**Mass Spectrometric Identification**

**Part I: Two-dimensional PAGE**

- Figure 1A (as provided in the manuscript) page 2

- Table with MS and MS/MS data page 3 - 4

(based on *C. oncophora* transcriptome database – Suppl. Information File 1)

- Full MS documentation page 5 - 208

**Part II: One-dimensional PAGE**

- Figure 1B (as provided in the manuscript) page 209

- Table with MS and MS/MS data page 210

(based on *C. oncophora* transcriptome database – Suppl. Information File 1)

- Full MS documentation page 211 - 346

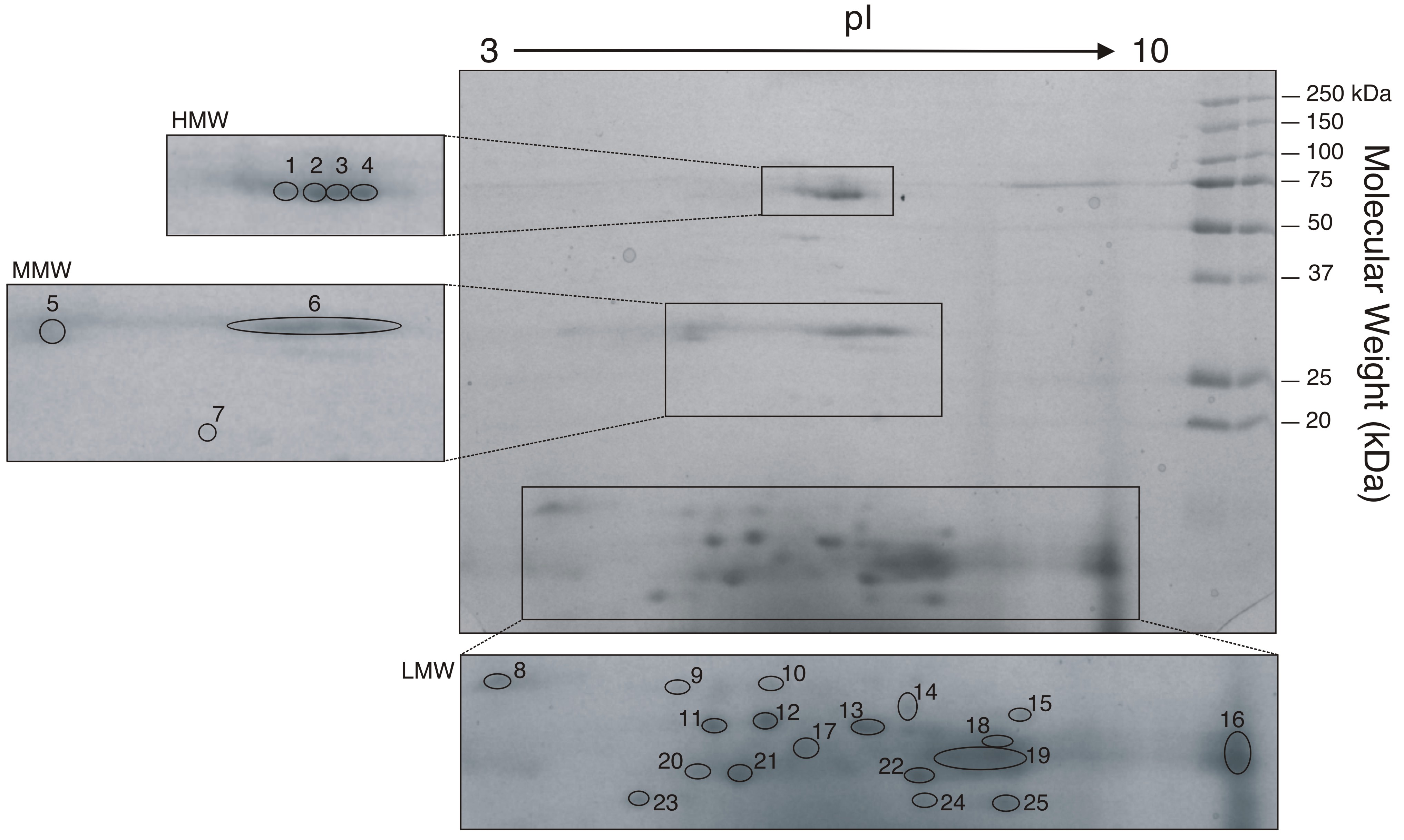
**Part III:**

- Isotig/contig ID list, used in full-length sequence determination, together with the page 347

corresponding <http://www.nematode.net> isotig codes of the top-hits (underlined)

**Part I:**

2D Gel Electrophoresis Spots (Figure 1A in the manuscript)



**Table.** MS-directed annotation of the *Cooperia oncophora* ES proteome, as revealed by 2D-PAGE (Fig. 1A and Table 1).

\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_

Spot N° Database ID GenBank Acc. N° Organism E-value MALDI-MS MS sequence Matched Unmatched MS2 sequence Description

(closest homology) BLASTP Mowse score coverage (%) peptides peptides coverage (%) (top BLASTP hit)

\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_

1 contig05709 AAK35199.1 *C. punctate* 3E-94 106 20 6 15 5 ASP-like protein

2 contig05709 AAK35199.1 *C. punctata* 3E-94 198 20 6 15 11 ASP-like protein

3 contig05709 AAK35199.1 *C. punctata* 3E-94 188 20 6 15 11 ASP-like protein

4 contig05709 AAK35199.1 *C. punctata* 3E-94 249 20 6 15 17 ASP-like protein

5 contig55746 AAO63577.1 *A. caninum* 2E-08 83 12 1 13 12 Secreted protein 5 precursor

6 isotig14500 XP\_003096841.1 *C. remanei*  4E-29 43 16 11 24 4 Innexin

7 isotig09291 CAD20737.1 *O. ostertagi* 5E-133 89 38 8 16 13 Thioredoxin peroxidase

8 isotig32303 86 32 3 8 32 /

9 isotig10739 108 12 2 15 12 /

10 isotig25459 AAD09212.1 *C. oncophora* 2E-10 115 24 4 11 11 14-kDa ES protein

11 isotig09711 AAD09213.1 *C. oncophora* 7E-62 189 52 18 35 12 ES antigen 2 protein

12 AAD09213.1 AAD09213.1 *C. oncophora* 0 128 38 5 10 15 ES antigen 2 protein

13 isotig11584 CAC38986.1 *C. oncophora* 3E-13 85 10 1 17 10 ES antigen 1

14 isotig11583 CAC38986.1 *C. oncophora* 3E-13 148 42 8 10 26 ES antigen 1

15 isotig14336 CAC38986.1 *C. oncophora* 5E-20 192 35 11 5 19 ES antigen 1

16 contig45229 CAC38986.1 *C. oncophora* 2E-21 100 35 6 9 8 ES antigen 1

17 no ID

18 CAC38986.1 CAC38986.1 *C. oncophora* 0 160 53 7 4 34 ES antigen 1

19 isotig09711 AAD09213.1 *C. oncophora* 7E-62 189 52 15 38 12 ES antigen 2 protein

20 isotig17160 CAC38986.1 *C. oncophora* 1E-13 90 41 4 14 8 ES antigen 1

21 isotig26364 CAC38986.1 *C. oncophora* 9E-91 74 46 5 6 23 ES antigen 1

22 no ID

23 isotig10740 162 32 5 11 13 /

24 isotig25459 AAD09212.1 *C. oncophora*  2E-10 37 10 1 14 10 14-kDa ES protein

25 no ID

\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_

**Page references for Figure 1A in the manuscript:**

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Spot 25: not identified

**Spot 1:**

**http://msmsms/mascot/images/88x31_logo_white.gifMascot Search Results**

**User :**

**Email :**

**Search title : SampleSetID: 341, AnalysisID: 561, MaldiWellID: 45038, SpectrumID: 137423, Path=\Jimmy\Cooperia Adult ES 20110221\20110221 MS en MSMS**

**Database : cooperia\_oncophora oncophora (33747 sequences; 5232511 residues)**

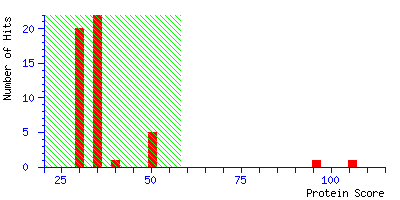
**Timestamp : 21 Feb 2011 at 15:35:40 GMT**

**Warning : A Peptide summary report will usually give a much clearer picture of MS/MS search results.**

**Top Score : 106 for contig05709, putative nuclear encoded protein Method: similarity and extension**

**Mascot Score Histogram**

Protein score is -10\*Log(P), where P is the probability that the observed match is a random event.  
Protein scores greater than 58 are significant (p<0.05).  
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



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**Protein Summary Report**

|  |  |  |  |
| --- | --- | --- | --- |
|  |  |  | [Help](http://msmsms/mascot/help/msms_summaries_help.html" \t "_blank) |
|  | Significance threshold p< | Max. number of hits |  |

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**Index**

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
|  | **Accession** | **Mass** | **Score** | **Description** |
| **1.** | [**contig05709**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20110221/F013477.dat#Hit1) | 23725 | 106 | putative nuclear encoded protein Method: similarity and extension |
| **2.** | [**contig63173**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20110221/F013477.dat#Hit2) | 22462 | 96 | putative nuclear encoded protein Method: similarity and extension |
| **3.** | [**isotig03031**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20110221/F013477.dat#Hit3) | 20758 | 51 | putative nuclear encoded protein Method: similarity and extension |
| **4.** | [**isotig03030**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20110221/F013477.dat#Hit4) | 20758 | 51 | putative nuclear encoded protein Method: similarity and extension |
| **5.** | [**isotig03029**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20110221/F013477.dat#Hit5) | 20758 | 51 | putative nuclear encoded protein Method: similarity and extension |
| **6.** | [**isotig03032**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20110221/F013477.dat#Hit6) | 20758 | 51 | putative nuclear encoded protein Method: similarity and extension |
| **7.** | [**isotig03033**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20110221/F013477.dat#Hit7) | 20758 | 51 | putative nuclear encoded protein Method: similarity and extension |
| **8.** | [**isotig30720**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20110221/F013477.dat#Hit8) | 8724 | 41 | putative nuclear encoded protein Method: Longest ORF |
| **9.** | [**isotig02635**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20110221/F013477.dat#Hit9) | 32723 | 36 | putative nuclear encoded protein Method: similarity and extension |
| **10.** | [**isotig04366**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20110221/F013477.dat#Hit10) | 16635 | 36 | putative nuclear encoded protein Method: similarity and extension |
| **11.** | [**isotig04367**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20110221/F013477.dat#Hit11) | 16635 | 36 | putative nuclear encoded protein Method: similarity and extension |
| **12.** | [**isotig13947**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20110221/F013477.dat#Hit12) | 10858 | 36 | putative nuclear encoded protein Method: Longest ORF |
| **13.** | [**isotig15829**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20110221/F013477.dat#Hit13) | 12327 | 35 | putative nuclear encoded protein Method: similarity and extension |
| **14.** | [**isotig11102**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20110221/F013477.dat#Hit14) | 23793 | 34 | putative nuclear encoded protein Method: similarity and extension |
| **15.** | [**isotig11103**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20110221/F013477.dat#Hit15) | 23793 | 34 | putative nuclear encoded protein Method: similarity and extension |
| **16.** | [**isotig23157**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20110221/F013477.dat#Hit16) | 15382 | 34 | putative nuclear encoded protein Method: similarity and extension |
| **17.** | [**isotig16877**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20110221/F013477.dat#Hit17) | 15891 | 34 | putative nuclear encoded protein Method: Longest ORF |
| **18.** | [**isotig20119**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20110221/F013477.dat#Hit18) | 12491 | 33 | putative nuclear encoded protein Method: similarity and extension |
| **19.** | [**isotig27043**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20110221/F013477.dat#Hit19) | 12123 | 33 | putative nuclear encoded protein Method: Longest ORF |
| **20.** | [**isotig03490**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20110221/F013477.dat#Hit20) | 26394 | 33 | putative nuclear encoded protein Method: similarity and extension |

**Results List**

|  |  |
| --- | --- |
| **1.** | [contig05709](http://msmsms/mascot/cgi/protein_view.pl?file=../data/20110221/F013477.dat&hit=1" \t "_blank)    **Mass:** 23725    **Score:** 106    **Expect:** 8.5e-007  **Matches:** 7 |
|  | putative nuclear encoded protein Method: similarity and extension |

|  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | **Observed** | **Mr(expt)** | **Mr(calc)** | **ppm** | **Start** |  | **End** | **Miss** | **Ions** | **Peptide** |
|  | 853.4938 | 852.4865 | 852.4566 | 35.1 | 97 | - | 103 | 2 | --- | K.SSKRYGR.N |
|  | 1311.6589 | 1310.6516 | 1310.6255 | 19.9 | 133 | - | 143 | 0 | --- | R.YGVPQDNVYTR.D |
|  | 1320.6975 | 1319.6902 | 1319.6622 | 21.2 | 37 | - | 46 | 1 | --- | K.VFLDKHNEYR.S |
|  | 1385.7184 | 1384.7111 | 1384.6735 | 27.1 | 52 | - | 65 | 0 | --- | K.GQAPNPQFGGSTPK.A |
|  | 1448.7664 | 1447.7591 | 1447.7572 | 1.35 | 36 | - | 46 | 2 | --- | R.KVFLDKHNEYR.S |
|  | 1448.7664 | 1447.7591 | 1447.7572 | 1.35 | 36 | - | 46 | 2 | 82 | R.KVFLDKHNEYR.S |
|  | 1467.7657 | 1466.7584 | 1466.7266 | 21.7 | 132 | - | 143 | 1 | --- | R.RYGVPQDNVYTR.D |

|  |  |
| --- | --- |
|  | **No match to:** 800.4802, 806.1047, 832.3173, 834.3154, 842.5109, 844.5518, 875.4531, 877.0513, 900.5539, 901.4774, 907.4500, 914.5042, 917.4774, 944.4880, 959.4749, 959.4749, 965.6496, 1003.5256, 1019.5261, 1035.5253, 1045.5900, 1046.5540, 1051.5642, 1052.5322, 1057.7086, 1100.6294, 1115.5885, 1115.5885, 1259.6727, 1347.6484, 1382.6008, 1390.7369, 1431.7339, 1478.7168, 1510.6722, 1514.8407, 1791.7594, 1886.9476, 1902.9481, 1925.8959, 2211.1448, 2284.2275, 2383.9880, 2663.3560, 2673.3643, 2673.3643, 2680.3914 |

|  |  |
| --- | --- |
| **2.** | [contig63173](http://msmsms/mascot/cgi/protein_view.pl?file=../data/20110221/F013477.dat&hit=2" \t "_blank)    **Mass:** 22462    **Score:** 96     **Expect:** 7.7e-006  **Matches:** 5 |
|  | putative nuclear encoded protein Method: similarity and extension |

|  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | **Observed** | **Mr(expt)** | **Mr(calc)** | **ppm** | **Start** |  | **End** | **Miss** | **Ions** | **Peptide** |
|  | 853.4938 | 852.4865 | 852.4817 | 5.62 | 117 | - | 125 | 0 | --- | K.TGLAPPAAR.M |
|  | 1448.7664 | 1447.7591 | 1447.7208 | 26.5 | 95 | - | 105 | 1 | --- | R.QVFLDKHNEYR.Q |
|  | 1448.7664 | 1447.7591 | 1447.7208 | 26.5 | 95 | - | 105 | 1 | 82 | R.QVFLDKHNEYR.Q |
|  | 1467.7657 | 1466.7584 | 1466.7577 | 0.51 | 34 | - | 47 | 1 | --- | K.PSTTTTKATTTTTR.P |
|  | 1510.6722 | 1509.6649 | 1509.7464 | -53.94 | 179 | - | 190 | 1 | --- | K.RSVDDWYIEVTK.Y |

|  |  |
| --- | --- |
|  | **No match to:** 800.4802, 806.1047, 832.3173, 834.3154, 842.5109, 844.5518, 875.4531, 877.0513, 900.5539, 901.4774, 907.4500, 914.5042, 917.4774, 944.4880, 959.4749, 959.4749, 965.6496, 1003.5256, 1019.5261, 1035.5253, 1045.5900, 1046.5540, 1051.5642, 1052.5322, 1057.7086, 1100.6294, 1115.5885, 1115.5885, 1259.6727, 1311.6589, 1320.6975, 1347.6484, 1382.6008, 1385.7184, 1390.7369, 1431.7339, 1478.7168, 1514.8407, 1791.7594, 1886.9476, 1902.9481, 1925.8959, 2211.1448, 2284.2275, 2383.9880, 2663.3560, 2673.3643, 2673.3643, 2680.3914 |

**http://msmsms/mascot/images/88x31_logo_white.gifMascot Search Results**

**Protein View**

Top of Form



Match to: **contig05709** Score: **106** Expect: **8.5e-007**

**putative nuclear encoded protein Method: similarity and extension**

Nominal mass (Mr): **23725**; Calculated pI value: **5.37**

NCBI BLAST search of [contig05709](http://www.ncbi.nlm.nih.gov/blast/Blast.cgi?ALIGNMENTS=50&ALIGNMENT_VIEW=Pairwise&AUTO_FORMAT=Semiauto&CDD_SEARCH=on&CLIENT=web&COMPOSITION_BASED_STATISTICS=on&DATABASE=nr&DESCRIPTIONS=100&ENTREZ_QUERY=(none)&EXPECT=10&FILTER=L&FORMAT_BLOCK_ON_RESPAGE=None&FORMAT_OBJECT=Alignment&FORMAT_TYPE=HTML&GAPCOSTS=11+1&I_THRESH=0.001&LAYOUT=TwoWindows&MATRIX_NAME=BLOSUM62&NCBI_GI=on&PAGE=Proteins&PROGRAM=blastp&QUERY=MLIALITVFCLILHHATVLGEELCSLDNGMTDEIRKVFLDKHNEYRSLVAKGQAPNPQFGGSTPKAARMLKAMYDCDVEEDMTKWAQAQCTYAPFKSSKRYGRNTWGMGVPNYNKTAAAESSVYDWFFELRRYGVPQDNVYTRDVDYSAYHYAQMVWQDSYKIGCVVAWCPSMTWVACGYSPAGDNIGSLIYELGEPCTKNEDCKCTDCT&SERVICE=plain&SET_DEFAULTS.x=9&SET_DEFAULTS.y=5&SHOW_OVERVIEW=on&WORD_SIZE=3&END_OF_HTTPGET=Yes" \t "_blank) against nr

Unformatted [sequence string](http://msmsms/mascot/cgi/getseq.pl?cooperia_oncophora+contig05709+seq" \t "_blank) for pasting into other applications

Variable modifications: Oxidation (HW),Oxidation (M)

Cleavage by Trypsin/P: cuts C-term side of KR

Sequence Coverage: **20%**

Matched peptides shown in **Bold Red**

**1** MLIALITVFC LILHHATVLG EELCSLDNGM TDEIR**KVFLD KHNEYR**SLVA

**51** K**GQAPNPQFG GSTPK**AARML KAMYDCDVEE DMTKWAQAQC TYAPFK**SSKR**

**101 YGR**NTWGMGV PNYNKTAAAE SSVYDWFFEL R**RYGVPQDNV YTR**DVDYSAY

**151** HYAQMVWQDS YKIGCVVAWC PSMTWVACGY SPAGDNIGSL IYELGEPCTK

**201** NEDCKCTDCT



  Residue Number  Increasing Mass  Decreasing Mass



**Start - End Observed Mr(expt) Mr(calc) ppm Miss Sequence**

**36 - 46 1448.7664 1447.7591 1447.7572 1 2 R.KVFLDKHNEYR.S**  ([No match](http://msmsms/mascot/cgi/peptide_view.pl?file=../data/20110221/F013477.dat&query=38&hit=1" \t "_blank))

**36 - 46 1448.7664 1447.7591 1447.7572 1 2 R.KVFLDKHNEYR.S**  ([Ions score 82](http://msmsms/mascot/cgi/peptide_view.pl?file=../data/20110221/F013477.dat&query=39&hit=1" \t "_blank))

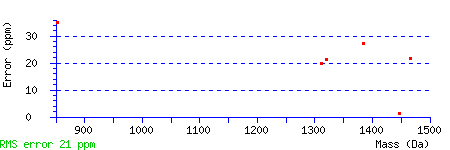
**37 - 46 1320.6975 1319.6902 1319.6622 21 1 K.VFLDKHNEYR.S**  ([No match](http://msmsms/mascot/cgi/peptide_view.pl?file=../data/20110221/F013477.dat&query=32&hit=1" \t "_blank))

**52 - 65 1385.7184 1384.7111 1384.6735 27 0 K.GQAPNPQFGGSTPK.A**  ([No match](http://msmsms/mascot/cgi/peptide_view.pl?file=../data/20110221/F013477.dat&query=35&hit=1" \t "_blank))

**97 - 103 853.4938 852.4865 852.4566 35 2 K.SSKRYGR.N**  ([No match](http://msmsms/mascot/cgi/peptide_view.pl?file=../data/20110221/F013477.dat&query=7&hit=1" \t "_blank))

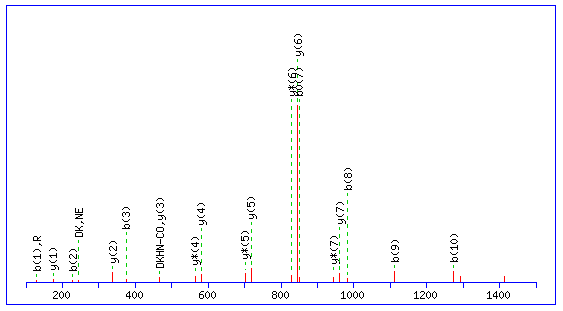
**132 - 143 1467.7657 1466.7584 1466.7266 22 1 R.RYGVPQDNVYTR.D**  ([No match](http://msmsms/mascot/cgi/peptide_view.pl?file=../data/20110221/F013477.dat&query=40&hit=1" \t "_blank))

**133 - 143 1311.6589 1310.6516 1310.6255 20 0 R.YGVPQDNVYTR.D**  ([No match](http://msmsms/mascot/cgi/peptide_view.pl?file=../data/20110221/F013477.dat&query=31&hit=1" \t "_blank))



Bottom of Form

🡪 Annotated MS2 spectrum for peptide KVFLDKHNEYR



**Monoisotopic mass of neutral peptide Mr(calc):** 1447.7572

**Ions Score:** 82 **Expect:** 5e-007

**Matches :** 22/160 fragment ions using 21 most intense peaks   ([help](http://msmsms/mascot/help/results_help.html" \l "PEP" \t "_blank))

|  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **#** | **Immon.** | **a** | **a\*** | **a0** | **b** | **b\*** | **b0** | **Seq.** | **v** | **w** | **y** | **y\*** | **y0** | **#** |
| **1** | 101.1073 | 101.1073 | 84.0808 |  | ***129.1022*** | 112.0757 |  | **K** |  |  |  |  |  | **11** |
| **2** | 72.0808 | 200.1757 | 183.1492 |  | ***228.1707*** | 211.1441 |  | **V** | 1276.6069 | 1289.6273 | 1320.6695 | 1303.6430 | 1302.6589 | **10** |
| **3** | 120.0808 | 347.2442 | 330.2176 |  | ***375.2391*** | 358.2125 |  | **F** | 1129.5385 |  | 1221.6011 | 1204.5745 | 1203.5905 | **9** |
| **4** | 86.0964 | 460.3282 | 443.3017 |  | 488.3231 | 471.2966 |  | **L** | 1016.4544 | 1015.4592 | 1074.5327 | 1057.5061 | 1056.5221 | **8** |
| **5** | 88.0393 | 575.3552 | 558.3286 | 557.3446 | 603.3501 | 586.3235 | 585.3395 | **D** | 901.4275 | 900.4322 | ***961.4486*** | 944.4221 | 943.4381 | **7** |
| **6** | 101.1073 | 703.4501 | 686.4236 | 685.4396 | 731.4450 | 714.4185 | 713.4345 | **K** | 773.3325 | 772.3373 | ***846.4217*** | 829.3951 | 828.4111 | **6** |
| **7** | 110.0713 | 840.5090 | 823.4825 | 822.4985 | 868.5039 | 851.4774 | 850.4934 | **H** | 636.2736 |  | ***718.3267*** | 701.3002 | 700.3161 | **5** |
| **8** | 87.0553 | 954.5520 | 937.5254 | 936.5414 | ***982.5469*** | 965.5203 | 964.5363 | **N** | 522.2307 | 521.2354 | ***581.2678*** | 564.2413 | 563.2572 | **4** |
| **9** | 102.0550 | 1083.5946 | 1066.5680 | 1065.5840 | ***1111.5895*** | 1094.5629 | 1093.5789 | **E** | 393.1881 | 392.1928 | ***467.2249*** | 450.1983 | 449.2143 | **3** |
| **10** | 136.0757 | 1246.6579 | 1229.6313 | 1228.6473 | ***1274.6528*** | 1257.6262 | 1256.6422 | **Y** | 230.1248 |  | ***338.1823*** | 321.1557 |  | **2** |
| **11** | 129.1135 |  |  |  |  |  |  | **R** | 74.0237 | 73.0284 | ***175.1190*** | 158.0924 |  | **1** |

|  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **Seq** | **ya** | **yb** | **Seq** | **ya** | **yb** | **Seq** | **ya** | **yb** |
| **VF** | 219.1492 | 247.1441 | **VFL** | 332.2333 | 360.2282 | **VFLD** | 447.2602 | 475.2551 |
| **VFLDK** | 575.3552 | 603.3501 | **FL** | 233.1648 | 261.1598 | **FLD** | 348.1918 | 376.1867 |
| **FLDK** | 476.2867 | 504.2817 | **FLDKH** | 613.3457 | 641.3406 | **LD** | 201.1234 | 229.1183 |
| **LDK** | 329.2183 | 357.2132 | **LDKH** | 466.2772 | 494.2722 | **LDKHN** | 580.3202 | 608.3151 |
| **DK** | 216.1343 | 244.1292 | **DKH** | 353.1932 | 381.1881 | **DKHN** | 467.2361 | 495.2310 |
| **DKHNE** | 596.2787 | 624.2736 | **KH** | 238.1662 | 266.1612 | **KHN** | 352.2092 | 380.2041 |
| **KHNE** | 481.2518 | 509.2467 | **KHNEY** | 644.3151 | 672.3100 | **HN** | 224.1142 | 252.1091 |
| **HNE** | 353.1568 | 381.1517 | **HNEY** | 516.2201 | 544.2150 | **NE** | 216.0979 | 244.0928 |
| **NEY** | 379.1612 | 407.1561 | **EY** | 265.1183 | 293.1132 |  |  |  |

**Spot 2:**

**http://msmsms/mascot/images/88x31_logo_white.gifMascot Search Results**

**User :**

**Email :**

**Search title : SampleSetID: 341, AnalysisID: 561, MaldiWellID: 45037, SpectrumID: 137418, Path=\Jimmy\Cooperia Adult ES 20110221\20110221 MS en MSMS**

**Database : cooperia\_oncophora oncophora (33747 sequences; 5232511 residues)**

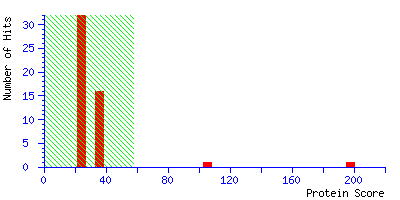
**Timestamp : 21 Feb 2011 at 15:35:24 GMT**

**Warning : A Peptide summary report will usually give a much clearer picture of MS/MS search results.**

**Top Score : 198 for contig05709, putative nuclear encoded protein Method: similarity and extension**

**Mascot Score Histogram**

Protein score is -10\*Log(P), where P is the probability that the observed match is a random event.  
Protein scores greater than 58 are significant (p<0.05).  
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



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**Protein Summary Report**

|  |  |  |  |
| --- | --- | --- | --- |
|  |  |  | [Help](http://msmsms/mascot/help/msms_summaries_help.html" \t "_blank) |
|  | Significance threshold p< | Max. number of hits |  |

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**Index**

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
|  | **Accession** | **Mass** | **Score** | **Description** |
| **1.** | [**contig05709**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20110221/F013476.dat#Hit1) | 23725 | 198 | putative nuclear encoded protein Method: similarity and extension |
| **2.** | [**contig63173**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20110221/F013476.dat#Hit2) | 22462 | 102 | putative nuclear encoded protein Method: similarity and extension |
| **3.** | [**isotig19477**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20110221/F013476.dat#Hit3) | 24321 | 41 | putative nuclear encoded protein Method: similarity and extension |
| **4.** | [**isotig04874**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20110221/F013476.dat#Hit4) | 9958 | 39 | putative nuclear encoded protein Method: Longest ORF |
| **5.** | [**isotig04875**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20110221/F013476.dat#Hit5) | 9958 | 39 | putative nuclear encoded protein Method: Longest ORF |
| **6.** | [**isotig22066**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20110221/F013476.dat#Hit6) | 21476 | 38 | putative nuclear encoded protein Method: similarity and extension |
| **7.** | [**isotig19223**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20110221/F013476.dat#Hit7) | 5943 | 38 | putative nuclear encoded protein Method: Longest ORF |
| **8.** | [**isotig09977**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20110221/F013476.dat#Hit8) | 27883 | 33 | putative nuclear encoded protein Method: similarity and extension |
| **9.** | [**isotig09976**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20110221/F013476.dat#Hit9) | 27883 | 33 | putative nuclear encoded protein Method: similarity and extension |
| **10.** | [**isotig11702**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20110221/F013476.dat#Hit10) | 24222 | 33 | putative nuclear encoded protein Method: similarity and extension |
| **11.** | [**isotig13961**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20110221/F013476.dat#Hit11) | 26563 | 32 | putative nuclear encoded protein Method: similarity and extension |
| **12.** | [**isotig19837**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20110221/F013476.dat#Hit12) | 15923 | 32 | putative nuclear encoded protein Method: Longest ORF |
| **13.** | [**isotig21421**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20110221/F013476.dat#Hit13) | 13362 | 32 | putative nuclear encoded protein Method: similarity and extension |
| **14.** | [**isotig21491**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20110221/F013476.dat#Hit14) | 17227 | 32 | putative nuclear encoded protein Method: Longest ORF |
| **15.** | [**isotig30720**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20110221/F013476.dat#Hit15) | 8724 | 31 | putative nuclear encoded protein Method: Longest ORF |
| **16.** | [**isotig12201**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20110221/F013476.dat#Hit16) | 33953 | 31 | putative nuclear encoded protein Method: similarity and extension |
| **17.** | [**isotig02453**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20110221/F013476.dat#Hit17) | 10135 | 30 | putative nuclear encoded protein Method: Longest ORF |
| **18.** | [**isotig02454**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20110221/F013476.dat#Hit18) | 10135 | 30 | putative nuclear encoded protein Method: Longest ORF |
| **19.** | [**isotig17412**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20110221/F013476.dat#Hit19) | 14526 | 30 | putative nuclear encoded protein Method: similarity and extension |
| **20.** | [**isotig03470**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20110221/F013476.dat#Hit20) | 8755 | 30 | putative nuclear encoded protein Method: Longest ORF |

**Results List**

|  |  |
| --- | --- |
| **1.** | [contig05709](http://msmsms/mascot/cgi/protein_view.pl?file=../data/20110221/F013476.dat&hit=1" \t "_blank)    **Mass:** 23725    **Score:** 198    **Expect:** 5.3e-016  **Matches:** 8 |
|  | putative nuclear encoded protein Method: similarity and extension |

|  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | **Observed** | **Mr(expt)** | **Mr(calc)** | **ppm** | **Start** |  | **End** | **Miss** | **Ions** | **Peptide** |
|  | 1311.6555 | 1310.6482 | 1310.6255 | 17.3 | 133 | - | 143 | 0 | --- | R.YGVPQDNVYTR.D |
|  | 1311.6555 | 1310.6482 | 1310.6255 | 17.3 | 133 | - | 143 | 0 | 79 | R.YGVPQDNVYTR.D |
|  | 1320.6906 | 1319.6833 | 1319.6622 | 16.0 | 37 | - | 46 | 1 | --- | K.VFLDKHNEYR.S |
|  | 1385.7109 | 1384.7036 | 1384.6735 | 21.7 | 52 | - | 65 | 0 | --- | K.GQAPNPQFGGSTPK.A |
|  | 1448.7579 | 1447.7506 | 1447.7572 | -4.52 | 36 | - | 46 | 2 | --- | R.KVFLDKHNEYR.S |
|  | 1448.7579 | 1447.7506 | 1447.7572 | -4.52 | 36 | - | 46 | 2 | 89 | R.KVFLDKHNEYR.S |
|  | 1467.7567 | 1466.7494 | 1466.7266 | 15.5 | 132 | - | 143 | 1 | --- | R.RYGVPQDNVYTR.D |
|  | 1834.8828 | 1833.8755 | 1833.9737 | -53.54 | 37 | - | 51 | 2 | --- | K.VFLDKHNEYRSLVAK.G + Oxidation (HW) |

|  |  |
| --- | --- |
|  | **No match to:** 806.0960, 832.3080, 850.0646, 875.4531, 877.0526, 881.2739, 899.2441, 901.4800, 917.2852, 959.4758, 1003.5462, 1035.5225, 1046.5385, 1052.5259, 1115.5867, 1115.5867, 1259.6699, 1347.6395, 1384.6108, 1390.7209, 1431.7340, 1761.7896, 1886.9374, 1886.9374, 1902.9310, 1918.9283, 1925.8993, 2212.1306, 2673.3560, 2680.3557 |

|  |  |
| --- | --- |
| **2.** | [contig63173](http://msmsms/mascot/cgi/protein_view.pl?file=../data/20110221/F013476.dat&hit=2" \t "_blank)    **Mass:** 22462    **Score:** 102    **Expect:** 2.1e-006  **Matches:** 4 |
|  | putative nuclear encoded protein Method: similarity and extension |

|  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | **Observed** | **Mr(expt)** | **Mr(calc)** | **ppm** | **Start** |  | **End** | **Miss** | **Ions** | **Peptide** |
|  | 881.2739 | 880.2666 | 880.4290 | -184.46 | 191 | - | 198 | 0 | --- | K.YGITADNK.I |
|  | 1448.7579 | 1447.7506 | 1447.7208 | 20.6 | 95 | - | 105 | 1 | --- | R.QVFLDKHNEYR.Q |
|  | 1448.7579 | 1447.7506 | 1447.7208 | 20.6 | 95 | - | 105 | 1 | 89 | R.QVFLDKHNEYR.Q |
|  | 1467.7567 | 1466.7494 | 1466.7577 | -5.63 | 34 | - | 47 | 1 | --- | K.PSTTTTKATTTTTR.P |

|  |  |
| --- | --- |
|  | **No match to:** 806.0960, 832.3080, 850.0646, 875.4531, 877.0526, 899.2441, 901.4800, 917.2852, 959.4758, 1003.5462, 1035.5225, 1046.5385, 1052.5259, 1115.5867, 1115.5867, 1259.6699, 1311.6555, 1311.6555, 1320.6906, 1347.6395, 1384.6108, 1385.7109, 1390.7209, 1431.7340, 1761.7896, 1834.8828, 1886.9374, 1886.9374, 1902.9310, 1918.9283, 1925.8993, 2212.1306, 2673.3560, 2680.3557 |

**http://msmsms/mascot/images/88x31_logo_white.gifMascot Search Results**

**Protein View**

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Match to: **contig05709** Score: **198** Expect: **5.3e-016**

**putative nuclear encoded protein Method: similarity and extension**

Nominal mass (Mr): **23725**; Calculated pI value: **5.37**

NCBI BLAST search of [contig05709](http://www.ncbi.nlm.nih.gov/blast/Blast.cgi?ALIGNMENTS=50&ALIGNMENT_VIEW=Pairwise&AUTO_FORMAT=Semiauto&CDD_SEARCH=on&CLIENT=web&COMPOSITION_BASED_STATISTICS=on&DATABASE=nr&DESCRIPTIONS=100&ENTREZ_QUERY=(none)&EXPECT=10&FILTER=L&FORMAT_BLOCK_ON_RESPAGE=None&FORMAT_OBJECT=Alignment&FORMAT_TYPE=HTML&GAPCOSTS=11+1&I_THRESH=0.001&LAYOUT=TwoWindows&MATRIX_NAME=BLOSUM62&NCBI_GI=on&PAGE=Proteins&PROGRAM=blastp&QUERY=MLIALITVFCLILHHATVLGEELCSLDNGMTDEIRKVFLDKHNEYRSLVAKGQAPNPQFGGSTPKAARMLKAMYDCDVEEDMTKWAQAQCTYAPFKSSKRYGRNTWGMGVPNYNKTAAAESSVYDWFFELRRYGVPQDNVYTRDVDYSAYHYAQMVWQDSYKIGCVVAWCPSMTWVACGYSPAGDNIGSLIYELGEPCTKNEDCKCTDCT&SERVICE=plain&SET_DEFAULTS.x=9&SET_DEFAULTS.y=5&SHOW_OVERVIEW=on&WORD_SIZE=3&END_OF_HTTPGET=Yes" \t "_blank) against nr

Unformatted [sequence string](http://msmsms/mascot/cgi/getseq.pl?cooperia_oncophora+contig05709+seq" \t "_blank) for pasting into other applications

Variable modifications: Oxidation (HW),Oxidation (M)

Cleavage by Trypsin/P: cuts C-term side of KR

Sequence Coverage: **20%**

Matched peptides shown in **Bold Red**

**1** MLIALITVFC LILHHATVLG EELCSLDNGM TDEIR**KVFLD KHNEYRSLVA**

**51 KGQAPNPQFG GSTPK**AARML KAMYDCDVEE DMTKWAQAQC TYAPFKSSKR

**101** YGRNTWGMGV PNYNKTAAAE SSVYDWFFEL R**RYGVPQDNV YTR**DVDYSAY

**151** HYAQMVWQDS YKIGCVVAWC PSMTWVACGY SPAGDNIGSL IYELGEPCTK

**201** NEDCKCTDCT



  Residue Number  Increasing Mass  Decreasing Mass



**Start - End Observed Mr(expt) Mr(calc) ppm Miss Sequence**

**36 - 46 1448.7579 1447.7506 1447.7572 -5 2 R.KVFLDKHNEYR.S**  ([No match](http://msmsms/mascot/cgi/peptide_view.pl?file=../data/20110221/F013476.dat&query=26&hit=1" \t "_blank))

**36 - 46 1448.7579 1447.7506 1447.7572 -5 2 R.KVFLDKHNEYR.S**  ([Ions score 89](http://msmsms/mascot/cgi/peptide_view.pl?file=../data/20110221/F013476.dat&query=27&hit=1" \t "_blank))

**37 - 46 1320.6906 1319.6833 1319.6622 16 1 K.VFLDKHNEYR.S**  ([No match](http://msmsms/mascot/cgi/peptide_view.pl?file=../data/20110221/F013476.dat&query=20&hit=1" \t "_blank))

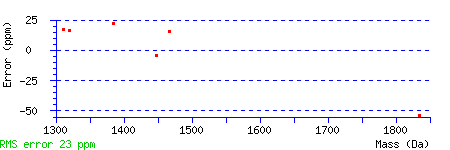
**37 - 51 1834.8828 1833.8755 1833.9737 -54 2 K.VFLDKHNEYRSLVAK.G**  Oxidation (HW) ([No match](http://msmsms/mascot/cgi/peptide_view.pl?file=../data/20110221/F013476.dat&query=30&hit=1" \t "_blank))

**52 - 65 1385.7109 1384.7036 1384.6735 22 0 K.GQAPNPQFGGSTPK.A**  ([No match](http://msmsms/mascot/cgi/peptide_view.pl?file=../data/20110221/F013476.dat&query=23&hit=1" \t "_blank))

**132 - 143 1467.7567 1466.7494 1466.7266 16 1 R.RYGVPQDNVYTR.D**  ([No match](http://msmsms/mascot/cgi/peptide_view.pl?file=../data/20110221/F013476.dat&query=28&hit=1" \t "_blank))

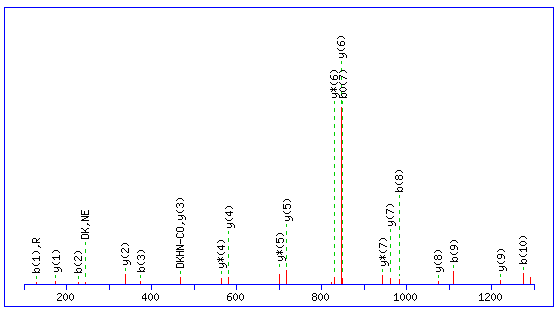
**133 - 143 1311.6555 1310.6482 1310.6255 17 0 R.YGVPQDNVYTR.D**  ([No match](http://msmsms/mascot/cgi/peptide_view.pl?file=../data/20110221/F013476.dat&query=18&hit=1" \t "_blank))

**133 - 143 1311.6555 1310.6482 1310.6255 17 0 R.YGVPQDNVYTR.D**  ([Ions score 79](http://msmsms/mascot/cgi/peptide_view.pl?file=../data/20110221/F013476.dat&query=19&hit=1" \t "_blank))



Bottom of Form

🡪 Annotated MS2 spectrum for peptide KVFLDKHNEYR



**Monoisotopic mass of neutral peptide Mr(calc):** 1447.7572

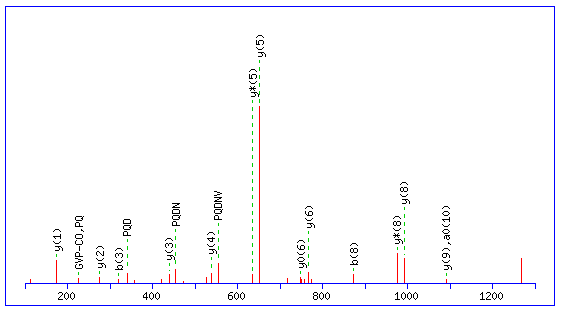
**Ions Score:** 89 **Expect:** 9.9e-008

**Matches :** 24/160 fragment ions using 23 most intense peaks   ([help](http://msmsms/mascot/help/results_help.html" \l "PEP" \t "_blank))

|  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **#** | **Immon.** | **a** | **a\*** | **a0** | **b** | **b\*** | **b0** | **Seq.** | **v** | **w** | **y** | **y\*** | **y0** | **#** |
| **1** | 101.1073 | 101.1073 | 84.0808 |  | **129.1022** | 112.0757 |  | **K** |  |  |  |  |  | **11** |
| **2** | 72.0808 | 200.1757 | 183.1492 |  | **228.1707** | 211.1441 |  | **V** | 1276.6069 | 1289.6273 | 1320.6695 | 1303.6430 | 1302.6589 | **10** |
| **3** | 120.0808 | 347.2442 | 330.2176 |  | **375.2391** | 358.2125 |  | **F** | 1129.5385 |  | ***1221.6011*** | 1204.5745 | 1203.5905 | **9** |
| **4** | 86.0964 | 460.3282 | 443.3017 |  | 488.3231 | 471.2966 |  | **L** | 1016.4544 | 1015.4592 | ***1074.5327*** | 1057.5061 | 1056.5221 | **8** |
| **5** | 88.0393 | 575.3552 | 558.3286 | 557.3446 | 603.3501 | 586.3235 | 585.3395 | **D** | 901.4275 | 900.4322 | ***961.4486*** | 944.4221 | 943.4381 | **7** |
| **6** | 101.1073 | 703.4501 | 686.4236 | 685.4396 | 731.4450 | 714.4185 | 713.4345 | **K** | 773.3325 | 772.3373 | ***846.4217*** | 829.3951 | 828.4111 | **6** |
| **7** | 110.0713 | 840.5090 | 823.4825 | 822.4985 | 868.5039 | 851.4774 | 850.4934 | **H** | 636.2736 |  | ***718.3267*** | 701.3002 | 700.3161 | **5** |
| **8** | 87.0553 | 954.5520 | 937.5254 | 936.5414 | **982.5469** | 965.5203 | 964.5363 | **N** | 522.2307 | 521.2354 | ***581.2678*** | 564.2413 | 563.2572 | **4** |
| **9** | 102.0550 | 1083.5946 | 1066.5680 | 1065.5840 | **1111.5895** | 1094.5629 | 1093.5789 | **E** | 393.1881 | 392.1928 | ***467.2249*** | 450.1983 | 449.2143 | **3** |
| **10** | 136.0757 | 1246.6579 | 1229.6313 | 1228.6473 | **1274.6528** | 1257.6262 | 1256.6422 | **Y** | 230.1248 |  | ***338.1823*** | 321.1557 |  | **2** |
| **11** | 129.1135 |  |  |  |  |  |  | **R** | 74.0237 | 73.0284 | ***175.1190*** | 158.0924 |  | **1** |

|  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **Seq** | **ya** | **yb** | **Seq** | **ya** | **yb** | **Seq** | **ya** | **yb** |
| **VF** | 219.1492 | 247.1441 | **VFL** | 332.2333 | 360.2282 | **VFLD** | 447.2602 | 475.2551 |
| **VFLDK** | 575.3552 | 603.3501 | **FL** | 233.1648 | 261.1598 | **FLD** | 348.1918 | 376.1867 |
| **FLDK** | 476.2867 | 504.2817 | **FLDKH** | 613.3457 | 641.3406 | **LD** | 201.1234 | 229.1183 |
| **LDK** | 329.2183 | 357.2132 | **LDKH** | 466.2772 | 494.2722 | **LDKHN** | 580.3202 | 608.3151 |
| **DK** | 216.1343 | 244.1292 | **DKH** | 353.1932 | 381.1881 | **DKHN** | 467.2361 | 495.2310 |
| **DKHNE** | 596.2787 | 624.2736 | **KH** | 238.1662 | 266.1612 | **KHN** | 352.2092 | 380.2041 |
| **KHNE** | 481.2518 | 509.2467 | **KHNEY** | 644.3151 | 672.3100 | **HN** | 224.1142 | 252.1091 |
| **HNE** | 353.1568 | 381.1517 | **HNEY** | 516.2201 | 544.2150 | **NE** | 216.0979 | 244.0928 |
| **NEY** | 379.1612 | 407.1561 | **EY** | 265.1183 | 293.1132 |  |  |  |

🡪 Annotated MS2 spectrum for peptide YGVPQDNVYTR



**Monoisotopic mass of neutral peptide Mr(calc):** 1310.6255

**Ions Score:** 79 **Expect:** 8.8e-007

**Matches :** 20/159 fragment ions using 19 most intense peaks   ([help](http://msmsms/mascot/help/results_help.html" \l "PEP" \t "_blank))

|  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **#** | **Immon.** | **a** | **a\*** | **a0** | **b** | **b\*** | **b0** | **Seq.** | **v** | **w** | **w'** | **y** | **y\*** | **y0** | **#** |
| **1** | 136.0757 | 136.0757 |  |  | 164.0706 |  |  | **Y** |  |  |  |  |  |  | **11** |
| **2** | 30.0338 | 193.0972 |  |  | 221.0921 |  |  | **G** |  |  |  | 1148.5695 | 1131.5429 | 1130.5589 | **10** |
| **3** | 72.0808 | 292.1656 |  |  | **320.1605** |  |  | **V** | 1047.4854 | 1060.5058 |  | ***1091.5480*** | 1074.5215 | 1073.5374 | **9** |
| **4** | 70.0651 | 389.2183 |  |  | 417.2132 |  |  | **P** | 950.4326 | 949.4374 |  | ***992.4796*** | 975.4530 | 974.4690 | **8** |
| **5** | 101.0709 | 517.2769 | 500.2504 |  | 545.2718 | 528.2453 |  | **Q** | 822.3741 | 821.3788 |  | 895.4268 | 878.4003 | 877.4163 | **7** |
| **6** | 88.0393 | 632.3039 | 615.2773 | 614.2933 | 660.2988 | 643.2722 | 642.2882 | **D** | 707.3471 | 706.3519 |  | ***767.3682*** | 750.3417 | 749.3577 | **6** |
| **7** | 87.0553 | 746.3468 | 729.3202 | 728.3362 | 774.3417 | 757.3151 | 756.3311 | **N** | 593.3042 | 592.3089 |  | ***652.3413*** | 635.3148 | 634.3307 | **5** |
| **8** | 72.0808 | 845.4152 | 828.3886 | 827.4046 | **873.4101** | 856.3836 | 855.3995 | **V** | 494.2358 | 507.2562 |  | ***538.2984*** | 521.2718 | 520.2878 | **4** |
| **9** | 136.0757 | 1008.4785 | 991.4520 | 990.4680 | 1036.4734 | 1019.4469 | 1018.4629 | **Y** | 331.1724 |  |  | ***439.2300*** | 422.2034 | 421.2194 | **3** |
| **10** | 74.0600 | 1109.5262 | 1092.4997 | 1091.5156 | 1137.5211 | 1120.4946 | 1119.5106 | **T** | 230.1248 | 243.1452 | 245.1244 | ***276.1666*** | 259.1401 | 258.1561 | **2** |
| **11** | 129.1135 |  |  |  |  |  |  | **R** | 74.0237 | 73.0284 |  | ***175.1190*** | 158.0924 |  | **1** |

|  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **Seq** | **ya** | **yb** | **Seq** | **ya** | **yb** | **Seq** | **ya** | **yb** |
| **GV** | 129.1022 | 157.0972 | **GVP** | 226.1550 | 254.1499 | **GVPQ** | 354.2136 | 382.2085 |
| **GVPQD** | 469.2405 | 497.2354 | **GVPQDN** | 583.2835 | 611.2784 | **GVPQDNV** | 682.3519 | 710.3468 |
| **VP** | 169.1335 | 197.1285 | **VPQ** | 297.1921 | 325.1870 | **VPQD** | 412.2191 | 440.2140 |
| **VPQDN** | 526.2620 | 554.2569 | **VPQDNV** | 625.3304 | 653.3253 | **PQ** | 198.1237 | 226.1186 |
| **PQD** | 313.1506 | 341.1456 | **PQDN** | 427.1936 | 455.1885 | **PQDNV** | 526.2620 | 554.2569 |
| **PQDNVY** | 689.3253 | 717.3202 | **QD** | 216.0979 | 244.0928 | **QDN** | 330.1408 | 358.1357 |
| **QDNV** | 429.2092 | 457.2041 | **QDNVY** | 592.2726 | 620.2675 | **QDNVYT** | 693.3202 | 721.3151 |
| **DN** | 202.0822 | 230.0771 | **DNV** | 301.1506 | 329.1456 | **DNVY** | 464.2140 | 492.2089 |
| **DNVYT** | 565.2617 | 593.2566 | **NV** | 186.1237 | 214.1186 | **NVY** | 349.1870 | 377.1819 |
| **NVYT** | 450.2347 | 478.2296 | **VY** | 235.1441 | 263.1390 | **VYT** | 336.1918 | 364.1867 |
| **YT** | 237.1234 | 265.1183 |  |  |  |  |  |  |

**Spot 3:**

**http://msmsms/mascot/images/88x31_logo_white.gifMascot Search Results**

**User :**

**Email :**

**Search title : SampleSetID: 341, AnalysisID: 800, MaldiWellID: 45037, SpectrumID: 175162, Path=\Jimmy\Cooperia Adult ES 20110221\20110509 1st experiment (repeat)**

**Database : cooperia\_oncophora oncophora\_20110405 (34373 sequences; 5289600 residues)**

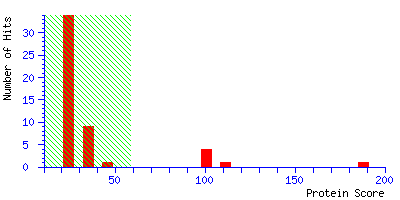
**Timestamp : 9 May 2011 at 12:37:45 GMT**

**Warning : A Peptide summary report will usually give a much clearer picture of MS/MS search results.**

**Top Score : 188 for contig05709, putative nuclear encoded protein Method: similarity and extension**

**Mascot Score Histogram**

Protein score is -10\*Log(P), where P is the probability that the observed match is a random event.  
Protein scores greater than 58 are significant (p<0.05).  
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



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**Protein Summary Report**

|  |  |  |  |
| --- | --- | --- | --- |
|  |  |  | [Help](http://msmsms/mascot/help/msms_summaries_help.html" \t "_blank) |
|  | Significance threshold p< | Max. number of hits |  |

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**Index**

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
|  | **Accession** | **Mass** | **Score** | **Description** |
| **1.** | [**contig05709**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20110509/F014795.dat#Hit1) | 23725 | 188 | putative nuclear encoded protein Method: similarity and extension |
| **2.** | [**contig63173**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20110509/F014795.dat#Hit2) | 22462 | 106 | putative nuclear encoded protein Method: similarity and extension |
| **3.** | [**gi|13625881|gb|AAK35185.1|AF352700\_1**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20110509/F014795.dat#Hit3) | 27510 | 105 | activation associated secreted protein-like protein [Cooperia punctata] |
| **4.** | [**gi|13625879|gb|AAK35184.1|AF352699\_1**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20110509/F014795.dat#Hit4) | 25808 | 104 | activation associated secreted protein-like protein [Cooperia punctata] |
| **5.** | [**gi|13625877|gb|AAK35183.1|AF352698\_1**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20110509/F014795.dat#Hit5) | 27540 | 101 | activation associated secreted protein-like protein [Cooperia punctata] |
| **6.** | [**gi|13625909|gb|AAK35199.1|AF352714\_1**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20110509/F014795.dat#Hit6) | 51596 | 96 | activation associated secreted protein-like protein [Cooperia punctata] |
| **7.** | [**isotig19477**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20110509/F014795.dat#Hit7) | 24321 | 45 | putative nuclear encoded protein Method: similarity and extension |
| **8.** | [**isotig09977**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20110509/F014795.dat#Hit8) | 27883 | 35 | putative nuclear encoded protein Method: similarity and extension |
| **9.** | [**isotig09976**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20110509/F014795.dat#Hit9) | 27883 | 35 | putative nuclear encoded protein Method: similarity and extension |
| **10.** | [**isotig22066**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20110509/F014795.dat#Hit10) | 21476 | 34 | putative nuclear encoded protein Method: similarity and extension |
| **11.** | [**isotig19223**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20110509/F014795.dat#Hit11) | 5943 | 34 | putative nuclear encoded protein Method: Longest ORF |
| **12.** | [**isotig04874**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20110509/F014795.dat#Hit12) | 9958 | 33 | putative nuclear encoded protein Method: Longest ORF |
| **13.** | [**isotig04875**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20110509/F014795.dat#Hit13) | 9958 | 33 | putative nuclear encoded protein Method: Longest ORF |
| **14.** | [**isotig13961**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20110509/F014795.dat#Hit14) | 26563 | 30 | putative nuclear encoded protein Method: similarity and extension |
| **15.** | [**isotig19837**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20110509/F014795.dat#Hit15) | 15923 | 29 | putative nuclear encoded protein Method: Longest ORF |
| **16.** | [**isotig23084**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20110509/F014795.dat#Hit16) | 19568 | 29 | putative nuclear encoded protein Method: similarity and extension |
| **17.** | [**isotig30720**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20110509/F014795.dat#Hit17) | 8724 | 29 | putative nuclear encoded protein Method: Longest ORF |
| **18.** | [**isotig12201**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20110509/F014795.dat#Hit18) | 33953 | 29 | putative nuclear encoded protein Method: similarity and extension |
| **19.** | [**isotig11702**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20110509/F014795.dat#Hit19) | 24222 | 28 | putative nuclear encoded protein Method: similarity and extension |
| **20.** | [**isotig17412**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20110509/F014795.dat#Hit20) | 14526 | 28 | putative nuclear encoded protein Method: similarity and extension |

**Results List**

|  |  |
| --- | --- |
| **1.** | [contig05709](http://msmsms/mascot/cgi/protein_view.pl?file=../data/20110509/F014795.dat&hit=1" \t "_blank)    **Mass:** 23725    **Score:** 188    **Expect:** 5.4e-015  **Matches:** 8 |
|  | putative nuclear encoded protein Method: similarity and extension |

|  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | **Observed** | **Mr(expt)** | **Mr(calc)** | **ppm** | **Start** |  | **End** | **Miss** | **Ions** | **Peptide** |
|  | 1311.6555 | 1310.6482 | 1310.6255 | 17.3 | 133 | - | 143 | 0 | --- | R.YGVPQDNVYTR.D |
|  | 1311.6555 | 1310.6482 | 1310.6255 | 17.3 | 133 | - | 143 | 0 | 79 | R.YGVPQDNVYTR.D |
|  | 1320.6906 | 1319.6833 | 1319.6622 | 16.0 | 37 | - | 46 | 1 | --- | K.VFLDKHNEYR.S |
|  | 1385.7109 | 1384.7036 | 1384.6735 | 21.7 | 52 | - | 65 | 0 | --- | K.GQAPNPQFGGSTPK.A |
|  | 1448.7579 | 1447.7506 | 1447.7572 | -4.52 | 36 | - | 46 | 2 | --- | R.KVFLDKHNEYR.S |
|  | 1448.7579 | 1447.7506 | 1447.7572 | -4.52 | 36 | - | 46 | 2 | 89 | R.KVFLDKHNEYR.S |
|  | 1467.7567 | 1466.7494 | 1466.7266 | 15.5 | 132 | - | 143 | 1 | --- | R.RYGVPQDNVYTR.D |
|  | 1834.8828 | 1833.8755 | 1833.9737 | -53.54 | 37 | - | 51 | 2 | --- | K.VFLDKHNEYRSLVAK.G + Oxidation (HW) |

|  |  |
| --- | --- |
|  | **No match to:** 806.0960, 832.3080, 850.0646, 875.4531, 877.0526, 881.2739, 899.2441, 901.4800, 917.2852, 959.4758, 1003.5462, 1035.5225, 1046.5385, 1052.5259, 1115.5867, 1115.5867, 1259.6699, 1347.6395, 1384.6108, 1390.7209, 1431.7340, 1761.7896, 1886.9374, 1886.9374, 1902.9310, 1918.9283, 1925.8993, 2212.1306, 2673.3560, 2680.3557 |

|  |  |
| --- | --- |
| **2.** | [contig63173](http://msmsms/mascot/cgi/protein_view.pl?file=../data/20110509/F014795.dat&hit=2" \t "_blank)    **Mass:** 22462    **Score:** 106    **Expect:** 8.6e-007  **Matches:** 5 |
|  | putative nuclear encoded protein Method: similarity and extension |

|  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | **Observed** | **Mr(expt)** | **Mr(calc)** | **ppm** | **Start** |  | **End** | **Miss** | **Ions** | **Peptide** |
|  | 881.2739 | 880.2666 | 880.4290 | -184.46 | 191 | - | 198 | 0 | --- | K.YGITADNK.I |
|  | 1347.6395 | 1346.6322 | 1346.6765 | -32.89 | 146 | - | 157 | 1 | --- | K.CKGGHSSFQVLK.G + Carbamidomethyl (C) |
|  | 1448.7579 | 1447.7506 | 1447.7208 | 20.6 | 95 | - | 105 | 1 | --- | R.QVFLDKHNEYR.Q |
|  | 1448.7579 | 1447.7506 | 1447.7208 | 20.6 | 95 | - | 105 | 1 | 89 | R.QVFLDKHNEYR.Q |
|  | 1467.7567 | 1466.7494 | 1466.7577 | -5.63 | 34 | - | 47 | 1 | --- | K.PSTTTTKATTTTTR.P |

|  |  |
| --- | --- |
|  | **No match to:** 806.0960, 832.3080, 850.0646, 875.4531, 877.0526, 899.2441, 901.4800, 917.2852, 959.4758, 1003.5462, 1035.5225, 1046.5385, 1052.5259, 1115.5867, 1115.5867, 1259.6699, 1311.6555, 1311.6555, 1320.6906, 1384.6108, 1385.7109, 1390.7209, 1431.7340, 1761.7896, 1834.8828, 1886.9374, 1886.9374, 1902.9310, 1918.9283, 1925.8993, 2212.1306, 2673.3560, 2680.3557 |

|  |  |
| --- | --- |
| **3.** | [gi|13625881|gb|AAK35185.1|AF352700\_1](http://msmsms/mascot/cgi/protein_view.pl?file=../data/20110509/F014795.dat&hit=3" \t "_blank)    **Mass:** 27510    **Score:** 105    **Expect:** 1.1e-006  **Matches:** 7 |
|  | activation associated secreted protein-like protein [Cooperia punctata] |

|  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | **Observed** | **Mr(expt)** | **Mr(calc)** | **ppm** | **Start** |  | **End** | **Miss** | **Ions** | **Peptide** |
|  | 881.2739 | 880.2666 | 880.4290 | -184.46 | 157 | - | 164 | 0 | --- | K.YGITADNK.I |
|  | 1259.6699 | 1258.6626 | 1258.4377 | 179 | 227 | - | 236 | 1 | --- | R.DEDCKCSSCR.C + 2 Carbamidomethyl (C) |
|  | 1347.6395 | 1346.6322 | 1346.6071 | 18.7 | 187 | - | 198 | 0 | --- | R.LGCAAVSCPEQR.R + 2 Carbamidomethyl (C) |
|  | 1384.6108 | 1383.6035 | 1383.6558 | -37.79 | 146 | - | 156 | 0 | --- | R.SVDDWYIELTK.Y + Oxidation (HW) |
|  | 1448.7579 | 1447.7506 | 1447.7208 | 20.6 | 61 | - | 71 | 1 | --- | R.QVFLDKHNEYR.Q |
|  | 1448.7579 | 1447.7506 | 1447.7208 | 20.6 | 61 | - | 71 | 1 | 89 | R.QVFLDKHNEYR.Q |
|  | 1761.7896 | 1760.7823 | 1760.7458 | 20.7 | 45 | - | 60 | 0 | --- | K.PVAHCTLDNGMTDEAR.Q + Oxidation (HW); Oxidation (M) |

|  |  |
| --- | --- |
|  | **No match to:** 806.0960, 832.3080, 850.0646, 875.4531, 877.0526, 899.2441, 901.4800, 917.2852, 959.4758, 1003.5462, 1035.5225, 1046.5385, 1052.5259, 1115.5867, 1115.5867, 1311.6555, 1311.6555, 1320.6906, 1385.7109, 1390.7209, 1431.7340, 1467.7567, 1834.8828, 1886.9374, 1886.9374, 1902.9310, 1918.9283, 1925.8993, 2212.1306, 2673.3560, 2680.3557 |

|  |  |
| --- | --- |
| **4.** | [gi|13625879|gb|AAK35184.1|AF352699\_1](http://msmsms/mascot/cgi/protein_view.pl?file=../data/20110509/F014795.dat&hit=4" \t "_blank)    **Mass:** 25808    **Score:** 104    **Expect:** 1.4e-006  **Matches:** 7 |
|  | activation associated secreted protein-like protein [Cooperia punctata] |

|  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | **Observed** | **Mr(expt)** | **Mr(calc)** | **ppm** | **Start** |  | **End** | **Miss** | **Ions** | **Peptide** |
|  | 881.2739 | 880.2666 | 880.4290 | -184.46 | 140 | - | 147 | 0 | --- | K.YGITADNK.I |
|  | 1259.6699 | 1258.6626 | 1258.4377 | 179 | 210 | - | 219 | 1 | --- | R.DEDCKCSSCR.C + 2 Carbamidomethyl (C) |
|  | 1347.6395 | 1346.6322 | 1346.6071 | 18.7 | 170 | - | 181 | 0 | --- | R.LGCAAVSCPEQR.K + 2 Carbamidomethyl (C) |
|  | 1384.6108 | 1383.6035 | 1383.6558 | -37.79 | 129 | - | 139 | 0 | --- | R.SVDDWYIELTK.Y + Oxidation (HW) |
|  | 1448.7579 | 1447.7506 | 1447.7208 | 20.6 | 44 | - | 54 | 1 | --- | R.QVFLDKHNEYR.Q |
|  | 1448.7579 | 1447.7506 | 1447.7208 | 20.6 | 44 | - | 54 | 1 | 89 | R.QVFLDKHNEYR.Q |
|  | 1761.7896 | 1760.7823 | 1760.7498 | 18.5 | 80 | - | 93 | 0 | --- | R.YDCDLEAHVMEHVK.T + Carbamidomethyl (C); Oxidation (M) |

|  |  |
| --- | --- |
|  | **No match to:** 806.0960, 832.3080, 850.0646, 875.4531, 877.0526, 899.2441, 901.4800, 917.2852, 959.4758, 1003.5462, 1035.5225, 1046.5385, 1052.5259, 1115.5867, 1115.5867, 1311.6555, 1311.6555, 1320.6906, 1385.7109, 1390.7209, 1431.7340, 1467.7567, 1834.8828, 1886.9374, 1886.9374, 1902.9310, 1918.9283, 1925.8993, 2212.1306, 2673.3560, 2680.3557 |

|  |  |
| --- | --- |
| **5.** | [gi|13625877|gb|AAK35183.1|AF352698\_1](http://msmsms/mascot/cgi/protein_view.pl?file=../data/20110509/F014795.dat&hit=5" \t "_blank)    **Mass:** 27540    **Score:** 101    **Expect:** 2.7e-006  **Matches:** 6 |
|  | activation associated secreted protein-like protein [Cooperia punctata] |

|  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | **Observed** | **Mr(expt)** | **Mr(calc)** | **ppm** | **Start** |  | **End** | **Miss** | **Ions** | **Peptide** |
|  | 881.2739 | 880.2666 | 880.4290 | -184.46 | 157 | - | 164 | 0 | --- | K.YGITADNK.I |
|  | 1259.6699 | 1258.6626 | 1258.4377 | 179 | 227 | - | 236 | 1 | --- | R.DEDCKCSSCR.C + 2 Carbamidomethyl (C) |
|  | 1347.6395 | 1346.6322 | 1346.6071 | 18.7 | 187 | - | 198 | 0 | --- | R.LGCAAVSCPEQR.R + 2 Carbamidomethyl (C) |
|  | 1448.7579 | 1447.7506 | 1447.7208 | 20.6 | 61 | - | 71 | 1 | --- | R.QVFLDKHNEYR.Q |
|  | 1448.7579 | 1447.7506 | 1447.7208 | 20.6 | 61 | - | 71 | 1 | 89 | R.QVFLDKHNEYR.Q |
|  | 1761.7896 | 1760.7823 | 1760.7458 | 20.7 | 45 | - | 60 | 0 | --- | K.PVAHCTLDNGMTDEAR.Q + Oxidation (HW); Oxidation (M) |

|  |  |
| --- | --- |
|  | **No match to:** 806.0960, 832.3080, 850.0646, 875.4531, 877.0526, 899.2441, 901.4800, 917.2852, 959.4758, 1003.5462, 1035.5225, 1046.5385, 1052.5259, 1115.5867, 1115.5867, 1311.6555, 1311.6555, 1320.6906, 1384.6108, 1385.7109, 1390.7209, 1431.7340, 1467.7567, 1834.8828, 1886.9374, 1886.9374, 1902.9310, 1918.9283, 1925.8993, 2212.1306, 2673.3560, 2680.3557 |

|  |  |
| --- | --- |
| **6.** | [gi|13625909|gb|AAK35199.1|AF352714\_1](http://msmsms/mascot/cgi/protein_view.pl?file=../data/20110509/F014795.dat&hit=6" \t "_blank)    **Mass:** 51596    **Score:** 96     **Expect:** 7.9e-006  **Matches:** 5 |
|  | activation associated secreted protein-like protein [Cooperia punctata] |

|  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | **Observed** | **Mr(expt)** | **Mr(calc)** | **ppm** | **Start** |  | **End** | **Miss** | **Ions** | **Peptide** |
|  | 881.2739 | 880.2666 | 880.4290 | -184.46 | 374 | - | 381 | 0 | --- | K.YGITADNK.I |
|  | 1259.6699 | 1258.6626 | 1258.4377 | 179 | 444 | - | 453 | 1 | --- | R.DEDCKCSSCR.C + 2 Carbamidomethyl (C) |
|  | 1384.6108 | 1383.6035 | 1383.6558 | -37.79 | 363 | - | 373 | 0 | --- | R.SVDDWYIELTK.Y + Oxidation (HW) |
|  | 1448.7579 | 1447.7506 | 1447.7208 | 20.6 | 278 | - | 288 | 1 | --- | R.QVFLDKHNEYR.Q |
|  | 1448.7579 | 1447.7506 | 1447.7208 | 20.6 | 278 | - | 288 | 1 | 89 | R.QVFLDKHNEYR.Q |

|  |  |
| --- | --- |
|  | **No match to:** 806.0960, 832.3080, 850.0646, 875.4531, 877.0526, 899.2441, 901.4800, 917.2852, 959.4758, 1003.5462, 1035.5225, 1046.5385, 1052.5259, 1115.5867, 1115.5867, 1311.6555, 1311.6555, 1320.6906, 1347.6395, 1385.7109, 1390.7209, 1431.7340, 1467.7567, 1761.7896, 1834.8828, 1886.9374, 1886.9374, 1902.9310, 1918.9283, 1925.8993, 2212.1306, 2673.3560, 2680.3557 |

**http://msmsms/mascot/images/88x31_logo_white.gifMascot Search Results**

**Protein View**

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Match to: **contig05709** Score: **188** Expect: **5.4e-015**

**putative nuclear encoded protein Method: similarity and extension**

Nominal mass (Mr): **23725**; Calculated pI value: **5.37**

NCBI BLAST search of [contig05709](http://www.ncbi.nlm.nih.gov/blast/Blast.cgi?ALIGNMENTS=50&ALIGNMENT_VIEW=Pairwise&AUTO_FORMAT=Semiauto&CDD_SEARCH=on&CLIENT=web&COMPOSITION_BASED_STATISTICS=on&DATABASE=nr&DESCRIPTIONS=100&ENTREZ_QUERY=(none)&EXPECT=10&FILTER=L&FORMAT_BLOCK_ON_RESPAGE=None&FORMAT_OBJECT=Alignment&FORMAT_TYPE=HTML&GAPCOSTS=11+1&I_THRESH=0.001&LAYOUT=TwoWindows&MATRIX_NAME=BLOSUM62&NCBI_GI=on&PAGE=Proteins&PROGRAM=blastp&QUERY=MLIALITVFCLILHHATVLGEELCSLDNGMTDEIRKVFLDKHNEYRSLVAKGQAPNPQFGGSTPKAARMLKAMYDCDVEEDMTKWAQAQCTYAPFKSSKRYGRNTWGMGVPNYNKTAAAESSVYDWFFELRRYGVPQDNVYTRDVDYSAYHYAQMVWQDSYKIGCVVAWCPSMTWVACGYSPAGDNIGSLIYELGEPCTKNEDCKCTDCT&SERVICE=plain&SET_DEFAULTS.x=9&SET_DEFAULTS.y=5&SHOW_OVERVIEW=on&WORD_SIZE=3&END_OF_HTTPGET=Yes" \t "_blank) against nr

Unformatted [sequence string](http://msmsms/mascot/cgi/getseq.pl?cooperia_oncophora+contig05709+seq" \t "_blank) for pasting into other applications

Variable modifications: Carbamidomethyl (C),Oxidation (HW),Oxidation (M)

Cleavage by Trypsin/P: cuts C-term side of KR

Sequence Coverage: **20%**

Matched peptides shown in **Bold Red**

**1** MLIALITVFC LILHHATVLG EELCSLDNGM TDEIR**KVFLD KHNEYRSLVA**

**51 KGQAPNPQFG GSTPK**AARML KAMYDCDVEE DMTKWAQAQC TYAPFKSSKR

**101** YGRNTWGMGV PNYNKTAAAE SSVYDWFFEL R**RYGVPQDNV YTR**DVDYSAY

**151** HYAQMVWQDS YKIGCVVAWC PSMTWVACGY SPAGDNIGSL IYELGEPCTK

**201** NEDCKCTDCT



  Residue Number  Increasing Mass  Decreasing Mass

**Start - End Observed Mr(expt) Mr(calc) ppm Miss Sequence**

**36 - 46 1448.7579 1447.7506 1447.7572 -5 2 R.KVFLDKHNEYR.S**  ([No match](http://msmsms/mascot/cgi/peptide_view.pl?file=../data/20110509/F014795.dat&query=26&hit=1" \t "_blank))

**36 - 46 1448.7579 1447.7506 1447.7572 -5 2 R.KVFLDKHNEYR.S**  ([Ions score 89](http://msmsms/mascot/cgi/peptide_view.pl?file=../data/20110509/F014795.dat&query=27&hit=1" \t "_blank))

**37 - 46 1320.6906 1319.6833 1319.6622 16 1 K.VFLDKHNEYR.S**  ([No match](http://msmsms/mascot/cgi/peptide_view.pl?file=../data/20110509/F014795.dat&query=20&hit=1" \t "_blank))

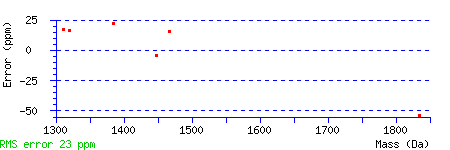
**37 - 51 1834.8828 1833.8755 1833.9737 -54 2 K.VFLDKHNEYRSLVAK.G**  Oxidation (HW) ([No match](http://msmsms/mascot/cgi/peptide_view.pl?file=../data/20110509/F014795.dat&query=30&hit=1" \t "_blank))

**52 - 65 1385.7109 1384.7036 1384.6735 22 0 K.GQAPNPQFGGSTPK.A**  ([No match](http://msmsms/mascot/cgi/peptide_view.pl?file=../data/20110509/F014795.dat&query=23&hit=1" \t "_blank))

**132 - 143 1467.7567 1466.7494 1466.7266 16 1 R.RYGVPQDNVYTR.D**  ([No match](http://msmsms/mascot/cgi/peptide_view.pl?file=../data/20110509/F014795.dat&query=28&hit=1" \t "_blank))

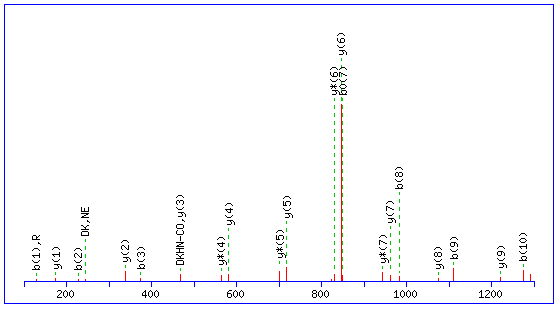
**133 - 143 1311.6555 1310.6482 1310.6255 17 0 R.YGVPQDNVYTR.D**  ([No match](http://msmsms/mascot/cgi/peptide_view.pl?file=../data/20110509/F014795.dat&query=18&hit=1" \t "_blank))

**133 - 143 1311.6555 1310.6482 1310.6255 17 0 R.YGVPQDNVYTR.D**  ([Ions score 79](http://msmsms/mascot/cgi/peptide_view.pl?file=../data/20110509/F014795.dat&query=19&hit=1" \t "_blank))



Bottom of Form

🡪 Annotated MS2 spectrum for peptide KVFLDKHNEYR



**Monoisotopic mass of neutral peptide Mr(calc):** 1447.7572

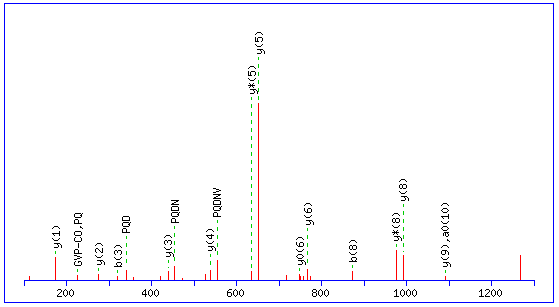
**Ions Score:** 89 **Expect:** 1.2e-007

**Matches :** 24/160 fragment ions using 23 most intense peaks   ([help](http://msmsms/mascot/help/results_help.html" \l "PEP" \t "_blank))

|  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **#** | **Immon.** | **a** | **a\*** | **a0** | **b** | **b\*** | **b0** | **Seq.** | **v** | **w** | **y** | **y\*** | **y0** | **#** |
| **1** | 101.1073 | 101.1073 | 84.0808 |  | **129.1022** | 112.0757 |  | **K** |  |  |  |  |  | **11** |
| **2** | 72.0808 | 200.1757 | 183.1492 |  | **228.1707** | 211.1441 |  | **V** | 1276.6069 | 1289.6273 | 1320.6695 | 1303.6430 | 1302.6589 | **10** |
| **3** | 120.0808 | 347.2442 | 330.2176 |  | **375.2391** | 358.2125 |  | **F** | 1129.5385 |  | ***1221.6011*** | 1204.5745 | 1203.5905 | **9** |
| **4** | 86.0964 | 460.3282 | 443.3017 |  | 488.3231 | 471.2966 |  | **L** | 1016.4544 | 1015.4592 | ***1074.5327*** | 1057.5061 | 1056.5221 | **8** |
| **5** | 88.0393 | 575.3552 | 558.3286 | 557.3446 | 603.3501 | 586.3235 | 585.3395 | **D** | 901.4275 | 900.4322 | ***961.4486*** | 944.4221 | 943.4381 | **7** |
| **6** | 101.1073 | 703.4501 | 686.4236 | 685.4396 | 731.4450 | 714.4185 | 713.4345 | **K** | 773.3325 | 772.3373 | ***846.4217*** | 829.3951 | 828.4111 | **6** |
| **7** | 110.0713 | 840.5090 | 823.4825 | 822.4985 | 868.5039 | 851.4774 | 850.4934 | **H** | 636.2736 |  | ***718.3267*** | 701.3002 | 700.3161 | **5** |
| **8** | 87.0553 | 954.5520 | 937.5254 | 936.5414 | **982.5469** | 965.5203 | 964.5363 | **N** | 522.2307 | 521.2354 | ***581.2678*** | 564.2413 | 563.2572 | **4** |
| **9** | 102.0550 | 1083.5946 | 1066.5680 | 1065.5840 | **1111.5895** | 1094.5629 | 1093.5789 | **E** | 393.1881 | 392.1928 | ***467.2249*** | 450.1983 | 449.2143 | **3** |
| **10** | 136.0757 | 1246.6579 | 1229.6313 | 1228.6473 | **1274.6528** | 1257.6262 | 1256.6422 | **Y** | 230.1248 |  | ***338.1823*** | 321.1557 |  | **2** |
| **11** | 129.1135 |  |  |  |  |  |  | **R** | 74.0237 | 73.0284 | ***175.1190*** | 158.0924 |  | **1** |

|  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **Seq** | **ya** | **yb** | **Seq** | **ya** | **yb** | **Seq** | **ya** | **yb** |
| **VF** | 219.1492 | 247.1441 | **VFL** | 332.2333 | 360.2282 | **VFLD** | 447.2602 | 475.2551 |
| **VFLDK** | 575.3552 | 603.3501 | **FL** | 233.1648 | 261.1598 | **FLD** | 348.1918 | 376.1867 |
| **FLDK** | 476.2867 | 504.2817 | **FLDKH** | 613.3457 | 641.3406 | **LD** | 201.1234 | 229.1183 |
| **LDK** | 329.2183 | 357.2132 | **LDKH** | 466.2772 | 494.2722 | **LDKHN** | 580.3202 | 608.3151 |
| **DK** | 216.1343 | 244.1292 | **DKH** | 353.1932 | 381.1881 | **DKHN** | 467.2361 | 495.2310 |
| **DKHNE** | 596.2787 | 624.2736 | **KH** | 238.1662 | 266.1612 | **KHN** | 352.2092 | 380.2041 |
| **KHNE** | 481.2518 | 509.2467 | **KHNEY** | 644.3151 | 672.3100 | **HN** | 224.1142 | 252.1091 |
| **HNE** | 353.1568 | 381.1517 | **HNEY** | 516.2201 | 544.2150 | **NE** | 216.0979 | 244.0928 |
| **NEY** | 379.1612 | 407.1561 | **EY** | 265.1183 | 293.1132 |  |  |  |

🡪 Annotated MS2 spectrum for peptide YGVPQDNVYTR



**Monoisotopic mass of neutral peptide Mr(calc):** 1310.6255

**Ions Score:** 79 **Expect:** 1.1e-006

**Matches :** 20/159 fragment ions using 19 most intense peaks   ([help](http://msmsms/mascot/help/results_help.html" \l "PEP" \t "_blank))

|  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **#** | **Immon.** | **a** | **a\*** | **a0** | **b** | **b\*** | **b0** | **Seq.** | **v** | **w** | **w'** | **y** | **y\*** | **y0** | **#** |
| **1** | 136.0757 | 136.0757 |  |  | 164.0706 |  |  | **Y** |  |  |  |  |  |  | **11** |
| **2** | 30.0338 | 193.0972 |  |  | 221.0921 |  |  | **G** |  |  |  | 1148.5695 | 1131.5429 | 1130.5589 | **10** |
| **3** | 72.0808 | 292.1656 |  |  | **320.1605** |  |  | **V** | 1047.4854 | 1060.5058 |  | ***1091.5480*** | 1074.5215 | 1073.5374 | **9** |
| **4** | 70.0651 | 389.2183 |  |  | 417.2132 |  |  | **P** | 950.4326 | 949.4374 |  | ***992.4796*** | 975.4530 | 974.4690 | **8** |
| **5** | 101.0709 | 517.2769 | 500.2504 |  | 545.2718 | 528.2453 |  | **Q** | 822.3741 | 821.3788 |  | 895.4268 | 878.4003 | 877.4163 | **7** |
| **6** | 88.0393 | 632.3039 | 615.2773 | 614.2933 | 660.2988 | 643.2722 | 642.2882 | **D** | 707.3471 | 706.3519 |  | ***767.3682*** | 750.3417 | 749.3577 | **6** |
| **7** | 87.0553 | 746.3468 | 729.3202 | 728.3362 | 774.3417 | 757.3151 | 756.3311 | **N** | 593.3042 | 592.3089 |  | ***652.3413*** | 635.3148 | 634.3307 | **5** |
| **8** | 72.0808 | 845.4152 | 828.3886 | 827.4046 | **873.4101** | 856.3836 | 855.3995 | **V** | 494.2358 | 507.2562 |  | ***538.2984*** | 521.2718 | 520.2878 | **4** |
| **9** | 136.0757 | 1008.4785 | 991.4520 | 990.4680 | 1036.4734 | 1019.4469 | 1018.4629 | **Y** | 331.1724 |  |  | ***439.2300*** | 422.2034 | 421.2194 | **3** |
| **10** | 74.0600 | 1109.5262 | 1092.4997 | 1091.5156 | 1137.5211 | 1120.4946 | 1119.5106 | **T** | 230.1248 | 243.1452 | 245.1244 | ***276.1666*** | 259.1401 | 258.1561 | **2** |
| **11** | 129.1135 |  |  |  |  |  |  | **R** | 74.0237 | 73.0284 |  | ***175.1190*** | 158.0924 |  | **1** |

|  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **Seq** | **ya** | **yb** | **Seq** | **ya** | **yb** | **Seq** | **ya** | **yb** |
| **GV** | 129.1022 | 157.0972 | **GVP** | 226.1550 | 254.1499 | **GVPQ** | 354.2136 | 382.2085 |
| **GVPQD** | 469.2405 | 497.2354 | **GVPQDN** | 583.2835 | 611.2784 | **GVPQDNV** | 682.3519 | 710.3468 |
| **VP** | 169.1335 | 197.1285 | **VPQ** | 297.1921 | 325.1870 | **VPQD** | 412.2191 | 440.2140 |
| **VPQDN** | 526.2620 | 554.2569 | **VPQDNV** | 625.3304 | 653.3253 | **PQ** | 198.1237 | 226.1186 |
| **PQD** | 313.1506 | 341.1456 | **PQDN** | 427.1936 | 455.1885 | **PQDNV** | 526.2620 | 554.2569 |
| **PQDNVY** | 689.3253 | 717.3202 | **QD** | 216.0979 | 244.0928 | **QDN** | 330.1408 | 358.1357 |
| **QDNV** | 429.2092 | 457.2041 | **QDNVY** | 592.2726 | 620.2675 | **QDNVYT** | 693.3202 | 721.3151 |
| **DN** | 202.0822 | 230.0771 | **DNV** | 301.1506 | 329.1456 | **DNVY** | 464.2140 | 492.2089 |
| **DNVYT** | 565.2617 | 593.2566 | **NV** | 186.1237 | 214.1186 | **NVY** | 349.1870 | 377.1819 |
| **NVYT** | 450.2347 | 478.2296 | **VY** | 235.1441 | 263.1390 | **VYT** | 336.1918 | 364.1867 |
| **YT** | 237.1234 | 265.1183 |  |  |  |  |  |  |

**Spot 4:**

**http://msmsms/mascot/images/88x31_logo_white.gifMascot Search Results**

**User :**

**Email :**

**Search title : SampleSetID: 341, AnalysisID: 561, MaldiWellID: 45035, SpectrumID: 137402, Path=\Jimmy\Cooperia Adult ES 20110221\20110221 MS en MSMS**

**Database : cooperia\_oncophora oncophora (33747 sequences; 5232511 residues)**

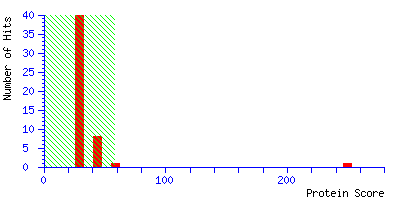
**Timestamp : 21 Feb 2011 at 15:34:50 GMT**

**Warning : A Peptide summary report will usually give a much clearer picture of MS/MS search results.**

**Top Score : 249 for contig05709, putative nuclear encoded protein Method: similarity and extension**

**Mascot Score Histogram**

Protein score is -10\*Log(P), where P is the probability that the observed match is a random event.  
Protein scores greater than 58 are significant (p<0.05).  
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



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**Protein Summary Report**

|  |  |  |  |
| --- | --- | --- | --- |
|  |  |  | [Help](http://msmsms/mascot/help/msms_summaries_help.html" \t "_blank) |
|  | Significance threshold p< | Max. number of hits |  |

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**Index**

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
|  | **Accession** | **Mass** | **Score** | **Description** |
| **1.** | [**contig05709**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20110221/F013474.dat#Hit1) | 23725 | 249 | putative nuclear encoded protein Method: similarity and extension |
| **2.** | [**contig63173**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20110221/F013474.dat#Hit2) | 22462 | 55 | putative nuclear encoded protein Method: similarity and extension |
| **3.** | [**isotig21491**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20110221/F013474.dat#Hit3) | 17227 | 46 | putative nuclear encoded protein Method: Longest ORF |
| **4.** | [**isotig17412**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20110221/F013474.dat#Hit4) | 14526 | 43 | putative nuclear encoded protein Method: similarity and extension |
| **5.** | [**isotig24052**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20110221/F013474.dat#Hit5) | 15248 | 42 | putative nuclear encoded protein Method: similarity and extension |
| **6.** | [**isotig32628**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20110221/F013474.dat#Hit6) | 11420 | 42 | putative nuclear encoded protein Method: similarity and extension |
| **7.** | [**isotig05806**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20110221/F013474.dat#Hit7) | 9102 | 39 | putative nuclear encoded protein Method: Longest ORF |
| **8.** | [**isotig31539**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20110221/F013474.dat#Hit8) | 18181 | 38 | putative nuclear encoded protein Method: Longest ORF |
| **9.** | [**isotig22461**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20110221/F013474.dat#Hit9) | 10364 | 37 | putative nuclear encoded protein Method: Longest ORF |
| **10.** | [**isotig31986**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20110221/F013474.dat#Hit10) | 11946 | 37 | putative nuclear encoded protein Method: similarity and extension |
| **11.** | [**isotig30345**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20110221/F013474.dat#Hit11) | 9062 | 37 | putative nuclear encoded protein Method: Longest ORF |
| **12.** | [**isotig19223**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20110221/F013474.dat#Hit12) | 5943 | 36 | putative nuclear encoded protein Method: Longest ORF |
| **13.** | [**isotig13961**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20110221/F013474.dat#Hit13) | 26563 | 36 | putative nuclear encoded protein Method: similarity and extension |
| **14.** | [**isotig10716**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20110221/F013474.dat#Hit14) | 17700 | 34 | putative nuclear encoded protein Method: Longest ORF |
| **15.** | [**isotig31572**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20110221/F013474.dat#Hit15) | 17413 | 34 | putative nuclear encoded protein Method: similarity and extension |
| **16.** | [**isotig01153**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20110221/F013474.dat#Hit16) | 38753 | 34 | putative nuclear encoded protein Method: similarity and extension |
| **17.** | [**isotig29700**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20110221/F013474.dat#Hit17) | 6743 | 34 | putative nuclear encoded protein Method: Longest ORF |
| **18.** | [**isotig01327**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20110221/F013474.dat#Hit18) | 36306 | 34 | putative nuclear encoded protein Method: similarity and extension |
| **19.** | [**isotig01318**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20110221/F013474.dat#Hit19) | 36262 | 34 | putative nuclear encoded protein Method: similarity and extension |
| **20.** | [**isotig01315**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20110221/F013474.dat#Hit20) | 36262 | 34 | putative nuclear encoded protein Method: similarity and extension |

**Results List**

|  |  |
| --- | --- |
| **1.** | [contig05709](http://msmsms/mascot/cgi/protein_view.pl?file=../data/20110221/F013474.dat&hit=1" \t "_blank)    **Mass:** 23725    **Score:** 249    **Expect:** 4.2e-021  **Matches:** 10 |
|  | putative nuclear encoded protein Method: similarity and extension |

|  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | **Observed** | **Mr(expt)** | **Mr(calc)** | **ppm** | **Start** |  | **End** | **Miss** | **Ions** | **Peptide** |
|  | 853.4781 | 852.4708 | 852.4566 | 16.7 | 97 | - | 103 | 2 | --- | K.SSKRYGR.N |
|  | 1311.6404 | 1310.6331 | 1310.6255 | 5.80 | 133 | - | 143 | 0 | --- | R.YGVPQDNVYTR.D |
|  | 1311.6404 | 1310.6331 | 1310.6255 | 5.80 | 133 | - | 143 | 0 | 66 | R.YGVPQDNVYTR.D |
|  | 1320.6779 | 1319.6706 | 1319.6622 | 6.37 | 37 | - | 46 | 1 | --- | K.VFLDKHNEYR.S |
|  | 1320.6779 | 1319.6706 | 1319.6622 | 6.37 | 37 | - | 46 | 1 | 70 | K.VFLDKHNEYR.S |
|  | 1385.6860 | 1384.6787 | 1384.6735 | 3.75 | 52 | - | 65 | 0 | --- | K.GQAPNPQFGGSTPK.A |
|  | 1385.6860 | 1384.6787 | 1384.6735 | 3.75 | 52 | - | 65 | 0 | 42 | K.GQAPNPQFGGSTPK.A |
|  | 1448.7411 | 1447.7338 | 1447.7572 | -16.13 | 36 | - | 46 | 2 | --- | R.KVFLDKHNEYR.S |
|  | 1448.7411 | 1447.7338 | 1447.7572 | -16.13 | 36 | - | 46 | 2 | 39 | R.KVFLDKHNEYR.S |
|  | 1467.7372 | 1466.7299 | 1466.7266 | 2.25 | 132 | - | 143 | 1 | --- | R.RYGVPQDNVYTR.D |

|  |  |
| --- | --- |
|  | **No match to:** 806.0900, 842.5046, 844.5453, 846.5433, 862.5406, 875.4469, 898.5488, 900.5500, 918.5851, 959.4695, 972.5956, 990.6068, 1045.5718, 1046.5311, 1052.5186, 1057.6875, 1113.7209, 1115.5706, 1131.7445, 1259.6584, 1259.6584, 1347.6282, 1363.6135, 1373.5630, 1382.5916, 1390.7085, 1431.7141, 1475.7330, 1761.7650, 1925.8682, 2211.1060, 2373.1096, 2673.3301 |

**http://msmsms/mascot/images/88x31_logo_white.gifMascot Search Results**

**Protein View**

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Match to: **contig05709** Score: **249** Expect: **4.2e-021**

**putative nuclear encoded protein Method: similarity and extension**

Nominal mass (Mr): **23725**; Calculated pI value: **5.37**

NCBI BLAST search of [contig05709](http://www.ncbi.nlm.nih.gov/blast/Blast.cgi?ALIGNMENTS=50&ALIGNMENT_VIEW=Pairwise&AUTO_FORMAT=Semiauto&CDD_SEARCH=on&CLIENT=web&COMPOSITION_BASED_STATISTICS=on&DATABASE=nr&DESCRIPTIONS=100&ENTREZ_QUERY=(none)&EXPECT=10&FILTER=L&FORMAT_BLOCK_ON_RESPAGE=None&FORMAT_OBJECT=Alignment&FORMAT_TYPE=HTML&GAPCOSTS=11+1&I_THRESH=0.001&LAYOUT=TwoWindows&MATRIX_NAME=BLOSUM62&NCBI_GI=on&PAGE=Proteins&PROGRAM=blastp&QUERY=MLIALITVFCLILHHATVLGEELCSLDNGMTDEIRKVFLDKHNEYRSLVAKGQAPNPQFGGSTPKAARMLKAMYDCDVEEDMTKWAQAQCTYAPFKSSKRYGRNTWGMGVPNYNKTAAAESSVYDWFFELRRYGVPQDNVYTRDVDYSAYHYAQMVWQDSYKIGCVVAWCPSMTWVACGYSPAGDNIGSLIYELGEPCTKNEDCKCTDCT&SERVICE=plain&SET_DEFAULTS.x=9&SET_DEFAULTS.y=5&SHOW_OVERVIEW=on&WORD_SIZE=3&END_OF_HTTPGET=Yes" \t "_blank) against nr

Unformatted [sequence string](http://msmsms/mascot/cgi/getseq.pl?cooperia_oncophora+contig05709+seq" \t "_blank) for pasting into other applications

Variable modifications: Oxidation (HW),Oxidation (M)

Cleavage by Trypsin/P: cuts C-term side of KR

Sequence Coverage: **20%**

Matched peptides shown in **Bold Red**

**1** MLIALITVFC LILHHATVLG EELCSLDNGM TDEIR**KVFLD KHNEYR**SLVA

**51** K**GQAPNPQFG GSTPK**AARML KAMYDCDVEE DMTKWAQAQC TYAPFK**SSKR**

**101 YGR**NTWGMGV PNYNKTAAAE SSVYDWFFEL R**RYGVPQDNV YTR**DVDYSAY

**151** HYAQMVWQDS YKIGCVVAWC PSMTWVACGY SPAGDNIGSL IYELGEPCTK

**201** NEDCKCTDCT



  Residue Number  Increasing Mass  Decreasing Mass



**Start - End Observed Mr(expt) Mr(calc) ppm Miss Sequence**

**36 - 46 1448.7411 1447.7338 1447.7572 -16 2 R.KVFLDKHNEYR.S**  ([No match](http://msmsms/mascot/cgi/peptide_view.pl?file=../data/20110221/F013474.dat&query=35&hit=1" \t "_blank))

**36 - 46 1448.7411 1447.7338 1447.7572 -16 2 R.KVFLDKHNEYR.S**  ([Ions score 39](http://msmsms/mascot/cgi/peptide_view.pl?file=../data/20110221/F013474.dat&query=36&hit=1" \t "_blank))

**37 - 46 1320.6779 1319.6706 1319.6622 6 1 K.VFLDKHNEYR.S**  ([No match](http://msmsms/mascot/cgi/peptide_view.pl?file=../data/20110221/F013474.dat&query=25&hit=1" \t "_blank))

**37 - 46 1320.6779 1319.6706 1319.6622 6 1 K.VFLDKHNEYR.S**  ([Ions score 70](http://msmsms/mascot/cgi/peptide_view.pl?file=../data/20110221/F013474.dat&query=26&hit=1" \t "_blank))

**52 - 65 1385.6860 1384.6787 1384.6735 4 0 K.GQAPNPQFGGSTPK.A**  ([No match](http://msmsms/mascot/cgi/peptide_view.pl?file=../data/20110221/F013474.dat&query=31&hit=1" \t "_blank))

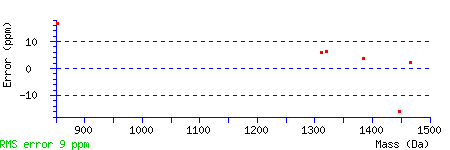
**52 - 65 1385.6860 1384.6787 1384.6735 4 0 K.GQAPNPQFGGSTPK.A**  ([Ions score 42](http://msmsms/mascot/cgi/peptide_view.pl?file=../data/20110221/F013474.dat&query=32&hit=1" \t "_blank))

**97 - 103 853.4781 852.4708 852.4566 17 2 K.SSKRYGR.N**  ([No match](http://msmsms/mascot/cgi/peptide_view.pl?file=../data/20110221/F013474.dat&query=5&hit=1" \t "_blank))

**132 - 143 1467.7372 1466.7299 1466.7266 2 1 R.RYGVPQDNVYTR.D**  ([No match](http://msmsms/mascot/cgi/peptide_view.pl?file=../data/20110221/F013474.dat&query=37&hit=1" \t "_blank))

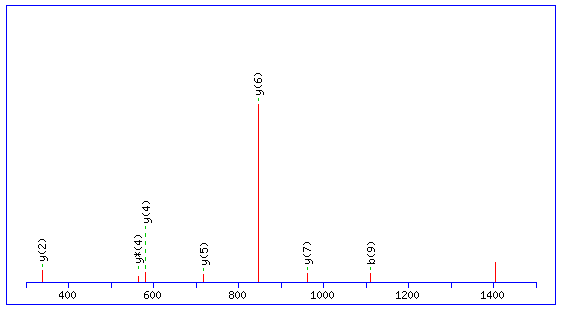
**133 - 143 1311.6404 1310.6331 1310.6255 6 0 R.YGVPQDNVYTR.D**  ([No match](http://msmsms/mascot/cgi/peptide_view.pl?file=../data/20110221/F013474.dat&query=23&hit=1" \t "_blank))

**133 - 143 1311.6404 1310.6331 1310.6255 6 0 R.YGVPQDNVYTR.D**  ([Ions score 66](http://msmsms/mascot/cgi/peptide_view.pl?file=../data/20110221/F013474.dat&query=24&hit=1" \t "_blank))



Bottom of Form

🡪 Annotated MS2 spectrum for peptide KVFLDKHNEYR



**Monoisotopic mass of neutral peptide Mr(calc):** 1447.7572

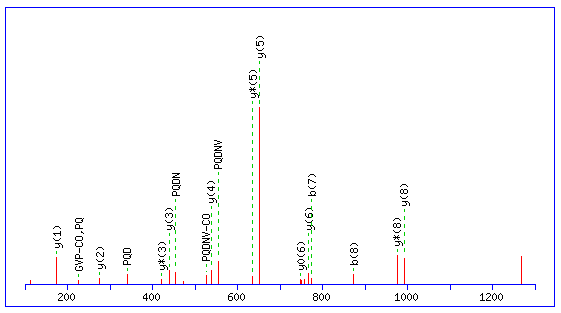
**Ions Score:** 39 **Expect:** 0.01

**Matches :** 7/160 fragment ions using 8 most intense peaks   ([help](http://msmsms/mascot/help/results_help.html" \l "PEP" \t "_blank))

|  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **#** | **Immon.** | **a** | **a\*** | **a0** | **b** | **b\*** | **b0** | **Seq.** | **v** | **w** | **y** | **y\*** | **y0** | **#** |
| **1** | 101.1073 | 101.1073 | 84.0808 |  | 129.1022 | 112.0757 |  | **K** |  |  |  |  |  | **11** |
| **2** | 72.0808 | 200.1757 | 183.1492 |  | 228.1707 | 211.1441 |  | **V** | 1276.6069 | 1289.6273 | 1320.6695 | 1303.6430 | 1302.6589 | **10** |
| **3** | 120.0808 | 347.2442 | 330.2176 |  | 375.2391 | 358.2125 |  | **F** | 1129.5385 |  | 1221.6011 | 1204.5745 | 1203.5905 | **9** |
| **4** | 86.0964 | 460.3282 | 443.3017 |  | 488.3231 | 471.2966 |  | **L** | 1016.4544 | 1015.4592 | 1074.5327 | 1057.5061 | 1056.5221 | **8** |
| **5** | 88.0393 | 575.3552 | 558.3286 | 557.3446 | 603.3501 | 586.3235 | 585.3395 | **D** | 901.4275 | 900.4322 | ***961.4486*** | 944.4221 | 943.4381 | **7** |
| **6** | 101.1073 | 703.4501 | 686.4236 | 685.4396 | 731.4450 | 714.4185 | 713.4345 | **K** | 773.3325 | 772.3373 | ***846.4217*** | 829.3951 | 828.4111 | **6** |
| **7** | 110.0713 | 840.5090 | 823.4825 | 822.4985 | 868.5039 | 851.4774 | 850.4934 | **H** | 636.2736 |  | ***718.3267*** | 701.3002 | 700.3161 | **5** |
| **8** | 87.0553 | 954.5520 | 937.5254 | 936.5414 | 982.5469 | 965.5203 | 964.5363 | **N** | 522.2307 | 521.2354 | ***581.2678*** | 564.2413 | 563.2572 | **4** |
| **9** | 102.0550 | 1083.5946 | 1066.5680 | 1065.5840 | 1111.5895 | 1094.5629 | 1093.5789 | **E** | 393.1881 | 392.1928 | 467.2249 | 450.1983 | 449.2143 | **3** |
| **10** | 136.0757 | 1246.6579 | 1229.6313 | 1228.6473 | 1274.6528 | 1257.6262 | 1256.6422 | **Y** | 230.1248 |  | ***338.1823*** | 321.1557 |  | **2** |
| **11** | 129.1135 |  |  |  |  |  |  | **R** | 74.0237 | 73.0284 | 175.1190 | 158.0924 |  | **1** |

|  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **Seq** | **ya** | **yb** | **Seq** | **ya** | **yb** | **Seq** | **ya** | **yb** |
| **VF** | 219.1492 | 247.1441 | **VFL** | 332.2333 | 360.2282 | **VFLD** | 447.2602 | 475.2551 |
| **VFLDK** | 575.3552 | 603.3501 | **FL** | 233.1648 | 261.1598 | **FLD** | 348.1918 | 376.1867 |
| **FLDK** | 476.2867 | 504.2817 | **FLDKH** | 613.3457 | 641.3406 | **LD** | 201.1234 | 229.1183 |
| **LDK** | 329.2183 | 357.2132 | **LDKH** | 466.2772 | 494.2722 | **LDKHN** | 580.3202 | 608.3151 |
| **DK** | 216.1343 | 244.1292 | **DKH** | 353.1932 | 381.1881 | **DKHN** | 467.2361 | 495.2310 |
| **DKHNE** | 596.2787 | 624.2736 | **KH** | 238.1662 | 266.1612 | **KHN** | 352.2092 | 380.2041 |
| **KHNE** | 481.2518 | 509.2467 | **KHNEY** | 644.3151 | 672.3100 | **HN** | 224.1142 | 252.1091 |
| **HNE** | 353.1568 | 381.1517 | **HNEY** | 516.2201 | 544.2150 | **NE** | 216.0979 | 244.0928 |
| **NEY** | 379.1612 | 407.1561 | **EY** | 265.1183 | 293.1132 |  |  |  |

🡪 Annotated MS2 spectrum for peptide YGVPQDNVYTR



**Monoisotopic mass of neutral peptide Mr(calc):** 1310.6255

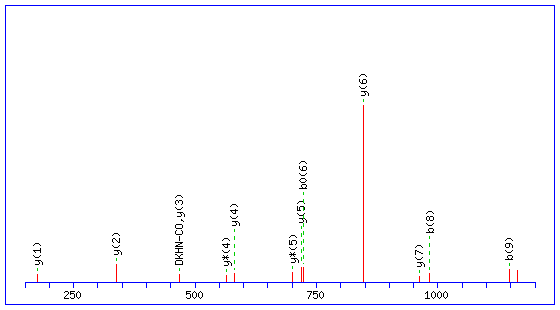
**Ions Score:** 66 **Expect:** 1.6e-005

**Matches :** 21/159 fragment ions using 20 most intense peaks   ([help](http://msmsms/mascot/help/results_help.html" \l "PEP" \t "_blank))

|  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **#** | **Immon.** | **a** | **a\*** | **a0** | **b** | **b\*** | **b0** | **Seq.** | **v** | **w** | **w'** | **y** | **y\*** | **y0** | **#** |
| **1** | 136.0757 | 136.0757 |  |  | 164.0706 |  |  | **Y** |  |  |  |  |  |  | **11** |
| **2** | 30.0338 | 193.0972 |  |  | 221.0921 |  |  | **G** |  |  |  | 1148.5695 | 1131.5429 | 1130.5589 | **10** |
| **3** | 72.0808 | 292.1656 |  |  | 320.1605 |  |  | **V** | 1047.4854 | 1060.5058 |  | 1091.5480 | 1074.5215 | 1073.5374 | **9** |
| **4** | 70.0651 | 389.2183 |  |  | 417.2132 |  |  | **P** | 950.4326 | 949.4374 |  | ***992.4796*** | 975.4530 | 974.4690 | **8** |
| **5** | 101.0709 | 517.2769 | 500.2504 |  | 545.2718 | 528.2453 |  | **Q** | 822.3741 | 821.3788 |  | 895.4268 | 878.4003 | 877.4163 | **7** |
| **6** | 88.0393 | 632.3039 | 615.2773 | 614.2933 | 660.2988 | 643.2722 | 642.2882 | **D** | 707.3471 | 706.3519 |  | ***767.3682*** | 750.3417 | 749.3577 | **6** |
| **7** | 87.0553 | 746.3468 | 729.3202 | 728.3362 | **774.3417** | 757.3151 | 756.3311 | **N** | 593.3042 | 592.3089 |  | ***652.3413*** | 635.3148 | 634.3307 | **5** |
| **8** | 72.0808 | 845.4152 | 828.3886 | 827.4046 | **873.4101** | 856.3836 | 855.3995 | **V** | 494.2358 | 507.2562 |  | ***538.2984*** | 521.2718 | 520.2878 | **4** |
| **9** | 136.0757 | 1008.4785 | 991.4520 | 990.4680 | 1036.4734 | 1019.4469 | 1018.4629 | **Y** | 331.1724 |  |  | ***439.2300*** | 422.2034 | 421.2194 | **3** |
| **10** | 74.0600 | 1109.5262 | 1092.4997 | 1091.5156 | 1137.5211 | 1120.4946 | 1119.5106 | **T** | 230.1248 | 243.1452 | 245.1244 | ***276.1666*** | 259.1401 | 258.1561 | **2** |
| **11** | 129.1135 |  |  |  |  |  |  | **R** | 74.0237 | 73.0284 |  | ***175.1190*** | 158.0924 |  | **1** |

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| --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **Seq** | **ya** | **yb** | **Seq** | **ya** | **yb** | **Seq** | **ya** | **yb** |
| **GV** | 129.1022 | 157.0972 | **GVP** | 226.1550 | 254.1499 | **GVPQ** | 354.2136 | 382.2085 |
| **GVPQD** | 469.2405 | 497.2354 | **GVPQDN** | 583.2835 | 611.2784 | **GVPQDNV** | 682.3519 | 710.3468 |
| **VP** | 169.1335 | 197.1285 | **VPQ** | 297.1921 | 325.1870 | **VPQD** | 412.2191 | 440.2140 |
| **VPQDN** | 526.2620 | 554.2569 | **VPQDNV** | 625.3304 | 653.3253 | **PQ** | 198.1237 | 226.1186 |
| **PQD** | 313.1506 | 341.1456 | **PQDN** | 427.1936 | 455.1885 | **PQDNV** | 526.2620 | 554.2569 |
| **PQDNVY** | 689.3253 | 717.3202 | **QD** | 216.0979 | 244.0928 | **QDN** | 330.1408 | 358.1357 |
| **QDNV** | 429.2092 | 457.2041 | **QDNVY** | 592.2726 | 620.2675 | **QDNVYT** | 693.3202 | 721.3151 |
| **DN** | 202.0822 | 230.0771 | **DNV** | 301.1506 | 329.1456 | **DNVY** | 464.2140 | 492.2089 |
| **DNVYT** | 565.2617 | 593.2566 | **NV** | 186.1237 | 214.1186 | **NVY** | 349.1870 | 377.1819 |
| **NVYT** | 450.2347 | 478.2296 | **VY** | 235.1441 | 263.1390 | **VYT** | 336.1918 | 364.1867 |
| **YT** | 237.1234 | 265.1183 |  |  |  |  |  |  |

🡪 Annotated MS2 spectrum for peptide VFLDKHNEYR



**Monoisotopic mass of neutral peptide Mr(calc):** 1319.6622

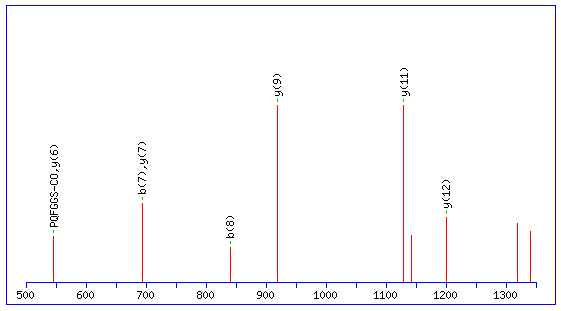
**Ions Score:** 70 **Expect:** 7.8e-006

**Matches :** 13/134 fragment ions using 13 most intense peaks   ([help](http://msmsms/mascot/help/results_help.html" \l "PEP" \t "_blank))

|  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **#** | **Immon.** | **a** | **a\*** | **a0** | **b** | **b\*** | **b0** | **Seq.** | **v** | **w** | **y** | **y\*** | **y0** | **#** |
| **1** | 72.0808 | 72.0808 |  |  | 100.0757 |  |  | **V** |  |  |  |  |  | **10** |
| **2** | 120.0808 | 219.1492 |  |  | 247.1441 |  |  | **F** | 1129.5385 |  | 1221.6011 | 1204.5745 | 1203.5905 | **9** |
| **3** | 86.0964 | 332.2333 |  |  | 360.2282 |  |  | **L** | 1016.4544 | 1015.4592 | 1074.5327 | 1057.5061 | 1056.5221 | **8** |
| **4** | 88.0393 | 447.2602 |  | 429.2496 | 475.2551 |  | 457.2445 | **D** | 901.4275 | 900.4322 | ***961.4486*** | 944.4221 | 943.4381 | **7** |
| **5** | 101.1073 | 575.3552 | 558.3286 | 557.3446 | 603.3501 | 586.3235 | 585.3395 | **K** | 773.3325 | 772.3373 | ***846.4217*** | 829.3951 | 828.4111 | **6** |
| **6** | 110.0713 | 712.4141 | 695.3875 | 694.4035 | 740.4090 | 723.3824 | 722.3984 | **H** | 636.2736 |  | ***718.3267*** | 701.3002 | 700.3161 | **5** |
| **7** | 87.0553 | 826.4570 | 809.4304 | 808.4464 | 854.4519 | 837.4254 | 836.4413 | **N** | 522.2307 | 521.2354 | ***581.2678*** | 564.2413 | 563.2572 | **4** |
| **8** | 102.0550 | 955.4996 | 938.4730 | 937.4890 | **983.4945** | 966.4680 | 965.4839 | **E** | 393.1881 | 392.1928 | ***467.2249*** | 450.1983 | 449.2143 | **3** |
| **9** | 136.0757 | 1118.5629 | 1101.5364 | 1100.5524 | **1146.5578** | 1129.5313 | 1128.5473 | **Y** | 230.1248 |  | ***338.1823*** | 321.1557 |  | **2** |
| **10** | 129.1135 |  |  |  |  |  |  | **R** | 74.0237 | 73.0284 | ***175.1190*** | 158.0924 |  | **1** |
|  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |

|  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **Seq** | **ya** | **yb** | **Seq** | **ya** | **yb** | **Seq** | **ya** | **yb** |
| **FL** | 233.1648 | 261.1598 | **FLD** | 348.1918 | 376.1867 | **FLDK** | 476.2867 | 504.2817 |
| **FLDKH** | 613.3457 | 641.3406 | **LD** | 201.1234 | 229.1183 | **LDK** | 329.2183 | 357.2132 |
| **LDKH** | 466.2772 | 494.2722 | **LDKHN** | 580.3202 | 608.3151 | **DK** | 216.1343 | 244.1292 |
| **DKH** | 353.1932 | 381.1881 | **DKHN** | 467.2361 | 495.2310 | **DKHNE** | 596.2787 | 624.2736 |
| **KH** | 238.1662 | 266.1612 | **KHN** | 352.2092 | 380.2041 | **KHNE** | 481.2518 | 509.2467 |
| **KHNEY** | 644.3151 | 672.3100 | **HN** | 224.1142 | 252.1091 | **HNE** | 353.1568 | 381.1517 |
| **HNEY** | 516.2201 | 544.2150 | **NE** | 216.0979 | 244.0928 | **NEY** | 379.1612 | 407.1561 |
| **EY** | 265.1183 | 293.1132 |  |  |  |  |  |  |

🡪 Annotated MS2 spectrum for peptide GQAPNPQFGGSTPK



**Monoisotopic mass of neutral peptide Mr(calc):** 1384.6735

**Ions Score:** 42 **Expect:** 0.0043

**Matches :** 8/206 fragment ions using 7 most intense peaks   ([help](http://msmsms/mascot/help/results_help.html" \l "PEP" \t "_blank))

|  |  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **#** | **Immon.** | **a** | **a\*** | **a0** | **b** | **b\*** | **b0** | **Seq.** | **y** | **y\*** | **y0** | **#** |
| **1** | 30.0338 | 30.0338 |  |  | 58.0287 |  |  | **G** |  |  |  | **14** |
| **2** | 101.0709 | 158.0924 | 141.0659 |  | 186.0873 | 169.0608 |  | **Q** | 1328.6593 | 1311.6328 | 1310.6488 | **13** |
| **3** | 44.0495 | 229.1295 | 212.1030 |  | 257.1244 | 240.0979 |  | **A** | ***1200.6008*** | 1183.5742 | 1182.5902 | **12** |
| **4** | 70.0651 | 326.1823 | 309.1557 |  | 354.1772 | 337.1506 |  | **P** | ***1129.5637*** | 1112.5371 | 1111.5531 | **11** |
| **5** | 87.0553 | 440.2252 | 423.1987 |  | 468.2201 | 451.1936 |  | **N** | 1032.5109 | 1015.4843 | 1014.5003 | **10** |
| **6** | 70.0651 | 537.2780 | 520.2514 |  | 565.2729 | 548.2463 |  | **P** | ***918.4680*** | 901.4414 | 900.4574 | **9** |
| **7** | 101.0709 | 665.3366 | 648.3100 |  | **693.3315** | 676.3049 |  | **Q** | 821.4152 | 804.3886 | 803.4046 | **8** |
| **8** | 120.0808 | 812.4050 | 795.3784 |  | **840.3999** | 823.3733 |  | **F** | ***693.3566*** | 676.3301 | 675.3461 | **7** |
| **9** | 30.0338 | 869.4264 | 852.3999 |  | 897.4213 | 880.3948 |  | **G** | ***546.2882*** | 529.2617 | 528.2776 | **6** |
| **10** | 30.0338 | 926.4479 | 909.4213 |  | 954.4428 | 937.4163 |  | **G** | 489.2667 | 472.2402 | 471.2562 | **5** |
| **11** | 60.0444 | 1013.4799 | 996.4534 | 995.4694 | 1041.4748 | 1024.4483 | 1023.4643 | **S** | 432.2453 | 415.2187 | 414.2347 | **4** |
| **12** | 74.0600 | 1114.5276 | 1097.5011 | 1096.5170 | 1142.5225 | 1125.4960 | 1124.5119 | **T** | 345.2132 | 328.1867 | 327.2027 | **3** |
| **13** | 70.0651 | 1211.5804 | 1194.5538 | 1193.5698 | 1239.5753 | 1222.5487 | 1221.5647 | **P** | 244.1656 | 227.1390 |  | **2** |
| **14** | 101.1073 |  |  |  |  |  |  | **K** | 147.1128 | 130.0863 |  | **1** |

|  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **Seq** | **ya** | **yb** | **Seq** | **ya** | **yb** | **Seq** | **ya** | **yb** |
| **QA** | 172.1081 | 200.1030 | **QAP** | 269.1608 | 297.1557 | **QAPN** | 383.2037 | 411.1987 |
| **QAPNP** | 480.2565 | 508.2514 | **QAPNPQ** | 608.3151 | 636.3100 | **AP** | 141.1022 | 169.0972 |
| **APN** | 255.1452 | 283.1401 | **APNP** | 352.1979 | 380.1928 | **APNPQ** | 480.2565 | 508.2514 |
| **APNPQF** | 627.3249 | 655.3198 | **APNPQFG** | 684.3464 | 712.3413 | **PN** | 184.1081 | 212.1030 |
| **PNP** | 281.1608 | 309.1557 | **PNPQ** | 409.2194 | 437.2143 | **PNPQF** | 556.2878 | 584.2827 |
| **PNPQFG** | 613.3093 | 641.3042 | **PNPQFGG** | 670.3307 | 698.3257 | **NP** | 184.1081 | 212.1030 |
| **NPQ** | 312.1666 | 340.1615 | **NPQF** | 459.2350 | 487.2300 | **NPQFG** | 516.2565 | 544.2514 |
| **NPQFGG** | 573.2780 | 601.2729 | **NPQFGGS** | 660.3100 | 688.3049 | **PQ** | 198.1237 | 226.1186 |
| **PQF** | 345.1921 | 373.1870 | **PQFG** | 402.2136 | 430.2085 | **PQFGG** | 459.2350 | 487.2300 |
| **PQFGGS** | 546.2671 | 574.2620 | **PQFGGST** | 647.3148 | 675.3097 | **QF** | 248.1394 | 276.1343 |
| **QFG** | 305.1608 | 333.1557 | **QFGG** | 362.1823 | 390.1772 | **QFGGS** | 449.2143 | 477.2092 |
| **QFGGST** | 550.2620 | 578.2569 | **QFGGSTP** | 647.3148 | 675.3097 | **FG** | 177.1022 | 205.0972 |
| **FGG** | 234.1237 | 262.1186 | **FGGS** | 321.1557 | 349.1506 | **FGGST** | 422.2034 | 450.1983 |
| **FGGSTP** | 519.2562 | 547.2511 | **GG** | 87.0553 | 115.0502 | **GGS** | 174.0873 | 202.0822 |
| **GGST** | 275.1350 | 303.1299 | **GGSTP** | 372.1878 | 400.1827 | **GS** | 117.0659 | 145.0608 |
| **GST** | 218.1135 | 246.1084 | **GSTP** | 315.1663 | 343.1612 | **ST** | 161.0921 | 189.0870 |
| **STP** | 258.1448 | 286.1397 | **TP** | 171.1128 | 199.1077 |  |  |  |

**Spot 5:**

**http://msmsms/mascot/images/88x31_logo_white.gifMascot Search Results**

**User :**

**Email :**

**Search title : SampleSetID: 341, AnalysisID: 561, MaldiWellID: 45044, SpectrumID: 137448, Path=\Jimmy\Cooperia Adult ES 20110221\20110221 MS en MSMS**

**Database : cooperia\_oncophora oncophora (33747 sequences; 5232511 residues)**

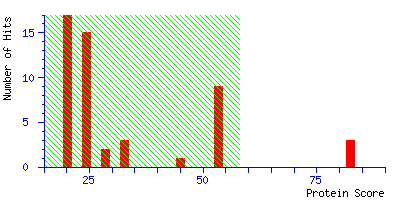
**Timestamp : 21 Feb 2011 at 15:36:45 GMT**

**Warning : A Peptide summary report will usually give a much clearer picture of MS/MS search results.**

**Top Score : 83 for contig55746, putative nuclear encoded protein Method: similarity and extension**

**Mascot Score Histogram**

Protein score is -10\*Log(P), where P is the probability that the observed match is a random event.  
Protein scores greater than 58 are significant (p<0.05).  
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



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**Protein Summary Report**

|  |  |  |  |
| --- | --- | --- | --- |
|  |  |  | [Help](http://msmsms/mascot/help/msms_summaries_help.html" \t "_blank) |
|  | Significance threshold p< | Max. number of hits |  |

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**Index**

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
|  | **Accession** | **Mass** | **Score** | **Description** |
| **1.** | [**contig55746**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20110221/F013482.dat#Hit1) | 17086 | 83 | putative nuclear encoded protein Method: similarity and extension |
| **2.** | [**isotig13456**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20110221/F013482.dat#Hit2) | 17575 | 82 | putative nuclear encoded protein Method: similarity and extension |
| **3.** | [**isotig13457**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20110221/F013482.dat#Hit3) | 17585 | 82 | putative nuclear encoded protein Method: similarity and extension |
| **4.** | [**isotig00350**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20110221/F013482.dat#Hit4) | 28465 | 55 | putative nuclear encoded protein Method: similarity and extension |
| **5.** | [**isotig00352**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20110221/F013482.dat#Hit5) | 28473 | 55 | putative nuclear encoded protein Method: similarity and extension |
| **6.** | [**isotig00338**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20110221/F013482.dat#Hit6) | 28674 | 55 | putative nuclear encoded protein Method: similarity and extension |
| **7.** | [**isotig00347**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20110221/F013482.dat#Hit7) | 28920 | 55 | putative nuclear encoded protein Method: similarity and extension |
| **8.** | [**isotig00335**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20110221/F013482.dat#Hit8) | 28600 | 55 | putative nuclear encoded protein Method: similarity and extension |
| **9.** | [**isotig00340**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20110221/F013482.dat#Hit9) | 28683 | 55 | putative nuclear encoded protein Method: similarity and extension |
| **10.** | [**isotig00346**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20110221/F013482.dat#Hit10) | 28929 | 55 | putative nuclear encoded protein Method: similarity and extension |
| **11.** | [**isotig00336**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20110221/F013482.dat#Hit11) | 28609 | 55 | putative nuclear encoded protein Method: similarity and extension |
| **12.** | [**isotig00355**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20110221/F013482.dat#Hit12) | 28656 | 55 | putative nuclear encoded protein Method: similarity and extension |
| **13.** | [**isotig25596**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20110221/F013482.dat#Hit13) | 8134 | 43 | putative nuclear encoded protein Method: Longest ORF |
| **14.** | [**isotig14592**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20110221/F013482.dat#Hit14) | 23294 | 32 | putative nuclear encoded protein Method: similarity and extension |
| **15.** | [**isotig13105**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20110221/F013482.dat#Hit15) | 15948 | 31 | putative nuclear encoded protein Method: similarity and extension |
| **16.** | [**isotig13106**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20110221/F013482.dat#Hit16) | 15942 | 31 | putative nuclear encoded protein Method: similarity and extension |
| **17.** | [**isotig13201**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20110221/F013482.dat#Hit17) | 16678 | 30 | putative nuclear encoded protein Method: Longest ORF |
| **18.** | [**isotig22025**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20110221/F013482.dat#Hit18) | 11682 | 28 | putative nuclear encoded protein Method: Longest ORF |
| **19.** | [**isotig23928**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20110221/F013482.dat#Hit19) | 16792 | 25 | putative nuclear encoded protein Method: similarity and extension |
| **20.** | [**isotig22102**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20110221/F013482.dat#Hit20) | 14103 | 25 | putative nuclear encoded protein Method: Longest ORF |

**Results List**

|  |  |
| --- | --- |
| **1.** | [contig55746](http://msmsms/mascot/cgi/protein_view.pl?file=../data/20110221/F013482.dat&hit=1" \t "_blank)    **Mass:** 17086    **Score:** 83     **Expect:** 0.00019  **Matches:** 2 |
|  | putative nuclear encoded protein Method: similarity and extension |

|  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | **Observed** | **Mr(expt)** | **Mr(calc)** | **ppm** | **Start** |  | **End** | **Miss** | **Ions** | **Peptide** |
|  | 2208.1555 | 2207.1482 | 2207.0858 | 28.3 | 4 | - | 22 | 0 | --- | K.NVYHDIVPEPVTENPSELR.M |
|  | 2208.1555 | 2207.1482 | 2207.0858 | 28.3 | 4 | - | 22 | 0 | 77 | K.NVYHDIVPEPVTENPSELR.M |

|  |  |
| --- | --- |
|  | **No match to:** 806.0997, 881.2771, 1151.6149, 1151.6149, 1163.6532, 1213.5425, 1442.7887, 1638.7351, 1652.7517, 1652.7517, 1729.7386, 1743.7522, 1743.7522, 2002.1176 |

|  |  |
| --- | --- |
| **2.** | [isotig13456](http://msmsms/mascot/cgi/protein_view.pl?file=../data/20110221/F013482.dat&hit=2" \t "_blank)    **Mass:** 17575    **Score:** 82     **Expect:** 0.00019  **Matches:** 2 |
|  | putative nuclear encoded protein Method: similarity and extension |

|  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | **Observed** | **Mr(expt)** | **Mr(calc)** | **ppm** | **Start** |  | **End** | **Miss** | **Ions** | **Peptide** |
|  | 2208.1555 | 2207.1482 | 2207.0858 | 28.3 | 8 | - | 26 | 0 | --- | K.NVYHDIVPEPVTENPSELR.M |
|  | 2208.1555 | 2207.1482 | 2207.0858 | 28.3 | 8 | - | 26 | 0 | 77 | K.NVYHDIVPEPVTENPSELR.M |

|  |  |
| --- | --- |
|  | **No match to:** 806.0997, 881.2771, 1151.6149, 1151.6149, 1163.6532, 1213.5425, 1442.7887, 1638.7351, 1652.7517, 1652.7517, 1729.7386, 1743.7522, 1743.7522, 2002.1176 |

|  |  |
| --- | --- |
| **3.** | [isotig13457](http://msmsms/mascot/cgi/protein_view.pl?file=../data/20110221/F013482.dat&hit=3" \t "_blank)    **Mass:** 17585    **Score:** 82     **Expect:** 0.00019  **Matches:** 2 |
|  | putative nuclear encoded protein Method: similarity and extension |

|  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | **Observed** | **Mr(expt)** | **Mr(calc)** | **ppm** | **Start** |  | **End** | **Miss** | **Ions** | **Peptide** |
|  | 2208.1555 | 2207.1482 | 2207.0858 | 28.3 | 8 | - | 26 | 0 | --- | K.NVYHDIVPEPVTENPSELR.M |
|  | 2208.1555 | 2207.1482 | 2207.0858 | 28.3 | 8 | - | 26 | 0 | 77 | K.NVYHDIVPEPVTENPSELR.M |

|  |  |
| --- | --- |
|  | **No match to:** 806.0997, 881.2771, 1151.6149, 1151.6149, 1163.6532, 1213.5425, 1442.7887, 1638.7351, 1652.7517, 1652.7517, 1729.7386, 1743.7522, 1743.7522, 2002.1176 |

**http://msmsms/mascot/images/88x31_logo_white.gifMascot Search Results**

**Protein View**

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Match to: **contig55746** Score: **83** Expect: **0.00019**

**putative nuclear encoded protein Method: similarity and extension**

Nominal mass (Mr): **17086**; Calculated pI value: **4.58**

NCBI BLAST search of [contig55746](http://www.ncbi.nlm.nih.gov/blast/Blast.cgi?ALIGNMENTS=50&ALIGNMENT_VIEW=Pairwise&AUTO_FORMAT=Semiauto&CDD_SEARCH=on&CLIENT=web&COMPOSITION_BASED_STATISTICS=on&DATABASE=nr&DESCRIPTIONS=100&ENTREZ_QUERY=(none)&EXPECT=10&FILTER=L&FORMAT_BLOCK_ON_RESPAGE=None&FORMAT_OBJECT=Alignment&FORMAT_TYPE=HTML&GAPCOSTS=11+1&I_THRESH=0.001&LAYOUT=TwoWindows&MATRIX_NAME=BLOSUM62&NCBI_GI=on&PAGE=Proteins&PROGRAM=blastp&QUERY=LGKNVYHDIVPEPVTENPSELRMRKYNFISAAIDDWLMPTETYPIQGDVRYKESLYSDSNLYTFANMAYDKIYEVGCNYEECPDGDETQASLICIYNTKVPDHTQLYQVGSKDPDHAGCNKDKTVCQFLGKANATCDDLLCKLPNVVSSFL&SERVICE=plain&SET_DEFAULTS.x=9&SET_DEFAULTS.y=5&SHOW_OVERVIEW=on&WORD_SIZE=3&END_OF_HTTPGET=Yes" \t "_blank) against nr

Unformatted [sequence string](http://msmsms/mascot/cgi/getseq.pl?cooperia_oncophora+contig55746+seq" \t "_blank) for pasting into other applications

Variable modifications: Oxidation (HW),Oxidation (M)

Cleavage by Trypsin/P: cuts C-term side of KR

Sequence Coverage: **12%**

Matched peptides shown in **Bold Red**

**1** LGK**NVYHDIV PEPVTENPSE LR**MRKYNFIS AAIDDWLMPT ETYPIQGDVR

**51** YKESLYSDSN LYTFANMAYD KIYEVGCNYE ECPDGDETQA SLICIYNTKV

**101** PDHTQLYQVG SKDPDHAGCN KDKTVCQFLG KANATCDDLL CKLPNVVSSF

**151** L



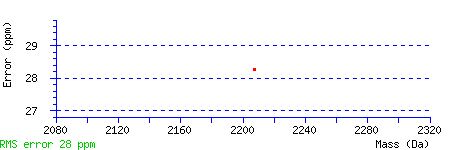
  Residue Number  Increasing Mass  Decreasing Mass



**Start - End Observed Mr(expt) Mr(calc) ppm Miss Sequence**

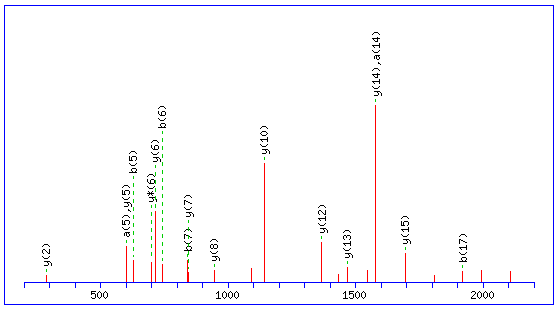
**4 - 22 2208.1555 2207.1482 2207.0858 28 0 K.NVYHDIVPEPVTENPSELR.M**  ([No match](http://msmsms/mascot/cgi/peptide_view.pl?file=../data/20110221/F013482.dat&query=15&hit=1" \t "_blank))

**4 - 22 2208.1555 2207.1482 2207.0858 28 0 K.NVYHDIVPEPVTENPSELR.M**  ([Ions score 77](http://msmsms/mascot/cgi/peptide_view.pl?file=../data/20110221/F013482.dat&query=16&hit=1" \t "_blank))



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🡪 Annotated MS2 spectrum for peptide NVYHDIVPEPVTENPSELR



**Monoisotopic mass of neutral peptide Mr(calc):** 2207.0858

**Ions Score:** 77 **Expect:** 1.5e-006

**Matches :** 17/346 fragment ions using 21 most intense peaks   ([help](http://msmsms/mascot/help/results_help.html" \l "PEP" \t "_blank))

|  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **#** | **Immon.** | **a** | **a\*** | **a0** | **b** | **b\*** | **b0** | **Seq.** | **v** | **w** | **w'** | **y** | **y\*** | **y0** | **#** |
| **1** | 87.0553 | 87.0553 | 70.0287 |  | 115.0502 | 98.0237 |  | **N** |  |  |  |  |  |  | **19** |
| **2** | 72.0808 | 186.1237 | 169.0972 |  | 214.1186 | 197.0921 |  | **V** | 2049.9876 | 2063.0080 |  | 2094.0502 | 2077.0237 | 2076.0396 | **18** |
| **3** | 136.0757 | 349.1870 | 332.1605 |  | 377.1819 | 360.1554 |  | **Y** | 1886.9243 |  |  | 1994.9818 | 1977.9552 | 1976.9712 | **17** |
| **4** | 110.0713 | 486.2459 | 469.2194 |  | 514.2409 | 497.2143 |  | **H** | 1749.8654 |  |  | 1831.9185 | 1814.8919 | 1813.9079 | **16** |
| **5** | 88.0393 | **601.2729** | 584.2463 | 583.2623 | **629.2678** | 612.2413 | 611.2572 | **D** | 1634.8384 | 1633.8432 |  | ***1694.8596*** | 1677.8330 | 1676.8490 | **15** |
| **6** | 86.0964 | 714.3569 | 697.3304 | 696.3464 | **742.3519** | 725.3253 | 724.3413 | **I** | 1521.7544 | 1534.7748 | 1548.7904 | ***1579.8326*** | 1562.8061 | 1561.8220 | **14** |
| **7** | 72.0808 | 813.4254 | 796.3988 | 795.4148 | **841.4203** | 824.3937 | 823.4097 | **V** | 1422.6859 | 1435.7064 |  | ***1466.7485*** | 1449.7220 | 1448.7380 | **13** |
| **8** | 70.0651 | 910.4781 | 893.4516 | 892.4676 | 938.4730 | 921.4465 | 920.4625 | **P** | 1325.6332 | 1324.6379 |  | ***1367.6801*** | 1350.6536 | 1349.6696 | **12** |
| **9** | 102.0550 | 1039.5207 | 1022.4942 | 1021.5102 | 1067.5156 | 1050.4891 | 1049.5051 | **E** | 1196.5906 | 1195.5953 |  | 1270.6274 | 1253.6008 | 1252.6168 | **11** |
| **10** | 70.0651 | 1136.5735 | 1119.5469 | 1118.5629 | 1164.5684 | 1147.5419 | 1146.5578 | **P** | 1099.5378 | 1098.5426 |  | ***1141.5848*** | 1124.5582 | 1123.5742 | **10** |
| **11** | 72.0808 | 1235.6419 | 1218.6154 | 1217.6313 | 1263.6368 | 1246.6103 | 1245.6262 | **V** | 1000.4694 | 1013.4898 |  | 1044.5320 | 1027.5055 | 1026.5214 | **9** |
| **12** | 74.0600 | 1336.6896 | 1319.6630 | 1318.6790 | 1364.6845 | 1347.6579 | 1346.6739 | **T** | 899.4217 | 912.4421 | 914.4214 | ***945.4636*** | 928.4371 | 927.4530 | **8** |
| **13** | 102.0550 | 1465.7322 | 1448.7056 | 1447.7216 | 1493.7271 | 1476.7005 | 1475.7165 | **E** | 770.3791 | 769.3839 |  | ***844.4159*** | 827.3894 | 826.4054 | **7** |
| **14** | 87.0553 | **1579.7751** | 1562.7485 | 1561.7645 | 1607.7700 | 1590.7435 | 1589.7594 | **N** | 656.3362 | 655.3410 |  | ***715.3733*** | 698.3468 | 697.3628 | **6** |
| **15** | 70.0651 | 1676.8279 | 1659.8013 | 1658.8173 | 1704.8228 | 1687.7962 | 1686.8122 | **P** | 559.2835 | 558.2882 |  | ***601.3304*** | 584.3039 | 583.3198 | **5** |
| **16** | 60.0444 | 1763.8599 | 1746.8333 | 1745.8493 | 1791.8548 | 1774.8283 | 1773.8442 | **S** | 472.2514 | 471.2562 |  | 504.2776 | 487.2511 | 486.2671 | **4** |
| **17** | 102.0550 | 1892.9025 | 1875.8759 | 1874.8919 | **1920.8974** | 1903.8708 | 1902.8868 | **E** | 343.2088 | 342.2136 |  | 417.2456 | 400.2191 | 399.2350 | **3** |
| **18** | 86.0964 | 2005.9865 | 1988.9600 | 1987.9760 | 2033.9815 | 2016.9549 | 2015.9709 | **L** | 230.1248 | 229.1295 |  | ***288.2030*** | 271.1765 |  | **2** |
| **19** | 129.1135 |  |  |  |  |  |  | **R** | 74.0237 | 73.0284 |  | 175.1190 | 158.0924 |  | **1** |

|  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **Seq** | **ya** | **yb** | **Seq** | **ya** | **yb** | **Seq** | **ya** | **yb** |
| **VY** | 235.1441 | 263.1390 | **VYH** | 372.2030 | 400.1979 | **VYHD** | 487.2300 | 515.2249 |
| **VYHDI** | 600.3140 | 628.3089 | **VYHDIV** | 699.3824 | 727.3774 | **YH** | 273.1346 | 301.1295 |
| **YHD** | 388.1615 | 416.1565 | **YHDI** | 501.2456 | 529.2405 | **YHDIV** | 600.3140 | 628.3089 |
| **YHDIVP** | 697.3668 | 725.3617 | **HD** | 225.0982 | 253.0931 | **HDI** | 338.1823 | 366.1772 |
| **HDIV** | 437.2507 | 465.2456 | **HDIVP** | 534.3035 | 562.2984 | **HDIVPE** | 663.3461 | 691.3410 |
| **DI** | 201.1234 | 229.1183 | **DIV** | 300.1918 | 328.1867 | **DIVP** | 397.2445 | 425.2395 |
| **DIVPE** | 526.2871 | 554.2821 | **DIVPEP** | 623.3399 | 651.3348 | **IV** | 185.1648 | 213.1598 |
| **IVP** | 282.2176 | 310.2125 | **IVPE** | 411.2602 | 439.2551 | **IVPEP** | 508.3130 | 536.3079 |
| **IVPEPV** | 607.3814 | 635.3763 | **VP** | 169.1335 | 197.1285 | **VPE** | 298.1761 | 326.1710 |
| **VPEP** | 395.2289 | 423.2238 | **VPEPV** | 494.2973 | 522.2922 | **VPEPVT** | 595.3450 | 623.3399 |
| **PE** | 199.1077 | 227.1026 | **PEP** | 296.1605 | 324.1554 | **PEPV** | 395.2289 | 423.2238 |
| **PEPVT** | 496.2766 | 524.2715 | **PEPVTE** | 625.3192 | 653.3141 | **EP** | 199.1077 | 227.1026 |
| **EPV** | 298.1761 | 326.1710 | **EPVT** | 399.2238 | 427.2187 | **EPVTE** | 528.2664 | 556.2613 |
| **EPVTEN** | 642.3093 | 670.3042 | **PV** | 169.1335 | 197.1285 | **PVT** | 270.1812 | 298.1761 |
| **PVTE** | 399.2238 | 427.2187 | **PVTEN** | 513.2667 | 541.2617 | **PVTENP** | 610.3195 | 638.3144 |
| **PVTENPS** | 697.3515 | 725.3464 | **VT** | 173.1285 | 201.1234 | **VTE** | 302.1710 | 330.1660 |
| **VTEN** | 416.2140 | 444.2089 | **VTENP** | 513.2667 | 541.2617 | **VTENPS** | 600.2988 | 628.2937 |
| **TE** | 203.1026 | 231.0975 | **TEN** | 317.1456 | 345.1405 | **TENP** | 414.1983 | 442.1932 |
| **TENPS** | 501.2304 | 529.2253 | **TENPSE** | 630.2729 | 658.2679 | **EN** | 216.0979 | 244.0928 |
| **ENP** | 313.1506 | 341.1456 | **ENPS** | 400.1827 | 428.1776 | **ENPSE** | 529.2253 | 557.2202 |
| **ENPSEL** | 642.3093 | 670.3042 | **NP** | 184.1081 | 212.1030 | **NPS** | 271.1401 | 299.1350 |
| **NPSE** | 400.1827 | 428.1776 | **NPSEL** | 513.2667 | 541.2617 | **PS** | 157.0972 | 185.0921 |
| **PSE** | 286.1397 | 314.1347 | **PSEL** | 399.2238 | 427.2187 | **SE** | 189.0870 | 217.0819 |
| **SEL** | 302.1710 | 330.1660 | **EL** | 215.1390 | 243.1339 |  |  |  |

**Spot 6:**

**http://msmsms/mascot/images/88x31_logo_white.gifMascot Search Results**

**User :**

**Email :**

**Search title : SampleSetID: 341, AnalysisID: 781, MaldiWellID: 45254, SpectrumID: 168736, Path=\Jimmy\Cooperia Adult ES 20110221\20110502 MS en MSMS (new DB)**

**Database : cooperia\_oncophora oncophora\_20110405 (34373 sequences; 5289600 residues)**

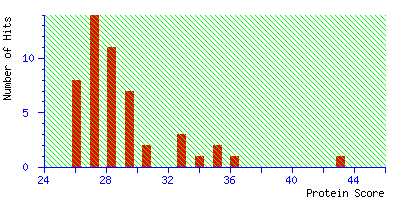
**Timestamp : 4 May 2011 at 11:12:58 GMT**

**Warning : A Peptide summary report will usually give a much clearer picture of MS/MS search results.**

**Top Score : 43 for isotig14500, putative nuclear encoded protein Method: similarity and extension**

**Mascot Score Histogram**

Protein score is -10\*Log(P), where P is the probability that the observed match is a random event.  
Protein scores greater than 58 are significant (p<0.05).  
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



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**Protein Summary Report**

|  |  |  |  |
| --- | --- | --- | --- |
|  |  |  | [Help](http://msmsms/mascot/help/msms_summaries_help.html" \t "_blank) |
|  | Significance threshold p< | Max. number of hits |  |

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**Index**

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
|  | **Accession** | **Mass** | **Score** | **Description** |
| **1.** | [**isotig14500**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20110504/F014678.dat#Hit1) | 32548 | 43 | putative nuclear encoded protein Method: similarity and extension |
| **2.** | [**isotig29679**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20110504/F014678.dat#Hit2) | 10992 | 36 | putative nuclear encoded protein Method: Longest ORF |
| **3.** | [**isotig27615**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20110504/F014678.dat#Hit3) | 19600 | 35 | putative nuclear encoded protein Method: similarity and extension |
| **4.** | [**isotig14501**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20110504/F014678.dat#Hit4) | 26337 | 35 | putative nuclear encoded protein Method: similarity and extension |
| **5.** | [**isotig04036**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20110504/F014678.dat#Hit5) | 19278 | 34 | putative nuclear encoded protein Method: ESTScan |
| **6.** | [**isotig25479**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20110504/F014678.dat#Hit6) | 13186 | 33 | putative nuclear encoded protein Method: Longest ORF |
| **7.** | [**isotig25978**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20110504/F014678.dat#Hit7) | 33882 | 33 | putative nuclear encoded protein Method: similarity and extension |
| **8.** | [**isotig15855**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20110504/F014678.dat#Hit8) | 24969 | 33 | putative nuclear encoded protein Method: similarity and extension |
| **9.** | [**isotig10705**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20110504/F014678.dat#Hit9) | 8764 | 31 | putative nuclear encoded protein Method: Longest ORF |
| **10.** | [**isotig13800**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20110504/F014678.dat#Hit10) | 12911 | 30 | putative nuclear encoded protein Method: Longest ORF |
| **11.** | [**isotig08881**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20110504/F014678.dat#Hit11) | 68383 | 30 | putative nuclear encoded protein Method: similarity and extension |
| **12.** | [**isotig29859**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20110504/F014678.dat#Hit12) | 9369 | 30 | putative nuclear encoded protein Method: similarity and extension |
| **13.** | [**isotig03119**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20110504/F014678.dat#Hit13) | 23382 | 29 | putative nuclear encoded protein Method: Longest ORF |
| **14.** | [**isotig03120**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20110504/F014678.dat#Hit14) | 23382 | 29 | putative nuclear encoded protein Method: Longest ORF |
| **15.** | [**isotig03125**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20110504/F014678.dat#Hit15) | 23382 | 29 | putative nuclear encoded protein Method: Longest ORF |
| **16.** | [**isotig08027**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20110504/F014678.dat#Hit16) | 16064 | 29 | putative nuclear encoded protein Method: similarity and extension |
| **17.** | [**isotig29854**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20110504/F014678.dat#Hit17) | 54091 | 29 | putative nuclear encoded protein Method: similarity and extension |
| **18.** | [**isotig19914**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20110504/F014678.dat#Hit18) | 10440 | 29 | putative nuclear encoded protein Method: ESTScan |
| **19.** | [**isotig32472**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20110504/F014678.dat#Hit19) | 9437 | 29 | putative nuclear encoded protein Method: similarity and extension |
| **20.** | [**isotig32694**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20110504/F014678.dat#Hit20) | 12734 | 29 | putative nuclear encoded protein Method: Longest ORF |

**Results List**

|  |  |
| --- | --- |
| **1.** | [isotig14500](http://msmsms/mascot/cgi/protein_view.pl?file=../data/20110504/F014678.dat&hit=1" \t "_blank)    **Mass:** 32548    **Score:** 43     **Expect:** 1.7  **Matches:** 9 |
|  | putative nuclear encoded protein Method: similarity and extension |

|  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | **Observed** | **Mr(expt)** | **Mr(calc)** | **ppm** | **Start** |  | **End** | **Miss** | **Ions** | **Peptide** |
|  | 982.4487 | 981.4414 | 981.5140 | -73.90 | 75 | - | 82 | 0 | --- | R.MMLAFLTR.K |
|  | 1034.4425 | 1033.4352 | 1033.4750 | -38.48 | 185 | - | 193 | 0 | --- | K.GDEMLINDK.H |
|  | 1163.6078 | 1162.6005 | 1162.6281 | -23.72 | 84 | - | 93 | 1 | --- | K.TFPRMIGGIR.I + Oxidation (M) |
|  | 1163.6078 | 1162.6005 | 1162.6281 | -23.72 | 84 | - | 93 | 1 | 22 | K.TFPRMIGGIR.I + Oxidation (M) |
|  | 1189.6263 | 1188.6190 | 1188.6040 | 12.7 | 232 | - | 240 | 1 | --- | R.VWTKYAHER.I |
|  | 1205.5714 | 1204.5641 | 1204.5989 | -28.86 | 232 | - | 240 | 1 | --- | R.VWTKYAHER.I + Oxidation (HW) |
|  | 1307.6539 | 1306.6466 | 1306.6075 | 30.0 | 183 | - | 193 | 1 | --- | R.EKGDEMLINDK.H + Oxidation (M) |
|  | 1627.6477 | 1626.6404 | 1626.8083 | -103.17 | 88 | - | 102 | 1 | --- | R.MIGGIRIPNHGGMAR.F + Oxidation (HW); 2 Oxidation (M) |
|  | 2097.0295 | 2096.0222 | 2096.0884 | -31.57 | 84 | - | 102 | 2 | --- | K.TFPRMIGGIRIPNHGGMAR.F + Oxidation (M) |

|  |  |
| --- | --- |
|  | **No match to:** 947.5775, 975.5327, 991.5988, 997.5219, 1045.5466, 1056.5677, 1081.5476, 1102.5668, 1107.5352, 1149.5884, 1161.5958, 1177.5823, 1179.5962, 1185.5912, 1209.5854, 1217.5344, 1225.5347, 1300.5806, 1316.5714, 1318.6465, 1322.5775, 1350.6320, 1390.6520, 1421.6548, 1434.7208, 1449.6526, 1454.7584, 1475.7511, 1493.7180, 1718.6548, 1718.6548, 2059.0479, 2075.0417, 2075.0417, 2082.9836, 2120.8721, 2148.0947, 2148.0947, 2160.1338, 2174.0063, 2182.0928, 2211.0537, 2276.1812, 2337.1794, 2734.0610 |

**http://msmsms/mascot/images/88x31_logo_white.gifMascot Search Results**

**Protein View**

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Match to: **isotig14500** Score: **43** Expect: **1.7**

**putative nuclear encoded protein Method: similarity and extension**

Nominal mass (Mr): **32548**; Calculated pI value: **9.57**

NCBI BLAST search of [isotig14500](http://www.ncbi.nlm.nih.gov/blast/Blast.cgi?ALIGNMENTS=50&ALIGNMENT_VIEW=Pairwise&AUTO_FORMAT=Semiauto&CDD_SEARCH=on&CLIENT=web&COMPOSITION_BASED_STATISTICS=on&DATABASE=nr&DESCRIPTIONS=100&ENTREZ_QUERY=(none)&EXPECT=10&FILTER=L&FORMAT_BLOCK_ON_RESPAGE=None&FORMAT_OBJECT=Alignment&FORMAT_TYPE=HTML&GAPCOSTS=11+1&I_THRESH=0.001&LAYOUT=TwoWindows&MATRIX_NAME=BLOSUM62&NCBI_GI=on&PAGE=Proteins&PROGRAM=blastp&QUERY=NRSSKLGNIADYIFSYFYYRKIARRGFISSVFRMPAVATVFYGITKFLYLMNAVLQLYLTTYFLGFPDMRWGLRMMLAFLTRKTFPRMIGGIRIPNHGGMARFPYFPLEVFCNYTRMVENNNLHTSSTQCMIPLNYINEKLFLFLWFWIVILIMVTMVNIVLFVGSIMNKSQREDTILSYLREKGDEMLINDKHGLATKFVHGFMGADGVLLTRFMTNKAGSLACRDVVQRVWTKYAHERIAALKADSDDEWSVPFSETCYSGIPLPATPYHDEDRKKSR&SERVICE=plain&SET_DEFAULTS.x=9&SET_DEFAULTS.y=5&SHOW_OVERVIEW=on&WORD_SIZE=3&END_OF_HTTPGET=Yes" \t "_blank) against nr

Unformatted [sequence string](http://msmsms/mascot/cgi/getseq.pl?cooperia_oncophora+isotig14500+seq" \t "_blank) for pasting into other applications

Variable modifications: Oxidation (HW),Oxidation (M)

Cleavage by Trypsin/P: cuts C-term side of KR

Sequence Coverage: **16%**

Matched peptides shown in **Bold Red**

**1** NRSSKLGNIA DYIFSYFYYR KIARRGFISS VFRMPAVATV FYGITKFLYL

**51** MNAVLQLYLT TYFLGFPDMR WGLR**MMLAFL TR**K**TFPRMIG GIRIPNHGGM**

**101 AR**FPYFPLEV FCNYTRMVEN NNLHTSSTQC MIPLNYINEK LFLFLWFWIV

**151** ILIMVTMVNI VLFVGSIMNK SQREDTILSY LR**EKGDEMLI NDK**HGLATKF

**201** VHGFMGADGV LLTRFMTNKA GSLACRDVVQ R**VWTKYAHER** IAALKADSDD

**251** EWSVPFSETC YSGIPLPATP YHDEDRKKSR



  Residue Number  Increasing Mass  Decreasing Mass

**Start - End Observed Mr(expt) Mr(calc) ppm Miss Sequence**

**75 - 82 982.4487 981.4414 981.5140 -74 0 R.MMLAFLTR.K**  ([No match](http://msmsms/mascot/cgi/peptide_view.pl?file=../data/20110504/F014678.dat&query=3&hit=1" \t "_blank))

**84 - 93 1163.6078 1162.6005 1162.6281 -24 1 K.TFPRMIGGIR.I**  Oxidation (M) ([No match](http://msmsms/mascot/cgi/peptide_view.pl?file=../data/20110504/F014678.dat&query=14&hit=1" \t "_blank))

**84 - 93 1163.6078 1162.6005 1162.6281 -24 1 K.TFPRMIGGIR.I**  Oxidation (M) ([Ions score 22](http://msmsms/mascot/cgi/peptide_view.pl?file=../data/20110504/F014678.dat&query=15&hit=1" \t "_blank))

**84 - 102 2097.0295 2096.0222 2096.0884 -32 2 K.TFPRMIGGIRIPNHGGMAR.F**  Oxidation (M) ([No match](http://msmsms/mascot/cgi/peptide_view.pl?file=../data/20110504/F014678.dat&query=44&hit=1" \t "_blank))

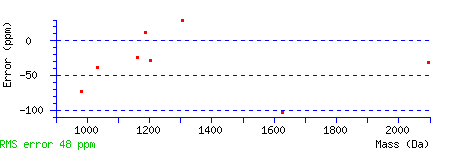
**88 - 102 1627.6477 1626.6404 1626.8083 -103 1 R.MIGGIRIPNHGGMAR.F**  Oxidation (HW); 2 Oxidation (M) ([No match](http://msmsms/mascot/cgi/peptide_view.pl?file=../data/20110504/F014678.dat&query=37&hit=1" \t "_blank))

**183 - 193 1307.6539 1306.6466 1306.6075 30 1 R.EKGDEMLINDK.H**  Oxidation (M) ([No match](http://msmsms/mascot/cgi/peptide_view.pl?file=../data/20110504/F014678.dat&query=25&hit=1" \t "_blank))

**185 - 193 1034.4425 1033.4352 1033.4750 -38 0 K.GDEMLINDK.H**  ([No match](http://msmsms/mascot/cgi/peptide_view.pl?file=../data/20110504/F014678.dat&query=6&hit=1" \t "_blank))

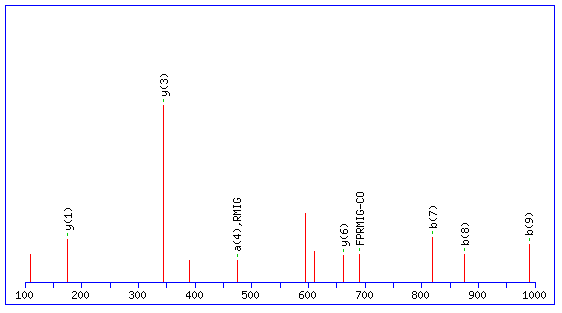
**232 - 240 1189.6263 1188.6190 1188.6040 13 1 R.VWTKYAHER.I**  ([No match](http://msmsms/mascot/cgi/peptide_view.pl?file=../data/20110504/F014678.dat&query=19&hit=1" \t "_blank))

**232 - 240 1205.5714 1204.5641 1204.5989 -29 1 R.VWTKYAHER.I**  Oxidation (HW) ([No match](http://msmsms/mascot/cgi/peptide_view.pl?file=../data/20110504/F014678.dat&query=20&hit=1" \t "_blank))



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🡪 Annotated MS2 spectrum for peptide TFPRMIGGIR



**Monoisotopic mass of neutral peptide Mr(calc):** 1162.6281

**Variable modifications:**

**M5 :** Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983

**Ions Score:** 22 **Expect:** 0.5

**Matches :** 9/225 fragment ions using 12 most intense peaks   ([help](http://msmsms/mascot/help/results_help.html" \l "PEP" \t "_blank))

|  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **#** | **Immon.** | **a** | **a\*** | **a0** | **b** | **b\*** | **b0** | **d** | **d'** | **Seq.** | **v** | **w** | **w'** | **y** | **y\*** | **#** |
| **1** | 74.0600 | 74.0600 |  | 56.0495 | 102.0550 |  | 84.0444 |  |  | **T** |  |  |  |  |  | **10** |
| **2** | 120.0808 | 221.1285 |  | 203.1179 | 249.1234 |  | 231.1128 |  |  | **F** | 970.5251 |  |  | 1062.5877 | 1045.5611 | **9** |
| **3** | 70.0651 | 318.1812 |  | 300.1707 | 346.1761 |  | 328.1656 |  |  | **P** | 873.4723 | 872.4771 |  | 915.5193 | 898.4927 | **8** |
| **4** | 129.1135 | 474.2823 | 457.2558 | 456.2718 | 502.2772 | 485.2507 | 484.2667 | 389.2183 |  | **R** | 717.3712 | 716.3760 |  | 818.4665 | 801.4400 | **7** |
| **5** | 120.0478 | 621.3177 | 604.2912 | 603.3072 | 649.3126 | 632.2861 | 631.3021 | 545.3194 |  | **M** | 570.3358 | 569.3406 |  | ***662.3654*** | 645.3389 | **6** |
| **6** | 86.0964 | 734.4018 | 717.3752 | 716.3912 | 762.3967 | 745.3702 | 744.3861 | 706.3705 | 720.3861 | **I** | 457.2518 | 470.2722 | 484.2878 | 515.3300 | 498.3035 | **5** |
| **7** | 30.0338 | 791.4233 | 774.3967 | 773.4127 | ***819.4182*** | 802.3916 | 801.4076 |  |  | **G** |  |  |  | 402.2459 | 385.2194 | **4** |
| **8** | 30.0338 | 848.4447 | 831.4182 | 830.4342 | ***876.4396*** | 859.4131 | 858.4291 |  |  | **G** |  |  |  | ***345.2245*** | 328.1979 | **3** |
| **9** | 86.0964 | 961.5288 | 944.5022 | 943.5182 | ***989.5237*** | 972.4972 | 971.5131 | 933.4975 | 947.5131 | **I** | 230.1248 | 243.1452 | 257.1608 | 288.2030 | 271.1765 | **2** |
| **10** | 129.1135 |  |  |  |  |  |  |  |  | **R** | 74.0237 | 73.0284 |  | ***175.1190*** | 158.0924 | **1** |

|  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **Seq** | **ya** | **yb** | **Seq** | **ya** | **yb** | **Seq** | **ya** | **yb** |
| **FP** | 217.1335 | 245.1285 | **FPR** | 373.2346 | 401.2296 | **FPRM** | 520.2701 | 548.2650 |
| **FPRMI** | 633.3541 | 661.3490 | **FPRMIG** | 690.3756 | 718.3705 | **PR** | 226.1662 | 254.1612 |
| **PRM** | 373.2016 | 401.1966 | **PRMI** | 486.2857 | 514.2806 | **PRMIG** | 543.3072 | 571.3021 |
| **PRMIGG** | 600.3286 | 628.3235 | **RM** | 276.1489 | 304.1438 | **RMI** | 389.2329 | 417.2279 |
| **RMIG** | 446.2544 | 474.2493 | **RMIGG** | 503.2759 | 531.2708 | **RMIGGI** | 616.3599 | 644.3548 |
| **MI** | 233.1318 | 261.1267 | **MIG** | 290.1533 | 318.1482 | **MIGG** | 347.1748 | 375.1697 |
| **MIGGI** | 460.2588 | 488.2537 | **IG** | 143.1179 | 171.1128 | **IGG** | 200.1394 | 228.1343 |
| **IGGI** | 313.2234 | 341.2183 | **GG** | 87.0553 | 115.0502 | **GGI** | 200.1394 | 228.1343 |
| **GI** | 143.1179 | 171.1128 |  |  |  |  |  |  |

**Spot 7:**

**http://msmsms/mascot/images/88x31_logo_white.gifMascot Search Results**

**User :**

**Email :**

**Search title : SampleSetID: 341, AnalysisID: 641, MaldiWellID: 45154, SpectrumID: 154688, Path=\Jimmy\Cooperia Adult ES 20110221\20110405 MS en MSMS (new DB)**

**Database : cooperia\_oncophora oncophora\_20110405 (34373 sequences; 5289600 residues)**

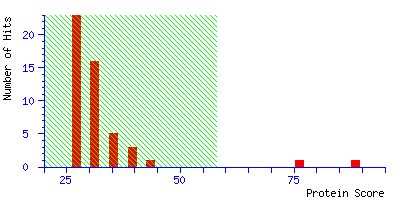
**Timestamp : 5 Apr 2011 at 12:35:21 GMT**

**Warning : A Peptide summary report will usually give a much clearer picture of MS/MS search results.**

**Top Score : 89 for isotig09291, putative nuclear encoded protein Method: similarity and extension**

**Mascot Score Histogram**

Protein score is -10\*Log(P), where P is the probability that the observed match is a random event.  
Protein scores greater than 58 are significant (p<0.05).  
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



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**Protein Summary Report**

|  |  |  |  |
| --- | --- | --- | --- |
|  |  |  | [Help](http://msmsms/mascot/help/msms_summaries_help.html" \t "_blank) |
|  | Significance threshold p< | Max. number of hits |  |

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**Index**

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
|  | **Accession** | **Mass** | **Score** | **Description** |
| **1.** | [**isotig09291**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20110405/F014357.dat#Hit1) | 21772 | 89 | putative nuclear encoded protein Method: similarity and extension |
| **2.** | [**isotig09292**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20110405/F014357.dat#Hit2) | 18619 | 75 | putative nuclear encoded protein Method: similarity and extension |
| **3.** | [**isotig20419**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20110405/F014357.dat#Hit3) | 15261 | 42 | putative nuclear encoded protein Method: Longest ORF |
| **4.** | [**isotig20827**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20110405/F014357.dat#Hit4) | 19110 | 40 | putative nuclear encoded protein Method: Longest ORF |
| **5.** | [**isotig08043**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20110405/F014357.dat#Hit5) | 13911 | 40 | putative nuclear encoded protein Method: similarity and extension |
| **6.** | [**isotig27210**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20110405/F014357.dat#Hit6) | 22064 | 38 | putative nuclear encoded protein Method: similarity and extension |
| **7.** | [**isotig19405**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20110405/F014357.dat#Hit7) | 9353 | 35 | putative nuclear encoded protein Method: similarity and extension |
| **8.** | [**isotig10710**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20110405/F014357.dat#Hit8) | 8925 | 35 | putative nuclear encoded protein Method: Longest ORF |
| **9.** | [**isotig21832**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20110405/F014357.dat#Hit9) | 29799 | 34 | putative nuclear encoded protein Method: similarity and extension |
| **10.** | [**isotig20397**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20110405/F014357.dat#Hit10) | 5790 | 34 | putative nuclear encoded protein Method: Longest ORF |
| **11.** | [**isotig11053**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20110405/F014357.dat#Hit11) | 8408 | 34 | putative nuclear encoded protein Method: Longest ORF |
| **12.** | [**isotig12572**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20110405/F014357.dat#Hit12) | 5718 | 33 | putative nuclear encoded protein Method: similarity and extension |
| **13.** | [**isotig24047**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20110405/F014357.dat#Hit13) | 20065 | 33 | putative nuclear encoded protein Method: ESTScan |
| **14.** | [**isotig03681**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20110405/F014357.dat#Hit14) | 37355 | 33 | putative nuclear encoded protein Method: similarity and extension |
| **15.** | [**isotig18424**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20110405/F014357.dat#Hit15) | 18810 | 32 | putative nuclear encoded protein Method: similarity and extension |
| **16.** | [**isotig27553**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20110405/F014357.dat#Hit16) | 22325 | 32 | putative nuclear encoded protein Method: similarity and extension |
| **17.** | [**isotig07485**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20110405/F014357.dat#Hit17) | 14404 | 31 | putative nuclear encoded protein Method: similarity and extension |
| **18.** | [**isotig07484**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20110405/F014357.dat#Hit18) | 14404 | 31 | putative nuclear encoded protein Method: similarity and extension |
| **19.** | [**isotig07483**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20110405/F014357.dat#Hit19) | 14389 | 31 | putative nuclear encoded protein Method: similarity and extension |
| **20.** | [**isotig13428**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20110405/F014357.dat#Hit20) | 15273 | 30 | putative nuclear encoded protein Method: Longest ORF |

**Results List**

|  |  |
| --- | --- |
| **1.** | [isotig09291](http://msmsms/mascot/cgi/protein_view.pl?file=../data/20110405/F014357.dat&hit=1" \t "_blank)    **Mass:** 21772    **Score:** 89     **Expect:** 4.9e-005  **Matches:** 10 |
|  | putative nuclear encoded protein Method: similarity and extension |

|  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | **Observed** | **Mr(expt)** | **Mr(calc)** | **ppm** | **Start** |  | **End** | **Miss** | **Ions** | **Peptide** |
|  | 810.3371 | 809.3298 | 809.4283 | -121.66 | 28 | - | 34 | 1 | --- | K.LSDYKGK.Y |
|  | 813.3815 | 812.3742 | 812.5120 | -169.54 | 179 | - | 186 | 1 | --- | K.ATIKPGVK.D |
|  | 819.3209 | 818.3136 | 818.4134 | -121.90 | 149 | - | 155 | 0 | --- | R.SVDETLR.L |
|  | 872.3945 | 871.3872 | 871.4439 | -65.08 | 190 | - | 196 | 1 | --- | K.EYFSKAK.- |
|  | 902.3931 | 901.3858 | 901.5273 | -156.93 | 126 | - | 133 | 0 | --- | R.GLFIIDPK.G |
|  | 1225.5122 | 1224.5049 | 1224.6826 | -145.11 | 138 | - | 148 | 0 | --- | R.QITINDLPVGR.S |
|  | 1225.5122 | 1224.5049 | 1224.6826 | -145.11 | 138 | - | 148 | 0 | 13 | R.QITINDLPVGR.S |
|  | 1404.5743 | 1403.5670 | 1403.7813 | -152.63 | 4 | - | 16 | 1 | --- | K.AFIGKPAPDFITK.A |
|  | 1613.5431 | 1612.5358 | 1612.7733 | -147.24 | 112 | - | 125 | 1 | --- | K.DYGVLKDDEGIAYR.G |
|  | 1613.5431 | 1612.5358 | 1612.7733 | -147.24 | 112 | - | 125 | 1 | 27 | K.DYGVLKDDEGIAYR.G |

|  |  |
| --- | --- |
|  | **No match to:** 802.3307, 803.3334, 805.3503, 812.3574, 814.3908, 816.3527, 820.3279, 824.3546, 826.3886, 828.3849, 829.3355, 832.3450, 842.3906, 844.4102, 848.3314, 856.4008, 857.3740, 858.3921, 859.3749, 860.3854, 862.4181, 870.4126, 882.3533, 898.3876, 900.4239, 904.3969, 909.3390, 916.4291, 918.4276, 941.3895, 952.3887, 972.4553, 990.4509, 1045.4087, 1045.4087, 1057.5328, 1072.4066, 1208.4889, 1209.4877, 1435.5748, 1812.6010, 2210.7847 |

|  |  |
| --- | --- |
| **2.** | [isotig09292](http://msmsms/mascot/cgi/protein_view.pl?file=../data/20110405/F014357.dat&hit=2" \t "_blank)    **Mass:** 18619    **Score:** 75     **Expect:** 0.0012  **Matches:** 8 |
|  | putative nuclear encoded protein Method: similarity and extension |

|  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | **Observed** | **Mr(expt)** | **Mr(calc)** | **ppm** | **Start** |  | **End** | **Miss** | **Ions** | **Peptide** |
|  | 813.3815 | 812.3742 | 812.5120 | -169.54 | 150 | - | 157 | 1 | --- | K.ATIKPGVK.D |
|  | 819.3209 | 818.3136 | 818.4134 | -121.90 | 120 | - | 126 | 0 | --- | R.SVDETLR.L |
|  | 872.3945 | 871.3872 | 871.4439 | -65.08 | 161 | - | 167 | 1 | --- | K.EYFSKAK.- |
|  | 902.3931 | 901.3858 | 901.5273 | -156.93 | 97 | - | 104 | 0 | --- | R.GLFIIDPK.G |
|  | 1225.5122 | 1224.5049 | 1224.6826 | -145.11 | 109 | - | 119 | 0 | --- | R.QITINDLPVGR.S |
|  | 1225.5122 | 1224.5049 | 1224.6826 | -145.11 | 109 | - | 119 | 0 | 13 | R.QITINDLPVGR.S |
|  | 1613.5431 | 1612.5358 | 1612.7733 | -147.24 | 83 | - | 96 | 1 | --- | K.DYGVLKDDEGIAYR.G |
|  | 1613.5431 | 1612.5358 | 1612.7733 | -147.24 | 83 | - | 96 | 1 | 27 | K.DYGVLKDDEGIAYR.G |

|  |  |
| --- | --- |
|  | **No match to:** 802.3307, 803.3334, 805.3503, 810.3371, 812.3574, 814.3908, 816.3527, 820.3279, 824.3546, 826.3886, 828.3849, 829.3355, 832.3450, 842.3906, 844.4102, 848.3314, 856.4008, 857.3740, 858.3921, 859.3749, 860.3854, 862.4181, 870.4126, 882.3533, 898.3876, 900.4239, 904.3969, 909.3390, 916.4291, 918.4276, 941.3895, 952.3887, 972.4553, 990.4509, 1045.4087, 1045.4087, 1057.5328, 1072.4066, 1208.4889, 1209.4877, 1404.5743, 1435.5748, 1812.6010, 2210.7847 |

**http://msmsms/mascot/images/88x31_logo_white.gifMascot Search Results**

**Protein View**

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Match to: **isotig09291** Score: **89** Expect: **4.9e-005**

**putative nuclear encoded protein Method: similarity and extension**

Nominal mass (Mr): **21772**; Calculated pI value: **6.89**

NCBI BLAST search of [isotig09291](http://www.ncbi.nlm.nih.gov/blast/Blast.cgi?ALIGNMENTS=50&ALIGNMENT_VIEW=Pairwise&AUTO_FORMAT=Semiauto&CDD_SEARCH=on&CLIENT=web&COMPOSITION_BASED_STATISTICS=on&DATABASE=nr&DESCRIPTIONS=100&ENTREZ_QUERY=(none)&EXPECT=10&FILTER=L&FORMAT_BLOCK_ON_RESPAGE=None&FORMAT_OBJECT=Alignment&FORMAT_TYPE=HTML&GAPCOSTS=11+1&I_THRESH=0.001&LAYOUT=TwoWindows&MATRIX_NAME=BLOSUM62&NCBI_GI=on&PAGE=Proteins&PROGRAM=blastp&QUERY=MSKAFIGKPAPDFITKAVYNGDFIDVKLSDYKGKYTVLFFYPLDFTFVCPTEIIAFSDRIEEFKKIDAAVLACSTDSVFSHLAWINTPRKHGGLGDMSIPVLADTNHQIAKDYGVLKDDEGIAYRGLFIIDPKGILRQITINDLPVGRSVDETLRLVQAFQFVDKHGEVCPAGWTPGKATIKPGVKDSKEYFSKAK&SERVICE=plain&SET_DEFAULTS.x=9&SET_DEFAULTS.y=5&SHOW_OVERVIEW=on&WORD_SIZE=3&END_OF_HTTPGET=Yes" \t "_blank) against nr

Unformatted [sequence string](http://msmsms/mascot/cgi/getseq.pl?cooperia_oncophora+isotig09291+seq" \t "_blank) for pasting into other applications

Variable modifications: Oxidation (HW),Oxidation (M)

Cleavage by Trypsin/P: cuts C-term side of KR

Sequence Coverage: **38%**

Matched peptides shown in **Bold Red**

**1** MSK**AFIGKPA PDFITK**AVYN GDFIDVK**LSD YKGK**YTVLFF YPLDFTFVCP

**51** TEIIAFSDRI EEFKKIDAAV LACSTDSVFS HLAWINTPRK HGGLGDMSIP

**101** VLADTNHQIA K**DYGVLKDDE GIAYRGLFII DPK**GILR**QIT INDLPVGRSV**

**151 DETLR**LVQAF QFVDKHGEVC PAGWTPGK**AT IKPGVK**DSK**E YFSKAK**



  Residue Number  Increasing Mass  Decreasing Mass

**Start - End Observed Mr(expt) Mr(calc) ppm Miss Sequence**

**4 - 16 1404.5743 1403.5670 1403.7813 -153 1 K.AFIGKPAPDFITK.A**  ([No match](http://msmsms/mascot/cgi/peptide_view.pl?file=../data/20110405/F014357.dat&query=47&hit=1" \t "_blank))

**28 - 34 810.3371 809.3298 809.4283 -122 1 K.LSDYKGK.Y**  ([No match](http://msmsms/mascot/cgi/peptide_view.pl?file=../data/20110405/F014357.dat&query=4&hit=1" \t "_blank))

**112 - 125 1613.5431 1612.5358 1612.7733 -147 1 K.DYGVLKDDEGIAYR.G**  ([No match](http://msmsms/mascot/cgi/peptide_view.pl?file=../data/20110405/F014357.dat&query=49&hit=1" \t "_blank))

**112 - 125 1613.5431 1612.5358 1612.7733 -147 1 K.DYGVLKDDEGIAYR.G**  ([Ions score 27](http://msmsms/mascot/cgi/peptide_view.pl?file=../data/20110405/F014357.dat&query=50&hit=1" \t "_blank))

**126 - 133 902.3931 901.3858 901.5273 -157 0 R.GLFIIDPK.G**  ([No match](http://msmsms/mascot/cgi/peptide_view.pl?file=../data/20110405/F014357.dat&query=30&hit=1" \t "_blank))

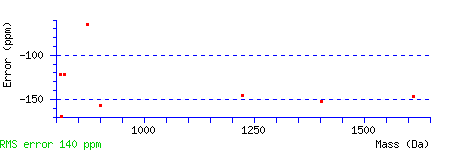
**138 - 148 1225.5122 1224.5049 1224.6826 -145 0 R.QITINDLPVGR.S**  ([No match](http://msmsms/mascot/cgi/peptide_view.pl?file=../data/20110405/F014357.dat&query=45&hit=1" \t "_blank))

**138 - 148 1225.5122 1224.5049 1224.6826 -145 0 R.QITINDLPVGR.S**  ([Ions score 13](http://msmsms/mascot/cgi/peptide_view.pl?file=../data/20110405/F014357.dat&query=46&hit=1" \t "_blank))

**149 - 155 819.3209 818.3136 818.4134 -122 0 R.SVDETLR.L**  ([No match](http://msmsms/mascot/cgi/peptide_view.pl?file=../data/20110405/F014357.dat&query=9&hit=1" \t "_blank))

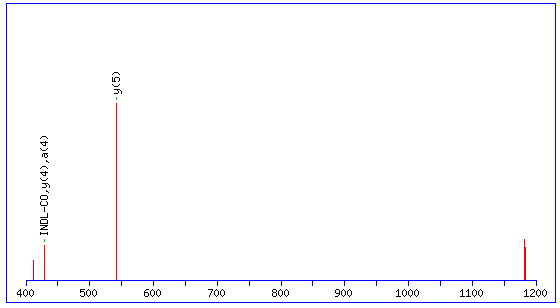
**179 - 186 813.3815 812.3742 812.5120 -170 1 K.ATIKPGVK.D**  ([No match](http://msmsms/mascot/cgi/peptide_view.pl?file=../data/20110405/F014357.dat&query=6&hit=1" \t "_blank))

**190 - 196 872.3945 871.3872 871.4439 -65 1 K.EYFSKAK.-**  ([No match](http://msmsms/mascot/cgi/peptide_view.pl?file=../data/20110405/F014357.dat&query=26&hit=1" \t "_blank))



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🡪 Annotated MS2 spectrum for peptide QITINDLPVGR



**Monoisotopic mass of neutral peptide Mr(calc):** 1224.6826

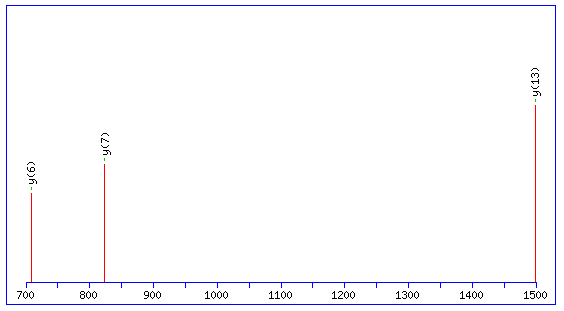
**Ions Score:** 13 **Expect:** 3.7

**Matches :** 4/174 fragment ions using 3 most intense peaks   ([help](http://msmsms/mascot/help/results_help.html" \l "PEP" \t "_blank))

|  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **#** | **Immon.** | **a** | **a\*** | **a0** | **b** | **b\*** | **b0** | **Seq.** | **v** | **w** | **w'** | **y** | **y\*** | **y0** | **#** |
| **1** | 101.0709 | 101.0709 | 84.0444 |  | 129.0659 | 112.0393 |  | **Q** |  |  |  |  |  |  | **11** |
| **2** | 86.0964 | 214.1550 | 197.1285 |  | 242.1499 | 225.1234 |  | **I** | 1039.5531 | 1052.5735 | 1066.5891 | 1097.6313 | 1080.6048 | 1079.6208 | **10** |
| **3** | 74.0600 | 315.2027 | 298.1761 | 297.1921 | 343.1976 | 326.1710 | 325.1870 | **T** | 938.5054 | 951.5258 | 953.5051 | 984.5473 | 967.5207 | 966.5367 | **9** |
| **4** | 86.0964 | **428.2867** | 411.2602 | 410.2762 | 456.2817 | 439.2551 | 438.2711 | **I** | 825.4213 | 838.4417 | 852.4574 | 883.4996 | 866.4730 | 865.4890 | **8** |
| **5** | 87.0553 | 542.3297 | 525.3031 | 524.3191 | 570.3246 | 553.2980 | 552.3140 | **N** | 711.3784 | 710.3832 |  | 770.4155 | 753.3890 | 752.4050 | **7** |
| **6** | 88.0393 | 657.3566 | 640.3301 | 639.3461 | 685.3515 | 668.3250 | 667.3410 | **D** | 596.3515 | 595.3562 |  | 656.3726 | 639.3461 | 638.3620 | **6** |
| **7** | 86.0964 | 770.4407 | 753.4141 | 752.4301 | 798.4356 | 781.4090 | 780.4250 | **L** | 483.2674 | 482.2722 |  | ***541.3457*** | 524.3191 |  | **5** |
| **8** | 70.0651 | 867.4934 | 850.4669 | 849.4829 | 895.4884 | 878.4618 | 877.4778 | **P** | 386.2146 | 385.2194 |  | ***428.2616*** | 411.2350 |  | **4** |
| **9** | 72.0808 | 966.5619 | 949.5353 | 948.5513 | 994.5568 | 977.5302 | 976.5462 | **V** | 287.1462 | 300.1666 |  | 331.2088 | 314.1823 |  | **3** |
| **10** | 30.0338 | 1023.5833 | 1006.5568 | 1005.5728 | 1051.5782 | 1034.5517 | 1033.5677 | **G** |  |  |  | 232.1404 | 215.1139 |  | **2** |
| **11** | 129.1135 |  |  |  |  |  |  | **R** | 74.0237 | 73.0284 |  | 175.1190 | 158.0924 |  | **1** |

|  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **Seq** | **ya** | **yb** | **Seq** | **ya** | **yb** | **Seq** | **ya** | **yb** |
| **IT** | 187.1441 | 215.1390 | **ITI** | 300.2282 | 328.2231 | **ITIN** | 414.2711 | 442.2660 |
| **ITIND** | 529.2980 | 557.2930 | **ITINDL** | 642.3821 | 670.3770 | **TI** | 187.1441 | 215.1390 |
| **TIN** | 301.1870 | 329.1819 | **TIND** | 416.2140 | 444.2089 | **TINDL** | 529.2980 | 557.2930 |
| **TINDLP** | 626.3508 | 654.3457 | **IN** | 200.1394 | 228.1343 | **IND** | 315.1663 | 343.1612 |
| **INDL** | 428.2504 | 456.2453 | **INDLP** | 525.3031 | 553.2980 | **INDLPV** | 624.3715 | 652.3665 |
| **INDLPVG** | 681.3930 | 709.3879 | **ND** | 202.0822 | 230.0771 | **NDL** | 315.1663 | 343.1612 |
| **NDLP** | 412.2191 | 440.2140 | **NDLPV** | 511.2875 | 539.2824 | **NDLPVG** | 568.3089 | 596.3039 |
| **DL** | 201.1234 | 229.1183 | **DLP** | 298.1761 | 326.1710 | **DLPV** | 397.2445 | 425.2395 |
| **DLPVG** | 454.2660 | 482.2609 | **LP** | 183.1492 | 211.1441 | **LPV** | 282.2176 | 310.2125 |
| **LPVG** | 339.2391 | 367.2340 | **PV** | 169.1335 | 197.1285 | **PVG** | 226.1550 | 254.1499 |
| **VG** | 129.1022 | 157.0972 |  |  |  |  |  |  |

🡪 Annotated MS2 spectrum for peptide DYGVLKDDEGIAYR



**Monoisotopic mass of neutral peptide Mr(calc):** 1612.7733

**Ions Score:** 27 **Expect:** 0.13

**Matches :** 3/225 fragment ions using 3 most intense peaks   ([help](http://msmsms/mascot/help/results_help.html" \l "PEP" \t "_blank))

|  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **#** | **Immon.** | **a** | **a\*** | **a0** | **b** | **b\*** | **b0** | **Seq.** | **v** | **w** | **w'** | **y** | **y\*** | **y0** | **#** |
| **1** | 88.0393 | 88.0393 |  | 70.0287 | 116.0342 |  | 98.0237 | **D** |  |  |  |  |  |  | **14** |
| **2** | 136.0757 | 251.1026 |  | 233.0921 | 279.0975 |  | 261.0870 | **Y** | 1390.6961 |  |  | ***1498.7536*** | 1481.7271 | 1480.7431 | **13** |
| **3** | 30.0338 | 308.1241 |  | 290.1135 | 336.1190 |  | 318.1084 | **G** |  |  |  | 1335.6903 | 1318.6638 | 1317.6797 | **12** |
| **4** | 72.0808 | 407.1925 |  | 389.1819 | 435.1874 |  | 417.1769 | **V** | 1234.6062 | 1247.6266 |  | 1278.6688 | 1261.6423 | 1260.6583 | **11** |
| **5** | 86.0964 | 520.2766 |  | 502.2660 | 548.2715 |  | 530.2609 | **L** | 1121.5222 | 1120.5269 |  | 1179.6004 | 1162.5739 | 1161.5899 | **10** |
| **6** | 101.1073 | 648.3715 | 631.3450 | 630.3610 | 676.3665 | 659.3399 | 658.3559 | **K** | 993.4272 | 992.4320 |  | 1066.5164 | 1049.4898 | 1048.5058 | **9** |
| **7** | 88.0393 | 763.3985 | 746.3719 | 745.3879 | 791.3934 | 774.3668 | 773.3828 | **D** | 878.4003 | 877.4050 |  | 938.4214 | 921.3949 | 920.4108 | **8** |
| **8** | 88.0393 | 878.4254 | 861.3989 | 860.4149 | 906.4203 | 889.3938 | 888.4098 | **D** | 763.3733 | 762.3781 |  | ***823.3945*** | 806.3679 | 805.3839 | **7** |
| **9** | 102.0550 | 1007.4680 | 990.4415 | 989.4575 | 1035.4629 | 1018.4364 | 1017.4524 | **E** | 634.3307 | 633.3355 |  | ***708.3675*** | 691.3410 | 690.3570 | **6** |
| **10** | 30.0338 | 1064.4895 | 1047.4629 | 1046.4789 | 1092.4844 | 1075.4578 | 1074.4738 | **G** |  |  |  | 579.3249 | 562.2984 |  | **5** |
| **11** | 86.0964 | 1177.5735 | 1160.5470 | 1159.5630 | 1205.5685 | 1188.5419 | 1187.5579 | **I** | 464.2252 | 477.2456 | 491.2613 | 522.3035 | 505.2769 |  | **4** |
| **12** | 44.0495 | 1248.6107 | 1231.5841 | 1230.6001 | 1276.6056 | 1259.5790 | 1258.5950 | **A** | 393.1881 |  |  | 409.2194 | 392.1928 |  | **3** |
| **13** | 136.0757 | 1411.6740 | 1394.6474 | 1393.6634 | 1439.6689 | 1422.6424 | 1421.6583 | **Y** | 230.1248 |  |  | 338.1823 | 321.1557 |  | **2** |
| **14** | 129.1135 |  |  |  |  |  |  | **R** | 74.0237 | 73.0284 |  | 175.1190 | 158.0924 |  | **1** |

|  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **Seq** | **ya** | **yb** | **Seq** | **ya** | **yb** | **Seq** | **ya** | **yb** |
| **YG** | 193.0972 | 221.0921 | **YGV** | 292.1656 | 320.1605 | **YGVL** | 405.2496 | 433.2445 |
| **YGVLK** | 533.3446 | 561.3395 | **YGVLKD** | 648.3715 | 676.3665 | **GV** | 129.1022 | 157.0972 |
| **GVL** | 242.1863 | 270.1812 | **GVLK** | 370.2813 | 398.2762 | **GVLKD** | 485.3082 | 513.3031 |
| **GVLKDD** | 600.3352 | 628.3301 | **VL** | 185.1648 | 213.1598 | **VLK** | 313.2598 | 341.2547 |
| **VLKD** | 428.2867 | 456.2817 | **VLKDD** | 543.3137 | 571.3086 | **VLKDDE** | 672.3563 | 700.3512 |
| **LK** | 214.1914 | 242.1863 | **LKD** | 329.2183 | 357.2132 | **LKDD** | 444.2453 | 472.2402 |
| **LKDDE** | 573.2879 | 601.2828 | **LKDDEG** | 630.3093 | 658.3042 | **KD** | 216.1343 | 244.1292 |
| **KDD** | 331.1612 | 359.1561 | **KDDE** | 460.2038 | 488.1987 | **KDDEG** | 517.2253 | 545.2202 |
| **KDDEGI** | 630.3093 | 658.3042 | **DD** | 203.0662 | 231.0612 | **DDE** | 332.1088 | 360.1038 |
| **DDEG** | 389.1303 | 417.1252 | **DDEGI** | 502.2144 | 530.2093 | **DDEGIA** | 573.2515 | 601.2464 |
| **DE** | 217.0819 | 245.0768 | **DEG** | 274.1034 | 302.0983 | **DEGI** | 387.1874 | 415.1823 |
| **DEGIA** | 458.2245 | 486.2195 | **DEGIAY** | 621.2879 | 649.2828 | **EG** | 159.0764 | 187.0713 |
| **EGI** | 272.1605 | 300.1554 | **EGIA** | 343.1976 | 371.1925 | **EGIAY** | 506.2609 | 534.2558 |
| **GI** | 143.1179 | 171.1128 | **GIA** | 214.1550 | 242.1499 | **GIAY** | 377.2183 | 405.2132 |
| **IA** | 157.1335 | 185.1285 | **IAY** | 320.1969 | 348.1918 | **AY** | 207.1128 | 235.1077 |

**Spot 8:**

**http://msmsms/mascot/images/88x31_logo_white.gifMascot Search Results**

**User :**

**Email :**

**Search title : SampleSetID: 341, AnalysisID: 800, MaldiWellID: 45055, SpectrumID: 175225, Path=\Jimmy\Cooperia Adult ES 20110221\20110509 1st experiment (repeat)**

**Database : cooperia\_oncophora oncophora\_20110405 (34373 sequences; 5289600 residues)**

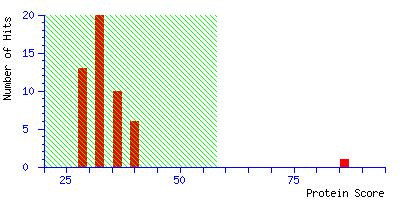
**Timestamp : 9 May 2011 at 12:39:00 GMT**

**Warning : A Peptide summary report will usually give a much clearer picture of MS/MS search results.**

**Top Score : 86 for isotig32303, putative nuclear encoded protein Method: Longest ORF**

**Mascot Score Histogram**

Protein score is -10\*Log(P), where P is the probability that the observed match is a random event.  
Protein scores greater than 58 are significant (p<0.05).  
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



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**Protein Summary Report**

|  |  |  |  |
| --- | --- | --- | --- |
|  |  |  | [Help](http://msmsms/mascot/help/msms_summaries_help.html" \t "_blank) |
|  | Significance threshold p< | Max. number of hits |  |

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**Index**

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
|  | **Accession** | **Mass** | **Score** | **Description** |
| **1.** | [**isotig32303**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20110509/F014808.dat#Hit1) | 12330 | 86 | putative nuclear encoded protein Method: Longest ORF |
| **2.** | [**isotig28102**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20110509/F014808.dat#Hit2) | 48142 | 42 | putative nuclear encoded protein Method: similarity and extension |
| **3.** | [**isotig06539**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20110509/F014808.dat#Hit3) | 21639 | 41 | putative nuclear encoded protein Method: ESTScan |
| **4.** | [**contig09094**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20110509/F014808.dat#Hit4) | 33134 | 40 | putative nuclear encoded protein Method: similarity and extension |
| **5.** | [**isotig15870**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20110509/F014808.dat#Hit5) | 16965 | 39 | putative nuclear encoded protein Method: similarity and extension |
| **6.** | [**contig04062**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20110509/F014808.dat#Hit6) | 35671 | 38 | putative nuclear encoded protein Method: similarity and extension |
| **7.** | [**isotig13441**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20110509/F014808.dat#Hit7) | 12150 | 38 | putative nuclear encoded protein Method: Longest ORF |
| **8.** | [**isotig07482**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20110509/F014808.dat#Hit8) | 15622 | 37 | putative nuclear encoded protein Method: similarity and extension |
| **9.** | [**isotig07486**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20110509/F014808.dat#Hit9) | 15622 | 37 | putative nuclear encoded protein Method: similarity and extension |
| **10.** | [**isotig15869**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20110509/F014808.dat#Hit10) | 16227 | 36 | putative nuclear encoded protein Method: similarity and extension |
| **11.** | [**contig24664**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20110509/F014808.dat#Hit11) | 6611 | 36 | putative nuclear encoded protein Method: similarity and extension |
| **12.** | [**isotig23409**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20110509/F014808.dat#Hit12) | 20858 | 36 | putative nuclear encoded protein Method: similarity and extension |
| **13.** | [**isotig17571**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20110509/F014808.dat#Hit13) | 16793 | 36 | putative nuclear encoded protein Method: similarity and extension |
| **14.** | [**isotig26954**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20110509/F014808.dat#Hit14) | 15407 | 35 | putative nuclear encoded protein Method: similarity and extension |
| **15.** | [**isotig27806**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20110509/F014808.dat#Hit15) | 18436 | 35 | putative nuclear encoded protein Method: Longest ORF |
| **16.** | [**isotig26948**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20110509/F014808.dat#Hit16) | 20872 | 35 | putative nuclear encoded protein Method: similarity and extension |
| **17.** | [**isotig26379**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20110509/F014808.dat#Hit17) | 12097 | 35 | putative nuclear encoded protein Method: similarity and extension |
| **18.** | [**isotig07268**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20110509/F014808.dat#Hit18) | 26750 | 34 | putative nuclear encoded protein Method: similarity and extension |
| **19.** | [**isotig07267**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20110509/F014808.dat#Hit19) | 26768 | 33 | putative nuclear encoded protein Method: similarity and extension |
| **20.** | [**isotig06592**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20110509/F014808.dat#Hit20) | 30041 | 33 | putative nuclear encoded protein Method: similarity and extension |

**Results List**

|  |  |
| --- | --- |
| **1.** | [isotig32303](http://msmsms/mascot/cgi/protein_view.pl?file=../data/20110509/F014808.dat&hit=1" \t "_blank)    **Mass:** 12330    **Score:** 86     **Expect:** 8.2e-005  **Matches:** 5 |
|  | putative nuclear encoded protein Method: Longest ORF |

|  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | **Observed** | **Mr(expt)** | **Mr(calc)** | **ppm** | **Start** |  | **End** | **Miss** | **Ions** | **Peptide** |
|  | 995.5329 | 994.5256 | 994.5236 | 2.03 | 33 | - | 40 | 1 | --- | K.VYKGEFPR.N |
|  | 995.5329 | 994.5256 | 994.5236 | 2.03 | 33 | - | 40 | 1 | 61 | K.VYKGEFPR.N |
|  | 1225.6587 | 1224.6514 | 1224.6462 | 4.23 | 81 | - | 92 | 0 | --- | K.IGSDAVAHQISK.E |
|  | 3015.3484 | 3014.3411 | 3014.3280 | 4.35 | 81 | - | 106 | 1 | --- | K.IGSDAVAHQISKEEYDSFYYDTCGLF.- + Carbamidomethyl (C) |
|  | 3015.3484 | 3014.3411 | 3014.3280 | 4.35 | 81 | - | 106 | 1 | 13 | K.IGSDAVAHQISKEEYDSFYYDTCGLF.- + Carbamidomethyl (C) |

|  |  |
| --- | --- |
|  | **No match to:** 830.4488, 832.3074, 842.5093, 844.5355, 891.4523, 905.4621, 914.5410, 948.4366, 963.4813, 977.5095, 978.5013, 980.5231, 982.4862, 993.5152, 994.5044, 1011.5246, 1017.5068, 1023.5268, 1037.5688, 1045.5640, 1057.4561, 1059.4611, 1065.5421, 1066.5282, 1121.5590, 1166.5670, 1169.5881, 1179.6106, 1182.5753, 1183.5983, 1203.5795, 1235.5421, 1260.5981, 1260.5981, 1267.7159, 1282.5739, 1307.6896, 1308.6794, 1320.5917, 1328.6589, 1353.6844, 1475.7649, 1493.7533, 1707.8007, 1791.7513, 1838.9320, 2211.1191, 2383.9729 |

**http://msmsms/mascot/images/88x31_logo_white.gifMascot Search Results**

**Protein View**

Top of Form



Match to: **isotig32303** Score: **86** Expect: **8.2e-005**

**putative nuclear encoded protein Method: Longest ORF**

Nominal mass (Mr): **12330**; Calculated pI value: **4.69**

NCBI BLAST search of [isotig32303](http://www.ncbi.nlm.nih.gov/blast/Blast.cgi?ALIGNMENTS=50&ALIGNMENT_VIEW=Pairwise&AUTO_FORMAT=Semiauto&CDD_SEARCH=on&CLIENT=web&COMPOSITION_BASED_STATISTICS=on&DATABASE=nr&DESCRIPTIONS=100&ENTREZ_QUERY=(none)&EXPECT=10&FILTER=L&FORMAT_BLOCK_ON_RESPAGE=None&FORMAT_OBJECT=Alignment&FORMAT_TYPE=HTML&GAPCOSTS=11+1&I_THRESH=0.001&LAYOUT=TwoWindows&MATRIX_NAME=BLOSUM62&NCBI_GI=on&PAGE=Proteins&PROGRAM=blastp&QUERY=HRRKMKLVTLAFLLYIAHSVMGDCQLLYSSFKVYKGEFPRNPFTVEYKDDDLVTLLWVQNEDSSLDVVDIQTDDGNVYYKIGSDAVAHQISKEEYDSFYYDTCGLF&SERVICE=plain&SET_DEFAULTS.x=9&SET_DEFAULTS.y=5&SHOW_OVERVIEW=on&WORD_SIZE=3&END_OF_HTTPGET=Yes" \t "_blank) against nr

Unformatted [sequence string](http://msmsms/mascot/cgi/getseq.pl?cooperia_oncophora+isotig32303+seq" \t "_blank) for pasting into other applications

Variable modifications: Carbamidomethyl (C),Oxidation (HW),Oxidation (M)

Cleavage by Trypsin/P: cuts C-term side of KR

Sequence Coverage: **32%**

Matched peptides shown in **Bold Red**

**1** HRRKMKLVTL AFLLYIAHSV MGDCQLLYSS FK**VYKGEFPR** NPFTVEYKDD

**51** DLVTLLWVQN EDSSLDVVDI QTDDGNVYYK **IGSDAVAHQI SKEEYDSFYY**

**101 DTCGLF**



  Residue Number  Increasing Mass  Decreasing Mass

**Start - End Observed Mr(expt) Mr(calc) ppm Miss Sequence**

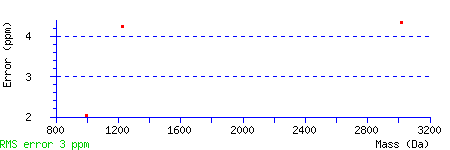
**33 - 40 995.5329 994.5256 994.5236 2 1 K.VYKGEFPR.N**  ([No match](http://msmsms/mascot/cgi/peptide_view.pl?file=../data/20110509/F014808.dat&query=16&hit=1" \t "_blank))

**33 - 40 995.5329 994.5256 994.5236 2 1 K.VYKGEFPR.N**  ([Ions score 61](http://msmsms/mascot/cgi/peptide_view.pl?file=../data/20110509/F014808.dat&query=17&hit=1" \t "_blank))

**81 - 92 1225.6587 1224.6514 1224.6462 4 0 K.IGSDAVAHQISK.E**  ([No match](http://msmsms/mascot/cgi/peptide_view.pl?file=../data/20110509/F014808.dat&query=34&hit=1" \t "_blank))

**81 - 106 3015.3484 3014.3411 3014.3280 4 1 K.IGSDAVAHQISKEEYDSFYYDTCGLF.-**  Carbamidomethyl (C) ([No match](http://msmsms/mascot/cgi/peptide_view.pl?file=../data/20110509/F014808.dat&query=52&hit=1" \t "_blank))

**81 - 106 3015.3484 3014.3411 3014.3280 4 1 K.IGSDAVAHQISKEEYDSFYYDTCGLF.-**  Carbamidomethyl (C) ([Ions score 13](http://msmsms/mascot/cgi/peptide_view.pl?file=../data/20110509/F014808.dat&query=53&hit=1" \t "_blank))



Bottom of Form

🡪 Annotated MS2 spectrum for peptide VYKGEFPR



**Monoisotopic mass of neutral peptide Mr(calc):** 994.5236

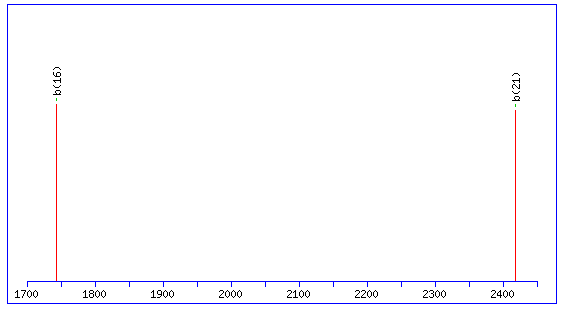
**Ions Score:** 61 **Expect:** 5.6e-005

**Matches :** 29/95 fragment ions using 36 most intense peaks   ([help](http://msmsms/mascot/help/results_help.html" \l "PEP" \t "_blank))

|  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **#** | **Immon.** | **a** | **a\*** | **a0** | **b** | **b\*** | **b0** | **Seq.** | **v** | **w** | **y** | **y\*** | **y0** | **#** |
| **1** | 72.0808 | 72.0808 |  |  | 100.0757 |  |  | **V** |  |  |  |  |  | **8** |
| **2** | 136.0757 | **235.1441** |  |  | 263.1390 |  |  | **Y** | 788.4050 |  | ***896.4625*** | 879.4359 | 878.4519 | **7** |
| **3** | 101.1073 | 363.2391 | 346.2125 |  | 391.2340 | 374.2074 |  | **K** | 660.3100 | 659.3148 | ***733.3992*** | 716.3726 | 715.3886 | **6** |
| **4** | 30.0338 | 420.2605 | 403.2340 |  | **448.2554** | 431.2289 |  | **G** |  |  | ***605.3042*** | 588.2776 | 587.2936 | **5** |
| **5** | 102.0550 | **549.3031** | 532.2766 | 531.2926 | **577.2980** | 560.2715 | 559.2875 | **E** | 474.2459 | 473.2507 | ***548.2827*** | 531.2562 | 530.2722 | **4** |
| **6** | 120.0808 | **696.3715** | 679.3450 | 678.3610 | **724.3665** | 707.3399 | 706.3559 | **F** | 327.1775 |  | ***419.2401*** | 402.2136 |  | **3** |
| **7** | 70.0651 | **793.4243** | 776.3978 | 775.4137 | **821.4192** | 804.3927 | 803.4087 | **P** | 230.1248 | 229.1295 | ***272.1717*** | 255.1452 |  | **2** |
| **8** | 129.1135 |  |  |  |  |  |  | **R** | 74.0237 | 73.0284 | ***175.1190*** | 158.0924 |  | **1** |

|  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **Seq** | **ya** | **yb** | **Seq** | **ya** | **yb** | **Seq** | **ya** | **yb** |
| **YK** | 264.1707 | 292.1656 | **YKG** | 321.1921 | 349.1870 | **YKGE** | 450.2347 | 478.2296 |
| **YKGEF** | 597.3031 | 625.2980 | **YKGEFP** | 694.3559 | 722.3508 | **KG** | 158.1288 | 186.1237 |
| **KGE** | 287.1714 | 315.1663 | **KGEF** | 434.2398 | 462.2347 | **KGEFP** | 531.2926 | 559.2875 |
| **GE** | 159.0764 | 187.0713 | **GEF** | 306.1448 | 334.1397 | **GEFP** | 403.1976 | 431.1925 |
| **EF** | 249.1234 | 277.1183 | **EFP** | 346.1761 | 374.1710 | **FP** | 217.1335 | 245.1285 |

🡪 Annotated MS2 spectrum for peptide IGSDAVAHQISKEEYDSFYYDTCGLF



**Monoisotopic mass of neutral peptide Mr(calc):** 3014.3280

**Variable modifications:**

**C23 :** Carbamidomethyl (C)

**Ions Score:** 13 **Expect:** 5.7

**Matches :** 2/403 fragment ions using 2 most intense peaks   ([help](http://msmsms/mascot/help/results_help.html" \l "PEP" \t "_blank))

|  |  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **#** | **Immon.** | **a** | **a\*** | **a0** | **b** | **b\*** | **b0** | **Seq.** | **y** | **y\*** | **y0** | **#** |
| **1** | 86.0964 | 86.0964 |  |  | 114.0913 |  |  | **I** |  |  |  | **26** |
| **2** | 30.0338 | 143.1179 |  |  | 171.1128 |  |  | **G** | 2902.2512 | 2885.2247 | 2884.2407 | **25** |
| **3** | 60.0444 | 230.1499 |  | 212.1394 | 258.1448 |  | 240.1343 | **S** | 2845.2298 | 2828.2032 | 2827.2192 | **24** |
| **4** | 88.0393 | 345.1769 |  | 327.1663 | 373.1718 |  | 355.1612 | **D** | 2758.1977 | 2741.1712 | 2740.1872 | **23** |
| **5** | 44.0495 | 416.2140 |  | 398.2034 | 444.2089 |  | 426.1983 | **A** | 2643.1708 | 2626.1442 | 2625.1602 | **22** |
| **6** | 72.0808 | 515.2824 |  | 497.2718 | 543.2773 |  | 525.2667 | **V** | 2572.1337 | 2555.1071 | 2554.1231 | **21** |
| **7** | 44.0495 | 586.3195 |  | 568.3089 | 614.3144 |  | 596.3039 | **A** | 2473.0653 | 2456.0387 | 2455.0547 | **20** |
| **8** | 110.0713 | 723.3784 |  | 705.3678 | 751.3733 |  | 733.3628 | **H** | 2402.0282 | 2385.0016 | 2384.0176 | **19** |
| **9** | 101.0709 | 851.4370 | 834.4104 | 833.4264 | 879.4319 | 862.4054 | 861.4213 | **Q** | 2264.9692 | 2247.9427 | 2246.9587 | **18** |
| **10** | 86.0964 | 964.5211 | 947.4945 | 946.5105 | 992.5160 | 975.4894 | 974.5054 | **I** | 2136.9107 | 2119.8841 | 2118.9001 | **17** |
| **11** | 60.0444 | 1051.5531 | 1034.5265 | 1033.5425 | 1079.5480 | 1062.5215 | 1061.5374 | **S** | 2023.8266 | 2006.8001 | 2005.8160 | **16** |
| **12** | 101.1073 | 1179.6480 | 1162.6215 | 1161.6375 | 1207.6430 | 1190.6164 | 1189.6324 | **K** | 1936.7946 | 1919.7680 | 1918.7840 | **15** |
| **13** | 102.0550 | 1308.6906 | 1291.6641 | 1290.6801 | 1336.6856 | 1319.6590 | 1318.6750 | **E** | 1808.6996 |  | 1790.6890 | **14** |
| **14** | 102.0550 | 1437.7332 | 1420.7067 | 1419.7227 | 1465.7281 | 1448.7016 | 1447.7176 | **E** | 1679.6570 |  | 1661.6465 | **13** |
| **15** | 136.0757 | 1600.7966 | 1583.7700 | 1582.7860 | 1628.7915 | 1611.7649 | 1610.7809 | **Y** | 1550.6144 |  | 1532.6039 | **12** |
| **16** | 88.0393 | 1715.8235 | 1698.7970 | 1697.8129 | ***1743.8184*** | 1726.7919 | 1725.8079 | **D** | 1387.5511 |  | 1369.5405 | **11** |
| **17** | 60.0444 | 1802.8555 | 1785.8290 | 1784.8450 | 1830.8504 | 1813.8239 | 1812.8399 | **S** | 1272.5242 |  | 1254.5136 | **10** |
| **18** | 120.0808 | 1949.9239 | 1932.8974 | 1931.9134 | 1977.9189 | 1960.8923 | 1959.9083 | **F** | 1185.4921 |  | 1167.4816 | **9** |
| **19** | 136.0757 | 2112.9873 | 2095.9607 | 2094.9767 | 2140.9822 | 2123.9556 | 2122.9716 | **Y** | 1038.4237 |  | 1020.4131 | **8** |
| **20** | 136.0757 | 2276.0506 | 2259.0241 | 2258.0400 | 2304.0455 | 2287.0190 | 2286.0350 | **Y** | 875.3604 |  | 857.3498 | **7** |
| **21** | 88.0393 | 2391.0775 | 2374.0510 | 2373.0670 | ***2419.0725*** | 2402.0459 | 2401.0619 | **D** | 712.2971 |  | 694.2865 | **6** |
| **22** | 74.0600 | 2492.1252 | 2475.0987 | 2474.1147 | 2520.1201 | 2503.0936 | 2502.1096 | **T** | 597.2701 |  | 579.2595 | **5** |
| **23** | 133.0430 | 2652.1559 | 2635.1293 | 2634.1453 | 2680.1508 | 2663.1242 | 2662.1402 | **C** | 496.2224 |  |  | **4** |
| **24** | 30.0338 | 2709.1773 | 2692.1508 | 2691.1668 | 2737.1723 | 2720.1457 | 2719.1617 | **G** | 336.1918 |  |  | **3** |
| **25** | 86.0964 | 2822.2614 | 2805.2349 | 2804.2508 | 2850.2563 | 2833.2298 | 2832.2458 | **L** | 279.1703 |  |  | **2** |
| **26** | 120.0808 |  |  |  |  |  |  | **F** | 166.0863 |  |  | **1** |

|  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **Seq** | **ya** | **yb** | **Seq** | **ya** | **yb** | **Seq** | **ya** | **yb** |
| **GS** | 117.0659 | 145.0608 | **GSD** | 232.0928 | 260.0877 | **GSDA** | 303.1299 | 331.1248 |
| **GSDAV** | 402.1983 | 430.1932 | **GSDAVA** | 473.2354 | 501.2304 | **GSDAVAH** | 610.2944 | 638.2893 |
| **SD** | 175.0713 | 203.0662 | **SDA** | 246.1084 | 274.1034 | **SDAV** | 345.1769 | 373.1718 |
| **SDAVA** | 416.2140 | 444.2089 | **SDAVAH** | 553.2729 | 581.2678 | **SDAVAHQ** | 681.3315 | 709.3264 |
| **DA** | 159.0764 | 187.0713 | **DAV** | 258.1448 | 286.1397 | **DAVA** | 329.1819 | 357.1769 |
| **DAVAH** | 466.2409 | 494.2358 | **DAVAHQ** | 594.2994 | 622.2944 | **AV** | 143.1179 | 171.1128 |
| **AVA** | 214.1550 | 242.1499 | **AVAH** | 351.2139 | 379.2088 | **AVAHQ** | 479.2725 | 507.2674 |
| **AVAHQI** | 592.3566 | 620.3515 | **AVAHQIS** | 679.3886 | 707.3835 | **VA** | 143.1179 | 171.1128 |
| **VAH** | 280.1768 | 308.1717 | **VAHQ** | 408.2354 | 436.2303 | **VAHQI** | 521.3194 | 549.3144 |
| **VAHQIS** | 608.3515 | 636.3464 | **AH** | 181.1084 | 209.1033 | **AHQ** | 309.1670 | 337.1619 |
| **AHQI** | 422.2510 | 450.2459 | **AHQIS** | 509.2831 | 537.2780 | **AHQISK** | 637.3780 | 665.3729 |
| **HQ** | 238.1299 | 266.1248 | **HQI** | 351.2139 | 379.2088 | **HQIS** | 438.2459 | 466.2409 |
| **HQISK** | 566.3409 | 594.3358 | **HQISKE** | 695.3835 | 723.3784 | **QI** | 214.1550 | 242.1499 |
| **QIS** | 301.1870 | 329.1819 | **QISK** | 429.2820 | 457.2769 | **QISKE** | 558.3246 | 586.3195 |
| **QISKEE** | 687.3672 | 715.3621 | **IS** | 173.1285 | 201.1234 | **ISK** | 301.2234 | 329.2183 |
| **ISKE** | 430.2660 | 458.2609 | **ISKEE** | 559.3086 | 587.3035 | **SK** | 188.1394 | 216.1343 |
| **SKE** | 317.1819 | 345.1769 | **SKEE** | 446.2245 | 474.2195 | **SKEEY** | 609.2879 | 637.2828 |
| **KE** | 230.1499 | 258.1448 | **KEE** | 359.1925 | 387.1874 | **KEEY** | 522.2558 | 550.2508 |
| **KEEYD** | 637.2828 | 665.2777 | **EE** | 231.0975 | 259.0925 | **EEY** | 394.1609 | 422.1558 |
| **EEYD** | 509.1878 | 537.1827 | **EEYDS** | 596.2198 | 624.2148 | **EY** | 265.1183 | 293.1132 |
| **EYD** | 380.1452 | 408.1401 | **EYDS** | 467.1773 | 495.1722 | **EYDSF** | 614.2457 | 642.2406 |
| **YD** | 251.1026 | 279.0975 | **YDS** | 338.1347 | 366.1296 | **YDSF** | 485.2031 | 513.1980 |
| **YDSFY** | 648.2664 | 676.2613 | **DS** | 175.0713 | 203.0662 | **DSF** | 322.1397 | 350.1347 |
| **DSFY** | 485.2031 | 513.1980 | **DSFYY** | 648.2664 | 676.2613 | **SF** | 207.1128 | 235.1077 |
| **SFY** | 370.1761 | 398.1710 | **SFYY** | 533.2395 | 561.2344 | **SFYYD** | 648.2664 | 676.2613 |
| **FY** | 283.1441 | 311.1390 | **FYY** | 446.2074 | 474.2023 | **FYYD** | 561.2344 | 589.2293 |
| **FYYDT** | 662.2821 | 690.2770 | **YY** | 299.1390 | 327.1339 | **YYD** | 414.1660 | 442.1609 |
| **YYDT** | 515.2136 | 543.2086 | **YYDTC** | 675.2443 | 703.2392 | **YD** | 251.1026 | 279.0975 |
| **YDT** | 352.1503 | 380.1452 | **YDTC** | 512.1810 | 540.1759 | **YDTCG** | 569.2024 | 597.1973 |
| **YDTCGL** | 682.2865 | 710.2814 | **DT** | 189.0870 | 217.0819 | **DTC** | 349.1176 | 377.1125 |
| **DTCG** | 406.1391 | 434.1340 | **DTCGL** | 519.2232 | 547.2181 | **TC** | 234.0907 | 262.0856 |
| **TCG** | 291.1122 | 319.1071 | **TCGL** | 404.1962 | 432.1911 | **CG** | 190.0645 | 218.0594 |
| **CGL** | 303.1485 | 331.1435 | **GL** | 143.1179 | 171.1128 |  |  |  |

**Spot 9:**

**http://msmsms/mascot/images/88x31_logo_white.gifMascot Search Results**

**User :**

**Email :**

**Search title : SampleSetID: 341, AnalysisID: 641, MaldiWellID: 45099, SpectrumID: 154499, Path=\Jimmy\Cooperia Adult ES 20110221\20110405 MS en MSMS (new DB)**

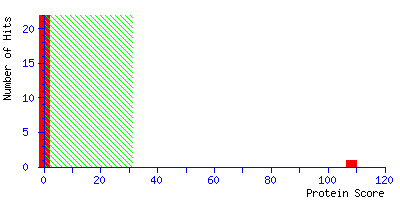
**Database : cooperia\_oncophora oncophora\_20110405 (34373 sequences; 5289600 residues)**

**Timestamp : 5 Apr 2011 at 12:32:16 GMT**

|  |  |  |
| --- | --- | --- |
| **Protein hits    :** | [**isotig10739**](http://msmsms/mascot/cgi/master_results.pl?file=..%2Fdata%2F20110405%2FF014320.dat#Hit1) | putative nuclear encoded protein Method: Longest ORF |
|  | [**isotig09337**](http://msmsms/mascot/cgi/master_results.pl?file=..%2Fdata%2F20110405%2FF014320.dat#Hit2) | putative nuclear encoded protein Method: Longest ORF |
|  | [**isotig16020**](http://msmsms/mascot/cgi/master_results.pl?file=..%2Fdata%2F20110405%2FF014320.dat#Hit3) | putative nuclear encoded protein Method: similarity and extension |
|  | [**isotig23582**](http://msmsms/mascot/cgi/master_results.pl?file=..%2Fdata%2F20110405%2FF014320.dat#Hit4) | putative nuclear encoded protein Method: ESTScan |
|  | [**isotig17021**](http://msmsms/mascot/cgi/master_results.pl?file=..%2Fdata%2F20110405%2FF014320.dat#Hit5) | putative nuclear encoded protein Method: Longest ORF |
|  | [**isotig25434**](http://msmsms/mascot/cgi/master_results.pl?file=..%2Fdata%2F20110405%2FF014320.dat#Hit6) | putative nuclear encoded protein Method: ESTScan |
|  | [**isotig02689**](http://msmsms/mascot/cgi/master_results.pl?file=..%2Fdata%2F20110405%2FF014320.dat#Hit7) | putative nuclear encoded protein Method: similarity and extension |
|  | [**isotig28352**](http://msmsms/mascot/cgi/master_results.pl?file=..%2Fdata%2F20110405%2FF014320.dat#Hit8) | putative nuclear encoded protein Method: ESTScan |
|  | [**isotig17564**](http://msmsms/mascot/cgi/master_results.pl?file=..%2Fdata%2F20110405%2FF014320.dat#Hit9) | putative nuclear encoded protein Method: ESTScan |
|  | [**isotig21656**](http://msmsms/mascot/cgi/master_results.pl?file=..%2Fdata%2F20110405%2FF014320.dat#Hit10) | putative nuclear encoded protein Method: ESTScan |
|  | [**isotig06878**](http://msmsms/mascot/cgi/master_results.pl?file=..%2Fdata%2F20110405%2FF014320.dat#Hit11) | putative nuclear encoded protein Method: Longest ORF |
|  | [**isotig13170**](http://msmsms/mascot/cgi/master_results.pl?file=..%2Fdata%2F20110405%2FF014320.dat#Hit12) | putative nuclear encoded protein Method: Longest ORF |
|  | [**isotig09910**](http://msmsms/mascot/cgi/master_results.pl?file=..%2Fdata%2F20110405%2FF014320.dat#Hit13) | putative nuclear encoded protein Method: Longest ORF |
|  | [**isotig15901**](http://msmsms/mascot/cgi/master_results.pl?file=..%2Fdata%2F20110405%2FF014320.dat#Hit14) | putative nuclear encoded protein Method: similarity and extension |
|  | [**isotig31987**](http://msmsms/mascot/cgi/master_results.pl?file=..%2Fdata%2F20110405%2FF014320.dat#Hit15) | putative nuclear encoded protein Method: ESTScan |
|  | [**isotig13354**](http://msmsms/mascot/cgi/master_results.pl?file=..%2Fdata%2F20110405%2FF014320.dat#Hit16) | putative nuclear encoded protein Method: ESTScan |
|  | [**isotig22109**](http://msmsms/mascot/cgi/master_results.pl?file=..%2Fdata%2F20110405%2FF014320.dat#Hit17) | putative nuclear encoded protein Method: similarity and extension |
|  | [**isotig27481**](http://msmsms/mascot/cgi/master_results.pl?file=..%2Fdata%2F20110405%2FF014320.dat#Hit18) | putative nuclear encoded protein Method: similarity and extension |
|  | [**isotig32958**](http://msmsms/mascot/cgi/master_results.pl?file=..%2Fdata%2F20110405%2FF014320.dat#Hit19) | putative nuclear encoded protein Method: similarity and extension |
|  | [**isotig23091**](http://msmsms/mascot/cgi/master_results.pl?file=..%2Fdata%2F20110405%2FF014320.dat#Hit20) | putative nuclear encoded protein Method: ESTScan |

**Mascot Score Histogram**

Ions score is -10\*Log(P), where P is the probability that the observed match is a random event.  
Individual ions scores > 31 indicate identity or extensive homology (p<0.05).  
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



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**Peptide Summary Report**

|  |  |  |  |
| --- | --- | --- | --- |
|  |  |  | [Help](http://msmsms/mascot/help/msms_summaries_help.html" \t "_blank) |
|  | Significance threshold p< | Max. number of hits |  |
|  | Standard scoring  MudPIT scoring | Ions score or expect cut-off | Show sub-sets |
|  | Show pop-ups  Suppress pop-ups | Sort unassigned | Require bold red |

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   **Error tolerant**

|  |  |
| --- | --- |
| **1.** | [isotig10739](http://msmsms/mascot/cgi/protein_view.pl?file=../data/20110405/F014320.dat&hit=isotig10739&db_idx=1&px=1&ave_thresh=31&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank)    **Mass:** 14670    **Score:** 108    **Matches:** 2(2)  **Sequences:** 2(2) |
|  | putative nuclear encoded protein Method: Longest ORF |

|  |  |
| --- | --- |
|  | Check to include this hit in error tolerant search or archive report |
|  |  |

|  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | **Query** | **Observed** | **Mr(expt)** | **Mr(calc)** | **ppm** | **Miss** | **Score** | **Expect** | **Rank** | **Unique** | **Peptide** |
|  | [29](http://msmsms/mascot/cgi/peptide_view.pl?file=../data/20110405/F014320.dat&query=29&hit=1&index=isotig10739&px=1&section=5&ave_thresh=31&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) | **1081.5131** | **1080.5058** | **1080.5088** | **-2.72** | **0** | **38** | **0.011** | **1** | **U** | **K.DSDFVTELR.I** |
|  | [47](http://msmsms/mascot/cgi/peptide_view.pl?file=../data/20110405/F014320.dat&query=47&hit=1&index=isotig10739&px=1&section=5&ave_thresh=31&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) | **1940.9703** | **1939.9630** | **1939.9428** | **10.4** | **1** | **100** | **8.4e-009** | **1** | **U** | **R.SHFVNFKDSDFVTELR.I** |

|  |  |
| --- | --- |
|  | |
|  | **Proteins matching the same set of peptides:** |

|  |  |
| --- | --- |
|  | [isotig10740](http://msmsms/mascot/cgi/protein_view.pl?file=../data/20110405/F014320.dat&hit=isotig10740&db_idx=1&px=1&ave_thresh=31&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank)    **Mass:** 14574    **Score:** 108    **Matches:** 2(2)  **Sequences:** 2(2) |
|  | putative nuclear encoded protein Method: Longest ORF |

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**http://msmsms/mascot/images/88x31_logo_white.gifMascot Search Results**

**Protein View**

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Match to: **isotig10739** Score: **108**

**putative nuclear encoded protein Method: Longest ORF**

Nominal mass (Mr): **14670**; Calculated pI value: **8.30**

NCBI BLAST search of [isotig10739](http://www.ncbi.nlm.nih.gov/blast/Blast.cgi?ALIGNMENTS=50&ALIGNMENT_VIEW=Pairwise&AUTO_FORMAT=Semiauto&CDD_SEARCH=on&CLIENT=web&COMPOSITION_BASED_STATISTICS=on&DATABASE=nr&DESCRIPTIONS=100&ENTREZ_QUERY=(none)&EXPECT=10&FILTER=L&FORMAT_BLOCK_ON_RESPAGE=None&FORMAT_OBJECT=Alignment&FORMAT_TYPE=HTML&GAPCOSTS=11+1&I_THRESH=0.001&LAYOUT=TwoWindows&MATRIX_NAME=BLOSUM62&NCBI_GI=on&PAGE=Proteins&PROGRAM=blastp&QUERY=PTRGSSTRARSLVLSPRYQHRRMKLVTLAFLLFIAHSVMGDDCQVSYTSFGVYNGDFPRNPFRSHFVNFKDSDFVTELRIHAKDTTLDVVEIQKDDDSRHYFIVGSDAVAKPIHKEEFSVYADKCGIF&SERVICE=plain&SET_DEFAULTS.x=9&SET_DEFAULTS.y=5&SHOW_OVERVIEW=on&WORD_SIZE=3&END_OF_HTTPGET=Yes" \t "_blank) against nr

Unformatted [sequence string](http://msmsms/mascot/cgi/getseq.pl?cooperia_oncophora+isotig10739+seq" \t "_blank) for pasting into other applications

Variable modifications: Oxidation (HW),Oxidation (M)

Cleavage by Trypsin/P: cuts C-term side of KR

Sequence Coverage: **12%**

Matched peptides shown in **Bold Red**

**1** PTRGSSTRAR SLVLSPRYQH RRMKLVTLAF LLFIAHSVMG DDCQVSYTSF

**51** GVYNGDFPRN PFR**SHFVNFK DSDFVTELR**I HAKDTTLDVV EIQKDDDSRH

**101** YFIVGSDAVA KPIHKEEFSV YADKCGIF

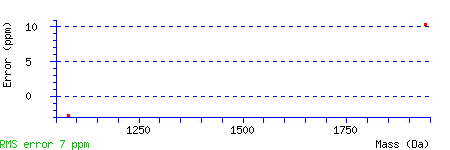


  Residue Number  Increasing Mass  Decreasing Mass

**Start - End Observed Mr(expt) Mr(calc) ppm Miss Sequence**

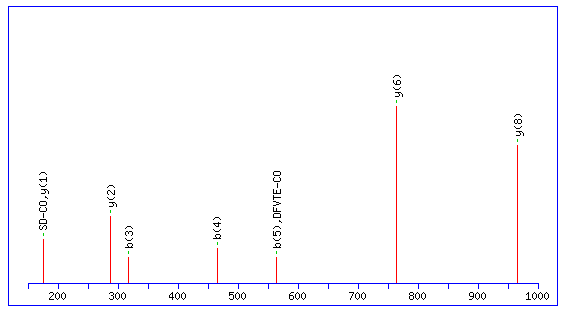
**64 - 79 1940.9703 1939.9630 1939.9428 10 1 R.SHFVNFKDSDFVTELR.I**  ([Ions score 100](http://msmsms/mascot/cgi/peptide_view.pl?file=../data/20110405/F014320.dat&query=47&hit=1&index=isotig10739&px=1&section=5&ave_thresh=31&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank))

**71 - 79 1081.5131 1080.5058 1080.5088 -3 0 K.DSDFVTELR.I**  ([Ions score 38](http://msmsms/mascot/cgi/peptide_view.pl?file=../data/20110405/F014320.dat&query=29&hit=1&index=isotig10739&px=1&section=5&ave_thresh=31&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank))



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🡪 Annotated MS2 spectrum for peptide DSDFVTELR



**Monoisotopic mass of neutral peptide Mr(calc):** 1080.5088

**Ions Score:** 44 **Expect:** 0.0032

**Matches :** 10/118 fragment ions using 7 most intense peaks   ([help](http://msmsms/mascot/help/results_help.html" \l "PEP" \t "_blank))

|  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **#** | **Immon.** | **a** | **a0** | **b** | **b0** | **Seq.** | **v** | **w** | **w'** | **y** | **y\*** | **y0** | **#** |
| **1** | 88.0393 | 88.0393 | 70.0287 | 116.0342 | 98.0237 | **D** |  |  |  |  |  |  | **9** |
| **2** | 60.0444 | 175.0713 | 157.0608 | 203.0662 | 185.0557 | **S** | 934.4629 | 933.4676 |  | ***966.4891*** | 949.4625 | 948.4785 | **8** |
| **3** | 88.0393 | 290.0983 | 272.0877 | ***318.0932*** | 300.0826 | **D** | 819.4359 | 818.4407 |  | 879.4571 | 862.4305 | 861.4465 | **7** |
| **4** | 120.0808 | 437.1667 | 419.1561 | ***465.1616*** | 447.1510 | **F** | 672.3675 |  |  | ***764.4301*** | 747.4036 | 746.4196 | **6** |
| **5** | 72.0808 | 536.2351 | 518.2245 | ***564.2300*** | 546.2195 | **V** | 573.2991 | 586.3195 |  | 617.3617 | 600.3352 | 599.3511 | **5** |
| **6** | 74.0600 | 637.2828 | 619.2722 | 665.2777 | 647.2671 | **T** | 472.2514 | 485.2718 | 487.2511 | 518.2933 | 501.2667 | 500.2827 | **4** |
| **7** | 102.0550 | 766.3254 | 748.3148 | 794.3203 | 776.3097 | **E** | 343.2088 | 342.2136 |  | 417.2456 | 400.2191 | 399.2350 | **3** |
| **8** | 86.0964 | 879.4094 | 861.3989 | 907.4044 | 889.3938 | **L** | 230.1248 | 229.1295 |  | ***288.2030*** | 271.1765 |  | **2** |
| **9** | 129.1135 |  |  |  |  | **R** | 74.0237 | 73.0284 |  | ***175.1190*** | 158.0924 |  | **1** |

|  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **Seq** | **ya** | **yb** | **Seq** | **ya** | **yb** | **Seq** | **ya** | **yb** |
| **SD** | 175.0713 | 203.0662 | **SDF** | 322.1397 | 350.1347 | **SDFV** | 421.2082 | 449.2031 |
| **SDFVT** | 522.2558 | 550.2508 | **SDFVTE** | 651.2984 | 679.2933 | **DF** | 235.1077 | 263.1026 |
| **DFV** | 334.1761 | 362.1710 | **DFVT** | 435.2238 | 463.2187 | **DFVTE** | 564.2664 | 592.2613 |
| **DFVTEL** | 677.3505 | 705.3454 | **FV** | 219.1492 | 247.1441 | **FVT** | 320.1969 | 348.1918 |
| **FVTE** | 449.2395 | 477.2344 | **FVTEL** | 562.3235 | 590.3184 | **VT** | 173.1285 | 201.1234 |
| **VTE** | 302.1710 | 330.1660 | **VTEL** | 415.2551 | 443.2500 | **TE** | 203.1026 | 231.0975 |
| **TEL** | 316.1867 | 344.1816 | **EL** | 215.1390 | 243.1339 |  |  |  |

**Spot 10:**

**http://msmsms/mascot/images/88x31_logo_white.gifMascot Search Results**

**User :**

**Email :**

**Search title : SampleSetID: 341, AnalysisID: 641, MaldiWellID: 45074, SpectrumID: 154421, Path=\Jimmy\Cooperia Adult ES 20110221\20110405 MS en MSMS (new DB)**

**Database : cooperia\_oncophora oncophora\_20110405 (34373 sequences; 5289600 residues)**

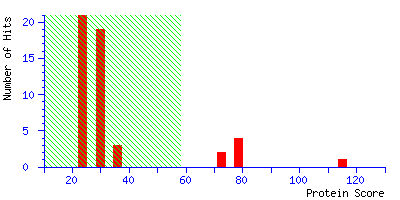
**Timestamp : 5 Apr 2011 at 12:30:49 GMT**

**Warning : A Peptide summary report will usually give a much clearer picture of MS/MS search results.**

**Top Score : 115 for isotig25459, putative nuclear encoded protein Method: Longest ORF**

**Mascot Score Histogram**

Protein score is -10\*Log(P), where P is the probability that the observed match is a random event.  
Protein scores greater than 58 are significant (p<0.05).  
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



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**Protein Summary Report**

|  |  |  |  |
| --- | --- | --- | --- |
|  |  |  | [Help](http://msmsms/mascot/help/msms_summaries_help.html" \t "_blank) |
|  | Significance threshold p< | Max. number of hits |  |

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**Index**

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
|  | **Accession** | **Mass** | **Score** | **Description** |
| **1.** | [**isotig25459**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20110405/F014303.dat#Hit1) | 15707 | 115 | putative nuclear encoded protein Method: Longest ORF |
| **2.** | [**contig45229**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20110405/F014303.dat#Hit2) | 14139 | 82 | putative nuclear encoded protein Method: similarity and extension |
| **3.** | [**isotig19733**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20110405/F014303.dat#Hit3) | 14161 | 77 | putative nuclear encoded protein Method: similarity and extension |
| **4.** | [**isotig21928**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20110405/F014303.dat#Hit4) | 14159 | 77 | putative nuclear encoded protein Method: similarity and extension |
| **5.** | [**isotig09197**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20110405/F014303.dat#Hit5) | 14129 | 77 | putative nuclear encoded protein Method: similarity and extension |
| **6.** | [**isotig14336**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20110405/F014303.dat#Hit6) | 14407 | 75 | putative nuclear encoded protein Method: similarity and extension |
| **7.** | [**isotig09196**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20110405/F014303.dat#Hit7) | 13826 | 71 | putative nuclear encoded protein Method: similarity and extension |
| **8.** | [**isotig26696**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20110405/F014303.dat#Hit8) | 24375 | 39 | putative nuclear encoded protein Method: similarity and extension |
| **9.** | [**isotig03072**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20110405/F014303.dat#Hit9) | 7053 | 37 | putative nuclear encoded protein Method: similarity and extension |
| **10.** | [**contig15387**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20110405/F014303.dat#Hit10) | 31507 | 36 | putative nuclear encoded protein Method: similarity and extension |
| **11.** | [**isotig11859**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20110405/F014303.dat#Hit11) | 34518 | 33 | putative nuclear encoded protein Method: similarity and extension |
| **12.** | [**isotig11481**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20110405/F014303.dat#Hit12) | 16071 | 31 | putative nuclear encoded protein Method: similarity and extension |
| **13.** | [**isotig11480**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20110405/F014303.dat#Hit13) | 16071 | 31 | putative nuclear encoded protein Method: similarity and extension |
| **14.** | [**isotig18643**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20110405/F014303.dat#Hit14) | 32787 | 31 | putative nuclear encoded protein Method: similarity and extension |
| **15.** | [**isotig18495**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20110405/F014303.dat#Hit15) | 22764 | 29 | putative nuclear encoded protein Method: similarity and extension |
| **16.** | [**isotig32704**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20110405/F014303.dat#Hit16) | 9699 | 29 | putative nuclear encoded protein Method: Longest ORF |
| **17.** | [**isotig03353**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20110405/F014303.dat#Hit17) | 13423 | 28 | putative nuclear encoded protein Method: Longest ORF |
| **18.** | [**isotig03358**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20110405/F014303.dat#Hit18) | 13423 | 28 | putative nuclear encoded protein Method: Longest ORF |
| **19.** | [**isotig03356**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20110405/F014303.dat#Hit19) | 13423 | 28 | putative nuclear encoded protein Method: Longest ORF |
| **20.** | [**isotig03354**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20110405/F014303.dat#Hit20) | 13423 | 28 | putative nuclear encoded protein Method: Longest ORF |

**Results List**

|  |  |
| --- | --- |
| **1.** | [isotig25459](http://msmsms/mascot/cgi/protein_view.pl?file=../data/20110405/F014303.dat&hit=1" \t "_blank)    **Mass:** 15707    **Score:** 115    **Expect:** 1.1e-007  **Matches:** 5 |
|  | putative nuclear encoded protein Method: Longest ORF |

|  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | **Observed** | **Mr(expt)** | **Mr(calc)** | **ppm** | **Start** |  | **End** | **Miss** | **Ions** | **Peptide** |
|  | 816.2845 | 815.2772 | 815.3636 | -105.92 | 43 | - | 48 | 0 | --- | R.MYPAYR.E + Oxidation (M) |
|  | 852.3268 | 851.3195 | 851.4613 | -166.55 | 108 | - | 114 | 1 | --- | K.GPKHEIR.E + Oxidation (HW) |
|  | 1520.5859 | 1519.5786 | 1519.7478 | -111.31 | 84 | - | 98 | 1 | --- | R.LEGEKEASTGSAVSR.A |
|  | 1520.5859 | 1519.5786 | 1519.7478 | -111.31 | 84 | - | 98 | 1 | 94 | R.LEGEKEASTGSAVSR.A |
|  | 1550.5552 | 1549.5479 | 1549.7169 | -109.07 | 37 | - | 48 | 1 | --- | K.CLTYNRMYPAYR.E |

|  |  |
| --- | --- |
|  | **No match to:** 806.3407, 809.3452, 823.3610, 825.3281, 832.2212, 834.3542, 837.3695, 844.3707, 844.3707, 880.3712, 883.4427, 896.3282, 906.3975, 909.3173, 925.3184, 940.4537, 941.3110, 951.3998, 994.3632, 1022.3755, 1033.4640, 1033.4640, 1059.4768, 1069.4094, 1074.4434, 1081.3636, 1107.4332, 1110.4032, 1131.4292, 1136.4779, 1147.4196, 1162.4556, 1165.4534, 1176.4463, 1182.4150, 1183.3877, 1197.4225, 1216.4884, 1296.4661, 1365.4880, 1449.5770, 1632.6456, 1632.6456, 1836.5803, 1898.6345, 1907.6085, 1989.6400, 2075.6670, 2100.7261 |

|  |  |
| --- | --- |
| **2.** | [contig45229](http://msmsms/mascot/cgi/protein_view.pl?file=../data/20110405/F014303.dat&hit=2" \t "_blank)    **Mass:** 14139    **Score:** 82     **Expect:** 0.00024  **Matches:** 6 |
|  | putative nuclear encoded protein Method: similarity and extension |

|  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | **Observed** | **Mr(expt)** | **Mr(calc)** | **ppm** | **Start** |  | **End** | **Miss** | **Ions** | **Peptide** |
|  | 834.3542 | 833.3469 | 833.4429 | -115.16 | 89 | - | 96 | 0 | --- | R.SALMAGLR.E + Oxidation (M) |
|  | 844.3707 | 843.3634 | 843.4562 | -110.04 | 97 | - | 103 | 1 | --- | R.EKGQLNR.A |
|  | 844.3707 | 843.3634 | 843.4562 | -110.04 | 97 | - | 103 | 1 | 16 | R.EKGQLNR.A |
|  | 1162.4556 | 1161.4483 | 1161.5778 | -111.51 | 74 | - | 84 | 0 | --- | R.TFPSGSSQPVR.S |
|  | 1632.6456 | 1631.6383 | 1631.8267 | -115.46 | 59 | - | 73 | 1 | --- | K.NPGTTTIPNKFTGER.T |
|  | 1632.6456 | 1631.6383 | 1631.8267 | -115.46 | 59 | - | 73 | 1 | 47 | K.NPGTTTIPNKFTGER.T |

|  |  |
| --- | --- |
|  | **No match to:** 806.3407, 809.3452, 816.2845, 823.3610, 825.3281, 832.2212, 837.3695, 852.3268, 880.3712, 883.4427, 896.3282, 906.3975, 909.3173, 925.3184, 940.4537, 941.3110, 951.3998, 994.3632, 1022.3755, 1033.4640, 1033.4640, 1059.4768, 1069.4094, 1074.4434, 1081.3636, 1107.4332, 1110.4032, 1131.4292, 1136.4779, 1147.4196, 1165.4534, 1176.4463, 1182.4150, 1183.3877, 1197.4225, 1216.4884, 1296.4661, 1365.4880, 1449.5770, 1520.5859, 1520.5859, 1550.5552, 1836.5803, 1898.6345, 1907.6085, 1989.6400, 2075.6670, 2100.7261 |

|  |  |
| --- | --- |
| **3.** | [isotig19733](http://msmsms/mascot/cgi/protein_view.pl?file=../data/20110405/F014303.dat&hit=3" \t "_blank)    **Mass:** 14161    **Score:** 77     **Expect:** 0.00065  **Matches:** 5 |
|  | putative nuclear encoded protein Method: similarity and extension |

|  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | **Observed** | **Mr(expt)** | **Mr(calc)** | **ppm** | **Start** |  | **End** | **Miss** | **Ions** | **Peptide** |
|  | 834.3542 | 833.3469 | 833.4429 | -115.16 | 89 | - | 96 | 0 | --- | R.SALMAGLR.E + Oxidation (M) |
|  | 844.3707 | 843.3634 | 843.4562 | -110.04 | 97 | - | 103 | 1 | --- | R.EKGQLNR.A |
|  | 844.3707 | 843.3634 | 843.4562 | -110.04 | 97 | - | 103 | 1 | 16 | R.EKGQLNR.A |
|  | 1632.6456 | 1631.6383 | 1631.8267 | -115.46 | 59 | - | 73 | 1 | --- | K.NPGTTTIPNKFTGER.S |
|  | 1632.6456 | 1631.6383 | 1631.8267 | -115.46 | 59 | - | 73 | 1 | 47 | K.NPGTTTIPNKFTGER.S |

|  |  |
| --- | --- |
|  | **No match to:** 806.3407, 809.3452, 816.2845, 823.3610, 825.3281, 832.2212, 837.3695, 852.3268, 880.3712, 883.4427, 896.3282, 906.3975, 909.3173, 925.3184, 940.4537, 941.3110, 951.3998, 994.3632, 1022.3755, 1033.4640, 1033.4640, 1059.4768, 1069.4094, 1074.4434, 1081.3636, 1107.4332, 1110.4032, 1131.4292, 1136.4779, 1147.4196, 1162.4556, 1165.4534, 1176.4463, 1182.4150, 1183.3877, 1197.4225, 1216.4884, 1296.4661, 1365.4880, 1449.5770, 1520.5859, 1520.5859, 1550.5552, 1836.5803, 1898.6345, 1907.6085, 1989.6400, 2075.6670, 2100.7261 |

|  |  |
| --- | --- |
| **4.** | [isotig21928](http://msmsms/mascot/cgi/protein_view.pl?file=../data/20110405/F014303.dat&hit=4" \t "_blank)    **Mass:** 14159    **Score:** 77     **Expect:** 0.00065  **Matches:** 5 |
|  | putative nuclear encoded protein Method: similarity and extension |

|  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | **Observed** | **Mr(expt)** | **Mr(calc)** | **ppm** | **Start** |  | **End** | **Miss** | **Ions** | **Peptide** |
|  | 834.3542 | 833.3469 | 833.4429 | -115.16 | 89 | - | 96 | 0 | --- | R.SALMAGLR.E + Oxidation (M) |
|  | 844.3707 | 843.3634 | 843.4562 | -110.04 | 97 | - | 103 | 1 | --- | R.EKGQLNR.A |
|  | 844.3707 | 843.3634 | 843.4562 | -110.04 | 97 | - | 103 | 1 | 16 | R.EKGQLNR.A |
|  | 1632.6456 | 1631.6383 | 1631.8267 | -115.46 | 59 | - | 73 | 1 | --- | K.NPGTTTIPNKFTGER.T |
|  | 1632.6456 | 1631.6383 | 1631.8267 | -115.46 | 59 | - | 73 | 1 | 47 | K.NPGTTTIPNKFTGER.T |

|  |  |
| --- | --- |
|  | **No match to:** 806.3407, 809.3452, 816.2845, 823.3610, 825.3281, 832.2212, 837.3695, 852.3268, 880.3712, 883.4427, 896.3282, 906.3975, 909.3173, 925.3184, 940.4537, 941.3110, 951.3998, 994.3632, 1022.3755, 1033.4640, 1033.4640, 1059.4768, 1069.4094, 1074.4434, 1081.3636, 1107.4332, 1110.4032, 1131.4292, 1136.4779, 1147.4196, 1162.4556, 1165.4534, 1176.4463, 1182.4150, 1183.3877, 1197.4225, 1216.4884, 1296.4661, 1365.4880, 1449.5770, 1520.5859, 1520.5859, 1550.5552, 1836.5803, 1898.6345, 1907.6085, 1989.6400, 2075.6670, 2100.7261 |

|  |  |
| --- | --- |
| **5.** | [isotig09197](http://msmsms/mascot/cgi/protein_view.pl?file=../data/20110405/F014303.dat&hit=5" \t "_blank)    **Mass:** 14129    **Score:** 77     **Expect:** 0.00065  **Matches:** 5 |
|  | putative nuclear encoded protein Method: similarity and extension |

|  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | **Observed** | **Mr(expt)** | **Mr(calc)** | **ppm** | **Start** |  | **End** | **Miss** | **Ions** | **Peptide** |
|  | 834.3542 | 833.3469 | 833.4429 | -115.16 | 89 | - | 96 | 0 | --- | R.SALMAGLR.E + Oxidation (M) |
|  | 844.3707 | 843.3634 | 843.4562 | -110.04 | 97 | - | 103 | 1 | --- | R.EKGQLNR.A |
|  | 844.3707 | 843.3634 | 843.4562 | -110.04 | 97 | - | 103 | 1 | 16 | R.EKGQLNR.A |
|  | 1632.6456 | 1631.6383 | 1631.8267 | -115.46 | 59 | - | 73 | 1 | --- | K.NPGTTTIPNKFTGER.T |
|  | 1632.6456 | 1631.6383 | 1631.8267 | -115.46 | 59 | - | 73 | 1 | 47 | K.NPGTTTIPNKFTGER.T |

|  |  |
| --- | --- |
|  | **No match to:** 806.3407, 809.3452, 816.2845, 823.3610, 825.3281, 832.2212, 837.3695, 852.3268, 880.3712, 883.4427, 896.3282, 906.3975, 909.3173, 925.3184, 940.4537, 941.3110, 951.3998, 994.3632, 1022.3755, 1033.4640, 1033.4640, 1059.4768, 1069.4094, 1074.4434, 1081.3636, 1107.4332, 1110.4032, 1131.4292, 1136.4779, 1147.4196, 1162.4556, 1165.4534, 1176.4463, 1182.4150, 1183.3877, 1197.4225, 1216.4884, 1296.4661, 1365.4880, 1449.5770, 1520.5859, 1520.5859, 1550.5552, 1836.5803, 1898.6345, 1907.6085, 1989.6400, 2075.6670, 2100.7261 |

|  |  |
| --- | --- |
| **6.** | [isotig14336](http://msmsms/mascot/cgi/protein_view.pl?file=../data/20110405/F014303.dat&hit=6" \t "_blank)    **Mass:** 14407    **Score:** 75     **Expect:** 0.0011  **Matches:** 5 |
|  | putative nuclear encoded protein Method: similarity and extension |

|  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | **Observed** | **Mr(expt)** | **Mr(calc)** | **ppm** | **Start** |  | **End** | **Miss** | **Ions** | **Peptide** |
|  | 844.3707 | 843.3634 | 843.4562 | -110.04 | 97 | - | 103 | 1 | --- | K.EKGQLNR.A |
|  | 844.3707 | 843.3634 | 843.4562 | -110.04 | 97 | - | 103 | 1 | 16 | K.EKGQLNR.A |
|  | 1632.6456 | 1631.6383 | 1631.8267 | -115.46 | 59 | - | 73 | 1 | --- | K.NPGTTTIPNKFTGER.T |
|  | 1632.6456 | 1631.6383 | 1631.8267 | -115.46 | 59 | - | 73 | 1 | 47 | K.NPGTTTIPNKFTGER.T |
|  | 2075.6670 | 2074.6597 | 2074.9962 | -162.16 | 104 | - | 123 | 2 | --- | R.ARLLPPGTKVGCDGMMDGNK.V + Oxidation (M) |

|  |  |
| --- | --- |
|  | **No match to:** 806.3407, 809.3452, 816.2845, 823.3610, 825.3281, 832.2212, 834.3542, 837.3695, 852.3268, 880.3712, 883.4427, 896.3282, 906.3975, 909.3173, 925.3184, 940.4537, 941.3110, 951.3998, 994.3632, 1022.3755, 1033.4640, 1033.4640, 1059.4768, 1069.4094, 1074.4434, 1081.3636, 1107.4332, 1110.4032, 1131.4292, 1136.4779, 1147.4196, 1162.4556, 1165.4534, 1176.4463, 1182.4150, 1183.3877, 1197.4225, 1216.4884, 1296.4661, 1365.4880, 1449.5770, 1520.5859, 1520.5859, 1550.5552, 1836.5803, 1898.6345, 1907.6085, 1989.6400, 2100.7261 |

|  |  |
| --- | --- |
| **7.** | [isotig09196](http://msmsms/mascot/cgi/protein_view.pl?file=../data/20110405/F014303.dat&hit=7" \t "_blank)    **Mass:** 13826    **Score:** 71     **Expect:** 0.0027  **Matches:** 4 |
|  | putative nuclear encoded protein Method: similarity and extension |

|  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | **Observed** | **Mr(expt)** | **Mr(calc)** | **ppm** | **Start** |  | **End** | **Miss** | **Ions** | **Peptide** |
|  | 844.3707 | 843.3634 | 843.4562 | -110.04 | 95 | - | 101 | 1 | --- | K.EKGQLNR.A |
|  | 844.3707 | 843.3634 | 843.4562 | -110.04 | 95 | - | 101 | 1 | 16 | K.EKGQLNR.A |
|  | 1632.6456 | 1631.6383 | 1631.8267 | -115.46 | 57 | - | 71 | 1 | --- | K.NPGTTTIPNKFTGER.T |
|  | 1632.6456 | 1631.6383 | 1631.8267 | -115.46 | 57 | - | 71 | 1 | 47 | K.NPGTTTIPNKFTGER.T |

|  |  |
| --- | --- |
|  | **No match to:** 806.3407, 809.3452, 816.2845, 823.3610, 825.3281, 832.2212, 834.3542, 837.3695, 852.3268, 880.3712, 883.4427, 896.3282, 906.3975, 909.3173, 925.3184, 940.4537, 941.3110, 951.3998, 994.3632, 1022.3755, 1033.4640, 1033.4640, 1059.4768, 1069.4094, 1074.4434, 1081.3636, 1107.4332, 1110.4032, 1131.4292, 1136.4779, 1147.4196, 1162.4556, 1165.4534, 1176.4463, 1182.4150, 1183.3877, 1197.4225, 1216.4884, 1296.4661, 1365.4880, 1449.5770, 1520.5859, 1520.5859, 1550.5552, 1836.5803, 1898.6345, 1907.6085, 1989.6400, 2075.6670, 2100.7261 |

**http://msmsms/mascot/images/88x31_logo_white.gifMascot Search Results**

**Protein View**

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Match to: **isotig25459** Score: **115** Expect: **1.1e-007**

**putative nuclear encoded protein Method: Longest ORF**

Nominal mass (Mr): **15707**; Calculated pI value: **7.62**

NCBI BLAST search of [isotig25459](http://www.ncbi.nlm.nih.gov/blast/Blast.cgi?ALIGNMENTS=50&ALIGNMENT_VIEW=Pairwise&AUTO_FORMAT=Semiauto&CDD_SEARCH=on&CLIENT=web&COMPOSITION_BASED_STATISTICS=on&DATABASE=nr&DESCRIPTIONS=100&ENTREZ_QUERY=(none)&EXPECT=10&FILTER=L&FORMAT_BLOCK_ON_RESPAGE=None&FORMAT_OBJECT=Alignment&FORMAT_TYPE=HTML&GAPCOSTS=11+1&I_THRESH=0.001&LAYOUT=TwoWindows&MATRIX_NAME=BLOSUM62&NCBI_GI=on&PAGE=Proteins&PROGRAM=blastp&QUERY=SDAGIAIEMSLALITLCLVLVNIHTFSQSSVVTQNKCLTYNRMYPAYREYHLTLNSNLVWDQQLHLEACEILNGIGSAESYYRLEGEKEASTGSAVSRARKALYQMKGPKHEIREFGEGYYGCNSIVVGNKAKVLCLYQR&SERVICE=plain&SET_DEFAULTS.x=9&SET_DEFAULTS.y=5&SHOW_OVERVIEW=on&WORD_SIZE=3&END_OF_HTTPGET=Yes" \t "_blank) against nr

Unformatted [sequence string](http://msmsms/mascot/cgi/getseq.pl?cooperia_oncophora+isotig25459+seq" \t "_blank) for pasting into other applications

Variable modifications: Oxidation (HW),Oxidation (M)

Cleavage by Trypsin/P: cuts C-term side of KR

Sequence Coverage: **24%**

Matched peptides shown in **Bold Red**

**1** SDAGIAIEMS LALITLCLVL VNIHTFSQSS VVTQNK**CLTY NRMYPAYR**EY

**51** HLTLNSNLVW DQQLHLEACE ILNGIGSAES YYR**LEGEKEA STGSAVSR**AR

**101** KALYQMK**GPK HEIR**EFGEGY YGCNSIVVGN KAKVLCLYQR



  Residue Number  Increasing Mass  Decreasing Mass

**Start - End Observed Mr(expt) Mr(calc) ppm Miss Sequence**

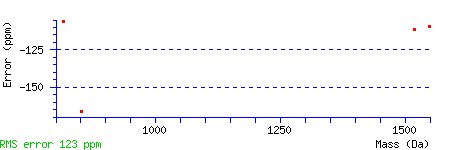
**37 - 48 1550.5552 1549.5479 1549.7169 -109 1 K.CLTYNRMYPAYR.E**  ([No match](http://msmsms/mascot/cgi/peptide_view.pl?file=../data/20110405/F014303.dat&query=46&hit=1" \t "_blank))

**43 - 48 816.2845 815.2772 815.3636 -106 0 R.MYPAYR.E**  Oxidation (M) ([No match](http://msmsms/mascot/cgi/peptide_view.pl?file=../data/20110405/F014303.dat&query=3&hit=1" \t "_blank))

**84 - 98 1520.5859 1519.5786 1519.7478 -111 1 R.LEGEKEASTGSAVSR.A**  ([No match](http://msmsms/mascot/cgi/peptide_view.pl?file=../data/20110405/F014303.dat&query=44&hit=1" \t "_blank))

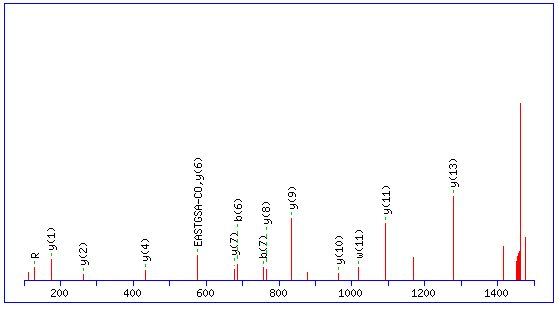
**84 - 98 1520.5859 1519.5786 1519.7478 -111 1 R.LEGEKEASTGSAVSR.A**  ([Ions score 94](http://msmsms/mascot/cgi/peptide_view.pl?file=../data/20110405/F014303.dat&query=45&hit=1" \t "_blank))

**108 - 114 852.3268 851.3195 851.4613 -167 1 K.GPKHEIR.E**  Oxidation (HW) ([No match](http://msmsms/mascot/cgi/peptide_view.pl?file=../data/20110405/F014303.dat&query=11&hit=1" \t "_blank))



Bottom of Form

🡪 Annotated MS2 spectrum for peptide LEGEKEASTGSAVSR



**Monoisotopic mass of neutral peptide Mr(calc):** 1519.7478

**Ions Score:** 94 **Expect:** 2.9e-008

**Matches :** 15/266 fragment ions using 18 most intense peaks   ([help](http://msmsms/mascot/help/results_help.html" \l "PEP" \t "_blank))

|  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **#** | **Immon.** | **a** | **a\*** | **a0** | **b** | **b\*** | **b0** | **Seq.** | **v** | **w** | **w'** | **y** | **y\*** | **y0** | **#** |
| **1** | 86.0964 | 86.0964 |  |  | 114.0913 |  |  | **L** |  |  |  |  |  |  | **15** |
| **2** | 102.0550 | 215.1390 |  | 197.1285 | 243.1339 |  | 225.1234 | **E** | 1333.6342 | 1332.6390 |  | 1407.6710 | 1390.6445 | 1389.6605 | **14** |
| **3** | 30.0338 | 272.1605 |  | 254.1499 | 300.1554 |  | 282.1448 | **G** |  |  |  | ***1278.6284*** | 1261.6019 | 1260.6179 | **13** |
| **4** | 102.0550 | 401.2031 |  | 383.1925 | 429.1980 |  | 411.1874 | **E** | 1147.5702 | 1146.5749 |  | 1221.6070 | 1204.5804 | 1203.5964 | **12** |
| **5** | 101.1073 | 529.2980 | 512.2715 | 511.2875 | 557.2930 | 540.2664 | 539.2824 | **K** | 1019.4752 | 1018.4800 |  | ***1092.5644*** | 1075.5378 | 1074.5538 | **11** |
| **6** | 102.0550 | 658.3406 | 641.3141 | 640.3301 | **686.3355** | 669.3090 | 668.3250 | **E** | 890.4326 | 889.4374 |  | ***964.4694*** | 947.4429 | 946.4588 | **10** |
| **7** | 44.0495 | 729.3777 | 712.3512 | 711.3672 | **757.3727** | 740.3461 | 739.3621 | **A** | 819.3955 |  |  | ***835.4268*** | 818.4003 | 817.4163 | **9** |
| **8** | 60.0444 | 816.4098 | 799.3832 | 798.3992 | 844.4047 | 827.3781 | 826.3941 | **S** | 732.3635 | 731.3682 |  | ***764.3897*** | 747.3632 | 746.3791 | **8** |
| **9** | 74.0600 | 917.4575 | 900.4309 | 899.4469 | 945.4524 | 928.4258 | 927.4418 | **T** | 631.3158 | 644.3362 | 646.3155 | ***677.3577*** | 660.3311 | 659.3471 | **7** |
| **10** | 30.0338 | 974.4789 | 957.4524 | 956.4684 | 1002.4738 | 985.4473 | 984.4633 | **G** |  |  |  | ***576.3100*** | 559.2835 | 558.2994 | **6** |
| **11** | 60.0444 | 1061.5109 | 1044.4844 | 1043.5004 | 1089.5059 | 1072.4793 | 1071.4953 | **S** | 487.2623 | 486.2671 |  | 519.2885 | 502.2620 | 501.2780 | **5** |
| **12** | 44.0495 | 1132.5481 | 1115.5215 | 1114.5375 | 1160.5430 | 1143.5164 | 1142.5324 | **A** | 416.2252 |  |  | ***432.2565*** | 415.2300 | 414.2459 | **4** |
| **13** | 72.0808 | 1231.6165 | 1214.5899 | 1213.6059 | 1259.6114 | 1242.5848 | 1241.6008 | **V** | 317.1568 | 330.1772 |  | 361.2194 | 344.1928 | 343.2088 | **3** |
| **14** | 60.0444 | 1318.6485 | 1301.6220 | 1300.6379 | 1346.6434 | 1329.6169 | 1328.6329 | **S** | 230.1248 | 229.1295 |  | ***262.1510*** | 245.1244 | 244.1404 | **2** |
| **15** | 129.1135 |  |  |  |  |  |  | **R** | 74.0237 | 73.0284 |  | ***175.1190*** | 158.0924 |  | **1** |

|  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **Seq** | **ya** | **yb** | **Seq** | **ya** | **yb** | **Seq** | **ya** | **yb** |
| **EG** | 159.0764 | 187.0713 | **EGE** | 288.1190 | 316.1139 | **EGEK** | 416.2140 | 444.2089 |
| **EGEKE** | 545.2566 | 573.2515 | **EGEKEA** | 616.2937 | 644.2886 | **GE** | 159.0764 | 187.0713 |
| **GEK** | 287.1714 | 315.1663 | **GEKE** | 416.2140 | 444.2089 | **GEKEA** | 487.2511 | 515.2460 |
| **GEKEAS** | 574.2831 | 602.2780 | **GEKEAST** | 675.3308 | 703.3257 | **EK** | 230.1499 | 258.1448 |
| **EKE** | 359.1925 | 387.1874 | **EKEA** | 430.2296 | 458.2245 | **EKEAS** | 517.2617 | 545.2566 |
| **EKEAST** | 618.3093 | 646.3042 | **EKEASTG** | 675.3308 | 703.3257 | **KE** | 230.1499 | 258.1448 |
| **KEA** | 301.1870 | 329.1819 | **KEAS** | 388.2191 | 416.2140 | **KEAST** | 489.2667 | 517.2617 |
| **KEASTG** | 546.2882 | 574.2831 | **KEASTGS** | 633.3202 | 661.3151 | **EA** | 173.0921 | 201.0870 |
| **EAS** | 260.1241 | 288.1190 | **EAST** | 361.1718 | 389.1667 | **EASTG** | 418.1932 | 446.1882 |
| **EASTGS** | 505.2253 | 533.2202 | **EASTGSA** | 576.2624 | 604.2573 | **EASTGSAV** | 675.3308 | 703.3257 |
| **AS** | 131.0815 | 159.0764 | **AST** | 232.1292 | 260.1241 | **ASTG** | 289.1506 | 317.1456 |
| **ASTGS** | 376.1827 | 404.1776 | **ASTGSA** | 447.2198 | 475.2147 | **ASTGSAV** | 546.2882 | 574.2831 |
| **ASTGSAVS** | 633.3202 | 661.3151 | **ST** | 161.0921 | 189.0870 | **STG** | 218.1135 | 246.1084 |
| **STGS** | 305.1456 | 333.1405 | **STGSA** | 376.1827 | 404.1776 | **STGSAV** | 475.2511 | 503.2460 |
| **STGSAVS** | 562.2831 | 590.2780 | **TG** | 131.0815 | 159.0764 | **TGS** | 218.1135 | 246.1084 |
| **TGSA** | 289.1506 | 317.1456 | **TGSAV** | 388.2191 | 416.2140 | **TGSAVS** | 475.2511 | 503.2460 |
| **GS** | 117.0659 | 145.0608 | **GSA** | 188.1030 | 216.0979 | **GSAV** | 287.1714 | 315.1663 |
| **GSAVS** | 374.2034 | 402.1983 | **SA** | 131.0815 | 159.0764 | **SAV** | 230.1499 | 258.1448 |
| **SAVS** | 317.1819 | 345.1769 | **AV** | 143.1179 | 171.1128 | **AVS** | 230.1499 | 258.1448 |
| **VS** | 159.1128 | 187.1077 |  |  |  |  |  |  |

**Spot 11:**

**http://msmsms/mascot/images/88x31_logo_white.gifMascot Search Results**

**User :**

**Email :**

**Search title : SampleSetID: 341, AnalysisID: 641, MaldiWellID: 45137, SpectrumID: 154599, Path=\Jimmy\Cooperia Adult ES 20110221\20110405 MS en MSMS (new DB)**

**Database : cooperia\_oncophora oncophora\_20110405 (34373 sequences; 5289600 residues)**

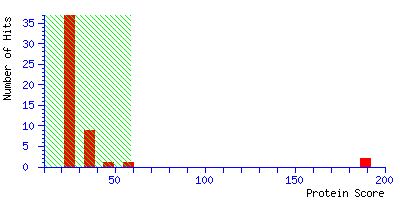
**Timestamp : 5 Apr 2011 at 12:34:06 GMT**

**Warning : A Peptide summary report will usually give a much clearer picture of MS/MS search results.**

**Top Score : 189 for isotig09711, putative nuclear encoded protein Method: similarity and extension**

**Mascot Score Histogram**

Protein score is -10\*Log(P), where P is the probability that the observed match is a random event.  
Protein scores greater than 58 are significant (p<0.05).  
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



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**Protein Summary Report**

|  |  |  |  |
| --- | --- | --- | --- |
|  |  |  | [Help](http://msmsms/mascot/help/msms_summaries_help.html" \t "_blank) |
|  | Significance threshold p< | Max. number of hits |  |

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**Index**

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
|  | **Accession** | **Mass** | **Score** | **Description** |
| **1.** | [**isotig09711**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20110405/F014342.dat#Hit1) | 28342 | 189 | putative nuclear encoded protein Method: similarity and extension |
| **2.** | [**isotig09712**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20110405/F014342.dat#Hit2) | 30518 | 189 | putative nuclear encoded protein Method: similarity and extension |
| **3.** | [**isotig21841**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20110405/F014342.dat#Hit3) | 13872 | 53 | putative nuclear encoded protein Method: similarity and extension |
| **4.** | [**isotig09440**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20110405/F014342.dat#Hit4) | 9370 | 41 | putative nuclear encoded protein Method: Longest ORF |
| **5.** | [**isotig20871**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20110405/F014342.dat#Hit5) | 15377 | 38 | putative nuclear encoded protein Method: similarity and extension |
| **6.** | [**contig08070**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20110405/F014342.dat#Hit6) | 20119 | 36 | putative nuclear encoded protein Method: similarity and extension |
| **7.** | [**isotig22185**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20110405/F014342.dat#Hit7) | 10408 | 34 | putative nuclear encoded protein Method: Longest ORF |
| **8.** | [**isotig19218**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20110405/F014342.dat#Hit8) | 11873 | 33 | putative nuclear encoded protein Method: Longest ORF |
| **9.** | [**isotig31798**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20110405/F014342.dat#Hit9) | 26201 | 33 | putative nuclear encoded protein Method: similarity and extension |
| **10.** | [**isotig18200**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20110405/F014342.dat#Hit10) | 14891 | 32 | putative nuclear encoded protein Method: similarity and extension |
| **11.** | [**isotig27142**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20110405/F014342.dat#Hit11) | 23236 | 32 | putative nuclear encoded protein Method: similarity and extension |
| **12.** | [**isotig10067**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20110405/F014342.dat#Hit12) | 22337 | 31 | putative nuclear encoded protein Method: similarity and extension |
| **13.** | [**isotig23822**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20110405/F014342.dat#Hit13) | 7764 | 30 | putative nuclear encoded protein Method: Longest ORF |
| **14.** | [**isotig09183**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20110405/F014342.dat#Hit14) | 15917 | 29 | putative nuclear encoded protein Method: similarity and extension |
| **15.** | [**isotig22068**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20110405/F014342.dat#Hit15) | 14276 | 29 | putative nuclear encoded protein Method: similarity and extension |
| **16.** | [**isotig11130**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20110405/F014342.dat#Hit16) | 16647 | 29 | putative nuclear encoded protein Method: Longest ORF |
| **17.** | [**isotig11131**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20110405/F014342.dat#Hit17) | 16647 | 29 | putative nuclear encoded protein Method: Longest ORF |
| **18.** | [**isotig11129**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20110405/F014342.dat#Hit18) | 16647 | 29 | putative nuclear encoded protein Method: Longest ORF |
| **19.** | [**isotig16778**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20110405/F014342.dat#Hit19) | 15285 | 28 | putative nuclear encoded protein Method: Longest ORF |
| **20.** | [**isotig14853**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20110405/F014342.dat#Hit20) | 55385 | 28 | putative nuclear encoded protein Method: similarity and extension |

**Results List**

|  |  |
| --- | --- |
| **1.** | [isotig09711](http://msmsms/mascot/cgi/protein_view.pl?file=../data/20110405/F014342.dat&hit=1" \t "_blank)    **Mass:** 28342    **Score:** 189    **Expect:** 4.3e-015  **Matches:** 20 |
|  | putative nuclear encoded protein Method: similarity and extension |

|  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | **Observed** | **Mr(expt)** | **Mr(calc)** | **ppm** | **Start** |  | **End** | **Miss** | **Ions** | **Peptide** |
|  | 1125.4938 | 1124.4865 | 1124.5349 | -43.06 | 112 | - | 121 | 1 | --- | K.ESGDKEGIYK.K |
|  | 1328.6719 | 1327.6646 | 1327.7248 | -45.32 | 15 | - | 25 | 1 | --- | R.HYIREILGAEK.A |
|  | 1371.6506 | 1370.6433 | 1370.7306 | -63.68 | 148 | - | 158 | 1 | --- | K.HYLREILGNEK.A |
|  | 1376.6470 | 1375.6397 | 1375.7095 | -50.76 | 19 | - | 30 | 1 | --- | R.EILGAEKADQFR.A |
|  | 1420.5522 | 1419.5449 | 1419.6994 | -108.79 | 152 | - | 163 | 1 | --- | R.EILGNEKADEFR.S |
|  | 1420.6383 | 1419.6310 | 1419.6994 | -48.14 | 152 | - | 163 | 1 | --- | R.EILGNEKADEFR.S |
|  | 1489.5988 | 1488.5915 | 1488.7572 | -111.32 | 82 | - | 94 | 0 | 27 | R.DHHPVTLEEALTK.Y |
|  | 1489.6842 | 1488.6769 | 1488.7572 | -53.95 | 82 | - | 94 | 0 | --- | R.DHHPVTLEEALTK.Y |
|  | 1535.6376 | 1534.6303 | 1534.7119 | -53.17 | 31 | - | 44 | 1 | --- | R.AMKESGTHMSEIAK.K + Oxidation (M) |
|  | 1546.6652 | 1545.6579 | 1545.7385 | -52.11 | 123 | - | 135 | 1 | --- | K.VMEYFEGITGEKK.E + Oxidation (M) |
|  | 1551.6384 | 1550.6311 | 1550.7068 | -48.83 | 31 | - | 44 | 1 | --- | R.AMKESGTHMSEIAK.K + 2 Oxidation (M) |
|  | 1618.7375 | 1617.7302 | 1617.8097 | -49.13 | 178 | - | 192 | 1 | --- | K.KVEEAIEGLTDESAK.M |
|  | 1646.7329 | 1645.7256 | 1645.7934 | -41.17 | 46 | - | 59 | 0 | --- | K.IEEAIEELTDEEVK.S |
|  | 1679.7544 | 1678.7471 | 1678.8018 | -32.57 | 31 | - | 45 | 2 | --- | R.AMKESGTHMSEIAKK.I + 2 Oxidation (M) |
|  | 1774.8002 | 1773.7929 | 1773.8883 | -53.79 | 45 | - | 59 | 1 | --- | K.KIEEAIEELTDEEVK.S |
|  | 1781.8120 | 1780.8047 | 1780.8883 | -46.92 | 95 | - | 108 | 1 | --- | K.YLTWLSDEQKEELK.S |
|  | 1803.7905 | 1802.7832 | 1802.8760 | -51.47 | 123 | - | 137 | 2 | --- | K.VMEYFEGITGEKKEK.A + Oxidation (M) |
|  | 1889.8527 | 1888.8454 | 1888.9265 | -42.93 | 46 | - | 61 | 1 | --- | K.IEEAIEELTDEEVKSR.A |
|  | 2017.8170 | 2016.8097 | 2017.0215 | -104.98 | 45 | - | 61 | 2 | 80 | K.KIEEAIEELTDEEVKSR.A |
|  | 2017.9396 | 2016.9323 | 2017.0215 | -44.20 | 45 | - | 61 | 2 | --- | K.KIEEAIEELTDEEVKSR.A |

|  |  |
| --- | --- |
|  | **No match to:** 1045.5198, 1131.4932, 1300.5394, 1455.6053, 1485.6249, 1499.6418, 1518.6420, 1550.6573, 1563.6421, 1581.7767, 1583.7233, 1605.7642, 1617.7091, 1619.5112, 1619.6438, 1626.7407, 1672.7253, 1708.6903, 1767.7891, 1775.7759, 2031.9420, 2210.9919 |

|  |  |
| --- | --- |
| **2.** | [isotig09712](http://msmsms/mascot/cgi/protein_view.pl?file=../data/20110405/F014342.dat&hit=2" \t "_blank)    **Mass:** 30518    **Score:** 189    **Expect:** 4.3e-015  **Matches:** 20 |
|  | putative nuclear encoded protein Method: similarity and extension |

|  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | **Observed** | **Mr(expt)** | **Mr(calc)** | **ppm** | **Start** |  | **End** | **Miss** | **Ions** | **Peptide** |
|  | 1125.4938 | 1124.4865 | 1124.5349 | -43.06 | 245 | - | 254 | 1 | --- | K.ESGDKEGIYK.K |
|  | 1328.6719 | 1327.6646 | 1327.7248 | -45.32 | 15 | - | 25 | 1 | --- | R.HYIREILGAEK.A |
|  | 1371.6506 | 1370.6433 | 1370.7306 | -63.68 | 148 | - | 158 | 1 | --- | K.HYLREILGNEK.A |
|  | 1376.6470 | 1375.6397 | 1375.7095 | -50.76 | 19 | - | 30 | 1 | --- | R.EILGAEKADQFR.A |
|  | 1420.5522 | 1419.5449 | 1419.6994 | -108.79 | 152 | - | 163 | 1 | --- | R.EILGNEKADEFR.S |
|  | 1420.6383 | 1419.6310 | 1419.6994 | -48.14 | 152 | - | 163 | 1 | --- | R.EILGNEKADEFR.S |
|  | 1489.5988 | 1488.5915 | 1488.7572 | -111.32 | 82 | - | 94 | 0 | 27 | R.DHHPVTLEEALTK.Y |
|  | 1489.6842 | 1488.6769 | 1488.7572 | -53.95 | 215 | - | 227 | 0 | --- | R.DHHPVTLEEALTK.Y |
|  | 1535.6376 | 1534.6303 | 1534.7119 | -53.17 | 31 | - | 44 | 1 | --- | R.AMKESGTHMSEIAK.K + Oxidation (M) |
|  | 1546.6652 | 1545.6579 | 1545.7385 | -52.11 | 123 | - | 135 | 1 | --- | K.VMEYFEGITGEKK.E + Oxidation (M) |
|  | 1551.6384 | 1550.6311 | 1550.7068 | -48.83 | 31 | - | 44 | 1 | --- | R.AMKESGTHMSEIAK.K + 2 Oxidation (M) |
|  | 1618.7375 | 1617.7302 | 1617.8097 | -49.13 | 178 | - | 192 | 1 | --- | K.KVEEAIEGLTDESAK.M |
|  | 1646.7329 | 1645.7256 | 1645.7934 | -41.17 | 46 | - | 59 | 0 | --- | K.IEEAIEELTDEEVK.S |
|  | 1679.7544 | 1678.7471 | 1678.8018 | -32.57 | 31 | - | 45 | 2 | --- | R.AMKESGTHMSEIAKK.I + 2 Oxidation (M) |
|  | 1774.8002 | 1773.7929 | 1773.8883 | -53.79 | 45 | - | 59 | 1 | --- | K.KIEEAIEELTDEEVK.S |
|  | 1781.8120 | 1780.8047 | 1780.8883 | -46.92 | 95 | - | 108 | 1 | --- | K.YLTWLSDEQKEELK.S |
|  | 1803.7905 | 1802.7832 | 1802.8760 | -51.47 | 123 | - | 137 | 2 | --- | K.VMEYFEGITGEKKEK.A + Oxidation (M) |
|  | 1889.8527 | 1888.8454 | 1888.9265 | -42.93 | 46 | - | 61 | 1 | --- | K.IEEAIEELTDEEVKSR.A |
|  | 2017.8170 | 2016.8097 | 2017.0215 | -104.98 | 45 | - | 61 | 2 | 80 | K.KIEEAIEELTDEEVKSR.A |
|  | 2017.9396 | 2016.9323 | 2017.0215 | -44.20 | 45 | - | 61 | 2 | --- | K.KIEEAIEELTDEEVKSR.A |

|  |  |
| --- | --- |
|  | **No match to:** 1045.5198, 1131.4932, 1300.5394, 1455.6053, 1485.6249, 1499.6418, 1518.6420, 1550.6573, 1563.6421, 1581.7767, 1583.7233, 1605.7642, 1617.7091, 1619.5112, 1619.6438, 1626.7407, 1672.7253, 1708.6903, 1767.7891, 1775.7759, 2031.9420, 2210.9919 |

**http://msmsms/mascot/images/88x31_logo_white.gifMascot Search Results**

**Protein View**

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Match to: **isotig09711** Score: **189** Expect: **4.3e-015**

**putative nuclear encoded protein Method: similarity and extension**

Nominal mass (Mr): **28342**; Calculated pI value: **8.24**

NCBI BLAST search of [isotig09711](http://www.ncbi.nlm.nih.gov/blast/Blast.cgi?ALIGNMENTS=50&ALIGNMENT_VIEW=Pairwise&AUTO_FORMAT=Semiauto&CDD_SEARCH=on&CLIENT=web&COMPOSITION_BASED_STATISTICS=on&DATABASE=nr&DESCRIPTIONS=100&ENTREZ_QUERY=(none)&EXPECT=10&FILTER=L&FORMAT_BLOCK_ON_RESPAGE=None&FORMAT_OBJECT=Alignment&FORMAT_TYPE=HTML&GAPCOSTS=11+1&I_THRESH=0.001&LAYOUT=TwoWindows&MATRIX_NAME=BLOSUM62&NCBI_GI=on&PAGE=Proteins&PROGRAM=blastp&QUERY=KKEKASEELQSGCRHYIREILGAEKADQFRAMKESGTHMSEIAKKIEEAIEELTDEEVKSRAKKASVACKRIFGVAHRFRRDHHPVTLEEALTKYLTWLSDEQKEELKSMKESGDKEGIYKKVMEYFEGITGEKKEKATEELRAACKHYLREILGNEKADEFRSMKESGTPEEEIAKKVEEAIEGLTDESAKMRGKKASAACKRIFGVARRFRRDHHPVTSGGGSHEVPHLAKRRAEGGIEVDERERR&SERVICE=plain&SET_DEFAULTS.x=9&SET_DEFAULTS.y=5&SHOW_OVERVIEW=on&WORD_SIZE=3&END_OF_HTTPGET=Yes" \t "_blank) against nr

Unformatted [sequence string](http://msmsms/mascot/cgi/getseq.pl?cooperia_oncophora+isotig09711+seq" \t "_blank) for pasting into other applications

Variable modifications: Oxidation (HW),Oxidation (M)

Cleavage by Trypsin/P: cuts C-term side of KR

Sequence Coverage: **52%**

Matched peptides shown in **Bold Red**

**1** KKEKASEELQ SGCR**HYIREI LGAEKADQFR AMKESGTHMS EIAKKIEEAI**

**51 EELTDEEVKS R**AKKASVACK RIFGVAHRFR R**DHHPVTLEE ALTKYLTWLS**

**101 DEQKEELK**SM K**ESGDKEGIY K**K**VMEYFEGI TGEKKEK**ATE ELRAACK**HYL**

**151 REILGNEKAD EFR**SMKESGT PEEEIAK**KVE EAIEGLTDES AK**MRGKKASA

**201** ACKRIFGVAR RFRRDHHPVT SGGGSHEVPH LAKRRAEGGI EVDERERR



  Residue Number  Increasing Mass  Decreasing Mass

**Start - End Observed Mr(expt) Mr(calc) ppm Miss Sequence**

**15 - 25 1328.6719 1327.6646 1327.7248 -45 1 R.HYIREILGAEK.A**  ([No match](http://msmsms/mascot/cgi/peptide_view.pl?file=../data/20110405/F014342.dat&query=5&hit=1" \t "_blank))

**19 - 30 1376.6470 1375.6397 1375.7095 -51 1 R.EILGAEKADQFR.A**  ([No match](http://msmsms/mascot/cgi/peptide_view.pl?file=../data/20110405/F014342.dat&query=7&hit=1" \t "_blank))

**31 - 44 1535.6376 1534.6303 1534.7119 -53 1 R.AMKESGTHMSEIAK.K**  Oxidation (M) ([No match](http://msmsms/mascot/cgi/peptide_view.pl?file=../data/20110405/F014342.dat&query=16&hit=1" \t "_blank))

**31 - 44 1551.6384 1550.6311 1550.7068 -49 1 R.AMKESGTHMSEIAK.K**  2 Oxidation (M) ([No match](http://msmsms/mascot/cgi/peptide_view.pl?file=../data/20110405/F014342.dat&query=19&hit=1" \t "_blank))

**31 - 45 1679.7544 1678.7471 1678.8018 -33 2 R.AMKESGTHMSEIAKK.I**  2 Oxidation (M) ([No match](http://msmsms/mascot/cgi/peptide_view.pl?file=../data/20110405/F014342.dat&query=31&hit=1" \t "_blank))

**45 - 59 1774.8002 1773.7929 1773.8883 -54 1 K.KIEEAIEELTDEEVK.S**  ([No match](http://msmsms/mascot/cgi/peptide_view.pl?file=../data/20110405/F014342.dat&query=34&hit=1" \t "_blank))

**45 - 61 2017.8170 2016.8097 2017.0215 -105 2 K.KIEEAIEELTDEEVKSR.A**  ([Ions score 80](http://msmsms/mascot/cgi/peptide_view.pl?file=../data/20110405/F014342.dat&query=39&hit=1" \t "_blank))

**45 - 61 2017.9396 2016.9323 2017.0215 -44 2 K.KIEEAIEELTDEEVKSR.A**  ([No match](http://msmsms/mascot/cgi/peptide_view.pl?file=../data/20110405/F014342.dat&query=40&hit=1" \t "_blank))

**46 - 59 1646.7329 1645.7256 1645.7934 -41 0 K.IEEAIEELTDEEVK.S**  ([No match](http://msmsms/mascot/cgi/peptide_view.pl?file=../data/20110405/F014342.dat&query=29&hit=1" \t "_blank))

**46 - 61 1889.8527 1888.8454 1888.9265 -43 1 K.IEEAIEELTDEEVKSR.A**  ([No match](http://msmsms/mascot/cgi/peptide_view.pl?file=../data/20110405/F014342.dat&query=38&hit=1" \t "_blank))

**82 - 94 1489.5988 1488.5915 1488.7572 -111 0 R.DHHPVTLEEALTK.Y**  ([Ions score 27](http://msmsms/mascot/cgi/peptide_view.pl?file=../data/20110405/F014342.dat&query=12&hit=1" \t "_blank))

**82 - 94 1489.6842 1488.6769 1488.7572 -54 0 R.DHHPVTLEEALTK.Y**  ([No match](http://msmsms/mascot/cgi/peptide_view.pl?file=../data/20110405/F014342.dat&query=13&hit=1" \t "_blank))

**95 - 108 1781.8120 1780.8047 1780.8883 -47 1 K.YLTWLSDEQKEELK.S**  ([No match](http://msmsms/mascot/cgi/peptide_view.pl?file=../data/20110405/F014342.dat&query=36&hit=1" \t "_blank))

**112 - 121 1125.4938 1124.4865 1124.5349 -43 1 K.ESGDKEGIYK.K**  ([No match](http://msmsms/mascot/cgi/peptide_view.pl?file=../data/20110405/F014342.dat&query=2&hit=1" \t "_blank))

**123 - 135 1546.6652 1545.6579 1545.7385 -52 1 K.VMEYFEGITGEKK.E**  Oxidation (M) ([No match](http://msmsms/mascot/cgi/peptide_view.pl?file=../data/20110405/F014342.dat&query=17&hit=1" \t "_blank))

**123 - 137 1803.7905 1802.7832 1802.8760 -51 2 K.VMEYFEGITGEKKEK.A**  Oxidation (M) ([No match](http://msmsms/mascot/cgi/peptide_view.pl?file=../data/20110405/F014342.dat&query=37&hit=1" \t "_blank))

**148 - 158 1371.6506 1370.6433 1370.7306 -64 1 K.HYLREILGNEK.A**  ([No match](http://msmsms/mascot/cgi/peptide_view.pl?file=../data/20110405/F014342.dat&query=6&hit=1" \t "_blank))

**152 - 163 1420.5522 1419.5449 1419.6994 -109 1 R.EILGNEKADEFR.S**  ([No match](http://msmsms/mascot/cgi/peptide_view.pl?file=../data/20110405/F014342.dat&query=8&hit=1" \t "_blank))

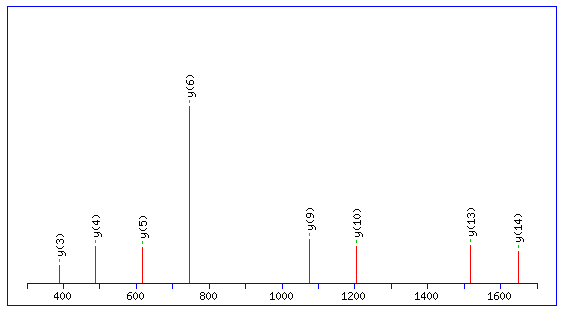
**152 - 163 1420.6383 1419.6310 1419.6994 -48 1 R.EILGNEKADEFR.S**  ([No match](http://msmsms/mascot/cgi/peptide_view.pl?file=../data/20110405/F014342.dat&query=9&hit=1" \t "_blank))

**178 - 192 1618.7375 1617.7302 1617.8097 -49 1 K.KVEEAIEGLTDESAK.M**  ([No match](http://msmsms/mascot/cgi/peptide_view.pl?file=../data/20110405/F014342.dat&query=25&hit=1" \t "_blank))



Bottom of Form

🡪 Annotated MS2 spectrum for peptide KIEEAIEELTDEEVKSR



**Monoisotopic mass of neutral peptide Mr(calc):** 2017.0215

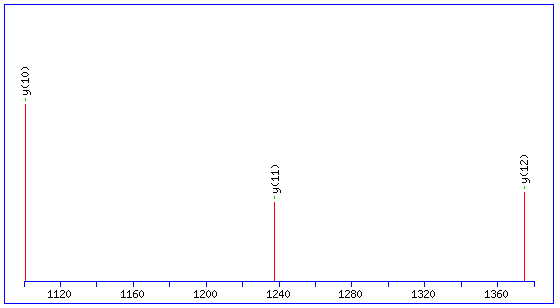
**Ions Score:** 80 **Expect:** 9.2e-007

**Matches :** 8/305 fragment ions using 8 most intense peaks   ([help](http://msmsms/mascot/help/results_help.html" \l "PEP" \t "_blank))

|  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **#** | **Immon.** | **a** | **a\*** | **a0** | **b** | **b\*** | **b0** | **Seq.** | **v** | **w** | **w'** | **y** | **y\*** | **y0** | **#** |
| **1** | 101.1073 | 101.1073 | 84.0808 |  | 129.1022 | 112.0757 |  | **K** |  |  |  |  |  |  | **17** |
| **2** | 86.0964 | 214.1914 | 197.1648 |  | 242.1863 | 225.1598 |  | **I** | 1831.8556 | 1844.8760 | 1858.8916 | 1889.9338 | 1872.9073 | 1871.9233 | **16** |
| **3** | 102.0550 | 343.2340 | 326.2074 | 325.2234 | 371.2289 | 354.2023 | 353.2183 | **E** | 1702.8130 | 1701.8178 |  | 1776.8498 | 1759.8232 | 1758.8392 | **15** |
| **4** | 102.0550 | 472.2766 | 455.2500 | 454.2660 | 500.2715 | 483.2449 | 482.2609 | **E** | 1573.7704 | 1572.7752 |  | ***1647.8072*** | 1630.7806 | 1629.7966 | **14** |
| **5** | 44.0495 | 543.3137 | 526.2871 | 525.3031 | 571.3086 | 554.2821 | 553.2980 | **A** | 1502.7333 |  |  | ***1518.7646*** | 1501.7380 | 1500.7540 | **13** |
| **6** | 86.0964 | 656.3978 | 639.3712 | 638.3872 | 684.3927 | 667.3661 | 666.3821 | **I** | 1389.6492 | 1402.6696 | 1416.6853 | 1447.7275 | 1430.7009 | 1429.7169 | **12** |
| **7** | 102.0550 | 785.4403 | 768.4138 | 767.4298 | 813.4353 | 796.4087 | 795.4247 | **E** | 1260.6066 | 1259.6114 |  | 1334.6434 | 1317.6169 | 1316.6329 | **11** |
| **8** | 102.0550 | 914.4829 | 897.4564 | 896.4724 | 942.4779 | 925.4513 | 924.4673 | **E** | 1131.5640 | 1130.5688 |  | ***1205.6008*** | 1188.5743 | 1187.5903 | **10** |
| **9** | 86.0964 | 1027.5670 | 1010.5405 | 1009.5564 | 1055.5619 | 1038.5354 | 1037.5514 | **L** | 1018.4800 | 1017.4847 |  | ***1076.5582*** | 1059.5317 | 1058.5477 | **9** |
| **10** | 74.0600 | 1128.6147 | 1111.5881 | 1110.6041 | 1156.6096 | 1139.5830 | 1138.5990 | **T** | 917.4323 | 930.4527 | 932.4320 | 963.4742 | 946.4476 | 945.4636 | **8** |
| **11** | 88.0393 | 1243.6416 | 1226.6151 | 1225.6311 | 1271.6365 | 1254.6100 | 1253.6260 | **D** | 802.4054 | 801.4101 |  | 862.4265 | 845.3999 | 844.4159 | **7** |
| **12** | 102.0550 | 1372.6842 | 1355.6577 | 1354.6737 | 1400.6791 | 1383.6526 | 1382.6686 | **E** | 673.3628 | 672.3675 |  | ***747.3995*** | 730.3730 | 729.3890 | **6** |
| **13** | 102.0550 | 1501.7268 | 1484.7003 | 1483.7162 | 1529.7217 | 1512.6952 | 1511.7112 | **E** | 544.3202 | 543.3249 |  | ***618.3570*** | 601.3304 | 600.3464 | **5** |
| **14** | 72.0808 | 1600.7952 | 1583.7687 | 1582.7847 | 1628.7901 | 1611.7636 | 1610.7796 | **V** | 445.2518 | 458.2722 |  | ***489.3144*** | 472.2878 | 471.3038 | **4** |
| **15** | 101.1073 | 1728.8902 | 1711.8636 | 1710.8796 | 1756.8851 | 1739.8586 | 1738.8745 | **K** | 317.1568 | 316.1615 |  | ***390.2459*** | 373.2194 | 372.2354 | **3** |
| **16** | 60.0444 | 1815.9222 | 1798.8957 | 1797.9117 | 1843.9171 | 1826.8906 | 1825.9066 | **S** | 230.1248 | 229.1295 |  | 262.1510 | 245.1244 | 244.1404 | **2** |
| **17** | 129.1135 |  |  |  |  |  |  | **R** | 74.0237 | 73.0284 |  | 175.1190 | 158.0924 |  | **1** |

|  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **Seq** | **ya** | **yb** | **Seq** | **ya** | **yb** | **Seq** | **ya** | **yb** |
| **IE** | 215.1390 | 243.1339 | **IEE** | 344.1816 | 372.1765 | **IEEA** | 415.2187 | 443.2136 |
| **IEEAI** | 528.3028 | 556.2977 | **IEEAIE** | 657.3454 | 685.3403 | **EE** | 231.0975 | 259.0925 |
| **EEA** | 302.1347 | 330.1296 | **EEAI** | 415.2187 | 443.2136 | **EEAIE** | 544.2613 | 572.2562 |
| **EEAIEE** | 673.3039 | 701.2988 | **EA** | 173.0921 | 201.0870 | **EAI** | 286.1761 | 314.1710 |
| **EAIE** | 415.2187 | 443.2136 | **EAIEE** | 544.2613 | 572.2562 | **EAIEEL** | 657.3454 | 685.3403 |
| **AI** | 157.1335 | 185.1285 | **AIE** | 286.1761 | 314.1710 | **AIEE** | 415.2187 | 443.2136 |
| **AIEEL** | 528.3028 | 556.2977 | **AIEELT** | 629.3505 | 657.3454 | **IE** | 215.1390 | 243.1339 |
| **IEE** | 344.1816 | 372.1765 | **IEEL** | 457.2657 | 485.2606 | **IEELT** | 558.3134 | 586.3083 |
| **IEELTD** | 673.3403 | 701.3352 | **EE** | 231.0975 | 259.0925 | **EEL** | 344.1816 | 372.1765 |
| **EELT** | 445.2293 | 473.2242 | **EELTD** | 560.2562 | 588.2511 | **EELTDE** | 689.2988 | 717.2937 |
| **EL** | 215.1390 | 243.1339 | **ELT** | 316.1867 | 344.1816 | **ELTD** | 431.2136 | 459.2086 |
| **ELTDE** | 560.2562 | 588.2511 | **ELTDEE** | 689.2988 | 717.2937 | **LT** | 187.1441 | 215.1390 |
| **LTD** | 302.1710 | 330.1660 | **LTDE** | 431.2136 | 459.2086 | **LTDEE** | 560.2562 | 588.2511 |
| **LTDEEV** | 659.3246 | 687.3196 | **TD** | 189.0870 | 217.0819 | **TDE** | 318.1296 | 346.1245 |
| **TDEE** | 447.1722 | 475.1671 | **TDEEV** | 546.2406 | 574.2355 | **TDEEVK** | 674.3355 | 702.3305 |
| **DE** | 217.0819 | 245.0768 | **DEE** | 346.1245 | 374.1194 | **DEEV** | 445.1929 | 473.1878 |
| **DEEVK** | 573.2879 | 601.2828 | **DEEVKS** | 660.3199 | 688.3148 | **EE** | 231.0975 | 259.0925 |
| **EEV** | 330.1660 | 358.1609 | **EEVK** | 458.2609 | 486.2558 | **EEVKS** | 545.2930 | 573.2879 |
| **EV** | 201.1234 | 229.1183 | **EVK** | 329.2183 | 357.2132 | **EVKS** | 416.2504 | 444.2453 |
| **VK** | 200.1757 | 228.1707 | **VKS** | 287.2078 | 315.2027 | **KS** | 188.1394 | 216.1343 |

🡪 Annotated MS2 spectrum for peptide DHHPVTLEEALTK



**Monoisotopic mass of neutral peptide Mr(calc):** 1488.7572

**Ions Score:** 27 **Expect:** 0.17

**Matches :** 3/176 fragment ions using 3 most intense peaks   ([help](http://msmsms/mascot/help/results_help.html" \l "PEP" \t "_blank))

|  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **#** | **Immon.** | **a** | **a0** | **b** | **b0** | **Seq.** | **y** | **y\*** | **y0** | **#** |
| **1** | 88.0393 | 88.0393 | 70.0287 | 116.0342 | 98.0237 | **D** |  |  |  | **13** |
| **2** | 110.0713 | 225.0982 | 207.0877 | 253.0931 | 235.0826 | **H** | ***1374.7376*** | 1357.7110 | 1356.7270 | **12** |
| **3** | 110.0713 | 362.1571 | 344.1466 | 390.1520 | 372.1415 | **H** | ***1237.6787*** | 1220.6521 | 1219.6681 | **11** |
| **4** | 70.0651 | 459.2099 | 441.1993 | 487.2048 | 469.1942 | **P** | ***1100.6198*** | 1083.5932 | 1082.6092 | **10** |
| **5** | 72.0808 | 558.2783 | 540.2677 | 586.2732 | 568.2627 | **V** | 1003.5670 | 986.5405 | 985.5564 | **9** |
| **6** | 74.0600 | 659.3260 | 641.3154 | 687.3209 | 669.3103 | **T** | 904.4986 | 887.4720 | 886.4880 | **8** |
| **7** | 86.0964 | 772.4100 | 754.3995 | 800.4050 | 782.3944 | **L** | 803.4509 | 786.4244 | 785.4403 | **7** |
| **8** | 102.0550 | 901.4526 | 883.4421 | 929.4476 | 911.4370 | **E** | 690.3668 | 673.3403 | 672.3563 | **6** |
| **9** | 102.0550 | 1030.4952 | 1012.4847 | 1058.4902 | 1040.4796 | **E** | 561.3243 | 544.2977 | 543.3137 | **5** |
| **10** | 44.0495 | 1101.5323 | 1083.5218 | 1129.5273 | 1111.5167 | **A** | 432.2817 | 415.2551 | 414.2711 | **4** |
| **11** | 86.0964 | 1214.6164 | 1196.6058 | 1242.6113 | 1224.6008 | **L** | 361.2445 | 344.2180 | 343.2340 | **3** |
| **12** | 74.0600 | 1315.6641 | 1297.6535 | 1343.6590 | 1325.6484 | **T** | 248.1605 | 231.1339 | 230.1499 | **2** |
| **13** | 101.1073 |  |  |  |  | **K** | 147.1128 | 130.0863 |  | **1** |

|  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **Seq** | **ya** | **yb** | **Seq** | **ya** | **yb** | **Seq** | **ya** | **yb** |
| **HH** | 247.1302 | 275.1251 | **HHP** | 344.1829 | 372.1779 | **HHPV** | 443.2514 | 471.2463 |
| **HHPVT** | 544.2990 | 572.2940 | **HHPVTL** | 657.3831 | 685.3780 | **HP** | 207.1240 | 235.1190 |
| **HPV** | 306.1925 | 334.1874 | **HPVT** | 407.2401 | 435.2350 | **HPVTL** | 520.3242 | 548.3191 |
| **HPVTLE** | 649.3668 | 677.3617 | **PV** | 169.1335 | 197.1285 | **PVT** | 270.1812 | 298.1761 |
| **PVTL** | 383.2653 | 411.2602 | **PVTLE** | 512.3079 | 540.3028 | **PVTLEE** | 641.3505 | 669.3454 |
| **VT** | 173.1285 | 201.1234 | **VTL** | 286.2125 | 314.2074 | **VTLE** | 415.2551 | 443.2500 |
| **VTLEE** | 544.2977 | 572.2926 | **VTLEEA** | 615.3348 | 643.3297 | **TL** | 187.1441 | 215.1390 |
| **TLE** | 316.1867 | 344.1816 | **TLEE** | 445.2293 | 473.2242 | **TLEEA** | 516.2664 | 544.2613 |
| **TLEEAL** | 629.3505 | 657.3454 | **LE** | 215.1390 | 243.1339 | **LEE** | 344.1816 | 372.1765 |
| **LEEA** | 415.2187 | 443.2136 | **LEEAL** | 528.3028 | 556.2977 | **LEEALT** | 629.3505 | 657.3454 |
| **EE** | 231.0975 | 259.0925 | **EEA** | 302.1347 | 330.1296 | **EEAL** | 415.2187 | 443.2136 |
| **EEALT** | 516.2664 | 544.2613 | **EA** | 173.0921 | 201.0870 | **EAL** | 286.1761 | 314.1710 |
| **EALT** | 387.2238 | 415.2187 | **AL** | 157.1335 | 185.1285 | **ALT** | 258.1812 | 286.1761 |
| **LT** | 187.1441 | 215.1390 |  |  |  |  |  |  |

**Spot 12:**

**http://msmsms/mascot/images/88x31_logo_white.gifMascot Search Results**

**User :**

**Email :**

**Search title : SampleSetID: 341, AnalysisID: 800, MaldiWellID: 45084, SpectrumID: 175241, Path=\Jimmy\Cooperia Adult ES 20110221\20110509 1st experiment (repeat)**

**Database : cooperia\_oncophora oncophora\_20110405 (34373 sequences; 5289600 residues)**

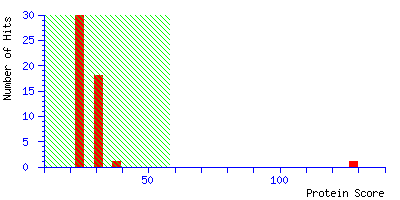
**Timestamp : 9 May 2011 at 12:39:15 GMT**

**Warning : A Peptide summary report will usually give a much clearer picture of MS/MS search results.**

**Top Score : 128 for gi|4097673|gb|AAD09213.1|, excretory/secretory antigen 2 protein [Cooperia oncophora]**

**Mascot Score Histogram**

Protein score is -10\*Log(P), where P is the probability that the observed match is a random event.  
Protein scores greater than 58 are significant (p<0.05).  
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



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**Protein Summary Report**

|  |  |  |  |
| --- | --- | --- | --- |
|  |  |  | [Help](http://msmsms/mascot/help/msms_summaries_help.html" \t "_blank) |
|  | Significance threshold p< | Max. number of hits |  |

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**Index**

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
|  | **Accession** | **Mass** | **Score** | **Description** |
| **1.** | [**gi|4097673|gb|AAD09213.1|**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20110509/F014811.dat#Hit1) | 13189 | 128 | excretory/secretory antigen 2 protein [Cooperia oncophora] |
| **2.** | [**isotig19986**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20110509/F014811.dat#Hit2) | 6560 | 40 | putative nuclear encoded protein Method: Longest ORF |
| **3.** | [**isotig10634**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20110509/F014811.dat#Hit3) | 10681 | 33 | putative nuclear encoded protein Method: similarity and extension |
| **4.** | [**isotig10632**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20110509/F014811.dat#Hit4) | 10681 | 33 | putative nuclear encoded protein Method: similarity and extension |
| **5.** | [**isotig10633**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20110509/F014811.dat#Hit5) | 9785 | 33 | putative nuclear encoded protein Method: similarity and extension |
| **6.** | [**isotig24026**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20110509/F014811.dat#Hit6) | 17365 | 33 | putative nuclear encoded protein Method: similarity and extension |
| **7.** | [**isotig22471**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20110509/F014811.dat#Hit7) | 18077 | 31 | putative nuclear encoded protein Method: similarity and extension |
| **8.** | [**isotig23485**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20110509/F014811.dat#Hit8) | 15829 | 31 | putative nuclear encoded protein Method: Longest ORF |
| **9.** | [**isotig16062**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20110509/F014811.dat#Hit9) | 33748 | 31 | putative nuclear encoded protein Method: similarity and extension |
| **10.** | [**isotig26959**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20110509/F014811.dat#Hit10) | 6563 | 31 | putative nuclear encoded protein Method: Longest ORF |
| **11.** | [**isotig27845**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20110509/F014811.dat#Hit11) | 14440 | 31 | putative nuclear encoded protein Method: similarity and extension |
| **12.** | [**isotig10440**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20110509/F014811.dat#Hit12) | 8031 | 29 | putative nuclear encoded protein Method: similarity and extension |
| **13.** | [**isotig11652**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20110509/F014811.dat#Hit13) | 15984 | 29 | putative nuclear encoded protein Method: Longest ORF |
| **14.** | [**isotig11651**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20110509/F014811.dat#Hit14) | 16154 | 29 | putative nuclear encoded protein Method: Longest ORF |
| **15.** | [**isotig24149**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20110509/F014811.dat#Hit15) | 8170 | 29 | putative nuclear encoded protein Method: Longest ORF |
| **16.** | [**isotig03962**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20110509/F014811.dat#Hit16) | 9606 | 28 | putative nuclear encoded protein Method: Longest ORF |
| **17.** | [**isotig21077**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20110509/F014811.dat#Hit17) | 9143 | 28 | putative nuclear encoded protein Method: Longest ORF |
| **18.** | [**isotig13186**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20110509/F014811.dat#Hit18) | 35810 | 27 | putative nuclear encoded protein Method: similarity and extension |
| **19.** | [**isotig05611**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20110509/F014811.dat#Hit19) | 12739 | 27 | putative nuclear encoded protein Method: Longest ORF |
| **20.** | [**isotig05613**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20110509/F014811.dat#Hit20) | 12784 | 27 | putative nuclear encoded protein Method: Longest ORF |

**Results List**

|  |  |
| --- | --- |
| **1.** | [gi|4097673|gb|AAD09213.1|](http://msmsms/mascot/cgi/protein_view.pl?file=../data/20110509/F014811.dat&hit=1" \t "_blank)    **Mass:** 13189    **Score:** 128    **Expect:** 5.4e-009  **Matches:** 6 |
|  | excretory/secretory antigen 2 protein [Cooperia oncophora] |

|  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | **Observed** | **Mr(expt)** | **Mr(calc)** | **ppm** | **Start** |  | **End** | **Miss** | **Ions** | **Peptide** |
|  | 862.4548 | 861.4475 | 861.4708 | -27.07 | 67 | - | 74 | 0 | --- | K.YSGLPLGR.R |
|  | 1013.4508 | 1012.4435 | 1012.4614 | -17.65 | 19 | - | 26 | 0 | --- | R.EYIDFNGR.Y |
|  | 1112.4934 | 1111.4861 | 1111.4968 | -9.61 | 10 | - | 18 | 0 | --- | K.CTTYEPVSR.E + Carbamidomethyl (C) |
|  | 1951.9337 | 1950.9264 | 1950.9357 | -4.75 | 91 | - | 108 | 0 | --- | K.SLAPQTIYGCNSLVDGEK.L + Carbamidomethyl (C) |
|  | 1951.9337 | 1950.9264 | 1950.9357 | -4.75 | 91 | - | 108 | 0 | 82 | K.SLAPQTIYGCNSLVDGEK.L + Carbamidomethyl (C) |
|  | 2193.1008 | 2192.0935 | 2192.1147 | -9.66 | 91 | - | 110 | 1 | --- | K.SLAPQTIYGCNSLVDGEKLK.V + Carbamidomethyl (C) |

|  |  |
| --- | --- |
|  | **No match to:** 813.4390, 924.3797, 926.3813, 995.4397, 996.4244, 1014.4385, 1076.3667, 1095.4683, 1111.4985, 1138.5271, 1138.5271, 1152.5383, 1729.8175, 1860.9214 |

**http://msmsms/mascot/images/88x31_logo_white.gifMascot Search Results**

**Protein View**

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Match to: **gi|4097673|gb|AAD09213.1|** Score: **128** Expect: **5.4e-009**

**excretory/secretory antigen 2 protein [Cooperia oncophora]**

Nominal mass (Mr): **13189**; Calculated pI value: **5.56**

NCBI BLAST search of [gi|4097673|gb|AAD09213.1|](http://www.ncbi.nlm.nih.gov/blast/Blast.cgi?ALIGNMENTS=50&ALIGNMENT_VIEW=Pairwise&AUTO_FORMAT=Semiauto&CDD_SEARCH=on&CLIENT=web&COMPOSITION_BASED_STATISTICS=on&DATABASE=nr&DESCRIPTIONS=100&ENTREZ_QUERY=(none)&EXPECT=10&FILTER=L&FORMAT_BLOCK_ON_RESPAGE=None&FORMAT_OBJECT=Alignment&FORMAT_TYPE=HTML&GAPCOSTS=11+1&I_THRESH=0.001&LAYOUT=TwoWindows&MATRIX_NAME=BLOSUM62&NCBI_GI=on&PAGE=Proteins&PROGRAM=blastp&QUERY=NEYTDALAKCTTYEPVSREYIDFNGRYNPNLEWDNELSYAACYDLVGLEPNNVNVRYEAERTFAGKYSGLPLGRRVRVALAAGSGKNKIKSLAPQTIYGCNSLVDGEKLKVLCLYWE&SERVICE=plain&SET_DEFAULTS.x=9&SET_DEFAULTS.y=5&SHOW_OVERVIEW=on&WORD_SIZE=3&END_OF_HTTPGET=Yes" \t "_blank) against nr

Unformatted [sequence string](http://msmsms/mascot/cgi/getseq.pl?cooperia_oncophora+gi%7c4097673%7cgb%7cAAD09213%2e1%7c+seq" \t "_blank) for pasting into other applications

Variable modifications: Carbamidomethyl (C),Oxidation (HW),Oxidation (M)

Cleavage by Trypsin/P: cuts C-term side of KR

Sequence Coverage: **38%**

Matched peptides shown in **Bold Red**

**1** NEYTDALAK**C TTYEPVSREY IDFNGR**YNPN LEWDNELSYA ACYDLVGLEP

**51** NNVNVRYEAE RTFAGK**YSGL PLGR**RVRVAL AAGSGKNKIK **SLAPQTIYGC**

**101 NSLVDGEKLK** VLCLYWE



  Residue Number  Increasing Mass  Decreasing Mass

**Start - End Observed Mr(expt) Mr(calc) ppm Miss Sequence**

**10 - 18 1112.4934 1111.4861 1111.4968 -10 0 K.CTTYEPVSR.E**  Carbamidomethyl (C) ([No match](http://msmsms/mascot/cgi/peptide_view.pl?file=../data/20110509/F014811.dat&query=12&hit=1" \t "_blank))

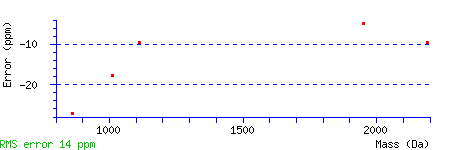
**19 - 26 1013.4508 1012.4435 1012.4614 -18 0 R.EYIDFNGR.Y**  ([No match](http://msmsms/mascot/cgi/peptide_view.pl?file=../data/20110509/F014811.dat&query=7&hit=1" \t "_blank))

**67 - 74 862.4548 861.4475 861.4708 -27 0 K.YSGLPLGR.R**  ([No match](http://msmsms/mascot/cgi/peptide_view.pl?file=../data/20110509/F014811.dat&query=2&hit=1" \t "_blank))

**91 - 108 1951.9337 1950.9264 1950.9357 -5 0 K.SLAPQTIYGCNSLVDGEK.L**  Carbamidomethyl (C) ([No match](http://msmsms/mascot/cgi/peptide_view.pl?file=../data/20110509/F014811.dat&query=18&hit=1" \t "_blank))

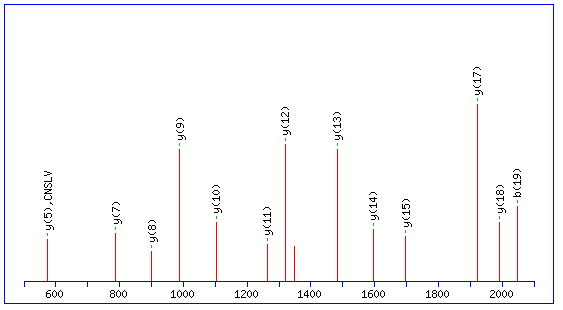
**91 - 108 1951.9337 1950.9264 1950.9357 -5 0 K.SLAPQTIYGCNSLVDGEK.L**  Carbamidomethyl (C) ([Ions score 82](http://msmsms/mascot/cgi/peptide_view.pl?file=../data/20110509/F014811.dat&query=19&hit=1" \t "_blank))

**91 - 110 2193.1008 2192.0935 2192.1147 -10 1 K.SLAPQTIYGCNSLVDGEKLK.V**  Carbamidomethyl (C) ([No match](http://msmsms/mascot/cgi/peptide_view.pl?file=../data/20110509/F014811.dat&query=20&hit=1" \t "_blank))



Bottom of Form

🡪 Annotated MS2 spectrum for peptide SLAPQTIYGCNSLVDGEK



**Monoisotopic mass of neutral peptide Mr(calc):** 2192.1147

**Variable modifications:**

**C10 :** Carbamidomethyl (C)

**Ions Score:** 116 **Expect:** 2.9e-010

**Matches :** 14/329 fragment ions using 14 most intense peaks   ([help](http://msmsms/mascot/help/results_help.html" \l "PEP" \t "_blank))

|  |  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **#** | **Immon.** | **a** | **a\*** | **a0** | **b** | **b\*** | **b0** | **Seq.** | **y** | **y\*** | **y0** | **#** |
| **1** | 60.0444 | 60.0444 |  | 42.0338 | 88.0393 |  | 70.0287 | **S** |  |  |  | **20** |
| **2** | 86.0964 | 173.1285 |  | 155.1179 | 201.1234 |  | 183.1128 | **L** | 2106.0900 | 2089.0634 | 2088.0794 | **19** |
| **3** | 44.0495 | 244.1656 |  | 226.1550 | 272.1605 |  | 254.1499 | **A** | ***1993.0059*** | 1975.9794 | 1974.9953 | **18** |
| **4** | 70.0651 | 341.2183 |  | 323.2078 | 369.2132 |  | 351.2027 | **P** | ***1921.9688*** | 1904.9422 | 1903.9582 | **17** |
| **5** | 101.0709 | 469.2769 | 452.2504 | 451.2663 | 497.2718 | 480.2453 | 479.2613 | **Q** | 1824.9160 | 1807.8895 | 1806.9055 | **16** |
| **6** | 74.0600 | 570.3246 | 553.2980 | 552.3140 | 598.3195 | 581.2930 | 580.3089 | **T** | ***1696.8574*** | 1679.8309 | 1678.8469 | **15** |
| **7** | 86.0964 | 683.4087 | 666.3821 | 665.3981 | 711.4036 | 694.3770 | 693.3930 | **I** | ***1595.8098*** | 1578.7832 | 1577.7992 | **14** |
| **8** | 136.0757 | 846.4720 | 829.4454 | 828.4614 | 874.4669 | 857.4403 | 856.4563 | **Y** | ***1482.7257*** | 1465.6992 | 1464.7151 | **13** |
| **9** | 30.0338 | 903.4934 | 886.4669 | 885.4829 | 931.4884 | 914.4618 | 913.4778 | **G** | ***1319.6624*** | 1302.6358 | 1301.6518 | **12** |
| **10** | 133.0430 | 1063.5241 | 1046.4975 | 1045.5135 | 1091.5190 | 1074.4925 | 1073.5084 | **C** | ***1262.6409*** | 1245.6144 | 1244.6303 | **11** |
| **11** | 87.0553 | 1177.5670 | 1160.5405 | 1159.5565 | 1205.5619 | 1188.5354 | 1187.5514 | **N** | ***1102.6103*** | 1085.5837 | 1084.5997 | **10** |
| **12** | 60.0444 | 1264.5990 | 1247.5725 | 1246.5885 | 1292.5940 | 1275.5674 | 1274.5834 | **S** | ***988.5673*** | 971.5408 | 970.5568 | **9** |
| **13** | 86.0964 | 1377.6831 | 1360.6566 | 1359.6725 | 1405.6780 | 1388.6515 | 1387.6675 | **L** | ***901.5353*** | 884.5088 | 883.5247 | **8** |
| **14** | 72.0808 | 1476.7515 | 1459.7250 | 1458.7410 | 1504.7464 | 1487.7199 | 1486.7359 | **V** | ***788.4512*** | 771.4247 | 770.4407 | **7** |
| **15** | 88.0393 | 1591.7785 | 1574.7519 | 1573.7679 | 1619.7734 | 1602.7468 | 1601.7628 | **D** | 689.3828 | 672.3563 | 671.3723 | **6** |
| **16** | 30.0338 | 1648.7999 | 1631.7734 | 1630.7894 | 1676.7948 | 1659.7683 | 1658.7843 | **G** | ***574.3559*** | 557.3293 | 556.3453 | **5** |
| **17** | 102.0550 | 1777.8425 | 1760.8160 | 1759.8320 | 1805.8374 | 1788.8109 | 1787.8269 | **E** | 517.3344 | 500.3079 | 499.3239 | **4** |
| **18** | 101.1073 | 1905.9375 | 1888.9109 | 1887.9269 | 1933.9324 | 1916.9059 | 1915.9218 | **K** | 388.2918 | 371.2653 |  | **3** |
| **19** | 86.0964 | 2019.0216 | 2001.9950 | 2001.0110 | 2047.0165 | 2029.9899 | 2029.0059 | **L** | 260.1969 | 243.1703 |  | **2** |
| **20** | 101.1073 |  |  |  |  |  |  | **K** | 147.1128 | 130.0863 |  | **1** |

|  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **Seq** | **ya** | **yb** | **Seq** | **ya** | **yb** | **Seq** | **ya** | **yb** |
| **LA** | 157.1335 | 185.1285 | **LAP** | 254.1863 | 282.1812 | **LAPQ** | 382.2449 | 410.2398 |
| **LAPQT** | 483.2926 | 511.2875 | **LAPQTI** | 596.3766 | 624.3715 | **AP** | 141.1022 | 169.0972 |
| **APQ** | 269.1608 | 297.1557 | **APQT** | 370.2085 | 398.2034 | **APQTI** | 483.2926 | 511.2875 |
| **APQTIY** | 646.3559 | 674.3508 | **PQ** | 198.1237 | 226.1186 | **PQT** | 299.1714 | 327.1663 |
| **PQTI** | 412.2554 | 440.2504 | **PQTIY** | 575.3188 | 603.3137 | **PQTIYG** | 632.3402 | 660.3352 |
| **QT** | 202.1186 | 230.1135 | **QTI** | 315.2027 | 343.1976 | **QTIY** | 478.2660 | 506.2609 |
| **QTIYG** | 535.2875 | 563.2824 | **QTIYGC** | 695.3181 | 723.3130 | **TI** | 187.1441 | 215.1390 |
| **TIY** | 350.2074 | 378.2023 | **TIYG** | 407.2289 | 435.2238 | **TIYGC** | 567.2595 | 595.2545 |
| **TIYGCN** | 681.3025 | 709.2974 | **IY** | 249.1598 | 277.1547 | **IYG** | 306.1812 | 334.1761 |
| **IYGC** | 466.2119 | 494.2068 | **IYGCN** | 580.2548 | 608.2497 | **IYGCNS** | 667.2868 | 695.2817 |
| **YG** | 193.0972 | 221.0921 | **YGC** | 353.1278 | 381.1227 | **YGCN** | 467.1707 | 495.1656 |
| **YGCNS** | 554.2028 | 582.1977 | **YGCNSL** | 667.2868 | 695.2817 | **GC** | 190.0645 | 218.0594 |
| **GCN** | 304.1074 | 332.1023 | **GCNS** | 391.1394 | 419.1343 | **GCNSL** | 504.2235 | 532.2184 |
| **GCNSLV** | 603.2919 | 631.2868 | **CN** | 247.0859 | 275.0809 | **CNS** | 334.1180 | 362.1129 |
| **CNSL** | 447.2020 | 475.1969 | **CNSLV** | 546.2704 | 574.2654 | **CNSLVD** | 661.2974 | 689.2923 |
| **NS** | 174.0873 | 202.0822 | **NSL** | 287.1714 | 315.1663 | **NSLV** | 386.2398 | 414.2347 |
| **NSLVD** | 501.2667 | 529.2617 | **NSLVDG** | 558.2882 | 586.2831 | **NSLVDGE** | 687.3308 | 715.3257 |
| **SL** | 173.1285 | 201.1234 | **SLV** | 272.1969 | 300.1918 | **SLVD** | 387.2238 | 415.2187 |
| **SLVDG** | 444.2453 | 472.2402 | **SLVDGE** | 573.2879 | 601.2828 | **LV** | 185.1648 | 213.1598 |
| **LVD** | 300.1918 | 328.1867 | **LVDG** | 357.2132 | 385.2082 | **LVDGE** | 486.2558 | 514.2508 |
| **LVDGEK** | 614.3508 | 642.3457 | **VD** | 187.1077 | 215.1026 | **VDG** | 244.1292 | 272.1241 |
| **VDGE** | 373.1718 | 401.1667 | **VDGEK** | 501.2667 | 529.2617 | **VDGEKL** | 614.3508 | 642.3457 |
| **DG** | 145.0608 | 173.0557 | **DGE** | 274.1034 | 302.0983 | **DGEK** | 402.1983 | 430.1932 |
| **DGEKL** | 515.2824 | 543.2773 | **GE** | 159.0764 | 187.0713 | **GEK** | 287.1714 | 315.1663 |
| **GEKL** | 400.2554 | 428.2504 | **EK** | 230.1499 | 258.1448 | **EKL** | 343.2340 | 371.2289 |
| **KL** | 214.1914 | 242.1863 |  |  |  |  |  |  |

**Spot 13:**

**http://msmsms/mascot/images/88x31_logo_white.gifMascot Search Results**

**User :**

**Email :**

**Search title : SampleSetID: 341, AnalysisID: 561, MaldiWellID: 45082, SpectrumID: 137487, Path=\Jimmy\Cooperia Adult ES 20110221\20110221 MS en MSMS**

**Database : cooperia\_oncophora oncophora (33747 sequences; 5232511 residues)**

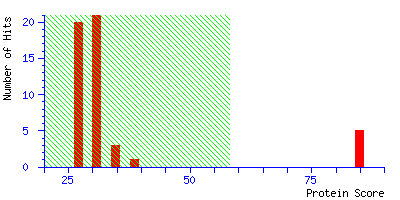
**Timestamp : 21 Feb 2011 at 15:38:16 GMT**

**Warning : A Peptide summary report will usually give a much clearer picture of MS/MS search results.**

**Top Score : 85 for isotig11584, putative nuclear encoded protein Method: similarity and extension**

**Mascot Score Histogram**

Protein score is -10\*Log(P), where P is the probability that the observed match is a random event.  
Protein scores greater than 58 are significant (p<0.05).  
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



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**Protein Summary Report**

|  |  |  |  |
| --- | --- | --- | --- |
|  |  |  | [Help](http://msmsms/mascot/help/msms_summaries_help.html" \t "_blank) |
|  | Significance threshold p< | Max. number of hits |  |

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**Index**

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
|  | **Accession** | **Mass** | **Score** | **Description** |
| **1.** | [**isotig11584**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20110221/F013490.dat#Hit1) | 14584 | 85 | putative nuclear encoded protein Method: similarity and extension |
| **2.** | [**isotig25277**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20110221/F013490.dat#Hit2) | 14624 | 85 | putative nuclear encoded protein Method: similarity and extension |
| **3.** | [**isotig26116**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20110221/F013490.dat#Hit3) | 14692 | 85 | putative nuclear encoded protein Method: similarity and extension |
| **4.** | [**isotig11583**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20110221/F013490.dat#Hit4) | 14759 | 85 | putative nuclear encoded protein Method: similarity and extension |
| **5.** | [**isotig11585**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20110221/F013490.dat#Hit5) | 14759 | 85 | putative nuclear encoded protein Method: similarity and extension |
| **6.** | [**isotig21970**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20110221/F013490.dat#Hit6) | 20044 | 37 | putative nuclear encoded protein Method: Longest ORF |
| **7.** | [**isotig12382**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20110221/F013490.dat#Hit7) | 9555 | 35 | putative nuclear encoded protein Method: Longest ORF |
| **8.** | [**isotig10145**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20110221/F013490.dat#Hit8) | 8103 | 33 | putative nuclear encoded protein Method: Longest ORF |
| **9.** | [**isotig10146**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20110221/F013490.dat#Hit9) | 8103 | 33 | putative nuclear encoded protein Method: Longest ORF |
| **10.** | [**isotig18536**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20110221/F013490.dat#Hit10) | 10824 | 33 | putative nuclear encoded protein Method: Longest ORF |
| **11.** | [**isotig28151**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20110221/F013490.dat#Hit11) | 24639 | 32 | putative nuclear encoded protein Method: similarity and extension |
| **12.** | [**isotig10633**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20110221/F013490.dat#Hit12) | 9785 | 32 | putative nuclear encoded protein Method: similarity and extension |
| **13.** | [**isotig18187**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20110221/F013490.dat#Hit13) | 11563 | 32 | putative nuclear encoded protein Method: Longest ORF |
| **14.** | [**isotig10634**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20110221/F013490.dat#Hit14) | 10681 | 31 | putative nuclear encoded protein Method: similarity and extension |
| **15.** | [**isotig10632**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20110221/F013490.dat#Hit15) | 10681 | 31 | putative nuclear encoded protein Method: similarity and extension |
| **16.** | [**isotig23275**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20110221/F013490.dat#Hit16) | 13558 | 31 | putative nuclear encoded protein Method: Longest ORF |
| **17.** | [**isotig28759**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20110221/F013490.dat#Hit17) | 12200 | 31 | putative nuclear encoded protein Method: ESTScan |
| **18.** | [**isotig32710**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20110221/F013490.dat#Hit18) | 24071 | 30 | putative nuclear encoded protein Method: ESTScan |
| **19.** | [**isotig22509**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20110221/F013490.dat#Hit19) | 15266 | 30 | putative nuclear encoded protein Method: ESTScan |
| **20.** | [**isotig12011**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20110221/F013490.dat#Hit20) | 6139 | 30 | putative nuclear encoded protein Method: Longest ORF |

**Results List**

|  |  |
| --- | --- |
| **1.** | [isotig11584](http://msmsms/mascot/cgi/protein_view.pl?file=../data/20110221/F013490.dat&hit=1" \t "_blank)    **Mass:** 14584    **Score:** 85     **Expect:** 0.00011  **Matches:** 2 |
|  | putative nuclear encoded protein Method: similarity and extension |

|  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | **Observed** | **Mr(expt)** | **Mr(calc)** | **ppm** | **Start** |  | **End** | **Miss** | **Ions** | **Peptide** |
|  | 1519.7924 | 1518.7851 | 1518.8154 | -19.94 | 88 | - | 100 | 2 | --- | R.AYKDKEAQVNVVR.N |
|  | 1519.7924 | 1518.7851 | 1518.8154 | -19.94 | 88 | - | 100 | 2 | 79 | R.AYKDKEAQVNVVR.N |

|  |  |
| --- | --- |
|  | **No match to:** 812.4753, 813.4131, 836.4561, 842.4882, 862.4514, 862.4514, 941.5311, 947.5113, 990.5525, 1013.4418, 1013.4418, 1014.4338, 1111.4664, 1112.4791, 1126.5089, 1138.5078, 1138.5078, 2075.8867, 2092.8987, 2193.0759 |

|  |  |
| --- | --- |
| **2.** | [isotig25277](http://msmsms/mascot/cgi/protein_view.pl?file=../data/20110221/F013490.dat&hit=2" \t "_blank)    **Mass:** 14624    **Score:** 85     **Expect:** 0.00011  **Matches:** 2 |
|  | putative nuclear encoded protein Method: similarity and extension |

|  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | **Observed** | **Mr(expt)** | **Mr(calc)** | **ppm** | **Start** |  | **End** | **Miss** | **Ions** | **Peptide** |
|  | 1519.7924 | 1518.7851 | 1518.8154 | -19.94 | 89 | - | 101 | 2 | --- | R.AYKDKEAQVNVVR.N |
|  | 1519.7924 | 1518.7851 | 1518.8154 | -19.94 | 89 | - | 101 | 2 | 79 | R.AYKDKEAQVNVVR.N |

|  |  |
| --- | --- |
|  | **No match to:** 812.4753, 813.4131, 836.4561, 842.4882, 862.4514, 862.4514, 941.5311, 947.5113, 990.5525, 1013.4418, 1013.4418, 1014.4338, 1111.4664, 1112.4791, 1126.5089, 1138.5078, 1138.5078, 2075.8867, 2092.8987, 2193.0759 |

|  |  |
| --- | --- |
| **3.** | [isotig26116](http://msmsms/mascot/cgi/protein_view.pl?file=../data/20110221/F013490.dat&hit=3" \t "_blank)    **Mass:** 14692    **Score:** 85     **Expect:** 0.00011  **Matches:** 2 |
|  | putative nuclear encoded protein Method: similarity and extension |

|  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | **Observed** | **Mr(expt)** | **Mr(calc)** | **ppm** | **Start** |  | **End** | **Miss** | **Ions** | **Peptide** |
|  | 1519.7924 | 1518.7851 | 1518.8154 | -19.94 | 89 | - | 101 | 2 | --- | R.AYKDKEAQVNVVR.N |
|  | 1519.7924 | 1518.7851 | 1518.8154 | -19.94 | 89 | - | 101 | 2 | 79 | R.AYKDKEAQVNVVR.N |

|  |  |
| --- | --- |
|  | **No match to:** 812.4753, 813.4131, 836.4561, 842.4882, 862.4514, 862.4514, 941.5311, 947.5113, 990.5525, 1013.4418, 1013.4418, 1014.4338, 1111.4664, 1112.4791, 1126.5089, 1138.5078, 1138.5078, 2075.8867, 2092.8987, 2193.0759 |

|  |  |
| --- | --- |
| **4.** | [isotig11583](http://msmsms/mascot/cgi/protein_view.pl?file=../data/20110221/F013490.dat&hit=4" \t "_blank)    **Mass:** 14759    **Score:** 85     **Expect:** 0.00011  **Matches:** 2 |
|  | putative nuclear encoded protein Method: similarity and extension |

|  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | **Observed** | **Mr(expt)** | **Mr(calc)** | **ppm** | **Start** |  | **End** | **Miss** | **Ions** | **Peptide** |
|  | 1519.7924 | 1518.7851 | 1518.8154 | -19.94 | 90 | - | 102 | 2 | --- | R.AYKDKEAQVNVVR.N |
|  | 1519.7924 | 1518.7851 | 1518.8154 | -19.94 | 90 | - | 102 | 2 | 79 | R.AYKDKEAQVNVVR.N |

|  |  |
| --- | --- |
|  | **No match to:** 812.4753, 813.4131, 836.4561, 842.4882, 862.4514, 862.4514, 941.5311, 947.5113, 990.5525, 1013.4418, 1013.4418, 1014.4338, 1111.4664, 1112.4791, 1126.5089, 1138.5078, 1138.5078, 2075.8867, 2092.8987, 2193.0759 |

|  |  |
| --- | --- |
| **5.** | [isotig11585](http://msmsms/mascot/cgi/protein_view.pl?file=../data/20110221/F013490.dat&hit=5" \t "_blank)    **Mass:** 14759    **Score:** 85     **Expect:** 0.00011  **Matches:** 2 |
|  | putative nuclear encoded protein Method: similarity and extension |

|  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | **Observed** | **Mr(expt)** | **Mr(calc)** | **ppm** | **Start** |  | **End** | **Miss** | **Ions** | **Peptide** |
|  | 1519.7924 | 1518.7851 | 1518.8154 | -19.94 | 90 | - | 102 | 2 | --- | R.AYKDKEAQVNVVR.N |
|  | 1519.7924 | 1518.7851 | 1518.8154 | -19.94 | 90 | - | 102 | 2 | 79 | R.AYKDKEAQVNVVR.N |

|  |  |
| --- | --- |
|  | **No match to:** 812.4753, 813.4131, 836.4561, 842.4882, 862.4514, 862.4514, 941.5311, 947.5113, 990.5525, 1013.4418, 1013.4418, 1014.4338, 1111.4664, 1112.4791, 1126.5089, 1138.5078, 1138.5078, 2075.8867, 2092.8987, 2193.0759 |

**http://msmsms/mascot/images/88x31_logo_white.gifMascot Search Results**

**Protein View**

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Match to: **isotig11584** Score: **85** Expect: **0.00011**

**putative nuclear encoded protein Method: similarity and extension**

Nominal mass (Mr): **14584**; Calculated pI value: **6.47**

NCBI BLAST search of [isotig11584](http://www.ncbi.nlm.nih.gov/blast/Blast.cgi?ALIGNMENTS=50&ALIGNMENT_VIEW=Pairwise&AUTO_FORMAT=Semiauto&CDD_SEARCH=on&CLIENT=web&COMPOSITION_BASED_STATISTICS=on&DATABASE=nr&DESCRIPTIONS=100&ENTREZ_QUERY=(none)&EXPECT=10&FILTER=L&FORMAT_BLOCK_ON_RESPAGE=None&FORMAT_OBJECT=Alignment&FORMAT_TYPE=HTML&GAPCOSTS=11+1&I_THRESH=0.001&LAYOUT=TwoWindows&MATRIX_NAME=BLOSUM62&NCBI_GI=on&PAGE=Proteins&PROGRAM=blastp&QUERY=LALTILCIFVMNAYANDCVPDFHQKHLYAKFHNGINNNLVWDEDLSERACEEAYGELGSHGFDKLEVEREVPKSLVRSSRIQRTLMRAYKDKEAQVNVVRNLPAGTKYGCNAVEIGDKTKVVCLYEKQ&SERVICE=plain&SET_DEFAULTS.x=9&SET_DEFAULTS.y=5&SHOW_OVERVIEW=on&WORD_SIZE=3&END_OF_HTTPGET=Yes" \t "_blank) against nr

Unformatted [sequence string](http://msmsms/mascot/cgi/getseq.pl?cooperia_oncophora+isotig11584+seq" \t "_blank) for pasting into other applications

Variable modifications: Oxidation (HW),Oxidation (M)

Cleavage by Trypsin/P: cuts C-term side of KR

Sequence Coverage: **10%**

Matched peptides shown in **Bold Red**

**1** LALTILCIFV MNAYANDCVP DFHQKHLYAK FHNGINNNLV WDEDLSERAC

**51** EEAYGELGSH GFDKLEVERE VPKSLVRSSR IQRTLMR**AYK DKEAQVNVVR**

**101** NLPAGTKYGC NAVEIGDKTK VVCLYEKQ



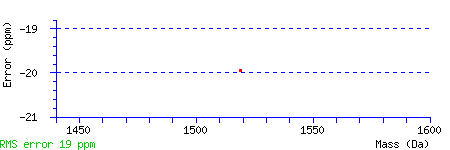
  Residue Number  Increasing Mass  Decreasing Mass



**Start - End Observed Mr(expt) Mr(calc) ppm Miss Sequence**

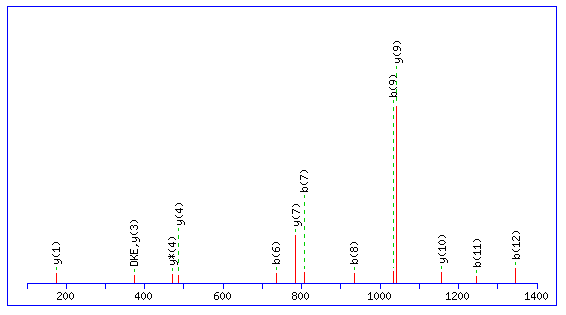
**88 - 100 1519.7924 1518.7851 1518.8154 -20 2 R.AYKDKEAQVNVVR.N**  ([No match](http://msmsms/mascot/cgi/peptide_view.pl?file=../data/20110221/F013490.dat&query=18&hit=1" \t "_blank))

**88 - 100 1519.7924 1518.7851 1518.8154 -20 2 R.AYKDKEAQVNVVR.N**  ([Ions score 79](http://msmsms/mascot/cgi/peptide_view.pl?file=../data/20110221/F013490.dat&query=19&hit=1" \t "_blank))



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🡪 Annotated MS2 spectrum for peptide AYKDKEAQVNVVR



**Monoisotopic mass of neutral peptide Mr(calc):** 1518.8154

**Ions Score:** 79 **Expect:** 9.5e-007

**Matches :** 14/203 fragment ions using 13 most intense peaks   ([help](http://msmsms/mascot/help/results_help.html" \l "PEP" \t "_blank))

|  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **#** | **Immon.** | **a** | **a\*** | **a0** | **b** | **b\*** | **b0** | **Seq.** | **v** | **w** | **y** | **y\*** | **y0** | **#** |
| **1** | 44.0495 | 44.0495 |  |  | 72.0444 |  |  | **A** |  |  |  |  |  | **13** |
| **2** | 136.0757 | 207.1128 |  |  | 235.1077 |  |  | **Y** | 1340.7281 |  | 1448.7856 | 1431.7591 | 1430.7750 | **12** |
| **3** | 101.1073 | 335.2078 | 318.1812 |  | 363.2027 | 346.1761 |  | **K** | 1212.6331 | 1211.6379 | 1285.7223 | 1268.6957 | 1267.7117 | **11** |
| **4** | 88.0393 | 450.2347 | 433.2082 | 432.2241 | 478.2296 | 461.2031 | 460.2191 | **D** | 1097.6062 | 1096.6109 | ***1157.6273*** | 1140.6008 | 1139.6167 | **10** |
| **5** | 101.1073 | 578.3297 | 561.3031 | 560.3191 | 606.3246 | 589.2980 | 588.3140 | **K** | 969.5112 | 968.5160 | ***1042.6004*** | 1025.5738 | 1024.5898 | **9** |
| **6** | 102.0550 | 707.3723 | 690.3457 | 689.3617 | ***735.3672*** | 718.3406 | 717.3566 | **E** | 840.4686 | 839.4734 | 914.5054 | 897.4789 | 896.4948 | **8** |
| **7** | 44.0495 | 778.4094 | 761.3828 | 760.3988 | ***806.4043*** | 789.3777 | 788.3937 | **A** | 769.4315 |  | ***785.4628*** | 768.4363 |  | **7** |
| **8** | 101.0709 | 906.4680 | 889.4414 | 888.4574 | ***934.4629*** | 917.4363 | 916.4523 | **Q** | 641.3729 | 640.3777 | 714.4257 | 697.3992 |  | **6** |
| **9** | 72.0808 | 1005.5364 | 988.5098 | 987.5258 | ***1033.5313*** | 1016.5047 | 1015.5207 | **V** | 542.3045 | 555.3249 | 586.3671 | 569.3406 |  | **5** |
| **10** | 87.0553 | 1119.5793 | 1102.5528 | 1101.5687 | 1147.5742 | 1130.5477 | 1129.5636 | **N** | 428.2616 | 427.2663 | ***487.2987*** | 470.2722 |  | **4** |
| **11** | 72.0808 | 1218.6477 | 1201.6212 | 1200.6371 | ***1246.6426*** | 1229.6161 | 1228.6321 | **V** | 329.1932 | 342.2136 | ***373.2558*** | 356.2292 |  | **3** |
| **12** | 72.0808 | 1317.7161 | 1300.6896 | 1299.7056 | ***1345.7110*** | 1328.6845 | 1327.7005 | **V** | 230.1248 | 243.1452 | 274.1874 | 257.1608 |  | **2** |
| **13** | 129.1135 |  |  |  |  |  |  | **R** | 74.0237 | 73.0284 | ***175.1190*** | 158.0924 |  | **1** |

|  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **Seq** | **ya** | **yb** | **Seq** | **ya** | **yb** | **Seq** | **ya** | **yb** |
| **YK** | 264.1707 | 292.1656 | **YKD** | 379.1976 | 407.1925 | **YKDK** | 507.2926 | 535.2875 |
| **YKDKE** | 636.3352 | 664.3301 | **KD** | 216.1343 | 244.1292 | **KDK** | 344.2292 | 372.2241 |
| **KDKE** | 473.2718 | 501.2667 | **KDKEA** | 544.3089 | 572.3039 | **KDKEAQ** | 672.3675 | 700.3624 |
| **DK** | 216.1343 | 244.1292 | **DKE** | 345.1769 | 373.1718 | **DKEA** | 416.2140 | 444.2089 |
| **DKEAQ** | 544.2726 | 572.2675 | **DKEAQV** | 643.3410 | 671.3359 | **KE** | 230.1499 | 258.1448 |
| **KEA** | 301.1870 | 329.1819 | **KEAQ** | 429.2456 | 457.2405 | **KEAQV** | 528.3140 | 556.3089 |
| **KEAQVN** | 642.3570 | 670.3519 | **EA** | 173.0921 | 201.0870 | **EAQ** | 301.1506 | 329.1456 |
| **EAQV** | 400.2191 | 428.2140 | **EAQVN** | 514.2620 | 542.2569 | **EAQVNV** | 613.3304 | 641.3253 |
| **AQ** | 172.1081 | 200.1030 | **AQV** | 271.1765 | 299.1714 | **AQVN** | 385.2194 | 413.2143 |
| **AQVNV** | 484.2878 | 512.2827 | **AQVNVV** | 583.3562 | 611.3511 | **QV** | 200.1394 | 228.1343 |
| **QVN** | 314.1823 | 342.1772 | **QVNV** | 413.2507 | 441.2456 | **QVNVV** | 512.3191 | 540.3140 |
| **VN** | 186.1237 | 214.1186 | **VNV** | 285.1921 | 313.1870 | **VNVV** | 384.2605 | 412.2554 |
| **NV** | 186.1237 | 214.1186 | **NVV** | 285.1921 | 313.1870 | **VV** | 171.1492 | 199.1441 |

**Spot 14:**

**http://msmsms/mascot/images/88x31_logo_white.gifMascot Search Results**

**User :**

**Email :**

**Search title : SampleSetID: 341, AnalysisID: 800, MaldiWellID: 45086, SpectrumID: 175246, Path=\Jimmy\Cooperia Adult ES 20110221\20110509 1st experiment (repeat)**

**Database : cooperia\_oncophora oncophora\_20110405 (34373 sequences; 5289600 residues)**

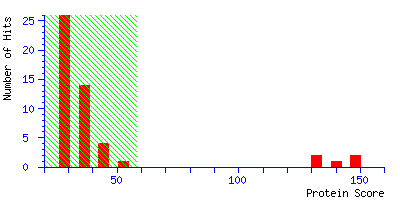
**Timestamp : 9 May 2011 at 12:39:20 GMT**

**Warning : A Peptide summary report will usually give a much clearer picture of MS/MS search results.**

**Top Score : 148 for isotig11583, putative nuclear encoded protein Method: similarity and extension**

**Mascot Score Histogram**

Protein score is -10\*Log(P), where P is the probability that the observed match is a random event.  
Protein scores greater than 58 are significant (p<0.05).  
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



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**Protein Summary Report**

|  |  |  |  |
| --- | --- | --- | --- |
|  |  |  | [Help](http://msmsms/mascot/help/msms_summaries_help.html" \t "_blank) |
|  | Significance threshold p< | Max. number of hits |  |

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**Index**

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
|  | **Accession** | **Mass** | **Score** | **Description** |
| **1.** | [**isotig11583**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20110509/F014812.dat#Hit1) | 14759 | 148 | putative nuclear encoded protein Method: similarity and extension |
| **2.** | [**isotig11585**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20110509/F014812.dat#Hit2) | 14759 | 148 | putative nuclear encoded protein Method: similarity and extension |
| **3.** | [**isotig11584**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20110509/F014812.dat#Hit3) | 14584 | 144 | putative nuclear encoded protein Method: similarity and extension |
| **4.** | [**isotig25277**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20110509/F014812.dat#Hit4) | 14624 | 135 | putative nuclear encoded protein Method: similarity and extension |
| **5.** | [**isotig26116**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20110509/F014812.dat#Hit5) | 14692 | 129 | putative nuclear encoded protein Method: similarity and extension |
| **6.** | [**isotig31779**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20110509/F014812.dat#Hit6) | 6879 | 51 | putative nuclear encoded protein Method: Longest ORF |
| **7.** | [**isotig12846**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20110509/F014812.dat#Hit7) | 14574 | 45 | putative nuclear encoded protein Method: similarity and extension |
| **8.** | [**isotig19163**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20110509/F014812.dat#Hit8) | 14654 | 44 | putative nuclear encoded protein Method: similarity and extension |
| **9.** | [**isotig06508**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20110509/F014812.dat#Hit9) | 15366 | 42 | putative nuclear encoded protein Method: similarity and extension |
| **10.** | [**isotig06509**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20110509/F014812.dat#Hit10) | 15395 | 42 | putative nuclear encoded protein Method: similarity and extension |
| **11.** | [**isotig14114**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20110509/F014812.dat#Hit11) | 39347 | 37 | putative nuclear encoded protein Method: similarity and extension |
| **12.** | [**isotig19585**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20110509/F014812.dat#Hit12) | 17201 | 36 | putative nuclear encoded protein Method: similarity and extension |
| **13.** | [**isotig00623**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20110509/F014812.dat#Hit13) | 17201 | 36 | putative nuclear encoded protein Method: similarity and extension |
| **14.** | [**isotig00625**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20110509/F014812.dat#Hit14) | 17201 | 36 | putative nuclear encoded protein Method: similarity and extension |
| **15.** | [**isotig26304**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20110509/F014812.dat#Hit15) | 17201 | 36 | putative nuclear encoded protein Method: similarity and extension |
| **16.** | [**isotig27906**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20110509/F014812.dat#Hit16) | 17201 | 36 | putative nuclear encoded protein Method: similarity and extension |
| **17.** | [**isotig00624**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20110509/F014812.dat#Hit17) | 17201 | 36 | putative nuclear encoded protein Method: similarity and extension |
| **18.** | [**isotig05260**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20110509/F014812.dat#Hit18) | 12016 | 36 | putative nuclear encoded protein Method: Longest ORF |
| **19.** | [**contig53292**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20110509/F014812.dat#Hit19) | 17589 | 35 | putative nuclear encoded protein Method: similarity and extension |
| **20.** | [**isotig29565**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20110509/F014812.dat#Hit20) | 13734 | 35 | putative nuclear encoded protein Method: Longest ORF |

**Results List**

|  |  |
| --- | --- |
| **1.** | [isotig11583](http://msmsms/mascot/cgi/protein_view.pl?file=../data/20110509/F014812.dat&hit=1" \t "_blank)    **Mass:** 14759    **Score:** 148    **Expect:** 5.4e-011  **Matches:** 10 |
|  | putative nuclear encoded protein Method: similarity and extension |

|  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | **Observed** | **Mr(expt)** | **Mr(calc)** | **ppm** | **Start** |  | **End** | **Miss** | **Ions** | **Peptide** |
|  | 910.4586 | 909.4513 | 909.4630 | -12.82 | 123 | - | 129 | 0 | --- | K.VVCLYEK.Q + Carbamidomethyl (C) |
|  | 914.5033 | 913.4960 | 913.4981 | -2.30 | 95 | - | 102 | 0 | --- | K.EAQVNVVR.N |
|  | 1038.5287 | 1037.5214 | 1037.5216 | -0.13 | 123 | - | 130 | 1 | --- | K.VVCLYEKQ.- + Carbamidomethyl (C) |
|  | 1157.6271 | 1156.6198 | 1156.6200 | -0.17 | 93 | - | 102 | 1 | --- | K.DKEAQVNVVR.N |
|  | 1168.5453 | 1167.5380 | 1167.5230 | 12.9 | 110 | - | 120 | 0 | --- | K.YGCNAVEIGDK.T |
|  | 1454.7159 | 1453.7086 | 1453.6871 | 14.8 | 110 | - | 122 | 1 | --- | K.YGCNAVEIGDKTK.V + Carbamidomethyl (C) |
|  | 1519.8379 | 1518.8306 | 1518.8154 | 10.0 | 90 | - | 102 | 2 | --- | R.AYKDKEAQVNVVR.N |
|  | 1519.8379 | 1518.8306 | 1518.8154 | 10.0 | 90 | - | 102 | 2 | 94 | R.AYKDKEAQVNVVR.N |
|  | 2396.0933 | 2395.0860 | 2395.0750 | 4.60 | 51 | - | 71 | 1 | --- | R.ACEEAYGELGSHGFDKLEVER.E + Carbamidomethyl (C) |
|  | 2396.0933 | 2395.0860 | 2395.0750 | 4.60 | 51 | - | 71 | 1 | 10 | R.ACEEAYGELGSHGFDKLEVER.E + Carbamidomethyl (C) |

|  |  |
| --- | --- |
|  | **No match to:** 804.2750, 813.4564, 819.4462, 832.2990, 834.3017, 836.4685, 842.5076, 844.5104, 862.4772, 874.4760, 906.4972, 941.5113, 947.5594, 982.4477, 990.5814, 994.4841, 1005.4525, 1013.4699, 1014.4618, 1022.4828, 1032.4540, 1041.5065, 1046.5094, 1061.5076, 1074.5604, 1081.4835, 1090.4644, 1094.5662, 1094.5662, 1122.5406, 1138.5386, 1171.6428, 1179.6052, 1232.6516, 1235.5463, 1259.5555, 1284.5836, 1430.8279, 1463.8141, 1475.7786, 1550.7454, 1587.6274, 1791.7573 |

|  |  |
| --- | --- |
| **2.** | [isotig11585](http://msmsms/mascot/cgi/protein_view.pl?file=../data/20110509/F014812.dat&hit=2" \t "_blank)    **Mass:** 14759    **Score:** 148    **Expect:** 5.4e-011  **Matches:** 10 |
|  | putative nuclear encoded protein Method: similarity and extension |

|  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | **Observed** | **Mr(expt)** | **Mr(calc)** | **ppm** | **Start** |  | **End** | **Miss** | **Ions** | **Peptide** |
|  | 910.4586 | 909.4513 | 909.4630 | -12.82 | 123 | - | 129 | 0 | --- | K.VVCLYEK.Q + Carbamidomethyl (C) |
|  | 914.5033 | 913.4960 | 913.4981 | -2.30 | 95 | - | 102 | 0 | --- | K.EAQVNVVR.N |
|  | 1038.5287 | 1037.5214 | 1037.5216 | -0.13 | 123 | - | 130 | 1 | --- | K.VVCLYEKQ.- + Carbamidomethyl (C) |
|  | 1157.6271 | 1156.6198 | 1156.6200 | -0.17 | 93 | - | 102 | 1 | --- | K.DKEAQVNVVR.N |
|  | 1168.5453 | 1167.5380 | 1167.5230 | 12.9 | 110 | - | 120 | 0 | --- | K.YGCNAVEIGDK.T |
|  | 1454.7159 | 1453.7086 | 1453.6871 | 14.8 | 110 | - | 122 | 1 | --- | K.YGCNAVEIGDKTK.V + Carbamidomethyl (C) |
|  | 1519.8379 | 1518.8306 | 1518.8154 | 10.0 | 90 | - | 102 | 2 | --- | R.AYKDKEAQVNVVR.N |
|  | 1519.8379 | 1518.8306 | 1518.8154 | 10.0 | 90 | - | 102 | 2 | 94 | R.AYKDKEAQVNVVR.N |
|  | 2396.0933 | 2395.0860 | 2395.0750 | 4.60 | 51 | - | 71 | 1 | --- | R.ACEEAYGELGSHGFDKLEVER.E + Carbamidomethyl (C) |
|  | 2396.0933 | 2395.0860 | 2395.0750 | 4.60 | 51 | - | 71 | 1 | 10 | R.ACEEAYGELGSHGFDKLEVER.E + Carbamidomethyl (C) |

|  |  |
| --- | --- |
|  | **No match to:** 804.2750, 813.4564, 819.4462, 832.2990, 834.3017, 836.4685, 842.5076, 844.5104, 862.4772, 874.4760, 906.4972, 941.5113, 947.5594, 982.4477, 990.5814, 994.4841, 1005.4525, 1013.4699, 1014.4618, 1022.4828, 1032.4540, 1041.5065, 1046.5094, 1061.5076, 1074.5604, 1081.4835, 1090.4644, 1094.5662, 1094.5662, 1122.5406, 1138.5386, 1171.6428, 1179.6052, 1232.6516, 1235.5463, 1259.5555, 1284.5836, 1430.8279, 1463.8141, 1475.7786, 1550.7454, 1587.6274, 1791.7573 |

|  |  |
| --- | --- |
| **3.** | [isotig11584](http://msmsms/mascot/cgi/protein_view.pl?file=../data/20110509/F014812.dat&hit=3" \t "_blank)    **Mass:** 14584    **Score:** 144    **Expect:** 1.4e-010  **Matches:** 10 |
|  | putative nuclear encoded protein Method: similarity and extension |

|  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | **Observed** | **Mr(expt)** | **Mr(calc)** | **ppm** | **Start** |  | **End** | **Miss** | **Ions** | **Peptide** |
|  | 910.4586 | 909.4513 | 909.4630 | -12.82 | 121 | - | 127 | 0 | --- | K.VVCLYEK.Q + Carbamidomethyl (C) |
|  | 914.5033 | 913.4960 | 913.4981 | -2.30 | 93 | - | 100 | 0 | --- | K.EAQVNVVR.N |
|  | 1038.5287 | 1037.5214 | 1037.5216 | -0.13 | 121 | - | 128 | 1 | --- | K.VVCLYEKQ.- + Carbamidomethyl (C) |
|  | 1157.6271 | 1156.6198 | 1156.6200 | -0.17 | 91 | - | 100 | 1 | --- | K.DKEAQVNVVR.N |
|  | 1168.5453 | 1167.5380 | 1167.5230 | 12.9 | 108 | - | 118 | 0 | --- | K.YGCNAVEIGDK.T |
|  | 1454.7159 | 1453.7086 | 1453.6871 | 14.8 | 108 | - | 120 | 1 | --- | K.YGCNAVEIGDKTK.V + Carbamidomethyl (C) |
|  | 1519.8379 | 1518.8306 | 1518.8154 | 10.0 | 88 | - | 100 | 2 | --- | R.AYKDKEAQVNVVR.N |
|  | 1519.8379 | 1518.8306 | 1518.8154 | 10.0 | 88 | - | 100 | 2 | 94 | R.AYKDKEAQVNVVR.N |
|  | 2396.0933 | 2395.0860 | 2395.0750 | 4.60 | 49 | - | 69 | 1 | --- | R.ACEEAYGELGSHGFDKLEVER.E + Carbamidomethyl (C) |
|  | 2396.0933 | 2395.0860 | 2395.0750 | 4.60 | 49 | - | 69 | 1 | 10 | R.ACEEAYGELGSHGFDKLEVER.E + Carbamidomethyl (C) |

|  |  |
| --- | --- |
|  | **No match to:** 804.2750, 813.4564, 819.4462, 832.2990, 834.3017, 836.4685, 842.5076, 844.5104, 862.4772, 874.4760, 906.4972, 941.5113, 947.5594, 982.4477, 990.5814, 994.4841, 1005.4525, 1013.4699, 1014.4618, 1022.4828, 1032.4540, 1041.5065, 1046.5094, 1061.5076, 1074.5604, 1081.4835, 1090.4644, 1094.5662, 1094.5662, 1122.5406, 1138.5386, 1171.6428, 1179.6052, 1232.6516, 1235.5463, 1259.5555, 1284.5836, 1430.8279, 1463.8141, 1475.7786, 1550.7454, 1587.6274, 1791.7573 |

|  |  |
| --- | --- |
| **4.** | [isotig25277](http://msmsms/mascot/cgi/protein_view.pl?file=../data/20110509/F014812.dat&hit=4" \t "_blank)    **Mass:** 14624    **Score:** 135    **Expect:** 1.1e-009  **Matches:** 8 |
|  | putative nuclear encoded protein Method: similarity and extension |

|  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | **Observed** | **Mr(expt)** | **Mr(calc)** | **ppm** | **Start** |  | **End** | **Miss** | **Ions** | **Peptide** |
|  | 910.4586 | 909.4513 | 909.4630 | -12.82 | 122 | - | 128 | 0 | --- | K.VVCLYEK.Q + Carbamidomethyl (C) |
|  | 914.5033 | 913.4960 | 913.4981 | -2.30 | 94 | - | 101 | 0 | --- | K.EAQVNVVR.N |
|  | 1038.5287 | 1037.5214 | 1037.5216 | -0.13 | 122 | - | 129 | 1 | --- | K.VVCLYEKQ.- + Carbamidomethyl (C) |
|  | 1157.6271 | 1156.6198 | 1156.6200 | -0.17 | 92 | - | 101 | 1 | --- | K.DKEAQVNVVR.N |
|  | 1519.8379 | 1518.8306 | 1518.8154 | 10.0 | 89 | - | 101 | 2 | --- | R.AYKDKEAQVNVVR.N |
|  | 1519.8379 | 1518.8306 | 1518.8154 | 10.0 | 89 | - | 101 | 2 | 94 | R.AYKDKEAQVNVVR.N |
|  | 2396.0933 | 2395.0860 | 2395.0750 | 4.60 | 50 | - | 70 | 1 | --- | R.ACEEAYGELGSHGFDKLEVER.E + Carbamidomethyl (C) |
|  | 2396.0933 | 2395.0860 | 2395.0750 | 4.60 | 50 | - | 70 | 1 | 10 | R.ACEEAYGELGSHGFDKLEVER.E + Carbamidomethyl (C) |

|  |  |
| --- | --- |
|  | **No match to:** 804.2750, 813.4564, 819.4462, 832.2990, 834.3017, 836.4685, 842.5076, 844.5104, 862.4772, 874.4760, 906.4972, 941.5113, 947.5594, 982.4477, 990.5814, 994.4841, 1005.4525, 1013.4699, 1014.4618, 1022.4828, 1032.4540, 1041.5065, 1046.5094, 1061.5076, 1074.5604, 1081.4835, 1090.4644, 1094.5662, 1094.5662, 1122.5406, 1138.5386, 1168.5453, 1171.6428, 1179.6052, 1232.6516, 1235.5463, 1259.5555, 1284.5836, 1430.8279, 1454.7159, 1463.8141, 1475.7786, 1550.7454, 1587.6274, 1791.7573 |

|  |  |
| --- | --- |
| **5.** | [isotig26116](http://msmsms/mascot/cgi/protein_view.pl?file=../data/20110509/F014812.dat&hit=5" \t "_blank)    **Mass:** 14692    **Score:** 129    **Expect:** 4.3e-009  **Matches:** 8 |
|  | putative nuclear encoded protein Method: similarity and extension |

|  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | **Observed** | **Mr(expt)** | **Mr(calc)** | **ppm** | **Start** |  | **End** | **Miss** | **Ions** | **Peptide** |
|  | 914.5033 | 913.4960 | 913.4981 | -2.30 | 94 | - | 101 | 0 | --- | K.EAQVNVVR.N |
|  | 1157.6271 | 1156.6198 | 1156.6200 | -0.17 | 92 | - | 101 | 1 | --- | K.DKEAQVNVVR.N |
|  | 1168.5453 | 1167.5380 | 1167.5230 | 12.9 | 109 | - | 119 | 0 | --- | K.YGCNAVEIGDK.T |
|  | 1454.7159 | 1453.7086 | 1453.6871 | 14.8 | 109 | - | 121 | 1 | --- | K.YGCNAVEIGDKTK.V + Carbamidomethyl (C) |
|  | 1519.8379 | 1518.8306 | 1518.8154 | 10.0 | 89 | - | 101 | 2 | --- | R.AYKDKEAQVNVVR.N |
|  | 1519.8379 | 1518.8306 | 1518.8154 | 10.0 | 89 | - | 101 | 2 | 94 | R.AYKDKEAQVNVVR.N |
|  | 2396.0933 | 2395.0860 | 2395.0750 | 4.60 | 50 | - | 70 | 1 | --- | R.ACEEAYGELGSHGFDKLEVER.E + Carbamidomethyl (C) |
|  | 2396.0933 | 2395.0860 | 2395.0750 | 4.60 | 50 | - | 70 | 1 | 10 | R.ACEEAYGELGSHGFDKLEVER.E + Carbamidomethyl (C) |

|  |  |
| --- | --- |
|  | **No match to:** 804.2750, 813.4564, 819.4462, 832.2990, 834.3017, 836.4685, 842.5076, 844.5104, 862.4772, 874.4760, 906.4972, 910.4586, 941.5113, 947.5594, 982.4477, 990.5814, 994.4841, 1005.4525, 1013.4699, 1014.4618, 1022.4828, 1032.4540, 1038.5287, 1041.5065, 1046.5094, 1061.5076, 1074.5604, 1081.4835, 1090.4644, 1094.5662, 1094.5662, 1122.5406, 1138.5386, 1171.6428, 1179.6052, 1232.6516, 1235.5463, 1259.5555, 1284.5836, 1430.8279, 1463.8141, 1475.7786, 1550.7454, 1587.6274, 1791.7573 |

# http://msmsms/mascot/images/88x31_logo_white.gifMascot Search Results

**Protein View**

Top of Form



Match to: **isotig11583** Score: **148** Expect: **5.4e-011**

**putative nuclear encoded protein Method: similarity and extension**

Nominal mass (Mr): **14759**; Calculated pI value: **6.29**

NCBI BLAST search of [isotig11583](http://www.ncbi.nlm.nih.gov/blast/Blast.cgi?ALIGNMENTS=50&ALIGNMENT_VIEW=Pairwise&AUTO_FORMAT=Semiauto&CDD_SEARCH=on&CLIENT=web&COMPOSITION_BASED_STATISTICS=on&DATABASE=nr&DESCRIPTIONS=100&ENTREZ_QUERY=(none)&EXPECT=10&FILTER=L&FORMAT_BLOCK_ON_RESPAGE=None&FORMAT_OBJECT=Alignment&FORMAT_TYPE=HTML&GAPCOSTS=11+1&I_THRESH=0.001&LAYOUT=TwoWindows&MATRIX_NAME=BLOSUM62&NCBI_GI=on&PAGE=Proteins&PROGRAM=blastp&QUERY=MLLALTVLCIFVINAYANDCVPDFHQKNLYAKFHNGLNNNLVWDDDLSERACEEAYGELGSHGFDKLEVEREVPKSLVRSSRIQRTLMRAYKDKEAQVNVVRNLPAGTKYGCNAVEIGDKTKVVCLYEKQ&SERVICE=plain&SET_DEFAULTS.x=9&SET_DEFAULTS.y=5&SHOW_OVERVIEW=on&WORD_SIZE=3&END_OF_HTTPGET=Yes" \t "_blank) against nr

Unformatted [sequence string](http://msmsms/mascot/cgi/getseq.pl?cooperia_oncophora+isotig11583+seq" \t "_blank) for pasting into other applications

Variable modifications: Carbamidomethyl (C),Oxidation (HW),Oxidation (M)

Cleavage by Trypsin/P: cuts C-term side of KR

Sequence Coverage: **42%**

Matched peptides shown in **Bold Red**

**1** MLLALTVLCI FVINAYANDC VPDFHQKNLY AKFHNGLNNN LVWDDDLSER

**51** **ACEEAYGELG SHGFDKLEVE R**EVPKSLVRS SRIQRTLMR**A YKDKEAQVNV**

**101 VR**NLPAGTK**Y GCNAVEIGDK TKVVCLYEKQ**



  Residue Number  Increasing Mass  Decreasing Mass

**Start - End Observed Mr(expt) Mr(calc) ppm Miss Sequence**

**51 - 71 2396.0933 2395.0860 2395.0750 5 1 R.ACEEAYGELGSHGFDKLEVER.E**  Carbamidomethyl (C) ([No match](http://msmsms/mascot/cgi/peptide_view.pl?file=../data/20110509/F014812.dat&query=52&hit=1" \t "_blank))

**51 - 71 2396.0933 2395.0860 2395.0750 5 1 R.ACEEAYGELGSHGFDKLEVER.E**  Carbamidomethyl (C) ([Ions score 10](http://msmsms/mascot/cgi/peptide_view.pl?file=../data/20110509/F014812.dat&query=53&hit=1" \t "_blank))

**90 - 102 1519.8379 1518.8306 1518.8154 10 2 R.AYKDKEAQVNVVR.N**  ([No match](http://msmsms/mascot/cgi/peptide_view.pl?file=../data/20110509/F014812.dat&query=47&hit=1" \t "_blank))

**90 - 102 1519.8379 1518.8306 1518.8154 10 2 R.AYKDKEAQVNVVR.N**  ([Ions score 94](http://msmsms/mascot/cgi/peptide_view.pl?file=../data/20110509/F014812.dat&query=48&hit=1" \t "_blank))

**93 - 102 1157.6271 1156.6198 1156.6200 -0 1 K.DKEAQVNVVR.N**  ([No match](http://msmsms/mascot/cgi/peptide_view.pl?file=../data/20110509/F014812.dat&query=35&hit=1" \t "_blank))

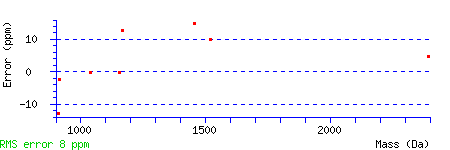
**95 - 102 914.5033 913.4960 913.4981 -2 0 K.EAQVNVVR.N**  ([No match](http://msmsms/mascot/cgi/peptide_view.pl?file=../data/20110509/F014812.dat&query=13&hit=1" \t "_blank))

**110 - 120 1168.5453 1167.5380 1167.5230 13 0 K.YGCNAVEIGDK.T**  ([No match](http://msmsms/mascot/cgi/peptide_view.pl?file=../data/20110509/F014812.dat&query=36&hit=1" \t "_blank))

**110 - 122 1454.7159 1453.7086 1453.6871 15 1 K.YGCNAVEIGDKTK.V**  Carbamidomethyl (C) ([No match](http://msmsms/mascot/cgi/peptide_view.pl?file=../data/20110509/F014812.dat&query=44&hit=1" \t "_blank))

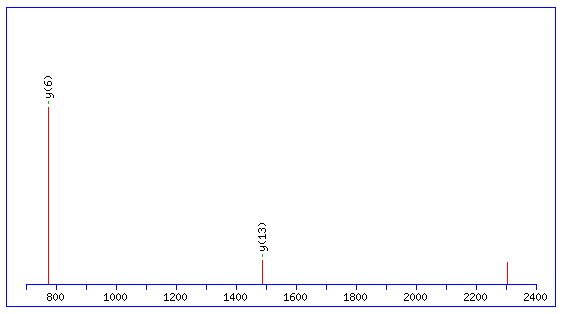
**123 - 129 910.4586 909.4513 909.4630 -13 0 K.VVCLYEK.Q**  Carbamidomethyl (C) ([No match](http://msmsms/mascot/cgi/peptide_view.pl?file=../data/20110509/F014812.dat&query=12&hit=1" \t "_blank))

**123 - 130 1038.5287 1037.5214 1037.5216 -0 1 K.VVCLYEKQ.-**  Carbamidomethyl (C) ([No match](http://msmsms/mascot/cgi/peptide_view.pl?file=../data/20110509/F014812.dat&query=24&hit=1" \t "_blank))



Bottom of Form

🡪 Annotated MS2 spectrum for peptide ACEEAYGELGSHGFDKLEVER



**Monoisotopic mass of neutral peptide Mr(calc):** 2395.0750

**Variable modifications:**

**C2 :** Carbamidomethyl (C)

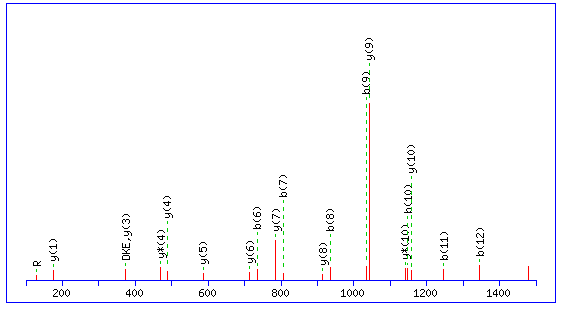
**Ions Score:** 10 **Expect:** 11

**Matches :** 2/358 fragment ions using 3 most intense peaks   ([help](http://msmsms/mascot/help/results_help.html" \l "PEP" \t "_blank))

|  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **#** | **Immon.** | **a** | **a\*** | **a0** | **b** | **b\*** | **b0** | **Seq.** | **v** | **w** | **y** | **y\*** | **y0** | **#** |
| **1** | 44.0495 | 44.0495 |  |  | 72.0444 |  |  | **A** |  |  |  |  |  | **21** |
| **2** | 133.0430 | 204.0801 |  |  | 232.0750 |  |  | **C** | 2220.0204 | 2219.0251 | 2325.0452 | 2308.0187 | 2307.0346 | **20** |
| **3** | 102.0550 | 333.1227 |  | 315.1122 | 361.1176 |  | 343.1071 | **E** | 2090.9778 | 2089.9825 | 2165.0146 | 2147.9880 | 2147.0040 | **19** |
| **4** | 102.0550 | 462.1653 |  | 444.1547 | 490.1602 |  | 472.1497 | **E** | 1961.9352 | 1960.9399 | 2035.9720 | 2018.9454 | 2017.9614 | **18** |
| **5** | 44.0495 | 533.2024 |  | 515.1919 | 561.1973 |  | 543.1868 | **A** | 1890.8981 |  | 1906.9294 | 1889.9028 | 1888.9188 | **17** |
| **6** | 136.0757 | 696.2658 |  | 678.2552 | 724.2607 |  | 706.2501 | **Y** | 1727.8347 |  | 1835.8923 | 1818.8657 | 1817.8817 | **16** |
| **7** | 30.0338 | 753.2872 |  | 735.2767 | 781.2821 |  | 763.2716 | **G** |  |  | 1672.8289 | 1655.8024 | 1654.8184 | **15** |
| **8** | 102.0550 | 882.3298 |  | 864.3192 | 910.3247 |  | 892.3142 | **E** | 1541.7707 | 1540.7754 | 1615.8075 | 1598.7809 | 1597.7969 | **14** |
| **9** | 86.0964 | 995.4139 |  | 977.4033 | 1023.4088 |  | 1005.3982 | **L** | 1428.6866 | 1427.6914 | ***1486.7649*** | 1469.7383 | 1468.7543 | **13** |
| **10** | 30.0338 | 1052.4353 |  | 1034.4248 | 1080.4303 |  | 1062.4197 | **G** |  |  | 1373.6808 | 1356.6543 | 1355.6702 | **12** |
| **11** | 60.0444 | 1139.4674 |  | 1121.4568 | 1167.4623 |  | 1149.4517 | **S** | 1284.6331 | 1283.6379 | 1316.6593 | 1299.6328 | 1298.6488 | **11** |
| **12** | 110.0713 | 1276.5263 |  | 1258.5157 | 1304.5212 |  | 1286.5106 | **H** | 1147.5742 |  | 1229.6273 | 1212.6008 | 1211.6167 | **10** |
| **13** | 30.0338 | 1333.5477 |  | 1315.5372 | 1361.5427 |  | 1343.5321 | **G** |  |  | 1092.5684 | 1075.5419 | 1074.5578 | **9** |
| **14** | 120.0808 | 1480.6162 |  | 1462.6056 | 1508.6111 |  | 1490.6005 | **F** | 943.4843 |  | 1035.5469 | 1018.5204 | 1017.5364 | **8** |
| **15** | 88.0393 | 1595.6431 |  | 1577.6325 | 1623.6380 |  | 1605.6274 | **D** | 828.4574 | 827.4621 | 888.4785 | 871.4520 | 870.4680 | **7** |
| **16** | 101.1073 | 1723.7381 | 1706.7115 | 1705.7275 | 1751.7330 | 1734.7064 | 1733.7224 | **K** | 700.3624 | 699.3672 | ***773.4516*** | 756.4250 | 755.4410 | **6** |
| **17** | 86.0964 | 1836.8221 | 1819.7956 | 1818.8116 | 1864.8170 | 1847.7905 | 1846.8065 | **L** | 587.2784 | 586.2831 | 645.3566 | 628.3301 | 627.3461 | **5** |
| **18** | 102.0550 | 1965.8647 | 1948.8382 | 1947.8542 | 1993.8596 | 1976.8331 | 1975.8491 | **E** | 458.2358 | 457.2405 | 532.2726 | 515.2460 | 514.2620 | **4** |
| **19** | 72.0808 | 2064.9331 | 2047.9066 | 2046.9226 | 2092.9280 | 2075.9015 | 2074.9175 | **V** | 359.1674 | 372.1878 | 403.2300 | 386.2034 | 385.2194 | **3** |
| **20** | 102.0550 | 2193.9757 | 2176.9492 | 2175.9652 | 2221.9706 | 2204.9441 | 2203.9601 | **E** | 230.1248 | 229.1295 | 304.1615 | 287.1350 | 286.1510 | **2** |
| **21** | 129.1135 |  |  |  |  |  |  | **R** | 74.0237 | 73.0284 | 175.1190 | 158.0924 |  | **1** |

|  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **Seq** | **ya** | **yb** | **Seq** | **ya** | **yb** | **Seq** | **ya** | **yb** |
| **CE** | 262.0856 | 290.0805 | **CEE** | 391.1282 | 419.1231 | **CEEA** | 462.1653 | 490.1602 |
| **CEEAY** | 625.2286 | 653.2236 | **CEEAYG** | 682.2501 | 710.2450 | **EE** | 231.0975 | 259.0925 |
| **EEA** | 302.1347 | 330.1296 | **EEAY** | 465.1980 | 493.1929 | **EEAYG** | 522.2195 | 550.2144 |
| **EEAYGE** | 651.2620 | 679.2570 | **EA** | 173.0921 | 201.0870 | **EAY** | 336.1554 | 364.1503 |
| **EAYG** | 393.1769 | 421.1718 | **EAYGE** | 522.2195 | 550.2144 | **EAYGEL** | 635.3035 | 663.2984 |
| **EAYGELG** | 692.3250 | 720.3199 | **AY** | 207.1128 | 235.1077 | **AYG** | 264.1343 | 292.1292 |
| **AYGE** | 393.1769 | 421.1718 | **AYGEL** | 506.2609 | 534.2558 | **AYGELG** | 563.2824 | 591.2773 |
| **AYGELGS** | 650.3144 | 678.3093 | **YG** | 193.0972 | 221.0921 | **YGE** | 322.1397 | 350.1347 |
| **YGEL** | 435.2238 | 463.2187 | **YGELG** | 492.2453 | 520.2402 | **YGELGS** | 579.2773 | 607.2722 |
| **GE** | 159.0764 | 187.0713 | **GEL** | 272.1605 | 300.1554 | **GELG** | 329.1819 | 357.1769 |
| **GELGS** | 416.2140 | 444.2089 | **GELGSH** | 553.2729 | 581.2678 | **GELGSHG** | 610.2944 | 638.2893 |
| **EL** | 215.1390 | 243.1339 | **ELG** | 272.1605 | 300.1554 | **ELGS** | 359.1925 | 387.1874 |
| **ELGSH** | 496.2514 | 524.2463 | **ELGSHG** | 553.2729 | 581.2678 | **LG** | 143.1179 | 171.1128 |
| **LGS** | 230.1499 | 258.1448 | **LGSH** | 367.2088 | 395.2037 | **LGSHG** | 424.2303 | 452.2252 |
| **LGSHGF** | 571.2987 | 599.2936 | **LGSHGFD** | 686.3257 | 714.3206 | **GS** | 117.0659 | 145.0608 |
| **GSH** | 254.1248 | 282.1197 | **GSHG** | 311.1462 | 339.1411 | **GSHGF** | 458.2146 | 486.2096 |
| **GSHGFD** | 573.2416 | 601.2365 | **SH** | 197.1033 | 225.0982 | **SHG** | 254.1248 | 282.1197 |
| **SHGF** | 401.1932 | 429.1881 | **SHGFD** | 516.2201 | 544.2150 | **SHGFDK** | 644.3151 | 672.3100 |
| **HG** | 167.0927 | 195.0877 | **HGF** | 314.1612 | 342.1561 | **HGFD** | 429.1881 | 457.1830 |
| **HGFDK** | 557.2831 | 585.2780 | **HGFDKL** | 670.3671 | 698.3620 | **GF** | 177.1022 | 205.0972 |
| **GFD** | 292.1292 | 320.1241 | **GFDK** | 420.2241 | 448.2191 | **GFDKL** | 533.3082 | 561.3031 |
| **GFDKLE** | 662.3508 | 690.3457 | **FD** | 235.1077 | 263.1026 | **FDK** | 363.2027 | 391.1976 |
| **FDKL** | 476.2867 | 504.2817 | **FDKLE** | 605.3293 | 633.3243 | **DK** | 216.1343 | 244.1292 |
| **DKL** | 329.2183 | 357.2132 | **DKLE** | 458.2609 | 486.2558 | **DKLEV** | 557.3293 | 585.3243 |
| **DKLEVE** | 686.3719 | 714.3668 | **KL** | 214.1914 | 242.1863 | **KLE** | 343.2340 | 371.2289 |
| **KLEV** | 442.3024 | 470.2973 | **KLEVE** | 571.3450 | 599.3399 | **LE** | 215.1390 | 243.1339 |
| **LEV** | 314.2074 | 342.2023 | **LEVE** | 443.2500 | 471.2449 | **EV** | 201.1234 | 229.1183 |
| **EVE** | 330.1660 | 358.1609 | **VE** | 201.1234 | 229.1183 |  |  |  |

🡪 Annotated MS2 spectrum for peptide AYKDKEAQVNVVR



**Monoisotopic mass of neutral peptide Mr(calc):** 1518.8154

**Ions Score:** 94 **Expect:** 3.8e-008

**Matches :** 20/203 fragment ions using 20 most intense peaks   ([help](http://msmsms/mascot/help/results_help.html" \l "PEP" \t "_blank))

|  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **#** | **Immon.** | **a** | **a\*** | **a0** | **b** | **b\*** | **b0** | **Seq.** | **v** | **w** | **y** | **y\*** | **y0** | **#** |
| **1** | 44.0495 | 44.0495 |  |  | 72.0444 |  |  | **A** |  |  |  |  |  | **13** |
| **2** | 136.0757 | 207.1128 |  |  | 235.1077 |  |  | **Y** | 1340.7281 |  | 1448.7856 | 1431.7591 | 1430.7750 | **12** |
| **3** | 101.1073 | 335.2078 | 318.1812 |  | 363.2027 | 346.1761 |  | **K** | 1212.6331 | 1211.6379 | 1285.7223 | 1268.6957 | 1267.7117 | **11** |
| **4** | 88.0393 | 450.2347 | 433.2082 | 432.2241 | 478.2296 | 461.2031 | 460.2191 | **D** | 1097.6062 | 1096.6109 | ***1157.6273*** | 1140.6008 | 1139.6167 | **10** |
| **5** | 101.1073 | 578.3297 | 561.3031 | 560.3191 | 606.3246 | 589.2980 | 588.3140 | **K** | 969.5112 | 968.5160 | ***1042.6004*** | 1025.5738 | 1024.5898 | **9** |
| **6** | 102.0550 | 707.3723 | 690.3457 | 689.3617 | ***735.3672*** | 718.3406 | 717.3566 | **E** | 840.4686 | 839.4734 | ***914.5054*** | 897.4789 | 896.4948 | **8** |
| **7** | 44.0495 | 778.4094 | 761.3828 | 760.3988 | ***806.4043*** | 789.3777 | 788.3937 | **A** | 769.4315 |  | ***785.4628*** | 768.4363 |  | **7** |
| **8** | 101.0709 | 906.4680 | 889.4414 | 888.4574 | ***934.4629*** | 917.4363 | 916.4523 | **Q** | 641.3729 | 640.3777 | ***714.4257*** | 697.3992 |  | **6** |
| **9** | 72.0808 | 1005.5364 | 988.5098 | 987.5258 | ***1033.5313*** | 1016.5047 | 1015.5207 | **V** | 542.3045 | 555.3249 | ***586.3671*** | 569.3406 |  | **5** |
| **10** | 87.0553 | 1119.5793 | 1102.5528 | 1101.5687 | ***1147.5742*** | 1130.5477 | 1129.5636 | **N** | 428.2616 | 427.2663 | ***487.2987*** | 470.2722 |  | **4** |
| **11** | 72.0808 | 1218.6477 | 1201.6212 | 1200.6371 | ***1246.6426*** | 1229.6161 | 1228.6321 | **V** | 329.1932 | 342.2136 | ***373.2558*** | 356.2292 |  | **3** |
| **12** | 72.0808 | 1317.7161 | 1300.6896 | 1299.7056 | ***1345.7110*** | 1328.6845 | 1327.7005 | **V** | 230.1248 | 243.1452 | 274.1874 | 257.1608 |  | **2** |
| **13** | 129.1135 |  |  |  |  |  |  | **R** | 74.0237 | 73.0284 | ***175.1190*** | 158.0924 |  | **1** |

|  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **Seq** | **ya** | **yb** | **Seq** | **ya** | **yb** | **Seq** | **ya** | **yb** |
| **YK** | 264.1707 | 292.1656 | **YKD** | 379.1976 | 407.1925 | **YKDK** | 507.2926 | 535.2875 |
| **YKDKE** | 636.3352 | 664.3301 | **KD** | 216.1343 | 244.1292 | **KDK** | 344.2292 | 372.2241 |
| **KDKE** | 473.2718 | 501.2667 | **KDKEA** | 544.3089 | 572.3039 | **KDKEAQ** | 672.3675 | 700.3624 |
| **DK** | 216.1343 | 244.1292 | **DKE** | 345.1769 | 373.1718 | **DKEA** | 416.2140 | 444.2089 |
| **DKEAQ** | 544.2726 | 572.2675 | **DKEAQV** | 643.3410 | 671.3359 | **KE** | 230.1499 | 258.1448 |
| **KEA** | 301.1870 | 329.1819 | **KEAQ** | 429.2456 | 457.2405 | **KEAQV** | 528.3140 | 556.3089 |
| **KEAQVN** | 642.3570 | 670.3519 | **EA** | 173.0921 | 201.0870 | **EAQ** | 301.1506 | 329.1456 |
| **EAQV** | 400.2191 | 428.2140 | **EAQVN** | 514.2620 | 542.2569 | **EAQVNV** | 613.3304 | 641.3253 |
| **AQ** | 172.1081 | 200.1030 | **AQV** | 271.1765 | 299.1714 | **AQVN** | 385.2194 | 413.2143 |
| **AQVNV** | 484.2878 | 512.2827 | **AQVNVV** | 583.3562 | 611.3511 | **QV** | 200.1394 | 228.1343 |
| **QVN** | 314.1823 | 342.1772 | **QVNV** | 413.2507 | 441.2456 | **QVNVV** | 512.3191 | 540.3140 |
| **VN** | 186.1237 | 214.1186 | **VNV** | 285.1921 | 313.1870 | **VNVV** | 384.2605 | 412.2554 |
| **NV** | 186.1237 | 214.1186 | **NVV** | 285.1921 | 313.1870 | **VV** | 171.1492 | 199.1441 |

**Spot 15:**

**http://msmsms/mascot/images/88x31_logo_white.gifMascot Search Results**

**User :**

**Email :**

**Search title : SampleSetID: 341, AnalysisID: 641, MaldiWellID: 45156, SpectrumID: 154694, Path=\Jimmy\Cooperia Adult ES 20110221\20110405 MS en MSMS (new DB)**

**Database : cooperia\_oncophora oncophora\_20110405 (34373 sequences; 5289600 residues)**

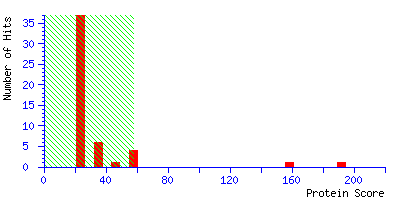
**Timestamp : 5 Apr 2011 at 12:35:26 GMT**

**Warning : A Peptide summary report will usually give a much clearer picture of MS/MS search results.**

**Top Score : 192 for isotig14336, putative nuclear encoded protein Method: similarity and extension**

**Mascot Score Histogram**

Protein score is -10\*Log(P), where P is the probability that the observed match is a random event.  
Protein scores greater than 58 are significant (p<0.05).  
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



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**Protein Summary Report**

|  |  |  |  |
| --- | --- | --- | --- |
|  |  |  | [Help](http://msmsms/mascot/help/msms_summaries_help.html" \t "_blank) |
|  | Significance threshold p< | Max. number of hits |  |

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**Index**

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
|  | **Accession** | **Mass** | **Score** | **Description** |
| **1.** | [**isotig14336**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20110405/F014358.dat#Hit1) | 14407 | 192 | putative nuclear encoded protein Method: similarity and extension |
| **2.** | [**isotig14337**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20110405/F014358.dat#Hit2) | 14387 | 153 | putative nuclear encoded protein Method: similarity and extension |
| **3.** | [**isotig19733**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20110405/F014358.dat#Hit3) | 14161 | 60 | putative nuclear encoded protein Method: similarity and extension |
| **4.** | [**isotig21928**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20110405/F014358.dat#Hit4) | 14159 | 60 | putative nuclear encoded protein Method: similarity and extension |
| **5.** | [**isotig09197**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20110405/F014358.dat#Hit5) | 14129 | 60 | putative nuclear encoded protein Method: similarity and extension |
| **6.** | [**contig45229**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20110405/F014358.dat#Hit6) | 14139 | 57 | putative nuclear encoded protein Method: similarity and extension |
| **7.** | [**isotig09196**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20110405/F014358.dat#Hit7) | 13826 | 52 | putative nuclear encoded protein Method: similarity and extension |
| **8.** | [**isotig22081**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20110405/F014358.dat#Hit8) | 10921 | 36 | putative nuclear encoded protein Method: Longest ORF |
| **9.** | [**contig16842**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20110405/F014358.dat#Hit9) | 40199 | 34 | putative nuclear encoded protein Method: similarity and extension |
| **10.** | [**contig02082**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20110405/F014358.dat#Hit10) | 46378 | 32 | putative nuclear encoded protein Method: similarity and extension |
| **11.** | [**isotig30345**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20110405/F014358.dat#Hit11) | 9062 | 31 | putative nuclear encoded protein Method: Longest ORF |
| **12.** | [**isotig25996**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20110405/F014358.dat#Hit12) | 7309 | 31 | putative nuclear encoded protein Method: similarity and extension |
| **13.** | [**isotig32856**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20110405/F014358.dat#Hit13) | 10343 | 31 | putative nuclear encoded protein Method: Longest ORF |
| **14.** | [**isotig20901**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20110405/F014358.dat#Hit14) | 13223 | 29 | putative nuclear encoded protein Method: Longest ORF |
| **15.** | [**isotig03878**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20110405/F014358.dat#Hit15) | 19409 | 29 | putative nuclear encoded protein Method: ESTScan |
| **16.** | [**isotig03881**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20110405/F014358.dat#Hit16) | 19435 | 29 | putative nuclear encoded protein Method: ESTScan |
| **17.** | [**isotig30639**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20110405/F014358.dat#Hit17) | 11876 | 29 | putative nuclear encoded protein Method: ESTScan |
| **18.** | [**isotig11259**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20110405/F014358.dat#Hit18) | 14821 | 29 | putative nuclear encoded protein Method: Longest ORF |
| **19.** | [**isotig14351**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20110405/F014358.dat#Hit19) | 33197 | 29 | putative nuclear encoded protein Method: similarity and extension |
| **20.** | [**isotig00419**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20110405/F014358.dat#Hit20) | 10546 | 29 | putative nuclear encoded protein Method: similarity and extension |

**Results List**

|  |  |
| --- | --- |
| **1.** | [isotig14336](http://msmsms/mascot/cgi/protein_view.pl?file=../data/20110405/F014358.dat&hit=1" \t "_blank)    **Mass:** 14407    **Score:** 192    **Expect:** 2.2e-015  **Matches:** 16 |
|  | putative nuclear encoded protein Method: similarity and extension |

|  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | **Observed** | **Mr(expt)** | **Mr(calc)** | **ppm** | **Start** |  | **End** | **Miss** | **Ions** | **Peptide** |
|  | 814.3730 | 813.3657 | 813.4569 | -112.10 | 99 | - | 105 | 1 | --- | K.GQLNRAR.L |
|  | 832.3800 | 831.3727 | 831.4888 | -139.58 | 89 | - | 96 | 0 | --- | R.LALMAGLK.E + Oxidation (M) |
|  | 844.3469 | 843.3396 | 843.4562 | -138.26 | 97 | - | 103 | 1 | --- | K.EKGQLNR.A |
|  | 844.3469 | 843.3396 | 843.4562 | -138.26 | 97 | - | 103 | 1 | 20 | K.EKGQLNR.A |
|  | 889.3837 | 888.3764 | 888.5029 | -142.29 | 81 | - | 88 | 1 | --- | R.ASLESKVR.L |
|  | 889.3837 | 888.3764 | 888.5029 | -142.29 | 81 | - | 88 | 1 | 19 | R.ASLESKVR.L |
|  | 952.4576 | 951.4503 | 951.5865 | -143.14 | 104 | - | 112 | 1 | --- | R.ARLLPPGTK.V |
|  | 952.4576 | 951.4503 | 951.5865 | -143.14 | 104 | - | 112 | 1 | 4 | R.ARLLPPGTK.V |
|  | 1087.5118 | 1086.5045 | 1086.6583 | -141.52 | 87 | - | 96 | 1 | --- | K.VRLALMAGLK.E + Oxidation (M) |
|  | 1089.4779 | 1088.4706 | 1088.6263 | -143.03 | 89 | - | 98 | 1 | --- | R.LALMAGLKEK.G + Oxidation (M) |
|  | 1089.4779 | 1088.4706 | 1088.6263 | -143.03 | 89 | - | 98 | 1 | 65 | R.LALMAGLKEK.G + Oxidation (M) |
|  | 1344.6171 | 1343.6098 | 1343.7959 | -138.44 | 87 | - | 98 | 2 | --- | K.VRLALMAGLKEK.G + Oxidation (M) |
|  | 1632.6080 | 1631.6007 | 1631.8267 | -138.50 | 59 | - | 73 | 1 | --- | K.NPGTTTIPNKFTGER.T |
|  | 1632.6080 | 1631.6007 | 1631.8267 | -138.50 | 59 | - | 73 | 1 | 8 | K.NPGTTTIPNKFTGER.T |
|  | 1657.7026 | 1656.6953 | 1656.9345 | -144.33 | 89 | - | 103 | 2 | --- | R.LALMAGLKEKGQLNR.A + Oxidation (M) |
|  | 1657.7026 | 1656.6953 | 1656.9345 | -144.33 | 89 | - | 103 | 2 | --- | R.LALMAGLKEKGQLNR.A + Oxidation (M) |

|  |  |
| --- | --- |
|  | **No match to:** 802.3357, 804.3039, 805.2978, 819.3575, 826.3769, 829.1153, 830.3461, 832.1935, 842.3950, 856.3993, 862.4095, 870.4163, 895.3223, 900.4395, 916.4443, 931.3651, 963.3280, 972.4426, 982.2914, 990.4576, 1037.4076, 1041.3606, 1045.4165, 1045.4165, 1065.3638, 1092.4343, 1111.4493, 1235.3622, 1379.4065, 1379.4065, 1395.4011, 1398.4814, 1406.4209, 1412.4938, 1421.5433, 1454.4219, 1470.3997, 1470.3997, 1486.3881, 1519.6093, 1791.4774, 1791.4774, 1974.6498, 2085.7327 |

|  |  |
| --- | --- |
| **2.** | [isotig14337](http://msmsms/mascot/cgi/protein_view.pl?file=../data/20110405/F014358.dat&hit=2" \t "_blank)    **Mass:** 14387    **Score:** 153    **Expect:** 1.7e-011  **Matches:** 13 |
|  | putative nuclear encoded protein Method: similarity and extension |

|  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | **Observed** | **Mr(expt)** | **Mr(calc)** | **ppm** | **Start** |  | **End** | **Miss** | **Ions** | **Peptide** |
|  | 814.3730 | 813.3657 | 813.4569 | -112.10 | 99 | - | 105 | 1 | --- | K.GQLNRAR.L |
|  | 832.3800 | 831.3727 | 831.4888 | -139.58 | 89 | - | 96 | 0 | --- | R.LALMAGLK.E + Oxidation (M) |
|  | 844.3469 | 843.3396 | 843.4562 | -138.26 | 97 | - | 103 | 1 | --- | K.EKGQLNR.A |
|  | 844.3469 | 843.3396 | 843.4562 | -138.26 | 97 | - | 103 | 1 | 20 | K.EKGQLNR.A |
|  | 952.4576 | 951.4503 | 951.5865 | -143.14 | 104 | - | 112 | 1 | --- | R.ARLLPPGTK.V |
|  | 952.4576 | 951.4503 | 951.5865 | -143.14 | 104 | - | 112 | 1 | 4 | R.ARLLPPGTK.V |
|  | 1087.5118 | 1086.5045 | 1086.6583 | -141.52 | 87 | - | 96 | 1 | --- | K.VRLALMAGLK.E + Oxidation (M) |
|  | 1089.4779 | 1088.4706 | 1088.6263 | -143.03 | 89 | - | 98 | 1 | --- | R.LALMAGLKEK.G + Oxidation (M) |
|  | 1089.4779 | 1088.4706 | 1088.6263 | -143.03 | 89 | - | 98 | 1 | 65 | R.LALMAGLKEK.G + Oxidation (M) |
|  | 1344.6171 | 1343.6098 | 1343.7959 | -138.44 | 87 | - | 98 | 2 | --- | K.VRLALMAGLKEK.G + Oxidation (M) |
|  | 1412.4938 | 1411.4865 | 1411.6943 | -147.19 | 74 | - | 86 | 1 | --- | R.TFSSSSRPSLESK.V |
|  | 1657.7026 | 1656.6953 | 1656.9345 | -144.33 | 89 | - | 103 | 2 | --- | R.LALMAGLKEKGQLNR.A + Oxidation (M) |
|  | 1657.7026 | 1656.6953 | 1656.9345 | -144.33 | 89 | - | 103 | 2 | --- | R.LALMAGLKEKGQLNR.A + Oxidation (M) |

|  |  |
| --- | --- |
|  | **No match to:** 802.3357, 804.3039, 805.2978, 819.3575, 826.3769, 829.1153, 830.3461, 832.1935, 842.3950, 856.3993, 862.4095, 870.4163, 889.3837, 889.3837, 895.3223, 900.4395, 916.4443, 931.3651, 963.3280, 972.4426, 982.2914, 990.4576, 1037.4076, 1041.3606, 1045.4165, 1045.4165, 1065.3638, 1092.4343, 1111.4493, 1235.3622, 1379.4065, 1379.4065, 1395.4011, 1398.4814, 1406.4209, 1421.5433, 1454.4219, 1470.3997, 1470.3997, 1486.3881, 1519.6093, 1632.6080, 1632.6080, 1791.4774, 1791.4774, 1974.6498, 2085.7327 |

**http://msmsms/mascot/images/88x31_logo_white.gifMascot Search Results**

**Protein View**

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Match to: **isotig14336** Score: **192** Expect: **2.2e-015**

**putative nuclear encoded protein Method: similarity and extension**

Nominal mass (Mr): **14407**; Calculated pI value: **6.73**

NCBI BLAST search of [isotig14336](http://www.ncbi.nlm.nih.gov/blast/Blast.cgi?ALIGNMENTS=50&ALIGNMENT_VIEW=Pairwise&AUTO_FORMAT=Semiauto&CDD_SEARCH=on&CLIENT=web&COMPOSITION_BASED_STATISTICS=on&DATABASE=nr&DESCRIPTIONS=100&ENTREZ_QUERY=(none)&EXPECT=10&FILTER=L&FORMAT_BLOCK_ON_RESPAGE=None&FORMAT_OBJECT=Alignment&FORMAT_TYPE=HTML&GAPCOSTS=11+1&I_THRESH=0.001&LAYOUT=TwoWindows&MATRIX_NAME=BLOSUM62&NCBI_GI=on&PAGE=Proteins&PROGRAM=blastp&QUERY=MLFAAITLSFLLANVGAEPECLTYHPLAGLYKEFNMRYINPDLDYDPTLIHDACDEAKNPGTTTIPNKFTGERTFSSSSRASLESKVRLALMAGLKEKGQLNRARLLPPGTKVGCDGMMDGNKVRVVCLYE&SERVICE=plain&SET_DEFAULTS.x=9&SET_DEFAULTS.y=5&SHOW_OVERVIEW=on&WORD_SIZE=3&END_OF_HTTPGET=Yes" \t "_blank) against nr

Unformatted [sequence string](http://msmsms/mascot/cgi/getseq.pl?cooperia_oncophora+isotig14336+seq" \t "_blank) for pasting into other applications

Variable modifications: Oxidation (HW),Oxidation (M)

Cleavage by Trypsin/P: cuts C-term side of KR

Sequence Coverage: **35%**

Matched peptides shown in **Bold Red**

**1** MLFAAITLSF LLANVGAEPE CLTYHPLAGL YKEFNMRYIN PDLDYDPTLI

**51** HDACDEAK**NP GTTTIPNKFT GER**TFSSSSR **ASLESKVRLA LMAGLKEKGQ**

**101 LNRARLLPPG TK**VGCDGMMD GNKVRVVCLY E



  Residue Number  Increasing Mass  Decreasing Mass

**Start - End Observed Mr(expt) Mr(calc) ppm Miss Sequence**

**59 - 73 1632.6080 1631.6007 1631.8267 -139 1 K.NPGTTTIPNKFTGER.T**  ([No match](http://msmsms/mascot/cgi/peptide_view.pl?file=../data/20110405/F014358.dat&query=53&hit=1" \t "_blank))

**59 - 73 1632.6080 1631.6007 1631.8267 -139 1 K.NPGTTTIPNKFTGER.T**  ([Ions score 8](http://msmsms/mascot/cgi/peptide_view.pl?file=../data/20110405/F014358.dat&query=54&hit=1" \t "_blank))

**81 - 88 889.3837 888.3764 888.5029 -142 1 R.ASLESKVR.L**  ([No match](http://msmsms/mascot/cgi/peptide_view.pl?file=../data/20110405/F014358.dat&query=17&hit=1" \t "_blank))

**81 - 88 889.3837 888.3764 888.5029 -142 1 R.ASLESKVR.L**  ([Ions score 19](http://msmsms/mascot/cgi/peptide_view.pl?file=../data/20110405/F014358.dat&query=18&hit=1" \t "_blank))

**87 - 96 1087.5118 1086.5045 1086.6583 -142 1 K.VRLALMAGLK.E**  Oxidation (M) ([No match](http://msmsms/mascot/cgi/peptide_view.pl?file=../data/20110405/F014358.dat&query=34&hit=1" \t "_blank))

**87 - 98 1344.6171 1343.6098 1343.7959 -138 2 K.VRLALMAGLKEK.G**  Oxidation (M) ([No match](http://msmsms/mascot/cgi/peptide_view.pl?file=../data/20110405/F014358.dat&query=40&hit=1" \t "_blank))

**89 - 96 832.3800 831.3727 831.4888 -140 0 R.LALMAGLK.E**  Oxidation (M) ([No match](http://msmsms/mascot/cgi/peptide_view.pl?file=../data/20110405/F014358.dat&query=10&hit=1" \t "_blank))

**89 - 98 1089.4779 1088.4706 1088.6263 -143 1 R.LALMAGLKEK.G**  Oxidation (M) ([No match](http://msmsms/mascot/cgi/peptide_view.pl?file=../data/20110405/F014358.dat&query=35&hit=1" \t "_blank))

**89 - 98 1089.4779 1088.4706 1088.6263 -143 1 R.LALMAGLKEK.G**  Oxidation (M) ([Ions score 65](http://msmsms/mascot/cgi/peptide_view.pl?file=../data/20110405/F014358.dat&query=36&hit=1" \t "_blank))

**89 - 103 1657.7026 1656.6953 1656.9345 -144 2 R.LALMAGLKEKGQLNR.A**  Oxidation (M) ([No match](http://msmsms/mascot/cgi/peptide_view.pl?file=../data/20110405/F014358.dat&query=55&hit=1" \t "_blank))

**89 - 103 1657.7026 1656.6953 1656.9345 -144 2 R.LALMAGLKEKGQLNR.A**  Oxidation (M) ([No match](http://msmsms/mascot/cgi/peptide_view.pl?file=../data/20110405/F014358.dat&query=56&hit=1" \t "_blank))

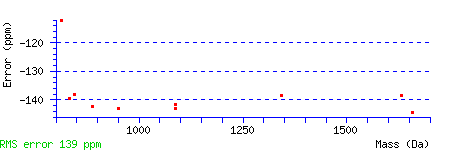
**97 - 103 844.3469 843.3396 843.4562 -138 1 K.EKGQLNR.A**  ([No match](http://msmsms/mascot/cgi/peptide_view.pl?file=../data/20110405/F014358.dat&query=12&hit=1" \t "_blank))

**97 - 103 844.3469 843.3396 843.4562 -138 1 K.EKGQLNR.A**  ([Ions score 20](http://msmsms/mascot/cgi/peptide_view.pl?file=../data/20110405/F014358.dat&query=13&hit=1" \t "_blank))

**99 - 105 814.3730 813.3657 813.4569 -112 1 K.GQLNRAR.L**  ([No match](http://msmsms/mascot/cgi/peptide_view.pl?file=../data/20110405/F014358.dat&query=4&hit=1" \t "_blank))

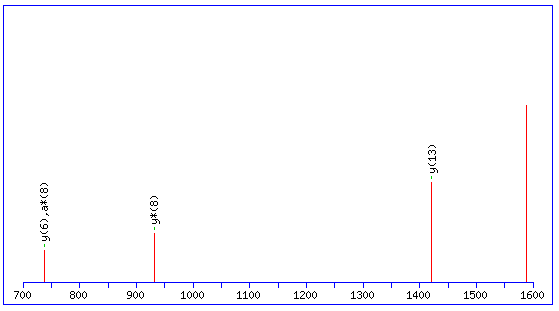
**104 - 112 952.4576 951.4503 951.5865 -143 1 R.ARLLPPGTK.V**  ([No match](http://msmsms/mascot/cgi/peptide_view.pl?file=../data/20110405/F014358.dat&query=23&hit=1" \t "_blank))

**104 - 112 952.4576 951.4503 951.5865 -143 1 R.ARLLPPGTK.V**  ([Ions score 4](http://msmsms/mascot/cgi/peptide_view.pl?file=../data/20110405/F014358.dat&query=24&hit=1" \t "_blank))



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🡪 Annotated MS2 spectrum for peptide NPGTTTIPNKFTGER



**Monoisotopic mass of neutral peptide Mr(calc):** 1631.8267

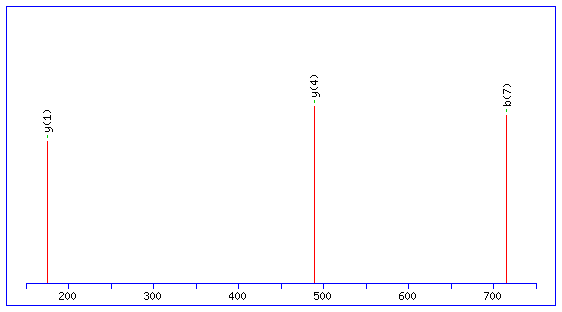
**Ions Score:** 8 **Expect:** 14

**Matches :** 4/264 fragment ions using 4 most intense peaks   ([help](http://msmsms/mascot/help/results_help.html" \l "PEP" \t "_blank))

|  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **#** | **Immon.** | **a** | **a\*** | **a0** | **b** | **b\*** | **b0** | **Seq.** | **v** | **w** | **w'** | **y** | **y\*** | **y0** | **#** |
| **1** | 87.0553 | 87.0553 | 70.0287 |  | 115.0502 | 98.0237 |  | **N** |  |  |  |  |  |  | **15** |
| **2** | 70.0651 | 184.1081 | 167.0815 |  | 212.1030 | 195.0764 |  | **P** | 1476.7441 | 1475.7489 |  | 1518.7911 | 1501.7645 | 1500.7805 | **14** |
| **3** | 30.0338 | 241.1295 | 224.1030 |  | 269.1244 | 252.0979 |  | **G** |  |  |  | ***1421.7383*** | 1404.7118 | 1403.7278 | **13** |
| **4** | 74.0600 | 342.1772 | 325.1506 | 324.1666 | 370.1721 | 353.1456 | 352.1615 | **T** | 1318.6750 | 1331.6954 | 1333.6747 | 1364.7169 | 1347.6903 | 1346.7063 | **12** |
| **5** | 74.0600 | 443.2249 | 426.1983 | 425.2143 | 471.2198 | 454.1932 | 453.2092 | **T** | 1217.6273 | 1230.6477 | 1232.6270 | 1263.6692 | 1246.6426 | 1245.6586 | **11** |
| **6** | 74.0600 | 544.2726 | 527.2460 | 526.2620 | 572.2675 | 555.2409 | 554.2569 | **T** | 1116.5796 | 1129.6000 | 1131.5793 | 1162.6215 | 1145.5950 | 1144.6109 | **10** |
| **7** | 86.0964 | 657.3566 | 640.3301 | 639.3461 | 685.3515 | 668.3250 | 667.3410 | **I** | 1003.4956 | 1016.5160 | 1030.5316 | 1061.5738 | 1044.5473 | 1043.5633 | **9** |
| **8** | 70.0651 | 754.4094 | 737.3828 | 736.3988 | 782.4043 | 765.3777 | 764.3937 | **P** | 906.4428 | 905.4476 |  | 948.4898 | 931.4632 | 930.4792 | **8** |
| **9** | 87.0553 | 868.4523 | 851.4258 | 850.4417 | 896.4472 | 879.4207 | 878.4367 | **N** | 792.3999 | 791.4046 |  | 851.4370 | 834.4104 | 833.4264 | **7** |
| **10** | 101.1073 | 996.5473 | 979.5207 | 978.5367 | 1024.5422 | 1007.5156 | 1006.5316 | **K** | 664.3049 | 663.3097 |  | ***737.3941*** | 720.3675 | 719.3835 | **6** |
| **11** | 120.0808 | 1143.6157 | 1126.5891 | 1125.6051 | 1171.6106 | 1154.5841 | 1153.6000 | **F** | 517.2365 |  |  | 609.2991 | 592.2726 | 591.2885 | **5** |
| **12** | 74.0600 | 1244.6634 | 1227.6368 | 1226.6528 | 1272.6583 | 1255.6317 | 1254.6477 | **T** | 416.1888 | 429.2092 | 431.1885 | 462.2307 | 445.2041 | 444.2201 | **4** |
| **13** | 30.0338 | 1301.6848 | 1284.6583 | 1283.6743 | 1329.6797 | 1312.6532 | 1311.6692 | **G** |  |  |  | 361.1830 | 344.1565 | 343.1724 | **3** |
| **14** | 102.0550 | 1430.7274 | 1413.7009 | 1412.7169 | 1458.7223 | 1441.6958 | 1440.7118 | **E** | 230.1248 | 229.1295 |  | 304.1615 | 287.1350 | 286.1510 | **2** |
| **15** | 129.1135 |  |  |  |  |  |  | **R** | 74.0237 | 73.0284 |  | 175.1190 | 158.0924 |  | **1** |

|  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **Seq** | **ya** | **yb** | **Seq** | **ya** | **yb** | **Seq** | **ya** | **yb** |
| **PG** | 127.0866 | 155.0815 | **PGT** | 228.1343 | 256.1292 | **PGTT** | 329.1819 | 357.1769 |
| **PGTTT** | 430.2296 | 458.2245 | **PGTTTI** | 543.3137 | 571.3086 | **PGTTTIP** | 640.3665 | 668.3614 |
| **GT** | 131.0815 | 159.0764 | **GTT** | 232.1292 | 260.1241 | **GTTT** | 333.1769 | 361.1718 |
| **GTTTI** | 446.2609 | 474.2558 | **GTTTIP** | 543.3137 | 571.3086 | **GTTTIPN** | 657.3566 | 685.3515 |
| **TT** | 175.1077 | 203.1026 | **TTT** | 276.1554 | 304.1503 | **TTTI** | 389.2395 | 417.2344 |
| **TTTIP** | 486.2922 | 514.2871 | **TTTIPN** | 600.3352 | 628.3301 | **TT** | 175.1077 | 203.1026 |
| **TTI** | 288.1918 | 316.1867 | **TTIP** | 385.2445 | 413.2395 | **TTIPN** | 499.2875 | 527.2824 |
| **TTIPNK** | 627.3824 | 655.3774 | **TI** | 187.1441 | 215.1390 | **TIP** | 284.1969 | 312.1918 |
| **TIPN** | 398.2398 | 426.2347 | **TIPNK** | 526.3348 | 554.3297 | **TIPNKF** | 673.4032 | 701.3981 |
| **IP** | 183.1492 | 211.1441 | **IPN** | 297.1921 | 325.1870 | **IPNK** | 425.2871 | 453.2820 |
| **IPNKF** | 572.3555 | 600.3504 | **IPNKFT** | 673.4032 | 701.3981 | **PN** | 184.1081 | 212.1030 |
| **PNK** | 312.2030 | 340.1979 | **PNKF** | 459.2714 | 487.2663 | **PNKFT** | 560.3191 | 588.3140 |
| **PNKFTG** | 617.3406 | 645.3355 | **NK** | 215.1503 | 243.1452 | **NKF** | 362.2187 | 390.2136 |
| **NKFT** | 463.2663 | 491.2613 | **NKFTG** | 520.2878 | 548.2827 | **NKFTGE** | 649.3304 | 677.3253 |
| **KF** | 248.1757 | 276.1707 | **KFT** | 349.2234 | 377.2183 | **KFTG** | 406.2449 | 434.2398 |
| **KFTGE** | 535.2875 | 563.2824 | **FT** | 221.1285 | 249.1234 | **FTG** | 278.1499 | 306.1448 |
| **FTGE** | 407.1925 | 435.1874 | **TG** | 131.0815 | 159.0764 | **TGE** | 260.1241 | 288.1190 |
| **GE** | 159.0764 | 187.0713 |  |  |  |  |  |  |

🡪 Annotated MS2 spectrum for peptide ASLESKVR



**Monoisotopic mass of neutral peptide Mr(calc):** 888.5029

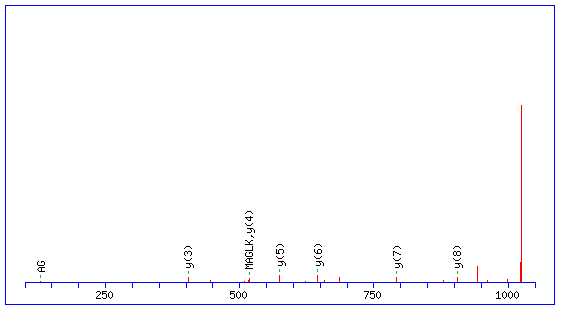
**Ions Score:** 19 **Expect:** 1.1

**Matches :** 3/100 fragment ions using 3 most intense peaks   ([help](http://msmsms/mascot/help/results_help.html" \l "PEP" \t "_blank))

|  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **#** | **Immon.** | **a** | **a\*** | **a0** | **b** | **b\*** | **b0** | **Seq.** | **v** | **w** | **y** | **y\*** | **y0** | **#** |
| **1** | 44.0495 | 44.0495 |  |  | 72.0444 |  |  | **A** |  |  |  |  |  | **8** |
| **2** | 60.0444 | 131.0815 |  | 113.0709 | 159.0764 |  | 141.0659 | **S** | 786.4468 | 785.4516 | 818.4730 | 801.4465 | 800.4625 | **7** |
| **3** | 86.0964 | 244.1656 |  | 226.1550 | 272.1605 |  | 254.1499 | **L** | 673.3628 | 672.3675 | 731.4410 | 714.4145 | 713.4304 | **6** |
| **4** | 102.0550 | 373.2082 |  | 355.1976 | 401.2031 |  | 383.1925 | **E** | 544.3202 | 543.3249 | 618.3570 | 601.3304 | 600.3464 | **5** |
| **5** | 60.0444 | 460.2402 |  | 442.2296 | 488.2351 |  | 470.2245 | **S** | 457.2881 | 456.2929 | ***489.3144*** | 472.2878 | 471.3038 | **4** |
| **6** | 101.1073 | 588.3352 | 571.3086 | 570.3246 | 616.3301 | 599.3035 | 598.3195 | **K** | 329.1932 | 328.1979 | 402.2823 | 385.2558 |  | **3** |
| **7** | 72.0808 | 687.4036 | 670.3770 | 669.3930 | **715.3985** | 698.3719 | 697.3879 | **V** | 230.1248 | 243.1452 | 274.1874 | 257.1608 |  | **2** |
| **8** | 129.1135 |  |  |  |  |  |  | **R** | 74.0237 | 73.0284 | ***175.1190*** | 158.0924 |  | **1** |

|  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **Seq** | **ya** | **yb** | **Seq** | **ya** | **yb** | **Seq** | **ya** | **yb** |
| **SL** | 173.1285 | 201.1234 | **SLE** | 302.1710 | 330.1660 | **SLES** | 389.2031 | 417.1980 |
| **SLESK** | 517.2980 | 545.2930 | **SLESKV** | 616.3665 | 644.3614 | **LE** | 215.1390 | 243.1339 |
| **LES** | 302.1710 | 330.1660 | **LESK** | 430.2660 | 458.2609 | **LESKV** | 529.3344 | 557.3293 |
| **ES** | 189.0870 | 217.0819 | **ESK** | 317.1819 | 345.1769 | **ESKV** | 416.2504 | 444.2453 |
| **SK** | 188.1394 | 216.1343 | **SKV** | 287.2078 | 315.2027 | **KV** | 200.1757 | 228.1707 |

🡪 Annotated MS2 spectrum for peptide LALMAGLKEK



**Monoisotopic mass of neutral peptide Mr(calc):** 1088.6263

**Variable modifications:**

**M4 :** Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983

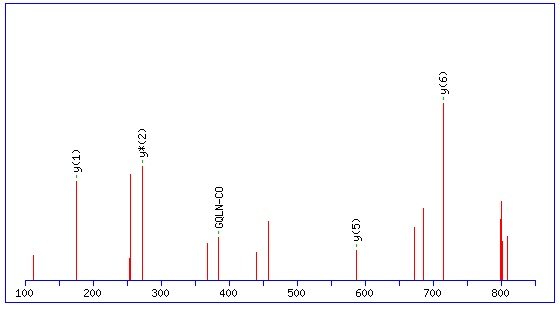
**Ions Score:** 65 **Expect:** 2.4e-005

**Matches :** 8/168 fragment ions using 8 most intense peaks   ([help](http://msmsms/mascot/help/results_help.html" \l "PEP" \t "_blank))

|  |  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **#** | **Immon.** | **a** | **a\*** | **a0** | **b** | **b\*** | **b0** | **Seq.** | **y** | **y\*** | **y0** | **#** |
| **1** | 86.0964 | 86.0964 |  |  | 114.0913 |  |  | **L** |  |  |  | **10** |
| **2** | 44.0495 | 157.1335 |  |  | 185.1285 |  |  | **A** | 976.5496 | 959.5230 | 958.5390 | **9** |
| **3** | 86.0964 | 270.2176 |  |  | 298.2125 |  |  | **L** | ***905.5125*** | 888.4859 | 887.5019 | **8** |
| **4** | 120.0478 | 417.2530 |  |  | 445.2479 |  |  | **M** | ***792.4284*** | 775.4019 | 774.4178 | **7** |
| **5** | 44.0495 | 488.2901 |  |  | 516.2850 |  |  | **A** | ***645.3930*** | 628.3665 | 627.3824 | **6** |
| **6** | 30.0338 | 545.3116 |  |  | 573.3065 |  |  | **G** | ***574.3559*** | 557.3293 | 556.3453 | **5** |
| **7** | 86.0964 | 658.3956 |  |  | 686.3906 |  |  | **L** | ***517.3344*** | 500.3079 | 499.3239 | **4** |
| **8** | 101.1073 | 786.4906 | 769.4641 |  | 814.4855 | 797.4590 |  | **K** | ***404.2504*** | 387.2238 | 386.2398 | **3** |
| **9** | 102.0550 | 915.5332 | 898.5067 | 897.5226 | 943.5281 | 926.5016 | 925.5176 | **E** | 276.1554 | 259.1288 | 258.1448 | **2** |
| **10** | 101.1073 |  |  |  |  |  |  | **K** | 147.1128 | 130.0863 |  | **1** |

|  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **Seq** | **ya** | **yb** | **Seq** | **ya** | **yb** | **Seq** | **ya** | **yb** |
| **AL** | 157.1335 | 185.1285 | **ALM** | 304.1689 | 332.1639 | **ALMA** | 375.2061 | 403.2010 |
| **ALMAG** | 432.2275 | 460.2224 | **ALMAGL** | 545.3116 | 573.3065 | **ALMAGLK** | 673.4065 | 701.4015 |
| **LM** | 233.1318 | 261.1267 | **LMA** | 304.1689 | 332.1639 | **LMAG** | 361.1904 | 389.1853 |
| **LMAGL** | 474.2745 | 502.2694 | **LMAGLK** | 602.3694 | 630.3643 | **MA** | 191.0849 | 219.0798 |
| **MAG** | 248.1063 | 276.1013 | **MAGL** | 361.1904 | 389.1853 | **MAGLK** | 489.2854 | 517.2803 |
| **MAGLKE** | 618.3280 | 646.3229 | **AG** | 101.0709 | 129.0659 | **AGL** | 214.1550 | 242.1499 |
| **AGLK** | 342.2500 | 370.2449 | **AGLKE** | 471.2926 | 499.2875 | **GL** | 143.1179 | 171.1128 |
| **GLK** | 271.2129 | 299.2078 | **GLKE** | 400.2554 | 428.2504 | **LK** | 214.1914 | 242.1863 |
| **LKE** | 343.2340 | 371.2289 | **KE** | 230.1499 | 258.1448 |  |  |  |

🡪 Annotated MS2 spectrum for peptide EKGQLNR



**Monoisotopic mass of neutral peptide Mr(calc):** 843.4562

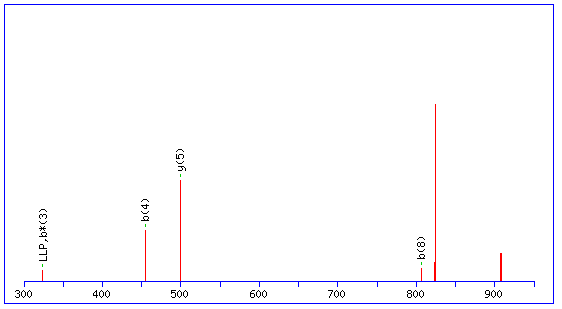
**Ions Score:** 20 **Expect:** 0.65

**Matches :** 6/83 fragment ions using 7 most intense peaks   ([help](http://msmsms/mascot/help/results_help.html" \l "PEP" \t "_blank))

|  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **#** | **Immon.** | **a** | **a\*** | **a0** | **b** | **b\*** | **b0** | **Seq.** | **v** | **w** | **y** | **y\*** | **#** |
| **1** | 102.0550 | 102.0550 |  | 84.0444 | 130.0499 |  | 112.0393 | **E** |  |  |  |  | **7** |
| **2** | 101.1073 | 230.1499 | 213.1234 | 212.1394 | 258.1448 | 241.1183 | 240.1343 | **K** | 642.3318 | 641.3366 | ***715.4209*** | 698.3944 | **6** |
| **3** | 30.0338 | 287.1714 | 270.1448 | 269.1608 | 315.1663 | 298.1397 | 297.1557 | **G** |  |  | ***587.3260*** | 570.2994 | **5** |
| **4** | 101.0709 | 415.2300 | 398.2034 | 397.2194 | 443.2249 | 426.1983 | 425.2143 | **Q** | 457.2518 | 456.2565 | 530.3045 | 513.2780 | **4** |
| **5** | 86.0964 | 528.3140 | 511.2875 | 510.3035 | 556.3089 | 539.2824 | 538.2984 | **L** | 344.1677 | 343.1724 | 402.2459 | 385.2194 | **3** |
| **6** | 87.0553 | 642.3569 | 625.3304 | 624.3464 | 670.3519 | 653.3253 | 652.3413 | **N** | 230.1248 | 229.1295 | 289.1619 | 272.1353 | **2** |
| **7** | 129.1135 |  |  |  |  |  |  | **R** | 74.0237 | 73.0284 | ***175.1190*** | 158.0924 | **1** |

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| --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **Seq** | **ya** | **yb** | **Seq** | **ya** | **yb** | **Seq** | **ya** | **yb** |
| **KG** | 158.1288 | 186.1237 | **KGQ** | 286.1874 | 314.1823 | **KGQL** | 399.2714 | 427.2663 |
| **KGQLN** | 513.3144 | 541.3093 | **GQ** | 158.0924 | 186.0873 | **GQL** | 271.1765 | 299.1714 |
| **GQLN** | 385.2194 | 413.2143 | **QL** | 214.1550 | 242.1499 | **QLN** | 328.1979 | 356.1928 |
| **LN** | 200.1394 | 228.1343 |  |  |  |  |  |  |

🡪 Annotated MS2 spectrum for peptide ARLLPPGTK



**Monoisotopic mass of neutral peptide Mr(calc):** 951.5865

**Ions Score:** 4 **Expect:** 28

**Matches :** 5/113 fragment ions using 7 most intense peaks   ([help](http://msmsms/mascot/help/results_help.html" \l "PEP" \t "_blank))

|  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **#** | **Immon.** | **a** | **a\*** | **a0** | **b** | **b\*** | **b0** | **d** | **d'** | **Seq.** | **v** | **w** | **y** | **y\*** | **y0** | **#** |
| **1** | 44.0495 | 44.0495 |  |  | 72.0444 |  |  |  |  | **A** |  |  |  |  |  | **9** |
| **2** | 129.1135 | 200.1506 | 183.1240 |  | 228.1455 | 211.1190 |  | 115.0866 |  | **R** | 780.4614 | 779.4662 | 881.5567 | 864.5302 | 863.5461 | **8** |
| **3** | 86.0964 | 313.2346 | 296.2081 |  | 341.2296 | 324.2030 |  | 271.1877 |  | **L** |  |  | 725.4556 | 708.4291 | 707.4450 | **7** |
| **4** | 86.0964 | 426.3187 | 409.2922 |  | ***454.3136*** | 437.2871 |  | 384.2718 |  | **L** |  |  | 612.3715 | 595.3450 | 594.3610 | **6** |
| **5** | 70.0651 | 523.3715 | 506.3449 |  | 551.3664 | 534.3398 |  | 497.3558 |  | **P** |  |  | 499.2875 | 482.2609 | 481.2769 | **5** |
| **6** | 70.0651 | 620.4242 | 603.3977 |  | 648.4192 | 631.3926 |  | 594.4086 |  | **P** |  |  | 402.2347 | 385.2082 | 384.2241 | **4** |
| **7** | 30.0338 | 677.4457 | 660.4192 |  | 705.4406 | 688.4141 |  |  |  | **G** |  |  | 305.1819 | 288.1554 | 287.1714 | **3** |
| **8** | 74.0600 | 778.4934 | 761.4668 | 760.4828 | ***806.4883*** | 789.4618 | 788.4777 | 762.4985 | 764.4777 | **T** |  |  | 248.1605 | 231.1339 | 230.1499 | **2** |
| **9** | 101.1073 |  |  |  |  |  |  |  |  | **K** |  |  | 147.1128 | 130.0863 |  | **1** |

|  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **Seq** | **ya** | **yb** | **Seq** | **ya** | **yb** | **Seq** | **ya** | **yb** |
| **RL** | 242.1975 | 270.1925 | **RLL** | 355.2816 | 383.2765 | **RLLP** | 452.3344 | 480.3293 |
| **RLLPP** | 549.3871 | 577.3820 | **RLLPPG** | 606.4086 | 634.4035 | **LL** | 199.1805 | 227.1754 |
| **LLP** | 296.2333 | 324.2282 | **LLPP** | 393.2860 | 421.2809 | **LLPPG** | 450.3075 | 478.3024 |
| **LLPPGT** | 551.3552 | 579.3501 | **LP** | 183.1492 | 211.1441 | **LPP** | 280.2020 | 308.1969 |
| **LPPG** | 337.2234 | 365.2183 | **LPPGT** | 438.2711 | 466.2660 | **PP** | 167.1179 | 195.1128 |
| **PPG** | 224.1394 | 252.1343 | **PPGT** | 325.1870 | 353.1819 | **PG** | 127.0866 | 155.0815 |
| **PGT** | 228.1343 | 256.1292 | **GT** | 131.0815 | 159.0764 |  |  |  |

**Spot 16:**

**http://msmsms/mascot/images/88x31_logo_white.gifMascot Search Results**

**User :**

**Email :**

**Search title : SampleSetID: 341, AnalysisID: 561, MaldiWellID: 45050, SpectrumID: 137465, Path=\Jimmy\Cooperia Adult ES 20110221\20110221 MS en MSMS**

**Database : cooperia\_oncophora oncophora (33747 sequences; 5232511 residues)**

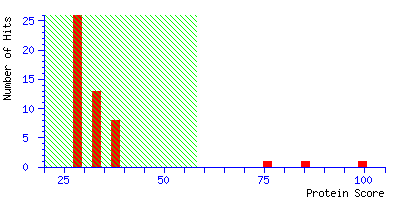
**Timestamp : 21 Feb 2011 at 15:37:18 GMT**

**Warning : A Peptide summary report will usually give a much clearer picture of MS/MS search results.**

**Top Score : 100 for contig45229, putative nuclear encoded protein Method: similarity and extension**

**Mascot Score Histogram**

Protein score is -10\*Log(P), where P is the probability that the observed match is a random event.  
Protein scores greater than 58 are significant (p<0.05).  
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Top of Form



**Protein Summary Report**

|  |  |  |  |
| --- | --- | --- | --- |
|  |  |  | [Help](http://msmsms/mascot/help/msms_summaries_help.html" \t "_blank) |
|  | Significance threshold p< | Max. number of hits |  |

Bottom of Form

Top of Form



Bottom of Form

**Index**

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
|  | **Accession** | **Mass** | **Score** | **Description** |
| **1.** | [**contig45229**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20110221/F013485.dat#Hit1) | 14139 | 100 | putative nuclear encoded protein Method: similarity and extension |
| **2.** | [**isotig17113**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20110221/F013485.dat#Hit2) | 14478 | 83 | putative nuclear encoded protein Method: similarity and extension |
| **3.** | [**isotig17160**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20110221/F013485.dat#Hit3) | 14996 | 77 | putative nuclear encoded protein Method: similarity and extension |
| **4.** | [**isotig21387**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20110221/F013485.dat#Hit4) | 12026 | 40 | putative nuclear encoded protein Method: Longest ORF |
| **5.** | [**isotig21928**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20110221/F013485.dat#Hit5) | 14159 | 38 | putative nuclear encoded protein Method: similarity and extension |
| **6.** | [**isotig09197**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20110221/F013485.dat#Hit6) | 14129 | 38 | putative nuclear encoded protein Method: similarity and extension |
| **7.** | [**isotig19764**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20110221/F013485.dat#Hit7) | 47568 | 37 | putative nuclear encoded protein Method: similarity and extension |
| **8.** | [**isotig26696**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20110221/F013485.dat#Hit8) | 24375 | 37 | putative nuclear encoded protein Method: similarity and extension |
| **9.** | [**isotig27927**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20110221/F013485.dat#Hit9) | 38685 | 37 | putative nuclear encoded protein Method: similarity and extension |
| **10.** | [**contig15387**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20110221/F013485.dat#Hit10) | 31507 | 37 | putative nuclear encoded protein Method: similarity and extension |
| **11.** | [**isotig14731**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20110221/F013485.dat#Hit11) | 15207 | 36 | putative nuclear encoded protein Method: similarity and extension |
| **12.** | [**isotig02635**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20110221/F013485.dat#Hit12) | 32723 | 34 | putative nuclear encoded protein Method: similarity and extension |
| **13.** | [**isotig18643**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20110221/F013485.dat#Hit13) | 32787 | 34 | putative nuclear encoded protein Method: similarity and extension |
| **14.** | [**isotig23672**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20110221/F013485.dat#Hit14) | 42082 | 33 | putative nuclear encoded protein Method: Longest ORF |
| **15.** | [**isotig06570**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20110221/F013485.dat#Hit15) | 11306 | 33 | putative nuclear encoded protein Method: Longest ORF |
| **16.** | [**isotig30478**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20110221/F013485.dat#Hit16) | 21312 | 32 | putative nuclear encoded protein Method: similarity and extension |
| **17.** | [**isotig27190**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20110221/F013485.dat#Hit17) | 12372 | 32 | putative nuclear encoded protein Method: similarity and extension |
| **18.** | [**isotig07058**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20110221/F013485.dat#Hit18) | 8610 | 32 | putative nuclear encoded protein Method: Longest ORF |
| **19.** | [**isotig07055**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20110221/F013485.dat#Hit19) | 8610 | 32 | putative nuclear encoded protein Method: Longest ORF |
| **20.** | [**isotig11021**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20110221/F013485.dat#Hit20) | 15114 | 31 | putative nuclear encoded protein Method: similarity and extension |

**Results List**

|  |  |
| --- | --- |
| **1.** | [contig45229](http://msmsms/mascot/cgi/protein_view.pl?file=../data/20110221/F013485.dat&hit=1" \t "_blank)    **Mass:** 14139    **Score:** 100    **Expect:** 3.8e-006  **Matches:** 7 |
|  | putative nuclear encoded protein Method: similarity and extension |

|  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | **Observed** | **Mr(expt)** | **Mr(calc)** | **ppm** | **Start** |  | **End** | **Miss** | **Ions** | **Peptide** |
|  | 834.4449 | 833.4376 | 833.4429 | -6.33 | 89 | - | 96 | 0 | --- | R.SALMAGLR.E + Oxidation (M) |
|  | 844.4680 | 843.4607 | 843.4562 | 5.32 | 97 | - | 103 | 1 | --- | R.EKGQLNR.A |
|  | 980.4872 | 979.4799 | 979.5161 | -36.92 | 124 | - | 131 | 1 | --- | K.VRVVCLYE.- |
|  | 1162.6044 | 1161.5971 | 1161.5778 | 16.6 | 74 | - | 84 | 0 | --- | R.TFPSGSSQPVR.S |
|  | 1162.6044 | 1161.5971 | 1161.5778 | 16.6 | 74 | - | 84 | 0 | 62 | R.TFPSGSSQPVR.S |
|  | 1520.7954 | 1519.7881 | 1519.8947 | -70.10 | 99 | - | 112 | 2 | --- | K.GQLNRARLLPPGTK.V |
|  | 1632.8737 | 1631.8664 | 1631.8744 | -4.86 | 74 | - | 88 | 2 | --- | R.TFPSGSSQPVRSKVR.S |

|  |  |
| --- | --- |
|  | **No match to:** 806.4286, 809.4370, 816.3771, 823.4503, 825.4399, 826.4092, 832.3274, 837.4684, 852.4302, 855.5543, 880.4735, 883.5497, 896.4417, 906.5044, 909.4255, 924.4424, 925.4297, 940.5698, 941.4376, 942.5769, 951.5180, 994.4857, 1003.5229, 1022.5051, 1033.5951, 1059.6152, 1074.5811, 1081.5057, 1107.5885, 1110.5526, 1131.5750, 1136.6251, 1136.6251, 1165.6107, 1171.6152, 1176.6025, 1182.5682, 1183.5448, 1197.5828, 1216.6537, 1296.6379, 1365.6832, 1449.7749, 1877.0337, 1989.9198, 1989.9198 |

|  |  |
| --- | --- |
| **2.** | [isotig17113](http://msmsms/mascot/cgi/protein_view.pl?file=../data/20110221/F013485.dat&hit=2" \t "_blank)    **Mass:** 14478    **Score:** 83     **Expect:** 0.00017  **Matches:** 4 |
|  | putative nuclear encoded protein Method: similarity and extension |

|  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | **Observed** | **Mr(expt)** | **Mr(calc)** | **ppm** | **Start** |  | **End** | **Miss** | **Ions** | **Peptide** |
|  | 1033.5951 | 1032.5878 | 1032.5750 | 12.5 | 76 | - | 84 | 2 | --- | R.KLAAKEMAR.Q + Oxidation (M) |
|  | 1136.6251 | 1135.6178 | 1135.5985 | 17.0 | 90 | - | 99 | 1 | --- | R.LKDSAYNVAR.M |
|  | 1136.6251 | 1135.6178 | 1135.5985 | 17.0 | 90 | - | 99 | 1 | 69 | R.LKDSAYNVAR.M |
|  | 1176.6025 | 1175.5952 | 1175.5724 | 19.5 | 55 | - | 65 | 0 | --- | K.GEANVFAGHFK.V |

|  |  |
| --- | --- |
|  | **No match to:** 806.4286, 809.4370, 816.3771, 823.4503, 825.4399, 826.4092, 832.3274, 834.4449, 837.4684, 844.4680, 852.4302, 855.5543, 880.4735, 883.5497, 896.4417, 906.5044, 909.4255, 924.4424, 925.4297, 940.5698, 941.4376, 942.5769, 951.5180, 980.4872, 994.4857, 1003.5229, 1022.5051, 1059.6152, 1074.5811, 1081.5057, 1107.5885, 1110.5526, 1131.5750, 1162.6044, 1162.6044, 1165.6107, 1171.6152, 1182.5682, 1183.5448, 1197.5828, 1216.6537, 1296.6379, 1365.6832, 1449.7749, 1520.7954, 1632.8737, 1877.0337, 1989.9198, 1989.9198 |

|  |  |
| --- | --- |
| **3.** | [isotig17160](http://msmsms/mascot/cgi/protein_view.pl?file=../data/20110221/F013485.dat&hit=3" \t "_blank)    **Mass:** 14996    **Score:** 77     **Expect:** 0.00063  **Matches:** 3 |
|  | putative nuclear encoded protein Method: similarity and extension |

|  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | **Observed** | **Mr(expt)** | **Mr(calc)** | **ppm** | **Start** |  | **End** | **Miss** | **Ions** | **Peptide** |
|  | 1059.6152 | 1058.6079 | 1058.5906 | 16.4 | 79 | - | 87 | 2 | --- | R.KLPAKEMAR.Q + Oxidation (M) |
|  | 1136.6251 | 1135.6178 | 1135.5985 | 17.0 | 93 | - | 102 | 1 | --- | R.LKDSAYNVAR.M |
|  | 1136.6251 | 1135.6178 | 1135.5985 | 17.0 | 93 | - | 102 | 1 | 69 | R.LKDSAYNVAR.M |

|  |  |
| --- | --- |
|  | **No match to:** 806.4286, 809.4370, 816.3771, 823.4503, 825.4399, 826.4092, 832.3274, 834.4449, 837.4684, 844.4680, 852.4302, 855.5543, 880.4735, 883.5497, 896.4417, 906.5044, 909.4255, 924.4424, 925.4297, 940.5698, 941.4376, 942.5769, 951.5180, 980.4872, 994.4857, 1003.5229, 1022.5051, 1033.5951, 1074.5811, 1081.5057, 1107.5885, 1110.5526, 1131.5750, 1162.6044, 1162.6044, 1165.6107, 1171.6152, 1176.6025, 1182.5682, 1183.5448, 1197.5828, 1216.6537, 1296.6379, 1365.6832, 1449.7749, 1520.7954, 1632.8737, 1877.0337, 1989.9198, 1989.9198 |

**http://msmsms/mascot/images/88x31_logo_white.gifMascot Search Results**

**Protein View**

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Match to: **contig45229** Score: **100** Expect: **3.8e-006**

**putative nuclear encoded protein Method: similarity and extension**

Nominal mass (Mr): **14139**; Calculated pI value: **7.64**

NCBI BLAST search of [contig45229](http://www.ncbi.nlm.nih.gov/blast/Blast.cgi?ALIGNMENTS=50&ALIGNMENT_VIEW=Pairwise&AUTO_FORMAT=Semiauto&CDD_SEARCH=on&CLIENT=web&COMPOSITION_BASED_STATISTICS=on&DATABASE=nr&DESCRIPTIONS=100&ENTREZ_QUERY=(none)&EXPECT=10&FILTER=L&FORMAT_BLOCK_ON_RESPAGE=None&FORMAT_OBJECT=Alignment&FORMAT_TYPE=HTML&GAPCOSTS=11+1&I_THRESH=0.001&LAYOUT=TwoWindows&MATRIX_NAME=BLOSUM62&NCBI_GI=on&PAGE=Proteins&PROGRAM=blastp&QUERY=MLFAAIALGLLLANVGAEPECLTFHALGELYKEFNLQFINNGLEYDPTLISYACDEAKNPGTTTIPNKFTGERTFPSGSSQPVRSKVRSALMAGLREKGQLNRARLLPPGTKVGCDGAVDGNKVRVVCLYE&SERVICE=plain&SET_DEFAULTS.x=9&SET_DEFAULTS.y=5&SHOW_OVERVIEW=on&WORD_SIZE=3&END_OF_HTTPGET=Yes" \t "_blank) against nr

Unformatted [sequence string](http://msmsms/mascot/cgi/getseq.pl?cooperia_oncophora+contig45229+seq" \t "_blank) for pasting into other applications

Variable modifications: Oxidation (HW),Oxidation (M)

Cleavage by Trypsin/P: cuts C-term side of KR

Sequence Coverage: **35%**

Matched peptides shown in **Bold Red**

**1** MLFAAIALGL LLANVGAEPE CLTFHALGEL YKEFNLQFIN NGLEYDPTLI

**51** SYACDEAKNP GTTTIPNKFT GER**TFPSGSS QPVRSKVRSA LMAGLREKGQ**

**101 LNRARLLPPG TK**VGCDGAVD GNK**VRVVCLY E**



  Residue Number  Increasing Mass  Decreasing Mass



**Start - End Observed Mr(expt) Mr(calc) ppm Miss Sequence**

**74 - 84 1162.6044 1161.5971 1161.5778 17 0 R.TFPSGSSQPVR.S**  ([No match](http://msmsms/mascot/cgi/peptide_view.pl?file=../data/20110221/F013485.dat&query=37&hit=1" \t "_blank))

**74 - 84 1162.6044 1161.5971 1161.5778 17 0 R.TFPSGSSQPVR.S**  ([Ions score 62](http://msmsms/mascot/cgi/peptide_view.pl?file=../data/20110221/F013485.dat&query=38&hit=1" \t "_blank))

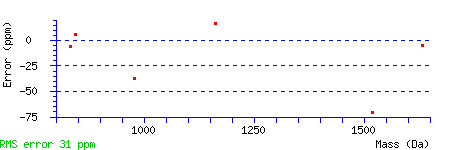
**74 - 88 1632.8737 1631.8664 1631.8744 -5 2 R.TFPSGSSQPVRSKVR.S**  ([No match](http://msmsms/mascot/cgi/peptide_view.pl?file=../data/20110221/F013485.dat&query=50&hit=1" \t "_blank))

**89 - 96 834.4449 833.4376 833.4429 -6 0 R.SALMAGLR.E**  Oxidation (M) ([No match](http://msmsms/mascot/cgi/peptide_view.pl?file=../data/20110221/F013485.dat&query=8&hit=1" \t "_blank))

**97 - 103 844.4680 843.4607 843.4562 5 1 R.EKGQLNR.A**  ([No match](http://msmsms/mascot/cgi/peptide_view.pl?file=../data/20110221/F013485.dat&query=10&hit=1" \t "_blank))

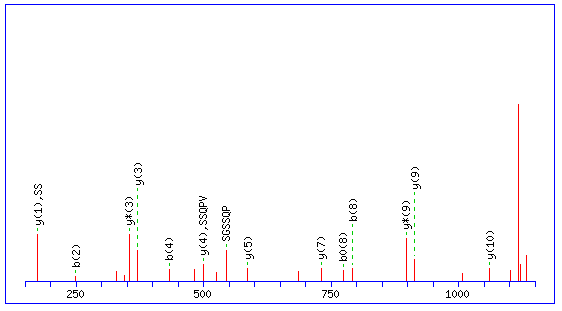
**99 - 112 1520.7954 1519.7881 1519.8947 -70 2 K.GQLNRARLLPPGTK.V**  ([No match](http://msmsms/mascot/cgi/peptide_view.pl?file=../data/20110221/F013485.dat&query=49&hit=1" \t "_blank))

**124 - 131 980.4872 979.4799 979.5161 -37 1 K.VRVVCLYE.-**  ([No match](http://msmsms/mascot/cgi/peptide_view.pl?file=../data/20110221/F013485.dat&query=24&hit=1" \t "_blank))



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🡪 Annotated MS2 spectrum for peptide TFPSGSSQPVR



**Monoisotopic mass of neutral peptide Mr(calc):** 1161.5778

**Ions Score:** 62 **Expect:** 5e-005

**Matches :** 17/166 fragment ions using 17 most intense peaks   ([help](http://msmsms/mascot/help/results_help.html" \l "PEP" \t "_blank))

|  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **#** | **Immon.** | **a** | **a\*** | **a0** | **b** | **b\*** | **b0** | **Seq.** | **v** | **w** | **y** | **y\*** | **y0** | **#** |
| **1** | 74.0600 | 74.0600 |  | 56.0495 | 102.0550 |  | 84.0444 | **T** |  |  |  |  |  | **11** |
| **2** | 120.0808 | 221.1285 |  | 203.1179 | **249.1234** |  | 231.1128 | **F** | 969.4748 |  | ***1061.5374*** | 1044.5109 | 1043.5269 | **10** |
| **3** | 70.0651 | 318.1812 |  | 300.1707 | 346.1761 |  | 328.1656 | **P** | 872.4221 | 871.4268 | ***914.4690*** | 897.4425 | 896.4585 | **9** |
| **4** | 60.0444 | 405.2132 |  | 387.2027 | **433.2082** |  | 415.1976 | **S** | 785.3900 | 784.3948 | 817.4163 | 800.3897 | 799.4057 | **8** |
| **5** | 30.0338 | 462.2347 |  | 444.2241 | 490.2296 |  | 472.2191 | **G** |  |  | ***730.3842*** | 713.3577 | 712.3737 | **7** |
| **6** | 60.0444 | 549.2667 |  | 531.2562 | 577.2617 |  | 559.2511 | **S** | 641.3366 | 640.3413 | 673.3628 | 656.3362 | 655.3522 | **6** |
| **7** | 60.0444 | 636.2988 |  | 618.2882 | 664.2937 |  | 646.2831 | **S** | 554.3045 | 553.3093 | ***586.3307*** | 569.3042 | 568.3202 | **5** |
| **8** | 101.0709 | 764.3573 | 747.3308 | 746.3468 | **792.3523** | 775.3257 | 774.3417 | **Q** | 426.2459 | 425.2507 | ***499.2987*** | 482.2722 |  | **4** |
| **9** | 70.0651 | 861.4101 | 844.3836 | 843.3995 | 889.4050 | 872.3785 | 871.3945 | **P** | 329.1932 | 328.1979 | ***371.2401*** | 354.2136 |  | **3** |
| **10** | 72.0808 | 960.4785 | 943.4520 | 942.4680 | 988.4734 | 971.4469 | 970.4629 | **V** | 230.1248 | 243.1452 | 274.1874 | 257.1608 |  | **2** |
| **11** | 129.1135 |  |  |  |  |  |  | **R** | 74.0237 | 73.0284 | ***175.1190*** | 158.0924 |  | **1** |

|  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **Seq** | **ya** | **yb** | **Seq** | **ya** | **yb** | **Seq** | **ya** | **yb** |
| **FP** | 217.1335 | 245.1285 | **FPS** | 304.1656 | 332.1605 | **FPSG** | 361.1870 | 389.1819 |
| **FPSGS** | 448.2191 | 476.2140 | **FPSGSS** | 535.2511 | 563.2460 | **FPSGSSQ** | 663.3097 | 691.3046 |
| **PS** | 157.0972 | 185.0921 | **PSG** | 214.1186 | 242.1135 | **PSGS** | 301.1506 | 329.1456 |
| **PSGSS** | 388.1827 | 416.1776 | **PSGSSQ** | 516.2413 | 544.2362 | **PSGSSQP** | 613.2940 | 641.2889 |
| **SG** | 117.0659 | 145.0608 | **SGS** | 204.0979 | 232.0928 | **SGSS** | 291.1299 | 319.1248 |
| **SGSSQ** | 419.1885 | 447.1834 | **SGSSQP** | 516.2413 | 544.2362 | **SGSSQPV** | 615.3097 | 643.3046 |
| **GS** | 117.0659 | 145.0608 | **GSS** | 204.0979 | 232.0928 | **GSSQ** | 332.1565 | 360.1514 |
| **GSSQP** | 429.2092 | 457.2041 | **GSSQPV** | 528.2776 | 556.2726 | **SS** | 147.0764 | 175.0713 |
| **SSQ** | 275.1350 | 303.1299 | **SSQP** | 372.1878 | 400.1827 | **SSQPV** | 471.2562 | 499.2511 |
| **SQ** | 188.1030 | 216.0979 | **SQP** | 285.1557 | 313.1506 | **SQPV** | 384.2241 | 412.2191 |
| **QP** | 198.1237 | 226.1186 | **QPV** | 297.1921 | 325.1870 | **PV** | 169.1335 | 197.1285 |

**Spot 18:**

**http://msmsms/mascot/images/88x31_logo_white.gifMascot Search Results**

**User :**

**Email :**

**Search title : SampleSetID: 341, AnalysisID: 800, MaldiWellID: 45096, SpectrumID: 175282, Path=\Jimmy\Cooperia Adult ES 20110221\20110509 1st experiment (repeat)**

**Database : cooperia\_oncophora oncophora\_20110405 (34373 sequences; 5289600 residues)**

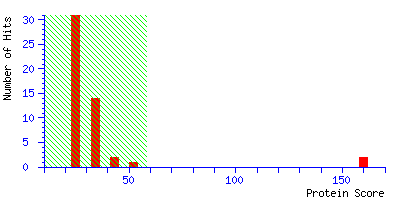
**Timestamp : 9 May 2011 at 12:40:03 GMT**

**Warning : A Peptide summary report will usually give a much clearer picture of MS/MS search results.**

**Top Score : 160 for gi|14140089|emb|CAC38986.1|, ES antigen 1 [Cooperia oncophora]**

**Mascot Score Histogram**

Protein score is -10\*Log(P), where P is the probability that the observed match is a random event.  
Protein scores greater than 58 are significant (p<0.05).  
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



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**Protein Summary Report**

|  |  |  |  |
| --- | --- | --- | --- |
|  |  |  | [Help](http://msmsms/mascot/help/msms_summaries_help.html" \t "_blank) |
|  | Significance threshold p< | Max. number of hits |  |

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**Index**

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
|  | **Accession** | **Mass** | **Score** | **Description** |
| **1.** | [**gi|14140089|emb|CAC38986.1|**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20110509/F014820.dat#Hit1) | 13887 | 160 | ES antigen 1 [Cooperia oncophora] |
| **2.** | [**isotig26364**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20110509/F014820.dat#Hit2) | 14131 | 160 | putative nuclear encoded protein Method: similarity and extension |
| **3.** | [**isotig22461**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20110509/F014820.dat#Hit3) | 10364 | 49 | putative nuclear encoded protein Method: Longest ORF |
| **4.** | [**isotig12469**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20110509/F014820.dat#Hit4) | 16851 | 39 | putative nuclear encoded protein Method: similarity and extension |
| **5.** | [**isotig12468**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20110509/F014820.dat#Hit5) | 16852 | 39 | putative nuclear encoded protein Method: similarity and extension |
| **6.** | [**isotig21342**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20110509/F014820.dat#Hit6) | 29194 | 34 | putative nuclear encoded protein Method: similarity and extension |
| **7.** | [**isotig28699**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20110509/F014820.dat#Hit7) | 21729 | 33 | putative nuclear encoded protein Method: similarity and extension |
| **8.** | [**isotig25394**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20110509/F014820.dat#Hit8) | 20007 | 32 | putative nuclear encoded protein Method: similarity and extension |
| **9.** | [**isotig12471**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20110509/F014820.dat#Hit9) | 15392 | 32 | putative nuclear encoded protein Method: similarity and extension |
| **10.** | [**isotig12470**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20110509/F014820.dat#Hit10) | 15393 | 32 | putative nuclear encoded protein Method: similarity and extension |
| **11.** | [**isotig03720**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20110509/F014820.dat#Hit11) | 9398 | 32 | putative nuclear encoded protein Method: Longest ORF |
| **12.** | [**isotig27965**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20110509/F014820.dat#Hit12) | 33029 | 31 | putative nuclear encoded protein Method: similarity and extension |
| **13.** | [**isotig19255**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20110509/F014820.dat#Hit13) | 11347 | 31 | putative nuclear encoded protein Method: similarity and extension |
| **14.** | [**isotig03718**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20110509/F014820.dat#Hit14) | 9181 | 31 | putative nuclear encoded protein Method: Longest ORF |
| **15.** | [**isotig17296**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20110509/F014820.dat#Hit15) | 32642 | 30 | putative nuclear encoded protein Method: similarity and extension |
| **16.** | [**isotig10283**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20110509/F014820.dat#Hit16) | 25622 | 30 | putative nuclear encoded protein Method: similarity and extension |
| **17.** | [**contig60560**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20110509/F014820.dat#Hit17) | 14131 | 30 | putative nuclear encoded protein Method: similarity and extension |
| **18.** | [**isotig14255**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20110509/F014820.dat#Hit18) | 12217 | 30 | putative nuclear encoded protein Method: Longest ORF |
| **19.** | [**isotig18268**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20110509/F014820.dat#Hit19) | 26997 | 30 | putative nuclear encoded protein Method: similarity and extension |
| **20.** | [**isotig24774**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20110509/F014820.dat#Hit20) | 11737 | 29 | putative nuclear encoded protein Method: Longest ORF |

**Results List**

|  |  |
| --- | --- |
| **1.** | [gi|14140089|emb|CAC38986.1|](http://msmsms/mascot/cgi/protein_view.pl?file=../data/20110509/F014820.dat&hit=1" \t "_blank)    **Mass:** 13887    **Score:** 160    **Expect:** 3.4e-012  **Matches:** 9 |
|  | ES antigen 1 [Cooperia oncophora] |

|  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | **Observed** | **Mr(expt)** | **Mr(calc)** | **ppm** | **Start** |  | **End** | **Miss** | **Ions** | **Peptide** |
|  | 806.4458 | 805.4385 | 805.4446 | -7.58 | 101 | - | 107 | 0 | --- | R.NLPPHTK.Y |
|  | 868.3972 | 867.3899 | 867.3909 | -1.11 | 19 | - | 25 | 0 | --- | R.CPTYTAR.K + Carbamidomethyl (C) |
|  | 993.5416 | 992.5343 | 992.5403 | -6.04 | 56 | - | 65 | 0 | --- | R.GIVASNAPHK.F |
|  | 1493.7401 | 1492.7328 | 1492.6656 | 45.0 | 108 | - | 120 | 0 | --- | K.YGCNSYFEGNLVK.V |
|  | 1550.7151 | 1549.7078 | 1549.6871 | 13.4 | 108 | - | 120 | 0 | --- | K.YGCNSYFEGNLVK.V + Carbamidomethyl (C) |
|  | 1550.7151 | 1549.7078 | 1549.6871 | 13.4 | 108 | - | 120 | 0 | 80 | K.YGCNSYFEGNLVK.V + Carbamidomethyl (C) |
|  | 3198.5354 | 3197.5281 | 3197.4857 | 13.3 | 71 | - | 100 | 0 | --- | K.TFASGGSVPVMIGETLMDGLQDETQTENVR.N + Oxidation (M) |
|  | 3214.5420 | 3213.5347 | 3213.4806 | 16.8 | 71 | - | 100 | 0 | --- | K.TFASGGSVPVMIGETLMDGLQDETQTENVR.N + 2 Oxidation (M) |
|  | 3214.5420 | 3213.5347 | 3213.4806 | 16.8 | 71 | - | 100 | 0 | 54 | K.TFASGGSVPVMIGETLMDGLQDETQTENVR.N + 2 Oxidation (M) |

|  |  |
| --- | --- |
|  | **No match to:** 832.3038, 834.3090, 842.5038, 844.5375, 851.3734, 877.4634, 881.2510, 884.4007, 1024.5048, 1047.5421, 1079.5164, 1081.5309, 1094.5413, 1097.5139, 1107.5577, 1109.4958, 1111.5244, 1118.5197, 1121.5320, 1136.5599, 1138.5508, 1138.5508, 1154.5435, 1179.6104, 1200.4836, 1216.4735, 1234.6937, 1300.6161, 1320.6035, 1418.6699, 1420.7212, 1422.7455, 1459.7029, 1475.7867, 1489.7762, 1536.7200, 1546.7617, 1618.8424, 1838.9387, 2211.1301, 3150.5532, 3197.5681, 3213.5476, 3228.5547 |

|  |  |
| --- | --- |
| **2.** | [isotig26364](http://msmsms/mascot/cgi/protein_view.pl?file=../data/20110509/F014820.dat&hit=2" \t "_blank)    **Mass:** 14131    **Score:** 160    **Expect:** 3.4e-012  **Matches:** 9 |
|  | putative nuclear encoded protein Method: similarity and extension |

|  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | **Observed** | **Mr(expt)** | **Mr(calc)** | **ppm** | **Start** |  | **End** | **Miss** | **Ions** | **Peptide** |
|  | 806.4458 | 805.4385 | 805.4446 | -7.58 | 103 | - | 109 | 0 | --- | R.NLPPHTK.Y |
|  | 868.3972 | 867.3899 | 867.3909 | -1.11 | 21 | - | 27 | 0 | --- | R.CPTYTAR.K + Carbamidomethyl (C) |
|  | 993.5416 | 992.5343 | 992.5403 | -6.04 | 58 | - | 67 | 0 | --- | R.GIVASNAPHK.F |
|  | 1493.7401 | 1492.7328 | 1492.6656 | 45.0 | 110 | - | 122 | 0 | --- | K.YGCNSYFEGNLVK.V |
|  | 1550.7151 | 1549.7078 | 1549.6871 | 13.4 | 110 | - | 122 | 0 | --- | K.YGCNSYFEGNLVK.V + Carbamidomethyl (C) |
|  | 1550.7151 | 1549.7078 | 1549.6871 | 13.4 | 110 | - | 122 | 0 | 80 | K.YGCNSYFEGNLVK.V + Carbamidomethyl (C) |
|  | 3198.5354 | 3197.5281 | 3197.4857 | 13.3 | 73 | - | 102 | 0 | --- | K.TFASGGSVPVMIGETLMDGLQDETQTENVR.N + Oxidation (M) |
|  | 3214.5420 | 3213.5347 | 3213.4806 | 16.8 | 73 | - | 102 | 0 | --- | K.TFASGGSVPVMIGETLMDGLQDETQTENVR.N + 2 Oxidation (M) |
|  | 3214.5420 | 3213.5347 | 3213.4806 | 16.8 | 73 | - | 102 | 0 | 54 | K.TFASGGSVPVMIGETLMDGLQDETQTENVR.N + 2 Oxidation (M) |

|  |  |
| --- | --- |
|  | **No match to:** 832.3038, 834.3090, 842.5038, 844.5375, 851.3734, 877.4634, 881.2510, 884.4007, 1024.5048, 1047.5421, 1079.5164, 1081.5309, 1094.5413, 1097.5139, 1107.5577, 1109.4958, 1111.5244, 1118.5197, 1121.5320, 1136.5599, 1138.5508, 1138.5508, 1154.5435, 1179.6104, 1200.4836, 1216.4735, 1234.6937, 1300.6161, 1320.6035, 1418.6699, 1420.7212, 1422.7455, 1459.7029, 1475.7867, 1489.7762, 1536.7200, 1546.7617, 1618.8424, 1838.9387, 2211.1301, 3150.5532, 3197.5681, 3213.5476, 3228.5547 |

**http://msmsms/mascot/images/88x31_logo_white.gifMascot Search Results**

**Protein View**

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Match to: **gi|14140089|emb|CAC38986.1|** Score: **160** Expect: **3.4e-012**

**ES antigen 1 [Cooperia oncophora]**

Nominal mass (Mr): **13887**; Calculated pI value: **5.30**

NCBI BLAST search of [gi|14140089|emb|CAC38986.1|](http://www.ncbi.nlm.nih.gov/blast/Blast.cgi?ALIGNMENTS=50&ALIGNMENT_VIEW=Pairwise&AUTO_FORMAT=Semiauto&CDD_SEARCH=on&CLIENT=web&COMPOSITION_BASED_STATISTICS=on&DATABASE=nr&DESCRIPTIONS=100&ENTREZ_QUERY=(none)&EXPECT=10&FILTER=L&FORMAT_BLOCK_ON_RESPAGE=None&FORMAT_OBJECT=Alignment&FORMAT_TYPE=HTML&GAPCOSTS=11+1&I_THRESH=0.001&LAYOUT=TwoWindows&MATRIX_NAME=BLOSUM62&NCBI_GI=on&PAGE=Proteins&PROGRAM=blastp&QUERY=FVLVPLCFLLINVAAGNRCPTYTARKEWYSSFNEFLNPALEWDPGLSSDACNEARGIVASNAPHKFIAEKTFASGGSVPVMIGETLMDGLQDETQTENVRNLPPHTKYGCNSYFEGNLVKVVCVYK&SERVICE=plain&SET_DEFAULTS.x=9&SET_DEFAULTS.y=5&SHOW_OVERVIEW=on&WORD_SIZE=3&END_OF_HTTPGET=Yes" \t "_blank) against nr

Unformatted [sequence string](http://msmsms/mascot/cgi/getseq.pl?cooperia_oncophora+gi%7c14140089%7cemb%7cCAC38986%2e1%7c+seq" \t "_blank) for pasting into other applications

Variable modifications: Carbamidomethyl (C),Oxidation (HW),Oxidation (M)

Cleavage by Trypsin/P: cuts C-term side of KR

Sequence Coverage: **53%**

Matched peptides shown in **Bold Red**

**1** FVLVPLCFLL INVAAGNR**CP TYTAR**KEWYS SFNEFLNPAL EWDPGLSSDA

**51** CNEAR**GIVAS NAPHK**FIAEK **TFASGGSVPV MIGETLMDGL QDETQTENVR**

**101 NLPPHTKYGC NSYFEGNLVK** VVCVYK



  Residue Number  Increasing Mass  Decreasing Mass

**Start - End Observed Mr(expt) Mr(calc) ppm Miss Sequence**

**19 - 25 868.3972 867.3899 867.3909 -1 0 R.CPTYTAR.K**  Carbamidomethyl (C) ([No match](http://msmsms/mascot/cgi/peptide_view.pl?file=../data/20110509/F014820.dat&query=7&hit=1" \t "_blank))

**56 - 65 993.5416 992.5343 992.5403 -6 0 R.GIVASNAPHK.F**  ([No match](http://msmsms/mascot/cgi/peptide_view.pl?file=../data/20110509/F014820.dat&query=11&hit=1" \t "_blank))

**71 - 100 3198.5354 3197.5281 3197.4857 13 0 K.TFASGGSVPVMIGETLMDGLQDETQTENVR.N**  Oxidation (M) ([No match](http://msmsms/mascot/cgi/peptide_view.pl?file=../data/20110509/F014820.dat&query=49&hit=1" \t "_blank))

**71 - 100 3214.5420 3213.5347 3213.4806 17 0 K.TFASGGSVPVMIGETLMDGLQDETQTENVR.N**  2 Oxidation (M) ([No match](http://msmsms/mascot/cgi/peptide_view.pl?file=../data/20110509/F014820.dat&query=51&hit=1" \t "_blank))

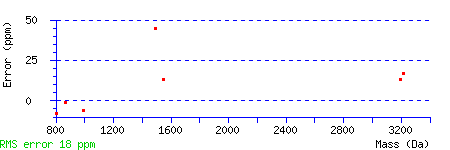
**71 - 100 3214.5420 3213.5347 3213.4806 17 0 K.TFASGGSVPVMIGETLMDGLQDETQTENVR.N**  2 Oxidation (M) ([Ions score 54](http://msmsms/mascot/cgi/peptide_view.pl?file=../data/20110509/F014820.dat&query=52&hit=1" \t "_blank))

**101 - 107 806.4458 805.4385 805.4446 -8 0 R.NLPPHTK.Y**  ([No match](http://msmsms/mascot/cgi/peptide_view.pl?file=../data/20110509/F014820.dat&query=1&hit=1" \t "_blank))

**108 - 120 1493.7401 1492.7328 1492.6656 45 0 K.YGCNSYFEGNLVK.V**  ([No match](http://msmsms/mascot/cgi/peptide_view.pl?file=../data/20110509/F014820.dat&query=39&hit=1" \t "_blank))

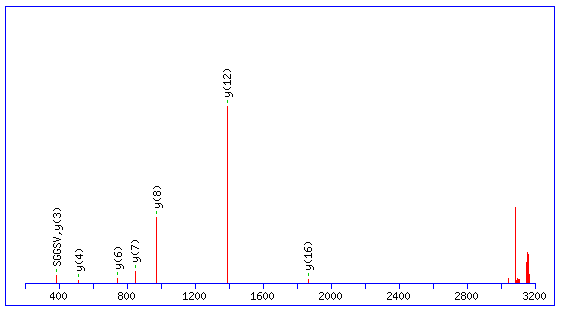
**108 - 120 1550.7151 1549.7078 1549.6871 13 0 K.YGCNSYFEGNLVK.V**  Carbamidomethyl (C) ([No match](http://msmsms/mascot/cgi/peptide_view.pl?file=../data/20110509/F014820.dat&query=42&hit=1" \t "_blank))

**108 - 120 1550.7151 1549.7078 1549.6871 13 0 K.YGCNSYFEGNLVK.V**  Carbamidomethyl (C) ([Ions score 80](http://msmsms/mascot/cgi/peptide_view.pl?file=../data/20110509/F014820.dat&query=43&hit=1" \t "_blank))



Bottom of Form

🡪 Annotated MS2 spectrum for peptide TFASGGSVPVMIGETLMDGLQDETQTENVR



**Monoisotopic mass of neutral peptide Mr(calc):** 3213.4806

**Variable modifications:**

**M11 :** Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983

**M17 :** Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983

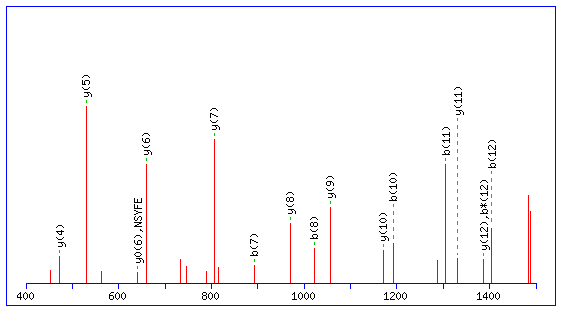
**Ions Score:** 54 **Expect:** 0.0005

**Matches :** 8/813 fragment ions using 9 most intense peaks   ([help](http://msmsms/mascot/help/results_help.html" \l "PEP" \t "_blank))

|  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **#** | **Immon.** | **a** | **a\*** | **a0** | **b** | **b\*** | **b0** | **Seq.** | **v** | **w** | **w'** | **y** | **y\*** | **y0** | **#** |
| **1** | 74.0600 | 74.0600 |  | 56.0495 | 102.0550 |  | 84.0444 | **T** |  |  |  |  |  |  | **30** |
| **2** | 120.0808 | 221.1285 |  | 203.1179 | 249.1234 |  | 231.1128 | **F** | 3021.3776 |  |  | 3113.4402 | 3096.4136 | 3095.4296 | **29** |
| **3** | 44.0495 | 292.1656 |  | 274.1550 | 320.1605 |  | 302.1499 | **A** | 2950.3405 |  |  | 2966.3718 | 2949.3452 | 2948.3612 | **28** |
| **4** | 60.0444 | 379.1976 |  | 361.1870 | 407.1925 |  | 389.1819 | **S** | 2863.3084 | 2862.3132 |  | 2895.3346 | 2878.3081 | 2877.3241 | **27** |
| **5** | 30.0338 | 436.2191 |  | 418.2085 | 464.2140 |  | 446.2034 | **G** |  |  |  | 2808.3026 | 2791.2761 | 2790.2921 | **26** |
| **6** | 30.0338 | 493.2405 |  | 475.2300 | 521.2354 |  | 503.2249 | **G** |  |  |  | 2751.2812 | 2734.2546 | 2733.2706 | **25** |
| **7** | 60.0444 | 580.2726 |  | 562.2620 | 608.2675 |  | 590.2569 | **S** | 2662.2335 | 2661.2382 |  | 2694.2597 | 2677.2331 | 2676.2491 | **24** |
| **8** | 72.0808 | 679.3410 |  | 661.3304 | 707.3359 |  | 689.3253 | **V** | 2563.1651 | 2576.1855 |  | 2607.2277 | 2590.2011 | 2589.2171 | **23** |
| **9** | 70.0651 | 776.3937 |  | 758.3832 | 804.3886 |  | 786.3781 | **P** | 2466.1123 | 2465.1170 |  | 2508.1592 | 2491.1327 | 2490.1487 | **22** |
| **10** | 72.0808 | 875.4621 |  | 857.4516 | 903.4571 |  | 885.4465 | **V** | 2367.0439 | 2380.0643 |  | 2411.1065 | 2394.0799 | 2393.0959 | **21** |
| **11** | 120.0478 | 1022.4975 |  | 1004.4870 | 1050.4925 |  | 1032.4819 | **M** | 2220.0085 | 2219.0132 |  | 2312.0381 | 2295.0115 | 2294.0275 | **20** |
| **12** | 86.0964 | 1135.5816 |  | 1117.5710 | 1163.5765 |  | 1145.5660 | **I** | 2106.9244 | 2119.9448 | 2133.9605 | 2165.0027 | 2147.9761 | 2146.9921 | **19** |
| **13** | 30.0338 | 1192.6031 |  | 1174.5925 | 1220.5980 |  | 1202.5874 | **G** |  |  |  | 2051.9186 | 2034.8921 | 2033.9080 | **18** |
| **14** | 102.0550 | 1321.6457 |  | 1303.6351 | 1349.6406 |  | 1331.6300 | **E** | 1920.8604 | 1919.8651 |  | 1994.8971 | 1977.8706 | 1976.8866 | **17** |
| **15** | 74.0600 | 1422.6933 |  | 1404.6828 | 1450.6883 |  | 1432.6777 | **T** | 1819.8127 | 1832.8331 | 1834.8124 | ***1865.8545*** | 1848.8280 | 1847.8440 | **16** |
| **16** | 86.0964 | 1535.7774 |  | 1517.7668 | 1563.7723 |  | 1545.7618 | **L** | 1706.7286 | 1705.7334 |  | 1764.8069 | 1747.7803 | 1746.7963 | **15** |
| **17** | 120.0478 | 1682.8128 |  | 1664.8022 | 1710.8077 |  | 1692.7972 | **M** | 1559.6932 | 1558.6980 |  | 1651.7228 | 1634.6963 | 1633.7122 | **14** |
| **18** | 88.0393 | 1797.8398 |  | 1779.8292 | 1825.8347 |  | 1807.8241 | **D** | 1444.6663 | 1443.6710 |  | 1504.6874 | 1487.6609 | 1486.6768 | **13** |
| **19** | 30.0338 | 1854.8612 |  | 1836.8506 | 1882.8561 |  | 1864.8456 | **G** |  |  |  | ***1389.6605*** | 1372.6339 | 1371.6499 | **12** |
| **20** | 86.0964 | 1967.9453 |  | 1949.9347 | 1995.9402 |  | 1977.9296 | **L** | 1274.5607 | 1273.5655 |  | 1332.6390 | 1315.6125 | 1314.6284 | **11** |
| **21** | 101.0709 | 2096.0039 | 2078.9773 | 2077.9933 | 2123.9988 | 2106.9722 | 2105.9882 | **Q** | 1146.5022 | 1145.5069 |  | 1219.5549 | 1202.5284 | 1201.5444 | **10** |
| **22** | 88.0393 | 2211.0308 | 2194.0043 | 2193.0202 | 2239.0257 | 2221.9992 | 2221.0151 | **D** | 1031.4752 | 1030.4800 |  | 1091.4964 | 1074.4698 | 1073.4858 | **9** |
| **23** | 102.0550 | 2340.0734 | 2323.0468 | 2322.0628 | 2368.0683 | 2351.0418 | 2350.0577 | **E** | 902.4326 | 901.4374 |  | ***976.4694*** | 959.4429 | 958.4588 | **8** |
| **24** | 74.0600 | 2441.1211 | 2424.0945 | 2423.1105 | 2469.1160 | 2452.0894 | 2451.1054 | **T** | 801.3850 | 814.4054 | 816.3846 | ***847.4268*** | 830.4003 | 829.4163 | **7** |
| **25** | 101.0709 | 2569.1796 | 2552.1531 | 2551.1691 | 2597.1746 | 2580.1480 | 2579.1640 | **Q** | 673.3264 | 672.3311 |  | ***746.3791*** | 729.3526 | 728.3686 | **6** |
| **26** | 74.0600 | 2670.2273 | 2653.2008 | 2652.2168 | 2698.2222 | 2681.1957 | 2680.2117 | **T** | 572.2787 | 585.2991 | 587.2784 | 618.3206 | 601.2940 | 600.3100 | **5** |
| **27** | 102.0550 | 2799.2699 | 2782.2434 | 2781.2594 | 2827.2648 | 2810.2383 | 2809.2543 | **E** | 443.2361 | 442.2409 |  | ***517.2729*** | 500.2463 | 499.2623 | **4** |
| **28** | 87.0553 | 2913.3128 | 2896.2863 | 2895.3023 | 2941.3078 | 2924.2812 | 2923.2972 | **N** | 329.1932 | 328.1979 |  | ***388.2303*** | 371.2037 |  | **3** |
| **29** | 72.0808 | 3012.3813 | 2995.3547 | 2994.3707 | 3040.3762 | 3023.3496 | 3022.3656 | **V** | 230.1248 | 243.1452 |  | 274.1874 | 257.1608 |  | **2** |
| **30** | 129.1135 |  |  |  |  |  |  | **R** | 74.0237 | 73.0284 |  | 175.1190 | 158.0924 |  | **1** |

|  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **Seq** | **ya** | **yb** | **Seq** | **ya** | **yb** | **Seq** | **ya** | **yb** |
| **FA** | 191.1179 | 219.1128 | **FAS** | 278.1499 | 306.1448 | **FASG** | 335.1714 | 363.1663 |
| **FASGG** | 392.1928 | 420.1878 | **FASGGS** | 479.2249 | 507.2198 | **FASGGSV** | 578.2933 | 606.2882 |
| **FASGGSVP** | 675.3461 | 703.3410 | **AS** | 131.0815 | 159.0764 | **ASG** | 188.1030 | 216.0979 |
| **ASGG** | 245.1244 | 273.1193 | **ASGGS** | 332.1565 | 360.1514 | **ASGGSV** | 431.2249 | 459.2198 |
| **ASGGSVP** | 528.2776 | 556.2726 | **ASGGSVPV** | 627.3461 | 655.3410 | **SG** | 117.0659 | 145.0608 |
| **SGG** | 174.0873 | 202.0822 | **SGGS** | 261.1193 | 289.1143 | **SGGSV** | 360.1878 | 388.1827 |
| **SGGSVP** | 457.2405 | 485.2354 | **SGGSVPV** | 556.3089 | 584.3039 | **GG** | 87.0553 | 115.0502 |
| **GGS** | 174.0873 | 202.0822 | **GGSV** | 273.1557 | 301.1506 | **GGSVP** | 370.2085 | 398.2034 |
| **GGSVPV** | 469.2769 | 497.2718 | **GGSVPVM** | 616.3123 | 644.3072 | **GS** | 117.0659 | 145.0608 |
| **GSV** | 216.1343 | 244.1292 | **GSVP** | 313.1870 | 341.1819 | **GSVPV** | 412.2554 | 440.2504 |
| **GSVPVM** | 559.2908 | 587.2858 | **GSVPVMI** | 672.3749 | 700.3698 | **SV** | 159.1128 | 187.1077 |
| **SVP** | 256.1656 | 284.1605 | **SVPV** | 355.2340 | 383.2289 | **SVPVM** | 502.2694 | 530.2643 |
| **SVPVMI** | 615.3534 | 643.3484 | **SVPVMIG** | 672.3749 | 700.3698 | **VP** | 169.1335 | 197.1285 |
| **VPV** | 268.2020 | 296.1969 | **VPVM** | 415.2374 | 443.2323 | **VPVMI** | 528.3214 | 556.3163 |
| **VPVMIG** | 585.3429 | 613.3378 | **PV** | 169.1335 | 197.1285 | **PVM** | 316.1689 | 344.1639 |
| **PVMI** | 429.2530 | 457.2479 | **PVMIG** | 486.2745 | 514.2694 | **PVMIGE** | 615.3171 | 643.3120 |
| **VM** | 219.1162 | 247.1111 | **VMI** | 332.2002 | 360.1952 | **VMIG** | 389.2217 | 417.2166 |
| **VMIGE** | 518.2643 | 546.2592 | **VMIGET** | 619.3120 | 647.3069 | **MI** | 233.1318 | 261.1267 |
| **MIG** | 290.1533 | 318.1482 | **MIGE** | 419.1959 | 447.1908 | **MIGET** | 520.2436 | 548.2385 |
| **MIGETL** | 633.3276 | 661.3225 | **IG** | 143.1179 | 171.1128 | **IGE** | 272.1605 | 300.1554 |
| **IGET** | 373.2082 | 401.2031 | **IGETL** | 486.2922 | 514.2871 | **IGETLM** | 633.3276 | 661.3225 |
| **GE** | 159.0764 | 187.0713 | **GET** | 260.1241 | 288.1190 | **GETL** | 373.2082 | 401.2031 |
| **GETLM** | 520.2436 | 548.2385 | **GETLMD** | 635.2705 | 663.2654 | **GETLMDG** | 692.2920 | 720.2869 |
| **ET** | 203.1026 | 231.0975 | **ETL** | 316.1867 | 344.1816 | **ETLM** | 463.2221 | 491.2170 |
| **ETLMD** | 578.2490 | 606.2440 | **ETLMDG** | 635.2705 | 663.2654 | **TL** | 187.1441 | 215.1390 |
| **TLM** | 334.1795 | 362.1744 | **TLMD** | 449.2064 | 477.2014 | **TLMDG** | 506.2279 | 534.2228 |
| **TLMDGL** | 619.3120 | 647.3069 | **LM** | 233.1318 | 261.1267 | **LMD** | 348.1588 | 376.1537 |
| **LMDG** | 405.1802 | 433.1751 | **LMDGL** | 518.2643 | 546.2592 | **LMDGLQ** | 646.3229 | 674.3178 |
| **MD** | 235.0747 | 263.0696 | **MDG** | 292.0962 | 320.0911 | **MDGL** | 405.1802 | 433.1751 |
| **MDGLQ** | 533.2388 | 561.2337 | **MDGLQD** | 648.2658 | 676.2607 | **DG** | 145.0608 | 173.0557 |
| **DGL** | 258.1448 | 286.1397 | **DGLQ** | 386.2034 | 414.1983 | **DGLQD** | 501.2304 | 529.2253 |
| **DGLQDE** | 630.2729 | 658.2679 | **GL** | 143.1179 | 171.1128 | **GLQ** | 271.1765 | 299.1714 |
| **GLQD** | 386.2034 | 414.1983 | **GLQDE** | 515.2460 | 543.2409 | **GLQDET** | 616.2937 | 644.2886 |
| **LQ** | 214.1550 | 242.1499 | **LQD** | 329.1819 | 357.1769 | **LQDE** | 458.2245 | 486.2195 |
| **LQDET** | 559.2722 | 587.2671 | **LQDETQ** | 687.3308 | 715.3257 | **QD** | 216.0979 | 244.0928 |
| **QDE** | 345.1405 | 373.1354 | **QDET** | 446.1882 | 474.1831 | **QDETQ** | 574.2467 | 602.2416 |
| **QDETQT** | 675.2944 | 703.2893 | **DE** | 217.0819 | 245.0768 | **DET** | 318.1296 | 346.1245 |
| **DETQ** | 446.1882 | 474.1831 | **DETQT** | 547.2358 | 575.2307 | **DETQTE** | 676.2784 | 704.2733 |
| **ET** | 203.1026 | 231.0975 | **ETQ** | 331.1612 | 359.1561 | **ETQT** | 432.2089 | 460.2038 |
| **ETQTE** | 561.2515 | 589.2464 | **ETQTEN** | 675.2944 | 703.2893 | **TQ** | 202.1186 | 230.1135 |
| **TQT** | 303.1663 | 331.1612 | **TQTE** | 432.2089 | 460.2038 | **TQTEN** | 546.2518 | 574.2467 |
| **TQTENV** | 645.3202 | 673.3151 | **QT** | 202.1186 | 230.1135 | **QTE** | 331.1612 | 359.1561 |
| **QTEN** | 445.2041 | 473.1991 | **QTENV** | 544.2726 | 572.2675 | **TE** | 203.1026 | 231.0975 |
| **TEN** | 317.1456 | 345.1405 | **TENV** | 416.2140 | 444.2089 | **EN** | 216.0979 | 244.0928 |
| **ENV** | 315.1663 | 343.1612 | **NV** | 186.1237 | 214.1186 |  |  |  |

🡪 Annotated MS2 spectrum for peptide YGCNSYFEGNLVK



**Monoisotopic mass of neutral peptide Mr(calc):** 1549.6871

**Variable modifications:**

**C3 :** Carbamidomethyl (C)

**Ions Score:** 80 **Expect:** 1e-006

**Matches :** 17/177 fragment ions using 20 most intense peaks   ([help](http://msmsms/mascot/help/results_help.html" \l "PEP" \t "_blank))

|  |  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **#** | **Immon.** | **a** | **a\*** | **a0** | **b** | **b\*** | **b0** | **Seq.** | **y** | **y\*** | **y0** | **#** |
| **1** | 136.0757 | 136.0757 |  |  | 164.0706 |  |  | **Y** |  |  |  | **13** |
| **2** | 30.0338 | 193.0972 |  |  | 221.0921 |  |  | **G** | ***1387.6311*** | 1370.6045 | 1369.6205 | **12** |
| **3** | 133.0430 | 353.1278 |  |  | 381.1227 |  |  | **C** | ***1330.6096*** | 1313.5831 | 1312.5990 | **11** |
| **4** | 87.0553 | 467.1707 | 450.1442 |  | 495.1656 | 478.1391 |  | **N** | ***1170.5790*** | 1153.5524 | 1152.5684 | **10** |
| **5** | 60.0444 | 554.2028 | 537.1762 | 536.1922 | 582.1977 | 565.1711 | 564.1871 | **S** | ***1056.5360*** | 1039.5095 | 1038.5255 | **9** |
| **6** | 136.0757 | 717.2661 | 700.2395 | 699.2555 | 745.2610 | 728.2345 | 727.2504 | **Y** | ***969.5040*** | 952.4775 | 951.4934 | **8** |
| **7** | 120.0808 | 864.3345 | 847.3080 | 846.3239 | ***892.3294*** | 875.3029 | 874.3189 | **F** | ***806.4407*** | 789.4141 | 788.4301 | **7** |
| **8** | 102.0550 | 993.3771 | 976.3505 | 975.3665 | ***1021.3720*** | 1004.3455 | 1003.3614 | **E** | ***659.3723*** | 642.3457 | 641.3617 | **6** |
| **9** | 30.0338 | 1050.3986 | 1033.3720 | 1032.3880 | 1078.3935 | 1061.3669 | 1060.3829 | **G** | ***530.3297*** | 513.3031 |  | **5** |
| **10** | 87.0553 | 1164.4415 | 1147.4149 | 1146.4309 | ***1192.4364*** | 1175.4099 | 1174.4258 | **N** | ***473.3082*** | 456.2817 |  | **4** |
| **11** | 86.0964 | 1277.5255 | 1260.4990 | 1259.5150 | ***1305.5205*** | 1288.4939 | 1287.5099 | **L** | 359.2653 | 342.2387 |  | **3** |
| **12** | 72.0808 | 1376.5940 | 1359.5674 | 1358.5834 | ***1404.5889*** | 1387.5623 | 1386.5783 | **V** | 246.1812 | 229.1547 |  | **2** |
| **13** | 101.1073 |  |  |  |  |  |  | **K** | 147.1128 | 130.0863 |  | **1** |

|  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **Seq** | **ya** | **yb** | **Seq** | **ya** | **yb** | **Seq** | **ya** | **yb** |
| **GC** | 190.0645 | 218.0594 | **GCN** | 304.1074 | 332.1023 | **GCNS** | 391.1394 | 419.1343 |
| **GCNSY** | 554.2028 | 582.1977 | **CN** | 247.0859 | 275.0809 | **CNS** | 334.1180 | 362.1129 |
| **CNSY** | 497.1813 | 525.1762 | **CNSYF** | 644.2497 | 672.2446 | **NS** | 174.0873 | 202.0822 |
| **NSY** | 337.1506 | 365.1456 | **NSYF** | 484.2191 | 512.2140 | **NSYFE** | 613.2617 | 641.2566 |
| **NSYFEG** | 670.2831 | 698.2780 | **SY** | 223.1077 | 251.1026 | **SYF** | 370.1761 | 398.1710 |
| **SYFE** | 499.2187 | 527.2136 | **SYFEG** | 556.2402 | 584.2351 | **SYFEGN** | 670.2831 | 698.2780 |
| **YF** | 283.1441 | 311.1390 | **YFE** | 412.1867 | 440.1816 | **YFEG** | 469.2082 | 497.2031 |
| **YFEGN** | 583.2511 | 611.2460 | **YFEGNL** | 696.3352 | 724.3301 | **FE** | 249.1234 | 277.1183 |
| **FEG** | 306.1448 | 334.1397 | **FEGN** | 420.1878 | 448.1827 | **FEGNL** | 533.2718 | 561.2667 |
| **FEGNLV** | 632.3402 | 660.3352 | **EG** | 159.0764 | 187.0713 | **EGN** | 273.1193 | 301.1143 |
| **EGNL** | 386.2034 | 414.1983 | **EGNLV** | 485.2718 | 513.2667 | **GN** | 144.0768 | 172.0717 |
| **GNL** | 257.1608 | 285.1557 | **GNLV** | 356.2292 | 384.2241 | **NL** | 200.1394 | 228.1343 |
| **NLV** | 299.2078 | 327.2027 | **LV** | 185.1648 | 213.1598 |  |  |  |

**Spot 19:**

**http://msmsms/mascot/images/88x31_logo_white.gifMascot Search Results**

**User :**

**Email :**

**Search title : SampleSetID: 341, AnalysisID: 804, MaldiWellID: 45137, SpectrumID: 175462, Path=\Jimmy\Cooperia Adult ES 20110221\20110509 2nd experiment (repeat)**

**Database : cooperia\_oncophora oncophora\_20110405 (34373 sequences; 5289600 residues)**

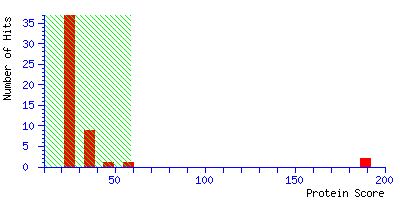
**Timestamp : 9 May 2011 at 13:41:24 GMT**

**Warning : A Peptide summary report will usually give a much clearer picture of MS/MS search results.**

**Top Score : 189 for isotig09711, putative nuclear encoded protein Method: similarity and extension**

**Mascot Score Histogram**

Protein score is -10\*Log(P), where P is the probability that the observed match is a random event.  
Protein scores greater than 58 are significant (p<0.05).  
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Top of Form



**Protein Summary Report**

|  |  |  |  |
| --- | --- | --- | --- |
|  |  |  | [Help](http://msmsms/mascot/help/msms_summaries_help.html" \t "_blank) |
|  | Significance threshold p< | Max. number of hits |  |

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**Index**

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
|  | **Accession** | **Mass** | **Score** | **Description** |
| **1.** | [**isotig09711**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20110509/F014873.dat#Hit1) | 28342 | 189 | putative nuclear encoded protein Method: similarity and extension |
| **2.** | [**isotig09712**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20110509/F014873.dat#Hit2) | 30518 | 189 | putative nuclear encoded protein Method: similarity and extension |

**http://msmsms/mascot/images/88x31_logo_white.gifMascot Search Results**

**Protein View**

Top of Form



Match to: **isotig09711** Score: **189** Expect: **4.3e-015**

**putative nuclear encoded protein Method: similarity and extension**

Nominal mass (Mr): **28342**; Calculated pI value: **8.24**

NCBI BLAST search of [isotig09711](http://www.ncbi.nlm.nih.gov/blast/Blast.cgi?ALIGNMENTS=50&ALIGNMENT_VIEW=Pairwise&AUTO_FORMAT=Semiauto&CDD_SEARCH=on&CLIENT=web&COMPOSITION_BASED_STATISTICS=on&DATABASE=nr&DESCRIPTIONS=100&ENTREZ_QUERY=(none)&EXPECT=10&FILTER=L&FORMAT_BLOCK_ON_RESPAGE=None&FORMAT_OBJECT=Alignment&FORMAT_TYPE=HTML&GAPCOSTS=11+1&I_THRESH=0.001&LAYOUT=TwoWindows&MATRIX_NAME=BLOSUM62&NCBI_GI=on&PAGE=Proteins&PROGRAM=blastp&QUERY=KKEKASEELQSGCRHYIREILGAEKADQFRAMKESGTHMSEIAKKIEEAIEELTDEEVKSRAKKASVACKRIFGVAHRFRRDHHPVTLEEALTKYLTWLSDEQKEELKSMKESGDKEGIYKKVMEYFEGITGEKKEKATEELRAACKHYLREILGNEKADEFRSMKESGTPEEEIAKKVEEAIEGLTDESAKMRGKKASAACKRIFGVARRFRRDHHPVTSGGGSHEVPHLAKRRAEGGIEVDERERR&SERVICE=plain&SET_DEFAULTS.x=9&SET_DEFAULTS.y=5&SHOW_OVERVIEW=on&WORD_SIZE=3&END_OF_HTTPGET=Yes" \t "_blank) against nr

Unformatted [sequence string](http://msmsms/mascot/cgi/getseq.pl?cooperia_oncophora+isotig09711+seq" \t "_blank) for pasting into other applications

Variable modifications: Oxidation (HW),Oxidation (M)

Cleavage by Trypsin/P: cuts C-term side of KR

Sequence Coverage: **52%**

Matched peptides shown in **Bold Red**

**1** KKEKASEELQ SGCR**HYIREI LGAEKADQFR AMKESGTHMS EIAKKIEEAI**

**51 EELTDEEVKS R**AKKASVACK RIFGVAHRFR R**DHHPVTLEE ALTKYLTWLS**

**101 DEQKEELK**SM K**ESGDKEGIY K**K**VMEYFEGI TGEKKEK**ATE ELRAACK**HYL**

**151 REILGNEKAD EFR**SMKESGT PEEEIAK**KVE EAIEGLTDES AK**MRGKKASA

**201** ACKRIFGVAR RFRRDHHPVT SGGGSHEVPH LAKRRAEGGI EVDERERR



  Residue Number  Increasing Mass  Decreasing Mass

**Start - End Observed Mr(expt) Mr(calc) ppm Miss Sequence**

**15 - 25 1328.6719 1327.6646 1327.7248 -45 1 R.HYIREILGAEK.A**  ([No match](http://msmsms/mascot/cgi/peptide_view.pl?file=../data/20110509/F014873.dat&query=5&hit=1" \t "_blank))

**19 - 30 1376.6470 1375.6397 1375.7095 -51 1 R.EILGAEKADQFR.A**  ([No match](http://msmsms/mascot/cgi/peptide_view.pl?file=../data/20110509/F014873.dat&query=7&hit=1" \t "_blank))

**31 - 44 1535.6376 1534.6303 1534.7119 -53 1 R.AMKESGTHMSEIAK.K**  Oxidation (M) ([No match](http://msmsms/mascot/cgi/peptide_view.pl?file=../data/20110509/F014873.dat&query=16&hit=1" \t "_blank))

**31 - 44 1551.6384 1550.6311 1550.7068 -49 1 R.AMKESGTHMSEIAK.K**  2 Oxidation (M) ([No match](http://msmsms/mascot/cgi/peptide_view.pl?file=../data/20110509/F014873.dat&query=19&hit=1" \t "_blank))

**31 - 45 1679.7544 1678.7471 1678.8018 -33 2 R.AMKESGTHMSEIAKK.I**  2 Oxidation (M) ([No match](http://msmsms/mascot/cgi/peptide_view.pl?file=../data/20110509/F014873.dat&query=31&hit=1" \t "_blank))

**45 - 59 1774.8002 1773.7929 1773.8883 -54 1 K.KIEEAIEELTDEEVK.S**  ([No match](http://msmsms/mascot/cgi/peptide_view.pl?file=../data/20110509/F014873.dat&query=34&hit=1" \t "_blank))

**45 - 61 2017.8170 2016.8097 2017.0215 -105 2 K.KIEEAIEELTDEEVKSR.A**  ([Ions score 80](http://msmsms/mascot/cgi/peptide_view.pl?file=../data/20110509/F014873.dat&query=39&hit=1" \t "_blank))

**45 - 61 2017.9396 2016.9323 2017.0215 -44 2 K.KIEEAIEELTDEEVKSR.A**  ([No match](http://msmsms/mascot/cgi/peptide_view.pl?file=../data/20110509/F014873.dat&query=40&hit=1" \t "_blank))

**46 - 59 1646.7329 1645.7256 1645.7934 -41 0 K.IEEAIEELTDEEVK.S**  ([No match](http://msmsms/mascot/cgi/peptide_view.pl?file=../data/20110509/F014873.dat&query=29&hit=1" \t "_blank))

**46 - 61 1889.8527 1888.8454 1888.9265 -43 1 K.IEEAIEELTDEEVKSR.A**  ([No match](http://msmsms/mascot/cgi/peptide_view.pl?file=../data/20110509/F014873.dat&query=38&hit=1" \t "_blank))

**82 - 94 1489.5988 1488.5915 1488.7572 -111 0 R.DHHPVTLEEALTK.Y**  ([Ions score 27](http://msmsms/mascot/cgi/peptide_view.pl?file=../data/20110509/F014873.dat&query=12&hit=1" \t "_blank))

**82 - 94 1489.6842 1488.6769 1488.7572 -54 0 R.DHHPVTLEEALTK.Y**  ([No match](http://msmsms/mascot/cgi/peptide_view.pl?file=../data/20110509/F014873.dat&query=13&hit=1" \t "_blank))

**95 - 108 1781.8120 1780.8047 1780.8883 -47 1 K.YLTWLSDEQKEELK.S**  ([No match](http://msmsms/mascot/cgi/peptide_view.pl?file=../data/20110509/F014873.dat&query=36&hit=1" \t "_blank))

**112 - 121 1125.4938 1124.4865 1124.5349 -43 1 K.ESGDKEGIYK.K**  ([No match](http://msmsms/mascot/cgi/peptide_view.pl?file=../data/20110509/F014873.dat&query=2&hit=1" \t "_blank))

**123 - 135 1546.6652 1545.6579 1545.7385 -52 1 K.VMEYFEGITGEKK.E**  Oxidation (M) ([No match](http://msmsms/mascot/cgi/peptide_view.pl?file=../data/20110509/F014873.dat&query=17&hit=1" \t "_blank))

**123 - 137 1803.7905 1802.7832 1802.8760 -51 2 K.VMEYFEGITGEKKEK.A**  Oxidation (M) ([No match](http://msmsms/mascot/cgi/peptide_view.pl?file=../data/20110509/F014873.dat&query=37&hit=1" \t "_blank))

**148 - 158 1371.6506 1370.6433 1370.7306 -64 1 K.HYLREILGNEK.A**  ([No match](http://msmsms/mascot/cgi/peptide_view.pl?file=../data/20110509/F014873.dat&query=6&hit=1" \t "_blank))

**152 - 163 1420.5522 1419.5449 1419.6994 -109 1 R.EILGNEKADEFR.S**  ([No match](http://msmsms/mascot/cgi/peptide_view.pl?file=../data/20110509/F014873.dat&query=8&hit=1" \t "_blank))

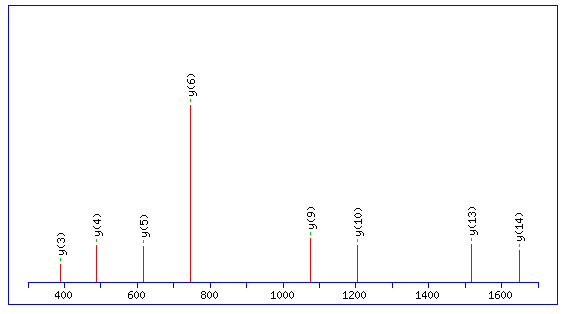
**152 - 163 1420.6383 1419.6310 1419.6994 -48 1 R.EILGNEKADEFR.S**  ([No match](http://msmsms/mascot/cgi/peptide_view.pl?file=../data/20110509/F014873.dat&query=9&hit=1" \t "_blank))

**178 - 192 1618.7375 1617.7302 1617.8097 -49 1 K.KVEEAIEGLTDESAK.M**  ([No match](http://msmsms/mascot/cgi/peptide_view.pl?file=../data/20110509/F014873.dat&query=25&hit=1" \t "_blank))



Bottom of Form

🡪 Annotated MS2 spectrum for peptide KIEEAIEELTDEEVKSR



**Monoisotopic mass of neutral peptide Mr(calc):** 2017.0215

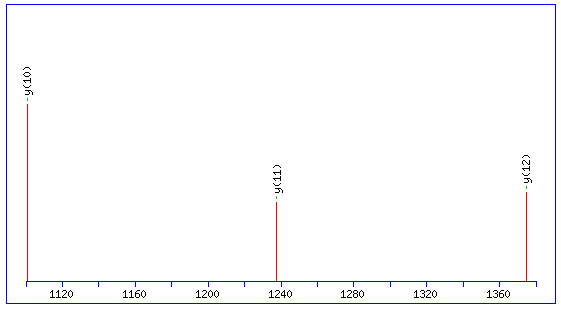
**Ions Score:** 80 **Expect:** 9.2e-007

**Matches :** 8/305 fragment ions using 8 most intense peaks   ([help](http://msmsms/mascot/help/results_help.html" \l "PEP" \t "_blank))

|  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **#** | **Immon.** | **a** | **a\*** | **a0** | **b** | **b\*** | **b0** | **Seq.** | **v** | **w** | **w'** | **y** | **y\*** | **y0** | **#** |
| **1** | 101.1073 | 101.1073 | 84.0808 |  | 129.1022 | 112.0757 |  | **K** |  |  |  |  |  |  | **17** |
| **2** | 86.0964 | 214.1914 | 197.1648 |  | 242.1863 | 225.1598 |  | **I** | 1831.8556 | 1844.8760 | 1858.8916 | 1889.9338 | 1872.9073 | 1871.9233 | **16** |
| **3** | 102.0550 | 343.2340 | 326.2074 | 325.2234 | 371.2289 | 354.2023 | 353.2183 | **E** | 1702.8130 | 1701.8178 |  | 1776.8498 | 1759.8232 | 1758.8392 | **15** |
| **4** | 102.0550 | 472.2766 | 455.2500 | 454.2660 | 500.2715 | 483.2449 | 482.2609 | **E** | 1573.7704 | 1572.7752 |  | ***1647.8072*** | 1630.7806 | 1629.7966 | **14** |
| **5** | 44.0495 | 543.3137 | 526.2871 | 525.3031 | 571.3086 | 554.2821 | 553.2980 | **A** | 1502.7333 |  |  | ***1518.7646*** | 1501.7380 | 1500.7540 | **13** |
| **6** | 86.0964 | 656.3978 | 639.3712 | 638.3872 | 684.3927 | 667.3661 | 666.3821 | **I** | 1389.6492 | 1402.6696 | 1416.6853 | 1447.7275 | 1430.7009 | 1429.7169 | **12** |
| **7** | 102.0550 | 785.4403 | 768.4138 | 767.4298 | 813.4353 | 796.4087 | 795.4247 | **E** | 1260.6066 | 1259.6114 |  | 1334.6434 | 1317.6169 | 1316.6329 | **11** |
| **8** | 102.0550 | 914.4829 | 897.4564 | 896.4724 | 942.4779 | 925.4513 | 924.4673 | **E** | 1131.5640 | 1130.5688 |  | ***1205.6008*** | 1188.5743 | 1187.5903 | **10** |
| **9** | 86.0964 | 1027.5670 | 1010.5405 | 1009.5564 | 1055.5619 | 1038.5354 | 1037.5514 | **L** | 1018.4800 | 1017.4847 |  | ***1076.5582*** | 1059.5317 | 1058.5477 | **9** |
| **10** | 74.0600 | 1128.6147 | 1111.5881 | 1110.6041 | 1156.6096 | 1139.5830 | 1138.5990 | **T** | 917.4323 | 930.4527 | 932.4320 | 963.4742 | 946.4476 | 945.4636 | **8** |
| **11** | 88.0393 | 1243.6416 | 1226.6151 | 1225.6311 | 1271.6365 | 1254.6100 | 1253.6260 | **D** | 802.4054 | 801.4101 |  | 862.4265 | 845.3999 | 844.4159 | **7** |
| **12** | 102.0550 | 1372.6842 | 1355.6577 | 1354.6737 | 1400.6791 | 1383.6526 | 1382.6686 | **E** | 673.3628 | 672.3675 |  | ***747.3995*** | 730.3730 | 729.3890 | **6** |
| **13** | 102.0550 | 1501.7268 | 1484.7003 | 1483.7162 | 1529.7217 | 1512.6952 | 1511.7112 | **E** | 544.3202 | 543.3249 |  | ***618.3570*** | 601.3304 | 600.3464 | **5** |
| **14** | 72.0808 | 1600.7952 | 1583.7687 | 1582.7847 | 1628.7901 | 1611.7636 | 1610.7796 | **V** | 445.2518 | 458.2722 |  | ***489.3144*** | 472.2878 | 471.3038 | **4** |
| **15** | 101.1073 | 1728.8902 | 1711.8636 | 1710.8796 | 1756.8851 | 1739.8586 | 1738.8745 | **K** | 317.1568 | 316.1615 |  | ***390.2459*** | 373.2194 | 372.2354 | **3** |
| **16** | 60.0444 | 1815.9222 | 1798.8957 | 1797.9117 | 1843.9171 | 1826.8906 | 1825.9066 | **S** | 230.1248 | 229.1295 |  | 262.1510 | 245.1244 | 244.1404 | **2** |
| **17** | 129.1135 |  |  |  |  |  |  | **R** | 74.0237 | 73.0284 |  | 175.1190 | 158.0924 |  | **1** |

|  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **Seq** | **ya** | **yb** | **Seq** | **ya** | **yb** | **Seq** | **ya** | **yb** |
| **IE** | 215.1390 | 243.1339 | **IEE** | 344.1816 | 372.1765 | **IEEA** | 415.2187 | 443.2136 |
| **IEEAI** | 528.3028 | 556.2977 | **IEEAIE** | 657.3454 | 685.3403 | **EE** | 231.0975 | 259.0925 |
| **EEA** | 302.1347 | 330.1296 | **EEAI** | 415.2187 | 443.2136 | **EEAIE** | 544.2613 | 572.2562 |
| **EEAIEE** | 673.3039 | 701.2988 | **EA** | 173.0921 | 201.0870 | **EAI** | 286.1761 | 314.1710 |
| **EAIE** | 415.2187 | 443.2136 | **EAIEE** | 544.2613 | 572.2562 | **EAIEEL** | 657.3454 | 685.3403 |
| **AI** | 157.1335 | 185.1285 | **AIE** | 286.1761 | 314.1710 | **AIEE** | 415.2187 | 443.2136 |
| **AIEEL** | 528.3028 | 556.2977 | **AIEELT** | 629.3505 | 657.3454 | **IE** | 215.1390 | 243.1339 |
| **IEE** | 344.1816 | 372.1765 | **IEEL** | 457.2657 | 485.2606 | **IEELT** | 558.3134 | 586.3083 |
| **IEELTD** | 673.3403 | 701.3352 | **EE** | 231.0975 | 259.0925 | **EEL** | 344.1816 | 372.1765 |
| **EELT** | 445.2293 | 473.2242 | **EELTD** | 560.2562 | 588.2511 | **EELTDE** | 689.2988 | 717.2937 |
| **EL** | 215.1390 | 243.1339 | **ELT** | 316.1867 | 344.1816 | **ELTD** | 431.2136 | 459.2086 |
| **ELTDE** | 560.2562 | 588.2511 | **ELTDEE** | 689.2988 | 717.2937 | **LT** | 187.1441 | 215.1390 |
| **LTD** | 302.1710 | 330.1660 | **LTDE** | 431.2136 | 459.2086 | **LTDEE** | 560.2562 | 588.2511 |
| **LTDEEV** | 659.3246 | 687.3196 | **TD** | 189.0870 | 217.0819 | **TDE** | 318.1296 | 346.1245 |
| **TDEE** | 447.1722 | 475.1671 | **TDEEV** | 546.2406 | 574.2355 | **TDEEVK** | 674.3355 | 702.3305 |
| **DE** | 217.0819 | 245.0768 | **DEE** | 346.1245 | 374.1194 | **DEEV** | 445.1929 | 473.1878 |
| **DEEVK** | 573.2879 | 601.2828 | **DEEVKS** | 660.3199 | 688.3148 | **EE** | 231.0975 | 259.0925 |
| **EEV** | 330.1660 | 358.1609 | **EEVK** | 458.2609 | 486.2558 | **EEVKS** | 545.2930 | 573.2879 |
| **EV** | 201.1234 | 229.1183 | **EVK** | 329.2183 | 357.2132 | **EVKS** | 416.2504 | 444.2453 |
| **VK** | 200.1757 | 228.1707 | **VKS** | 287.2078 | 315.2027 | **KS** | 188.1394 | 216.1343 |

🡪 Annotated MS2 spectrum for peptide DHHPVTLEEALTK



**Monoisotopic mass of neutral peptide Mr(calc):** 1488.7572

**Ions Score:** 27 **Expect:** 0.17

**Matches :** 3/176 fragment ions using 3 most intense peaks   ([help](http://msmsms/mascot/help/results_help.html" \l "PEP" \t "_blank))

|  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **#** | **Immon.** | **a** | **a0** | **b** | **b0** | **Seq.** | **y** | **y\*** | **y0** | **#** |
| **1** | 88.0393 | 88.0393 | 70.0287 | 116.0342 | 98.0237 | **D** |  |  |  | **13** |
| **2** | 110.0713 | 225.0982 | 207.0877 | 253.0931 | 235.0826 | **H** | ***1374.7376*** | 1357.7110 | 1356.7270 | **12** |
| **3** | 110.0713 | 362.1571 | 344.1466 | 390.1520 | 372.1415 | **H** | ***1237.6787*** | 1220.6521 | 1219.6681 | **11** |
| **4** | 70.0651 | 459.2099 | 441.1993 | 487.2048 | 469.1942 | **P** | ***1100.6198*** | 1083.5932 | 1082.6092 | **10** |
| **5** | 72.0808 | 558.2783 | 540.2677 | 586.2732 | 568.2627 | **V** | 1003.5670 | 986.5405 | 985.5564 | **9** |
| **6** | 74.0600 | 659.3260 | 641.3154 | 687.3209 | 669.3103 | **T** | 904.4986 | 887.4720 | 886.4880 | **8** |
| **7** | 86.0964 | 772.4100 | 754.3995 | 800.4050 | 782.3944 | **L** | 803.4509 | 786.4244 | 785.4403 | **7** |
| **8** | 102.0550 | 901.4526 | 883.4421 | 929.4476 | 911.4370 | **E** | 690.3668 | 673.3403 | 672.3563 | **6** |
| **9** | 102.0550 | 1030.4952 | 1012.4847 | 1058.4902 | 1040.4796 | **E** | 561.3243 | 544.2977 | 543.3137 | **5** |
| **10** | 44.0495 | 1101.5323 | 1083.5218 | 1129.5273 | 1111.5167 | **A** | 432.2817 | 415.2551 | 414.2711 | **4** |
| **11** | 86.0964 | 1214.6164 | 1196.6058 | 1242.6113 | 1224.6008 | **L** | 361.2445 | 344.2180 | 343.2340 | **3** |
| **12** | 74.0600 | 1315.6641 | 1297.6535 | 1343.6590 | 1325.6484 | **T** | 248.1605 | 231.1339 | 230.1499 | **2** |
| **13** | 101.1073 |  |  |  |  | **K** | 147.1128 | 130.0863 |  | **1** |

|  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **Seq** | **ya** | **yb** | **Seq** | **ya** | **yb** | **Seq** | **ya** | **yb** |
| **HH** | 247.1302 | 275.1251 | **HHP** | 344.1829 | 372.1779 | **HHPV** | 443.2514 | 471.2463 |
| **HHPVT** | 544.2990 | 572.2940 | **HHPVTL** | 657.3831 | 685.3780 | **HP** | 207.1240 | 235.1190 |
| **HPV** | 306.1925 | 334.1874 | **HPVT** | 407.2401 | 435.2350 | **HPVTL** | 520.3242 | 548.3191 |
| **HPVTLE** | 649.3668 | 677.3617 | **PV** | 169.1335 | 197.1285 | **PVT** | 270.1812 | 298.1761 |
| **PVTL** | 383.2653 | 411.2602 | **PVTLE** | 512.3079 | 540.3028 | **PVTLEE** | 641.3505 | 669.3454 |
| **VT** | 173.1285 | 201.1234 | **VTL** | 286.2125 | 314.2074 | **VTLE** | 415.2551 | 443.2500 |
| **VTLEE** | 544.2977 | 572.2926 | **VTLEEA** | 615.3348 | 643.3297 | **TL** | 187.1441 | 215.1390 |
| **TLE** | 316.1867 | 344.1816 | **TLEE** | 445.2293 | 473.2242 | **TLEEA** | 516.2664 | 544.2613 |
| **TLEEAL** | 629.3505 | 657.3454 | **LE** | 215.1390 | 243.1339 | **LEE** | 344.1816 | 372.1765 |
| **LEEA** | 415.2187 | 443.2136 | **LEEAL** | 528.3028 | 556.2977 | **LEEALT** | 629.3505 | 657.3454 |
| **EE** | 231.0975 | 259.0925 | **EEA** | 302.1347 | 330.1296 | **EEAL** | 415.2187 | 443.2136 |
| **EEALT** | 516.2664 | 544.2613 | **EA** | 173.0921 | 201.0870 | **EAL** | 286.1761 | 314.1710 |
| **EALT** | 387.2238 | 415.2187 | **AL** | 157.1335 | 185.1285 | **ALT** | 258.1812 | 286.1761 |
| **LT** | 187.1441 | 215.1390 |  |  |  |  |  |  |

**Bottom of Form**

**Spot 20:**

**http://msmsms/mascot/images/88x31_logo_white.gifMascot Search Results**

**User :**

**Email :**

**Search title : SampleSetID: 341, AnalysisID: 621, MaldiWellID: 45141, SpectrumID: 150979, Path=\Jimmy\Cooperia Adult ES 20110221\20110330 MS en MSMS**

**Database : cooperia\_oncophora oncophora (33747 sequences; 5232511 residues)**

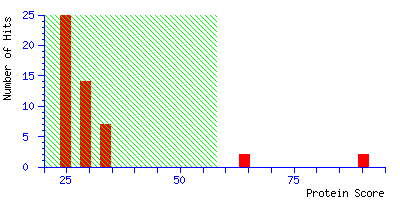
**Timestamp : 30 Mar 2011 at 12:16:41 GMT**

**Warning : A Peptide summary report will usually give a much clearer picture of MS/MS search results.**

**Top Score : 90 for isotig17160, putative nuclear encoded protein Method: similarity and extension**

**Mascot Score Histogram**

Protein score is -10\*Log(P), where P is the probability that the observed match is a random event.  
Protein scores greater than 58 are significant (p<0.05).  
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



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**Protein Summary Report**

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**Index**

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
|  | **Accession** | **Mass** | **Score** | **Description** |
| **1.** | [**isotig17160**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20110330/F014226.dat#Hit1) | 14996 | 90 | putative nuclear encoded protein Method: similarity and extension |
| **2.** | [**isotig17113**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20110330/F014226.dat#Hit2) | 14478 | 90 | putative nuclear encoded protein Method: similarity and extension |
| **3.** | [**isotig21044**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20110330/F014226.dat#Hit3) | 15109 | 62 | putative nuclear encoded protein Method: similarity and extension |
| **4.** | [**isotig29536**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20110330/F014226.dat#Hit4) | 15107 | 62 | putative nuclear encoded protein Method: similarity and extension |
| **5.** | [**isotig32720**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20110330/F014226.dat#Hit5) | 6830 | 35 | putative nuclear encoded protein Method: Longest ORF |
| **6.** | [**isotig22734**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20110330/F014226.dat#Hit6) | 13630 | 33 | putative nuclear encoded protein Method: similarity and extension |
| **7.** | [**isotig25489**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20110330/F014226.dat#Hit7) | 39226 | 32 | putative nuclear encoded protein Method: similarity and extension |
| **8.** | [**isotig30794**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20110330/F014226.dat#Hit8) | 17046 | 32 | putative nuclear encoded protein Method: Longest ORF |
| **9.** | [**isotig23281**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20110330/F014226.dat#Hit9) | 29512 | 32 | putative nuclear encoded protein Method: similarity and extension |
| **10.** | [**isotig19741**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20110330/F014226.dat#Hit10) | 51146 | 32 | putative nuclear encoded protein Method: similarity and extension |
| **11.** | [**isotig14197**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20110330/F014226.dat#Hit11) | 20833 | 32 | putative nuclear encoded protein Method: similarity and extension |
| **12.** | [**isotig00500**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20110330/F014226.dat#Hit12) | 14131 | 31 | putative nuclear encoded protein Method: similarity and extension |
| **13.** | [**isotig19508**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20110330/F014226.dat#Hit13) | 5563 | 31 | putative nuclear encoded protein Method: similarity and extension |
| **14.** | [**isotig07454**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20110330/F014226.dat#Hit14) | 27617 | 30 | putative nuclear encoded protein Method: similarity and extension |
| **15.** | [**isotig28402**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20110330/F014226.dat#Hit15) | 17999 | 30 | putative nuclear encoded protein Method: similarity and extension |
| **16.** | [**isotig15682**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20110330/F014226.dat#Hit16) | 17070 | 29 | putative nuclear encoded protein Method: Longest ORF |
| **17.** | [**isotig01159**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20110330/F014226.dat#Hit17) | 7068 | 29 | putative nuclear encoded protein Method: Longest ORF |
| **18.** | [**isotig24316**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20110330/F014226.dat#Hit18) | 12965 | 29 | putative nuclear encoded protein Method: Longest ORF |
| **19.** | [**isotig21636**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20110330/F014226.dat#Hit19) | 16937 | 28 | putative nuclear encoded protein Method: similarity and extension |
| **20.** | [**isotig32929**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20110330/F014226.dat#Hit20) | 6722 | 28 | putative nuclear encoded protein Method: similarity and extension |

**Results List**

|  |  |
| --- | --- |
| **1.** | [isotig17160](http://msmsms/mascot/cgi/protein_view.pl?file=../data/20110330/F014226.dat&hit=1" \t "_blank)    **Mass:** 14996    **Score:** 90     **Expect:** 3.2e-005  **Matches:** 5 |
|  | putative nuclear encoded protein Method: similarity and extension |

|  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | **Observed** | **Mr(expt)** | **Mr(calc)** | **ppm** | **Start** |  | **End** | **Miss** | **Ions** | **Peptide** |
|  | 1059.4877 | 1058.4804 | 1058.5906 | -104.08 | 79 | - | 87 | 2 | --- | R.KLPAKEMAR.Q + Oxidation (M) |
|  | 1136.4873 | 1135.4800 | 1135.5985 | -104.37 | 93 | - | 102 | 1 | --- | R.LKDSAYNVAR.M |
|  | 1136.4873 | 1135.4800 | 1135.5985 | -104.37 | 93 | - | 102 | 1 | 71 | R.LKDSAYNVAR.M |
|  | 1630.6591 | 1629.6518 | 1629.8263 | -107.07 | 37 | - | 50 | 0 | --- | R.QFNPSLVWANDLAR.E |
|  | 2500.9897 | 2499.9824 | 2500.1589 | -70.59 | 108 | - | 128 | 2 | --- | R.PEFGCNSFYKDSVMKVVCLYR.D + Oxidation (M) |

|  |  |
| --- | --- |
|  | **No match to:** 909.3253, 940.4577, 947.4646, 999.3598, 1003.3516, 1006.3755, 1013.3722, 1014.3467, 1022.3751, 1081.3639, 1156.4233, 1162.4653, 1171.4778, 1179.4668, 1197.4698, 1231.5547, 1300.4603, 1345.5773, 1360.5850, 1493.5785, 1501.6617, 1520.6561, 1550.5662, 1593.6445, 1607.5867, 1608.5759, 1608.5759, 1613.6451, 1632.6639, 1638.6909, 1667.6569, 1678.6509, 1707.5918, 1805.7639, 1823.7509, 1823.7509, 1876.7913, 1898.6672, 1921.6617, 1947.6467, 1948.7231, 1984.7021, 2003.6857, 2003.6857, 2077.7314, 2089.7151, 2104.8235, 2215.8914, 2872.1096 |

|  |  |
| --- | --- |
| **2.** | [isotig17113](http://msmsms/mascot/cgi/protein_view.pl?file=../data/20110330/F014226.dat&hit=2" \t "_blank)    **Mass:** 14478    **Score:** 90     **Expect:** 3.6e-005  **Matches:** 5 |
|  | putative nuclear encoded protein Method: similarity and extension |

|  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | **Observed** | **Mr(expt)** | **Mr(calc)** | **ppm** | **Start** |  | **End** | **Miss** | **Ions** | **Peptide** |
|  | 1136.4873 | 1135.4800 | 1135.5985 | -104.37 | 90 | - | 99 | 1 | --- | R.LKDSAYNVAR.M |
|  | 1136.4873 | 1135.4800 | 1135.5985 | -104.37 | 90 | - | 99 | 1 | 71 | R.LKDSAYNVAR.M |
|  | 1550.5662 | 1549.5589 | 1549.8398 | -181.26 | 77 | - | 89 | 2 | --- | K.LAAKEMARQTLFR.L + Oxidation (M) |
|  | 1630.6591 | 1629.6518 | 1629.8263 | -107.07 | 34 | - | 47 | 0 | --- | R.QFNPSLVWANDLAR.E |
|  | 2089.7151 | 2088.7078 | 2088.9397 | -111.02 | 102 | - | 119 | 1 | --- | K.SPQPEFGCNSFFKNNVMK.V + Oxidation (M) |

|  |  |
| --- | --- |
|  | **No match to:** 909.3253, 940.4577, 947.4646, 999.3598, 1003.3516, 1006.3755, 1013.3722, 1014.3467, 1022.3751, 1059.4877, 1081.3639, 1156.4233, 1162.4653, 1171.4778, 1179.4668, 1197.4698, 1231.5547, 1300.4603, 1345.5773, 1360.5850, 1493.5785, 1501.6617, 1520.6561, 1593.6445, 1607.5867, 1608.5759, 1608.5759, 1613.6451, 1632.6639, 1638.6909, 1667.6569, 1678.6509, 1707.5918, 1805.7639, 1823.7509, 1823.7509, 1876.7913, 1898.6672, 1921.6617, 1947.6467, 1948.7231, 1984.7021, 2003.6857, 2003.6857, 2077.7314, 2104.8235, 2215.8914, 2500.9897, 2872.1096 |

**http://msmsms/mascot/images/88x31_logo_white.gifMascot Search Results**

**Protein View**

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Match to: **isotig17160** Score: **90** Expect: **3.2e-005**

**putative nuclear encoded protein Method: similarity and extension**

Nominal mass (Mr): **14996**; Calculated pI value: **8.62**

NCBI BLAST search of [isotig17160](http://www.ncbi.nlm.nih.gov/blast/Blast.cgi?ALIGNMENTS=50&ALIGNMENT_VIEW=Pairwise&AUTO_FORMAT=Semiauto&CDD_SEARCH=on&CLIENT=web&COMPOSITION_BASED_STATISTICS=on&DATABASE=nr&DESCRIPTIONS=100&ENTREZ_QUERY=(none)&EXPECT=10&FILTER=L&FORMAT_BLOCK_ON_RESPAGE=None&FORMAT_OBJECT=Alignment&FORMAT_TYPE=HTML&GAPCOSTS=11+1&I_THRESH=0.001&LAYOUT=TwoWindows&MATRIX_NAME=BLOSUM62&NCBI_GI=on&PAGE=Proteins&PROGRAM=blastp&QUERY=MFFTLIVLCFFLVNVNADSGCVDYHGLSGYYIQRNRQFNPSLVWANDLAREACDVAKGEANVFAGQFKVEAERNFAGRKLPAKEMARQTLFRLKDSAYNVARMKSSRPEFGCNSFYKDSVMKVVCLYRDEE&SERVICE=plain&SET_DEFAULTS.x=9&SET_DEFAULTS.y=5&SHOW_OVERVIEW=on&WORD_SIZE=3&END_OF_HTTPGET=Yes" \t "_blank) against nr

Unformatted [sequence string](http://msmsms/mascot/cgi/getseq.pl?cooperia_oncophora+isotig17160+seq" \t "_blank) for pasting into other applications

Variable modifications: Oxidation (HW),Oxidation (M)

Cleavage by Trypsin/P: cuts C-term side of KR

Sequence Coverage: **41%**

Matched peptides shown in **Bold Red**

**1** MFFTLIVLCF FLVNVNADSG CVDYHGLSGY YIQRNR**QFNP SLVWANDLAR**

**51** EACDVAKGEA NVFAGQFKVE AERNFAGR**KL PAKEMAR**QTL FR**LKDSAYNV**

**101 AR**MKSSR**PEF GCNSFYKDSV MKVVCLYR**DE E

**Error! Not a valid embedded object.**

**Start - End Observed Mr(expt) Mr(calc) ppm Miss Sequence**

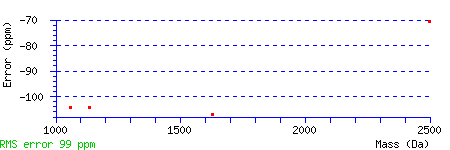
**37 - 50 1630.6591 1629.6518 1629.8263 -107 0 R.QFNPSLVWANDLAR.E**  ([No match](http://msmsms/mascot/cgi/peptide_view.pl?file=../data/20110330/F014226.dat&query=32&hit=1" \t "_blank))

**79 - 87 1059.4877 1058.4804 1058.5906 -104 2 R.KLPAKEMAR.Q**  Oxidation (M) ([No match](http://msmsms/mascot/cgi/peptide_view.pl?file=../data/20110330/F014226.dat&query=10&hit=1" \t "_blank))

**93 - 102 1136.4873 1135.4800 1135.5985 -104 1 R.LKDSAYNVAR.M**  ([No match](http://msmsms/mascot/cgi/peptide_view.pl?file=../data/20110330/F014226.dat&query=12&hit=1" \t "_blank))

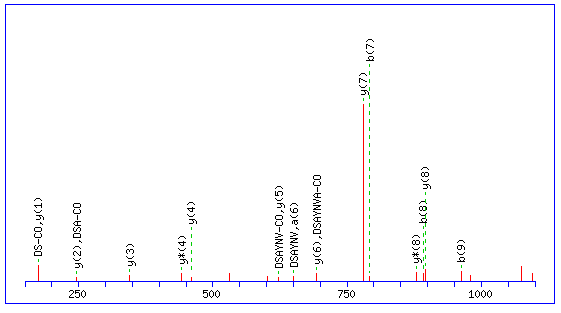
**93 - 102 1136.4873 1135.4800 1135.5985 -104 1 R.LKDSAYNVAR.M**  ([Ions score 71](http://msmsms/mascot/cgi/peptide_view.pl?file=../data/20110330/F014226.dat&query=13&hit=1" \t "_blank))

**108 - 128 2500.9897 2499.9824 2500.1589 -71 2 R.PEFGCNSFYKDSVMKVVCLYR.D**  Oxidation (M) ([No match](http://msmsms/mascot/cgi/peptide_view.pl?file=../data/20110330/F014226.dat&query=53&hit=1" \t "_blank))



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🡪 Annotated MS2 spectrum for peptide LKDSAYNVAR



**Monoisotopic mass of neutral peptide Mr(calc):** 1135.5985

**Ions Score:** 71 **Expect:** 5.4e-006

**Matches :** 19/145 fragment ions using 19 most intense peaks   ([help](http://msmsms/mascot/help/results_help.html" \l "PEP" \t "_blank))

|  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **#** | **Immon.** | **a** | **a\*** | **a0** | **b** | **b\*** | **b0** | **Seq.** | **v** | **w** | **y** | **y\*** | **y0** | **#** |
| **1** | 86.0964 | 86.0964 |  |  | 114.0913 |  |  | **L** |  |  |  |  |  | **10** |
| **2** | 101.1073 | 214.1914 | 197.1648 |  | 242.1863 | 225.1598 |  | **K** | 950.4326 | 949.4374 | 1023.5218 | 1006.4952 | 1005.5112 | **9** |
| **3** | 88.0393 | 329.2183 | 312.1918 | 311.2078 | 357.2132 | 340.1867 | 339.2027 | **D** | 835.4057 | 834.4104 | ***895.4268*** | 878.4003 | 877.4163 | **8** |
| **4** | 60.0444 | 416.2504 | 399.2238 | 398.2398 | 444.2453 | 427.2187 | 426.2347 | **S** | 748.3737 | 747.3784 | ***780.3999*** | 763.3733 | 762.3893 | **7** |
| **5** | 44.0495 | 487.2875 | 470.2609 | 469.2769 | 515.2824 | 498.2558 | 497.2718 | **A** | 677.3366 |  | ***693.3679*** | 676.3413 |  | **6** |
| **6** | 136.0757 | 650.3508 | 633.3243 | 632.3402 | 678.3457 | 661.3192 | 660.3352 | **Y** | 514.2732 |  | ***622.3307*** | 605.3042 |  | **5** |
| **7** | 87.0553 | 764.3937 | 747.3672 | 746.3832 | **792.3886** | 775.3621 | 774.3781 | **N** | 400.2303 | 399.2350 | ***459.2674*** | 442.2409 |  | **4** |
| **8** | 72.0808 | 863.4621 | 846.4356 | 845.4516 | **891.4571** | 874.4305 | 873.4465 | **V** | 301.1619 | 314.1823 | ***345.2245*** | 328.1979 |  | **3** |
| **9** | 44.0495 | 934.4993 | 917.4727 | 916.4887 | **962.4942** | 945.4676 | 944.4836 | **A** | 230.1248 |  | ***246.1561*** | 229.1295 |  | **2** |
| **10** | 129.1135 |  |  |  |  |  |  | **R** | 74.0237 | 73.0284 | ***175.1190*** | 158.0924 |  | **1** |

|  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **Seq** | **ya** | **yb** | **Seq** | **ya** | **yb** | **Seq** | **ya** | **yb** |
| **KD** | 216.1343 | 244.1292 | **KDS** | 303.1663 | 331.1612 | **KDSA** | 374.2034 | 402.1983 |
| **KDSAY** | 537.2667 | 565.2617 | **KDSAYN** | 651.3097 | 679.3046 | **DS** | 175.0713 | 203.0662 |
| **DSA** | 246.1084 | 274.1034 | **DSAY** | 409.1718 | 437.1667 | **DSAYN** | 523.2147 | 551.2096 |
| **DSAYNV** | 622.2831 | 650.2780 | **DSAYNVA** | 693.3202 | 721.3151 | **SA** | 131.0815 | 159.0764 |
| **SAY** | 294.1448 | 322.1397 | **SAYN** | 408.1878 | 436.1827 | **SAYNV** | 507.2562 | 535.2511 |
| **SAYNVA** | 578.2933 | 606.2882 | **AY** | 207.1128 | 235.1077 | **AYN** | 321.1557 | 349.1506 |
| **AYNV** | 420.2241 | 448.2191 | **AYNVA** | 491.2613 | 519.2562 | **YN** | 250.1186 | 278.1135 |
| **YNV** | 349.1870 | 377.1819 | **YNVA** | 420.2241 | 448.2191 | **NV** | 186.1237 | 214.1186 |
| **NVA** | 257.1608 | 285.1557 | **VA** | 143.1179 | 171.1128 |  |  |  |

**Spot 21:**

**http://msmsms/mascot/images/88x31_logo_white.gifMascot Search Results**

**User :**

**Email :**

**Search title : SampleSetID: 341, AnalysisID: 561, MaldiWellID: 45096, SpectrumID: 137538, Path=\Jimmy\Cooperia Adult ES 20110221\20110221 MS en MSMS**

**Database : cooperia\_oncophora oncophora (33747 sequences; 5232511 residues)**

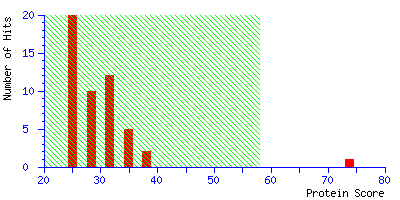
**Timestamp : 21 Feb 2011 at 15:40:24 GMT**

**Warning : A Peptide summary report will usually give a much clearer picture of MS/MS search results.**

**Top Score : 74 for isotig26364, putative nuclear encoded protein Method: similarity and extension**

**Mascot Score Histogram**

Protein score is -10\*Log(P), where P is the probability that the observed match is a random event.  
Protein scores greater than 58 are significant (p<0.05).  
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



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**Protein Summary Report**

|  |  |  |  |
| --- | --- | --- | --- |
|  |  |  | [Help](http://msmsms/mascot/help/msms_summaries_help.html" \t "_blank) |
|  | Significance threshold p< | Max. number of hits |  |

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**Index**

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
|  | **Accession** | **Mass** | **Score** | **Description** |
| **1.** | [**isotig26364**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20110221/F013501.dat#Hit1) | 14131 | 74 | putative nuclear encoded protein Method: similarity and extension |
| **2.** | [**isotig12469**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20110221/F013501.dat#Hit2) | 16851 | 40 | putative nuclear encoded protein Method: similarity and extension |
| **3.** | [**isotig12468**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20110221/F013501.dat#Hit3) | 16852 | 40 | putative nuclear encoded protein Method: similarity and extension |
| **4.** | [**isotig28699**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20110221/F013501.dat#Hit4) | 21729 | 35 | putative nuclear encoded protein Method: similarity and extension |
| **5.** | [**isotig27965**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20110221/F013501.dat#Hit5) | 33029 | 34 | putative nuclear encoded protein Method: similarity and extension |
| **6.** | [**isotig19255**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20110221/F013501.dat#Hit6) | 11347 | 34 | putative nuclear encoded protein Method: similarity and extension |
| **7.** | [**isotig12471**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20110221/F013501.dat#Hit7) | 15392 | 33 | putative nuclear encoded protein Method: similarity and extension |
| **8.** | [**isotig12470**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20110221/F013501.dat#Hit8) | 15393 | 33 | putative nuclear encoded protein Method: similarity and extension |
| **9.** | [**isotig27376**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20110221/F013501.dat#Hit9) | 20179 | 33 | putative nuclear encoded protein Method: Longest ORF |
| **10.** | [**isotig15924**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20110221/F013501.dat#Hit10) | 24521 | 32 | putative nuclear encoded protein Method: similarity and extension |
| **11.** | [**isotig10283**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20110221/F013501.dat#Hit11) | 25622 | 31 | putative nuclear encoded protein Method: similarity and extension |
| **12.** | [**isotig06393**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20110221/F013501.dat#Hit12) | 20948 | 31 | putative nuclear encoded protein Method: similarity and extension |
| **13.** | [**isotig06392**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20110221/F013501.dat#Hit13) | 20948 | 31 | putative nuclear encoded protein Method: similarity and extension |
| **14.** | [**isotig06397**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20110221/F013501.dat#Hit14) | 20948 | 31 | putative nuclear encoded protein Method: similarity and extension |
| **15.** | [**isotig06398**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20110221/F013501.dat#Hit15) | 20948 | 31 | putative nuclear encoded protein Method: similarity and extension |
| **16.** | [**isotig06396**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20110221/F013501.dat#Hit16) | 20948 | 31 | putative nuclear encoded protein Method: similarity and extension |
| **17.** | [**isotig06395**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20110221/F013501.dat#Hit17) | 20948 | 31 | putative nuclear encoded protein Method: similarity and extension |
| **18.** | [**isotig06391**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20110221/F013501.dat#Hit18) | 20948 | 31 | putative nuclear encoded protein Method: similarity and extension |
| **19.** | [**isotig24304**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20110221/F013501.dat#Hit19) | 7673 | 30 | putative nuclear encoded protein Method: similarity and extension |
| **20.** | [**isotig21265**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20110221/F013501.dat#Hit20) | 6115 | 30 | putative nuclear encoded protein Method: similarity and extension |

**Results List**

|  |  |
| --- | --- |
| **1.** | [isotig26364](http://msmsms/mascot/cgi/protein_view.pl?file=../data/20110221/F013501.dat&hit=1" \t "_blank)    **Mass:** 14131    **Score:** 74     **Expect:** 0.0014  **Matches:** 6 |
|  | putative nuclear encoded protein Method: similarity and extension |

|  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | **Observed** | **Mr(expt)** | **Mr(calc)** | **ppm** | **Start** |  | **End** | **Miss** | **Ions** | **Peptide** |
|  | 806.4458 | 805.4385 | 805.4446 | -7.58 | 103 | - | 109 | 0 | --- | R.NLPPHTK.Y |
|  | 993.5416 | 992.5343 | 992.5403 | -6.04 | 58 | - | 67 | 0 | --- | R.GIVASNAPHK.F |
|  | 1493.7401 | 1492.7328 | 1492.6656 | 45.0 | 110 | - | 122 | 0 | --- | K.YGCNSYFEGNLVK.V |
|  | 3198.5354 | 3197.5281 | 3197.4857 | 13.3 | 73 | - | 102 | 0 | --- | K.TFASGGSVPVMIGETLMDGLQDETQTENVR.N + Oxidation (M) |
|  | 3214.5420 | 3213.5347 | 3213.4806 | 16.8 | 73 | - | 102 | 0 | --- | K.TFASGGSVPVMIGETLMDGLQDETQTENVR.N + 2 Oxidation (M) |
|  | 3214.5420 | 3213.5347 | 3213.4806 | 16.8 | 73 | - | 102 | 0 | 54 | K.TFASGGSVPVMIGETLMDGLQDETQTENVR.N + 2 Oxidation (M) |

|  |  |
| --- | --- |
|  | **No match to:** 832.3038, 834.3090, 842.5038, 844.5375, 851.3734, 868.3972, 877.4634, 881.2510, 884.4007, 1024.5048, 1047.5421, 1079.5164, 1081.5309, 1094.5413, 1097.5139, 1107.5577, 1109.4958, 1111.5244, 1118.5197, 1121.5320, 1136.5599, 1138.5508, 1138.5508, 1154.5435, 1179.6104, 1200.4836, 1216.4735, 1234.6937, 1300.6161, 1320.6035, 1418.6699, 1420.7212, 1422.7455, 1459.7029, 1475.7867, 1489.7762, 1536.7200, 1546.7617, 1550.7151, 1550.7151, 1618.8424, 1838.9387, 2211.1301, 3150.5532, 3197.5681, 3213.5476, 3228.5547 |

**http://msmsms/mascot/images/88x31_logo_white.gifMascot Search Results**

**Protein View**

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Match to: **isotig26364** Score: **74** Expect: **0.0014**

**putative nuclear encoded protein Method: similarity and extension**

Nominal mass (Mr): **14131**; Calculated pI value: **5.29**

NCBI BLAST search of [isotig26364](http://www.ncbi.nlm.nih.gov/blast/Blast.cgi?ALIGNMENTS=50&ALIGNMENT_VIEW=Pairwise&AUTO_FORMAT=Semiauto&CDD_SEARCH=on&CLIENT=web&COMPOSITION_BASED_STATISTICS=on&DATABASE=nr&DESCRIPTIONS=100&ENTREZ_QUERY=(none)&EXPECT=10&FILTER=L&FORMAT_BLOCK_ON_RESPAGE=None&FORMAT_OBJECT=Alignment&FORMAT_TYPE=HTML&GAPCOSTS=11+1&I_THRESH=0.001&LAYOUT=TwoWindows&MATRIX_NAME=BLOSUM62&NCBI_GI=on&PAGE=Proteins&PROGRAM=blastp&QUERY=MLFVLVPLCFLLINVAAGNRCPTYTARKEWYSSFNEFLNPALEWDPGLSSDACNEARGIVASNAPHKFIAEKTFASGGSVPVMIGETLMDGLQDETQTENVRNLPPHTKYGCNSYFEGNLVKVVCVYK&SERVICE=plain&SET_DEFAULTS.x=9&SET_DEFAULTS.y=5&SHOW_OVERVIEW=on&WORD_SIZE=3&END_OF_HTTPGET=Yes" \t "_blank) against nr

Unformatted [sequence string](http://msmsms/mascot/cgi/getseq.pl?cooperia_oncophora+isotig26364+seq" \t "_blank) for pasting into other applications

Variable modifications: Oxidation (HW),Oxidation (M)

Cleavage by Trypsin/P: cuts C-term side of KR

Sequence Coverage: **46%**

Matched peptides shown in **Bold Red**

**1** MLFVLVPLCF LLINVAAGNR CPTYTARKEW YSSFNEFLNP ALEWDPGLSS

**51** DACNEAR**GIV ASNAPHK**FIA EK**TFASGGSV PVMIGETLMD GLQDETQTEN**

**101 VRNLPPHTKY GCNSYFEGNL VK**VVCVYK



  Residue Number  Increasing Mass  Decreasing Mass



**Start - End Observed Mr(expt) Mr(calc) ppm Miss Sequence**

**58 - 67 993.5416 992.5343 992.5403 -6 0 R.GIVASNAPHK.F**  ([No match](http://msmsms/mascot/cgi/peptide_view.pl?file=../data/20110221/F013501.dat&query=11&hit=1" \t "_blank))

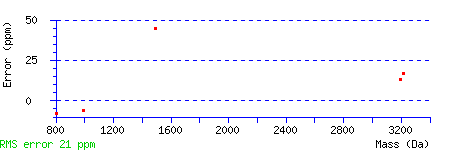
**73 - 102 3198.5354 3197.5281 3197.4857 13 0 K.TFASGGSVPVMIGETLMDGLQDETQTENVR.N**  Oxidation (M) ([No match](http://msmsms/mascot/cgi/peptide_view.pl?file=../data/20110221/F013501.dat&query=49&hit=1" \t "_blank))

**73 - 102 3214.5420 3213.5347 3213.4806 17 0 K.TFASGGSVPVMIGETLMDGLQDETQTENVR.N**  2 Oxidation (M) ([No match](http://msmsms/mascot/cgi/peptide_view.pl?file=../data/20110221/F013501.dat&query=51&hit=1" \t "_blank))

**73 - 102 3214.5420 3213.5347 3213.4806 17 0 K.TFASGGSVPVMIGETLMDGLQDETQTENVR.N**  2 Oxidation (M) ([Ions score 54](http://msmsms/mascot/cgi/peptide_view.pl?file=../data/20110221/F013501.dat&query=52&hit=1" \t "_blank))

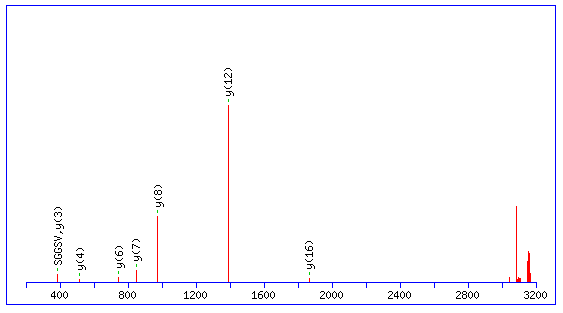
**103 - 109 806.4458 805.4385 805.4446 -8 0 R.NLPPHTK.Y**  ([No match](http://msmsms/mascot/cgi/peptide_view.pl?file=../data/20110221/F013501.dat&query=1&hit=1" \t "_blank))

**110 - 122 1493.7401 1492.7328 1492.6656 45 0 K.YGCNSYFEGNLVK.V**  ([No match](http://msmsms/mascot/cgi/peptide_view.pl?file=../data/20110221/F013501.dat&query=39&hit=1" \t "_blank))



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🡪 Annotated MS2 spectrum for peptide TFASGGSVPVMIGETLMDGLQDETQTENVR



**Monoisotopic mass of neutral peptide Mr(calc):** 3213.4806

**Variable modifications:**

**M11 :** Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983

**M17 :** Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983

**Ions Score:** 54 **Expect:** 0.0005

**Matches :** 8/813 fragment ions using 9 most intense peaks   ([help](http://msmsms/mascot/help/results_help.html" \l "PEP" \t "_blank))

|  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **#** | **Immon.** | **a** | **a\*** | **a0** | **b** | **b\*** | **b0** | **Seq.** | **v** | **w** | **w'** | **y** | **y\*** | **y0** | **#** |
| **1** | 74.0600 | 74.0600 |  | 56.0495 | 102.0550 |  | 84.0444 | **T** |  |  |  |  |  |  | **30** |
| **2** | 120.0808 | 221.1285 |  | 203.1179 | 249.1234 |  | 231.1128 | **F** | 3021.3776 |  |  | 3113.4402 | 3096.4136 | 3095.4296 | **29** |
| **3** | 44.0495 | 292.1656 |  | 274.1550 | 320.1605 |  | 302.1499 | **A** | 2950.3405 |  |  | 2966.3718 | 2949.3452 | 2948.3612 | **28** |
| **4** | 60.0444 | 379.1976 |  | 361.1870 | 407.1925 |  | 389.1819 | **S** | 2863.3084 | 2862.3132 |  | 2895.3346 | 2878.3081 | 2877.3241 | **27** |
| **5** | 30.0338 | 436.2191 |  | 418.2085 | 464.2140 |  | 446.2034 | **G** |  |  |  | 2808.3026 | 2791.2761 | 2790.2921 | **26** |
| **6** | 30.0338 | 493.2405 |  | 475.2300 | 521.2354 |  | 503.2249 | **G** |  |  |  | 2751.2812 | 2734.2546 | 2733.2706 | **25** |
| **7** | 60.0444 | 580.2726 |  | 562.2620 | 608.2675 |  | 590.2569 | **S** | 2662.2335 | 2661.2382 |  | 2694.2597 | 2677.2331 | 2676.2491 | **24** |
| **8** | 72.0808 | 679.3410 |  | 661.3304 | 707.3359 |  | 689.3253 | **V** | 2563.1651 | 2576.1855 |  | 2607.2277 | 2590.2011 | 2589.2171 | **23** |
| **9** | 70.0651 | 776.3937 |  | 758.3832 | 804.3886 |  | 786.3781 | **P** | 2466.1123 | 2465.1170 |  | 2508.1592 | 2491.1327 | 2490.1487 | **22** |
| **10** | 72.0808 | 875.4621 |  | 857.4516 | 903.4571 |  | 885.4465 | **V** | 2367.0439 | 2380.0643 |  | 2411.1065 | 2394.0799 | 2393.0959 | **21** |
| **11** | 120.0478 | 1022.4975 |  | 1004.4870 | 1050.4925 |  | 1032.4819 | **M** | 2220.0085 | 2219.0132 |  | 2312.0381 | 2295.0115 | 2294.0275 | **20** |
| **12** | 86.0964 | 1135.5816 |  | 1117.5710 | 1163.5765 |  | 1145.5660 | **I** | 2106.9244 | 2119.9448 | 2133.9605 | 2165.0027 | 2147.9761 | 2146.9921 | **19** |
| **13** | 30.0338 | 1192.6031 |  | 1174.5925 | 1220.5980 |  | 1202.5874 | **G** |  |  |  | 2051.9186 | 2034.8921 | 2033.9080 | **18** |
| **14** | 102.0550 | 1321.6457 |  | 1303.6351 | 1349.6406 |  | 1331.6300 | **E** | 1920.8604 | 1919.8651 |  | 1994.8971 | 1977.8706 | 1976.8866 | **17** |
| **15** | 74.0600 | 1422.6933 |  | 1404.6828 | 1450.6883 |  | 1432.6777 | **T** | 1819.8127 | 1832.8331 | 1834.8124 | ***1865.8545*** | 1848.8280 | 1847.8440 | **16** |
| **16** | 86.0964 | 1535.7774 |  | 1517.7668 | 1563.7723 |  | 1545.7618 | **L** | 1706.7286 | 1705.7334 |  | 1764.8069 | 1747.7803 | 1746.7963 | **15** |
| **17** | 120.0478 | 1682.8128 |  | 1664.8022 | 1710.8077 |  | 1692.7972 | **M** | 1559.6932 | 1558.6980 |  | 1651.7228 | 1634.6963 | 1633.7122 | **14** |
| **18** | 88.0393 | 1797.8398 |  | 1779.8292 | 1825.8347 |  | 1807.8241 | **D** | 1444.6663 | 1443.6710 |  | 1504.6874 | 1487.6609 | 1486.6768 | **13** |
| **19** | 30.0338 | 1854.8612 |  | 1836.8506 | 1882.8561 |  | 1864.8456 | **G** |  |  |  | ***1389.6605*** | 1372.6339 | 1371.6499 | **12** |
| **20** | 86.0964 | 1967.9453 |  | 1949.9347 | 1995.9402 |  | 1977.9296 | **L** | 1274.5607 | 1273.5655 |  | 1332.6390 | 1315.6125 | 1314.6284 | **11** |
| **21** | 101.0709 | 2096.0039 | 2078.9773 | 2077.9933 | 2123.9988 | 2106.9722 | 2105.9882 | **Q** | 1146.5022 | 1145.5069 |  | 1219.5549 | 1202.5284 | 1201.5444 | **10** |
| **22** | 88.0393 | 2211.0308 | 2194.0043 | 2193.0202 | 2239.0257 | 2221.9992 | 2221.0151 | **D** | 1031.4752 | 1030.4800 |  | 1091.4964 | 1074.4698 | 1073.4858 | **9** |
| **23** | 102.0550 | 2340.0734 | 2323.0468 | 2322.0628 | 2368.0683 | 2351.0418 | 2350.0577 | **E** | 902.4326 | 901.4374 |  | ***976.4694*** | 959.4429 | 958.4588 | **8** |
| **24** | 74.0600 | 2441.1211 | 2424.0945 | 2423.1105 | 2469.1160 | 2452.0894 | 2451.1054 | **T** | 801.3850 | 814.4054 | 816.3846 | ***847.4268*** | 830.4003 | 829.4163 | **7** |
| **25** | 101.0709 | 2569.1796 | 2552.1531 | 2551.1691 | 2597.1746 | 2580.1480 | 2579.1640 | **Q** | 673.3264 | 672.3311 |  | ***746.3791*** | 729.3526 | 728.3686 | **6** |
| **26** | 74.0600 | 2670.2273 | 2653.2008 | 2652.2168 | 2698.2222 | 2681.1957 | 2680.2117 | **T** | 572.2787 | 585.2991 | 587.2784 | 618.3206 | 601.2940 | 600.3100 | **5** |
| **27** | 102.0550 | 2799.2699 | 2782.2434 | 2781.2594 | 2827.2648 | 2810.2383 | 2809.2543 | **E** | 443.2361 | 442.2409 |  | ***517.2729*** | 500.2463 | 499.2623 | **4** |
| **28** | 87.0553 | 2913.3128 | 2896.2863 | 2895.3023 | 2941.3078 | 2924.2812 | 2923.2972 | **N** | 329.1932 | 328.1979 |  | ***388.2303*** | 371.2037 |  | **3** |
| **29** | 72.0808 | 3012.3813 | 2995.3547 | 2994.3707 | 3040.3762 | 3023.3496 | 3022.3656 | **V** | 230.1248 | 243.1452 |  | 274.1874 | 257.1608 |  | **2** |
| **30** | 129.1135 |  |  |  |  |  |  | **R** | 74.0237 | 73.0284 |  | 175.1190 | 158.0924 |  | **1** |

|  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **Seq** | **ya** | **yb** | **Seq** | **ya** | **yb** | **Seq** | **ya** | **yb** |
| **FA** | 191.1179 | 219.1128 | **FAS** | 278.1499 | 306.1448 | **FASG** | 335.1714 | 363.1663 |
| **FASGG** | 392.1928 | 420.1878 | **FASGGS** | 479.2249 | 507.2198 | **FASGGSV** | 578.2933 | 606.2882 |
| **FASGGSVP** | 675.3461 | 703.3410 | **AS** | 131.0815 | 159.0764 | **ASG** | 188.1030 | 216.0979 |
| **ASGG** | 245.1244 | 273.1193 | **ASGGS** | 332.1565 | 360.1514 | **ASGGSV** | 431.2249 | 459.2198 |
| **ASGGSVP** | 528.2776 | 556.2726 | **ASGGSVPV** | 627.3461 | 655.3410 | **SG** | 117.0659 | 145.0608 |
| **SGG** | 174.0873 | 202.0822 | **SGGS** | 261.1193 | 289.1143 | **SGGSV** | 360.1878 | 388.1827 |
| **SGGSVP** | 457.2405 | 485.2354 | **SGGSVPV** | 556.3089 | 584.3039 | **GG** | 87.0553 | 115.0502 |
| **GGS** | 174.0873 | 202.0822 | **GGSV** | 273.1557 | 301.1506 | **GGSVP** | 370.2085 | 398.2034 |
| **GGSVPV** | 469.2769 | 497.2718 | **GGSVPVM** | 616.3123 | 644.3072 | **GS** | 117.0659 | 145.0608 |
| **GSV** | 216.1343 | 244.1292 | **GSVP** | 313.1870 | 341.1819 | **GSVPV** | 412.2554 | 440.2504 |
| **GSVPVM** | 559.2908 | 587.2858 | **GSVPVMI** | 672.3749 | 700.3698 | **SV** | 159.1128 | 187.1077 |
| **SVP** | 256.1656 | 284.1605 | **SVPV** | 355.2340 | 383.2289 | **SVPVM** | 502.2694 | 530.2643 |
| **SVPVMI** | 615.3534 | 643.3484 | **SVPVMIG** | 672.3749 | 700.3698 | **VP** | 169.1335 | 197.1285 |
| **VPV** | 268.2020 | 296.1969 | **VPVM** | 415.2374 | 443.2323 | **VPVMI** | 528.3214 | 556.3163 |
| **VPVMIG** | 585.3429 | 613.3378 | **PV** | 169.1335 | 197.1285 | **PVM** | 316.1689 | 344.1639 |
| **PVMI** | 429.2530 | 457.2479 | **PVMIG** | 486.2745 | 514.2694 | **PVMIGE** | 615.3171 | 643.3120 |
| **VM** | 219.1162 | 247.1111 | **VMI** | 332.2002 | 360.1952 | **VMIG** | 389.2217 | 417.2166 |
| **VMIGE** | 518.2643 | 546.2592 | **VMIGET** | 619.3120 | 647.3069 | **MI** | 233.1318 | 261.1267 |
| **MIG** | 290.1533 | 318.1482 | **MIGE** | 419.1959 | 447.1908 | **MIGET** | 520.2436 | 548.2385 |
| **MIGETL** | 633.3276 | 661.3225 | **IG** | 143.1179 | 171.1128 | **IGE** | 272.1605 | 300.1554 |
| **IGET** | 373.2082 | 401.2031 | **IGETL** | 486.2922 | 514.2871 | **IGETLM** | 633.3276 | 661.3225 |
| **GE** | 159.0764 | 187.0713 | **GET** | 260.1241 | 288.1190 | **GETL** | 373.2082 | 401.2031 |
| **GETLM** | 520.2436 | 548.2385 | **GETLMD** | 635.2705 | 663.2654 | **GETLMDG** | 692.2920 | 720.2869 |
| **ET** | 203.1026 | 231.0975 | **ETL** | 316.1867 | 344.1816 | **ETLM** | 463.2221 | 491.2170 |
| **ETLMD** | 578.2490 | 606.2440 | **ETLMDG** | 635.2705 | 663.2654 | **TL** | 187.1441 | 215.1390 |
| **TLM** | 334.1795 | 362.1744 | **TLMD** | 449.2064 | 477.2014 | **TLMDG** | 506.2279 | 534.2228 |
| **TLMDGL** | 619.3120 | 647.3069 | **LM** | 233.1318 | 261.1267 | **LMD** | 348.1588 | 376.1537 |
| **LMDG** | 405.1802 | 433.1751 | **LMDGL** | 518.2643 | 546.2592 | **LMDGLQ** | 646.3229 | 674.3178 |
| **MD** | 235.0747 | 263.0696 | **MDG** | 292.0962 | 320.0911 | **MDGL** | 405.1802 | 433.1751 |
| **MDGLQ** | 533.2388 | 561.2337 | **MDGLQD** | 648.2658 | 676.2607 | **DG** | 145.0608 | 173.0557 |
| **DGL** | 258.1448 | 286.1397 | **DGLQ** | 386.2034 | 414.1983 | **DGLQD** | 501.2304 | 529.2253 |
| **DGLQDE** | 630.2729 | 658.2679 | **GL** | 143.1179 | 171.1128 | **GLQ** | 271.1765 | 299.1714 |
| **GLQD** | 386.2034 | 414.1983 | **GLQDE** | 515.2460 | 543.2409 | **GLQDET** | 616.2937 | 644.2886 |
| **LQ** | 214.1550 | 242.1499 | **LQD** | 329.1819 | 357.1769 | **LQDE** | 458.2245 | 486.2195 |
| **LQDET** | 559.2722 | 587.2671 | **LQDETQ** | 687.3308 | 715.3257 | **QD** | 216.0979 | 244.0928 |
| **QDE** | 345.1405 | 373.1354 | **QDET** | 446.1882 | 474.1831 | **QDETQ** | 574.2467 | 602.2416 |
| **QDETQT** | 675.2944 | 703.2893 | **DE** | 217.0819 | 245.0768 | **DET** | 318.1296 | 346.1245 |
| **DETQ** | 446.1882 | 474.1831 | **DETQT** | 547.2358 | 575.2307 | **DETQTE** | 676.2784 | 704.2733 |
| **ET** | 203.1026 | 231.0975 | **ETQ** | 331.1612 | 359.1561 | **ETQT** | 432.2089 | 460.2038 |
| **ETQTE** | 561.2515 | 589.2464 | **ETQTEN** | 675.2944 | 703.2893 | **TQ** | 202.1186 | 230.1135 |
| **TQT** | 303.1663 | 331.1612 | **TQTE** | 432.2089 | 460.2038 | **TQTEN** | 546.2518 | 574.2467 |
| **TQTENV** | 645.3202 | 673.3151 | **QT** | 202.1186 | 230.1135 | **QTE** | 331.1612 | 359.1561 |
| **QTEN** | 445.2041 | 473.1991 | **QTENV** | 544.2726 | 572.2675 | **TE** | 203.1026 | 231.0975 |
| **TEN** | 317.1456 | 345.1405 | **TENV** | 416.2140 | 444.2089 | **EN** | 216.0979 | 244.0928 |
| **ENV** | 315.1663 | 343.1612 | **NV** | 186.1237 | 214.1186 |  |  |  |

**Spot 23:**

**http://msmsms/mascot/images/88x31_logo_white.gifMascot Search Results**

**User :**

**Email :**

**Search title : SampleSetID: 341, AnalysisID: 561, MaldiWellID: 45099, SpectrumID: 137547, Path=\Jimmy\Cooperia Adult ES 20110221\20110221 MS en MSMS**

**Database : cooperia\_oncophora oncophora (33747 sequences; 5232511 residues)**

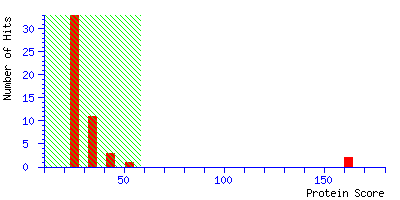
**Timestamp : 21 Feb 2011 at 15:40:46 GMT**

**Warning : A Peptide summary report will usually give a much clearer picture of MS/MS search results.**

**Top Score : 162 for isotig10740, putative nuclear encoded protein Method: Longest ORF**

**Mascot Score Histogram**

Protein score is -10\*Log(P), where P is the probability that the observed match is a random event.  
Protein scores greater than 58 are significant (p<0.05).  
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Top of Form

**Protein Summary Report**

|  |  |  |  |
| --- | --- | --- | --- |
|  |  |  |  |
|  |  |  |  |

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Bottom of Form

**Index**

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
|  | **Accession** | **Mass** | **Score** | **Description** |
| **1.** | [**isotig10740**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20110221/F013503.dat#Hit1) | 14574 | 162 | putative nuclear encoded protein Method: Longest ORF |
| **2.** | [**isotig10739**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20110221/F013503.dat#Hit2) | 14670 | 161 | putative nuclear encoded protein Method: Longest ORF |
| **3.** | [**isotig10741**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20110221/F013503.dat#Hit3) | 14118 | 54 | putative nuclear encoded protein Method: Longest ORF |
| **4.** | [**isotig01629**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20110221/F013503.dat#Hit4) | 14274 | 43 | putative nuclear encoded protein Method: Longest ORF |
| **5.** | [**isotig30345**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20110221/F013503.dat#Hit5) | 9062 | 41 | putative nuclear encoded protein Method: Longest ORF |
| **6.** | [**isotig31421**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20110221/F013503.dat#Hit6) | 16194 | 39 | putative nuclear encoded protein Method: similarity and extension |
| **7.** | [**isotig22787**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20110221/F013503.dat#Hit7) | 8345 | 38 | putative nuclear encoded protein Method: Longest ORF |
| **8.** | [**isotig02566**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20110221/F013503.dat#Hit8) | 8220 | 36 | putative nuclear encoded protein Method: Longest ORF |
| **9.** | [**isotig27615**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20110221/F013503.dat#Hit9) | 19600 | 34 | putative nuclear encoded protein Method: similarity and extension |
| **10.** | [**isotig20531**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20110221/F013503.dat#Hit10) | 13912 | 33 | putative nuclear encoded protein Method: Longest ORF |
| **11.** | [**isotig11405**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20110221/F013503.dat#Hit11) | 18761 | 32 | putative nuclear encoded protein Method: similarity and extension |
| **12.** | [**isotig11404**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20110221/F013503.dat#Hit12) | 18761 | 32 | putative nuclear encoded protein Method: similarity and extension |
| **13.** | [**isotig23908**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20110221/F013503.dat#Hit13) | 16377 | 32 | putative nuclear encoded protein Method: similarity and extension |
| **14.** | [**isotig22272**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20110221/F013503.dat#Hit14) | 17504 | 32 | putative nuclear encoded protein Method: similarity and extension |
| **15.** | [**isotig20757**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20110221/F013503.dat#Hit15) | 6829 | 31 | putative nuclear encoded protein Method: Longest ORF |
| **16.** | [**isotig28435**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20110221/F013503.dat#Hit16) | 7744 | 30 | putative nuclear encoded protein Method: similarity and extension |
| **17.** | [**isotig18838**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20110221/F013503.dat#Hit17) | 30548 | 30 | putative nuclear encoded protein Method: similarity and extension |
| **18.** | [**isotig11765**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20110221/F013503.dat#Hit18) | 8852 | 29 | putative nuclear encoded protein Method: similarity and extension |
| **19.** | [**isotig11766**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20110221/F013503.dat#Hit19) | 8852 | 29 | putative nuclear encoded protein Method: similarity and extension |
| **20.** | [**isotig26845**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20110221/F013503.dat#Hit20) | 13463 | 29 | putative nuclear encoded protein Method: similarity and extension |

**Results List**

|  |  |
| --- | --- |
| **1.** | [isotig10740](http://msmsms/mascot/cgi/protein_view.pl?file=../data/20110221/F013503.dat&hit=1" \t "_blank)    **Mass:** 14574    **Score:** 162    **Expect:** 2.1e-012  **Matches:** 7 |
|  | putative nuclear encoded protein Method: Longest ORF |

|  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | **Observed** | **Mr(expt)** | **Mr(calc)** | **ppm** | **Start** |  | **End** | **Miss** | **Ions** | **Peptide** |
|  | 878.4468 | 877.4395 | 877.4446 | -5.83 | 64 | - | 70 | 0 | --- | R.SHFVNFK.D |
|  | 1081.5131 | 1080.5058 | 1080.5088 | -2.72 | 71 | - | 79 | 0 | --- | K.DSDFVTELR.V |
|  | 1081.5131 | 1080.5058 | 1080.5088 | -2.72 | 71 | - | 79 | 0 | 38 | K.DSDFVTELR.V |
|  | 1087.4998 | 1086.4925 | 1086.4869 | 5.14 | 116 | - | 124 | 0 | --- | K.EEFSVYADK.C |
|  | 1848.9025 | 1847.8952 | 1847.8749 | 11.0 | 84 | - | 99 | 1 | --- | K.DTTLDVVEIQKDDDSR.H |
|  | 1940.9703 | 1939.9630 | 1939.9428 | 10.4 | 64 | - | 79 | 1 | --- | R.SHFVNFKDSDFVTELR.V |
|  | 1940.9703 | 1939.9630 | 1939.9428 | 10.4 | 64 | - | 79 | 1 | 100 | R.SHFVNFKDSDFVTELR.V |

|  |  |
| --- | --- |
|  | **No match to:** 802.4386, 806.0862, 807.4161, 812.4821, 813.4646, 826.5312, 832.3059, 842.4998, 844.5246, 846.5546, 850.0470, 856.5141, 862.4819, 870.5353, 877.0353, 895.4453, 897.4238, 900.5753, 916.5585, 967.5015, 982.4359, 990.5743, 1013.4728, 1014.4600, 1045.5632, 1065.5116, 1090.5238, 1107.5322, 1109.4791, 1112.5322, 1131.7393, 1138.5345, 1179.6049, 1234.6849, 1235.5470, 1300.5835, 1307.6910, 1475.7622, 1493.7522, 1791.7568, 2135.9456, 2136.9409, 2211.1240, 2226.9631, 2226.9631, 2227.9517 |

|  |  |
| --- | --- |
| **2.** | [isotig10739](http://msmsms/mascot/cgi/protein_view.pl?file=../data/20110221/F013503.dat&hit=2" \t "_blank)    **Mass:** 14670    **Score:** 161    **Expect:** 2.7e-012  **Matches:** 7 |
|  | putative nuclear encoded protein Method: Longest ORF |

|  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | **Observed** | **Mr(expt)** | **Mr(calc)** | **ppm** | **Start** |  | **End** | **Miss** | **Ions** | **Peptide** |
|  | 878.4468 | 877.4395 | 877.4446 | -5.83 | 64 | - | 70 | 0 | --- | R.SHFVNFK.D |
|  | 1081.5131 | 1080.5058 | 1080.5088 | -2.72 | 71 | - | 79 | 0 | --- | K.DSDFVTELR.I |
|  | 1081.5131 | 1080.5058 | 1080.5088 | -2.72 | 71 | - | 79 | 0 | 38 | K.DSDFVTELR.I |
|  | 1087.4998 | 1086.4925 | 1086.4869 | 5.14 | 116 | - | 124 | 0 | --- | K.EEFSVYADK.C |
|  | 1848.9025 | 1847.8952 | 1847.8749 | 11.0 | 84 | - | 99 | 1 | --- | K.DTTLDVVEIQKDDDSR.H |
|  | 1940.9703 | 1939.9630 | 1939.9428 | 10.4 | 64 | - | 79 | 1 | --- | R.SHFVNFKDSDFVTELR.I |
|  | 1940.9703 | 1939.9630 | 1939.9428 | 10.4 | 64 | - | 79 | 1 | 100 | R.SHFVNFKDSDFVTELR.I |

|  |  |
| --- | --- |
|  | **No match to:** 802.4386, 806.0862, 807.4161, 812.4821, 813.4646, 826.5312, 832.3059, 842.4998, 844.5246, 846.5546, 850.0470, 856.5141, 862.4819, 870.5353, 877.0353, 895.4453, 897.4238, 900.5753, 916.5585, 967.5015, 982.4359, 990.5743, 1013.4728, 1014.4600, 1045.5632, 1065.5116, 1090.5238, 1107.5322, 1109.4791, 1112.5322, 1131.7393, 1138.5345, 1179.6049, 1234.6849, 1235.5470, 1300.5835, 1307.6910, 1475.7622, 1493.7522, 1791.7568, 2135.9456, 2136.9409, 2211.1240, 2226.9631, 2226.9631, 2227.9517 |

**http://msmsms/mascot/images/88x31_logo_white.gifMascot Search Results**

**Protein View**

Top of Form

Match to: **isotig10740** Score: **162** Expect: **2.1e-012**

**putative nuclear encoded protein Method: Longest ORF**

Nominal mass (Mr): **14574**; Calculated pI value: **6.56**

NCBI BLAST search of [isotig10740](http://www.ncbi.nlm.nih.gov/blast/Blast.cgi?ALIGNMENTS=50&ALIGNMENT_VIEW=Pairwise&AUTO_FORMAT=Semiauto&CDD_SEARCH=on&CLIENT=web&COMPOSITION_BASED_STATISTICS=on&DATABASE=nr&DESCRIPTIONS=100&ENTREZ_QUERY=(none)&EXPECT=10&FILTER=L&FORMAT_BLOCK_ON_RESPAGE=None&FORMAT_OBJECT=Alignment&FORMAT_TYPE=HTML&GAPCOSTS=11+1&I_THRESH=0.001&LAYOUT=TwoWindows&MATRIX_NAME=BLOSUM62&NCBI_GI=on&PAGE=Proteins&PROGRAM=blastp&QUERY=SDAGSSNRARSLVLSPRYQHRRMKLVTLAFLLCIAHSVMGDDCQVSYTSFGVYNGDFPRNPFRSHFVNFKDSDFVTELRVHTKDTTLDVVEIQKDDDSRHYFIVGSDAVAKPIHKEEFSVYADKCGIF&SERVICE=plain&SET_DEFAULTS.x=9&SET_DEFAULTS.y=5&SHOW_OVERVIEW=on&WORD_SIZE=3&END_OF_HTTPGET=Yes" \t "_blank) against nr

Unformatted [sequence string](http://msmsms/mascot/cgi/getseq.pl?cooperia_oncophora+isotig10740+seq" \t "_blank) for pasting into other applications

Variable modifications: Oxidation (HW),Oxidation (M)

Cleavage by Trypsin/P: cuts C-term side of KR

Sequence Coverage: **32%**

Matched peptides shown in **Bold Red**

**1** SDAGSSNRAR SLVLSPRYQH RRMKLVTLAF LLCIAHSVMG DDCQVSYTSF

**51** GVYNGDFPRN PFR**SHFVNFK DSDFVTELR**V HTK**DTTLDVV EIQKDDDSR**H

**101** YFIVGSDAVA KPIHK**EEFSV YADK**CGIF

**Error! Not a valid embedded object.**  **Error! Not a valid embedded object.**Residue Number  **Error! Not a valid embedded object.**Increasing Mass  **Error! Not a valid embedded object.**Decreasing Mass

**Start - End Observed Mr(expt) Mr(calc) ppm Miss Sequence**

**64 - 70 878.4468 877.4395 877.4446 -6 0 R.SHFVNFK.D**  ([No match](http://msmsms/mascot/cgi/peptide_view.pl?file=../data/20110221/F013503.dat&query=16&hit=1" \t "_blank))

**64 - 79 1940.9703 1939.9630 1939.9428 10 1 R.SHFVNFKDSDFVTELR.V**  ([No match](http://msmsms/mascot/cgi/peptide_view.pl?file=../data/20110221/F013503.dat&query=46&hit=1" \t "_blank))

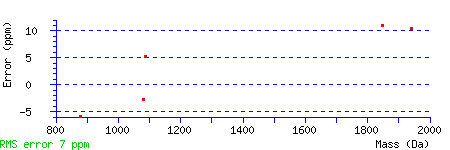
**64 - 79 1940.9703 1939.9630 1939.9428 10 1 R.SHFVNFKDSDFVTELR.V**  ([Ions score 100](http://msmsms/mascot/cgi/peptide_view.pl?file=../data/20110221/F013503.dat&query=47&hit=1" \t "_blank))

**71 - 79 1081.5131 1080.5058 1080.5088 -3 0 K.DSDFVTELR.V**  ([No match](http://msmsms/mascot/cgi/peptide_view.pl?file=../data/20110221/F013503.dat&query=28&hit=1" \t "_blank))

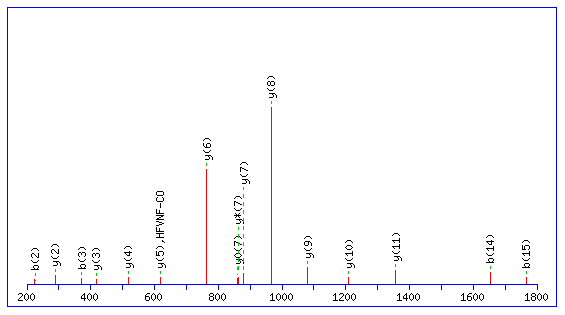
**71 - 79 1081.5131 1080.5058 1080.5088 -3 0 K.DSDFVTELR.V**  ([Ions score 38](http://msmsms/mascot/cgi/peptide_view.pl?file=../data/20110221/F013503.dat&query=29&hit=1" \t "_blank))

**84 - 99 1848.9025 1847.8952 1847.8749 11 1 K.DTTLDVVEIQKDDDSR.H**  ([No match](http://msmsms/mascot/cgi/peptide_view.pl?file=../data/20110221/F013503.dat&query=45&hit=1" \t "_blank))

**116 - 124 1087.4998 1086.4925 1086.4869 5 0 K.EEFSVYADK.C**  ([No match](http://msmsms/mascot/cgi/peptide_view.pl?file=../data/20110221/F013503.dat&query=30&hit=1" \t "_blank))



🡪 Annotated MS2 spectrum for peptide SHFVNFKDSDFVTELR



**Monoisotopic mass of neutral peptide Mr(calc):** 1939.9428

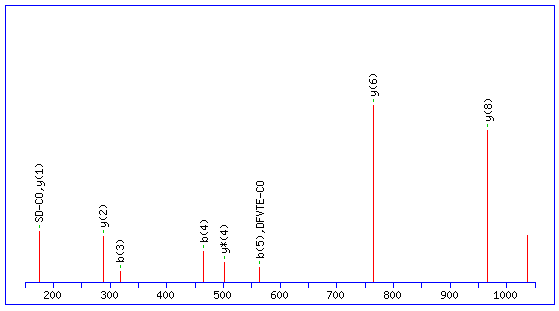
**Ions Score:** 100 **Expect:** 8.4e-009

**Matches :** 17/270 fragment ions using 17 most intense peaks   ([help](http://msmsms/mascot/help/results_help.html" \l "PEP" \t "_blank))

|  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **#** | **Immon.** | **a** | **a\*** | **a0** | **b** | **b\*** | **b0** | **Seq.** | **v** | **w** | **w'** | **y** | **y\*** | **y0** | **#** |
| **1** | 60.0444 | 60.0444 |  | 42.0338 | 88.0393 |  | 70.0287 | **S** |  |  |  |  |  |  | **16** |
| **2** | 110.0713 | 197.1033 |  | 179.0927 | **225.0982** |  | 207.0877 | **H** | 1771.8650 |  |  | 1853.9181 | 1836.8915 | 1835.9075 | **15** |
| **3** | 120.0808 | 344.1717 |  | 326.1612 | **372.1666** |  | 354.1561 | **F** | 1624.7966 |  |  | 1716.8592 | 1699.8326 | 1698.8486 | **14** |
| **4** | 72.0808 | 443.2401 |  | 425.2296 | 471.2350 |  | 453.2245 | **V** | 1525.7281 | 1538.7485 |  | 1569.7907 | 1552.7642 | 1551.7802 | **13** |
| **5** | 87.0553 | 557.2831 | 540.2565 | 539.2725 | 585.2780 | 568.2514 | 567.2674 | **N** | 1411.6852 | 1410.6900 |  | 1470.7223 | 1453.6958 | 1452.7118 | **12** |
| **6** | 120.0808 | 704.3515 | 687.3249 | 686.3409 | 732.3464 | 715.3198 | 714.3358 | **F** | 1264.6168 |  |  | ***1356.6794*** | 1339.6529 | 1338.6688 | **11** |
| **7** | 101.1073 | 832.4464 | 815.4199 | 814.4359 | 860.4413 | 843.4148 | 842.4308 | **K** | 1136.5218 | 1135.5266 |  | ***1209.6110*** | 1192.5844 | 1191.6004 | **10** |
| **8** | 88.0393 | 947.4734 | 930.4468 | 929.4628 | 975.4683 | 958.4417 | 957.4577 | **D** | 1021.4949 | 1020.4997 |  | ***1081.5160*** | 1064.4895 | 1063.5055 | **9** |
| **9** | 60.0444 | 1034.5054 | 1017.4789 | 1016.4948 | 1062.5003 | 1045.4738 | 1044.4898 | **S** | 934.4629 | 933.4676 |  | ***966.4891*** | 949.4625 | 948.4785 | **8** |
| **10** | 88.0393 | 1149.5323 | 1132.5058 | 1131.5218 | 1177.5273 | 1160.5007 | 1159.5167 | **D** | 819.4359 | 818.4407 |  | ***879.4571*** | 862.4305 | 861.4465 | **7** |
| **11** | 120.0808 | 1296.6008 | 1279.5742 | 1278.5902 | 1324.5957 | 1307.5691 | 1306.5851 | **F** | 672.3675 |  |  | ***764.4301*** | 747.4036 | 746.4196 | **6** |
| **12** | 72.0808 | 1395.6692 | 1378.6426 | 1377.6586 | 1423.6641 | 1406.6375 | 1405.6535 | **V** | 573.2991 | 586.3195 |  | ***617.3617*** | 600.3352 | 599.3511 | **5** |
| **13** | 74.0600 | 1496.7169 | 1479.6903 | 1478.7063 | 1524.7118 | 1507.6852 | 1506.7012 | **T** | 472.2514 | 485.2718 | 487.2511 | ***518.2933*** | 501.2667 | 500.2827 | **4** |
| **14** | 102.0550 | 1625.7594 | 1608.7329 | 1607.7489 | **1653.7544** | 1636.7278 | 1635.7438 | **E** | 343.2088 | 342.2136 |  | ***417.2456*** | 400.2191 | 399.2350 | **3** |
| **15** | 86.0964 | 1738.8435 | 1721.8170 | 1720.8329 | **1766.8384** | 1749.8119 | 1748.8279 | **L** | 230.1248 | 229.1295 |  | ***288.2030*** | 271.1765 |  | **2** |
| **16** | 129.1135 |  |  |  |  |  |  | **R** | 74.0237 | 73.0284 |  | 175.1190 | 158.0924 |  | **1** |

|  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **Seq** | **ya** | **yb** | **Seq** | **ya** | **yb** | **Seq** | **ya** | **yb** |
| **HF** | 257.1397 | 285.1346 | **HFV** | 356.2081 | 384.2030 | **HFVN** | 470.2510 | 498.2459 |
| **HFVNF** | 617.3194 | 645.3144 | **FV** | 219.1492 | 247.1441 | **FVN** | 333.1921 | 361.1870 |
| **FVNF** | 480.2605 | 508.2554 | **FVNFK** | 608.3555 | 636.3504 | **VN** | 186.1237 | 214.1186 |
| **VNF** | 333.1921 | 361.1870 | **VNFK** | 461.2871 | 489.2820 | **VNFKD** | 576.3140 | 604.3089 |
| **VNFKDS** | 663.3460 | 691.3410 | **NF** | 234.1237 | 262.1186 | **NFK** | 362.2187 | 390.2136 |
| **NFKD** | 477.2456 | 505.2405 | **NFKDS** | 564.2776 | 592.2726 | **NFKDSD** | 679.3046 | 707.2995 |
| **FK** | 248.1757 | 276.1707 | **FKD** | 363.2027 | 391.1976 | **FKDS** | 450.2347 | 478.2296 |
| **FKDSD** | 565.2617 | 593.2566 | **KD** | 216.1343 | 244.1292 | **KDS** | 303.1663 | 331.1612 |
| **KDSD** | 418.1932 | 446.1882 | **KDSDF** | 565.2617 | 593.2566 | **KDSDFV** | 664.3301 | 692.3250 |
| **DS** | 175.0713 | 203.0662 | **DSD** | 290.0983 | 318.0932 | **DSDF** | 437.1667 | 465.1616 |
| **DSDFV** | 536.2351 | 564.2300 | **DSDFVT** | 637.2828 | 665.2777 | **SD** | 175.0713 | 203.0662 |
| **SDF** | 322.1397 | 350.1347 | **SDFV** | 421.2082 | 449.2031 | **SDFVT** | 522.2558 | 550.2508 |
| **SDFVTE** | 651.2984 | 679.2933 | **DF** | 235.1077 | 263.1026 | **DFV** | 334.1761 | 362.1710 |
| **DFVT** | 435.2238 | 463.2187 | **DFVTE** | 564.2664 | 592.2613 | **DFVTEL** | 677.3505 | 705.3454 |
| **FV** | 219.1492 | 247.1441 | **FVT** | 320.1969 | 348.1918 | **FVTE** | 449.2395 | 477.2344 |
| **FVTEL** | 562.3235 | 590.3184 | **VT** | 173.1285 | 201.1234 | **VTE** | 302.1710 | 330.1660 |
| **VTEL** | 415.2551 | 443.2500 | **TE** | 203.1026 | 231.0975 | **TEL** | 316.1867 | 344.1816 |
| **EL** | 215.1390 | 243.1339 |  |  |  |  |  |  |

🡪 Annotated MS2 spectrum for peptide DSDFVTELR



**Monoisotopic mass of neutral peptide Mr(calc):** 1080.5088

**Ions Score:** 38 **Expect:** 0.011

**Matches :** 11/118 fragment ions using 9 most intense peaks   ([help](http://msmsms/mascot/help/results_help.html" \l "PEP" \t "_blank))

|  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **#** | **Immon.** | **a** | **a0** | **b** | **b0** | **Seq.** | **v** | **w** | **w'** | **y** | **y\*** | **y0** | **#** |
| **1** | 88.0393 | 88.0393 | 70.0287 | 116.0342 | 98.0237 | **D** |  |  |  |  |  |  | **9** |
| **2** | 60.0444 | 175.0713 | 157.0608 | 203.0662 | 185.0557 | **S** | 934.4629 | 933.4676 |  | ***966.4891*** | 949.4625 | 948.4785 | **8** |
| **3** | 88.0393 | 290.0983 | 272.0877 | ***318.0932*** | 300.0826 | **D** | 819.4359 | 818.4407 |  | 879.4571 | 862.4305 | 861.4465 | **7** |
| **4** | 120.0808 | 437.1667 | 419.1561 | ***465.1616*** | 447.1510 | **F** | 672.3675 |  |  | ***764.4301*** | 747.4036 | 746.4196 | **6** |
| **5** | 72.0808 | 536.2351 | 518.2245 | ***564.2300*** | 546.2195 | **V** | 573.2991 | 586.3195 |  | 617.3617 | 600.3352 | 599.3511 | **5** |
| **6** | 74.0600 | 637.2828 | 619.2722 | 665.2777 | 647.2671 | **T** | 472.2514 | 485.2718 | 487.2511 | 518.2933 | 501.2667 | 500.2827 | **4** |
| **7** | 102.0550 | 766.3254 | 748.3148 | 794.3203 | 776.3097 | **E** | 343.2088 | 342.2136 |  | 417.2456 | 400.2191 | 399.2350 | **3** |
| **8** | 86.0964 | 879.4094 | 861.3989 | 907.4044 | 889.3938 | **L** | 230.1248 | 229.1295 |  | ***288.2030*** | 271.1765 |  | **2** |
| **9** | 129.1135 |  |  |  |  | **R** | 74.0237 | 73.0284 |  | ***175.1190*** | 158.0924 |  | **1** |

|  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **Seq** | **ya** | **yb** | **Seq** | **ya** | **yb** | **Seq** | **ya** | **yb** |
| **SD** | 175.0713 | 203.0662 | **SDF** | 322.1397 | 350.1347 | **SDFV** | 421.2082 | 449.2031 |
| **SDFVT** | 522.2558 | 550.2508 | **SDFVTE** | 651.2984 | 679.2933 | **DF** | 235.1077 | 263.1026 |
| **DFV** | 334.1761 | 362.1710 | **DFVT** | 435.2238 | 463.2187 | **DFVTE** | 564.2664 | 592.2613 |
| **DFVTEL** | 677.3505 | 705.3454 | **FV** | 219.1492 | 247.1441 | **FVT** | 320.1969 | 348.1918 |
| **FVTE** | 449.2395 | 477.2344 | **FVTEL** | 562.3235 | 590.3184 | **VT** | 173.1285 | 201.1234 |
| **VTE** | 302.1710 | 330.1660 | **VTEL** | 415.2551 | 443.2500 | **TE** | 203.1026 | 231.0975 |
| **TEL** | 316.1867 | 344.1816 | **EL** | 215.1390 | 243.1339 |  |  |  |

**Bottom of Form**

**Spot 24:**

**http://msmsms/mascot/images/88x31_logo_white.gifMascot Search Results**

**User :**

**Email :**

**Search title : SampleSetID: 341, AnalysisID: 641, MaldiWellID: 45125, SpectrumID: 154579, Path=\Jimmy\Cooperia Adult ES 20110221\20110405 MS en MSMS (new DB)**

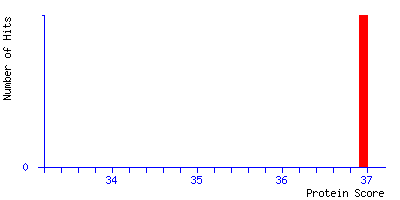
**Database : cooperia\_oncophora oncophora\_20110405 (34373 sequences; 5289600 residues)**

**Timestamp : 5 Apr 2011 at 12:33:46 GMT**

|  |  |  |
| --- | --- | --- |
| **Protein hits    :** | [**isotig25459**](http://msmsms/mascot/cgi/master_results.pl?file=..%2Fdata%2F20110405%2FF014338.dat#Hit1) | putative nuclear encoded protein Method: Longest ORF |

**Mascot Score Histogram**

Ions score is -10\*Log(P), where P is the probability that the observed match is a random event.  
Individual ions scores > 31 indicate identity or extensive homology (p<0.05).  
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Top of Form



**Peptide Summary Report**

|  |  |  |  |
| --- | --- | --- | --- |
|  |  |  | [Help](http://msmsms/mascot/help/msms_summaries_help.html" \t "_blank) |
|  | Significance threshold p< | Max. number of hits |  |
|  | Standard scoring  MudPIT scoring | Ions score or expect cut-off | Show sub-sets |
|  | Show pop-ups  Suppress pop-ups | Sort unassigned | Require bold red |

Bottom of Form

Top of Form



   **Error tolerant**

|  |  |
| --- | --- |
| **1.** | [isotig25459](http://msmsms/mascot/cgi/protein_view.pl?file=../data/20110405/F014338.dat&hit=isotig25459&db_idx=1&px=1&ave_thresh=31&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank)    **Mass:** 15707    **Score:** 37     **Matches:** 1(1)  **Sequences:** 1(1) |
|  | putative nuclear encoded protein Method: Longest ORF |

|  |  |
| --- | --- |
|  | Check to include this hit in error tolerant search or archive report |
|  |  |

|  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | **Query** | **Observed** | **Mr(expt)** | **Mr(calc)** | **ppm** | **Miss** | **Score** | **Expect** | **Rank** | **Unique** | **Peptide** |
|  | [40](http://msmsms/mascot/cgi/peptide_view.pl?file=../data/20110405/F014338.dat&query=40&hit=1&index=isotig25459&px=1&section=5&ave_thresh=31&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) | **1520.5432** | **1519.5359** | **1519.7478** | **-139.41** | **1** | **37** | **0.014** | **1** | **U** | **R.LEGEKEASTGSAVSR.A** |

Bottom of Form

**http://msmsms/mascot/images/88x31_logo_white.gifMascot Search Results**

**Protein View**

Top of Form



Match to: **isotig25459** Score: **37**

**putative nuclear encoded protein Method: Longest ORF**

Nominal mass (Mr): **15707**; Calculated pI value: **7.62**

NCBI BLAST search of [isotig25459](http://www.ncbi.nlm.nih.gov/blast/Blast.cgi?ALIGNMENTS=50&ALIGNMENT_VIEW=Pairwise&AUTO_FORMAT=Semiauto&CDD_SEARCH=on&CLIENT=web&COMPOSITION_BASED_STATISTICS=on&DATABASE=nr&DESCRIPTIONS=100&ENTREZ_QUERY=(none)&EXPECT=10&FILTER=L&FORMAT_BLOCK_ON_RESPAGE=None&FORMAT_OBJECT=Alignment&FORMAT_TYPE=HTML&GAPCOSTS=11+1&I_THRESH=0.001&LAYOUT=TwoWindows&MATRIX_NAME=BLOSUM62&NCBI_GI=on&PAGE=Proteins&PROGRAM=blastp&QUERY=SDAGIAIEMSLALITLCLVLVNIHTFSQSSVVTQNKCLTYNRMYPAYREYHLTLNSNLVWDQQLHLEACEILNGIGSAESYYRLEGEKEASTGSAVSRARKALYQMKGPKHEIREFGEGYYGCNSIVVGNKAKVLCLYQR&SERVICE=plain&SET_DEFAULTS.x=9&SET_DEFAULTS.y=5&SHOW_OVERVIEW=on&WORD_SIZE=3&END_OF_HTTPGET=Yes" \t "_blank) against nr

Unformatted [sequence string](http://msmsms/mascot/cgi/getseq.pl?cooperia_oncophora+isotig25459+seq" \t "_blank) for pasting into other applications

Variable modifications: Oxidation (HW),Oxidation (M)

Cleavage by Trypsin/P: cuts C-term side of KR

Sequence Coverage: **10%**

Matched peptides shown in **Bold Red**

**1** SDAGIAIEMS LALITLCLVL VNIHTFSQSS VVTQNKCLTY NRMYPAYREY

**51** HLTLNSNLVW DQQLHLEACE ILNGIGSAES YYR**LEGEKEA STGSAVSR**AR

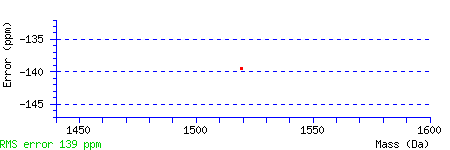
**101** KALYQMKGPK HEIREFGEGY YGCNSIVVGN KAKVLCLYQR



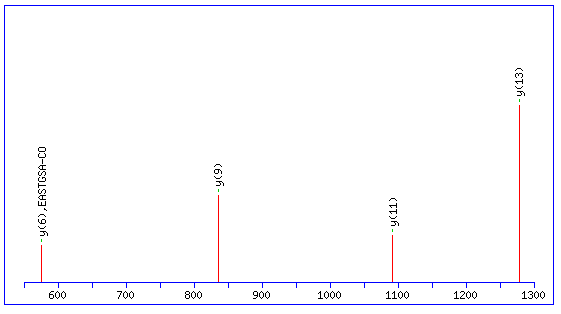
  Residue Number  Increasing Mass  Decreasing Mass

**Start - End Observed Mr(expt) Mr(calc) ppm Miss Sequence**

**84 - 98 1520.5432 1519.5359 1519.7478 -139 1 R.LEGEKEASTGSAVSR.A**  ([Ions score 37](http://msmsms/mascot/cgi/peptide_view.pl?file=../data/20110405/F014338.dat&query=40&hit=1&index=isotig25459&px=1&section=5&ave_thresh=31&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank))



🡪 Annotated MS2 spectrum for peptide LEGEKEASTGSAVSR



**Monoisotopic mass of neutral peptide Mr(calc):** 1519.7478

**Ions Score:** 37 **Expect:** 0.014

**Matches :** 5/266 fragment ions using 4 most intense peaks   ([help](http://msmsms/mascot/help/results_help.html" \l "PEP" \t "_blank))

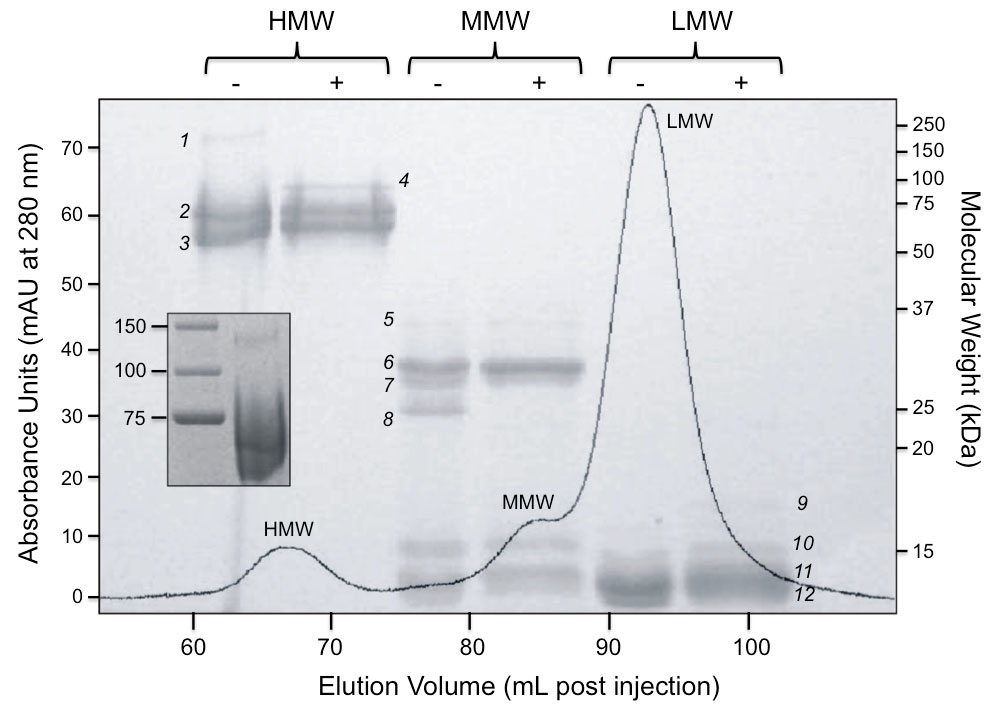
|  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **#** | **Immon.** | **a** | **a\*** | **a0** | **b** | **b\*** | **b0** | **Seq.** | **v** | **w** | **w'** | **y** | **y\*** | **y0** | **#** |
| **1** | 86.0964 | 86.0964 |  |  | 114.0913 |  |  | **L** |  |  |  |  |  |  | **15** |
| **2** | 102.0550 | 215.1390 |  | 197.1285 | 243.1339 |  | 225.1234 | **E** | 1333.6342 | 1332.6390 |  | 1407.6710 | 1390.6445 | 1389.6605 | **14** |
| **3** | 30.0338 | 272.1605 |  | 254.1499 | 300.1554 |  | 282.1448 | **G** |  |  |  | ***1278.6284*** | 1261.6019 | 1260.6179 | **13** |
| **4** | 102.0550 | 401.2031 |  | 383.1925 | 429.1980 |  | 411.1874 | **E** | 1147.5702 | 1146.5749 |  | 1221.6070 | 1204.5804 | 1203.5964 | **12** |
| **5** | 101.1073 | 529.2980 | 512.2715 | 511.2875 | 557.2930 | 540.2664 | 539.2824 | **K** | 1019.4752 | 1018.4800 |  | ***1092.5644*** | 1075.5378 | 1074.5538 | **11** |
| **6** | 102.0550 | 658.3406 | 641.3141 | 640.3301 | 686.3355 | 669.3090 | 668.3250 | **E** | 890.4326 | 889.4374 |  | 964.4694 | 947.4429 | 946.4588 | **10** |
| **7** | 44.0495 | 729.3777 | 712.3512 | 711.3672 | 757.3727 | 740.3461 | 739.3621 | **A** | 819.3955 |  |  | ***835.4268*** | 818.4003 | 817.4163 | **9** |
| **8** | 60.0444 | 816.4098 | 799.3832 | 798.3992 | 844.4047 | 827.3781 | 826.3941 | **S** | 732.3635 | 731.3682 |  | 764.3897 | 747.3632 | 746.3791 | **8** |
| **9** | 74.0600 | 917.4575 | 900.4309 | 899.4469 | 945.4524 | 928.4258 | 927.4418 | **T** | 631.3158 | 644.3362 | 646.3155 | 677.3577 | 660.3311 | 659.3471 | **7** |
| **10** | 30.0338 | 974.4789 | 957.4524 | 956.4684 | 1002.4738 | 985.4473 | 984.4633 | **G** |  |  |  | ***576.3100*** | 559.2835 | 558.2994 | **6** |
| **11** | 60.0444 | 1061.5109 | 1044.4844 | 1043.5004 | 1089.5059 | 1072.4793 | 1071.4953 | **S** | 487.2623 | 486.2671 |  | 519.2885 | 502.2620 | 501.2780 | **5** |
| **12** | 44.0495 | 1132.5481 | 1115.5215 | 1114.5375 | 1160.5430 | 1143.5164 | 1142.5324 | **A** | 416.2252 |  |  | 432.2565 | 415.2300 | 414.2459 | **4** |
| **13** | 72.0808 | 1231.6165 | 1214.5899 | 1213.6059 | 1259.6114 | 1242.5848 | 1241.6008 | **V** | 317.1568 | 330.1772 |  | 361.2194 | 344.1928 | 343.2088 | **3** |
| **14** | 60.0444 | 1318.6485 | 1301.6220 | 1300.6379 | 1346.6434 | 1329.6169 | 1328.6329 | **S** | 230.1248 | 229.1295 |  | 262.1510 | 245.1244 | 244.1404 | **2** |
| **15** | 129.1135 |  |  |  |  |  |  | **R** | 74.0237 | 73.0284 |  | 175.1190 | 158.0924 |  | **1** |

|  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **Seq** | **ya** | **yb** | **Seq** | **ya** | **yb** | **Seq** | **ya** | **yb** |
| **EG** | 159.0764 | 187.0713 | **EGE** | 288.1190 | 316.1139 | **EGEK** | 416.2140 | 444.2089 |
| **EGEKE** | 545.2566 | 573.2515 | **EGEKEA** | 616.2937 | 644.2886 | **GE** | 159.0764 | 187.0713 |
| **GEK** | 287.1714 | 315.1663 | **GEKE** | 416.2140 | 444.2089 | **GEKEA** | 487.2511 | 515.2460 |
| **GEKEAS** | 574.2831 | 602.2780 | **GEKEAST** | 675.3308 | 703.3257 | **EK** | 230.1499 | 258.1448 |
| **EKE** | 359.1925 | 387.1874 | **EKEA** | 430.2296 | 458.2245 | **EKEAS** | 517.2617 | 545.2566 |
| **EKEAST** | 618.3093 | 646.3042 | **EKEASTG** | 675.3308 | 703.3257 | **KE** | 230.1499 | 258.1448 |
| **KEA** | 301.1870 | 329.1819 | **KEAS** | 388.2191 | 416.2140 | **KEAST** | 489.2667 | 517.2617 |
| **KEASTG** | 546.2882 | 574.2831 | **KEASTGS** | 633.3202 | 661.3151 | **EA** | 173.0921 | 201.0870 |
| **EAS** | 260.1241 | 288.1190 | **EAST** | 361.1718 | 389.1667 | **EASTG** | 418.1932 | 446.1882 |
| **EASTGS** | 505.2253 | 533.2202 | **EASTGSA** | 576.2624 | 604.2573 | **EASTGSAV** | 675.3308 | 703.3257 |
| **AS** | 131.0815 | 159.0764 | **AST** | 232.1292 | 260.1241 | **ASTG** | 289.1506 | 317.1456 |
| **ASTGS** | 376.1827 | 404.1776 | **ASTGSA** | 447.2198 | 475.2147 | **ASTGSAV** | 546.2882 | 574.2831 |
| **ASTGSAVS** | 633.3202 | 661.3151 | **ST** | 161.0921 | 189.0870 | **STG** | 218.1135 | 246.1084 |
| **STGS** | 305.1456 | 333.1405 | **STGSA** | 376.1827 | 404.1776 | **STGSAV** | 475.2511 | 503.2460 |
| **STGSAVS** | 562.2831 | 590.2780 | **TG** | 131.0815 | 159.0764 | **TGS** | 218.1135 | 246.1084 |
| **TGSA** | 289.1506 | 317.1456 | **TGSAV** | 388.2191 | 416.2140 | **TGSAVS** | 475.2511 | 503.2460 |
| **GS** | 117.0659 | 145.0608 | **GSA** | 188.1030 | 216.0979 | **GSAV** | 287.1714 | 315.1663 |
| **GSAVS** | 374.2034 | 402.1983 | **SA** | 131.0815 | 159.0764 | **SAV** | 230.1499 | 258.1448 |
| **SAVS** | 317.1819 | 345.1769 | **AV** | 143.1179 | 171.1128 | **AVS** | 230.1499 | 258.1448 |
| **VS** | 159.1128 | 187.1077 |  |  |  |  |  |  |

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**Part II:**

Spots from 1D Gel Electrophoresis after SEC Fractionation of ES material (Figure 1B in the manuscript)



**Table.** MS identification of protein bands found in the three SEC fractions (Fig. 1B and Table 1).

\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_

Band N° Database ID GenBank Acc. N° Organism E-value MALDI-MS MS sequence Matched Unmatched MS2 sequence Description

(closest homology) BLASTP Mowse score coverage (%) peptides peptides coverage (%) (top BLASTP hit)

\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_

1 contig05709 AAK35199.1 *C. punctate* 3E-94 315 17 5 16 17 ASP-like protein

2 contig63173 AAK35185.1 *C. punctate*  1E-89 245 35 7 19 15 ASP-like protein

3 contig05709 AAK35199.1 *C. punctate*  3E-94 276 30 8 13 19 ASP-like protein

4 isotig24792 XP-003114672.1 *C. remanei* 5E-13 59 9 2 19 8 Hypothetical protein

5 isotig01086 NP-509242.1 *C. elegans* 4E-119 345 50 22 15 16 Aldose reductase

6 isotig13456 AAO63577.1 *A. caninum* 1E-09 180 12 1 14 12 Secreted protein 5 precursor

7 isotig13456 AAO63577.1 *A. caninum* 1E-09 154 12 1 14 12 Secreted protein 5 precursor

8 isotig00466 ADN00784.1 *H. contortus* 4E-53 61 65 11 7 0 Parasitic stage specif. prot. 2

9 isotig32303 75 18 2 9 7 /

10 isotig11584 CAC38986.1 *C. oncophora* 3E-13 119 13 3 15 10 ES antigen 1

11 isotig21044 AAK35204.1 *C. punctata* 7E-18 159 33 7 10 12 14-kDa ES protein

12 CAC38986.1 CAC38986.1 *C. oncophora* 0 125 23 1 10 23 ES antigen 1

\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_

**Page references for Figure 1B in the manuscript:**

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**Band 1:**

**http://msmsms/mascot/images/88x31_logo_white.gifMascot Search Results**

**User :**

**Email :**

**Search title : SampleSetID: 683, AnalysisID: 1071, MaldiWellID: 82745, SpectrumID: 217077, Path=\Jimmy\Cooperia 3\Co ES Conc 3 Frac 13012012 (strict)**

**Database : cooperia\_oncophora oncophora\_20110405 (34373 sequences; 5289600 residues)**

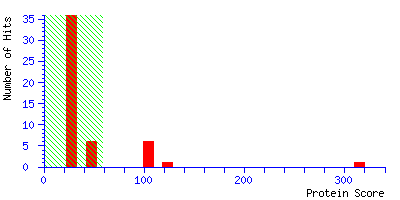
**Timestamp : 13 Jan 2012 at 14:32:15 GMT**

**Warning : A Peptide summary report will usually give a much clearer picture of MS/MS search results.**

**Top Score : 315 for contig05709, putative nuclear encoded protein Method: similarity and extension**

**Mascot Score Histogram**

Protein score is -10\*Log(P), where P is the probability that the observed match is a random event.  
Protein scores greater than 58 are significant (p<0.05).  
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Top of Form



**Protein Summary Report**

|  |  |  |  |
| --- | --- | --- | --- |
|  |  |  | [Help](http://msmsms/mascot/help/msms_summaries_help.html" \t "_blank) |
|  | Significance threshold p< | Max. number of hits |  |

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**Index**

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
|  | **Accession** | **Mass** | **Score** | **Description** |
| **1.** | [**contig05709**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20120113/F018129.dat#Hit1) | 23725 | 315 | putative nuclear encoded protein Method: similarity and extension |
| **2.** | [**contig63173**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20120113/F018129.dat#Hit2) | 22462 | 122 | putative nuclear encoded protein Method: similarity and extension |
| **3.** | [**gi|13625881|gb|AAK35185.1|AF352700\_1**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20120113/F018129.dat#Hit3) | 27510 | 110 | activation associated secreted protein-like protein [Cooperia punctata] |
| **4.** | [**gi|13625877|gb|AAK35183.1|AF352698\_1**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20120113/F018129.dat#Hit4) | 27540 | 105 | activation associated secreted protein-like protein [Cooperia punctata] |
| **5.** | [**gi|13625909|gb|AAK35199.1|AF352714\_1**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20120113/F018129.dat#Hit5) | 51596 | 103 | activation associated secreted protein-like protein [Cooperia punctata] |
| **6.** | [**gi|13625911|gb|AAK35200.1|AF352715\_1**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20120113/F018129.dat#Hit6) | 9724 | 101 | activation associated secreted protein-like protein [Cooperia punctata] |
| **7.** | [**gi|13625885|gb|AAK35187.1|AF352702\_1**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20120113/F018129.dat#Hit7) | 55209 | 101 | activation associated secreted protein-like protein [Cooperia punctata] |
| **8.** | [**gi|13625879|gb|AAK35184.1|AF352699\_1**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20120113/F018129.dat#Hit8) | 25808 | 98 | activation associated secreted protein-like protein [Cooperia punctata] |
| **9.** | [**isotig19055**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20120113/F018129.dat#Hit9) | 17485 | 46 | putative nuclear encoded protein Method: similarity and extension |
| **10.** | [**isotig27922**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20120113/F018129.dat#Hit10) | 18314 | 43 | putative nuclear encoded protein Method: Longest ORF |
| **11.** | [**isotig30720**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20120113/F018129.dat#Hit11) | 8724 | 42 | putative nuclear encoded protein Method: Longest ORF |
| **12.** | [**isotig19561**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20120113/F018129.dat#Hit12) | 27902 | 42 | putative nuclear encoded protein Method: similarity and extension |
| **13.** | [**isotig00873**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20120113/F018129.dat#Hit13) | 9124 | 41 | putative nuclear encoded protein Method: Longest ORF |
| **14.** | [**isotig15276**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20120113/F018129.dat#Hit14) | 12135 | 39 | putative nuclear encoded protein Method: similarity and extension |
| **15.** | [**isotig00871**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20120113/F018129.dat#Hit15) | 9637 | 37 | putative nuclear encoded protein Method: Longest ORF |
| **16.** | [**isotig31853**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20120113/F018129.dat#Hit16) | 21527 | 37 | putative nuclear encoded protein Method: ESTScan |
| **17.** | [**isotig17976**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20120113/F018129.dat#Hit17) | 17166 | 36 | putative nuclear encoded protein Method: similarity and extension |
| **18.** | [**isotig00325**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20120113/F018129.dat#Hit18) | 11031 | 36 | putative nuclear encoded protein Method: Longest ORF |
| **19.** | [**isotig16946**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20120113/F018129.dat#Hit19) | 33072 | 36 | putative nuclear encoded protein Method: similarity and extension |
| **20.** | [**isotig06877**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20120113/F018129.dat#Hit20) | 10511 | 35 | putative nuclear encoded protein Method: Longest ORF |

**Results List**

|  |  |
| --- | --- |
| **1.** | [contig05709](http://msmsms/mascot/cgi/protein_view.pl?file=../data/20120113/F018129.dat&hit=1" \t "_blank)    **Mass:** 23725    **Score:** 315    **Expect:** 1.1e-027  **Matches:** 9 |
|  | putative nuclear encoded protein Method: similarity and extension |

|  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | **Observed** | **Mr(expt)** | **Mr(calc)** | **ppm** | **Start** |  | **End** | **Miss** | **Ions** | **Peptide** |
|  | 1311.6515 | 1310.6442 | 1310.6255 | 14.3 | 133 | - | 143 | 0 | --- | R.YGVPQDNVYTR.D |
|  | 1311.6515 | 1310.6442 | 1310.6255 | 14.3 | 133 | - | 143 | 0 | 78 | R.YGVPQDNVYTR.D |
|  | 1320.6891 | 1319.6818 | 1319.6622 | 14.9 | 37 | - | 46 | 1 | --- | K.VFLDKHNEYR.S |
|  | 1320.6891 | 1319.6818 | 1319.6622 | 14.9 | 37 | - | 46 | 1 | 52 | K.VFLDKHNEYR.S |
|  | 1385.6836 | 1384.6763 | 1384.6735 | 2.01 | 52 | - | 65 | 0 | --- | K.GQAPNPQFGGSTPK.A |
|  | 1385.6836 | 1384.6763 | 1384.6735 | 2.01 | 52 | - | 65 | 0 | 79 | K.GQAPNPQFGGSTPK.A |
|  | 1448.7543 | 1447.7470 | 1447.7572 | -7.01 | 36 | - | 46 | 2 | --- | R.KVFLDKHNEYR.S |
|  | 1448.7543 | 1447.7470 | 1447.7572 | -7.01 | 36 | - | 46 | 2 | 89 | R.KVFLDKHNEYR.S |
|  | 1467.7462 | 1466.7389 | 1466.7266 | 8.39 | 132 | - | 143 | 1 | --- | R.RYGVPQDNVYTR.D |

|  |  |
| --- | --- |
|  | **No match to:** 901.4816, 904.4781, 917.4740, 919.4605, 934.4749, 936.4710, 948.4430, 950.4682, 966.4713, 971.5641, 982.4548, 1003.5497, 1033.5271, 1045.5751, 1046.5530, 1059.5961, 1060.5720, 1065.5469, 1092.5292, 1100.6106, 1115.5874, 1116.5972, 1179.6349, 1231.5663, 1233.5846, 1235.6046, 1238.6145, 1259.6625, 1308.6830, 1332.6801, 1334.7019, 1354.6564, 1390.6996, 1430.7495, 1431.7217, 1431.7217, 1462.8020, 1475.7579, 1493.7649, 1498.8232, 1686.7849, 1686.7849, 1791.7388, 2373.1147 |

|  |  |
| --- | --- |
| **2.** | [contig63173](http://msmsms/mascot/cgi/protein_view.pl?file=../data/20120113/F018129.dat&hit=2" \t "_blank)    **Mass:** 22462    **Score:** 122    **Expect:** 2.2e-008  **Matches:** 11 |
|  | putative nuclear encoded protein Method: similarity and extension |

|  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | **Observed** | **Mr(expt)** | **Mr(calc)** | **ppm** | **Start** |  | **End** | **Miss** | **Ions** | **Peptide** |
|  | 919.4605 | 918.4532 | 918.4447 | 9.31 | 69 | - | 76 | 0 | --- | R.AAWEESVK.R |
|  | 936.4710 | 935.4637 | 935.4495 | 15.2 | 87 | - | 94 | 1 | --- | K.NGMTDKVR.Q + Oxidation (M) |
|  | 971.5641 | 970.5568 | 970.5560 | 0.90 | 106 | - | 114 | 1 | --- | R.QIVARGEAK.N |
|  | 1059.5961 | 1058.5888 | 1058.5509 | 35.8 | 148 | - | 157 | 0 | --- | K.GGHSSFQVLK.G |
|  | 1354.6564 | 1353.6491 | 1353.6452 | 2.86 | 180 | - | 190 | 0 | --- | R.SVDDWYIEVTK.Y |
|  | 1448.7543 | 1447.7470 | 1447.7208 | 18.1 | 95 | - | 105 | 1 | --- | R.QVFLDKHNEYR.Q |
|  | 1448.7543 | 1447.7470 | 1447.7208 | 18.1 | 95 | - | 105 | 1 | 89 | R.QVFLDKHNEYR.Q |
|  | 1467.7462 | 1466.7389 | 1466.7577 | -12.78 | 34 | - | 47 | 1 | --- | K.PSTTTTKATTTTTR.P |
|  | 1686.7849 | 1685.7776 | 1685.8597 | -48.70 | 101 | - | 114 | 2 | --- | K.HNEYRQIVARGEAK.N + Oxidation (HW) |
|  | 1686.7849 | 1685.7776 | 1685.8597 | -48.70 | 101 | - | 114 | 2 | --- | K.HNEYRQIVARGEAK.N + Oxidation (HW) |
|  | 2373.1147 | 2372.1074 | 2372.1648 | -24.20 | 179 | - | 198 | 2 | --- | K.RSVDDWYIEVTKYGITADNK.I |

|  |  |
| --- | --- |
|  | **No match to:** 901.4816, 904.4781, 917.4740, 934.4749, 948.4430, 950.4682, 966.4713, 982.4548, 1003.5497, 1033.5271, 1045.5751, 1046.5530, 1060.5720, 1065.5469, 1092.5292, 1100.6106, 1115.5874, 1116.5972, 1179.6349, 1231.5663, 1233.5846, 1235.6046, 1238.6145, 1259.6625, 1308.6830, 1311.6515, 1311.6515, 1320.6891, 1320.6891, 1332.6801, 1334.7019, 1385.6836, 1385.6836, 1390.6996, 1430.7495, 1431.7217, 1431.7217, 1462.8020, 1475.7579, 1493.7649, 1498.8232, 1791.7388 |

|  |  |
| --- | --- |
| **3.** | [gi|13625881|gb|AAK35185.1|AF352700\_1](http://msmsms/mascot/cgi/protein_view.pl?file=../data/20120113/F018129.dat&hit=3" \t "_blank)    **Mass:** 27510    **Score:** 110    **Expect:** 3.4e-007  **Matches:** 8 |
|  | activation associated secreted protein-like protein [Cooperia punctata] |

|  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | **Observed** | **Mr(expt)** | **Mr(calc)** | **ppm** | **Start** |  | **End** | **Miss** | **Ions** | **Peptide** |
|  | 919.4605 | 918.4532 | 918.4447 | 9.31 | 36 | - | 43 | 0 | --- | R.AAWEESVK.K |
|  | 1060.5720 | 1059.5647 | 1059.5349 | 28.1 | 114 | - | 123 | 0 | --- | K.GGHSTFDVLK.G |
|  | 1092.5292 | 1091.5219 | 1091.5822 | -55.26 | 1 | - | 11 | 1 | --- | -.KPATTSSTTAK.T |
|  | 1233.5846 | 1232.5773 | 1232.5642 | 10.7 | 187 | - | 198 | 0 | --- | R.LGCAAVSCPEQR.R |
|  | 1332.6801 | 1331.6728 | 1331.6622 | 7.94 | 173 | - | 183 | 0 | --- | K.TGHYSQVVWQK.S |
|  | 1448.7543 | 1447.7470 | 1447.7208 | 18.1 | 61 | - | 71 | 1 | --- | R.QVFLDKHNEYR.Q |
|  | 1448.7543 | 1447.7470 | 1447.7208 | 18.1 | 61 | - | 71 | 1 | 89 | R.QVFLDKHNEYR.Q |
|  | 1791.7388 | 1790.7315 | 1790.7604 | -16.10 | 97 | - | 111 | 0 | --- | R.YDCDLEAHVMEHVAK.C + Oxidation (HW); Oxidation (M) |

|  |  |
| --- | --- |
|  | **No match to:** 901.4816, 904.4781, 917.4740, 934.4749, 936.4710, 948.4430, 950.4682, 966.4713, 971.5641, 982.4548, 1003.5497, 1033.5271, 1045.5751, 1046.5530, 1059.5961, 1065.5469, 1100.6106, 1115.5874, 1116.5972, 1179.6349, 1231.5663, 1235.6046, 1238.6145, 1259.6625, 1308.6830, 1311.6515, 1311.6515, 1320.6891, 1320.6891, 1334.7019, 1354.6564, 1385.6836, 1385.6836, 1390.6996, 1430.7495, 1431.7217, 1431.7217, 1462.8020, 1467.7462, 1475.7579, 1493.7649, 1498.8232, 1686.7849, 1686.7849, 2373.1147 |

|  |  |
| --- | --- |
| **4.** | [gi|13625877|gb|AAK35183.1|AF352698\_1](http://msmsms/mascot/cgi/protein_view.pl?file=../data/20120113/F018129.dat&hit=4" \t "_blank)    **Mass:** 27540    **Score:** 105    **Expect:** 1.1e-006  **Matches:** 7 |
|  | activation associated secreted protein-like protein [Cooperia punctata] |

|  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | **Observed** | **Mr(expt)** | **Mr(calc)** | **ppm** | **Start** |  | **End** | **Miss** | **Ions** | **Peptide** |
|  | 919.4605 | 918.4532 | 918.4447 | 9.31 | 36 | - | 43 | 0 | --- | R.AAWEESVK.K |
|  | 1092.5292 | 1091.5219 | 1091.5822 | -55.26 | 1 | - | 11 | 1 | --- | -.KPATTSSTTAK.T |
|  | 1233.5846 | 1232.5773 | 1232.5642 | 10.7 | 187 | - | 198 | 0 | --- | R.LGCAAVSCPEQR.R |
|  | 1332.6801 | 1331.6728 | 1331.6622 | 7.94 | 173 | - | 183 | 0 | --- | K.TGHYSQVVWQK.S |
|  | 1448.7543 | 1447.7470 | 1447.7208 | 18.1 | 61 | - | 71 | 1 | --- | R.QVFLDKHNEYR.Q |
|  | 1448.7543 | 1447.7470 | 1447.7208 | 18.1 | 61 | - | 71 | 1 | 89 | R.QVFLDKHNEYR.Q |
|  | 1791.7388 | 1790.7315 | 1790.7604 | -16.10 | 97 | - | 111 | 0 | --- | R.YDCDLEAHVMEHVAK.C + Oxidation (HW); Oxidation (M) |

|  |  |
| --- | --- |
|  | **No match to:** 901.4816, 904.4781, 917.4740, 934.4749, 936.4710, 948.4430, 950.4682, 966.4713, 971.5641, 982.4548, 1003.5497, 1033.5271, 1045.5751, 1046.5530, 1059.5961, 1060.5720, 1065.5469, 1100.6106, 1115.5874, 1116.5972, 1179.6349, 1231.5663, 1235.6046, 1238.6145, 1259.6625, 1308.6830, 1311.6515, 1311.6515, 1320.6891, 1320.6891, 1334.7019, 1354.6564, 1385.6836, 1385.6836, 1390.6996, 1430.7495, 1431.7217, 1431.7217, 1462.8020, 1467.7462, 1475.7579, 1493.7649, 1498.8232, 1686.7849, 1686.7849, 2373.1147 |

|  |  |
| --- | --- |
| **5.** | [gi|13625909|gb|AAK35199.1|AF352714\_1](http://msmsms/mascot/cgi/protein_view.pl?file=../data/20120113/F018129.dat&hit=5" \t "_blank)    **Mass:** 51596    **Score:** 103    **Expect:** 1.7e-006  **Matches:** 8 |
|  | activation associated secreted protein-like protein [Cooperia punctata] |

|  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | **Observed** | **Mr(expt)** | **Mr(calc)** | **ppm** | **Start** |  | **End** | **Miss** | **Ions** | **Peptide** |
|  | 971.5641 | 970.5568 | 970.5560 | 0.90 | 289 | - | 297 | 1 | --- | R.QLVARGEAK.N |
|  | 1332.6801 | 1331.6728 | 1331.6622 | 7.94 | 390 | - | 400 | 0 | --- | K.TGHYSQVVWQK.S |
|  | 1334.7019 | 1333.6946 | 1333.6779 | 12.6 | 30 | - | 39 | 1 | --- | K.LFLDKHNEYR.S |
|  | 1448.7543 | 1447.7470 | 1447.7208 | 18.1 | 278 | - | 288 | 1 | --- | R.QVFLDKHNEYR.Q |
|  | 1448.7543 | 1447.7470 | 1447.7208 | 18.1 | 278 | - | 288 | 1 | 89 | R.QVFLDKHNEYR.Q |
|  | 1462.8020 | 1461.7947 | 1461.7728 | 15.0 | 29 | - | 39 | 2 | --- | R.KLFLDKHNEYR.S |
|  | 1686.7849 | 1685.7776 | 1685.7719 | 3.39 | 314 | - | 327 | 0 | --- | R.YDCDLEAHVLEHVK.T + Oxidation (HW) |
|  | 1686.7849 | 1685.7776 | 1685.8597 | -48.70 | 284 | - | 297 | 2 | --- | K.HNEYRQLVARGEAK.N + Oxidation (HW) |

|  |  |
| --- | --- |
|  | **No match to:** 901.4816, 904.4781, 917.4740, 919.4605, 934.4749, 936.4710, 948.4430, 950.4682, 966.4713, 982.4548, 1003.5497, 1033.5271, 1045.5751, 1046.5530, 1059.5961, 1060.5720, 1065.5469, 1092.5292, 1100.6106, 1115.5874, 1116.5972, 1179.6349, 1231.5663, 1233.5846, 1235.6046, 1238.6145, 1259.6625, 1308.6830, 1311.6515, 1311.6515, 1320.6891, 1320.6891, 1354.6564, 1385.6836, 1385.6836, 1390.6996, 1430.7495, 1431.7217, 1431.7217, 1467.7462, 1475.7579, 1493.7649, 1498.8232, 1791.7388, 2373.1147 |

|  |  |
| --- | --- |
| **6.** | [gi|13625911|gb|AAK35200.1|AF352715\_1](http://msmsms/mascot/cgi/protein_view.pl?file=../data/20120113/F018129.dat&hit=6" \t "_blank)    **Mass:** 9724     **Score:** 101    **Expect:** 2.7e-006  **Matches:** 4 |
|  | activation associated secreted protein-like protein [Cooperia punctata] |

|  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | **Observed** | **Mr(expt)** | **Mr(calc)** | **ppm** | **Start** |  | **End** | **Miss** | **Ions** | **Peptide** |
|  | 904.4781 | 903.4708 | 903.4563 | 16.1 | 30 | - | 37 | 0 | --- | R.NTWGTGIR.N |
|  | 1493.7649 | 1492.7576 | 1492.7647 | -4.76 | 26 | - | 37 | 2 | --- | R.RYNRNTWGTGIR.N |
|  | 1686.7849 | 1685.7776 | 1685.7685 | 5.40 | 44 | - | 57 | 0 | --- | K.AAESSVYDWFNEIR.K |
|  | 1686.7849 | 1685.7776 | 1685.7685 | 5.40 | 44 | - | 57 | 0 | 83 | K.AAESSVYDWFNEIR.K |

|  |  |
| --- | --- |
|  | **No match to:** 901.4816, 917.4740, 919.4605, 934.4749, 936.4710, 948.4430, 950.4682, 966.4713, 971.5641, 982.4548, 1003.5497, 1033.5271, 1045.5751, 1046.5530, 1059.5961, 1060.5720, 1065.5469, 1092.5292, 1100.6106, 1115.5874, 1116.5972, 1179.6349, 1231.5663, 1233.5846, 1235.6046, 1238.6145, 1259.6625, 1308.6830, 1311.6515, 1311.6515, 1320.6891, 1320.6891, 1332.6801, 1334.7019, 1354.6564, 1385.6836, 1385.6836, 1390.6996, 1430.7495, 1431.7217, 1431.7217, 1448.7543, 1448.7543, 1462.8020, 1467.7462, 1475.7579, 1498.8232, 1791.7388, 2373.1147 |

|  |  |
| --- | --- |
| **7.** | [gi|13625885|gb|AAK35187.1|AF352702\_1](http://msmsms/mascot/cgi/protein_view.pl?file=../data/20120113/F018129.dat&hit=7" \t "_blank)    **Mass:** 55209    **Score:** 101    **Expect:** 2.7e-006  **Matches:** 8 |
|  | activation associated secreted protein-like protein [Cooperia punctata] |

|  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | **Observed** | **Mr(expt)** | **Mr(calc)** | **ppm** | **Start** |  | **End** | **Miss** | **Ions** | **Peptide** |
|  | 919.4605 | 918.4532 | 918.4447 | 9.31 | 278 | - | 285 | 0 | --- | R.AAWEESVK.H |
|  | 971.5641 | 970.5568 | 970.5560 | 0.90 | 315 | - | 323 | 1 | --- | R.QIVARGEAK.N |
|  | 1059.5961 | 1058.5888 | 1058.5509 | 35.8 | 357 | - | 366 | 0 | --- | K.GGHSQFSVLK.G |
|  | 1233.5846 | 1232.5773 | 1232.5642 | 10.7 | 430 | - | 441 | 0 | --- | R.LGCAAVSCPEQR.R |
|  | 1334.7019 | 1333.6946 | 1333.6779 | 12.6 | 26 | - | 35 | 1 | --- | K.IFLDKHNEYR.S |
|  | 1462.8020 | 1461.7947 | 1461.7728 | 15.0 | 25 | - | 35 | 2 | --- | R.KIFLDKHNEYR.S |
|  | 1686.7849 | 1685.7776 | 1685.7685 | 5.40 | 107 | - | 120 | 0 | --- | K.AAESSVYDWFNEIR.T |
|  | 1686.7849 | 1685.7776 | 1685.7685 | 5.40 | 107 | - | 120 | 0 | 83 | K.AAESSVYDWFNEIR.T |

|  |  |
| --- | --- |
|  | **No match to:** 901.4816, 904.4781, 917.4740, 934.4749, 936.4710, 948.4430, 950.4682, 966.4713, 982.4548, 1003.5497, 1033.5271, 1045.5751, 1046.5530, 1060.5720, 1065.5469, 1092.5292, 1100.6106, 1115.5874, 1116.5972, 1179.6349, 1231.5663, 1235.6046, 1238.6145, 1259.6625, 1308.6830, 1311.6515, 1311.6515, 1320.6891, 1320.6891, 1332.6801, 1354.6564, 1385.6836, 1385.6836, 1390.6996, 1430.7495, 1431.7217, 1431.7217, 1448.7543, 1448.7543, 1467.7462, 1475.7579, 1493.7649, 1498.8232, 1791.7388, 2373.1147 |

|  |  |
| --- | --- |
| **8.** | [gi|13625879|gb|AAK35184.1|AF352699\_1](http://msmsms/mascot/cgi/protein_view.pl?file=../data/20120113/F018129.dat&hit=8" \t "_blank)    **Mass:** 25808    **Score:** 98     **Expect:** 6.1e-006  **Matches:** 4 |
|  | activation associated secreted protein-like protein [Cooperia punctata] |

|  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | **Observed** | **Mr(expt)** | **Mr(calc)** | **ppm** | **Start** |  | **End** | **Miss** | **Ions** | **Peptide** |
|  | 1233.5846 | 1232.5773 | 1232.5642 | 10.7 | 170 | - | 181 | 0 | --- | R.LGCAAVSCPEQR.K |
|  | 1332.6801 | 1331.6728 | 1331.6622 | 7.94 | 156 | - | 166 | 0 | --- | K.TGHYSQVVWQK.S |
|  | 1448.7543 | 1447.7470 | 1447.7208 | 18.1 | 44 | - | 54 | 1 | --- | R.QVFLDKHNEYR.Q |
|  | 1448.7543 | 1447.7470 | 1447.7208 | 18.1 | 44 | - | 54 | 1 | 89 | R.QVFLDKHNEYR.Q |

|  |  |
| --- | --- |
|  | **No match to:** 901.4816, 904.4781, 917.4740, 919.4605, 934.4749, 936.4710, 948.4430, 950.4682, 966.4713, 971.5641, 982.4548, 1003.5497, 1033.5271, 1045.5751, 1046.5530, 1059.5961, 1060.5720, 1065.5469, 1092.5292, 1100.6106, 1115.5874, 1116.5972, 1179.6349, 1231.5663, 1235.6046, 1238.6145, 1259.6625, 1308.6830, 1311.6515, 1311.6515, 1320.6891, 1320.6891, 1334.7019, 1354.6564, 1385.6836, 1385.6836, 1390.6996, 1430.7495, 1431.7217, 1431.7217, 1462.8020, 1467.7462, 1475.7579, 1493.7649, 1498.8232, 1686.7849, 1686.7849, 1791.7388, 2373.1147 |

**http://msmsms/mascot/images/88x31_logo_white.gifMascot Search Results**

**Protein View**

Top of Form



Match to: **contig05709** Score: **315** Expect: **1.1e-027**

**putative nuclear encoded protein Method: similarity and extension**

Nominal mass (Mr): **23725**; Calculated pI value: **5.37**

NCBI BLAST search of [contig05709](http://www.ncbi.nlm.nih.gov/blast/Blast.cgi?ALIGNMENTS=50&ALIGNMENT_VIEW=Pairwise&AUTO_FORMAT=Semiauto&CDD_SEARCH=on&CLIENT=web&COMPOSITION_BASED_STATISTICS=on&DATABASE=nr&DESCRIPTIONS=100&ENTREZ_QUERY=(none)&EXPECT=10&FILTER=L&FORMAT_BLOCK_ON_RESPAGE=None&FORMAT_OBJECT=Alignment&FORMAT_TYPE=HTML&GAPCOSTS=11+1&I_THRESH=0.001&LAYOUT=TwoWindows&MATRIX_NAME=BLOSUM62&NCBI_GI=on&PAGE=Proteins&PROGRAM=blastp&QUERY=MLIALITVFCLILHHATVLGEELCSLDNGMTDEIRKVFLDKHNEYRSLVAKGQAPNPQFGGSTPKAARMLKAMYDCDVEEDMTKWAQAQCTYAPFKSSKRYGRNTWGMGVPNYNKTAAAESSVYDWFFELRRYGVPQDNVYTRDVDYSAYHYAQMVWQDSYKIGCVVAWCPSMTWVACGYSPAGDNIGSLIYELGEPCTKNEDCKCTDCT&SERVICE=plain&SET_DEFAULTS.x=9&SET_DEFAULTS.y=5&SHOW_OVERVIEW=on&WORD_SIZE=3&END_OF_HTTPGET=Yes" \t "_blank) against nr

Unformatted [sequence string](http://msmsms/mascot/cgi/getseq.pl?cooperia_oncophora+contig05709+seq" \t "_blank) for pasting into other applications

Variable modifications: Oxidation (HW),Oxidation (M)

Cleavage by Trypsin/P: cuts C-term side of KR

Sequence Coverage: **17%**

Matched peptides shown in **Bold Red**

**1** MLIALITVFC LILHHATVLG EELCSLDNGM TDEIR**KVFLD KHNEYR**SLVA

**51** K**GQAPNPQFG GSTPK**AARML KAMYDCDVEE DMTKWAQAQC TYAPFKSSKR

**101** YGRNTWGMGV PNYNKTAAAE SSVYDWFFEL R**RYGVPQDNV YTR**DVDYSAY

**151** HYAQMVWQDS YKIGCVVAWC PSMTWVACGY SPAGDNIGSL IYELGEPCTK

**201** NEDCKCTDCT



  Residue Number  Increasing Mass  Decreasing Mass

**Start - End Observed Mr(expt) Mr(calc) ppm Miss Sequence**

**36 - 46 1448.7543 1447.7470 1447.7572 -7 2 R.KVFLDKHNEYR.S**  ([No match](http://msmsms/mascot/cgi/peptide_view.pl?file=../data/20120113/F018129.dat&query=43&hit=1" \t "_blank))

**36 - 46 1448.7543 1447.7470 1447.7572 -7 2 R.KVFLDKHNEYR.S**  ([Ions score 89](http://msmsms/mascot/cgi/peptide_view.pl?file=../data/20120113/F018129.dat&query=44&hit=1" \t "_blank))

**37 - 46 1320.6891 1319.6818 1319.6622 15 1 K.VFLDKHNEYR.S**  ([No match](http://msmsms/mascot/cgi/peptide_view.pl?file=../data/20120113/F018129.dat&query=32&hit=1" \t "_blank))

**37 - 46 1320.6891 1319.6818 1319.6622 15 1 K.VFLDKHNEYR.S**  ([Ions score 52](http://msmsms/mascot/cgi/peptide_view.pl?file=../data/20120113/F018129.dat&query=33&hit=1" \t "_blank))

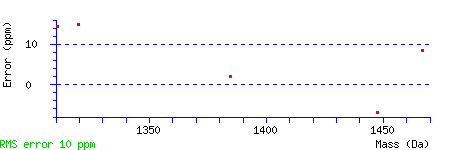
**52 - 65 1385.6836 1384.6763 1384.6735 2 0 K.GQAPNPQFGGSTPK.A**  ([No match](http://msmsms/mascot/cgi/peptide_view.pl?file=../data/20120113/F018129.dat&query=37&hit=1" \t "_blank))

**52 - 65 1385.6836 1384.6763 1384.6735 2 0 K.GQAPNPQFGGSTPK.A**  ([Ions score 79](http://msmsms/mascot/cgi/peptide_view.pl?file=../data/20120113/F018129.dat&query=38&hit=1" \t "_blank))

**132 - 143 1467.7462 1466.7389 1466.7266 8 1 R.RYGVPQDNVYTR.D**  ([No match](http://msmsms/mascot/cgi/peptide_view.pl?file=../data/20120113/F018129.dat&query=46&hit=1" \t "_blank))

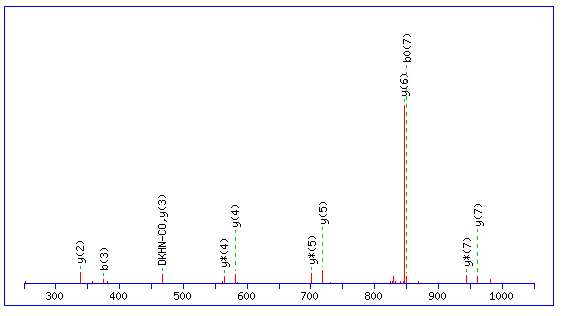
**133 - 143 1311.6515 1310.6442 1310.6255 14 0 R.YGVPQDNVYTR.D**  ([No match](http://msmsms/mascot/cgi/peptide_view.pl?file=../data/20120113/F018129.dat&query=30&hit=1" \t "_blank))

**133 - 143 1311.6515 1310.6442 1310.6255 14 0 R.YGVPQDNVYTR.D**  ([Ions score 78](http://msmsms/mascot/cgi/peptide_view.pl?file=../data/20120113/F018129.dat&query=31&hit=1" \t "_blank))



Bottom of Form

🡪 Annotated MS2 spectrum for peptide KVFLDKHNEYR



**Monoisotopic mass of neutral peptide Mr(calc):** 1447.7572

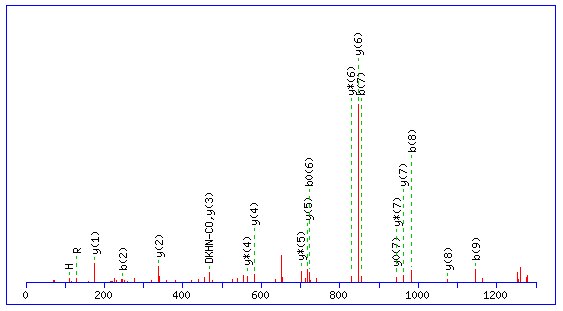
**Ions Score:** 89 **Expect:** 1.1e-007

**Matches :** 23/160 fragment ions using 23 most intense peaks   ([help](http://msmsms/mascot/help/results_help.html" \l "PEP" \t "_blank))

|  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **#** | **Immon.** | **a** | **a\*** | **a0** | **b** | **b\*** | **b0** | **Seq.** | **v** | **w** | **y** | **y\*** | **y0** | **#** |
| **1** | 101.1073 | 101.1073 | 84.0808 |  | **129.1022** | 112.0757 |  | **K** |  |  |  |  |  | **11** |
| **2** | 72.0808 | 200.1757 | 183.1492 |  | **228.1707** | 211.1441 |  | **V** | 1276.6069 | 1289.6273 | 1320.6695 | 1303.6430 | 1302.6589 | **10** |
| **3** | 120.0808 | 347.2442 | 330.2176 |  | **375.2391** | 358.2125 |  | **F** | 1129.5385 |  | ***1221.6011*** | 1204.5745 | 1203.5905 | **9** |
| **4** | 86.0964 | 460.3282 | 443.3017 |  | 488.3231 | 471.2966 |  | **L** | 1016.4544 | 1015.4592 | ***1074.5327*** | 1057.5061 | 1056.5221 | **8** |
| **5** | 88.0393 | 575.3552 | 558.3286 | 557.3446 | 603.3501 | 586.3235 | 585.3395 | **D** | 901.4275 | 900.4322 | ***961.4486*** | 944.4221 | 943.4381 | **7** |
| **6** | 101.1073 | 703.4501 | 686.4236 | 685.4396 | 731.4450 | 714.4185 | 713.4345 | **K** | 773.3325 | 772.3373 | ***846.4217*** | 829.3951 | 828.4111 | **6** |
| **7** | 110.0713 | 840.5090 | 823.4825 | 822.4985 | 868.5039 | 851.4774 | 850.4934 | **H** | 636.2736 |  | ***718.3267*** | 701.3002 | 700.3161 | **5** |
| **8** | 87.0553 | 954.5520 | 937.5254 | 936.5414 | 982.5469 | 965.5203 | 964.5363 | **N** | 522.2307 | 521.2354 | ***581.2678*** | 564.2413 | 563.2572 | **4** |
| **9** | 102.0550 | 1083.5946 | 1066.5680 | 1065.5840 | **1111.5895** | 1094.5629 | 1093.5789 | **E** | 393.1881 | 392.1928 | ***467.2249*** | 450.1983 | 449.2143 | **3** |
| **10** | 136.0757 | 1246.6579 | 1229.6313 | 1228.6473 | **1274.6528** | 1257.6262 | 1256.6422 | **Y** | 230.1248 |  | ***338.1823*** | 321.1557 |  | **2** |
| **11** | 129.1135 |  |  |  |  |  |  | **R** | 74.0237 | 73.0284 | ***175.1190*** | 158.0924 |  | **1** |

|  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **Seq** | **ya** | **yb** | **Seq** | **ya** | **yb** | **Seq** | **ya** | **yb** |
| **VF** | 219.1492 | 247.1441 | **VFL** | 332.2333 | 360.2282 | **VFLD** | 447.2602 | 475.2551 |
| **VFLDK** | 575.3552 | 603.3501 | **FL** | 233.1648 | 261.1598 | **FLD** | 348.1918 | 376.1867 |
| **FLDK** | 476.2867 | 504.2817 | **FLDKH** | 613.3457 | 641.3406 | **LD** | 201.1234 | 229.1183 |
| **LDK** | 329.2183 | 357.2132 | **LDKH** | 466.2772 | 494.2722 | **LDKHN** | 580.3202 | 608.3151 |
| **DK** | 216.1343 | 244.1292 | **DKH** | 353.1932 | 381.1881 | **DKHN** | 467.2361 | 495.2310 |
| **DKHNE** | 596.2787 | 624.2736 | **KH** | 238.1662 | 266.1612 | **KHN** | 352.2092 | 380.2041 |
| **KHNE** | 481.2518 | 509.2467 | **KHNEY** | 644.3151 | 672.3100 | **HN** | 224.1142 | 252.1091 |
| **HNE** | 353.1568 | 381.1517 | **HNEY** | 516.2201 | 544.2150 | **NE** | 216.0979 | 244.0928 |
| **NEY** | 379.1612 | 407.1561 | **EY** | 265.1183 | 293.1132 |  |  |  |

🡪 Annotated MS2 spectrum for peptide VFLDKHNEYR



**Monoisotopic mass of neutral peptide Mr(calc):** 1319.6622

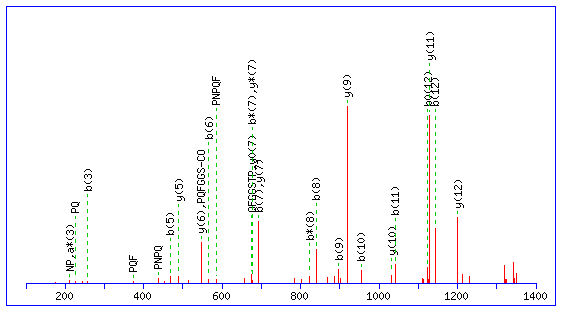
**Ions Score:** 52 **Expect:** 0.00047

**Matches :** 21/134 fragment ions using 36 most intense peaks   ([help](http://msmsms/mascot/help/results_help.html" \l "PEP" \t "_blank))

|  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **#** | **Immon.** | **a** | **a\*** | **a0** | **b** | **b\*** | **b0** | **Seq.** | **v** | **w** | **y** | **y\*** | **y0** | **#** |
| **1** | 72.0808 | 72.0808 |  |  | 100.0757 |  |  | **V** |  |  |  |  |  | **10** |
| **2** | 120.0808 | 219.1492 |  |  | **247.1441** |  |  | **F** | 1129.5385 |  | 1221.6011 | 1204.5745 | 1203.5905 | **9** |
| **3** | 86.0964 | 332.2333 |  |  | 360.2282 |  |  | **L** | 1016.4544 | 1015.4592 | ***1074.5327*** | 1057.5061 | 1056.5221 | **8** |
| **4** | 88.0393 | 447.2602 |  | 429.2496 | 475.2551 |  | 457.2445 | **D** | 901.4275 | 900.4322 | ***961.4486*** | 944.4221 | 943.4381 | **7** |
| **5** | 101.1073 | 575.3552 | 558.3286 | 557.3446 | 603.3501 | 586.3235 | 585.3395 | **K** | 773.3325 | 772.3373 | ***846.4217*** | 829.3951 | 828.4111 | **6** |
| **6** | 110.0713 | 712.4141 | 695.3875 | 694.4035 | 740.4090 | 723.3824 | 722.3984 | **H** | 636.2736 |  | ***718.3267*** | 701.3002 | 700.3161 | **5** |
| **7** | 87.0553 | 826.4570 | 809.4304 | 808.4464 | **854.4519** | 837.4254 | 836.4413 | **N** | 522.2307 | 521.2354 | ***581.2678*** | 564.2413 | 563.2572 | **4** |
| **8** | 102.0550 | 955.4996 | 938.4730 | 937.4890 | **983.4945** | 966.4680 | 965.4839 | **E** | 393.1881 | 392.1928 | ***467.2249*** | 450.1983 | 449.2143 | **3** |
| **9** | 136.0757 | 1118.5629 | 1101.5364 | 1100.5524 | **1146.5578** | 1129.5313 | 1128.5473 | **Y** | 230.1248 |  | ***338.1823*** | 321.1557 |  | **2** |
| **10** | 129.1135 |  |  |  |  |  |  | **R** | 74.0237 | 73.0284 | ***175.1190*** | 158.0924 |  | **1** |

|  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **Seq** | **ya** | **yb** | **Seq** | **ya** | **yb** | **Seq** | **ya** | **yb** |
| **FL** | 233.1648 | 261.1598 | **FLD** | 348.1918 | 376.1867 | **FLDK** | 476.2867 | 504.2817 |
| **FLDKH** | 613.3457 | 641.3406 | **LD** | 201.1234 | 229.1183 | **LDK** | 329.2183 | 357.2132 |
| **LDKH** | 466.2772 | 494.2722 | **LDKHN** | 580.3202 | 608.3151 | **DK** | 216.1343 | 244.1292 |
| **DKH** | 353.1932 | 381.1881 | **DKHN** | 467.2361 | 495.2310 | **DKHNE** | 596.2787 | 624.2736 |
| **KH** | 238.1662 | 266.1612 | **KHN** | 352.2092 | 380.2041 | **KHNE** | 481.2518 | 509.2467 |
| **KHNEY** | 644.3151 | 672.3100 | **HN** | 224.1142 | 252.1091 | **HNE** | 353.1568 | 381.1517 |
| **HNEY** | 516.2201 | 544.2150 | **NE** | 216.0979 | 244.0928 | **NEY** | 379.1612 | 407.1561 |
| **EY** | 265.1183 | 293.1132 |  |  |  |  |  |  |

🡪 Annotated MS2 spectrum for peptide GQAPNPQFGGSTPK



**Monoisotopic mass of neutral peptide Mr(calc):** 1384.6735

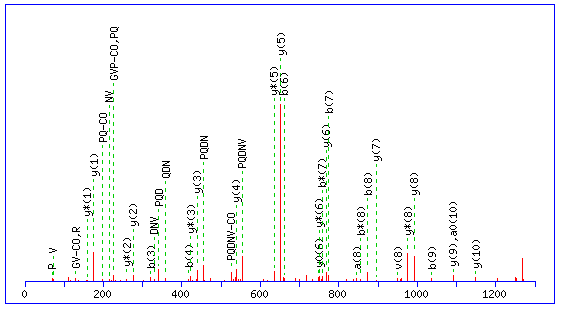
**Ions Score:** 79 **Expect:** 1e-006

**Matches :** 31/206 fragment ions using 32 most intense peaks   ([help](http://msmsms/mascot/help/results_help.html" \l "PEP" \t "_blank))

|  |  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **#** | **Immon.** | **a** | **a\*** | **a0** | **b** | **b\*** | **b0** | **Seq.** | **y** | **y\*** | **y0** | **#** |
| **1** | 30.0338 | 30.0338 |  |  | 58.0287 |  |  | **G** |  |  |  | **14** |
| **2** | 101.0709 | 158.0924 | 141.0659 |  | 186.0873 | 169.0608 |  | **Q** | 1328.6593 | 1311.6328 | 1310.6488 | **13** |
| **3** | 44.0495 | 229.1295 | 212.1030 |  | ***257.1244*** | 240.0979 |  | **A** | ***1200.6008*** | 1183.5742 | 1182.5902 | **12** |
| **4** | 70.0651 | 326.1823 | 309.1557 |  | 354.1772 | 337.1506 |  | **P** | ***1129.5637*** | 1112.5371 | 1111.5531 | **11** |
| **5** | 87.0553 | 440.2252 | 423.1987 |  | ***468.2201*** | 451.1936 |  | **N** | ***1032.5109*** | 1015.4843 | 1014.5003 | **10** |
| **6** | 70.0651 | 537.2780 | 520.2514 |  | ***565.2729*** | 548.2463 |  | **P** | ***918.4680*** | 901.4414 | 900.4574 | **9** |
| **7** | 101.0709 | 665.3366 | 648.3100 |  | ***693.3315*** | 676.3049 |  | **Q** | 821.4152 | 804.3886 | 803.4046 | **8** |
| **8** | 120.0808 | 812.4050 | 795.3784 |  | ***840.3999*** | 823.3733 |  | **F** | ***693.3566*** | 676.3301 | 675.3461 | **7** |
| **9** | 30.0338 | 869.4264 | 852.3999 |  | ***897.4213*** | 880.3948 |  | **G** | ***546.2882*** | 529.2617 | 528.2776 | **6** |
| **10** | 30.0338 | 926.4479 | 909.4213 |  | ***954.4428*** | 937.4163 |  | **G** | ***489.2667*** | 472.2402 | 471.2562 | **5** |
| **11** | 60.0444 | 1013.4799 | 996.4534 | 995.4694 | ***1041.4748*** | 1024.4483 | 1023.4643 | **S** | 432.2453 | 415.2187 | 414.2347 | **4** |
| **12** | 74.0600 | 1114.5276 | 1097.5011 | 1096.5170 | ***1142.5225*** | 1125.4960 | 1124.5119 | **T** | 345.2132 | 328.1867 | 327.2027 | **3** |
| **13** | 70.0651 | 1211.5804 | 1194.5538 | 1193.5698 | 1239.5753 | 1222.5487 | 1221.5647 | **P** | 244.1656 | 227.1390 |  | **2** |
| **14** | 101.1073 |  |  |  |  |  |  | **K** | 147.1128 | 130.0863 |  | **1** |

|  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **Seq** | **ya** | **yb** | **Seq** | **ya** | **yb** | **Seq** | **ya** | **yb** |
| **QA** | 172.1081 | 200.1030 | **QAP** | 269.1608 | 297.1557 | **QAPN** | 383.2037 | 411.1987 |
| **QAPNP** | 480.2565 | 508.2514 | **QAPNPQ** | 608.3151 | 636.3100 | **AP** | 141.1022 | 169.0972 |
| **APN** | 255.1452 | 283.1401 | **APNP** | 352.1979 | 380.1928 | **APNPQ** | 480.2565 | 508.2514 |
| **APNPQF** | 627.3249 | 655.3198 | **APNPQFG** | 684.3464 | 712.3413 | **PN** | 184.1081 | 212.1030 |
| **PNP** | 281.1608 | 309.1557 | **PNPQ** | 409.2194 | 437.2143 | **PNPQF** | 556.2878 | 584.2827 |
| **PNPQFG** | 613.3093 | 641.3042 | **PNPQFGG** | 670.3307 | 698.3257 | **NP** | 184.1081 | 212.1030 |
| **NPQ** | 312.1666 | 340.1615 | **NPQF** | 459.2350 | 487.2300 | **NPQFG** | 516.2565 | 544.2514 |
| **NPQFGG** | 573.2780 | 601.2729 | **NPQFGGS** | 660.3100 | 688.3049 | **PQ** | 198.1237 | 226.1186 |
| **PQF** | 345.1921 | 373.1870 | **PQFG** | 402.2136 | 430.2085 | **PQFGG** | 459.2350 | 487.2300 |
| **PQFGGS** | 546.2671 | 574.2620 | **PQFGGST** | 647.3148 | 675.3097 | **QF** | 248.1394 | 276.1343 |
| **QFG** | 305.1608 | 333.1557 | **QFGG** | 362.1823 | 390.1772 | **QFGGS** | 449.2143 | 477.2092 |
| **QFGGST** | 550.2620 | 578.2569 | **QFGGSTP** | 647.3148 | 675.3097 | **FG** | 177.1022 | 205.0972 |
| **FGG** | 234.1237 | 262.1186 | **FGGS** | 321.1557 | 349.1506 | **FGGST** | 422.2034 | 450.1983 |
| **FGGSTP** | 519.2562 | 547.2511 | **GG** | 87.0553 | 115.0502 | **GGS** | 174.0873 | 202.0822 |
| **GGST** | 275.1350 | 303.1299 | **GGSTP** | 372.1878 | 400.1827 | **GS** | 117.0659 | 145.0608 |
| **GST** | 218.1135 | 246.1084 | **GSTP** | 315.1663 | 343.1612 | **ST** | 161.0921 | 189.0870 |
| **STP** | 258.1448 | 286.1397 | **TP** | 171.1128 | 199.1077 |  |  |  |

🡪 Annotated MS2 spectrum for peptide YGVPQDNVYTR



**Monoisotopic mass of neutral peptide Mr(calc):** 1310.6255

**Ions Score:** 78 **Expect:** 1.1e-006

**Matches :** 45/159 fragment ions using 55 most intense peaks   ([help](http://msmsms/mascot/help/results_help.html" \l "PEP" \t "_blank))

|  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **#** | **Immon.** | **a** | **a\*** | **a0** | **b** | **b\*** | **b0** | **Seq.** | **v** | **w** | **w'** | **y** | **y\*** | **y0** | **#** |
| **1** | 136.0757 | 136.0757 |  |  | 164.0706 |  |  | **Y** |  |  |  |  |  |  | **11** |
| **2** | 30.0338 | 193.0972 |  |  | 221.0921 |  |  | **G** |  |  |  | ***1148.5695*** | 1131.5429 | 1130.5589 | **10** |
| **3** | 72.0808 | 292.1656 |  |  | **320.1605** |  |  | **V** | 1047.4854 | 1060.5058 |  | ***1091.5480*** | 1074.5215 | 1073.5374 | **9** |
| **4** | 70.0651 | 389.2183 |  |  | **417.2132** |  |  | **P** | 950.4326 | 949.4374 |  | ***992.4796*** | 975.4530 | 974.4690 | **8** |
| **5** | 101.0709 | 517.2769 | 500.2504 |  | 545.2718 | 528.2453 |  | **Q** | 822.3741 | 821.3788 |  | ***895.4268*** | 878.4003 | 877.4163 | **7** |
| **6** | 88.0393 | 632.3039 | 615.2773 | 614.2933 | **660.2988** | 643.2722 | 642.2882 | **D** | 707.3471 | 706.3519 |  | ***767.3682*** | 750.3417 | 749.3577 | **6** |
| **7** | 87.0553 | 746.3468 | 729.3202 | 728.3362 | **774.3417** | 757.3151 | 756.3311 | **N** | 593.3042 | 592.3089 |  | ***652.3413*** | 635.3148 | 634.3307 | **5** |
| **8** | 72.0808 | 845.4152 | 828.3886 | 827.4046 | **873.4101** | 856.3836 | 855.3995 | **V** | 494.2358 | 507.2562 |  | ***538.2984*** | 521.2718 | 520.2878 | **4** |
| **9** | 136.0757 | 1008.4785 | 991.4520 | 990.4680 | **1036.4734** | 1019.4469 | 1018.4629 | **Y** | 331.1724 |  |  | ***439.2300*** | 422.2034 | 421.2194 | **3** |
| **10** | 74.0600 | 1109.5262 | 1092.4997 | 1091.5156 | 1137.5211 | 1120.4946 | 1119.5106 | **T** | 230.1248 | 243.1452 | 245.1244 | ***276.1666*** | 259.1401 | 258.1561 | **2** |
| **11** | 129.1135 |  |  |  |  |  |  | **R** | 74.0237 | 73.0284 |  | ***175.1190*** | 158.0924 |  | **1** |

|  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **Seq** | **ya** | **yb** | **Seq** | **ya** | **yb** | **Seq** | **ya** | **yb** |
| **GV** | 129.1022 | 157.0972 | **GVP** | 226.1550 | 254.1499 | **GVPQ** | 354.2136 | 382.2085 |
| **GVPQD** | 469.2405 | 497.2354 | **GVPQDN** | 583.2835 | 611.2784 | **GVPQDNV** | 682.3519 | 710.3468 |
| **VP** | 169.1335 | 197.1285 | **VPQ** | 297.1921 | 325.1870 | **VPQD** | 412.2191 | 440.2140 |
| **VPQDN** | 526.2620 | 554.2569 | **VPQDNV** | 625.3304 | 653.3253 | **PQ** | 198.1237 | 226.1186 |
| **PQD** | 313.1506 | 341.1456 | **PQDN** | 427.1936 | 455.1885 | **PQDNV** | 526.2620 | 554.2569 |
| **PQDNVY** | 689.3253 | 717.3202 | **QD** | 216.0979 | 244.0928 | **QDN** | 330.1408 | 358.1357 |
| **QDNV** | 429.2092 | 457.2041 | **QDNVY** | 592.2726 | 620.2675 | **QDNVYT** | 693.3202 | 721.3151 |
| **DN** | 202.0822 | 230.0771 | **DNV** | 301.1506 | 329.1456 | **DNVY** | 464.2140 | 492.2089 |
| **DNVYT** | 565.2617 | 593.2566 | **NV** | 186.1237 | 214.1186 | **NVY** | 349.1870 | 377.1819 |
| **NVYT** | 450.2347 | 478.2296 | **VY** | 235.1441 | 263.1390 | **VYT** | 336.1918 | 364.1867 |
| **YT** | 237.1234 | 265.1183 |  |  |  |  |  |  |

**Band 2:**

**http://msmsms/mascot/images/88x31_logo_white.gifMascot Search Results**

**User :**

**Email :**

**Search title : SampleSetID: 683, AnalysisID: 1071, MaldiWellID: 82746, SpectrumID: 217084, Path=\Jimmy\Cooperia 3\Co ES Conc 3 Frac 13012012 (strict)**

**Database : cooperia\_oncophora oncophora\_20110405 (34373 sequences; 5289600 residues)**

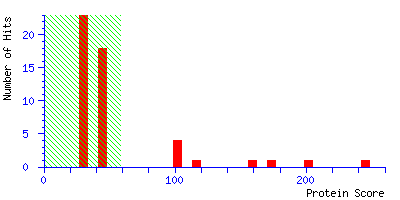
**Timestamp : 13 Jan 2012 at 14:32:28 GMT**

**Warning : A Peptide summary report will usually give a much clearer picture of MS/MS search results.**

**Top Score : 245 for contig63173, putative nuclear encoded protein Method: similarity and extension**

**Mascot Score Histogram**

Protein score is -10\*Log(P), where P is the probability that the observed match is a random event.  
Protein scores greater than 58 are significant (p<0.05).  
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Top of Form



**Protein Summary Report**

|  |  |  |  |
| --- | --- | --- | --- |
|  |  |  | [Help](http://msmsms/mascot/help/msms_summaries_help.html" \t "_blank) |
|  | Significance threshold p< | Max. number of hits |  |

Bottom of Form

Top of Form





Bottom of Form

**Index**

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
|  | **Accession** | **Mass** | **Score** | **Description** |
| **1.** | [**contig63173**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20120113/F018130.dat#Hit1) | 22462 | 245 | putative nuclear encoded protein Method: similarity and extension |
| **2.** | [**gi|13625885|gb|AAK35187.1|AF352702\_1**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20120113/F018130.dat#Hit2) | 55209 | 201 | activation associated secreted protein-like protein [Cooperia punctata] |
| **3.** | [**gi|13625909|gb|AAK35199.1|AF352714\_1**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20120113/F018130.dat#Hit3) | 51596 | 174 | activation associated secreted protein-like protein [Cooperia punctata] |
| **4.** | [**isotig31886**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20120113/F018130.dat#Hit4) | 15295 | 157 | putative nuclear encoded protein Method: similarity and extension |
| **5.** | [**gi|13625911|gb|AAK35200.1|AF352715\_1**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20120113/F018130.dat#Hit5) | 9724 | 122 | activation associated secreted protein-like protein [Cooperia punctata] |
| **6.** | [**gi|13625881|gb|AAK35185.1|AF352700\_1**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20120113/F018130.dat#Hit6) | 27510 | 107 | activation associated secreted protein-like protein [Cooperia punctata] |
| **7.** | [**contig05709**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20120113/F018130.dat#Hit7) | 23725 | 105 | putative nuclear encoded protein Method: similarity and extension |
| **8.** | [**gi|13625879|gb|AAK35184.1|AF352699\_1**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20120113/F018130.dat#Hit8) | 25808 | 100 | activation associated secreted protein-like protein [Cooperia punctata] |
| **9.** | [**gi|13625877|gb|AAK35183.1|AF352698\_1**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20120113/F018130.dat#Hit9) | 27540 | 97 | activation associated secreted protein-like protein [Cooperia punctata] |
| **10.** | [**isotig04210**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20120113/F018130.dat#Hit10) | 26899 | 49 | putative nuclear encoded protein Method: similarity and extension |
| **11.** | [**isotig04205**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20120113/F018130.dat#Hit11) | 26898 | 49 | putative nuclear encoded protein Method: similarity and extension |
| **12.** | [**isotig04209**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20120113/F018130.dat#Hit12) | 26899 | 49 | putative nuclear encoded protein Method: similarity and extension |
| **13.** | [**isotig04206**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20120113/F018130.dat#Hit13) | 26898 | 49 | putative nuclear encoded protein Method: similarity and extension |
| **14.** | [**isotig04211**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20120113/F018130.dat#Hit14) | 18030 | 45 | putative nuclear encoded protein Method: similarity and extension |
| **15.** | [**isotig04212**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20120113/F018130.dat#Hit15) | 18030 | 45 | putative nuclear encoded protein Method: similarity and extension |
| **16.** | [**isotig04217**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20120113/F018130.dat#Hit16) | 16347 | 44 | putative nuclear encoded protein Method: similarity and extension |
| **17.** | [**isotig04218**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20120113/F018130.dat#Hit17) | 16347 | 44 | putative nuclear encoded protein Method: similarity and extension |
| **18.** | [**isotig04215**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20120113/F018130.dat#Hit18) | 11800 | 43 | putative nuclear encoded protein Method: similarity and extension |
| **19.** | [**isotig04216**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20120113/F018130.dat#Hit19) | 11800 | 43 | putative nuclear encoded protein Method: similarity and extension |
| **20.** | [**isotig04214**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20120113/F018130.dat#Hit20) | 26769 | 41 | putative nuclear encoded protein Method: similarity and extension |

**Results List**

|  |  |
| --- | --- |
| **1.** | [contig63173](http://msmsms/mascot/cgi/protein_view.pl?file=../data/20120113/F018130.dat&hit=1" \t "_blank)    **Mass:** 22462    **Score:** 245    **Expect:** 1.1e-020  **Matches:** 11 |
|  | putative nuclear encoded protein Method: similarity and extension |

|  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | **Observed** | **Mr(expt)** | **Mr(calc)** | **ppm** | **Start** |  | **End** | **Miss** | **Ions** | **Peptide** |
|  | 1354.6582 | 1353.6509 | 1353.6452 | 4.19 | 180 | - | 190 | 0 | --- | R.SVDDWYIEVTK.Y |
|  | 1448.7404 | 1447.7331 | 1447.7208 | 8.52 | 95 | - | 105 | 1 | --- | R.QVFLDKHNEYR.Q |
|  | 1448.7404 | 1447.7331 | 1447.7208 | 8.52 | 95 | - | 105 | 1 | 88 | R.QVFLDKHNEYR.Q |
|  | 1467.7362 | 1466.7289 | 1466.7577 | -19.60 | 34 | - | 47 | 1 | --- | K.PSTTTTKATTTTTR.P |
|  | 1686.7777 | 1685.7704 | 1685.8597 | -52.97 | 101 | - | 114 | 2 | --- | K.HNEYRQIVARGEAK.N + Oxidation (HW) |
|  | 1686.7777 | 1685.7704 | 1685.8597 | -52.97 | 101 | - | 114 | 2 | --- | K.HNEYRQIVARGEAK.N + Oxidation (HW) |
|  | 2016.0723 | 2015.0650 | 2015.0701 | -2.50 | 95 | - | 110 | 2 | --- | R.QVFLDKHNEYRQIVAR.G |
|  | 2181.1772 | 2180.1699 | 2180.1702 | -0.11 | 160 | - | 179 | 2 | --- | R.GQNIWGITVPNLDKAEAAKR.S |
|  | 2181.1772 | 2180.1699 | 2180.1702 | -0.11 | 160 | - | 179 | 2 | 140 | R.GQNIWGITVPNLDKAEAAKR.S |
|  | 2373.1367 | 2372.1294 | 2372.1648 | -14.92 | 179 | - | 198 | 2 | --- | K.RSVDDWYIEVTKYGITADNK.I |
|  | 2373.1367 | 2372.1294 | 2372.1648 | -14.92 | 179 | - | 198 | 2 | --- | K.RSVDDWYIEVTKYGITADNK.I |

|  |  |
| --- | --- |
|  | **No match to:** 901.4799, 917.4655, 934.4561, 944.5021, 950.4550, 959.4774, 985.5931, 1003.5372, 1019.5316, 1035.5262, 1036.5310, 1036.5310, 1052.5254, 1097.5887, 1098.5793, 1100.6066, 1115.5808, 1115.5808, 1228.6597, 1228.6597, 1231.5714, 1259.6527, 1311.6396, 1320.6768, 1332.6744, 1334.6930, 1334.6930, 1366.7074, 1367.6774, 1383.6606, 1384.7648, 1384.7648, 1427.7333, 1430.7317, 1431.7069, 1447.7339, 1462.7825, 1476.7115, 1488.6875, 1492.6952, 1508.7031, 1524.7134, 1573.8041, 1701.9031, 1883.9982, 1886.9141, 2673.3201, 2673.3201, 2940.4924 |

|  |  |
| --- | --- |
| **2.** | [gi|13625885|gb|AAK35187.1|AF352702\_1](http://msmsms/mascot/cgi/protein_view.pl?file=../data/20120113/F018130.dat&hit=2" \t "_blank)    **Mass:** 55209    **Score:** 201    **Expect:** 2.7e-016  **Matches:** 10 |
|  | activation associated secreted protein-like protein [Cooperia punctata] |

|  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | **Observed** | **Mr(expt)** | **Mr(calc)** | **ppm** | **Start** |  | **End** | **Miss** | **Ions** | **Peptide** |
|  | 1334.6930 | 1333.6857 | 1333.6779 | 5.90 | 26 | - | 35 | 1 | --- | K.IFLDKHNEYR.S |
|  | 1334.6930 | 1333.6857 | 1333.6779 | 5.90 | 26 | - | 35 | 1 | 70 | K.IFLDKHNEYR.S |
|  | 1462.7825 | 1461.7752 | 1461.7728 | 1.65 | 25 | - | 35 | 2 | --- | R.KIFLDKHNEYR.S |
|  | 1488.6875 | 1487.6802 | 1487.6827 | -1.67 | 121 | - | 132 | 1 | --- | R.TYGVPRDNMYTR.D + Oxidation (M) |
|  | 1573.8041 | 1572.7968 | 1572.8121 | -9.69 | 31 | - | 44 | 2 | --- | K.HNEYRSLVARGGAK.D + Oxidation (HW) |
|  | 1686.7777 | 1685.7704 | 1685.7685 | 1.13 | 107 | - | 120 | 0 | --- | K.AAESSVYDWFNEIR.T |
|  | 1686.7777 | 1685.7704 | 1685.7685 | 1.13 | 107 | - | 120 | 0 | 117 | K.AAESSVYDWFNEIR.T |
|  | 1883.9982 | 1882.9909 | 1882.9148 | 40.4 | 442 | - | 457 | 1 | --- | R.RLYVGCEYWPGGNTLR.H |
|  | 2016.0723 | 2015.0650 | 2014.9795 | 42.4 | 90 | - | 105 | 2 | --- | R.YNRNTWGIGIRNFNMK.K + Oxidation (HW); Oxidation (M) |
|  | 2940.4924 | 2939.4851 | 2939.3654 | 40.7 | 278 | - | 303 | 2 | --- | R.AAWEESVKHPVAHCTVNKNGMTDEVR.Q + Oxidation (HW); Oxidation (M) |

|  |  |
| --- | --- |
|  | **No match to:** 901.4799, 917.4655, 934.4561, 944.5021, 950.4550, 959.4774, 985.5931, 1003.5372, 1019.5316, 1035.5262, 1036.5310, 1036.5310, 1052.5254, 1097.5887, 1098.5793, 1100.6066, 1115.5808, 1115.5808, 1228.6597, 1228.6597, 1231.5714, 1259.6527, 1311.6396, 1320.6768, 1332.6744, 1354.6582, 1366.7074, 1367.6774, 1383.6606, 1384.7648, 1384.7648, 1427.7333, 1430.7317, 1431.7069, 1447.7339, 1448.7404, 1448.7404, 1467.7362, 1476.7115, 1492.6952, 1508.7031, 1524.7134, 1701.9031, 1886.9141, 2181.1772, 2181.1772, 2373.1367, 2373.1367, 2673.3201, 2673.3201 |

|  |  |
| --- | --- |
| **3.** | [gi|13625909|gb|AAK35199.1|AF352714\_1](http://msmsms/mascot/cgi/protein_view.pl?file=../data/20120113/F018130.dat&hit=3" \t "_blank)    **Mass:** 51596    **Score:** 174    **Expect:** 1.4e-013  **Matches:** 15 |
|  | activation associated secreted protein-like protein [Cooperia punctata] |

|  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | **Observed** | **Mr(expt)** | **Mr(calc)** | **ppm** | **Start** |  | **End** | **Miss** | **Ions** | **Peptide** |
|  | 944.5021 | 943.4948 | 943.5749 | -84.87 | 59 | - | 66 | 2 | --- | K.AARMLKVR.Y |
|  | 1332.6744 | 1331.6671 | 1331.6622 | 3.66 | 390 | - | 400 | 0 | --- | K.TGHYSQVVWQK.S |
|  | 1334.6930 | 1333.6857 | 1333.6779 | 5.90 | 30 | - | 39 | 1 | --- | K.LFLDKHNEYR.S |
|  | 1334.6930 | 1333.6857 | 1333.6779 | 5.90 | 30 | - | 39 | 1 | 70 | K.LFLDKHNEYR.S |
|  | 1383.6606 | 1382.6533 | 1382.6441 | 6.66 | 78 | - | 89 | 0 | --- | K.WAQAQCAYAPFK.S |
|  | 1384.7648 | 1383.7575 | 1383.6558 | 73.5 | 363 | - | 373 | 0 | --- | R.SVDDWYIELTK.Y + Oxidation (HW) |
|  | 1384.7648 | 1383.7575 | 1383.6558 | 73.5 | 363 | - | 373 | 0 | --- | R.SVDDWYIELTK.Y + Oxidation (HW) |
|  | 1448.7404 | 1447.7331 | 1447.7208 | 8.52 | 278 | - | 288 | 1 | --- | R.QVFLDKHNEYR.Q |
|  | 1448.7404 | 1447.7331 | 1447.7208 | 8.52 | 278 | - | 288 | 1 | 88 | R.QVFLDKHNEYR.Q |
|  | 1462.7825 | 1461.7752 | 1461.7728 | 1.65 | 29 | - | 39 | 2 | --- | R.KLFLDKHNEYR.S |
|  | 1524.7134 | 1523.7061 | 1523.7620 | -36.67 | 362 | - | 373 | 1 | --- | K.RSVDDWYIELTK.Y |
|  | 1573.8041 | 1572.7968 | 1572.8195 | -14.41 | 328 | - | 342 | 2 | --- | K.TCKGGHSPFSVLKGR.G |
|  | 1686.7777 | 1685.7704 | 1685.7719 | -0.88 | 314 | - | 327 | 0 | --- | R.YDCDLEAHVLEHVK.T + Oxidation (HW) |
|  | 1686.7777 | 1685.7704 | 1685.8597 | -52.97 | 284 | - | 297 | 2 | --- | K.HNEYRQLVARGEAK.N + Oxidation (HW) |
|  | 2016.0723 | 2015.0650 | 2015.0701 | -2.50 | 278 | - | 293 | 2 | --- | R.QVFLDKHNEYRQLVAR.G |

|  |  |
| --- | --- |
|  | **No match to:** 901.4799, 917.4655, 934.4561, 950.4550, 959.4774, 985.5931, 1003.5372, 1019.5316, 1035.5262, 1036.5310, 1036.5310, 1052.5254, 1097.5887, 1098.5793, 1100.6066, 1115.5808, 1115.5808, 1228.6597, 1228.6597, 1231.5714, 1259.6527, 1311.6396, 1320.6768, 1354.6582, 1366.7074, 1367.6774, 1427.7333, 1430.7317, 1431.7069, 1447.7339, 1467.7362, 1476.7115, 1488.6875, 1492.6952, 1508.7031, 1701.9031, 1883.9982, 1886.9141, 2181.1772, 2181.1772, 2373.1367, 2373.1367, 2673.3201, 2673.3201, 2940.4924 |

|  |  |
| --- | --- |
| **4.** | [isotig31886](http://msmsms/mascot/cgi/protein_view.pl?file=../data/20120113/F018130.dat&hit=4" \t "_blank)    **Mass:** 15295    **Score:** 157    **Expect:** 6.9e-012  **Matches:** 8 |
|  | putative nuclear encoded protein Method: similarity and extension |

|  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | **Observed** | **Mr(expt)** | **Mr(calc)** | **ppm** | **Start** |  | **End** | **Miss** | **Ions** | **Peptide** |
|  | 1332.6744 | 1331.6671 | 1331.6622 | 3.66 | 62 | - | 72 | 0 | --- | K.TGHYSQVVWQK.S |
|  | 1354.6582 | 1353.6509 | 1353.6452 | 4.19 | 35 | - | 45 | 0 | --- | R.SVDDWYIEVTK.Y |
|  | 1476.7115 | 1475.7042 | 1475.7521 | -32.46 | 61 | - | 72 | 1 | --- | K.KTGHYSQVVWQK.S + Oxidation (HW) |
|  | 1492.6952 | 1491.6879 | 1491.7470 | -39.63 | 61 | - | 72 | 1 | --- | K.KTGHYSQVVWQK.S + 2 Oxidation (HW) |
|  | 2181.1772 | 2180.1699 | 2180.1702 | -0.11 | 15 | - | 34 | 2 | --- | R.GQNIWGITVPNLDKAEAAKR.S |
|  | 2181.1772 | 2180.1699 | 2180.1702 | -0.11 | 15 | - | 34 | 2 | 140 | R.GQNIWGITVPNLDKAEAAKR.S |
|  | 2373.1367 | 2372.1294 | 2372.1648 | -14.92 | 34 | - | 53 | 2 | --- | K.RSVDDWYIEVTKYGITADNK.I |
|  | 2373.1367 | 2372.1294 | 2372.1648 | -14.92 | 34 | - | 53 | 2 | --- | K.RSVDDWYIEVTKYGITADNK.I |

|  |  |
| --- | --- |
|  | **No match to:** 901.4799, 917.4655, 934.4561, 944.5021, 950.4550, 959.4774, 985.5931, 1003.5372, 1019.5316, 1035.5262, 1036.5310, 1036.5310, 1052.5254, 1097.5887, 1098.5793, 1100.6066, 1115.5808, 1115.5808, 1228.6597, 1228.6597, 1231.5714, 1259.6527, 1311.6396, 1320.6768, 1334.6930, 1334.6930, 1366.7074, 1367.6774, 1383.6606, 1384.7648, 1384.7648, 1427.7333, 1430.7317, 1431.7069, 1447.7339, 1448.7404, 1448.7404, 1462.7825, 1467.7362, 1488.6875, 1508.7031, 1524.7134, 1573.8041, 1686.7777, 1686.7777, 1701.9031, 1883.9982, 1886.9141, 2016.0723, 2673.3201, 2673.3201, 2940.4924 |

|  |  |
| --- | --- |
| **5.** | [gi|13625911|gb|AAK35200.1|AF352715\_1](http://msmsms/mascot/cgi/protein_view.pl?file=../data/20120113/F018130.dat&hit=5" \t "_blank)    **Mass:** 9724     **Score:** 122    **Expect:** 2.2e-008  **Matches:** 2 |
|  | activation associated secreted protein-like protein [Cooperia punctata] |

|  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | **Observed** | **Mr(expt)** | **Mr(calc)** | **ppm** | **Start** |  | **End** | **Miss** | **Ions** | **Peptide** |
|  | 1686.7777 | 1685.7704 | 1685.7685 | 1.13 | 44 | - | 57 | 0 | --- | K.AAESSVYDWFNEIR.K |
|  | 1686.7777 | 1685.7704 | 1685.7685 | 1.13 | 44 | - | 57 | 0 | 117 | K.AAESSVYDWFNEIR.K |

|  |  |
| --- | --- |
|  | **No match to:** 901.4799, 917.4655, 934.4561, 944.5021, 950.4550, 959.4774, 985.5931, 1003.5372, 1019.5316, 1035.5262, 1036.5310, 1036.5310, 1052.5254, 1097.5887, 1098.5793, 1100.6066, 1115.5808, 1115.5808, 1228.6597, 1228.6597, 1231.5714, 1259.6527, 1311.6396, 1320.6768, 1332.6744, 1334.6930, 1334.6930, 1354.6582, 1366.7074, 1367.6774, 1383.6606, 1384.7648, 1384.7648, 1427.7333, 1430.7317, 1431.7069, 1447.7339, 1448.7404, 1448.7404, 1462.7825, 1467.7362, 1476.7115, 1488.6875, 1492.6952, 1508.7031, 1524.7134, 1573.8041, 1701.9031, 1883.9982, 1886.9141, 2016.0723, 2181.1772, 2181.1772, 2373.1367, 2373.1367, 2673.3201, 2673.3201, 2940.4924 |

|  |  |
| --- | --- |
| **6.** | [gi|13625881|gb|AAK35185.1|AF352700\_1](http://msmsms/mascot/cgi/protein_view.pl?file=../data/20120113/F018130.dat&hit=6" \t "_blank)    **Mass:** 27510    **Score:** 107    **Expect:** 6.9e-007  **Matches:** 8 |
|  | activation associated secreted protein-like protein [Cooperia punctata] |

|  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | **Observed** | **Mr(expt)** | **Mr(calc)** | **ppm** | **Start** |  | **End** | **Miss** | **Ions** | **Peptide** |
|  | 1332.6744 | 1331.6671 | 1331.6622 | 3.66 | 173 | - | 183 | 0 | --- | K.TGHYSQVVWQK.S |
|  | 1384.7648 | 1383.7575 | 1383.6558 | 73.5 | 146 | - | 156 | 0 | --- | R.SVDDWYIELTK.Y + Oxidation (HW) |
|  | 1384.7648 | 1383.7575 | 1383.6558 | 73.5 | 146 | - | 156 | 0 | --- | R.SVDDWYIELTK.Y + Oxidation (HW) |
|  | 1448.7404 | 1447.7331 | 1447.7208 | 8.52 | 61 | - | 71 | 1 | --- | R.QVFLDKHNEYR.Q |
|  | 1448.7404 | 1447.7331 | 1447.7208 | 8.52 | 61 | - | 71 | 1 | 88 | R.QVFLDKHNEYR.Q |
|  | 1524.7134 | 1523.7061 | 1523.7620 | -36.67 | 145 | - | 156 | 1 | --- | K.RSVDDWYIELTK.Y |
|  | 1883.9982 | 1882.9909 | 1882.9148 | 40.4 | 199 | - | 214 | 1 | --- | R.RLYVGCEYWPGGNTLR.H |
|  | 2016.0723 | 2015.0650 | 2015.0701 | -2.50 | 61 | - | 76 | 2 | --- | R.QVFLDKHNEYRQLVAR.G |

|  |  |
| --- | --- |
|  | **No match to:** 901.4799, 917.4655, 934.4561, 944.5021, 950.4550, 959.4774, 985.5931, 1003.5372, 1019.5316, 1035.5262, 1036.5310, 1036.5310, 1052.5254, 1097.5887, 1098.5793, 1100.6066, 1115.5808, 1115.5808, 1228.6597, 1228.6597, 1231.5714, 1259.6527, 1311.6396, 1320.6768, 1334.6930, 1334.6930, 1354.6582, 1366.7074, 1367.6774, 1383.6606, 1427.7333, 1430.7317, 1431.7069, 1447.7339, 1462.7825, 1467.7362, 1476.7115, 1488.6875, 1492.6952, 1508.7031, 1573.8041, 1686.7777, 1686.7777, 1701.9031, 1886.9141, 2181.1772, 2181.1772, 2373.1367, 2373.1367, 2673.3201, 2673.3201, 2940.4924 |

|  |  |
| --- | --- |
| **7.** | [contig05709](http://msmsms/mascot/cgi/protein_view.pl?file=../data/20120113/F018130.dat&hit=7" \t "_blank)    **Mass:** 23725    **Score:** 105    **Expect:** 1.1e-006  **Matches:** 6 |
|  | putative nuclear encoded protein Method: similarity and extension |

|  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | **Observed** | **Mr(expt)** | **Mr(calc)** | **ppm** | **Start** |  | **End** | **Miss** | **Ions** | **Peptide** |
|  | 1311.6396 | 1310.6323 | 1310.6255 | 5.19 | 133 | - | 143 | 0 | --- | R.YGVPQDNVYTR.D |
|  | 1320.6768 | 1319.6695 | 1319.6622 | 5.54 | 37 | - | 46 | 1 | --- | K.VFLDKHNEYR.S |
|  | 1448.7404 | 1447.7331 | 1447.7572 | -16.61 | 36 | - | 46 | 2 | --- | R.KVFLDKHNEYR.S |
|  | 1448.7404 | 1447.7331 | 1447.7572 | -16.61 | 36 | - | 46 | 2 | 88 | R.KVFLDKHNEYR.S |
|  | 1467.7362 | 1466.7289 | 1466.7266 | 1.57 | 132 | - | 143 | 1 | --- | R.RYGVPQDNVYTR.D |
|  | 1883.9982 | 1882.9909 | 1882.9901 | 0.43 | 47 | - | 65 | 1 | --- | R.SLVAKGQAPNPQFGGSTPK.A |

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| --- | --- |
|  | **No match to:** 901.4799, 917.4655, 934.4561, 944.5021, 950.4550, 959.4774, 985.5931, 1003.5372, 1019.5316, 1035.5262, 1036.5310, 1036.5310, 1052.5254, 1097.5887, 1098.5793, 1100.6066, 1115.5808, 1115.5808, 1228.6597, 1228.6597, 1231.5714, 1259.6527, 1332.6744, 1334.6930, 1334.6930, 1354.6582, 1366.7074, 1367.6774, 1383.6606, 1384.7648, 1384.7648, 1427.7333, 1430.7317, 1431.7069, 1447.7339, 1462.7825, 1476.7115, 1488.6875, 1492.6952, 1508.7031, 1524.7134, 1573.8041, 1686.7777, 1686.7777, 1701.9031, 1886.9141, 2016.0723, 2181.1772, 2181.1772, 2373.1367, 2373.1367, 2673.3201, 2673.3201, 2940.4924 |

|  |  |
| --- | --- |
| **8.** | [gi|13625879|gb|AAK35184.1|AF352699\_1](http://msmsms/mascot/cgi/protein_view.pl?file=../data/20120113/F018130.dat&hit=8" \t "_blank)    **Mass:** 25808    **Score:** 100    **Expect:** 3.8e-006  **Matches:** 8 |
|  | activation associated secreted protein-like protein [Cooperia punctata] |

|  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | **Observed** | **Mr(expt)** | **Mr(calc)** | **ppm** | **Start** |  | **End** | **Miss** | **Ions** | **Peptide** |
|  | 1332.6744 | 1331.6671 | 1331.6622 | 3.66 | 156 | - | 166 | 0 | --- | K.TGHYSQVVWQK.S |
|  | 1384.7648 | 1383.7575 | 1383.6558 | 73.5 | 129 | - | 139 | 0 | --- | R.SVDDWYIELTK.Y + Oxidation (HW) |
|  | 1384.7648 | 1383.7575 | 1383.6558 | 73.5 | 129 | - | 139 | 0 | --- | R.SVDDWYIELTK.Y + Oxidation (HW) |
|  | 1448.7404 | 1447.7331 | 1447.7208 | 8.52 | 44 | - | 54 | 1 | --- | R.QVFLDKHNEYR.Q |
|  | 1448.7404 | 1447.7331 | 1447.7208 | 8.52 | 44 | - | 54 | 1 | 88 | R.QVFLDKHNEYR.Q |
|  | 1524.7134 | 1523.7061 | 1523.7620 | -36.67 | 128 | - | 139 | 1 | --- | K.RSVDDWYIELTK.Y |
|  | 1573.8041 | 1572.7968 | 1572.8195 | -14.41 | 94 | - | 108 | 2 | --- | K.TCKGGHSPFSVLKGR.G |
|  | 2016.0723 | 2015.0650 | 2015.0701 | -2.50 | 44 | - | 59 | 2 | --- | R.QVFLDKHNEYRQLVAR.G |

|  |  |
| --- | --- |
|  | **No match to:** 901.4799, 917.4655, 934.4561, 944.5021, 950.4550, 959.4774, 985.5931, 1003.5372, 1019.5316, 1035.5262, 1036.5310, 1036.5310, 1052.5254, 1097.5887, 1098.5793, 1100.6066, 1115.5808, 1115.5808, 1228.6597, 1228.6597, 1231.5714, 1259.6527, 1311.6396, 1320.6768, 1334.6930, 1334.6930, 1354.6582, 1366.7074, 1367.6774, 1383.6606, 1427.7333, 1430.7317, 1431.7069, 1447.7339, 1462.7825, 1467.7362, 1476.7115, 1488.6875, 1492.6952, 1508.7031, 1686.7777, 1686.7777, 1701.9031, 1883.9982, 1886.9141, 2181.1772, 2181.1772, 2373.1367, 2373.1367, 2673.3201, 2673.3201, 2940.4924 |

|  |  |
| --- | --- |
| **9.** | [gi|13625877|gb|AAK35183.1|AF352698\_1](http://msmsms/mascot/cgi/protein_view.pl?file=../data/20120113/F018130.dat&hit=9" \t "_blank)    **Mass:** 27540    **Score:** 97     **Expect:** 6.3e-006  **Matches:** 5 |
|  | activation associated secreted protein-like protein [Cooperia punctata] |

|  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | **Observed** | **Mr(expt)** | **Mr(calc)** | **ppm** | **Start** |  | **End** | **Miss** | **Ions** | **Peptide** |
|  | 1332.6744 | 1331.6671 | 1331.6622 | 3.66 | 173 | - | 183 | 0 | --- | K.TGHYSQVVWQK.S |
|  | 1448.7404 | 1447.7331 | 1447.7208 | 8.52 | 61 | - | 71 | 1 | --- | R.QVFLDKHNEYR.Q |
|  | 1448.7404 | 1447.7331 | 1447.7208 | 8.52 | 61 | - | 71 | 1 | 88 | R.QVFLDKHNEYR.Q |
|  | 1883.9982 | 1882.9909 | 1882.9148 | 40.4 | 199 | - | 214 | 1 | --- | R.RLYVGCEYWPGGNTLR.H |
|  | 2016.0723 | 2015.0650 | 2015.0701 | -2.50 | 61 | - | 76 | 2 | --- | R.QVFLDKHNEYRQLVAR.G |

|  |  |
| --- | --- |
|  | **No match to:** 901.4799, 917.4655, 934.4561, 944.5021, 950.4550, 959.4774, 985.5931, 1003.5372, 1019.5316, 1035.5262, 1036.5310, 1036.5310, 1052.5254, 1097.5887, 1098.5793, 1100.6066, 1115.5808, 1115.5808, 1228.6597, 1228.6597, 1231.5714, 1259.6527, 1311.6396, 1320.6768, 1334.6930, 1334.6930, 1354.6582, 1366.7074, 1367.6774, 1383.6606, 1384.7648, 1384.7648, 1427.7333, 1430.7317, 1431.7069, 1447.7339, 1462.7825, 1467.7362, 1476.7115, 1488.6875, 1492.6952, 1508.7031, 1524.7134, 1573.8041, 1686.7777, 1686.7777, 1701.9031, 1886.9141, 2181.1772, 2181.1772, 2373.1367, 2373.1367, 2673.3201, 2673.3201, 2940.4924 |

**http://msmsms/mascot/images/88x31_logo_white.gifMascot Search Results**

**Protein View**

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Match to: **contig63173** Score: **245** Expect: **1.1e-020**

**putative nuclear encoded protein Method: similarity and extension**

Nominal mass (Mr): **22462**; Calculated pI value: **9.65**

NCBI BLAST search of [contig63173](http://www.ncbi.nlm.nih.gov/blast/Blast.cgi?ALIGNMENTS=50&ALIGNMENT_VIEW=Pairwise&AUTO_FORMAT=Semiauto&CDD_SEARCH=on&CLIENT=web&COMPOSITION_BASED_STATISTICS=on&DATABASE=nr&DESCRIPTIONS=100&ENTREZ_QUERY=(none)&EXPECT=10&FILTER=L&FORMAT_BLOCK_ON_RESPAGE=None&FORMAT_OBJECT=Alignment&FORMAT_TYPE=HTML&GAPCOSTS=11+1&I_THRESH=0.001&LAYOUT=TwoWindows&MATRIX_NAME=BLOSUM62&NCBI_GI=on&PAGE=Proteins&PROGRAM=blastp&QUERY=KEALCVPPGETKPASTATTTTKTTTKTTTTTTKPSTTTTKATTTTTRPTTTTTKPTTTTAKPTTTFNRAAWEESVKRPVAHCTVNKNGMTDKVRQVFLDKHNEYRQIVARGEAKNKTGLAPPAARMLQMRYDCDLEAHVMEHLVKCKGGHSSFQVLKGRGQNIWGITVPNLDKAEAAKRSVDDWYIEVTKYGITADNKISMENAA&SERVICE=plain&SET_DEFAULTS.x=9&SET_DEFAULTS.y=5&SHOW_OVERVIEW=on&WORD_SIZE=3&END_OF_HTTPGET=Yes" \t "_blank) against nr

Unformatted [sequence string](http://msmsms/mascot/cgi/getseq.pl?cooperia_oncophora+contig63173+seq" \t "_blank) for pasting into other applications

Variable modifications: Oxidation (HW),Oxidation (M)

Cleavage by Trypsin/P: cuts C-term side of KR

Sequence Coverage: **35%**

Matched peptides shown in **Bold Red**

**1** KEALCVPPGE TKPASTATTT TKTTTKTTTT TTK**PSTTTTK ATTTTTR**PTT

**51** TTTKPTTTTA KPTTTFNRAA WEESVKRPVA HCTVNKNGMT DKVR**QVFLDK**

**101 HNEYRQIVAR GEAK**NKTGLA PPAARMLQMR YDCDLEAHVM EHLVKCKGGH

**151** SSFQVLKGR**G QNIWGITVPN LDKAEAAKRS VDDWYIEVTK YGITADNK**IS

**201** MENAA



  Residue Number  Increasing Mass  Decreasing Mass

**Start - End Observed Mr(expt) Mr(calc) ppm Miss Sequence**

**34 - 47 1467.7362 1466.7289 1466.7577 -20 1 K.PSTTTTKATTTTTR.P**  ([No match](http://msmsms/mascot/cgi/peptide_view.pl?file=../data/20120113/F018130.dat&query=41&hit=1" \t "_blank))

**95 - 105 1448.7404 1447.7331 1447.7208 9 1 R.QVFLDKHNEYR.Q**  ([No match](http://msmsms/mascot/cgi/peptide_view.pl?file=../data/20120113/F018130.dat&query=38&hit=1" \t "_blank))

**95 - 105 1448.7404 1447.7331 1447.7208 9 1 R.QVFLDKHNEYR.Q**  ([Ions score 88](http://msmsms/mascot/cgi/peptide_view.pl?file=../data/20120113/F018130.dat&query=39&hit=1" \t "_blank))

**95 - 110 2016.0723 2015.0650 2015.0701 -3 2 R.QVFLDKHNEYRQIVAR.G**  ([No match](http://msmsms/mascot/cgi/peptide_view.pl?file=../data/20120113/F018130.dat&query=53&hit=1" \t "_blank))

**101 - 114 1686.7777 1685.7704 1685.8597 -53 2 K.HNEYRQIVARGEAK.N**  Oxidation (HW) ([No match](http://msmsms/mascot/cgi/peptide_view.pl?file=../data/20120113/F018130.dat&query=48&hit=1" \t "_blank))

**101 - 114 1686.7777 1685.7704 1685.8597 -53 2 K.HNEYRQIVARGEAK.N**  Oxidation (HW) ([No match](http://msmsms/mascot/cgi/peptide_view.pl?file=../data/20120113/F018130.dat&query=49&hit=1" \t "_blank))

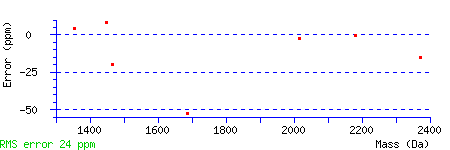
**160 - 179 2181.1772 2180.1699 2180.1702 -0 2 R.GQNIWGITVPNLDKAEAAKR.S**  ([No match](http://msmsms/mascot/cgi/peptide_view.pl?file=../data/20120113/F018130.dat&query=54&hit=1" \t "_blank))

**160 - 179 2181.1772 2180.1699 2180.1702 -0 2 R.GQNIWGITVPNLDKAEAAKR.S**  ([Ions score 140](http://msmsms/mascot/cgi/peptide_view.pl?file=../data/20120113/F018130.dat&query=55&hit=1" \t "_blank))

**179 - 198 2373.1367 2372.1294 2372.1648 -15 2 K.RSVDDWYIEVTKYGITADNK.I**  ([No match](http://msmsms/mascot/cgi/peptide_view.pl?file=../data/20120113/F018130.dat&query=56&hit=1" \t "_blank))

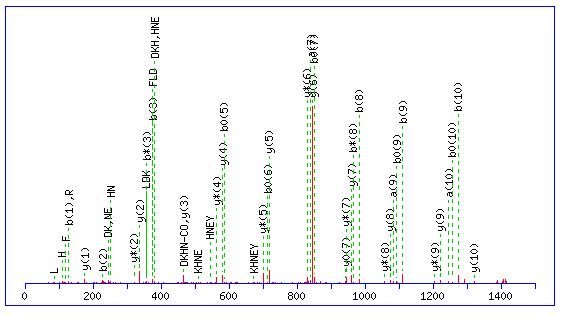
**179 - 198 2373.1367 2372.1294 2372.1648 -15 2 K.RSVDDWYIEVTKYGITADNK.I**  ([No match](http://msmsms/mascot/cgi/peptide_view.pl?file=../data/20120113/F018130.dat&query=57&hit=1" \t "_blank))

**180 - 190 1354.6582 1353.6509 1353.6452 4 0 R.SVDDWYIEVTK.Y**  ([No match](http://msmsms/mascot/cgi/peptide_view.pl?file=../data/20120113/F018130.dat&query=28&hit=1" \t "_blank))



Bottom of Form

🡪 Annotated MS2 spectrum for peptide QVFLDKHNEYR



**Monoisotopic mass of neutral peptide Mr(calc):** 1447.7208

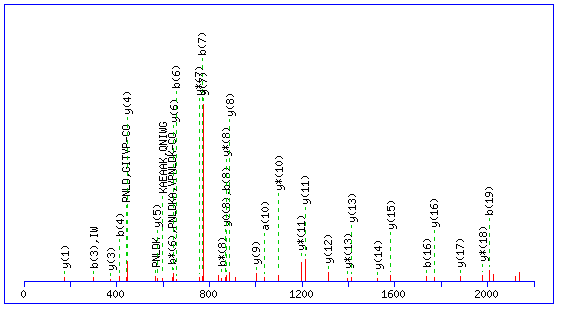
**Ions Score:** 88 **Expect:** 1.5e-007

**Matches :** 49/160 fragment ions using 54 most intense peaks   ([help](http://msmsms/mascot/help/results_help.html" \l "PEP" \t "_blank))

|  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **#** | **Immon.** | **a** | **a\*** | **a0** | **b** | **b\*** | **b0** | **Seq.** | **v** | **w** | **y** | **y\*** | **y0** | **#** |
| **1** | 101.0709 | 101.0709 | 84.0444 |  | **129.0659** | 112.0393 |  | **Q** |  |  |  |  |  | **11** |
| **2** | 72.0808 | 200.1394 | 183.1128 |  | **228.1343** | 211.1077 |  | **V** | 1276.6069 | 1289.6273 | ***1320.6695*** | 1303.6430 | 1302.6589 | **10** |
| **3** | 120.0808 | 347.2078 | 330.1812 |  | **375.2027** | 358.1761 |  | **F** | 1129.5385 |  | ***1221.6011*** | 1204.5745 | 1203.5905 | **9** |
| **4** | 86.0964 | 460.2918 | 443.2653 |  | 488.2867 | 471.2602 |  | **L** | 1016.4544 | 1015.4592 | ***1074.5327*** | 1057.5061 | 1056.5221 | **8** |
| **5** | 88.0393 | 575.3188 | 558.2922 | 557.3082 | 603.3137 | 586.2871 | 585.3031 | **D** | 901.4275 | 900.4322 | ***961.4486*** | 944.4221 | 943.4381 | **7** |
| **6** | 101.1073 | 703.4137 | 686.3872 | 685.4032 | 731.4087 | 714.3821 | 713.3981 | **K** | 773.3325 | 772.3373 | ***846.4217*** | 829.3951 | 828.4111 | **6** |
| **7** | 110.0713 | **840.4726** | 823.4461 | 822.4621 | 868.4676 | 851.4410 | 850.4570 | **H** | 636.2736 |  | ***718.3267*** | 701.3002 | 700.3161 | **5** |
| **8** | 87.0553 | 954.5156 | 937.4890 | 936.5050 | **982.5105** | 965.4839 | 964.4999 | **N** | 522.2307 | 521.2354 | ***581.2678*** | 564.2413 | 563.2572 | **4** |
| **9** | 102.0550 | **1083.5582** | 1066.5316 | 1065.5476 | **1111.5531** | 1094.5265 | 1093.5425 | **E** | 393.1881 | 392.1928 | ***467.2249*** | 450.1983 | 449.2143 | **3** |
| **10** | 136.0757 | **1246.6215** | 1229.5949 | 1228.6109 | **1274.6164** | 1257.5899 | 1256.6058 | **Y** | 230.1248 |  | ***338.1823*** | 321.1557 |  | **2** |
| **11** | 129.1135 |  |  |  |  |  |  | **R** | 74.0237 | 73.0284 | ***175.1190*** | 158.0924 |  | **1** |

|  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **Seq** | **ya** | **yb** | **Seq** | **ya** | **yb** | **Seq** | **ya** | **yb** |
| **VF** | 219.1492 | 247.1441 | **VFL** | 332.2333 | 360.2282 | **VFLD** | 447.2602 | 475.2551 |
| **VFLDK** | 575.3552 | 603.3501 | **FL** | 233.1648 | 261.1598 | **FLD** | 348.1918 | 376.1867 |
| **FLDK** | 476.2867 | 504.2817 | **FLDKH** | 613.3457 | 641.3406 | **LD** | 201.1234 | 229.1183 |
| **LDK** | 329.2183 | 357.2132 | **LDKH** | 466.2772 | 494.2722 | **LDKHN** | 580.3202 | 608.3151 |
| **DK** | 216.1343 | 244.1292 | **DKH** | 353.1932 | 381.1881 | **DKHN** | 467.2361 | 495.2310 |
| **DKHNE** | 596.2787 | 624.2736 | **KH** | 238.1662 | 266.1612 | **KHN** | 352.2092 | 380.2041 |
| **KHNE** | 481.2518 | 509.2467 | **KHNEY** | 644.3151 | 672.3100 | **HN** | 224.1142 | 252.1091 |
| **HNE** | 353.1568 | 381.1517 | **HNEY** | 516.2201 | 544.2150 | **NE** | 216.0979 | 244.0928 |
| **NEY** | 379.1612 | 407.1561 | **EY** | 265.1183 | 293.1132 |  |  |  |

🡪 Annotated MS2 spectrum for peptide GQNIWGITVPNLDKAEAAKR



**Monoisotopic mass of neutral peptide Mr(calc):** 2180.1702

**Ions Score:** 140 **Expect:** 7.4e-013

**Matches :** 42/360 fragment ions using 40 most intense peaks   ([help](http://msmsms/mascot/help/results_help.html" \l "PEP" \t "_blank))

|  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **#** | **Immon.** | **a** | **a\*** | **a0** | **b** | **b\*** | **b0** | **Seq.** | **v** | **w** | **w'** | **y** | **y\*** | **y0** | **#** |
| **1** | 30.0338 | 30.0338 |  |  | 58.0287 |  |  | **G** |  |  |  |  |  |  | **20** |
| **2** | 101.0709 | 158.0924 | 141.0659 |  | 186.0873 | 169.0608 |  | **Q** | 2051.1032 | 2050.1080 |  | 2124.1560 | 2107.1295 | 2106.1454 | **19** |
| **3** | 87.0553 | 272.1353 | 255.1088 |  | **300.1302** | 283.1037 |  | **N** | 1937.0603 | 1936.0651 |  | 1996.0974 | 1979.0709 | 1978.0869 | **18** |
| **4** | 86.0964 | 385.2194 | 368.1928 |  | **413.2143** | 396.1878 |  | **I** | 1823.9763 | 1836.9967 | 1851.0123 | ***1882.0545*** | 1865.0280 | 1864.0439 | **17** |
| **5** | 159.0917 | 571.2987 | 554.2722 |  | **599.2936** | 582.2671 |  | **W** | 1637.8969 |  |  | ***1768.9704*** | 1751.9439 | 1750.9599 | **16** |
| **6** | 30.0338 | 628.3202 | 611.2936 |  | **656.3151** | 639.2885 |  | **G** |  |  |  | ***1582.8911*** | 1565.8646 | 1564.8806 | **15** |
| **7** | 86.0964 | 741.4042 | 724.3777 |  | **769.3992** | 752.3726 |  | **I** | 1467.7914 | 1480.8118 | 1494.8275 | ***1525.8697*** | 1508.8431 | 1507.8591 | **14** |
| **8** | 74.0600 | 842.4519 | 825.4254 | 824.4413 | **870.4468** | 853.4203 | 852.4363 | **T** | 1366.7437 | 1379.7641 | 1381.7434 | ***1412.7856*** | 1395.7591 | 1394.7750 | **13** |
| **9** | 72.0808 | 941.5203 | 924.4938 | 923.5098 | 969.5152 | 952.4887 | 951.5047 | **V** | 1267.6753 | 1280.6957 |  | ***1311.7379*** | 1294.7114 | 1293.7274 | **12** |
| **10** | 70.0651 | 1038.5731 | 1021.5465 | 1020.5625 | 1066.5680 | 1049.5415 | 1048.5574 | **P** | 1170.6226 | 1169.6273 |  | ***1212.6695*** | 1195.6430 | 1194.6589 | **11** |
| **11** | 87.0553 | 1152.6160 | 1135.5895 | 1134.6055 | 1180.6109 | 1163.5844 | 1162.6004 | **N** | 1056.5796 | 1055.5844 |  | 1115.6167 | 1098.5902 | 1097.6062 | **10** |
| **12** | 86.0964 | 1265.7001 | 1248.6735 | 1247.6895 | 1293.6950 | 1276.6684 | 1275.6844 | **L** | 943.4956 | 942.5003 |  | ***1001.5738*** | 984.5473 | 983.5633 | **9** |
| **13** | 88.0393 | 1380.7270 | 1363.7005 | 1362.7165 | 1408.7219 | 1391.6954 | 1390.7114 | **D** | 828.4686 | 827.4734 |  | ***888.4898*** | 871.4632 | 870.4792 | **8** |
| **14** | 101.1073 | 1508.8220 | 1491.7954 | 1490.8114 | 1536.8169 | 1519.7904 | 1518.8063 | **K** | 700.3737 | 699.3784 |  | ***773.4628*** | 756.4363 | 755.4522 | **7** |
| **15** | 44.0495 | 1579.8591 | 1562.8326 | 1561.8485 | 1607.8540 | 1590.8275 | 1589.8435 | **A** | 629.3365 |  |  | ***645.3678*** | 628.3413 | 627.3573 | **6** |
| **16** | 102.0550 | 1708.9017 | 1691.8751 | 1690.8911 | **1736.8966** | 1719.8701 | 1718.8860 | **E** | 500.2940 | 499.2987 |  | ***574.3307*** | 557.3042 | 556.3202 | **5** |
| **17** | 44.0495 | 1779.9388 | 1762.9123 | 1761.9282 | 1807.9337 | 1790.9072 | 1789.9232 | **A** | 429.2568 |  |  | ***445.2881*** | 428.2616 |  | **4** |
| **18** | 44.0495 | 1850.9759 | 1833.9494 | 1832.9654 | 1878.9708 | 1861.9443 | 1860.9603 | **A** | 358.2197 |  |  | ***374.2510*** | 357.2245 |  | **3** |
| **19** | 101.1073 | 1979.0709 | 1962.0443 | 1961.0603 | **2007.0658** | 1990.0393 | 1989.0552 | **K** | 230.1248 | 229.1295 |  | 303.2139 | 286.1874 |  | **2** |
| **20** | 129.1135 |  |  |  |  |  |  | **R** | 74.0237 | 73.0284 |  | ***175.1190*** | 158.0924 |  | **1** |

|  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **Seq** | **ya** | **yb** | **Seq** | **ya** | **yb** | **Seq** | **ya** | **yb** |
| **QN** | 215.1139 | 243.1088 | **QNI** | 328.1979 | 356.1928 | **QNIW** | 514.2772 | 542.2722 |
| **QNIWG** | 571.2987 | 599.2936 | **QNIWGI** | 684.3828 | 712.3777 | **NI** | 200.1394 | 228.1343 |
| **NIW** | 386.2187 | 414.2136 | **NIWG** | 443.2401 | 471.2350 | **NIWGI** | 556.3242 | 584.3191 |
| **NIWGIT** | 657.3719 | 685.3668 | **IW** | 272.1757 | 300.1707 | **IWG** | 329.1972 | 357.1921 |
| **IWGI** | 442.2813 | 470.2762 | **IWGIT** | 543.3289 | 571.3239 | **IWGITV** | 642.3974 | 670.3923 |
| **WG** | 216.1131 | 244.1081 | **WGI** | 329.1972 | 357.1921 | **WGIT** | 430.2449 | 458.2398 |
| **WGITV** | 529.3133 | 557.3082 | **WGITVP** | 626.3661 | 654.3610 | **GI** | 143.1179 | 171.1128 |
| **GIT** | 244.1656 | 272.1605 | **GITV** | 343.2340 | 371.2289 | **GITVP** | 440.2867 | 468.2817 |
| **GITVPN** | 554.3297 | 582.3246 | **GITVPNL** | 667.4137 | 695.4087 | **IT** | 187.1441 | 215.1390 |
| **ITV** | 286.2125 | 314.2074 | **ITVP** | 383.2653 | 411.2602 | **ITVPN** | 497.3082 | 525.3031 |
| **ITVPNL** | 610.3923 | 638.3872 | **TV** | 173.1285 | 201.1234 | **TVP** | 270.1812 | 298.1761 |
| **TVPN** | 384.2241 | 412.2191 | **TVPNL** | 497.3082 | 525.3031 | **TVPNLD** | 612.3352 | 640.3301 |
| **VP** | 169.1335 | 197.1285 | **VPN** | 283.1765 | 311.1714 | **VPNL** | 396.2605 | 424.2554 |
| **VPNLD** | 511.2875 | 539.2824 | **VPNLDK** | 639.3824 | 667.3774 | **PN** | 184.1081 | 212.1030 |
| **PNL** | 297.1921 | 325.1870 | **PNLD** | 412.2191 | 440.2140 | **PNLDK** | 540.3140 | 568.3089 |
| **PNLDKA** | 611.3511 | 639.3461 | **NL** | 200.1394 | 228.1343 | **NLD** | 315.1663 | 343.1612 |
| **NLDK** | 443.2613 | 471.2562 | **NLDKA** | 514.2984 | 542.2933 | **NLDKAE** | 643.3410 | 671.3359 |
| **LD** | 201.1234 | 229.1183 | **LDK** | 329.2183 | 357.2132 | **LDKA** | 400.2554 | 428.2504 |
| **LDKAE** | 529.2980 | 557.2930 | **LDKAEA** | 600.3352 | 628.3301 | **LDKAEAA** | 671.3723 | 699.3672 |
| **DK** | 216.1343 | 244.1292 | **DKA** | 287.1714 | 315.1663 | **DKAE** | 416.2140 | 444.2089 |
| **DKAEA** | 487.2511 | 515.2460 | **DKAEAA** | 558.2882 | 586.2831 | **DKAEAAK** | 686.3832 | 714.3781 |
| **KA** | 172.1444 | 200.1394 | **KAE** | 301.1870 | 329.1819 | **KAEA** | 372.2241 | 400.2191 |
| **KAEAA** | 443.2613 | 471.2562 | **KAEAAK** | 571.3562 | 599.3511 | **AE** | 173.0921 | 201.0870 |
| **AEA** | 244.1292 | 272.1241 | **AEAA** | 315.1663 | 343.1612 | **AEAAK** | 443.2613 | 471.2562 |
| **EA** | 173.0921 | 201.0870 | **EAA** | 244.1292 | 272.1241 | **EAAK** | 372.2241 | 400.2191 |
| **AA** | 115.0866 | 143.0815 | **AAK** | 243.1816 | 271.1765 | **AK** | 172.1444 | 200.1394 |

**Band 3:**

**http://msmsms/mascot/images/88x31_logo_white.gifMascot Search Results**

**User :**

**Email :**

**Search title : SampleSetID: 683, AnalysisID: 1071, MaldiWellID: 82747, SpectrumID: 217095, Path=\Jimmy\Cooperia 3\Co ES Conc 3 Frac 13012012 (strict)**

**Database : cooperia\_oncophora oncophora\_20110405 (34373 sequences; 5289600 residues)**

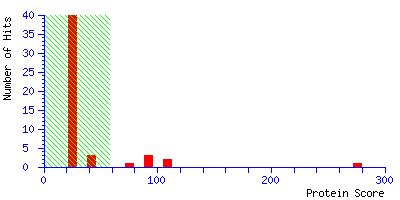
**Timestamp : 13 Jan 2012 at 14:32:43 GMT**

**Warning : A Peptide summary report will usually give a much clearer picture of MS/MS search results.**

**Top Score : 276 for contig05709, putative nuclear encoded protein Method: similarity and extension**

**Mascot Score Histogram**

Protein score is -10\*Log(P), where P is the probability that the observed match is a random event.  
Protein scores greater than 58 are significant (p<0.05).  
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Top of Form



**Protein Summary Report**

|  |  |  |  |
| --- | --- | --- | --- |
|  |  |  | [Help](http://msmsms/mascot/help/msms_summaries_help.html" \t "_blank) |
|  | Significance threshold p< | Max. number of hits |  |

Bottom of Form

Top of Form





Bottom of Form

**Index**

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
|  | **Accession** | **Mass** | **Score** | **Description** |
| **1.** | [**contig05709**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20120113/F018131.dat#Hit1) | 23725 | 276 | putative nuclear encoded protein Method: similarity and extension |
| **2.** | [**gi|13625881|gb|AAK35185.1|AF352700\_1**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20120113/F018131.dat#Hit2) | 27510 | 102 | activation associated secreted protein-like protein [Cooperia punctata] |
| **3.** | [**gi|13625909|gb|AAK35199.1|AF352714\_1**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20120113/F018131.dat#Hit3) | 51596 | 101 | activation associated secreted protein-like protein [Cooperia punctata] |
| **4.** | [**gi|13625879|gb|AAK35184.1|AF352699\_1**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20120113/F018131.dat#Hit4) | 25808 | 99 | activation associated secreted protein-like protein [Cooperia punctata] |
| **5.** | [**contig63173**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20120113/F018131.dat#Hit5) | 22462 | 97 | putative nuclear encoded protein Method: similarity and extension |
| **6.** | [**gi|13625877|gb|AAK35183.1|AF352698\_1**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20120113/F018131.dat#Hit6) | 27540 | 95 | activation associated secreted protein-like protein [Cooperia punctata] |
| **7.** | [**isotig00099**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20120113/F018131.dat#Hit7) | 12511 | 73 | putative nuclear encoded protein Method: similarity and extension |
| **8.** | [**isotig31853**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20120113/F018131.dat#Hit8) | 21527 | 38 | putative nuclear encoded protein Method: ESTScan |
| **9.** | [**isotig25613**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20120113/F018131.dat#Hit9) | 11649 | 35 | putative nuclear encoded protein Method: Longest ORF |
| **10.** | [**isotig19705**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20120113/F018131.dat#Hit10) | 14597 | 35 | putative nuclear encoded protein Method: similarity and extension |
| **11.** | [**isotig11704**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20120113/F018131.dat#Hit11) | 24236 | 33 | putative nuclear encoded protein Method: similarity and extension |
| **12.** | [**isotig11702**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20120113/F018131.dat#Hit12) | 24222 | 33 | putative nuclear encoded protein Method: similarity and extension |
| **13.** | [**isotig20235**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20120113/F018131.dat#Hit13) | 11486 | 33 | putative nuclear encoded protein Method: similarity and extension |
| **14.** | [**isotig10344**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20120113/F018131.dat#Hit14) | 6461 | 32 | putative nuclear encoded protein Method: Longest ORF |
| **15.** | [**isotig24071**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20120113/F018131.dat#Hit15) | 8570 | 31 | putative nuclear encoded protein Method: similarity and extension |
| **16.** | [**isotig27236**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20120113/F018131.dat#Hit16) | 21555 | 31 | putative nuclear encoded protein Method: similarity and extension |
| **17.** | [**isotig19223**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20120113/F018131.dat#Hit17) | 5943 | 31 | putative nuclear encoded protein Method: Longest ORF |
| **18.** | [**isotig04036**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20120113/F018131.dat#Hit18) | 19278 | 31 | putative nuclear encoded protein Method: ESTScan |
| **19.** | [**isotig16444**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20120113/F018131.dat#Hit19) | 13936 | 30 | putative nuclear encoded protein Method: Longest ORF |
| **20.** | [**isotig30720**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20120113/F018131.dat#Hit20) | 8724 | 30 | putative nuclear encoded protein Method: Longest ORF |

**Results List**

|  |  |
| --- | --- |
| **1.** | [contig05709](http://msmsms/mascot/cgi/protein_view.pl?file=../data/20120113/F018131.dat&hit=1" \t "_blank)    **Mass:** 23725    **Score:** 276    **Expect:** 8.6e-024  **Matches:** 11 |
|  | putative nuclear encoded protein Method: similarity and extension |

|  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | **Observed** | **Mr(expt)** | **Mr(calc)** | **ppm** | **Start** |  | **End** | **Miss** | **Ions** | **Peptide** |
|  | 1311.6479 | 1310.6406 | 1310.6255 | 11.5 | 133 | - | 143 | 0 | --- | R.YGVPQDNVYTR.D |
|  | 1311.6479 | 1310.6406 | 1310.6255 | 11.5 | 133 | - | 143 | 0 | 79 | R.YGVPQDNVYTR.D |
|  | 1320.6832 | 1319.6759 | 1319.6622 | 10.4 | 37 | - | 46 | 1 | --- | K.VFLDKHNEYR.S |
|  | 1385.6823 | 1384.6750 | 1384.6735 | 1.07 | 52 | - | 65 | 0 | --- | K.GQAPNPQFGGSTPK.A |
|  | 1396.6498 | 1395.6425 | 1395.6241 | 13.2 | 104 | - | 115 | 0 | --- | R.NTWGMGVPNYNK.T + Oxidation (M) |
|  | 1448.7441 | 1447.7368 | 1447.7572 | -14.05 | 36 | - | 46 | 2 | --- | R.KVFLDKHNEYR.S |
|  | 1448.7441 | 1447.7368 | 1447.7572 | -14.05 | 36 | - | 46 | 2 | 89 | R.KVFLDKHNEYR.S |
|  | 1467.7302 | 1466.7229 | 1466.7266 | -2.52 | 132 | - | 143 | 1 | --- | R.RYGVPQDNVYTR.D |
|  | 1891.8846 | 1890.8773 | 1890.8788 | -0.79 | 116 | - | 131 | 0 | --- | K.TAAAESSVYDWFFELR.R |
|  | 2047.9758 | 2046.9685 | 2046.9799 | -5.57 | 116 | - | 132 | 1 | --- | K.TAAAESSVYDWFFELRR.Y |
|  | 2047.9758 | 2046.9685 | 2046.9799 | -5.57 | 116 | - | 132 | 1 | 73 | K.TAAAESSVYDWFFELRR.Y |

|  |  |
| --- | --- |
|  | **No match to:** 901.4788, 917.4667, 944.5056, 959.4774, 986.4898, 1003.5240, 1019.5211, 1035.5203, 1036.5298, 1046.5328, 1052.5233, 1100.5947, 1115.5746, 1115.5746, 1116.5812, 1156.6023, 1231.5630, 1238.6171, 1259.6561, 1334.6826, 1390.6980, 1390.6980, 1401.6981, 1427.7306, 1430.7336, 1431.7059, 1476.7136, 1498.8071, 1508.7194, 1514.8020, 1524.7190, 1730.7977, 1781.9600, 1886.8986, 1886.8986, 1902.8888, 2011.9779, 2164.9978, 2673.3113, 2673.3113, 2740.2971, 2756.2961, 3027.4219, 3059.4282, 3205.4954, 3205.4954, 3418.6208 |

|  |  |
| --- | --- |
| **2.** | [gi|13625881|gb|AAK35185.1|AF352700\_1](http://msmsms/mascot/cgi/protein_view.pl?file=../data/20120113/F018131.dat&hit=2" \t "_blank)    **Mass:** 27510    **Score:** 102    **Expect:** 2.2e-006  **Matches:** 7 |
|  | activation associated secreted protein-like protein [Cooperia punctata] |

|  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | **Observed** | **Mr(expt)** | **Mr(calc)** | **ppm** | **Start** |  | **End** | **Miss** | **Ions** | **Peptide** |
|  | 1448.7441 | 1447.7368 | 1447.7208 | 11.1 | 61 | - | 71 | 1 | --- | R.QVFLDKHNEYR.Q |
|  | 1448.7441 | 1447.7368 | 1447.7208 | 11.1 | 61 | - | 71 | 1 | 89 | R.QVFLDKHNEYR.Q |
|  | 1524.7190 | 1523.7117 | 1523.7620 | -32.99 | 145 | - | 156 | 1 | --- | K.RSVDDWYIELTK.Y |
|  | 1781.9600 | 1780.9527 | 1780.9584 | -3.19 | 124 | - | 139 | 1 | --- | K.GRGQNIWAITVPNLDK.A |
|  | 2047.9758 | 2046.9685 | 2047.1286 | -78.21 | 72 | - | 91 | 2 | --- | R.QLVARGEAQNKTGLAPPAAR.M |
|  | 2047.9758 | 2046.9685 | 2047.1286 | -78.21 | 72 | - | 91 | 2 | --- | R.QLVARGEAQNKTGLAPPAAR.M |
|  | 3059.4282 | 3058.4209 | 3058.5135 | -30.26 | 146 | - | 172 | 2 | --- | R.SVDDWYIELTKYGITADNKISIDNAAK.T + Oxidation (HW) |

|  |  |
| --- | --- |
|  | **No match to:** 901.4788, 917.4667, 944.5056, 959.4774, 986.4898, 1003.5240, 1019.5211, 1035.5203, 1036.5298, 1046.5328, 1052.5233, 1100.5947, 1115.5746, 1115.5746, 1116.5812, 1156.6023, 1231.5630, 1238.6171, 1259.6561, 1311.6479, 1311.6479, 1320.6832, 1334.6826, 1385.6823, 1390.6980, 1390.6980, 1396.6498, 1401.6981, 1427.7306, 1430.7336, 1431.7059, 1467.7302, 1476.7136, 1498.8071, 1508.7194, 1514.8020, 1730.7977, 1886.8986, 1886.8986, 1891.8846, 1902.8888, 2011.9779, 2164.9978, 2673.3113, 2673.3113, 2740.2971, 2756.2961, 3027.4219, 3205.4954, 3205.4954, 3418.6208 |

|  |  |
| --- | --- |
| **3.** | [gi|13625909|gb|AAK35199.1|AF352714\_1](http://msmsms/mascot/cgi/protein_view.pl?file=../data/20120113/F018131.dat&hit=3" \t "_blank)    **Mass:** 51596    **Score:** 101    **Expect:** 2.7e-006  **Matches:** 12 |
|  | activation associated secreted protein-like protein [Cooperia punctata] |

|  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | **Observed** | **Mr(expt)** | **Mr(calc)** | **ppm** | **Start** |  | **End** | **Miss** | **Ions** | **Peptide** |
|  | 944.5056 | 943.4983 | 943.5749 | -81.16 | 59 | - | 66 | 2 | --- | K.AARMLKVR.Y |
|  | 1334.6826 | 1333.6753 | 1333.6779 | -1.90 | 30 | - | 39 | 1 | --- | K.LFLDKHNEYR.S |
|  | 1396.6498 | 1395.6425 | 1395.6783 | -25.61 | 125 | - | 136 | 1 | --- | R.SYGVPPDNKYTR.N |
|  | 1448.7441 | 1447.7368 | 1447.7208 | 11.1 | 278 | - | 288 | 1 | --- | R.QVFLDKHNEYR.Q |
|  | 1448.7441 | 1447.7368 | 1447.7208 | 11.1 | 278 | - | 288 | 1 | 89 | R.QVFLDKHNEYR.Q |
|  | 1524.7190 | 1523.7117 | 1523.7620 | -32.99 | 362 | - | 373 | 1 | --- | K.RSVDDWYIELTK.Y |
|  | 1781.9600 | 1780.9527 | 1780.9584 | -3.19 | 341 | - | 356 | 1 | --- | K.GRGQNIWAITVPNLDK.A |
|  | 2756.2961 | 2755.2888 | 2755.1426 | 53.1 | 67 | - | 89 | 1 | --- | R.YDCEVEEDMMKWAQAQCAYAPFK.S |
|  | 3027.4219 | 3026.4146 | 3026.3071 | 35.5 | 65 | - | 89 | 2 | --- | K.VRYDCEVEEDMMKWAQAQCAYAPFK.S + Oxidation (M) |
|  | 3059.4282 | 3058.4209 | 3058.5135 | -30.26 | 363 | - | 389 | 2 | --- | R.SVDDWYIELTKYGITADNKISIDNAAK.T + Oxidation (HW) |
|  | 3205.4954 | 3204.4881 | 3204.4636 | 7.66 | 109 | - | 136 | 2 | --- | K.TAAAESSVDDWFDELRSYGVPPDNKYTR.N + Oxidation (HW) |
|  | 3205.4954 | 3204.4881 | 3204.4636 | 7.66 | 109 | - | 136 | 2 | --- | K.TAAAESSVDDWFDELRSYGVPPDNKYTR.N + Oxidation (HW) |

|  |  |
| --- | --- |
|  | **No match to:** 901.4788, 917.4667, 959.4774, 986.4898, 1003.5240, 1019.5211, 1035.5203, 1036.5298, 1046.5328, 1052.5233, 1100.5947, 1115.5746, 1115.5746, 1116.5812, 1156.6023, 1231.5630, 1238.6171, 1259.6561, 1311.6479, 1311.6479, 1320.6832, 1385.6823, 1390.6980, 1390.6980, 1401.6981, 1427.7306, 1430.7336, 1431.7059, 1467.7302, 1476.7136, 1498.8071, 1508.7194, 1514.8020, 1730.7977, 1886.8986, 1886.8986, 1891.8846, 1902.8888, 2011.9779, 2047.9758, 2047.9758, 2164.9978, 2673.3113, 2673.3113, 2740.2971, 3418.6208 |

|  |  |
| --- | --- |
| **4.** | [gi|13625879|gb|AAK35184.1|AF352699\_1](http://msmsms/mascot/cgi/protein_view.pl?file=../data/20120113/F018131.dat&hit=4" \t "_blank)    **Mass:** 25808    **Score:** 99     **Expect:** 4.3e-006  **Matches:** 5 |
|  | activation associated secreted protein-like protein [Cooperia punctata] |

|  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | **Observed** | **Mr(expt)** | **Mr(calc)** | **ppm** | **Start** |  | **End** | **Miss** | **Ions** | **Peptide** |
|  | 1448.7441 | 1447.7368 | 1447.7208 | 11.1 | 44 | - | 54 | 1 | --- | R.QVFLDKHNEYR.Q |
|  | 1448.7441 | 1447.7368 | 1447.7208 | 11.1 | 44 | - | 54 | 1 | 89 | R.QVFLDKHNEYR.Q |
|  | 1524.7190 | 1523.7117 | 1523.7620 | -32.99 | 128 | - | 139 | 1 | --- | K.RSVDDWYIELTK.Y |
|  | 1781.9600 | 1780.9527 | 1780.9584 | -3.19 | 107 | - | 122 | 1 | --- | K.GRGQNIWAITVPNLDK.A |
|  | 3059.4282 | 3058.4209 | 3058.5135 | -30.26 | 129 | - | 155 | 2 | --- | R.SVDDWYIELTKYGITADNKISIDNAAK.T + Oxidation (HW) |

|  |  |
| --- | --- |
|  | **No match to:** 901.4788, 917.4667, 944.5056, 959.4774, 986.4898, 1003.5240, 1019.5211, 1035.5203, 1036.5298, 1046.5328, 1052.5233, 1100.5947, 1115.5746, 1115.5746, 1116.5812, 1156.6023, 1231.5630, 1238.6171, 1259.6561, 1311.6479, 1311.6479, 1320.6832, 1334.6826, 1385.6823, 1390.6980, 1390.6980, 1396.6498, 1401.6981, 1427.7306, 1430.7336, 1431.7059, 1467.7302, 1476.7136, 1498.8071, 1508.7194, 1514.8020, 1730.7977, 1886.8986, 1886.8986, 1891.8846, 1902.8888, 2011.9779, 2047.9758, 2047.9758, 2164.9978, 2673.3113, 2673.3113, 2740.2971, 2756.2961, 3027.4219, 3205.4954, 3205.4954, 3418.6208 |

|  |  |
| --- | --- |
| **5.** | [contig63173](http://msmsms/mascot/cgi/protein_view.pl?file=../data/20120113/F018131.dat&hit=5" \t "_blank)    **Mass:** 22462    **Score:** 97     **Expect:** 7.7e-006  **Matches:** 5 |
|  | putative nuclear encoded protein Method: similarity and extension |

|  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | **Observed** | **Mr(expt)** | **Mr(calc)** | **ppm** | **Start** |  | **End** | **Miss** | **Ions** | **Peptide** |
|  | 1448.7441 | 1447.7368 | 1447.7208 | 11.1 | 95 | - | 105 | 1 | --- | R.QVFLDKHNEYR.Q |
|  | 1448.7441 | 1447.7368 | 1447.7208 | 11.1 | 95 | - | 105 | 1 | 89 | R.QVFLDKHNEYR.Q |
|  | 1467.7302 | 1466.7229 | 1466.7577 | -23.69 | 34 | - | 47 | 1 | --- | K.PSTTTTKATTTTTR.P |
|  | 2740.2971 | 2739.2898 | 2739.2311 | 21.4 | 126 | - | 147 | 2 | --- | R.MLQMRYDCDLEAHVMEHLVKCK.G + 3 Oxidation (M) |
|  | 2756.2961 | 2755.2888 | 2755.2260 | 22.8 | 126 | - | 147 | 2 | --- | R.MLQMRYDCDLEAHVMEHLVKCK.G + Oxidation (HW); 3 Oxidation (M) |

|  |  |
| --- | --- |
|  | **No match to:** 901.4788, 917.4667, 944.5056, 959.4774, 986.4898, 1003.5240, 1019.5211, 1035.5203, 1036.5298, 1046.5328, 1052.5233, 1100.5947, 1115.5746, 1115.5746, 1116.5812, 1156.6023, 1231.5630, 1238.6171, 1259.6561, 1311.6479, 1311.6479, 1320.6832, 1334.6826, 1385.6823, 1390.6980, 1390.6980, 1396.6498, 1401.6981, 1427.7306, 1430.7336, 1431.7059, 1476.7136, 1498.8071, 1508.7194, 1514.8020, 1524.7190, 1730.7977, 1781.9600, 1886.8986, 1886.8986, 1891.8846, 1902.8888, 2011.9779, 2047.9758, 2047.9758, 2164.9978, 2673.3113, 2673.3113, 3027.4219, 3059.4282, 3205.4954, 3205.4954, 3418.6208 |

|  |  |
| --- | --- |
| **6.** | [gi|13625877|gb|AAK35183.1|AF352698\_1](http://msmsms/mascot/cgi/protein_view.pl?file=../data/20120113/F018131.dat&hit=6" \t "_blank)    **Mass:** 27540    **Score:** 95     **Expect:** 1e-005  **Matches:** 5 |
|  | activation associated secreted protein-like protein [Cooperia punctata] |

|  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | **Observed** | **Mr(expt)** | **Mr(calc)** | **ppm** | **Start** |  | **End** | **Miss** | **Ions** | **Peptide** |
|  | 1448.7441 | 1447.7368 | 1447.7208 | 11.1 | 61 | - | 71 | 1 | --- | R.QVFLDKHNEYR.Q |
|  | 1448.7441 | 1447.7368 | 1447.7208 | 11.1 | 61 | - | 71 | 1 | 89 | R.QVFLDKHNEYR.Q |
|  | 1781.9600 | 1780.9527 | 1780.9584 | -3.19 | 124 | - | 139 | 1 | --- | K.GRGQNIWAITVPNLDK.A |
|  | 2047.9758 | 2046.9685 | 2047.1286 | -78.21 | 72 | - | 91 | 2 | --- | R.QLVARGEAQNKTGLAPPAAR.M |
|  | 2047.9758 | 2046.9685 | 2047.1286 | -78.21 | 72 | - | 91 | 2 | --- | R.QLVARGEAQNKTGLAPPAAR.M |

|  |  |
| --- | --- |
|  | **No match to:** 901.4788, 917.4667, 944.5056, 959.4774, 986.4898, 1003.5240, 1019.5211, 1035.5203, 1036.5298, 1046.5328, 1052.5233, 1100.5947, 1115.5746, 1115.5746, 1116.5812, 1156.6023, 1231.5630, 1238.6171, 1259.6561, 1311.6479, 1311.6479, 1320.6832, 1334.6826, 1385.6823, 1390.6980, 1390.6980, 1396.6498, 1401.6981, 1427.7306, 1430.7336, 1431.7059, 1467.7302, 1476.7136, 1498.8071, 1508.7194, 1514.8020, 1524.7190, 1730.7977, 1886.8986, 1886.8986, 1891.8846, 1902.8888, 2011.9779, 2164.9978, 2673.3113, 2673.3113, 2740.2971, 2756.2961, 3027.4219, 3059.4282, 3205.4954, 3205.4954, 3418.6208 |

|  |  |
| --- | --- |
| **7.** | [isotig00099](http://msmsms/mascot/cgi/protein_view.pl?file=../data/20120113/F018131.dat&hit=7" \t "_blank)    **Mass:** 12511    **Score:** 73     **Expect:** 0.0017  **Matches:** 5 |
|  | putative nuclear encoded protein Method: similarity and extension |

|  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | **Observed** | **Mr(expt)** | **Mr(calc)** | **ppm** | **Start** |  | **End** | **Miss** | **Ions** | **Peptide** |
|  | 1390.6980 | 1389.6907 | 1389.6929 | -1.53 | 12 | - | 22 | 0 | --- | R.SVHDWYIELTK.Y |
|  | 1390.6980 | 1389.6907 | 1389.6929 | -1.53 | 12 | - | 22 | 0 | 62 | R.SVHDWYIELTK.Y |
|  | 2164.9978 | 2163.9905 | 2164.0007 | -4.72 | 31 | - | 49 | 0 | --- | K.ISMDNAANTGHYSQVVWQK.S + Oxidation (M) |
|  | 3027.4219 | 3026.4146 | 3026.4192 | -1.52 | 23 | - | 49 | 1 | --- | K.YGITADNKISMDNAANTGHYSQVVWQK.S + Oxidation (M) |
|  | 3059.4282 | 3058.4209 | 3058.4091 | 3.88 | 23 | - | 49 | 1 | --- | K.YGITADNKISMDNAANTGHYSQVVWQK.S + 2 Oxidation (HW); Oxidation (M) |

|  |  |
| --- | --- |
|  | **No match to:** 901.4788, 917.4667, 944.5056, 959.4774, 986.4898, 1003.5240, 1019.5211, 1035.5203, 1036.5298, 1046.5328, 1052.5233, 1100.5947, 1115.5746, 1115.5746, 1116.5812, 1156.6023, 1231.5630, 1238.6171, 1259.6561, 1311.6479, 1311.6479, 1320.6832, 1334.6826, 1385.6823, 1396.6498, 1401.6981, 1427.7306, 1430.7336, 1431.7059, 1448.7441, 1448.7441, 1467.7302, 1476.7136, 1498.8071, 1508.7194, 1514.8020, 1524.7190, 1730.7977, 1781.9600, 1886.8986, 1886.8986, 1891.8846, 1902.8888, 2011.9779, 2047.9758, 2047.9758, 2673.3113, 2673.3113, 2740.2971, 2756.2961, 3205.4954, 3205.4954, 3418.6208 |

**http://msmsms/mascot/images/88x31_logo_white.gifMascot Search Results**

**Protein View**

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Match to: **contig05709** Score: **276** Expect: **8.6e-024**

**putative nuclear encoded protein Method: similarity and extension**

Nominal mass (Mr): **23725**; Calculated pI value: **5.37**

NCBI BLAST search of [contig05709](http://www.ncbi.nlm.nih.gov/blast/Blast.cgi?ALIGNMENTS=50&ALIGNMENT_VIEW=Pairwise&AUTO_FORMAT=Semiauto&CDD_SEARCH=on&CLIENT=web&COMPOSITION_BASED_STATISTICS=on&DATABASE=nr&DESCRIPTIONS=100&ENTREZ_QUERY=(none)&EXPECT=10&FILTER=L&FORMAT_BLOCK_ON_RESPAGE=None&FORMAT_OBJECT=Alignment&FORMAT_TYPE=HTML&GAPCOSTS=11+1&I_THRESH=0.001&LAYOUT=TwoWindows&MATRIX_NAME=BLOSUM62&NCBI_GI=on&PAGE=Proteins&PROGRAM=blastp&QUERY=MLIALITVFCLILHHATVLGEELCSLDNGMTDEIRKVFLDKHNEYRSLVAKGQAPNPQFGGSTPKAARMLKAMYDCDVEEDMTKWAQAQCTYAPFKSSKRYGRNTWGMGVPNYNKTAAAESSVYDWFFELRRYGVPQDNVYTRDVDYSAYHYAQMVWQDSYKIGCVVAWCPSMTWVACGYSPAGDNIGSLIYELGEPCTKNEDCKCTDCT&SERVICE=plain&SET_DEFAULTS.x=9&SET_DEFAULTS.y=5&SHOW_OVERVIEW=on&WORD_SIZE=3&END_OF_HTTPGET=Yes" \t "_blank) against nr

Unformatted [sequence string](http://msmsms/mascot/cgi/getseq.pl?cooperia_oncophora+contig05709+seq" \t "_blank) for pasting into other applications

Variable modifications: Oxidation (HW),Oxidation (M)

Cleavage by Trypsin/P: cuts C-term side of KR

Sequence Coverage: **30%**

Matched peptides shown in **Bold Red**

**1** MLIALITVFC LILHHATVLG EELCSLDNGM TDEIR**KVFLD KHNEYR**SLVA

**51** K**GQAPNPQFG GSTPK**AARML KAMYDCDVEE DMTKWAQAQC TYAPFKSSKR

**101** YGR**NTWGMGV PNYNKTAAAE SSVYDWFFEL RRYGVPQDNV YTR**DVDYSAY

**151** HYAQMVWQDS YKIGCVVAWC PSMTWVACGY SPAGDNIGSL IYELGEPCTK

**201** NEDCKCTDCT



  Residue Number  Increasing Mass  Decreasing Mass

**Start - End Observed Mr(expt) Mr(calc) ppm Miss Sequence**

**36 - 46 1448.7441 1447.7368 1447.7572 -14 2 R.KVFLDKHNEYR.S**  ([No match](http://msmsms/mascot/cgi/peptide_view.pl?file=../data/20120113/F018131.dat&query=32&hit=1" \t "_blank))

**36 - 46 1448.7441 1447.7368 1447.7572 -14 2 R.KVFLDKHNEYR.S**  ([Ions score 89](http://msmsms/mascot/cgi/peptide_view.pl?file=../data/20120113/F018131.dat&query=33&hit=1" \t "_blank))

**37 - 46 1320.6832 1319.6759 1319.6622 10 1 K.VFLDKHNEYR.S**  ([No match](http://msmsms/mascot/cgi/peptide_view.pl?file=../data/20120113/F018131.dat&query=22&hit=1" \t "_blank))

**52 - 65 1385.6823 1384.6750 1384.6735 1 0 K.GQAPNPQFGGSTPK.A**  ([No match](http://msmsms/mascot/cgi/peptide_view.pl?file=../data/20120113/F018131.dat&query=24&hit=1" \t "_blank))

**104 - 115 1396.6498 1395.6425 1395.6241 13 0 R.NTWGMGVPNYNK.T**  Oxidation (M) ([No match](http://msmsms/mascot/cgi/peptide_view.pl?file=../data/20120113/F018131.dat&query=27&hit=1" \t "_blank))

**116 - 131 1891.8846 1890.8773 1890.8788 -1 0 K.TAAAESSVYDWFFELR.R**  ([No match](http://msmsms/mascot/cgi/peptide_view.pl?file=../data/20120113/F018131.dat&query=44&hit=1" \t "_blank))

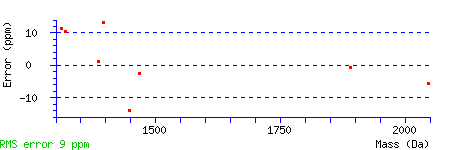
**116 - 132 2047.9758 2046.9685 2046.9799 -6 1 K.TAAAESSVYDWFFELRR.Y**  ([No match](http://msmsms/mascot/cgi/peptide_view.pl?file=../data/20120113/F018131.dat&query=47&hit=1" \t "_blank))

**116 - 132 2047.9758 2046.9685 2046.9799 -6 1 K.TAAAESSVYDWFFELRR.Y**  ([Ions score 73](http://msmsms/mascot/cgi/peptide_view.pl?file=../data/20120113/F018131.dat&query=48&hit=1" \t "_blank))

**132 - 143 1467.7302 1466.7229 1466.7266 -3 1 R.RYGVPQDNVYTR.D**  ([No match](http://msmsms/mascot/cgi/peptide_view.pl?file=../data/20120113/F018131.dat&query=34&hit=1" \t "_blank))

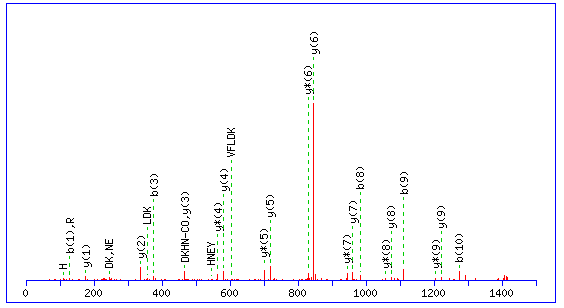
**133 - 143 1311.6479 1310.6406 1310.6255 12 0 R.YGVPQDNVYTR.D**  ([No match](http://msmsms/mascot/cgi/peptide_view.pl?file=../data/20120113/F018131.dat&query=20&hit=1" \t "_blank))

**133 - 143 1311.6479 1310.6406 1310.6255 12 0 R.YGVPQDNVYTR.D**  ([Ions score 79](http://msmsms/mascot/cgi/peptide_view.pl?file=../data/20120113/F018131.dat&query=21&hit=1" \t "_blank))



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🡪 Annotated MS2 spectrum for peptide KVFLDKHNEYR



**Monoisotopic mass of neutral peptide Mr(calc):** 1447.7572

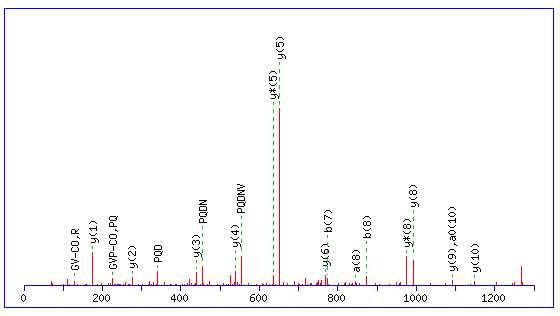
**Ions Score:** 89 **Expect:** 1.1e-007

**Matches :** 29/160 fragment ions using 28 most intense peaks   ([help](http://msmsms/mascot/help/results_help.html" \l "PEP" \t "_blank))

|  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **#** | **Immon.** | **a** | **a\*** | **a0** | **b** | **b\*** | **b0** | **Seq.** | **v** | **w** | **y** | **y\*** | **y0** | **#** |
| **1** | 101.1073 | 101.1073 | 84.0808 |  | **129.1022** | 112.0757 |  | **K** |  |  |  |  |  | **11** |
| **2** | 72.0808 | 200.1757 | 183.1492 |  | 228.1707 | 211.1441 |  | **V** | 1276.6069 | 1289.6273 | 1320.6695 | 1303.6430 | 1302.6589 | **10** |
| **3** | 120.0808 | 347.2442 | 330.2176 |  | **375.2391** | 358.2125 |  | **F** | 1129.5385 |  | ***1221.6011*** | 1204.5745 | 1203.5905 | **9** |
| **4** | 86.0964 | 460.3282 | 443.3017 |  | 488.3231 | 471.2966 |  | **L** | 1016.4544 | 1015.4592 | ***1074.5327*** | 1057.5061 | 1056.5221 | **8** |
| **5** | 88.0393 | 575.3552 | 558.3286 | 557.3446 | **603.3501** | 586.3235 | 585.3395 | **D** | 901.4275 | 900.4322 | ***961.4486*** | 944.4221 | 943.4381 | **7** |
| **6** | 101.1073 | 703.4501 | 686.4236 | 685.4396 | 731.4450 | 714.4185 | 713.4345 | **K** | 773.3325 | 772.3373 | ***846.4217*** | 829.3951 | 828.4111 | **6** |
| **7** | 110.0713 | 840.5090 | 823.4825 | 822.4985 | 868.5039 | 851.4774 | 850.4934 | **H** | 636.2736 |  | ***718.3267*** | 701.3002 | 700.3161 | **5** |
| **8** | 87.0553 | 954.5520 | 937.5254 | 936.5414 | **982.5469** | 965.5203 | 964.5363 | **N** | 522.2307 | 521.2354 | ***581.2678*** | 564.2413 | 563.2572 | **4** |
| **9** | 102.0550 | 1083.5946 | 1066.5680 | 1065.5840 | **1111.5895** | 1094.5629 | 1093.5789 | **E** | 393.1881 | 392.1928 | ***467.2249*** | 450.1983 | 449.2143 | **3** |
| **10** | 136.0757 | 1246.6579 | 1229.6313 | 1228.6473 | **1274.6528** | 1257.6262 | 1256.6422 | **Y** | 230.1248 |  | ***338.1823*** | 321.1557 |  | **2** |
| **11** | 129.1135 |  |  |  |  |  |  | **R** | 74.0237 | 73.0284 | ***175.1190*** | 158.0924 |  | **1** |

|  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **Seq** | **ya** | **yb** | **Seq** | **ya** | **yb** | **Seq** | **ya** | **yb** |
| **VF** | 219.1492 | 247.1441 | **VFL** | 332.2333 | 360.2282 | **VFLD** | 447.2602 | 475.2551 |
| **VFLDK** | 575.3552 | 603.3501 | **FL** | 233.1648 | 261.1598 | **FLD** | 348.1918 | 376.1867 |
| **FLDK** | 476.2867 | 504.2817 | **FLDKH** | 613.3457 | 641.3406 | **LD** | 201.1234 | 229.1183 |
| **LDK** | 329.2183 | 357.2132 | **LDKH** | 466.2772 | 494.2722 | **LDKHN** | 580.3202 | 608.3151 |
| **DK** | 216.1343 | 244.1292 | **DKH** | 353.1932 | 381.1881 | **DKHN** | 467.2361 | 495.2310 |
| **DKHNE** | 596.2787 | 624.2736 | **KH** | 238.1662 | 266.1612 | **KHN** | 352.2092 | 380.2041 |
| **KHNE** | 481.2518 | 509.2467 | **KHNEY** | 644.3151 | 672.3100 | **HN** | 224.1142 | 252.1091 |
| **HNE** | 353.1568 | 381.1517 | **HNEY** | 516.2201 | 544.2150 | **NE** | 216.0979 | 244.0928 |
| **NEY** | 379.1612 | 407.1561 | **EY** | 265.1183 | 293.1132 |  |  |  |

🡪 Annotated MS2 spectrum for peptide YGVPQDNVYTR



**Monoisotopic mass of neutral peptide Mr(calc):** 1310.6255

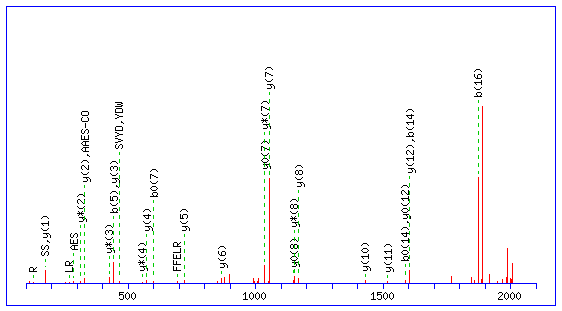
**Ions Score:** 79 **Expect:** 8.2e-007

**Matches :** 23/159 fragment ions using 24 most intense peaks   ([help](http://msmsms/mascot/help/results_help.html" \l "PEP" \t "_blank))

|  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **#** | **Immon.** | **a** | **a\*** | **a0** | **b** | **b\*** | **b0** | **Seq.** | **v** | **w** | **w'** | **y** | **y\*** | **y0** | **#** |
| **1** | 136.0757 | 136.0757 |  |  | 164.0706 |  |  | **Y** |  |  |  |  |  |  | **11** |
| **2** | 30.0338 | 193.0972 |  |  | 221.0921 |  |  | **G** |  |  |  | ***1148.5695*** | 1131.5429 | 1130.5589 | **10** |
| **3** | 72.0808 | 292.1656 |  |  | 320.1605 |  |  | **V** | 1047.4854 | 1060.5058 |  | ***1091.5480*** | 1074.5215 | 1073.5374 | **9** |
| **4** | 70.0651 | 389.2183 |  |  | 417.2132 |  |  | **P** | 950.4326 | 949.4374 |  | ***992.4796*** | 975.4530 | 974.4690 | **8** |
| **5** | 101.0709 | 517.2769 | 500.2504 |  | 545.2718 | 528.2453 |  | **Q** | 822.3741 | 821.3788 |  | 895.4268 | 878.4003 | 877.4163 | **7** |
| **6** | 88.0393 | 632.3039 | 615.2773 | 614.2933 | 660.2988 | 643.2722 | 642.2882 | **D** | 707.3471 | 706.3519 |  | ***767.3682*** | 750.3417 | 749.3577 | **6** |
| **7** | 87.0553 | 746.3468 | 729.3202 | 728.3362 | **774.3417** | 757.3151 | 756.3311 | **N** | 593.3042 | 592.3089 |  | ***652.3413*** | 635.3148 | 634.3307 | **5** |
| **8** | 72.0808 | 845.4152 | 828.3886 | 827.4046 | **873.4101** | 856.3836 | 855.3995 | **V** | 494.2358 | 507.2562 |  | ***538.2984*** | 521.2718 | 520.2878 | **4** |
| **9** | 136.0757 | 1008.4785 | 991.4520 | 990.4680 | 1036.4734 | 1019.4469 | 1018.4629 | **Y** | 331.1724 |  |  | ***439.2300*** | 422.2034 | 421.2194 | **3** |
| **10** | 74.0600 | 1109.5262 | 1092.4997 | 1091.5156 | 1137.5211 | 1120.4946 | 1119.5106 | **T** | 230.1248 | 243.1452 | 245.1244 | ***276.1666*** | 259.1401 | 258.1561 | **2** |
| **11** | 129.1135 |  |  |  |  |  |  | **R** | 74.0237 | 73.0284 |  | ***175.1190*** | 158.0924 |  | **1** |

|  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **Seq** | **ya** | **yb** | **Seq** | **ya** | **yb** | **Seq** | **ya** | **yb** |
| **GV** | 129.1022 | 157.0972 | **GVP** | 226.1550 | 254.1499 | **GVPQ** | 354.2136 | 382.2085 |
| **GVPQD** | 469.2405 | 497.2354 | **GVPQDN** | 583.2835 | 611.2784 | **GVPQDNV** | 682.3519 | 710.3468 |
| **VP** | 169.1335 | 197.1285 | **VPQ** | 297.1921 | 325.1870 | **VPQD** | 412.2191 | 440.2140 |
| **VPQDN** | 526.2620 | 554.2569 | **VPQDNV** | 625.3304 | 653.3253 | **PQ** | 198.1237 | 226.1186 |
| **PQD** | 313.1506 | 341.1456 | **PQDN** | 427.1936 | 455.1885 | **PQDNV** | 526.2620 | 554.2569 |
| **PQDNVY** | 689.3253 | 717.3202 | **QD** | 216.0979 | 244.0928 | **QDN** | 330.1408 | 358.1357 |
| **QDNV** | 429.2092 | 457.2041 | **QDNVY** | 592.2726 | 620.2675 | **QDNVYT** | 693.3202 | 721.3151 |
| **DN** | 202.0822 | 230.0771 | **DNV** | 301.1506 | 329.1456 | **DNVY** | 464.2140 | 492.2089 |
| **DNVYT** | 565.2617 | 593.2566 | **NV** | 186.1237 | 214.1186 | **NVY** | 349.1870 | 377.1819 |
| **NVYT** | 450.2347 | 478.2296 | **VY** | 235.1441 | 263.1390 | **VYT** | 336.1918 | 364.1867 |
| **YT** | 237.1234 | 265.1183 |  |  |  |  |  |  |

🡪 Annotated MS2 spectrum for peptide TAAAESSVYDWFFELRR



**Monoisotopic mass of neutral peptide Mr(calc):** 2046.9799

**Ions Score:** 73 **Expect:** 4e-006

**Matches :** 33/260 fragment ions using 40 most intense peaks   ([help](http://msmsms/mascot/help/results_help.html" \l "PEP" \t "_blank))

|  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **#** | **Immon.** | **a** | **a\*** | **a0** | **b** | **b\*** | **b0** | **d** | **Seq.** | **v** | **w** | **y** | **y\*** | **y0** | **#** |
| **1** | 74.0600 | 74.0600 |  | 56.0495 | 102.0550 |  | 84.0444 |  | **T** |  |  |  |  |  | **17** |
| **2** | 44.0495 | 145.0972 |  | 127.0866 | 173.0921 |  | 155.0815 |  | **A** | 1930.9082 |  | 1946.9395 | 1929.9130 | 1928.9290 | **16** |
| **3** | 44.0495 | 216.1343 |  | 198.1237 | 244.1292 |  | 226.1186 |  | **A** | 1859.8711 |  | 1875.9024 | 1858.8759 | 1857.8919 | **15** |
| **4** | 44.0495 | 287.1714 |  | 269.1608 | 315.1663 |  | 297.1557 |  | **A** | 1788.8340 |  | 1804.8653 | 1787.8388 | 1786.8547 | **14** |
| **5** | 102.0550 | 416.2140 |  | 398.2034 | **444.2089** |  | 426.1983 |  | **E** | 1659.7914 | 1658.7962 | 1733.8282 | 1716.8016 | 1715.8176 | **13** |
| **6** | 60.0444 | 503.2460 |  | 485.2354 | 531.2409 |  | 513.2304 |  | **S** | 1572.7594 | 1571.7641 | ***1604.7856*** | 1587.7591 | 1586.7750 | **12** |
| **7** | 60.0444 | 590.2780 |  | 572.2675 | 618.2729 |  | 600.2624 |  | **S** | 1485.7274 | 1484.7321 | ***1517.7536*** | 1500.7270 | 1499.7430 | **11** |
| **8** | 72.0808 | 689.3464 |  | 671.3359 | 717.3414 |  | 699.3308 |  | **V** | 1386.6589 | 1399.6793 | ***1430.7215*** | 1413.6950 | 1412.7110 | **10** |
| **9** | 136.0757 | 852.4098 |  | 834.3992 | 880.4047 |  | 862.3941 |  | **Y** | 1223.5956 |  | 1331.6531 | 1314.6266 | 1313.6426 | **9** |
| **10** | 88.0393 | 967.4367 |  | 949.4262 | 995.4316 |  | 977.4211 |  | **D** | 1108.5687 | 1107.5734 | ***1168.5898*** | 1151.5633 | 1150.5792 | **8** |
| **11** | 159.0917 | 1153.5160 |  | 1135.5055 | 1181.5109 |  | 1163.5004 |  | **W** | 922.4894 |  | ***1053.5629*** | 1036.5363 | 1035.5523 | **7** |
| **12** | 120.0808 | 1300.5844 |  | 1282.5739 | 1328.5794 |  | 1310.5688 |  | **F** | 775.4209 |  | ***867.4835*** | 850.4570 | 849.4730 | **6** |
| **13** | 120.0808 | 1447.6529 |  | 1429.6423 | 1475.6478 |  | 1457.6372 |  | **F** | 628.3525 |  | ***720.4151*** | 703.3886 | 702.4046 | **5** |
| **14** | 102.0550 | 1576.6955 |  | 1558.6849 | **1604.6904** |  | 1586.6798 |  | **E** | 499.3099 | 498.3147 | ***573.3467*** | 556.3202 | 555.3362 | **4** |
| **15** | 86.0964 | 1689.7795 |  | 1671.7689 | 1717.7744 |  | 1699.7639 |  | **L** | 386.2259 | 385.2306 | ***444.3041*** | 427.2776 |  | **3** |
| **16** | 129.1135 | 1845.8806 | 1828.8541 | 1827.8701 | **1873.8755** | 1856.8490 | 1855.8650 | 1760.8166 | **R** | 230.1248 | 229.1295 | ***331.2201*** | 314.1935 |  | **2** |
| **17** | 129.1135 |  |  |  |  |  |  |  | **R** | 74.0237 | 73.0284 | ***175.1190*** | 158.0924 |  | **1** |

|  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **Seq** | **ya** | **yb** | **Seq** | **ya** | **yb** | **Seq** | **ya** | **yb** |
| **AA** | 115.0866 | 143.0815 | **AAA** | 186.1237 | 214.1186 | **AAAE** | 315.1663 | 343.1612 |
| **AAAES** | 402.1983 | 430.1932 | **AAAESS** | 489.2304 | 517.2253 | **AAAESSV** | 588.2988 | 616.2937 |
| **AA** | 115.0866 | 143.0815 | **AAE** | 244.1292 | 272.1241 | **AAES** | 331.1612 | 359.1561 |
| **AAESS** | 418.1932 | 446.1882 | **AAESSV** | 517.2617 | 545.2566 | **AAESSVY** | 680.3250 | 708.3199 |
| **AE** | 173.0921 | 201.0870 | **AES** | 260.1241 | 288.1190 | **AESS** | 347.1561 | 375.1510 |
| **AESSV** | 446.2245 | 474.2195 | **AESSVY** | 609.2879 | 637.2828 | **ES** | 189.0870 | 217.0819 |
| **ESS** | 276.1190 | 304.1139 | **ESSV** | 375.1874 | 403.1823 | **ESSVY** | 538.2508 | 566.2457 |
| **ESSVYD** | 653.2777 | 681.2726 | **SS** | 147.0764 | 175.0713 | **SSV** | 246.1448 | 274.1397 |
| **SSVY** | 409.2082 | 437.2031 | **SSVYD** | 524.2351 | 552.2300 | **SV** | 159.1128 | 187.1077 |
| **SVY** | 322.1761 | 350.1710 | **SVYD** | 437.2031 | 465.1980 | **SVYDW** | 623.2824 | 651.2773 |
| **VY** | 235.1441 | 263.1390 | **VYD** | 350.1710 | 378.1660 | **VYDW** | 536.2504 | 564.2453 |
| **VYDWF** | 683.3188 | 711.3137 | **YD** | 251.1026 | 279.0975 | **YDW** | 437.1819 | 465.1769 |
| **YDWF** | 584.2504 | 612.2453 | **DW** | 274.1186 | 302.1135 | **DWF** | 421.1870 | 449.1819 |
| **DWFF** | 568.2554 | 596.2504 | **DWFFE** | 697.2980 | 725.2930 | **WF** | 306.1601 | 334.1550 |
| **WFF** | 453.2285 | 481.2234 | **WFFE** | 582.2711 | 610.2660 | **WFFEL** | 695.3552 | 723.3501 |
| **FF** | 267.1492 | 295.1441 | **FFE** | 396.1918 | 424.1867 | **FFEL** | 509.2758 | 537.2708 |
| **FFELR** | 665.3770 | 693.3719 | **FE** | 249.1234 | 277.1183 | **FEL** | 362.2074 | 390.2023 |
| **FELR** | 518.3085 | 546.3035 | **EL** | 215.1390 | 243.1339 | **ELR** | 371.2401 | 399.2350 |
| **LR** | 242.1975 | 270.1925 |  |  |  |  |  |  |

**Band 4:**

**http://msmsms/mascot/images/88x31_logo_white.gifMascot Search Results**

**User :**

**Email :**

**Search title : SampleSetID: 683, AnalysisID: 1069, MaldiWellID: 82748, SpectrumID: 217006, Path=\Jimmy\Cooperia 3\Co ES Conc 3 Frac 13012012 (good database)**

**Database : cooperia\_oncophora oncophora\_20110405 (34373 sequences; 5289600 residues)**

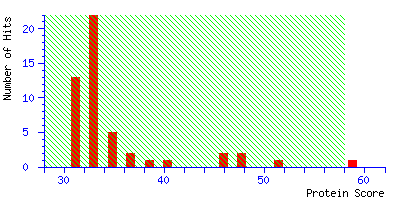
**Timestamp : 13 Jan 2012 at 14:15:58 GMT**

**Warning : A Peptide summary report will usually give a much clearer picture of MS/MS search results.**

**Top Score : 59 for isotig24792, putative nuclear encoded protein Method: similarity and extension**

**Mascot Score Histogram**

Protein score is -10\*Log(P), where P is the probability that the observed match is a random event.  
Protein scores greater than 58 are significant (p<0.05).  
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



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**Protein Summary Report**

|  |  |  |  |
| --- | --- | --- | --- |
|  |  |  | [Help](http://msmsms/mascot/help/msms_summaries_help.html" \t "_blank) |
|  | Significance threshold p< | Max. number of hits |  |

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**Index**

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
|  | **Accession** | **Mass** | **Score** | **Description** |
| **1.** | [**isotig24792**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20120113/F018120.dat#Hit1) | 13502 | 59 | putative nuclear encoded protein Method: similarity and extension |
| **2.** | [**isotig03127**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20120113/F018120.dat#Hit2) | 25801 | 52 | putative nuclear encoded protein Method: ESTScan |
| **3.** | [**isotig03118**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20120113/F018120.dat#Hit3) | 63532 | 48 | putative nuclear encoded protein Method: ESTScan |
| **4.** | [**isotig30340**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20120113/F018120.dat#Hit4) | 11088 | 47 | putative nuclear encoded protein Method: Longest ORF |
| **5.** | [**isotig23367**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20120113/F018120.dat#Hit5) | 13511 | 47 | putative nuclear encoded protein Method: similarity and extension |
| **6.** | [**isotig29232**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20120113/F018120.dat#Hit6) | 14163 | 45 | putative nuclear encoded protein Method: Longest ORF |
| **7.** | [**isotig29345**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20120113/F018120.dat#Hit7) | 9150 | 40 | putative nuclear encoded protein Method: similarity and extension |
| **8.** | [**isotig10859**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20120113/F018120.dat#Hit8) | 23922 | 38 | putative nuclear encoded protein Method: similarity and extension |
| **9.** | [**isotig16489**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20120113/F018120.dat#Hit9) | 11638 | 37 | putative nuclear encoded protein Method: Longest ORF |
| **10.** | [**isotig16421**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20120113/F018120.dat#Hit10) | 17483 | 36 | putative nuclear encoded protein Method: similarity and extension |
| **11.** | [**isotig12127**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20120113/F018120.dat#Hit11) | 39875 | 35 | putative nuclear encoded protein Method: similarity and extension |
| **12.** | [**isotig07651**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20120113/F018120.dat#Hit12) | 16893 | 35 | putative nuclear encoded protein Method: similarity and extension |
| **13.** | [**isotig07652**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20120113/F018120.dat#Hit13) | 16893 | 35 | putative nuclear encoded protein Method: similarity and extension |
| **14.** | [**isotig20304**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20120113/F018120.dat#Hit14) | 23306 | 35 | putative nuclear encoded protein Method: similarity and extension |
| **15.** | [**isotig27190**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20120113/F018120.dat#Hit15) | 12372 | 34 | putative nuclear encoded protein Method: similarity and extension |
| **16.** | [**isotig21841**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20120113/F018120.dat#Hit16) | 13872 | 34 | putative nuclear encoded protein Method: similarity and extension |
| **17.** | [**isotig23959**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20120113/F018120.dat#Hit17) | 20681 | 34 | putative nuclear encoded protein Method: similarity and extension |
| **18.** | [**isotig28868**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20120113/F018120.dat#Hit18) | 13474 | 33 | putative nuclear encoded protein Method: similarity and extension |
| **19.** | [**isotig07620**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20120113/F018120.dat#Hit19) | 13287 | 33 | putative nuclear encoded protein Method: Longest ORF |
| **20.** | [**isotig24985**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20120113/F018120.dat#Hit20) | 16916 | 33 | putative nuclear encoded protein Method: similarity and extension |

**Results List**

|  |  |
| --- | --- |
| **1.** | [isotig24792](http://msmsms/mascot/cgi/protein_view.pl?file=../data/20120113/F018120.dat&hit=1" \t "_blank)    **Mass:** 13502    **Score:** 59     **Expect:** 0.045  **Matches:** 3 |
|  | putative nuclear encoded protein Method: similarity and extension |

|  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | **Observed** | **Mr(expt)** | **Mr(calc)** | **ppm** | **Start** |  | **End** | **Miss** | **Ions** | **Peptide** |
|  | 1045.6033 | 1044.5960 | 1044.5927 | 3.16 | 62 | - | 70 | 1 | --- | K.EANLTKLTR.I |
|  | 1045.6033 | 1044.5960 | 1044.5927 | 3.16 | 62 | - | 70 | 1 | 48 | K.EANLTKLTR.I |
|  | 1320.7537 | 1319.7464 | 1319.7231 | 17.7 | 60 | - | 70 | 2 | --- | K.MKEANLTKLTR.I + Oxidation (M) |

|  |  |
| --- | --- |
|  | **No match to:** 901.5146, 917.4919, 959.5128, 985.6264, 1014.6115, 1036.5636, 1044.6050, 1052.5431, 1061.6178, 1098.6035, 1115.6179, 1115.6179, 1228.7057, 1318.7819, 1334.7267, 1355.6682, 1384.8320, 1384.8320, 1414.7671, 1430.7645, 1431.7363, 1446.8677, 1447.7860, 1597.9486, 1601.8423, 1617.8313, 1775.9160, 1775.9160, 1778.1108, 1784.8877 |

**http://msmsms/mascot/images/88x31_logo_white.gifMascot Search Results**

**Protein View**

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Match to: **isotig24792** Score: **59** Expect: **0.045**

**putative nuclear encoded protein Method: similarity and extension**

Nominal mass (Mr): **13502**; Calculated pI value: **7.98**

NCBI BLAST search of [isotig24792](http://www.ncbi.nlm.nih.gov/blast/Blast.cgi?ALIGNMENTS=50&ALIGNMENT_VIEW=Pairwise&AUTO_FORMAT=Semiauto&CDD_SEARCH=on&CLIENT=web&COMPOSITION_BASED_STATISTICS=on&DATABASE=nr&DESCRIPTIONS=100&ENTREZ_QUERY=(none)&EXPECT=10&FILTER=L&FORMAT_BLOCK_ON_RESPAGE=None&FORMAT_OBJECT=Alignment&FORMAT_TYPE=HTML&GAPCOSTS=11+1&I_THRESH=0.001&LAYOUT=TwoWindows&MATRIX_NAME=BLOSUM62&NCBI_GI=on&PAGE=Proteins&PROGRAM=blastp&QUERY=WDRLRELDTMKKEWQREHIADLLAELLLARAITLMALKVIEWGELTTETTACLKRMFAKMKEANLTKLTRIFECIMDVKKNRLLHDGLRIFLQMHFDDDPVYAKIENTFATWR&SERVICE=plain&SET_DEFAULTS.x=9&SET_DEFAULTS.y=5&SHOW_OVERVIEW=on&WORD_SIZE=3&END_OF_HTTPGET=Yes" \t "_blank) against nr

Unformatted [sequence string](http://msmsms/mascot/cgi/getseq.pl?cooperia_oncophora+isotig24792+seq" \t "_blank) for pasting into other applications

Variable modifications: Oxidation (HW),Oxidation (M)

Cleavage by Trypsin/P: cuts C-term side of KR

Sequence Coverage: **9%**

Matched peptides shown in **Bold Red**

**1** WDRLRELDTM KKEWQREHIA DLLAELLLAR AITLMALKVI EWGELTTETT

**51** ACLKRMFAK**M KEANLTKLTR** IFECIMDVKK NRLLHDGLRI FLQMHFDDDP

**101** VYAKIENTFA TWR



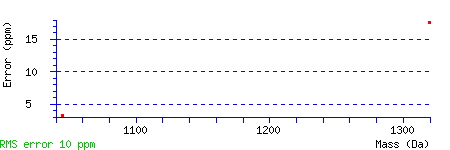
  Residue Number  Increasing Mass  Decreasing Mass

**Start - End Observed Mr(expt) Mr(calc) ppm Miss Sequence**

**60 - 70 1320.7537 1319.7464 1319.7231 18 2 K.MKEANLTKLTR.I**  Oxidation (M) ([No match](http://msmsms/mascot/cgi/peptide_view.pl?file=../data/20120113/F018120.dat&query=17&hit=1" \t "_blank))

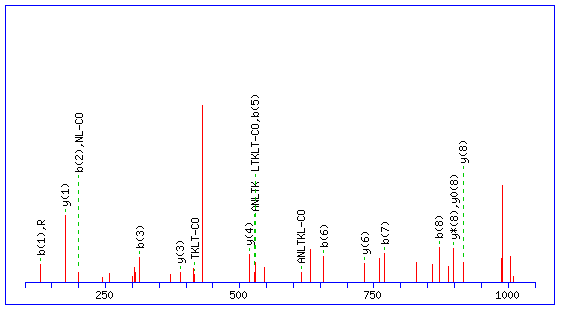
**62 - 70 1045.6033 1044.5960 1044.5927 3 1 K.EANLTKLTR.I**  ([No match](http://msmsms/mascot/cgi/peptide_view.pl?file=../data/20120113/F018120.dat&query=8&hit=1" \t "_blank))

**62 - 70 1045.6033 1044.5960 1044.5927 3 1 K.EANLTKLTR.I**  ([Ions score 48](http://msmsms/mascot/cgi/peptide_view.pl?file=../data/20120113/F018120.dat&query=9&hit=1" \t "_blank))



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🡪 Annotated MS2 spectrum for peptide EANLTKLTR



**Monoisotopic mass of neutral peptide Mr(calc):** 1044.5927

**Ions Score:** 48 **Expect:** 0.0013

**Matches :** 20/133 fragment ions using 26 most intense peaks   ([help](http://msmsms/mascot/help/results_help.html" \l "PEP" \t "_blank))

|  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **#** | **Immon.** | **a** | **a\*** | **a0** | **b** | **b\*** | **b0** | **Seq.** | **v** | **w** | **w'** | **y** | **y\*** | **y0** | **#** |
| **1** | 102.0550 | 102.0550 |  | 84.0444 | ***130.0499*** |  | 112.0393 | **E** |  |  |  |  |  |  | **9** |
| **2** | 44.0495 | 173.0921 |  | 155.0815 | ***201.0870*** |  | 183.0764 | **A** | 900.5261 |  |  | **916.5574** | 899.5309 | 898.5469 | **8** |
| **3** | 87.0553 | 287.1350 | 270.1084 | 269.1244 | ***315.1299*** | 298.1034 | 297.1193 | **N** | 786.4832 | 785.4880 |  | 845.5203 | 828.4938 | 827.5098 | **7** |
| **4** | 86.0964 | 400.2191 | 383.1925 | 382.2085 | 428.2140 | 411.1874 | 410.2034 | **L** | 673.3992 | 672.4039 |  | **731.4774** | 714.4509 | 713.4668 | **6** |
| **5** | 74.0600 | 501.2667 | 484.2402 | 483.2562 | ***529.2617*** | 512.2351 | 511.2511 | **T** | 572.3515 | 585.3719 | 587.3511 | 618.3933 | 601.3668 | 600.3828 | **5** |
| **6** | 101.1073 | 629.3617 | 612.3352 | 611.3511 | ***657.3566*** | 640.3301 | 639.3461 | **K** | 444.2565 | 443.2613 |  | **517.3457** | 500.3191 | 499.3351 | **4** |
| **7** | 86.0964 | 742.4458 | 725.4192 | 724.4352 | ***770.4407*** | 753.4141 | 752.4301 | **L** | 331.1724 | 330.1772 |  | **389.2507** | 372.2241 | 371.2401 | **3** |
| **8** | 74.0600 | 843.4934 | 826.4669 | 825.4829 | ***871.4884*** | 854.4618 | 853.4778 | **T** | 230.1248 | 243.1452 | 245.1244 | 276.1666 | 259.1401 | 258.1561 | **2** |
| **9** | 129.1135 |  |  |  |  |  |  | **R** | 74.0237 | 73.0284 |  | **175.1190** | 158.0924 |  | **1** |

|  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **Seq** | **ya** | **yb** | **Seq** | **ya** | **yb** | **Seq** | **ya** | **yb** |
| **AN** | 158.0924 | 186.0873 | **ANL** | 271.1765 | 299.1714 | **ANLT** | 372.2241 | 400.2191 |
| **ANLTK** | 500.3191 | 528.3140 | **ANLTKL** | 613.4032 | 641.3981 | **NL** | 200.1394 | 228.1343 |
| **NLT** | 301.1870 | 329.1819 | **NLTK** | 429.2820 | 457.2769 | **NLTKL** | 542.3661 | 570.3610 |
| **NLTKLT** | 643.4137 | 671.4087 | **LT** | 187.1441 | 215.1390 | **LTK** | 315.2391 | 343.2340 |
| **LTKL** | 428.3231 | 456.3180 | **LTKLT** | 529.3708 | 557.3657 | **TK** | 202.1550 | 230.1499 |
| **TKL** | 315.2391 | 343.2340 | **TKLT** | 416.2867 | 444.2817 | **KL** | 214.1914 | 242.1863 |
| **KLT** | 315.2391 | 343.2340 | **LT** | 187.1441 | 215.1390 |  |  |  |

**Band 5:**

**http://msmsms/mascot/images/88x31_logo_white.gifMascot Search Results**

**User :**

**Email :**

**Search title : SampleSetID: 683, AnalysisID: 1071, MaldiWellID: 82749, SpectrumID: 217109, Path=\Jimmy\Cooperia 3\Co ES Conc 3 Frac 13012012 (strict)**

**Database : cooperia\_oncophora oncophora\_20110405 (34373 sequences; 5289600 residues)**

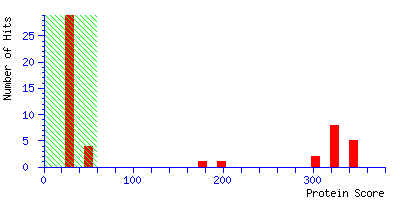
**Timestamp : 13 Jan 2012 at 14:33:10 GMT**

**Warning : A Peptide summary report will usually give a much clearer picture of MS/MS search results.**

**Top Score : 345 for isotig01086, putative nuclear encoded protein Method: similarity and extension**

**Mascot Score Histogram**

Protein score is -10\*Log(P), where P is the probability that the observed match is a random event.  
Protein scores greater than 58 are significant (p<0.05).  
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



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**Protein Summary Report**

|  |  |  |  |
| --- | --- | --- | --- |
|  |  |  | [Help](http://msmsms/mascot/help/msms_summaries_help.html" \t "_blank) |
|  | Significance threshold p< | Max. number of hits |  |

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**Index**

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
|  | **Accession** | **Mass** | **Score** | **Description** |
| **1.** | [**isotig01086**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20120113/F018133.dat#Hit1) | 30794 | 345 | putative nuclear encoded protein Method: similarity and extension |
| **2.** | [**isotig01075**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20120113/F018133.dat#Hit2) | 30780 | 336 | putative nuclear encoded protein Method: similarity and extension |
| **3.** | [**isotig01083**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20120113/F018133.dat#Hit3) | 30780 | 336 | putative nuclear encoded protein Method: similarity and extension |
| **4.** | [**isotig01085**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20120113/F018133.dat#Hit4) | 30780 | 336 | putative nuclear encoded protein Method: similarity and extension |
| **5.** | [**isotig01076**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20120113/F018133.dat#Hit5) | 30780 | 336 | putative nuclear encoded protein Method: similarity and extension |
| **6.** | [**isotig01087**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20120113/F018133.dat#Hit6) | 30817 | 334 | putative nuclear encoded protein Method: similarity and extension |
| **7.** | [**isotig01088**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20120113/F018133.dat#Hit7) | 30798 | 334 | putative nuclear encoded protein Method: similarity and extension |
| **8.** | [**isotig01082**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20120113/F018133.dat#Hit8) | 30803 | 326 | putative nuclear encoded protein Method: similarity and extension |
| **9.** | [**isotig01074**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20120113/F018133.dat#Hit9) | 30803 | 326 | putative nuclear encoded protein Method: similarity and extension |
| **10.** | [**isotig01084**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20120113/F018133.dat#Hit10) | 30803 | 326 | putative nuclear encoded protein Method: similarity and extension |
| **11.** | [**isotig01077**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20120113/F018133.dat#Hit11) | 30803 | 326 | putative nuclear encoded protein Method: similarity and extension |
| **12.** | [**isotig01080**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20120113/F018133.dat#Hit12) | 30766 | 318 | putative nuclear encoded protein Method: similarity and extension |
| **13.** | [**isotig01079**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20120113/F018133.dat#Hit13) | 30766 | 318 | putative nuclear encoded protein Method: similarity and extension |
| **14.** | [**isotig01081**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20120113/F018133.dat#Hit14) | 30789 | 309 | putative nuclear encoded protein Method: similarity and extension |
| **15.** | [**isotig01078**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20120113/F018133.dat#Hit15) | 30789 | 309 | putative nuclear encoded protein Method: similarity and extension |
| **16.** | [**isotig20646**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20120113/F018133.dat#Hit16) | 11793 | 189 | putative nuclear encoded protein Method: similarity and extension |
| **17.** | [**isotig01089**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20120113/F018133.dat#Hit17) | 10048 | 166 | putative nuclear encoded protein Method: similarity and extension |
| **18.** | [**isotig31867**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20120113/F018133.dat#Hit18) | 9186 | 58 | putative nuclear encoded protein Method: similarity and extension |
| **19.** | [**contig17607**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20120113/F018133.dat#Hit19) | 8734 | 45 | putative nuclear encoded protein Method: similarity and extension |
| **20.** | [**isotig24138**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20120113/F018133.dat#Hit20) | 12446 | 45 | putative nuclear encoded protein Method: similarity and extension |

**Results List**

|  |  |
| --- | --- |
| **1.** | [isotig01086](http://msmsms/mascot/cgi/protein_view.pl?file=../data/20120113/F018133.dat&hit=1" \t "_blank)    **Mass:** 30794    **Score:** 345    **Expect:** 1.1e-030  **Matches:** 27 |
|  | putative nuclear encoded protein Method: similarity and extension |

|  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | **Observed** | **Mr(expt)** | **Mr(calc)** | **ppm** | **Start** |  | **End** | **Miss** | **Ions** | **Peptide** |
|  | 911.5567 | 910.5494 | 910.5600 | -11.60 | 196 | - | 203 | 0 | --- | K.TPAQILLR.Y |
|  | 999.4901 | 998.4828 | 998.5509 | -68.15 | 240 | - | 247 | 1 | --- | K.LLESTKHR.Q + Oxidation (HW) |
|  | 1016.4747 | 1015.4674 | 1015.4685 | -1.03 | 250 | - | 257 | 0 | --- | R.LFTDDFMK.G |
|  | 1032.4697 | 1031.4624 | 1031.4634 | -0.94 | 250 | - | 257 | 0 | --- | R.LFTDDFMK.G + Oxidation (M) |
|  | 1103.5808 | 1102.5735 | 1102.5771 | -3.26 | 83 | - | 91 | 0 | --- | K.SVTVQDIWR.G |
|  | 1103.5808 | 1102.5735 | 1102.5771 | -3.26 | 83 | - | 91 | 0 | 62 | K.SVTVQDIWR.G |
|  | 1119.5797 | 1118.5724 | 1118.5720 | 0.35 | 83 | - | 91 | 0 | --- | K.SVTVQDIWR.G + Oxidation (HW) |
|  | 1225.5549 | 1224.5476 | 1224.5523 | -3.85 | 258 | - | 268 | 0 | --- | K.GHPEDPFAAER.- |
|  | 1225.5549 | 1224.5476 | 1224.5523 | -3.85 | 258 | - | 268 | 0 | 51 | K.GHPEDPFAAER.- |
|  | 1283.6632 | 1282.6559 | 1282.7106 | -42.59 | 240 | - | 249 | 2 | --- | K.LLESTKHRQR.L + Oxidation (HW) |
|  | 1289.7469 | 1288.7396 | 1288.7503 | -8.28 | 193 | - | 203 | 1 | --- | K.YSKTPAQILLR.Y |
|  | 1300.6488 | 1299.6415 | 1299.6282 | 10.3 | 248 | - | 257 | 1 | --- | R.QRLFTDDFMK.G |
|  | 1340.6504 | 1339.6431 | 1339.6619 | -14.05 | 176 | - | 187 | 1 | --- | K.EAPKDLDDPNVK.Q |
|  | 1354.6492 | 1353.6419 | 1353.6540 | -8.90 | 165 | - | 175 | 1 | --- | R.AQFMPDKFGWK.E |
|  | 1363.7800 | 1362.7727 | 1362.7871 | -10.53 | 25 | - | 35 | 2 | --- | K.IKREDLFITTK.V |
|  | 1370.6603 | 1369.6530 | 1369.6489 | 3.01 | 165 | - | 175 | 1 | --- | R.AQFMPDKFGWK.E + Oxidation (M) |
|  | 1386.7076 | 1385.7003 | 1385.6438 | 40.8 | 165 | - | 175 | 1 | --- | R.AQFMPDKFGWK.E + Oxidation (HW); Oxidation (M) |
|  | 1386.7076 | 1385.7003 | 1385.6438 | 40.8 | 165 | - | 175 | 1 | 2 | R.AQFMPDKFGWK.E + Oxidation (HW); Oxidation (M) |
|  | 1417.7721 | 1416.7648 | 1416.8452 | -56.76 | 192 | - | 203 | 2 | --- | K.KYSKTPAQILLR.Y |
|  | 1572.7612 | 1571.7539 | 1571.7692 | -9.72 | 104 | - | 117 | 0 | --- | K.AIGVSNWNGEQIER.V |
|  | 1572.7612 | 1571.7539 | 1571.7692 | -9.72 | 104 | - | 117 | 0 | 83 | K.AIGVSNWNGEQIER.V |
|  | 1588.7607 | 1587.7534 | 1587.7641 | -6.73 | 104 | - | 117 | 0 | --- | K.AIGVSNWNGEQIER.V + Oxidation (HW) |
|  | 1589.7434 | 1588.7361 | 1588.8759 | -87.97 | 196 | - | 208 | 1 | --- | K.TPAQILLRYVMER.G |
|  | 1659.8221 | 1658.8148 | 1658.8376 | -13.75 | 149 | - | 164 | 0 | --- | K.HNVSLTSYATLGSPGR.A |
|  | 1875.8829 | 1874.8756 | 1874.8911 | -8.27 | 36 | - | 51 | 0 | --- | K.VWITHEHPDDTEGAIR.E |
|  | 2238.9758 | 2237.9685 | 2238.0052 | -16.38 | 250 | - | 268 | 1 | --- | R.LFTDDFMKGHPEDPFAAER.- + Oxidation (M) |
|  | 2238.9758 | 2237.9685 | 2238.0052 | -16.38 | 250 | - | 268 | 1 | 55 | R.LFTDDFMKGHPEDPFAAER.- + Oxidation (M) |

|  |  |
| --- | --- |
|  | **No match to:** 905.4774, 907.4572, 935.4518, 994.4860, 1036.5116, 1045.5576, 1052.5287, 1062.4561, 1118.5878, 1135.5676, 1151.5809, 1163.6130, 1170.6744, 1189.6440, 1190.5983, 1192.6528, 1299.6344, 1349.6703, 1385.7020, 1416.7092, 1571.7432, 1573.7526, 1604.7560, 1621.8300, 1728.8385, 1771.8662, 1888.8778, 2208.0649 |

|  |  |
| --- | --- |
| **2.** | [isotig01075](http://msmsms/mascot/cgi/protein_view.pl?file=../data/20120113/F018133.dat&hit=2" \t "_blank)    **Mass:** 30780    **Score:** 336    **Expect:** 8.6e-030  **Matches:** 26 |
|  | putative nuclear encoded protein Method: similarity and extension |

|  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | **Observed** | **Mr(expt)** | **Mr(calc)** | **ppm** | **Start** |  | **End** | **Miss** | **Ions** | **Peptide** |
|  | 911.5567 | 910.5494 | 910.5600 | -11.60 | 196 | - | 203 | 0 | --- | K.TPAQILLR.Y |
|  | 999.4901 | 998.4828 | 998.5509 | -68.15 | 240 | - | 247 | 1 | --- | K.LLESTKHR.Q + Oxidation (HW) |
|  | 1016.4747 | 1015.4674 | 1015.4685 | -1.03 | 250 | - | 257 | 0 | --- | R.LFTDDFMK.G |
|  | 1032.4697 | 1031.4624 | 1031.4634 | -0.94 | 250 | - | 257 | 0 | --- | R.LFTDDFMK.G + Oxidation (M) |
|  | 1103.5808 | 1102.5735 | 1102.5771 | -3.26 | 83 | - | 91 | 0 | --- | K.SVTVQDIWR.G |
|  | 1103.5808 | 1102.5735 | 1102.5771 | -3.26 | 83 | - | 91 | 0 | 62 | K.SVTVQDIWR.G |
|  | 1119.5797 | 1118.5724 | 1118.5720 | 0.35 | 83 | - | 91 | 0 | --- | K.SVTVQDIWR.G + Oxidation (HW) |
|  | 1225.5549 | 1224.5476 | 1224.5523 | -3.85 | 258 | - | 268 | 0 | --- | K.GHPEDPFAAER.- |
|  | 1225.5549 | 1224.5476 | 1224.5523 | -3.85 | 258 | - | 268 | 0 | 51 | K.GHPEDPFAAER.- |
|  | 1283.6632 | 1282.6559 | 1282.7106 | -42.59 | 240 | - | 249 | 2 | --- | K.LLESTKHRQR.L + Oxidation (HW) |
|  | 1289.7469 | 1288.7396 | 1288.7503 | -8.28 | 193 | - | 203 | 1 | --- | K.YSKTPAQILLR.Y |
|  | 1300.6488 | 1299.6415 | 1299.6282 | 10.3 | 248 | - | 257 | 1 | --- | R.QRLFTDDFMK.G |
|  | 1340.6504 | 1339.6431 | 1339.6619 | -14.05 | 176 | - | 187 | 1 | --- | K.EAPKDLDDPNVK.Q |
|  | 1354.6492 | 1353.6419 | 1353.6540 | -8.90 | 165 | - | 175 | 1 | --- | R.AQFMPDKFGWK.E |
|  | 1363.7800 | 1362.7727 | 1362.7871 | -10.53 | 25 | - | 35 | 2 | --- | K.IKREDLFITTK.V |
|  | 1370.6603 | 1369.6530 | 1369.6489 | 3.01 | 165 | - | 175 | 1 | --- | R.AQFMPDKFGWK.E + Oxidation (M) |
|  | 1386.7076 | 1385.7003 | 1385.6438 | 40.8 | 165 | - | 175 | 1 | --- | R.AQFMPDKFGWK.E + Oxidation (HW); Oxidation (M) |
|  | 1386.7076 | 1385.7003 | 1385.6438 | 40.8 | 165 | - | 175 | 1 | 2 | R.AQFMPDKFGWK.E + Oxidation (HW); Oxidation (M) |
|  | 1417.7721 | 1416.7648 | 1416.8452 | -56.76 | 192 | - | 203 | 2 | --- | K.KYSKTPAQILLR.Y |
|  | 1572.7612 | 1571.7539 | 1571.7692 | -9.72 | 104 | - | 117 | 0 | --- | K.AIGVSNWNGEQIER.V |
|  | 1572.7612 | 1571.7539 | 1571.7692 | -9.72 | 104 | - | 117 | 0 | 83 | K.AIGVSNWNGEQIER.V |
|  | 1588.7607 | 1587.7534 | 1587.7641 | -6.73 | 104 | - | 117 | 0 | --- | K.AIGVSNWNGEQIER.V + Oxidation (HW) |
|  | 1659.8221 | 1658.8148 | 1658.8376 | -13.75 | 149 | - | 164 | 0 | --- | K.HNVSLTSYATLGSPGR.A |
|  | 1875.8829 | 1874.8756 | 1874.8911 | -8.27 | 36 | - | 51 | 0 | --- | K.VWITHEHPDDTEGAIR.E |
|  | 2238.9758 | 2237.9685 | 2238.0052 | -16.38 | 250 | - | 268 | 1 | --- | R.LFTDDFMKGHPEDPFAAER.- + Oxidation (M) |
|  | 2238.9758 | 2237.9685 | 2238.0052 | -16.38 | 250 | - | 268 | 1 | 55 | R.LFTDDFMKGHPEDPFAAER.- + Oxidation (M) |

|  |  |
| --- | --- |
|  | **No match to:** 905.4774, 907.4572, 935.4518, 994.4860, 1036.5116, 1045.5576, 1052.5287, 1062.4561, 1118.5878, 1135.5676, 1151.5809, 1163.6130, 1170.6744, 1189.6440, 1190.5983, 1192.6528, 1299.6344, 1349.6703, 1385.7020, 1416.7092, 1571.7432, 1573.7526, 1589.7434, 1604.7560, 1621.8300, 1728.8385, 1771.8662, 1888.8778, 2208.0649 |

|  |  |
| --- | --- |
| **3.** | [isotig01083](http://msmsms/mascot/cgi/protein_view.pl?file=../data/20120113/F018133.dat&hit=3" \t "_blank)    **Mass:** 30780    **Score:** 336    **Expect:** 8.6e-030  **Matches:** 26 |
|  | putative nuclear encoded protein Method: similarity and extension |

|  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | **Observed** | **Mr(expt)** | **Mr(calc)** | **ppm** | **Start** |  | **End** | **Miss** | **Ions** | **Peptide** |
|  | 911.5567 | 910.5494 | 910.5600 | -11.60 | 196 | - | 203 | 0 | --- | K.TPAQILLR.Y |
|  | 999.4901 | 998.4828 | 998.5509 | -68.15 | 240 | - | 247 | 1 | --- | K.LLESTKHR.Q + Oxidation (HW) |
|  | 1016.4747 | 1015.4674 | 1015.4685 | -1.03 | 250 | - | 257 | 0 | --- | R.LFTDDFMK.G |
|  | 1032.4697 | 1031.4624 | 1031.4634 | -0.94 | 250 | - | 257 | 0 | --- | R.LFTDDFMK.G + Oxidation (M) |
|  | 1103.5808 | 1102.5735 | 1102.5771 | -3.26 | 83 | - | 91 | 0 | --- | K.SVTVQDIWR.G |
|  | 1103.5808 | 1102.5735 | 1102.5771 | -3.26 | 83 | - | 91 | 0 | 62 | K.SVTVQDIWR.G |
|  | 1119.5797 | 1118.5724 | 1118.5720 | 0.35 | 83 | - | 91 | 0 | --- | K.SVTVQDIWR.G + Oxidation (HW) |
|  | 1225.5549 | 1224.5476 | 1224.5523 | -3.85 | 258 | - | 268 | 0 | --- | K.GHPEDPFAAER.- |
|  | 1225.5549 | 1224.5476 | 1224.5523 | -3.85 | 258 | - | 268 | 0 | 51 | K.GHPEDPFAAER.- |
|  | 1283.6632 | 1282.6559 | 1282.7106 | -42.59 | 240 | - | 249 | 2 | --- | K.LLESTKHRQR.L + Oxidation (HW) |
|  | 1289.7469 | 1288.7396 | 1288.7503 | -8.28 | 193 | - | 203 | 1 | --- | K.YSKTPAQILLR.Y |
|  | 1300.6488 | 1299.6415 | 1299.6282 | 10.3 | 248 | - | 257 | 1 | --- | R.QRLFTDDFMK.G |
|  | 1340.6504 | 1339.6431 | 1339.6619 | -14.05 | 176 | - | 187 | 1 | --- | K.EAPKDLDDPNVK.Q |
|  | 1354.6492 | 1353.6419 | 1353.6540 | -8.90 | 165 | - | 175 | 1 | --- | R.AQFMPDKFGWK.E |
|  | 1363.7800 | 1362.7727 | 1362.7871 | -10.53 | 25 | - | 35 | 2 | --- | K.IKREDLFITTK.V |
|  | 1370.6603 | 1369.6530 | 1369.6489 | 3.01 | 165 | - | 175 | 1 | --- | R.AQFMPDKFGWK.E + Oxidation (M) |
|  | 1386.7076 | 1385.7003 | 1385.6438 | 40.8 | 165 | - | 175 | 1 | --- | R.AQFMPDKFGWK.E + Oxidation (HW); Oxidation (M) |
|  | 1386.7076 | 1385.7003 | 1385.6438 | 40.8 | 165 | - | 175 | 1 | 2 | R.AQFMPDKFGWK.E + Oxidation (HW); Oxidation (M) |
|  | 1417.7721 | 1416.7648 | 1416.8452 | -56.76 | 192 | - | 203 | 2 | --- | K.KYSKTPAQILLR.Y |
|  | 1572.7612 | 1571.7539 | 1571.7692 | -9.72 | 104 | - | 117 | 0 | --- | K.AIGVSNWNGEQIER.V |
|  | 1572.7612 | 1571.7539 | 1571.7692 | -9.72 | 104 | - | 117 | 0 | 83 | K.AIGVSNWNGEQIER.V |
|  | 1588.7607 | 1587.7534 | 1587.7641 | -6.73 | 104 | - | 117 | 0 | --- | K.AIGVSNWNGEQIER.V + Oxidation (HW) |
|  | 1659.8221 | 1658.8148 | 1658.8376 | -13.75 | 149 | - | 164 | 0 | --- | K.HNVSLTSYATLGSPGR.A |
|  | 1875.8829 | 1874.8756 | 1874.8911 | -8.27 | 36 | - | 51 | 0 | --- | K.VWITHEHPDDTEGAIR.E |
|  | 2238.9758 | 2237.9685 | 2238.0052 | -16.38 | 250 | - | 268 | 1 | --- | R.LFTDDFMKGHPEDPFAAER.- + Oxidation (M) |
|  | 2238.9758 | 2237.9685 | 2238.0052 | -16.38 | 250 | - | 268 | 1 | 55 | R.LFTDDFMKGHPEDPFAAER.- + Oxidation (M) |

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|  | **No match to:** 905.4774, 907.4572, 935.4518, 994.4860, 1036.5116, 1045.5576, 1052.5287, 1062.4561, 1118.5878, 1135.5676, 1151.5809, 1163.6130, 1170.6744, 1189.6440, 1190.5983, 1192.6528, 1299.6344, 1349.6703, 1385.7020, 1416.7092, 1571.7432, 1573.7526, 1589.7434, 1604.7560, 1621.8300, 1728.8385, 1771.8662, 1888.8778, 2208.0649 |

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| **4.** | [isotig01085](http://msmsms/mascot/cgi/protein_view.pl?file=../data/20120113/F018133.dat&hit=4" \t "_blank)    **Mass:** 30780    **Score:** 336    **Expect:** 8.6e-030  **Matches:** 26 |
|  | putative nuclear encoded protein Method: similarity and extension |

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| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | **Observed** | **Mr(expt)** | **Mr(calc)** | **ppm** | **Start** |  | **End** | **Miss** | **Ions** | **Peptide** |
|  | 911.5567 | 910.5494 | 910.5600 | -11.60 | 196 | - | 203 | 0 | --- | K.TPAQILLR.Y |
|  | 999.4901 | 998.4828 | 998.5509 | -68.15 | 240 | - | 247 | 1 | --- | K.LLESTKHR.Q + Oxidation (HW) |
|  | 1016.4747 | 1015.4674 | 1015.4685 | -1.03 | 250 | - | 257 | 0 | --- | R.LFTDDFMK.G |
|  | 1032.4697 | 1031.4624 | 1031.4634 | -0.94 | 250 | - | 257 | 0 | --- | R.LFTDDFMK.G + Oxidation (M) |
|  | 1103.5808 | 1102.5735 | 1102.5771 | -3.26 | 83 | - | 91 | 0 | --- | K.SVTVQDIWR.G |
|  | 1103.5808 | 1102.5735 | 1102.5771 | -3.26 | 83 | - | 91 | 0 | 62 | K.SVTVQDIWR.G |
|  | 1119.5797 | 1118.5724 | 1118.5720 | 0.35 | 83 | - | 91 | 0 | --- | K.SVTVQDIWR.G + Oxidation (HW) |
|  | 1225.5549 | 1224.5476 | 1224.5523 | -3.85 | 258 | - | 268 | 0 | --- | K.GHPEDPFAAER.- |
|  | 1225.5549 | 1224.5476 | 1224.5523 | -3.85 | 258 | - | 268 | 0 | 51 | K.GHPEDPFAAER.- |
|  | 1283.6632 | 1282.6559 | 1282.7106 | -42.59 | 240 | - | 249 | 2 | --- | K.LLESTKHRQR.L + Oxidation (HW) |
|  | 1289.7469 | 1288.7396 | 1288.7503 | -8.28 | 193 | - | 203 | 1 | --- | K.YSKTPAQILLR.Y |
|  | 1300.6488 | 1299.6415 | 1299.6282 | 10.3 | 248 | - | 257 | 1 | --- | R.QRLFTDDFMK.G |
|  | 1340.6504 | 1339.6431 | 1339.6619 | -14.05 | 176 | - | 187 | 1 | --- | K.EAPKDLDDPNVK.Q |
|  | 1354.6492 | 1353.6419 | 1353.6540 | -8.90 | 165 | - | 175 | 1 | --- | R.AQFMPDKFGWK.E |
|  | 1363.7800 | 1362.7727 | 1362.7871 | -10.53 | 25 | - | 35 | 2 | --- | K.IKREDLFITTK.V |
|  | 1370.6603 | 1369.6530 | 1369.6489 | 3.01 | 165 | - | 175 | 1 | --- | R.AQFMPDKFGWK.E + Oxidation (M) |
|  | 1386.7076 | 1385.7003 | 1385.6438 | 40.8 | 165 | - | 175 | 1 | --- | R.AQFMPDKFGWK.E + Oxidation (HW); Oxidation (M) |
|  | 1386.7076 | 1385.7003 | 1385.6438 | 40.8 | 165 | - | 175 | 1 | 2 | R.AQFMPDKFGWK.E + Oxidation (HW); Oxidation (M) |
|  | 1417.7721 | 1416.7648 | 1416.8452 | -56.76 | 192 | - | 203 | 2 | --- | K.KYSKTPAQILLR.Y |
|  | 1572.7612 | 1571.7539 | 1571.7692 | -9.72 | 104 | - | 117 | 0 | --- | K.AIGVSNWNGEQIER.V |
|  | 1572.7612 | 1571.7539 | 1571.7692 | -9.72 | 104 | - | 117 | 0 | 83 | K.AIGVSNWNGEQIER.V |
|  | 1588.7607 | 1587.7534 | 1587.7641 | -6.73 | 104 | - | 117 | 0 | --- | K.AIGVSNWNGEQIER.V + Oxidation (HW) |
|  | 1659.8221 | 1658.8148 | 1658.8376 | -13.75 | 149 | - | 164 | 0 | --- | K.HNVSLTSYATLGSPGR.A |
|  | 1875.8829 | 1874.8756 | 1874.8911 | -8.27 | 36 | - | 51 | 0 | --- | K.VWITHEHPDDTEGAIR.E |
|  | 2238.9758 | 2237.9685 | 2238.0052 | -16.38 | 250 | - | 268 | 1 | --- | R.LFTDDFMKGHPEDPFAAER.- + Oxidation (M) |
|  | 2238.9758 | 2237.9685 | 2238.0052 | -16.38 | 250 | - | 268 | 1 | 55 | R.LFTDDFMKGHPEDPFAAER.- + Oxidation (M) |

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| --- | --- |
|  | **No match to:** 905.4774, 907.4572, 935.4518, 994.4860, 1036.5116, 1045.5576, 1052.5287, 1062.4561, 1118.5878, 1135.5676, 1151.5809, 1163.6130, 1170.6744, 1189.6440, 1190.5983, 1192.6528, 1299.6344, 1349.6703, 1385.7020, 1416.7092, 1571.7432, 1573.7526, 1589.7434, 1604.7560, 1621.8300, 1728.8385, 1771.8662, 1888.8778, 2208.0649 |

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| **5.** | [isotig01076](http://msmsms/mascot/cgi/protein_view.pl?file=../data/20120113/F018133.dat&hit=5" \t "_blank)    **Mass:** 30780    **Score:** 336    **Expect:** 8.6e-030  **Matches:** 26 |
|  | putative nuclear encoded protein Method: similarity and extension |

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| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | **Observed** | **Mr(expt)** | **Mr(calc)** | **ppm** | **Start** |  | **End** | **Miss** | **Ions** | **Peptide** |
|  | 911.5567 | 910.5494 | 910.5600 | -11.60 | 196 | - | 203 | 0 | --- | K.TPAQILLR.Y |
|  | 999.4901 | 998.4828 | 998.5509 | -68.15 | 240 | - | 247 | 1 | --- | K.LLESTKHR.Q + Oxidation (HW) |
|  | 1016.4747 | 1015.4674 | 1015.4685 | -1.03 | 250 | - | 257 | 0 | --- | R.LFTDDFMK.G |
|  | 1032.4697 | 1031.4624 | 1031.4634 | -0.94 | 250 | - | 257 | 0 | --- | R.LFTDDFMK.G + Oxidation (M) |
|  | 1103.5808 | 1102.5735 | 1102.5771 | -3.26 | 83 | - | 91 | 0 | --- | K.SVTVQDIWR.G |
|  | 1103.5808 | 1102.5735 | 1102.5771 | -3.26 | 83 | - | 91 | 0 | 62 | K.SVTVQDIWR.G |
|  | 1119.5797 | 1118.5724 | 1118.5720 | 0.35 | 83 | - | 91 | 0 | --- | K.SVTVQDIWR.G + Oxidation (HW) |
|  | 1225.5549 | 1224.5476 | 1224.5523 | -3.85 | 258 | - | 268 | 0 | --- | K.GHPEDPFAAER.- |
|  | 1225.5549 | 1224.5476 | 1224.5523 | -3.85 | 258 | - | 268 | 0 | 51 | K.GHPEDPFAAER.- |
|  | 1283.6632 | 1282.6559 | 1282.7106 | -42.59 | 240 | - | 249 | 2 | --- | K.LLESTKHRQR.L + Oxidation (HW) |
|  | 1289.7469 | 1288.7396 | 1288.7503 | -8.28 | 193 | - | 203 | 1 | --- | K.YSKTPAQILLR.Y |
|  | 1300.6488 | 1299.6415 | 1299.6282 | 10.3 | 248 | - | 257 | 1 | --- | R.QRLFTDDFMK.G |
|  | 1340.6504 | 1339.6431 | 1339.6619 | -14.05 | 176 | - | 187 | 1 | --- | K.EAPKDLDDPNVK.Q |
|  | 1354.6492 | 1353.6419 | 1353.6540 | -8.90 | 165 | - | 175 | 1 | --- | R.AQFMPDKFGWK.E |
|  | 1363.7800 | 1362.7727 | 1362.7871 | -10.53 | 25 | - | 35 | 2 | --- | K.IKREDLFITTK.V |
|  | 1370.6603 | 1369.6530 | 1369.6489 | 3.01 | 165 | - | 175 | 1 | --- | R.AQFMPDKFGWK.E + Oxidation (M) |
|  | 1386.7076 | 1385.7003 | 1385.6438 | 40.8 | 165 | - | 175 | 1 | --- | R.AQFMPDKFGWK.E + Oxidation (HW); Oxidation (M) |
|  | 1386.7076 | 1385.7003 | 1385.6438 | 40.8 | 165 | - | 175 | 1 | 2 | R.AQFMPDKFGWK.E + Oxidation (HW); Oxidation (M) |
|  | 1417.7721 | 1416.7648 | 1416.8452 | -56.76 | 192 | - | 203 | 2 | --- | K.KYSKTPAQILLR.Y |
|  | 1572.7612 | 1571.7539 | 1571.7692 | -9.72 | 104 | - | 117 | 0 | --- | K.AIGVSNWNGEQIER.V |
|  | 1572.7612 | 1571.7539 | 1571.7692 | -9.72 | 104 | - | 117 | 0 | 83 | K.AIGVSNWNGEQIER.V |
|  | 1588.7607 | 1587.7534 | 1587.7641 | -6.73 | 104 | - | 117 | 0 | --- | K.AIGVSNWNGEQIER.V + Oxidation (HW) |
|  | 1659.8221 | 1658.8148 | 1658.8376 | -13.75 | 149 | - | 164 | 0 | --- | K.HNVSLTSYATLGSPGR.A |
|  | 1875.8829 | 1874.8756 | 1874.8911 | -8.27 | 36 | - | 51 | 0 | --- | K.VWITHEHPDDTEGAIR.E |
|  | 2238.9758 | 2237.9685 | 2238.0052 | -16.38 | 250 | - | 268 | 1 | --- | R.LFTDDFMKGHPEDPFAAER.- + Oxidation (M) |
|  | 2238.9758 | 2237.9685 | 2238.0052 | -16.38 | 250 | - | 268 | 1 | 55 | R.LFTDDFMKGHPEDPFAAER.- + Oxidation (M) |

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| --- | --- |
|  | **No match to:** 905.4774, 907.4572, 935.4518, 994.4860, 1036.5116, 1045.5576, 1052.5287, 1062.4561, 1118.5878, 1135.5676, 1151.5809, 1163.6130, 1170.6744, 1189.6440, 1190.5983, 1192.6528, 1299.6344, 1349.6703, 1385.7020, 1416.7092, 1571.7432, 1573.7526, 1589.7434, 1604.7560, 1621.8300, 1728.8385, 1771.8662, 1888.8778, 2208.0649 |

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| **6.** | [isotig01087](http://msmsms/mascot/cgi/protein_view.pl?file=../data/20120113/F018133.dat&hit=6" \t "_blank)    **Mass:** 30817    **Score:** 334    **Expect:** 1.4e-029  **Matches:** 26 |
|  | putative nuclear encoded protein Method: similarity and extension |

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| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | **Observed** | **Mr(expt)** | **Mr(calc)** | **ppm** | **Start** |  | **End** | **Miss** | **Ions** | **Peptide** |
|  | 911.5567 | 910.5494 | 910.5600 | -11.60 | 196 | - | 203 | 0 | --- | K.TPAQILLR.Y |
|  | 999.4901 | 998.4828 | 998.5509 | -68.15 | 240 | - | 247 | 1 | --- | K.LLESTKHR.Q + Oxidation (HW) |
|  | 1016.4747 | 1015.4674 | 1015.4685 | -1.03 | 250 | - | 257 | 0 | --- | R.LFTDDFMK.G |
|  | 1032.4697 | 1031.4624 | 1031.4634 | -0.94 | 250 | - | 257 | 0 | --- | R.LFTDDFMK.G + Oxidation (M) |
|  | 1103.5808 | 1102.5735 | 1102.5771 | -3.26 | 83 | - | 91 | 0 | --- | K.SVTVQDIWR.G |
|  | 1103.5808 | 1102.5735 | 1102.5771 | -3.26 | 83 | - | 91 | 0 | 62 | K.SVTVQDIWR.G |
|  | 1119.5797 | 1118.5724 | 1118.5720 | 0.35 | 83 | - | 91 | 0 | --- | K.SVTVQDIWR.G + Oxidation (HW) |
|  | 1225.5549 | 1224.5476 | 1224.5523 | -3.85 | 258 | - | 268 | 0 | --- | K.GHPEDPFAAER.- |
|  | 1225.5549 | 1224.5476 | 1224.5523 | -3.85 | 258 | - | 268 | 0 | 51 | K.GHPEDPFAAER.- |
|  | 1283.6632 | 1282.6559 | 1282.7106 | -42.59 | 240 | - | 249 | 2 | --- | K.LLESTKHRQR.L + Oxidation (HW) |
|  | 1289.7469 | 1288.7396 | 1288.7503 | -8.28 | 193 | - | 203 | 1 | --- | K.YSKTPAQILLR.Y |
|  | 1300.6488 | 1299.6415 | 1299.6282 | 10.3 | 248 | - | 257 | 1 | --- | R.QRLFTDDFMK.G |
|  | 1354.6492 | 1353.6419 | 1353.6540 | -8.90 | 165 | - | 175 | 1 | --- | R.AQFMPDKFGWK.E |
|  | 1363.7800 | 1362.7727 | 1362.7871 | -10.53 | 25 | - | 35 | 2 | --- | K.IKREDLFITTK.V |
|  | 1370.6603 | 1369.6530 | 1369.6489 | 3.01 | 165 | - | 175 | 1 | --- | R.AQFMPDKFGWK.E + Oxidation (M) |
|  | 1386.7076 | 1385.7003 | 1385.6438 | 40.8 | 165 | - | 175 | 1 | --- | R.AQFMPDKFGWK.E + Oxidation (HW); Oxidation (M) |
|  | 1386.7076 | 1385.7003 | 1385.6438 | 40.8 | 165 | - | 175 | 1 | 2 | R.AQFMPDKFGWK.E + Oxidation (HW); Oxidation (M) |
|  | 1417.7721 | 1416.7648 | 1416.8452 | -56.76 | 192 | - | 203 | 2 | --- | K.KYSKTPAQILLR.Y |
|  | 1572.7612 | 1571.7539 | 1571.7692 | -9.72 | 104 | - | 117 | 0 | --- | K.AIGVSNWNGEQIER.V |
|  | 1572.7612 | 1571.7539 | 1571.7692 | -9.72 | 104 | - | 117 | 0 | 83 | K.AIGVSNWNGEQIER.V |
|  | 1588.7607 | 1587.7534 | 1587.7641 | -6.73 | 104 | - | 117 | 0 | --- | K.AIGVSNWNGEQIER.V + Oxidation (HW) |
|  | 1589.7434 | 1588.7361 | 1588.8759 | -87.97 | 196 | - | 208 | 1 | --- | K.TPAQILLRYVMER.G |
|  | 1659.8221 | 1658.8148 | 1658.8376 | -13.75 | 149 | - | 164 | 0 | --- | K.HNVSLTSYATLGSPGR.A |
|  | 1875.8829 | 1874.8756 | 1874.8911 | -8.27 | 36 | - | 51 | 0 | --- | K.VWITHEHPDDTEGAIR.E |
|  | 2238.9758 | 2237.9685 | 2238.0052 | -16.38 | 250 | - | 268 | 1 | --- | R.LFTDDFMKGHPEDPFAAER.- + Oxidation (M) |
|  | 2238.9758 | 2237.9685 | 2238.0052 | -16.38 | 250 | - | 268 | 1 | 55 | R.LFTDDFMKGHPEDPFAAER.- + Oxidation (M) |

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| --- | --- |
|  | **No match to:** 905.4774, 907.4572, 935.4518, 994.4860, 1036.5116, 1045.5576, 1052.5287, 1062.4561, 1118.5878, 1135.5676, 1151.5809, 1163.6130, 1170.6744, 1189.6440, 1190.5983, 1192.6528, 1299.6344, 1340.6504, 1349.6703, 1385.7020, 1416.7092, 1571.7432, 1573.7526, 1604.7560, 1621.8300, 1728.8385, 1771.8662, 1888.8778, 2208.0649 |

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| **7.** | [isotig01088](http://msmsms/mascot/cgi/protein_view.pl?file=../data/20120113/F018133.dat&hit=7" \t "_blank)    **Mass:** 30798    **Score:** 334    **Expect:** 1.4e-029  **Matches:** 26 |
|  | putative nuclear encoded protein Method: similarity and extension |

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| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | **Observed** | **Mr(expt)** | **Mr(calc)** | **ppm** | **Start** |  | **End** | **Miss** | **Ions** | **Peptide** |
|  | 911.5567 | 910.5494 | 910.5600 | -11.60 | 196 | - | 203 | 0 | --- | K.TPAQILLR.Y |
|  | 999.4901 | 998.4828 | 998.5509 | -68.15 | 240 | - | 247 | 1 | --- | K.LLESTKHR.Q + Oxidation (HW) |
|  | 1016.4747 | 1015.4674 | 1015.4685 | -1.03 | 250 | - | 257 | 0 | --- | R.LFTDDFMK.G |
|  | 1032.4697 | 1031.4624 | 1031.4634 | -0.94 | 250 | - | 257 | 0 | --- | R.LFTDDFMK.G + Oxidation (M) |
|  | 1103.5808 | 1102.5735 | 1102.5771 | -3.26 | 83 | - | 91 | 0 | --- | K.SVTVQDIWR.G |
|  | 1103.5808 | 1102.5735 | 1102.5771 | -3.26 | 83 | - | 91 | 0 | 62 | K.SVTVQDIWR.G |
|  | 1119.5797 | 1118.5724 | 1118.5720 | 0.35 | 83 | - | 91 | 0 | --- | K.SVTVQDIWR.G + Oxidation (HW) |
|  | 1225.5549 | 1224.5476 | 1224.5523 | -3.85 | 258 | - | 268 | 0 | --- | K.GHPEDPFAAER.- |
|  | 1225.5549 | 1224.5476 | 1224.5523 | -3.85 | 258 | - | 268 | 0 | 51 | K.GHPEDPFAAER.- |
|  | 1283.6632 | 1282.6559 | 1282.7106 | -42.59 | 240 | - | 249 | 2 | --- | K.LLESTKHRQR.L + Oxidation (HW) |
|  | 1289.7469 | 1288.7396 | 1288.7503 | -8.28 | 193 | - | 203 | 1 | --- | K.YSKTPAQILLR.Y |
|  | 1300.6488 | 1299.6415 | 1299.6282 | 10.3 | 248 | - | 257 | 1 | --- | R.QRLFTDDFMK.G |
|  | 1340.6504 | 1339.6431 | 1339.6619 | -14.05 | 176 | - | 187 | 1 | --- | K.EAPKDLDDPNVK.Q |
|  | 1354.6492 | 1353.6419 | 1353.6540 | -8.90 | 165 | - | 175 | 1 | --- | R.AQFMPDKFGWK.E |
|  | 1363.7800 | 1362.7727 | 1362.7871 | -10.53 | 25 | - | 35 | 2 | --- | K.IKREDLFITTK.V |
|  | 1370.6603 | 1369.6530 | 1369.6489 | 3.01 | 165 | - | 175 | 1 | --- | R.AQFMPDKFGWK.E + Oxidation (M) |
|  | 1386.7076 | 1385.7003 | 1385.6438 | 40.8 | 165 | - | 175 | 1 | --- | R.AQFMPDKFGWK.E + Oxidation (HW); Oxidation (M) |
|  | 1386.7076 | 1385.7003 | 1385.6438 | 40.8 | 165 | - | 175 | 1 | 2 | R.AQFMPDKFGWK.E + Oxidation (HW); Oxidation (M) |
|  | 1417.7721 | 1416.7648 | 1416.8452 | -56.76 | 192 | - | 203 | 2 | --- | K.KYSKTPAQILLR.Y |
|  | 1572.7612 | 1571.7539 | 1571.7692 | -9.72 | 104 | - | 117 | 0 | --- | K.AIGVSNWNGEQIER.V |
|  | 1572.7612 | 1571.7539 | 1571.7692 | -9.72 | 104 | - | 117 | 0 | 83 | K.AIGVSNWNGEQIER.V |
|  | 1588.7607 | 1587.7534 | 1587.7641 | -6.73 | 104 | - | 117 | 0 | --- | K.AIGVSNWNGEQIER.V + Oxidation (HW) |
|  | 1659.8221 | 1658.8148 | 1658.8376 | -13.75 | 149 | - | 164 | 0 | --- | K.HNVSLTSYATLGSPGR.A |
|  | 1875.8829 | 1874.8756 | 1874.8911 | -8.27 | 36 | - | 51 | 0 | --- | K.VWITHEHPDDTEGAIR.E |
|  | 2238.9758 | 2237.9685 | 2238.0052 | -16.38 | 250 | - | 268 | 1 | --- | R.LFTDDFMKGHPEDPFAAER.- + Oxidation (M) |
|  | 2238.9758 | 2237.9685 | 2238.0052 | -16.38 | 250 | - | 268 | 1 | 55 | R.LFTDDFMKGHPEDPFAAER.- + Oxidation (M) |

|  |  |
| --- | --- |
|  | **No match to:** 905.4774, 907.4572, 935.4518, 994.4860, 1036.5116, 1045.5576, 1052.5287, 1062.4561, 1118.5878, 1135.5676, 1151.5809, 1163.6130, 1170.6744, 1189.6440, 1190.5983, 1192.6528, 1299.6344, 1349.6703, 1385.7020, 1416.7092, 1571.7432, 1573.7526, 1589.7434, 1604.7560, 1621.8300, 1728.8385, 1771.8662, 1888.8778, 2208.0649 |

|  |  |
| --- | --- |
| **8.** | [isotig01082](http://msmsms/mascot/cgi/protein_view.pl?file=../data/20120113/F018133.dat&hit=8" \t "_blank)    **Mass:** 30803    **Score:** 326    **Expect:** 8.6e-029  **Matches:** 25 |
|  | putative nuclear encoded protein Method: similarity and extension |

|  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | **Observed** | **Mr(expt)** | **Mr(calc)** | **ppm** | **Start** |  | **End** | **Miss** | **Ions** | **Peptide** |
|  | 911.5567 | 910.5494 | 910.5600 | -11.60 | 196 | - | 203 | 0 | --- | K.TPAQILLR.Y |
|  | 999.4901 | 998.4828 | 998.5509 | -68.15 | 240 | - | 247 | 1 | --- | K.LLESTKHR.Q + Oxidation (HW) |
|  | 1016.4747 | 1015.4674 | 1015.4685 | -1.03 | 250 | - | 257 | 0 | --- | R.LFTDDFMK.G |
|  | 1032.4697 | 1031.4624 | 1031.4634 | -0.94 | 250 | - | 257 | 0 | --- | R.LFTDDFMK.G + Oxidation (M) |
|  | 1103.5808 | 1102.5735 | 1102.5771 | -3.26 | 83 | - | 91 | 0 | --- | K.SVTVQDIWR.G |
|  | 1103.5808 | 1102.5735 | 1102.5771 | -3.26 | 83 | - | 91 | 0 | 62 | K.SVTVQDIWR.G |
|  | 1119.5797 | 1118.5724 | 1118.5720 | 0.35 | 83 | - | 91 | 0 | --- | K.SVTVQDIWR.G + Oxidation (HW) |
|  | 1225.5549 | 1224.5476 | 1224.5523 | -3.85 | 258 | - | 268 | 0 | --- | K.GHPEDPFAAER.- |
|  | 1225.5549 | 1224.5476 | 1224.5523 | -3.85 | 258 | - | 268 | 0 | 51 | K.GHPEDPFAAER.- |
|  | 1283.6632 | 1282.6559 | 1282.7106 | -42.59 | 240 | - | 249 | 2 | --- | K.LLESTKHRQR.L + Oxidation (HW) |
|  | 1289.7469 | 1288.7396 | 1288.7503 | -8.28 | 193 | - | 203 | 1 | --- | K.YSKTPAQILLR.Y |
|  | 1300.6488 | 1299.6415 | 1299.6282 | 10.3 | 248 | - | 257 | 1 | --- | R.QRLFTDDFMK.G |
|  | 1354.6492 | 1353.6419 | 1353.6540 | -8.90 | 165 | - | 175 | 1 | --- | R.AQFMPDKFGWK.E |
|  | 1363.7800 | 1362.7727 | 1362.7871 | -10.53 | 25 | - | 35 | 2 | --- | K.IKREDLFITTK.V |
|  | 1370.6603 | 1369.6530 | 1369.6489 | 3.01 | 165 | - | 175 | 1 | --- | R.AQFMPDKFGWK.E + Oxidation (M) |
|  | 1386.7076 | 1385.7003 | 1385.6438 | 40.8 | 165 | - | 175 | 1 | --- | R.AQFMPDKFGWK.E + Oxidation (HW); Oxidation (M) |
|  | 1386.7076 | 1385.7003 | 1385.6438 | 40.8 | 165 | - | 175 | 1 | 2 | R.AQFMPDKFGWK.E + Oxidation (HW); Oxidation (M) |
|  | 1417.7721 | 1416.7648 | 1416.8452 | -56.76 | 192 | - | 203 | 2 | --- | K.KYSKTPAQILLR.Y |
|  | 1572.7612 | 1571.7539 | 1571.7692 | -9.72 | 104 | - | 117 | 0 | --- | K.AIGVSNWNGEQIER.V |
|  | 1572.7612 | 1571.7539 | 1571.7692 | -9.72 | 104 | - | 117 | 0 | 83 | K.AIGVSNWNGEQIER.V |
|  | 1588.7607 | 1587.7534 | 1587.7641 | -6.73 | 104 | - | 117 | 0 | --- | K.AIGVSNWNGEQIER.V + Oxidation (HW) |
|  | 1659.8221 | 1658.8148 | 1658.8376 | -13.75 | 149 | - | 164 | 0 | --- | K.HNVSLTSYATLGSPGR.A |
|  | 1875.8829 | 1874.8756 | 1874.8911 | -8.27 | 36 | - | 51 | 0 | --- | K.VWITHEHPDDTEGAIR.E |
|  | 2238.9758 | 2237.9685 | 2238.0052 | -16.38 | 250 | - | 268 | 1 | --- | R.LFTDDFMKGHPEDPFAAER.- + Oxidation (M) |
|  | 2238.9758 | 2237.9685 | 2238.0052 | -16.38 | 250 | - | 268 | 1 | 55 | R.LFTDDFMKGHPEDPFAAER.- + Oxidation (M) |

|  |  |
| --- | --- |
|  | **No match to:** 905.4774, 907.4572, 935.4518, 994.4860, 1036.5116, 1045.5576, 1052.5287, 1062.4561, 1118.5878, 1135.5676, 1151.5809, 1163.6130, 1170.6744, 1189.6440, 1190.5983, 1192.6528, 1299.6344, 1340.6504, 1349.6703, 1385.7020, 1416.7092, 1571.7432, 1573.7526, 1589.7434, 1604.7560, 1621.8300, 1728.8385, 1771.8662, 1888.8778, 2208.0649 |

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| --- | --- |
| **9.** | [isotig01074](http://msmsms/mascot/cgi/protein_view.pl?file=../data/20120113/F018133.dat&hit=9" \t "_blank)    **Mass:** 30803    **Score:** 326    **Expect:** 8.6e-029  **Matches:** 25 |
|  | putative nuclear encoded protein Method: similarity and extension |

|  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | **Observed** | **Mr(expt)** | **Mr(calc)** | **ppm** | **Start** |  | **End** | **Miss** | **Ions** | **Peptide** |
|  | 911.5567 | 910.5494 | 910.5600 | -11.60 | 196 | - | 203 | 0 | --- | K.TPAQILLR.Y |
|  | 999.4901 | 998.4828 | 998.5509 | -68.15 | 240 | - | 247 | 1 | --- | K.LLESTKHR.Q + Oxidation (HW) |
|  | 1016.4747 | 1015.4674 | 1015.4685 | -1.03 | 250 | - | 257 | 0 | --- | R.LFTDDFMK.G |
|  | 1032.4697 | 1031.4624 | 1031.4634 | -0.94 | 250 | - | 257 | 0 | --- | R.LFTDDFMK.G + Oxidation (M) |
|  | 1103.5808 | 1102.5735 | 1102.5771 | -3.26 | 83 | - | 91 | 0 | --- | K.SVTVQDIWR.G |
|  | 1103.5808 | 1102.5735 | 1102.5771 | -3.26 | 83 | - | 91 | 0 | 62 | K.SVTVQDIWR.G |
|  | 1119.5797 | 1118.5724 | 1118.5720 | 0.35 | 83 | - | 91 | 0 | --- | K.SVTVQDIWR.G + Oxidation (HW) |
|  | 1225.5549 | 1224.5476 | 1224.5523 | -3.85 | 258 | - | 268 | 0 | --- | K.GHPEDPFAAER.- |
|  | 1225.5549 | 1224.5476 | 1224.5523 | -3.85 | 258 | - | 268 | 0 | 51 | K.GHPEDPFAAER.- |
|  | 1283.6632 | 1282.6559 | 1282.7106 | -42.59 | 240 | - | 249 | 2 | --- | K.LLESTKHRQR.L + Oxidation (HW) |
|  | 1289.7469 | 1288.7396 | 1288.7503 | -8.28 | 193 | - | 203 | 1 | --- | K.YSKTPAQILLR.Y |
|  | 1300.6488 | 1299.6415 | 1299.6282 | 10.3 | 248 | - | 257 | 1 | --- | R.QRLFTDDFMK.G |
|  | 1354.6492 | 1353.6419 | 1353.6540 | -8.90 | 165 | - | 175 | 1 | --- | R.AQFMPDKFGWK.E |
|  | 1363.7800 | 1362.7727 | 1362.7871 | -10.53 | 25 | - | 35 | 2 | --- | K.IKREDLFITTK.V |
|  | 1370.6603 | 1369.6530 | 1369.6489 | 3.01 | 165 | - | 175 | 1 | --- | R.AQFMPDKFGWK.E + Oxidation (M) |
|  | 1386.7076 | 1385.7003 | 1385.6438 | 40.8 | 165 | - | 175 | 1 | --- | R.AQFMPDKFGWK.E + Oxidation (HW); Oxidation (M) |
|  | 1386.7076 | 1385.7003 | 1385.6438 | 40.8 | 165 | - | 175 | 1 | 2 | R.AQFMPDKFGWK.E + Oxidation (HW); Oxidation (M) |
|  | 1417.7721 | 1416.7648 | 1416.8452 | -56.76 | 192 | - | 203 | 2 | --- | K.KYSKTPAQILLR.Y |
|  | 1572.7612 | 1571.7539 | 1571.7692 | -9.72 | 104 | - | 117 | 0 | --- | K.AIGVSNWNGEQIER.V |
|  | 1572.7612 | 1571.7539 | 1571.7692 | -9.72 | 104 | - | 117 | 0 | 83 | K.AIGVSNWNGEQIER.V |
|  | 1588.7607 | 1587.7534 | 1587.7641 | -6.73 | 104 | - | 117 | 0 | --- | K.AIGVSNWNGEQIER.V + Oxidation (HW) |
|  | 1659.8221 | 1658.8148 | 1658.8376 | -13.75 | 149 | - | 164 | 0 | --- | K.HNVSLTSYATLGSPGR.A |
|  | 1875.8829 | 1874.8756 | 1874.8911 | -8.27 | 36 | - | 51 | 0 | --- | K.VWITHEHPDDTEGAIR.E |
|  | 2238.9758 | 2237.9685 | 2238.0052 | -16.38 | 250 | - | 268 | 1 | --- | R.LFTDDFMKGHPEDPFAAER.- + Oxidation (M) |
|  | 2238.9758 | 2237.9685 | 2238.0052 | -16.38 | 250 | - | 268 | 1 | 55 | R.LFTDDFMKGHPEDPFAAER.- + Oxidation (M) |

|  |  |
| --- | --- |
|  | **No match to:** 905.4774, 907.4572, 935.4518, 994.4860, 1036.5116, 1045.5576, 1052.5287, 1062.4561, 1118.5878, 1135.5676, 1151.5809, 1163.6130, 1170.6744, 1189.6440, 1190.5983, 1192.6528, 1299.6344, 1340.6504, 1349.6703, 1385.7020, 1416.7092, 1571.7432, 1573.7526, 1589.7434, 1604.7560, 1621.8300, 1728.8385, 1771.8662, 1888.8778, 2208.0649 |

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| --- | --- |
| **10.** | [isotig01084](http://msmsms/mascot/cgi/protein_view.pl?file=../data/20120113/F018133.dat&hit=10" \t "_blank)    **Mass:** 30803    **Score:** 326    **Expect:** 8.6e-029  **Matches:** 25 |
|  | putative nuclear encoded protein Method: similarity and extension |

|  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | **Observed** | **Mr(expt)** | **Mr(calc)** | **ppm** | **Start** |  | **End** | **Miss** | **Ions** | **Peptide** |
|  | 911.5567 | 910.5494 | 910.5600 | -11.60 | 196 | - | 203 | 0 | --- | K.TPAQILLR.Y |
|  | 999.4901 | 998.4828 | 998.5509 | -68.15 | 240 | - | 247 | 1 | --- | K.LLESTKHR.Q + Oxidation (HW) |
|  | 1016.4747 | 1015.4674 | 1015.4685 | -1.03 | 250 | - | 257 | 0 | --- | R.LFTDDFMK.G |
|  | 1032.4697 | 1031.4624 | 1031.4634 | -0.94 | 250 | - | 257 | 0 | --- | R.LFTDDFMK.G + Oxidation (M) |
|  | 1103.5808 | 1102.5735 | 1102.5771 | -3.26 | 83 | - | 91 | 0 | --- | K.SVTVQDIWR.G |
|  | 1103.5808 | 1102.5735 | 1102.5771 | -3.26 | 83 | - | 91 | 0 | 62 | K.SVTVQDIWR.G |
|  | 1119.5797 | 1118.5724 | 1118.5720 | 0.35 | 83 | - | 91 | 0 | --- | K.SVTVQDIWR.G + Oxidation (HW) |
|  | 1225.5549 | 1224.5476 | 1224.5523 | -3.85 | 258 | - | 268 | 0 | --- | K.GHPEDPFAAER.- |
|  | 1225.5549 | 1224.5476 | 1224.5523 | -3.85 | 258 | - | 268 | 0 | 51 | K.GHPEDPFAAER.- |
|  | 1283.6632 | 1282.6559 | 1282.7106 | -42.59 | 240 | - | 249 | 2 | --- | K.LLESTKHRQR.L + Oxidation (HW) |
|  | 1289.7469 | 1288.7396 | 1288.7503 | -8.28 | 193 | - | 203 | 1 | --- | K.YSKTPAQILLR.Y |
|  | 1300.6488 | 1299.6415 | 1299.6282 | 10.3 | 248 | - | 257 | 1 | --- | R.QRLFTDDFMK.G |
|  | 1354.6492 | 1353.6419 | 1353.6540 | -8.90 | 165 | - | 175 | 1 | --- | R.AQFMPDKFGWK.E |
|  | 1363.7800 | 1362.7727 | 1362.7871 | -10.53 | 25 | - | 35 | 2 | --- | K.IKREDLFITTK.V |
|  | 1370.6603 | 1369.6530 | 1369.6489 | 3.01 | 165 | - | 175 | 1 | --- | R.AQFMPDKFGWK.E + Oxidation (M) |
|  | 1386.7076 | 1385.7003 | 1385.6438 | 40.8 | 165 | - | 175 | 1 | --- | R.AQFMPDKFGWK.E + Oxidation (HW); Oxidation (M) |
|  | 1386.7076 | 1385.7003 | 1385.6438 | 40.8 | 165 | - | 175 | 1 | 2 | R.AQFMPDKFGWK.E + Oxidation (HW); Oxidation (M) |
|  | 1417.7721 | 1416.7648 | 1416.8452 | -56.76 | 192 | - | 203 | 2 | --- | K.KYSKTPAQILLR.Y |
|  | 1572.7612 | 1571.7539 | 1571.7692 | -9.72 | 104 | - | 117 | 0 | --- | K.AIGVSNWNGEQIER.V |
|  | 1572.7612 | 1571.7539 | 1571.7692 | -9.72 | 104 | - | 117 | 0 | 83 | K.AIGVSNWNGEQIER.V |
|  | 1588.7607 | 1587.7534 | 1587.7641 | -6.73 | 104 | - | 117 | 0 | --- | K.AIGVSNWNGEQIER.V + Oxidation (HW) |
|  | 1659.8221 | 1658.8148 | 1658.8376 | -13.75 | 149 | - | 164 | 0 | --- | K.HNVSLTSYATLGSPGR.A |
|  | 1875.8829 | 1874.8756 | 1874.8911 | -8.27 | 36 | - | 51 | 0 | --- | K.VWITHEHPDDTEGAIR.E |
|  | 2238.9758 | 2237.9685 | 2238.0052 | -16.38 | 250 | - | 268 | 1 | --- | R.LFTDDFMKGHPEDPFAAER.- + Oxidation (M) |
|  | 2238.9758 | 2237.9685 | 2238.0052 | -16.38 | 250 | - | 268 | 1 | 55 | R.LFTDDFMKGHPEDPFAAER.- + Oxidation (M) |

|  |  |
| --- | --- |
|  | **No match to:** 905.4774, 907.4572, 935.4518, 994.4860, 1036.5116, 1045.5576, 1052.5287, 1062.4561, 1118.5878, 1135.5676, 1151.5809, 1163.6130, 1170.6744, 1189.6440, 1190.5983, 1192.6528, 1299.6344, 1340.6504, 1349.6703, 1385.7020, 1416.7092, 1571.7432, 1573.7526, 1589.7434, 1604.7560, 1621.8300, 1728.8385, 1771.8662, 1888.8778, 2208.0649 |

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| **11.** | [isotig01077](http://msmsms/mascot/cgi/protein_view.pl?file=../data/20120113/F018133.dat&hit=11" \t "_blank)    **Mass:** 30803    **Score:** 326    **Expect:** 8.6e-029  **Matches:** 25 |
|  | putative nuclear encoded protein Method: similarity and extension |

|  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | **Observed** | **Mr(expt)** | **Mr(calc)** | **ppm** | **Start** |  | **End** | **Miss** | **Ions** | **Peptide** |
|  | 911.5567 | 910.5494 | 910.5600 | -11.60 | 196 | - | 203 | 0 | --- | K.TPAQILLR.Y |
|  | 999.4901 | 998.4828 | 998.5509 | -68.15 | 240 | - | 247 | 1 | --- | K.LLESTKHR.Q + Oxidation (HW) |
|  | 1016.4747 | 1015.4674 | 1015.4685 | -1.03 | 250 | - | 257 | 0 | --- | R.LFTDDFMK.G |
|  | 1032.4697 | 1031.4624 | 1031.4634 | -0.94 | 250 | - | 257 | 0 | --- | R.LFTDDFMK.G + Oxidation (M) |
|  | 1103.5808 | 1102.5735 | 1102.5771 | -3.26 | 83 | - | 91 | 0 | --- | K.SVTVQDIWR.G |
|  | 1103.5808 | 1102.5735 | 1102.5771 | -3.26 | 83 | - | 91 | 0 | 62 | K.SVTVQDIWR.G |
|  | 1119.5797 | 1118.5724 | 1118.5720 | 0.35 | 83 | - | 91 | 0 | --- | K.SVTVQDIWR.G + Oxidation (HW) |
|  | 1225.5549 | 1224.5476 | 1224.5523 | -3.85 | 258 | - | 268 | 0 | --- | K.GHPEDPFAAER.- |
|  | 1225.5549 | 1224.5476 | 1224.5523 | -3.85 | 258 | - | 268 | 0 | 51 | K.GHPEDPFAAER.- |
|  | 1283.6632 | 1282.6559 | 1282.7106 | -42.59 | 240 | - | 249 | 2 | --- | K.LLESTKHRQR.L + Oxidation (HW) |
|  | 1289.7469 | 1288.7396 | 1288.7503 | -8.28 | 193 | - | 203 | 1 | --- | K.YSKTPAQILLR.Y |
|  | 1300.6488 | 1299.6415 | 1299.6282 | 10.3 | 248 | - | 257 | 1 | --- | R.QRLFTDDFMK.G |
|  | 1354.6492 | 1353.6419 | 1353.6540 | -8.90 | 165 | - | 175 | 1 | --- | R.AQFMPDKFGWK.E |
|  | 1363.7800 | 1362.7727 | 1362.7871 | -10.53 | 25 | - | 35 | 2 | --- | K.IKREDLFITTK.V |
|  | 1370.6603 | 1369.6530 | 1369.6489 | 3.01 | 165 | - | 175 | 1 | --- | R.AQFMPDKFGWK.E + Oxidation (M) |
|  | 1386.7076 | 1385.7003 | 1385.6438 | 40.8 | 165 | - | 175 | 1 | --- | R.AQFMPDKFGWK.E + Oxidation (HW); Oxidation (M) |
|  | 1386.7076 | 1385.7003 | 1385.6438 | 40.8 | 165 | - | 175 | 1 | 2 | R.AQFMPDKFGWK.E + Oxidation (HW); Oxidation (M) |
|  | 1417.7721 | 1416.7648 | 1416.8452 | -56.76 | 192 | - | 203 | 2 | --- | K.KYSKTPAQILLR.Y |
|  | 1572.7612 | 1571.7539 | 1571.7692 | -9.72 | 104 | - | 117 | 0 | --- | K.AIGVSNWNGEQIER.V |
|  | 1572.7612 | 1571.7539 | 1571.7692 | -9.72 | 104 | - | 117 | 0 | 83 | K.AIGVSNWNGEQIER.V |
|  | 1588.7607 | 1587.7534 | 1587.7641 | -6.73 | 104 | - | 117 | 0 | --- | K.AIGVSNWNGEQIER.V + Oxidation (HW) |
|  | 1659.8221 | 1658.8148 | 1658.8376 | -13.75 | 149 | - | 164 | 0 | --- | K.HNVSLTSYATLGSPGR.A |
|  | 1875.8829 | 1874.8756 | 1874.8911 | -8.27 | 36 | - | 51 | 0 | --- | K.VWITHEHPDDTEGAIR.E |
|  | 2238.9758 | 2237.9685 | 2238.0052 | -16.38 | 250 | - | 268 | 1 | --- | R.LFTDDFMKGHPEDPFAAER.- + Oxidation (M) |
|  | 2238.9758 | 2237.9685 | 2238.0052 | -16.38 | 250 | - | 268 | 1 | 55 | R.LFTDDFMKGHPEDPFAAER.- + Oxidation (M) |

|  |  |
| --- | --- |
|  | **No match to:** 905.4774, 907.4572, 935.4518, 994.4860, 1036.5116, 1045.5576, 1052.5287, 1062.4561, 1118.5878, 1135.5676, 1151.5809, 1163.6130, 1170.6744, 1189.6440, 1190.5983, 1192.6528, 1299.6344, 1340.6504, 1349.6703, 1385.7020, 1416.7092, 1571.7432, 1573.7526, 1589.7434, 1604.7560, 1621.8300, 1728.8385, 1771.8662, 1888.8778, 2208.0649 |

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| **12.** | [isotig01080](http://msmsms/mascot/cgi/protein_view.pl?file=../data/20120113/F018133.dat&hit=12" \t "_blank)    **Mass:** 30766    **Score:** 318    **Expect:** 5.4e-028  **Matches:** 24 |
|  | putative nuclear encoded protein Method: similarity and extension |

|  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | **Observed** | **Mr(expt)** | **Mr(calc)** | **ppm** | **Start** |  | **End** | **Miss** | **Ions** | **Peptide** |
|  | 911.5567 | 910.5494 | 910.5600 | -11.60 | 196 | - | 203 | 0 | --- | K.TPAQILLR.Y |
|  | 1016.4747 | 1015.4674 | 1015.4685 | -1.03 | 250 | - | 257 | 0 | --- | R.LFTDDFMK.G |
|  | 1032.4697 | 1031.4624 | 1031.4634 | -0.94 | 250 | - | 257 | 0 | --- | R.LFTDDFMK.G + Oxidation (M) |
|  | 1103.5808 | 1102.5735 | 1102.5771 | -3.26 | 83 | - | 91 | 0 | --- | K.SVTVQDIWR.G |
|  | 1103.5808 | 1102.5735 | 1102.5771 | -3.26 | 83 | - | 91 | 0 | 62 | K.SVTVQDIWR.G |
|  | 1119.5797 | 1118.5724 | 1118.5720 | 0.35 | 83 | - | 91 | 0 | --- | K.SVTVQDIWR.G + Oxidation (HW) |
|  | 1225.5549 | 1224.5476 | 1224.5523 | -3.85 | 258 | - | 268 | 0 | --- | K.GHPEDPFAAER.- |
|  | 1225.5549 | 1224.5476 | 1224.5523 | -3.85 | 258 | - | 268 | 0 | 51 | K.GHPEDPFAAER.- |
|  | 1289.7469 | 1288.7396 | 1288.7503 | -8.28 | 193 | - | 203 | 1 | --- | K.YSKTPAQILLR.Y |
|  | 1300.6488 | 1299.6415 | 1299.6282 | 10.3 | 248 | - | 257 | 1 | --- | R.QRLFTDDFMK.G |
|  | 1340.6504 | 1339.6431 | 1339.6619 | -14.05 | 176 | - | 187 | 1 | --- | K.EAPKDLDDPNVK.Q |
|  | 1354.6492 | 1353.6419 | 1353.6540 | -8.90 | 165 | - | 175 | 1 | --- | R.AQFMPDKFGWK.E |
|  | 1363.7800 | 1362.7727 | 1362.7871 | -10.53 | 25 | - | 35 | 2 | --- | K.IKREDLFITTK.V |
|  | 1370.6603 | 1369.6530 | 1369.6489 | 3.01 | 165 | - | 175 | 1 | --- | R.AQFMPDKFGWK.E + Oxidation (M) |
|  | 1386.7076 | 1385.7003 | 1385.6438 | 40.8 | 165 | - | 175 | 1 | --- | R.AQFMPDKFGWK.E + Oxidation (HW); Oxidation (M) |
|  | 1386.7076 | 1385.7003 | 1385.6438 | 40.8 | 165 | - | 175 | 1 | 2 | R.AQFMPDKFGWK.E + Oxidation (HW); Oxidation (M) |
|  | 1417.7721 | 1416.7648 | 1416.8452 | -56.76 | 192 | - | 203 | 2 | --- | K.KYSKTPAQILLR.Y |
|  | 1572.7612 | 1571.7539 | 1571.7692 | -9.72 | 104 | - | 117 | 0 | --- | K.AIGVSNWNGEQIER.V |
|  | 1572.7612 | 1571.7539 | 1571.7692 | -9.72 | 104 | - | 117 | 0 | 83 | K.AIGVSNWNGEQIER.V |
|  | 1588.7607 | 1587.7534 | 1587.7641 | -6.73 | 104 | - | 117 | 0 | --- | K.AIGVSNWNGEQIER.V + Oxidation (HW) |
|  | 1659.8221 | 1658.8148 | 1658.8376 | -13.75 | 149 | - | 164 | 0 | --- | K.HNVSLTSYATLGSPGR.A |
|  | 1875.8829 | 1874.8756 | 1874.8911 | -8.27 | 36 | - | 51 | 0 | --- | K.VWITHEHPDDTEGAIR.E |
|  | 2238.9758 | 2237.9685 | 2238.0052 | -16.38 | 250 | - | 268 | 1 | --- | R.LFTDDFMKGHPEDPFAAER.- + Oxidation (M) |
|  | 2238.9758 | 2237.9685 | 2238.0052 | -16.38 | 250 | - | 268 | 1 | 55 | R.LFTDDFMKGHPEDPFAAER.- + Oxidation (M) |

|  |  |
| --- | --- |
|  | **No match to:** 905.4774, 907.4572, 935.4518, 994.4860, 999.4901, 1036.5116, 1045.5576, 1052.5287, 1062.4561, 1118.5878, 1135.5676, 1151.5809, 1163.6130, 1170.6744, 1189.6440, 1190.5983, 1192.6528, 1283.6632, 1299.6344, 1349.6703, 1385.7020, 1416.7092, 1571.7432, 1573.7526, 1589.7434, 1604.7560, 1621.8300, 1728.8385, 1771.8662, 1888.8778, 2208.0649 |

|  |  |
| --- | --- |
| **13.** | [isotig01079](http://msmsms/mascot/cgi/protein_view.pl?file=../data/20120113/F018133.dat&hit=13" \t "_blank)    **Mass:** 30766    **Score:** 318    **Expect:** 5.4e-028  **Matches:** 24 |
|  | putative nuclear encoded protein Method: similarity and extension |

|  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | **Observed** | **Mr(expt)** | **Mr(calc)** | **ppm** | **Start** |  | **End** | **Miss** | **Ions** | **Peptide** |
|  | 911.5567 | 910.5494 | 910.5600 | -11.60 | 196 | - | 203 | 0 | --- | K.TPAQILLR.Y |
|  | 1016.4747 | 1015.4674 | 1015.4685 | -1.03 | 250 | - | 257 | 0 | --- | R.LFTDDFMK.G |
|  | 1032.4697 | 1031.4624 | 1031.4634 | -0.94 | 250 | - | 257 | 0 | --- | R.LFTDDFMK.G + Oxidation (M) |
|  | 1103.5808 | 1102.5735 | 1102.5771 | -3.26 | 83 | - | 91 | 0 | --- | K.SVTVQDIWR.G |
|  | 1103.5808 | 1102.5735 | 1102.5771 | -3.26 | 83 | - | 91 | 0 | 62 | K.SVTVQDIWR.G |
|  | 1119.5797 | 1118.5724 | 1118.5720 | 0.35 | 83 | - | 91 | 0 | --- | K.SVTVQDIWR.G + Oxidation (HW) |
|  | 1225.5549 | 1224.5476 | 1224.5523 | -3.85 | 258 | - | 268 | 0 | --- | K.GHPEDPFAAER.- |
|  | 1225.5549 | 1224.5476 | 1224.5523 | -3.85 | 258 | - | 268 | 0 | 51 | K.GHPEDPFAAER.- |
|  | 1289.7469 | 1288.7396 | 1288.7503 | -8.28 | 193 | - | 203 | 1 | --- | K.YSKTPAQILLR.Y |
|  | 1300.6488 | 1299.6415 | 1299.6282 | 10.3 | 248 | - | 257 | 1 | --- | R.QRLFTDDFMK.G |
|  | 1340.6504 | 1339.6431 | 1339.6619 | -14.05 | 176 | - | 187 | 1 | --- | K.EAPKDLDDPNVK.Q |
|  | 1354.6492 | 1353.6419 | 1353.6540 | -8.90 | 165 | - | 175 | 1 | --- | R.AQFMPDKFGWK.E |
|  | 1363.7800 | 1362.7727 | 1362.7871 | -10.53 | 25 | - | 35 | 2 | --- | K.IKREDLFITTK.V |
|  | 1370.6603 | 1369.6530 | 1369.6489 | 3.01 | 165 | - | 175 | 1 | --- | R.AQFMPDKFGWK.E + Oxidation (M) |
|  | 1386.7076 | 1385.7003 | 1385.6438 | 40.8 | 165 | - | 175 | 1 | --- | R.AQFMPDKFGWK.E + Oxidation (HW); Oxidation (M) |
|  | 1386.7076 | 1385.7003 | 1385.6438 | 40.8 | 165 | - | 175 | 1 | 2 | R.AQFMPDKFGWK.E + Oxidation (HW); Oxidation (M) |
|  | 1417.7721 | 1416.7648 | 1416.8452 | -56.76 | 192 | - | 203 | 2 | --- | K.KYSKTPAQILLR.Y |
|  | 1572.7612 | 1571.7539 | 1571.7692 | -9.72 | 104 | - | 117 | 0 | --- | K.AIGVSNWNGEQIER.V |
|  | 1572.7612 | 1571.7539 | 1571.7692 | -9.72 | 104 | - | 117 | 0 | 83 | K.AIGVSNWNGEQIER.V |
|  | 1588.7607 | 1587.7534 | 1587.7641 | -6.73 | 104 | - | 117 | 0 | --- | K.AIGVSNWNGEQIER.V + Oxidation (HW) |
|  | 1659.8221 | 1658.8148 | 1658.8376 | -13.75 | 149 | - | 164 | 0 | --- | K.HNVSLTSYATLGSPGR.A |
|  | 1875.8829 | 1874.8756 | 1874.8911 | -8.27 | 36 | - | 51 | 0 | --- | K.VWITHEHPDDTEGAIR.E |
|  | 2238.9758 | 2237.9685 | 2238.0052 | -16.38 | 250 | - | 268 | 1 | --- | R.LFTDDFMKGHPEDPFAAER.- + Oxidation (M) |
|  | 2238.9758 | 2237.9685 | 2238.0052 | -16.38 | 250 | - | 268 | 1 | 55 | R.LFTDDFMKGHPEDPFAAER.- + Oxidation (M) |

|  |  |
| --- | --- |
|  | **No match to:** 905.4774, 907.4572, 935.4518, 994.4860, 999.4901, 1036.5116, 1045.5576, 1052.5287, 1062.4561, 1118.5878, 1135.5676, 1151.5809, 1163.6130, 1170.6744, 1189.6440, 1190.5983, 1192.6528, 1283.6632, 1299.6344, 1349.6703, 1385.7020, 1416.7092, 1571.7432, 1573.7526, 1589.7434, 1604.7560, 1621.8300, 1728.8385, 1771.8662, 1888.8778, 2208.0649 |

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| --- | --- |
| **14.** | [isotig01081](http://msmsms/mascot/cgi/protein_view.pl?file=../data/20120113/F018133.dat&hit=14" \t "_blank)    **Mass:** 30789    **Score:** 309    **Expect:** 4.3e-027  **Matches:** 23 |
|  | putative nuclear encoded protein Method: similarity and extension |

|  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | **Observed** | **Mr(expt)** | **Mr(calc)** | **ppm** | **Start** |  | **End** | **Miss** | **Ions** | **Peptide** |
|  | 911.5567 | 910.5494 | 910.5600 | -11.60 | 196 | - | 203 | 0 | --- | K.TPAQILLR.Y |
|  | 1016.4747 | 1015.4674 | 1015.4685 | -1.03 | 250 | - | 257 | 0 | --- | R.LFTDDFMK.G |
|  | 1032.4697 | 1031.4624 | 1031.4634 | -0.94 | 250 | - | 257 | 0 | --- | R.LFTDDFMK.G + Oxidation (M) |
|  | 1103.5808 | 1102.5735 | 1102.5771 | -3.26 | 83 | - | 91 | 0 | --- | K.SVTVQDIWR.G |
|  | 1103.5808 | 1102.5735 | 1102.5771 | -3.26 | 83 | - | 91 | 0 | 62 | K.SVTVQDIWR.G |
|  | 1119.5797 | 1118.5724 | 1118.5720 | 0.35 | 83 | - | 91 | 0 | --- | K.SVTVQDIWR.G + Oxidation (HW) |
|  | 1225.5549 | 1224.5476 | 1224.5523 | -3.85 | 258 | - | 268 | 0 | --- | K.GHPEDPFAAER.- |
|  | 1225.5549 | 1224.5476 | 1224.5523 | -3.85 | 258 | - | 268 | 0 | 51 | K.GHPEDPFAAER.- |
|  | 1289.7469 | 1288.7396 | 1288.7503 | -8.28 | 193 | - | 203 | 1 | --- | K.YSKTPAQILLR.Y |
|  | 1300.6488 | 1299.6415 | 1299.6282 | 10.3 | 248 | - | 257 | 1 | --- | R.QRLFTDDFMK.G |
|  | 1354.6492 | 1353.6419 | 1353.6540 | -8.90 | 165 | - | 175 | 1 | --- | R.AQFMPDKFGWK.E |
|  | 1363.7800 | 1362.7727 | 1362.7871 | -10.53 | 25 | - | 35 | 2 | --- | K.IKREDLFITTK.V |
|  | 1370.6603 | 1369.6530 | 1369.6489 | 3.01 | 165 | - | 175 | 1 | --- | R.AQFMPDKFGWK.E + Oxidation (M) |
|  | 1386.7076 | 1385.7003 | 1385.6438 | 40.8 | 165 | - | 175 | 1 | --- | R.AQFMPDKFGWK.E + Oxidation (HW); Oxidation (M) |
|  | 1386.7076 | 1385.7003 | 1385.6438 | 40.8 | 165 | - | 175 | 1 | 2 | R.AQFMPDKFGWK.E + Oxidation (HW); Oxidation (M) |
|  | 1417.7721 | 1416.7648 | 1416.8452 | -56.76 | 192 | - | 203 | 2 | --- | K.KYSKTPAQILLR.Y |
|  | 1572.7612 | 1571.7539 | 1571.7692 | -9.72 | 104 | - | 117 | 0 | --- | K.AIGVSNWNGEQIER.V |
|  | 1572.7612 | 1571.7539 | 1571.7692 | -9.72 | 104 | - | 117 | 0 | 83 | K.AIGVSNWNGEQIER.V |
|  | 1588.7607 | 1587.7534 | 1587.7641 | -6.73 | 104 | - | 117 | 0 | --- | K.AIGVSNWNGEQIER.V + Oxidation (HW) |
|  | 1659.8221 | 1658.8148 | 1658.8376 | -13.75 | 149 | - | 164 | 0 | --- | K.HNVSLTSYATLGSPGR.A |
|  | 1875.8829 | 1874.8756 | 1874.8911 | -8.27 | 36 | - | 51 | 0 | --- | K.VWITHEHPDDTEGAIR.E |
|  | 2238.9758 | 2237.9685 | 2238.0052 | -16.38 | 250 | - | 268 | 1 | --- | R.LFTDDFMKGHPEDPFAAER.- + Oxidation (M) |
|  | 2238.9758 | 2237.9685 | 2238.0052 | -16.38 | 250 | - | 268 | 1 | 55 | R.LFTDDFMKGHPEDPFAAER.- + Oxidation (M) |

|  |  |
| --- | --- |
|  | **No match to:** 905.4774, 907.4572, 935.4518, 994.4860, 999.4901, 1036.5116, 1045.5576, 1052.5287, 1062.4561, 1118.5878, 1135.5676, 1151.5809, 1163.6130, 1170.6744, 1189.6440, 1190.5983, 1192.6528, 1283.6632, 1299.6344, 1340.6504, 1349.6703, 1385.7020, 1416.7092, 1571.7432, 1573.7526, 1589.7434, 1604.7560, 1621.8300, 1728.8385, 1771.8662, 1888.8778, 2208.0649 |

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| --- | --- |
| **15.** | [isotig01078](http://msmsms/mascot/cgi/protein_view.pl?file=../data/20120113/F018133.dat&hit=15" \t "_blank)    **Mass:** 30789    **Score:** 309    **Expect:** 4.3e-027  **Matches:** 23 |
|  | putative nuclear encoded protein Method: similarity and extension |

|  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | **Observed** | **Mr(expt)** | **Mr(calc)** | **ppm** | **Start** |  | **End** | **Miss** | **Ions** | **Peptide** |
|  | 911.5567 | 910.5494 | 910.5600 | -11.60 | 196 | - | 203 | 0 | --- | K.TPAQILLR.Y |
|  | 1016.4747 | 1015.4674 | 1015.4685 | -1.03 | 250 | - | 257 | 0 | --- | R.LFTDDFMK.G |
|  | 1032.4697 | 1031.4624 | 1031.4634 | -0.94 | 250 | - | 257 | 0 | --- | R.LFTDDFMK.G + Oxidation (M) |
|  | 1103.5808 | 1102.5735 | 1102.5771 | -3.26 | 83 | - | 91 | 0 | --- | K.SVTVQDIWR.G |
|  | 1103.5808 | 1102.5735 | 1102.5771 | -3.26 | 83 | - | 91 | 0 | 62 | K.SVTVQDIWR.G |
|  | 1119.5797 | 1118.5724 | 1118.5720 | 0.35 | 83 | - | 91 | 0 | --- | K.SVTVQDIWR.G + Oxidation (HW) |
|  | 1225.5549 | 1224.5476 | 1224.5523 | -3.85 | 258 | - | 268 | 0 | --- | K.GHPEDPFAAER.- |
|  | 1225.5549 | 1224.5476 | 1224.5523 | -3.85 | 258 | - | 268 | 0 | 51 | K.GHPEDPFAAER.- |
|  | 1289.7469 | 1288.7396 | 1288.7503 | -8.28 | 193 | - | 203 | 1 | --- | K.YSKTPAQILLR.Y |
|  | 1300.6488 | 1299.6415 | 1299.6282 | 10.3 | 248 | - | 257 | 1 | --- | R.QRLFTDDFMK.G |
|  | 1354.6492 | 1353.6419 | 1353.6540 | -8.90 | 165 | - | 175 | 1 | --- | R.AQFMPDKFGWK.E |
|  | 1363.7800 | 1362.7727 | 1362.7871 | -10.53 | 25 | - | 35 | 2 | --- | K.IKREDLFITTK.V |
|  | 1370.6603 | 1369.6530 | 1369.6489 | 3.01 | 165 | - | 175 | 1 | --- | R.AQFMPDKFGWK.E + Oxidation (M) |
|  | 1386.7076 | 1385.7003 | 1385.6438 | 40.8 | 165 | - | 175 | 1 | --- | R.AQFMPDKFGWK.E + Oxidation (HW); Oxidation (M) |
|  | 1386.7076 | 1385.7003 | 1385.6438 | 40.8 | 165 | - | 175 | 1 | 2 | R.AQFMPDKFGWK.E + Oxidation (HW); Oxidation (M) |
|  | 1417.7721 | 1416.7648 | 1416.8452 | -56.76 | 192 | - | 203 | 2 | --- | K.KYSKTPAQILLR.Y |
|  | 1572.7612 | 1571.7539 | 1571.7692 | -9.72 | 104 | - | 117 | 0 | --- | K.AIGVSNWNGEQIER.V |
|  | 1572.7612 | 1571.7539 | 1571.7692 | -9.72 | 104 | - | 117 | 0 | 83 | K.AIGVSNWNGEQIER.V |
|  | 1588.7607 | 1587.7534 | 1587.7641 | -6.73 | 104 | - | 117 | 0 | --- | K.AIGVSNWNGEQIER.V + Oxidation (HW) |
|  | 1659.8221 | 1658.8148 | 1658.8376 | -13.75 | 149 | - | 164 | 0 | --- | K.HNVSLTSYATLGSPGR.A |
|  | 1875.8829 | 1874.8756 | 1874.8911 | -8.27 | 36 | - | 51 | 0 | --- | K.VWITHEHPDDTEGAIR.E |
|  | 2238.9758 | 2237.9685 | 2238.0052 | -16.38 | 250 | - | 268 | 1 | --- | R.LFTDDFMKGHPEDPFAAER.- + Oxidation (M) |
|  | 2238.9758 | 2237.9685 | 2238.0052 | -16.38 | 250 | - | 268 | 1 | 55 | R.LFTDDFMKGHPEDPFAAER.- + Oxidation (M) |

|  |  |
| --- | --- |
|  | **No match to:** 905.4774, 907.4572, 935.4518, 994.4860, 999.4901, 1036.5116, 1045.5576, 1052.5287, 1062.4561, 1118.5878, 1135.5676, 1151.5809, 1163.6130, 1170.6744, 1189.6440, 1190.5983, 1192.6528, 1283.6632, 1299.6344, 1340.6504, 1349.6703, 1385.7020, 1416.7092, 1571.7432, 1573.7526, 1589.7434, 1604.7560, 1621.8300, 1728.8385, 1771.8662, 1888.8778, 2208.0649 |

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| --- | --- |
| **16.** | [isotig20646](http://msmsms/mascot/cgi/protein_view.pl?file=../data/20120113/F018133.dat&hit=16" \t "_blank)    **Mass:** 11793    **Score:** 189    **Expect:** 4.3e-015  **Matches:** 15 |
|  | putative nuclear encoded protein Method: similarity and extension |

|  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | **Observed** | **Mr(expt)** | **Mr(calc)** | **ppm** | **Start** |  | **End** | **Miss** | **Ions** | **Peptide** |
|  | 911.5567 | 910.5494 | 910.5600 | -11.60 | 29 | - | 36 | 0 | --- | K.TPAQILLR.Y |
|  | 999.4901 | 998.4828 | 998.5509 | -68.15 | 73 | - | 80 | 1 | --- | K.LLESTKHR.Q + Oxidation (HW) |
|  | 1016.4747 | 1015.4674 | 1015.4685 | -1.03 | 83 | - | 90 | 0 | --- | R.LFTDDFMK.G |
|  | 1032.4697 | 1031.4624 | 1031.4634 | -0.94 | 83 | - | 90 | 0 | --- | R.LFTDDFMK.G + Oxidation (M) |
|  | 1225.5549 | 1224.5476 | 1224.5523 | -3.85 | 91 | - | 101 | 0 | --- | K.GHPEDPFAAER.- |
|  | 1225.5549 | 1224.5476 | 1224.5523 | -3.85 | 91 | - | 101 | 0 | 51 | K.GHPEDPFAAER.- |
|  | 1283.6632 | 1282.6559 | 1282.7106 | -42.59 | 73 | - | 82 | 2 | --- | K.LLESTKHRQR.L + Oxidation (HW) |
|  | 1289.7469 | 1288.7396 | 1288.7503 | -8.28 | 26 | - | 36 | 1 | --- | K.YSKTPAQILLR.Y |
|  | 1300.6488 | 1299.6415 | 1299.6282 | 10.3 | 81 | - | 90 | 1 | --- | R.QRLFTDDFMK.G |
|  | 1349.6703 | 1348.6630 | 1348.6259 | 27.5 | 9 | - | 20 | 0 | --- | K.EAPNDLDDPHVK.E |
|  | 1363.7800 | 1362.7727 | 1362.8711 | -72.16 | 42 | - | 54 | 2 | --- | R.GIAIIPKSIKPAR.V |
|  | 1417.7721 | 1416.7648 | 1416.8452 | -56.76 | 25 | - | 36 | 2 | --- | K.KYSKTPAQILLR.Y |
|  | 2208.0649 | 2207.0576 | 2207.0647 | -3.22 | 2 | - | 20 | 2 | --- | M.PDKFGWKEAPNDLDDPHVK.E |
|  | 2238.9758 | 2237.9685 | 2238.0052 | -16.38 | 83 | - | 101 | 1 | --- | R.LFTDDFMKGHPEDPFAAER.- + Oxidation (M) |
|  | 2238.9758 | 2237.9685 | 2238.0052 | -16.38 | 83 | - | 101 | 1 | 55 | R.LFTDDFMKGHPEDPFAAER.- + Oxidation (M) |

|  |  |
| --- | --- |
|  | **No match to:** 905.4774, 907.4572, 935.4518, 994.4860, 1036.5116, 1045.5576, 1052.5287, 1062.4561, 1103.5808, 1103.5808, 1118.5878, 1119.5797, 1135.5676, 1151.5809, 1163.6130, 1170.6744, 1189.6440, 1190.5983, 1192.6528, 1299.6344, 1340.6504, 1354.6492, 1370.6603, 1385.7020, 1386.7076, 1386.7076, 1416.7092, 1571.7432, 1572.7612, 1572.7612, 1573.7526, 1588.7607, 1589.7434, 1604.7560, 1621.8300, 1659.8221, 1728.8385, 1771.8662, 1875.8829, 1888.8778 |

|  |  |
| --- | --- |
| **17.** | [isotig01089](http://msmsms/mascot/cgi/protein_view.pl?file=../data/20120113/F018133.dat&hit=17" \t "_blank)    **Mass:** 10048    **Score:** 166    **Expect:** 8.6e-013  **Matches:** 12 |
|  | putative nuclear encoded protein Method: similarity and extension |

|  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | **Observed** | **Mr(expt)** | **Mr(calc)** | **ppm** | **Start** |  | **End** | **Miss** | **Ions** | **Peptide** |
|  | 911.5567 | 910.5494 | 910.5600 | -11.60 | 14 | - | 21 | 0 | --- | K.TPAQILLR.Y |
|  | 1016.4747 | 1015.4674 | 1015.4685 | -1.03 | 68 | - | 75 | 0 | --- | R.LFTDDFMK.G |
|  | 1032.4697 | 1031.4624 | 1031.4634 | -0.94 | 68 | - | 75 | 0 | --- | R.LFTDDFMK.G + Oxidation (M) |
|  | 1163.6130 | 1162.6057 | 1162.6822 | -65.79 | 1 | - | 10 | 2 | --- | -.DPHVKQLAKK.Y |
|  | 1225.5549 | 1224.5476 | 1224.5523 | -3.85 | 76 | - | 86 | 0 | --- | K.GHPEDPFAAER.- |
|  | 1225.5549 | 1224.5476 | 1224.5523 | -3.85 | 76 | - | 86 | 0 | 51 | K.GHPEDPFAAER.- |
|  | 1289.7469 | 1288.7396 | 1288.7503 | -8.28 | 11 | - | 21 | 1 | --- | K.YSKTPAQILLR.Y |
|  | 1300.6488 | 1299.6415 | 1299.6282 | 10.3 | 66 | - | 75 | 1 | --- | R.QRLFTDDFMK.G |
|  | 1363.7800 | 1362.7727 | 1362.8711 | -72.16 | 27 | - | 39 | 2 | --- | R.GIAIIPKSIKPAR.V |
|  | 1417.7721 | 1416.7648 | 1416.8452 | -56.76 | 10 | - | 21 | 2 | --- | K.KYSKTPAQILLR.Y |
|  | 2238.9758 | 2237.9685 | 2238.0052 | -16.38 | 68 | - | 86 | 1 | --- | R.LFTDDFMKGHPEDPFAAER.- + Oxidation (M) |
|  | 2238.9758 | 2237.9685 | 2238.0052 | -16.38 | 68 | - | 86 | 1 | 55 | R.LFTDDFMKGHPEDPFAAER.- + Oxidation (M) |

|  |  |
| --- | --- |
|  | **No match to:** 905.4774, 907.4572, 935.4518, 994.4860, 999.4901, 1036.5116, 1045.5576, 1052.5287, 1062.4561, 1103.5808, 1103.5808, 1118.5878, 1119.5797, 1135.5676, 1151.5809, 1170.6744, 1189.6440, 1190.5983, 1192.6528, 1283.6632, 1299.6344, 1340.6504, 1349.6703, 1354.6492, 1370.6603, 1385.7020, 1386.7076, 1386.7076, 1416.7092, 1571.7432, 1572.7612, 1572.7612, 1573.7526, 1588.7607, 1589.7434, 1604.7560, 1621.8300, 1659.8221, 1728.8385, 1771.8662, 1875.8829, 1888.8778, 2208.0649 |

**http://msmsms/mascot/images/88x31_logo_white.gifMascot Search Results**

**Protein View**

Top of Form



Match to: **isotig01086** Score: **345** Expect: **1.1e-030**

**putative nuclear encoded protein Method: similarity and extension**

Nominal mass (Mr): **30794**; Calculated pI value: **7.33**

NCBI BLAST search of [isotig01086](http://www.ncbi.nlm.nih.gov/blast/Blast.cgi?ALIGNMENTS=50&ALIGNMENT_VIEW=Pairwise&AUTO_FORMAT=Semiauto&CDD_SEARCH=on&CLIENT=web&COMPOSITION_BASED_STATISTICS=on&DATABASE=nr&DESCRIPTIONS=100&ENTREZ_QUERY=(none)&EXPECT=10&FILTER=L&FORMAT_BLOCK_ON_RESPAGE=None&FORMAT_OBJECT=Alignment&FORMAT_TYPE=HTML&GAPCOSTS=11+1&I_THRESH=0.001&LAYOUT=TwoWindows&MATRIX_NAME=BLOSUM62&NCBI_GI=on&PAGE=Proteins&PROGRAM=blastp&QUERY=DTAAVYQNEEAIGEAIKELISAGKIKREDLFITTKVWITHEHPDDTEGAIRESLRKLQMTYVDLYLSHMPTCFNHDMSAQNKSVTVQDIWRGLEGVYKKGLTKAIGVSNWNGEQIERVLKTATVPIHNNQVELHLYWPQHELHEICKKHNVSLTSYATLGSPGRAQFMPDKFGWKEAPKDLDDPNVKQLAKKYSKTPAQILLRYVMERGIAIIPKSIKPARVIENFQLFDFSLTKEDIKLLESTKHRQRLFTDDFMKGHPEDPFAAER&SERVICE=plain&SET_DEFAULTS.x=9&SET_DEFAULTS.y=5&SHOW_OVERVIEW=on&WORD_SIZE=3&END_OF_HTTPGET=Yes" \t "_blank) against nr

Unformatted [sequence string](http://msmsms/mascot/cgi/getseq.pl?cooperia_oncophora+isotig01086+seq" \t "_blank) for pasting into other applications

Variable modifications: Oxidation (HW),Oxidation (M)

Cleavage by Trypsin/P: cuts C-term side of KR

Sequence Coverage: **50%**

Matched peptides shown in **Bold Red**

**1** DTAAVYQNEE AIGEAIKELI SAGK**IKREDL FITTKVWITH EHPDDTEGAI**

**51 R**ESLRKLQMT YVDLYLSHMP TCFNHDMSAQ NK**SVTVQDIW R**GLEGVYKKG

**101** LTK**AIGVSNW NGEQIER**VLK TATVPIHNNQ VELHLYWPQH ELHEICKK**HN**

**151 VSLTSYATLG SPGRAQFMPD KFGWKEAPKD LDDPNVK**QLA K**KYSKTPAQI**

**201 LLRYVMER**GI AIIPKSIKPA RVIENFQLFD FSLTKEDIK**L LESTKHRQRL**

**251 FTDDFMKGHP EDPFAAER**



  Residue Number  Increasing Mass  Decreasing Mass

**Start - End Observed Mr(expt) Mr(calc) ppm Miss Sequence**

**25 - 35 1363.7800 1362.7727 1362.7871 -11 2 K.IKREDLFITTK.V**  ([No match](http://msmsms/mascot/cgi/peptide_view.pl?file=../data/20120113/F018133.dat&query=33&hit=1" \t "_blank))

**36 - 51 1875.8829 1874.8756 1874.8911 -8 0 K.VWITHEHPDDTEGAIR.E**  ([No match](http://msmsms/mascot/cgi/peptide_view.pl?file=../data/20120113/F018133.dat&query=51&hit=1" \t "_blank))

**83 - 91 1103.5808 1102.5735 1102.5771 -3 0 K.SVTVQDIWR.G**  ([No match](http://msmsms/mascot/cgi/peptide_view.pl?file=../data/20120113/F018133.dat&query=13&hit=1" \t "_blank))

**83 - 91 1103.5808 1102.5735 1102.5771 -3 0 K.SVTVQDIWR.G**  ([Ions score 62](http://msmsms/mascot/cgi/peptide_view.pl?file=../data/20120113/F018133.dat&query=14&hit=1" \t "_blank))

**83 - 91 1119.5797 1118.5724 1118.5720 0 0 K.SVTVQDIWR.G**  Oxidation (HW) ([No match](http://msmsms/mascot/cgi/peptide_view.pl?file=../data/20120113/F018133.dat&query=16&hit=1" \t "_blank))

**104 - 117 1572.7612 1571.7539 1571.7692 -10 0 K.AIGVSNWNGEQIER.V**  ([No match](http://msmsms/mascot/cgi/peptide_view.pl?file=../data/20120113/F018133.dat&query=41&hit=1" \t "_blank))

**104 - 117 1572.7612 1571.7539 1571.7692 -10 0 K.AIGVSNWNGEQIER.V**  ([Ions score 83](http://msmsms/mascot/cgi/peptide_view.pl?file=../data/20120113/F018133.dat&query=42&hit=1" \t "_blank))

**104 - 117 1588.7607 1587.7534 1587.7641 -7 0 K.AIGVSNWNGEQIER.V**  Oxidation (HW) ([No match](http://msmsms/mascot/cgi/peptide_view.pl?file=../data/20120113/F018133.dat&query=44&hit=1" \t "_blank))

**149 - 164 1659.8221 1658.8148 1658.8376 -14 0 K.HNVSLTSYATLGSPGR.A**  ([No match](http://msmsms/mascot/cgi/peptide_view.pl?file=../data/20120113/F018133.dat&query=48&hit=1" \t "_blank))

**165 - 175 1354.6492 1353.6419 1353.6540 -9 1 R.AQFMPDKFGWK.E**  ([No match](http://msmsms/mascot/cgi/peptide_view.pl?file=../data/20120113/F018133.dat&query=32&hit=1" \t "_blank))

**165 - 175 1370.6603 1369.6530 1369.6489 3 1 R.AQFMPDKFGWK.E**  Oxidation (M) ([No match](http://msmsms/mascot/cgi/peptide_view.pl?file=../data/20120113/F018133.dat&query=34&hit=1" \t "_blank))

**165 - 175 1386.7076 1385.7003 1385.6438 41 1 R.AQFMPDKFGWK.E**  Oxidation (HW); Oxidation (M) ([No match](http://msmsms/mascot/cgi/peptide_view.pl?file=../data/20120113/F018133.dat&query=36&hit=1" \t "_blank))

**165 - 175 1386.7076 1385.7003 1385.6438 41 1 R.AQFMPDKFGWK.E**  Oxidation (HW); Oxidation (M) ([Ions score 2](http://msmsms/mascot/cgi/peptide_view.pl?file=../data/20120113/F018133.dat&query=37&hit=1" \t "_blank))

**176 - 187 1340.6504 1339.6431 1339.6619 -14 1 K.EAPKDLDDPNVK.Q**  ([No match](http://msmsms/mascot/cgi/peptide_view.pl?file=../data/20120113/F018133.dat&query=30&hit=1" \t "_blank))

**192 - 203 1417.7721 1416.7648 1416.8452 -57 2 K.KYSKTPAQILLR.Y**  ([No match](http://msmsms/mascot/cgi/peptide_view.pl?file=../data/20120113/F018133.dat&query=39&hit=1" \t "_blank))

**193 - 203 1289.7469 1288.7396 1288.7503 -8 1 K.YSKTPAQILLR.Y**  ([No match](http://msmsms/mascot/cgi/peptide_view.pl?file=../data/20120113/F018133.dat&query=27&hit=1" \t "_blank))

**196 - 203 911.5567 910.5494 910.5600 -12 0 K.TPAQILLR.Y**  ([No match](http://msmsms/mascot/cgi/peptide_view.pl?file=../data/20120113/F018133.dat&query=3&hit=1" \t "_blank))

**196 - 208 1589.7434 1588.7361 1588.8759 -88 1 K.TPAQILLRYVMER.G**  ([No match](http://msmsms/mascot/cgi/peptide_view.pl?file=../data/20120113/F018133.dat&query=45&hit=1" \t "_blank))

**240 - 247 999.4901 998.4828 998.5509 -68 1 K.LLESTKHR.Q**  Oxidation (HW) ([No match](http://msmsms/mascot/cgi/peptide_view.pl?file=../data/20120113/F018133.dat&query=6&hit=1" \t "_blank))

**240 - 249 1283.6632 1282.6559 1282.7106 -43 2 K.LLESTKHRQR.L**  Oxidation (HW) ([No match](http://msmsms/mascot/cgi/peptide_view.pl?file=../data/20120113/F018133.dat&query=26&hit=1" \t "_blank))

**248 - 257 1300.6488 1299.6415 1299.6282 10 1 R.QRLFTDDFMK.G**  ([No match](http://msmsms/mascot/cgi/peptide_view.pl?file=../data/20120113/F018133.dat&query=29&hit=1" \t "_blank))

**250 - 257 1016.4747 1015.4674 1015.4685 -1 0 R.LFTDDFMK.G**  ([No match](http://msmsms/mascot/cgi/peptide_view.pl?file=../data/20120113/F018133.dat&query=7&hit=1" \t "_blank))

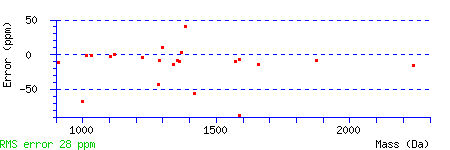
**250 - 257 1032.4697 1031.4624 1031.4634 -1 0 R.LFTDDFMK.G**  Oxidation (M) ([No match](http://msmsms/mascot/cgi/peptide_view.pl?file=../data/20120113/F018133.dat&query=8&hit=1" \t "_blank))

**250 - 268 2238.9758 2237.9685 2238.0052 -16 1 R.LFTDDFMKGHPEDPFAAER.-**  Oxidation (M) ([No match](http://msmsms/mascot/cgi/peptide_view.pl?file=../data/20120113/F018133.dat&query=54&hit=1" \t "_blank))

**250 - 268 2238.9758 2237.9685 2238.0052 -16 1 R.LFTDDFMKGHPEDPFAAER.-**  Oxidation (M) ([Ions score 55](http://msmsms/mascot/cgi/peptide_view.pl?file=../data/20120113/F018133.dat&query=55&hit=1" \t "_blank))

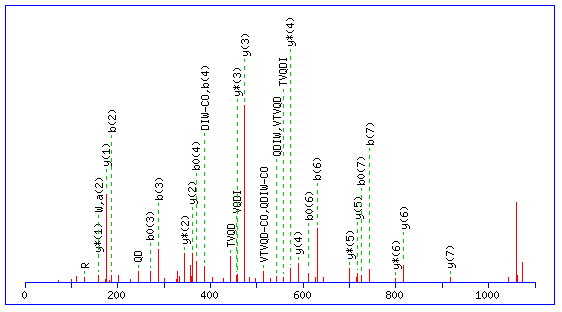
**258 - 268 1225.5549 1224.5476 1224.5523 -4 0 K.GHPEDPFAAER.-**  ([No match](http://msmsms/mascot/cgi/peptide_view.pl?file=../data/20120113/F018133.dat&query=24&hit=1" \t "_blank))

**258 - 268 1225.5549 1224.5476 1224.5523 -4 0 K.GHPEDPFAAER.-**  ([Ions score 51](http://msmsms/mascot/cgi/peptide_view.pl?file=../data/20120113/F018133.dat&query=25&hit=1" \t "_blank))



Bottom of Form

🡪 Annotated MS2 spectrum for peptide SVTVQDIWR



**Monoisotopic mass of neutral peptide Mr(calc):** 1102.5771

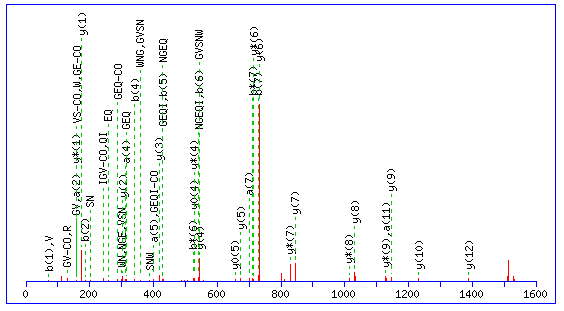
**Ions Score:** 62 **Expect:** 4.6e-005

**Matches :** 35/125 fragment ions using 35 most intense peaks   ([help](http://msmsms/mascot/help/results_help.html" \l "PEP" \t "_blank))

|  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **#** | **Immon.** | **a** | **a\*** | **a0** | **b** | **b\*** | **b0** | **Seq.** | **v** | **w** | **w'** | **y** | **y\*** | **y0** | **#** |
| **1** | 60.0444 | 60.0444 |  | 42.0338 | 88.0393 |  | 70.0287 | **S** |  |  |  |  |  |  | **9** |
| **2** | 72.0808 | 159.1128 |  | 141.1022 | **187.1077** |  | 169.0972 | **V** | 972.4898 | 985.5102 |  | 1016.5524 | 999.5258 | 998.5418 | **8** |
| **3** | 74.0600 | 260.1605 |  | 242.1499 | **288.1554** |  | 270.1448 | **T** | 871.4421 | 884.4625 | 886.4417 | ***917.4839*** | 900.4574 | 899.4734 | **7** |
| **4** | 72.0808 | 359.2289 |  | 341.2183 | **387.2238** |  | 369.2132 | **V** | 772.3737 | 785.3941 |  | ***816.4363*** | 799.4097 | 798.4257 | **6** |
| **5** | 101.0709 | 487.2875 | 470.2609 | 469.2769 | **515.2824** | 498.2558 | 497.2718 | **Q** | 644.3151 | 643.3198 |  | ***717.3679*** | 700.3413 | 699.3573 | **5** |
| **6** | 88.0393 | 602.3144 | 585.2879 | 584.3039 | **630.3093** | 613.2828 | 612.2988 | **D** | 529.2881 | 528.2929 |  | ***589.3093*** | 572.2827 | 571.2987 | **4** |
| **7** | 86.0964 | 715.3985 | 698.3719 | 697.3879 | **743.3934** | 726.3668 | 725.3828 | **I** | 416.2041 | 429.2245 | 443.2401 | ***474.2823*** | 457.2558 |  | **3** |
| **8** | 159.0917 | 901.4778 | 884.4512 | 883.4672 | 929.4727 | 912.4462 | 911.4621 | **W** | 230.1248 |  |  | ***361.1983*** | 344.1717 |  | **2** |
| **9** | 129.1135 |  |  |  |  |  |  | **R** | 74.0237 | 73.0284 |  | ***175.1190*** | 158.0924 |  | **1** |

|  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **Seq** | **ya** | **yb** | **Seq** | **ya** | **yb** | **Seq** | **ya** | **yb** |
| **VT** | 173.1285 | 201.1234 | **VTV** | 272.1969 | 300.1918 | **VTVQ** | 400.2554 | 428.2504 |
| **VTVQD** | 515.2824 | 543.2773 | **VTVQDI** | 628.3665 | 656.3614 | **TV** | 173.1285 | 201.1234 |
| **TVQ** | 301.1870 | 329.1819 | **TVQD** | 416.2140 | 444.2089 | **TVQDI** | 529.2980 | 557.2930 |
| **VQ** | 200.1394 | 228.1343 | **VQD** | 315.1663 | 343.1612 | **VQDI** | 428.2504 | 456.2453 |
| **VQDIW** | 614.3297 | 642.3246 | **QD** | 216.0979 | 244.0928 | **QDI** | 329.1819 | 357.1769 |
| **QDIW** | 515.2613 | 543.2562 | **DI** | 201.1234 | 229.1183 | **DIW** | 387.2027 | 415.1976 |
| **IW** | 272.1757 | 300.1707 |  |  |  |  |  |  |

🡪 Annotated MS2 spectrum for peptide AIGVSNWNGEQIER



**Monoisotopic mass of neutral peptide Mr(calc):** 1571.7692

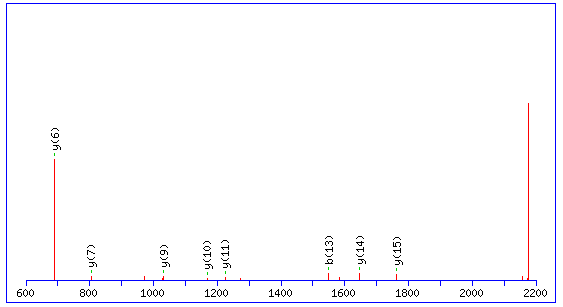
**Ions Score:** 83 **Expect:** 4.4e-007

**Matches :** 60/222 fragment ions using 60 most intense peaks   ([help](http://msmsms/mascot/help/results_help.html" \l "PEP" \t "_blank))

|  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **#** | **Immon.** | **a** | **a\*** | **a0** | **b** | **b\*** | **b0** | **Seq.** | **v** | **w** | **w'** | **y** | **y\*** | **y0** | **#** |
| **1** | 44.0495 | 44.0495 |  |  | **72.0444** |  |  | **A** |  |  |  |  |  |  | **14** |
| **2** | 86.0964 | **157.1335** |  |  | **185.1285** |  |  | **I** | 1443.6611 | 1456.6815 | 1470.6972 | 1501.7394 | 1484.7128 | 1483.7288 | **13** |
| **3** | 30.0338 | 214.1550 |  |  | **242.1499** |  |  | **G** |  |  |  | ***1388.6553*** | 1371.6288 | 1370.6448 | **12** |
| **4** | 72.0808 | **313.2234** |  |  | **341.2183** |  |  | **V** | 1287.5713 | 1300.5917 |  | 1331.6339 | 1314.6073 | 1313.6233 | **11** |
| **5** | 60.0444 | **400.2554** |  | 382.2449 | **428.2504** |  | 410.2398 | **S** | 1200.5392 | 1199.5440 |  | ***1232.5654*** | 1215.5389 | 1214.5549 | **10** |
| **6** | 87.0553 | 514.2984 | 497.2718 | 496.2878 | **542.2933** | 525.2667 | 524.2827 | **N** | 1086.4963 | 1085.5010 |  | ***1145.5334*** | 1128.5069 | 1127.5228 | **9** |
| **7** | 159.0917 | **700.3777** | 683.3511 | 682.3671 | **728.3726** | 711.3461 | 710.3620 | **W** | 900.4170 |  |  | ***1031.4905*** | 1014.4639 | 1013.4799 | **8** |
| **8** | 87.0553 | 814.4206 | 797.3941 | 796.4100 | 842.4155 | 825.3890 | 824.4050 | **N** | 786.3741 | 785.3788 |  | ***845.4112*** | 828.3846 | 827.4006 | **7** |
| **9** | 30.0338 | 871.4421 | 854.4155 | 853.4315 | 899.4370 | 882.4104 | 881.4264 | **G** |  |  |  | ***731.3682*** | 714.3417 | 713.3577 | **6** |
| **10** | 102.0550 | 1000.4847 | 983.4581 | 982.4741 | 1028.4796 | 1011.4530 | 1010.4690 | **E** | 600.3100 | 599.3148 |  | ***674.3468*** | 657.3202 | 656.3362 | **5** |
| **11** | 101.0709 | **1128.5432** | 1111.5167 | 1110.5327 | 1156.5382 | 1139.5116 | 1138.5276 | **Q** | 472.2514 | 471.2562 |  | ***545.3042*** | 528.2776 | 527.2936 | **4** |
| **12** | 86.0964 | 1241.6273 | 1224.6008 | 1223.6167 | 1269.6222 | 1252.5957 | 1251.6117 | **I** | 359.1674 | 372.1878 | 386.2034 | ***417.2456*** | 400.2191 | 399.2350 | **3** |
| **13** | 102.0550 | 1370.6699 | 1353.6434 | 1352.6593 | 1398.6648 | 1381.6383 | 1380.6543 | **E** | 230.1248 | 229.1295 |  | ***304.1615*** | 287.1350 | 286.1510 | **2** |
| **14** | 129.1135 |  |  |  |  |  |  | **R** | 74.0237 | 73.0284 |  | ***175.1190*** | 158.0924 |  | **1** |

|  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **Seq** | **ya** | **yb** | **Seq** | **ya** | **yb** | **Seq** | **ya** | **yb** |
| **IG** | 143.1179 | 171.1128 | **IGV** | 242.1863 | 270.1812 | **IGVS** | 329.2183 | 357.2132 |
| **IGVSN** | 443.2613 | 471.2562 | **IGVSNW** | 629.3406 | 657.3355 | **GV** | 129.1022 | 157.0972 |
| **GVS** | 216.1343 | 244.1292 | **GVSN** | 330.1772 | 358.1721 | **GVSNW** | 516.2565 | 544.2514 |
| **GVSNWN** | 630.2994 | 658.2943 | **GVSNWNG** | 687.3209 | 715.3158 | **VS** | 159.1128 | 187.1077 |
| **VSN** | 273.1557 | 301.1506 | **VSNW** | 459.2350 | 487.2300 | **VSNWN** | 573.2780 | 601.2729 |
| **VSNWNG** | 630.2994 | 658.2943 | **SN** | 174.0873 | 202.0822 | **SNW** | 360.1666 | 388.1615 |
| **SNWN** | 474.2096 | 502.2045 | **SNWNG** | 531.2310 | 559.2259 | **SNWNGE** | 660.2736 | 688.2685 |
| **NW** | 273.1346 | 301.1295 | **NWN** | 387.1775 | 415.1724 | **NWNG** | 444.1990 | 472.1939 |
| **NWNGE** | 573.2416 | 601.2365 | **WN** | 273.1346 | 301.1295 | **WNG** | 330.1561 | 358.1510 |
| **WNGE** | 459.1987 | 487.1936 | **WNGEQ** | 587.2572 | 615.2522 | **NG** | 144.0768 | 172.0717 |
| **NGE** | 273.1193 | 301.1143 | **NGEQ** | 401.1779 | 429.1728 | **NGEQI** | 514.2620 | 542.2569 |
| **NGEQIE** | 643.3046 | 671.2995 | **GE** | 159.0764 | 187.0713 | **GEQ** | 287.1350 | 315.1299 |
| **GEQI** | 400.2191 | 428.2140 | **GEQIE** | 529.2617 | 557.2566 | **EQ** | 230.1135 | 258.1084 |
| **EQI** | 343.1976 | 371.1925 | **EQIE** | 472.2402 | 500.2351 | **QI** | 214.1550 | 242.1499 |
| **QIE** | 343.1976 | 371.1925 | **IE** | 215.1390 | 243.1339 |  |  |  |

🡪 Annotated MS2 spectrum for peptide LFTDDFMKGHPEDPFAAER



**Monoisotopic mass of neutral peptide Mr(calc):** 2238.0052

**Variable modifications:**

**M7 :** Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983

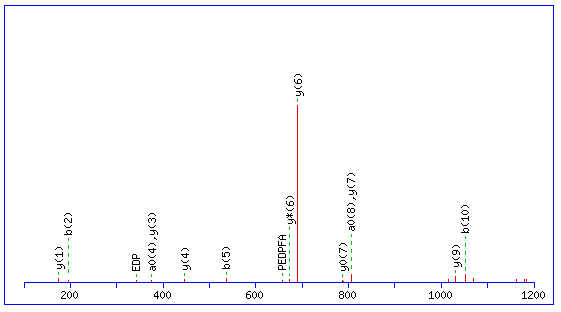
**Ions Score:** 55 **Expect:** 0.00022

**Matches :** 8/452 fragment ions using 10 most intense peaks   ([help](http://msmsms/mascot/help/results_help.html" \l "PEP" \t "_blank))

|  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **#** | **Immon.** | **a** | **a\*** | **a0** | **b** | **b\*** | **b0** | **Seq.** | **v** | **w** | **w'** | **y** | **y\*** | **y0** | **#** |
| **1** | 86.0964 | 86.0964 |  |  | 114.0913 |  |  | **L** |  |  |  |  |  |  | **19** |
| **2** | 120.0808 | 233.1648 |  |  | 261.1598 |  |  | **F** | 2033.8658 |  |  | 2125.9284 | 2108.9018 | 2107.9178 | **18** |
| **3** | 74.0600 | 334.2125 |  | 316.2020 | 362.2074 |  | 344.1969 | **T** | 1932.8181 | 1945.8385 | 1947.8178 | 1978.8600 | 1961.8334 | 1960.8494 | **17** |
| **4** | 88.0393 | 449.2395 |  | 431.2289 | 477.2344 |  | 459.2238 | **D** | 1817.7912 | 1816.7959 |  | 1877.8123 | 1860.7857 | 1859.8017 | **16** |
| **5** | 88.0393 | 564.2664 |  | 546.2558 | 592.2613 |  | 574.2508 | **D** | 1702.7642 | 1701.7690 |  | ***1762.7853*** | 1745.7588 | 1744.7748 | **15** |
| **6** | 120.0808 | 711.3348 |  | 693.3243 | 739.3297 |  | 721.3192 | **F** | 1555.6958 |  |  | ***1647.7584*** | 1630.7319 | 1629.7478 | **14** |
| **7** | 120.0478 | 858.3702 |  | 840.3597 | 886.3651 |  | 868.3546 | **M** | 1408.6604 | 1407.6652 |  | 1500.6900 | 1483.6634 | 1482.6794 | **13** |
| **8** | 101.1073 | 986.4652 | 969.4386 | 968.4546 | 1014.4601 | 997.4335 | 996.4495 | **K** | 1280.5654 | 1279.5702 |  | 1353.6546 | 1336.6280 | 1335.6440 | **12** |
| **9** | 30.0338 | 1043.4866 | 1026.4601 | 1025.4761 | 1071.4816 | 1054.4550 | 1053.4710 | **G** |  |  |  | ***1225.5596*** | 1208.5331 | 1207.5491 | **11** |
| **10** | 110.0713 | 1180.5456 | 1163.5190 | 1162.5350 | 1208.5405 | 1191.5139 | 1190.5299 | **H** | 1086.4851 |  |  | ***1168.5382*** | 1151.5116 | 1150.5276 | **10** |
| **11** | 70.0651 | 1277.5983 | 1260.5718 | 1259.5878 | 1305.5932 | 1288.5667 | 1287.5827 | **P** | 989.4323 | 988.4371 |  | ***1031.4793*** | 1014.4527 | 1013.4687 | **9** |
| **12** | 102.0550 | 1406.6409 | 1389.6144 | 1388.6303 | 1434.6358 | 1417.6093 | 1416.6253 | **E** | 860.3897 | 859.3945 |  | 934.4265 | 917.3999 | 916.4159 | **8** |
| **13** | 88.0393 | 1521.6679 | 1504.6413 | 1503.6573 | 1549.6628 | 1532.6362 | 1531.6522 | **D** | 745.3628 | 744.3675 |  | ***805.3839*** | 788.3573 | 787.3733 | **7** |
| **14** | 70.0651 | 1618.7206 | 1601.6941 | 1600.7101 | 1646.7155 | 1629.6890 | 1628.7050 | **P** | 648.3100 | 647.3148 |  | ***690.3570*** | 673.3304 | 672.3464 | **6** |
| **15** | 120.0808 | 1765.7890 | 1748.7625 | 1747.7785 | 1793.7840 | 1776.7574 | 1775.7734 | **F** | 501.2416 |  |  | 593.3042 | 576.2776 | 575.2936 | **5** |
| **16** | 44.0495 | 1836.8261 | 1819.7996 | 1818.8156 | 1864.8211 | 1847.7945 | 1846.8105 | **A** | 430.2045 |  |  | 446.2358 | 429.2092 | 428.2252 | **4** |
| **17** | 44.0495 | 1907.8633 | 1890.8367 | 1889.8527 | 1935.8582 | 1918.8316 | 1917.8476 | **A** | 359.1674 |  |  | 375.1987 | 358.1721 | 357.1881 | **3** |
| **18** | 102.0550 | 2036.9059 | 2019.8793 | 2018.8953 | 2064.9008 | 2047.8742 | 2046.8902 | **E** | 230.1248 | 229.1295 |  | 304.1615 | 287.1350 | 286.1510 | **2** |
| **19** | 129.1135 |  |  |  |  |  |  | **R** | 74.0237 | 73.0284 |  | 175.1190 | 158.0924 |  | **1** |

|  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **Seq** | **ya** | **yb** | **Seq** | **ya** | **yb** | **Seq** | **ya** | **yb** |
| **FT** | 221.1285 | 249.1234 | **FTD** | 336.1554 | 364.1503 | **FTDD** | 451.1823 | 479.1773 |
| **FTDDF** | 598.2508 | 626.2457 | **TD** | 189.0870 | 217.0819 | **TDD** | 304.1139 | 332.1088 |
| **TDDF** | 451.1823 | 479.1773 | **TDDFM** | 598.2177 | 626.2127 | **DD** | 203.0662 | 231.0612 |
| **DDF** | 350.1347 | 378.1296 | **DDFM** | 497.1701 | 525.1650 | **DDFMK** | 625.2650 | 653.2599 |
| **DDFMKG** | 682.2865 | 710.2814 | **DF** | 235.1077 | 263.1026 | **DFM** | 382.1431 | 410.1380 |
| **DFMK** | 510.2381 | 538.2330 | **DFMKG** | 567.2595 | 595.2545 | **FM** | 267.1162 | 295.1111 |
| **FMK** | 395.2111 | 423.2061 | **FMKG** | 452.2326 | 480.2275 | **FMKGH** | 589.2915 | 617.2864 |
| **FMKGHP** | 686.3443 | 714.3392 | **MK** | 248.1427 | 276.1376 | **MKG** | 305.1642 | 333.1591 |
| **MKGH** | 442.2231 | 470.2180 | **MKGHP** | 539.2759 | 567.2708 | **MKGHPE** | 668.3185 | 696.3134 |
| **KG** | 158.1288 | 186.1237 | **KGH** | 295.1877 | 323.1826 | **KGHP** | 392.2405 | 420.2354 |
| **KGHPE** | 521.2831 | 549.2780 | **KGHPED** | 636.3100 | 664.3049 | **GH** | 167.0927 | 195.0877 |
| **GHP** | 264.1455 | 292.1404 | **GHPE** | 393.1881 | 421.1830 | **GHPED** | 508.2150 | 536.2100 |
| **GHPEDP** | 605.2678 | 633.2627 | **HP** | 207.1240 | 235.1190 | **HPE** | 336.1666 | 364.1615 |
| **HPED** | 451.1936 | 479.1885 | **HPEDP** | 548.2463 | 576.2413 | **HPEDPF** | 695.3148 | 723.3097 |
| **PE** | 199.1077 | 227.1026 | **PED** | 314.1347 | 342.1296 | **PEDP** | 411.1874 | 439.1823 |
| **PEDPF** | 558.2558 | 586.2508 | **PEDPFA** | 629.2930 | 657.2879 | **ED** | 217.0819 | 245.0768 |
| **EDP** | 314.1347 | 342.1296 | **EDPF** | 461.2031 | 489.1980 | **EDPFA** | 532.2402 | 560.2351 |
| **EDPFAA** | 603.2773 | 631.2722 | **DP** | 185.0921 | 213.0870 | **DPF** | 332.1605 | 360.1554 |
| **DPFA** | 403.1976 | 431.1925 | **DPFAA** | 474.2347 | 502.2296 | **DPFAAE** | 603.2773 | 631.2722 |
| **PF** | 217.1335 | 245.1285 | **PFA** | 288.1707 | 316.1656 | **PFAA** | 359.2078 | 387.2027 |
| **PFAAE** | 488.2504 | 516.2453 | **FA** | 191.1179 | 219.1128 | **FAA** | 262.1550 | 290.1499 |
| **FAAE** | 391.1976 | 419.1925 | **AA** | 115.0866 | 143.0815 | **AAE** | 244.1292 | 272.1241 |
| **AE** | 173.0921 | 201.0870 |  |  |  |  |  |  |

🡪 Annotated MS2 spectrum for peptide GHPEDPFAAER



**Monoisotopic mass of neutral peptide Mr(calc):** 1224.5523

**Ions Score:** 51 **Expect:** 0.00058

**Matches :** 16/149 fragment ions using 16 most intense peaks   ([help](http://msmsms/mascot/help/results_help.html" \l "PEP" \t "_blank))

|  |  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **#** | **Immon.** | **a** | **a0** | **b** | **b0** | **Seq.** | **v** | **w** | **y** | **y\*** | **y0** | **#** |
| **1** | 30.0338 | 30.0338 |  | 58.0287 |  | **G** |  |  |  |  |  | **11** |
| **2** | 110.0713 | 167.0927 |  | **195.0877** |  | **H** | 1086.4851 |  | 1168.5382 | 1151.5116 | 1150.5276 | **10** |
| **3** | 70.0651 | 264.1455 |  | 292.1404 |  | **P** | 989.4323 | 988.4371 | ***1031.4793*** | 1014.4527 | 1013.4687 | **9** |
| **4** | 102.0550 | 393.1881 | 375.1775 | 421.1830 | 403.1724 | **E** | 860.3897 | 859.3945 | 934.4265 | 917.3999 | 916.4159 | **8** |
| **5** | 88.0393 | 508.2150 | 490.2045 | **536.2100** | 518.1994 | **D** | 745.3628 | 744.3675 | ***805.3839*** | 788.3573 | 787.3733 | **7** |
| **6** | 70.0651 | 605.2678 | 587.2572 | 633.2627 | 615.2522 | **P** | 648.3100 | 647.3148 | ***690.3570*** | 673.3304 | 672.3464 | **6** |
| **7** | 120.0808 | 752.3362 | 734.3257 | 780.3311 | 762.3206 | **F** | 501.2416 |  | 593.3042 | 576.2776 | 575.2936 | **5** |
| **8** | 44.0495 | 823.3733 | 805.3628 | 851.3682 | 833.3577 | **A** | 430.2045 |  | ***446.2358*** | 429.2092 | 428.2252 | **4** |
| **9** | 44.0495 | 894.4104 | 876.3999 | 922.4054 | 904.3948 | **A** | 359.1674 |  | ***375.1987*** | 358.1721 | 357.1881 | **3** |
| **10** | 102.0550 | 1023.4530 | 1005.4425 | **1051.4480** | 1033.4374 | **E** | 230.1248 | 229.1295 | 304.1615 | 287.1350 | 286.1510 | **2** |
| **11** | 129.1135 |  |  |  |  | **R** | 74.0237 | 73.0284 | ***175.1190*** | 158.0924 |  | **1** |

|  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **Seq** | **ya** | **yb** | **Seq** | **ya** | **yb** | **Seq** | **ya** | **yb** |
| **HP** | 207.1240 | 235.1190 | **HPE** | 336.1666 | 364.1615 | **HPED** | 451.1936 | 479.1885 |
| **HPEDP** | 548.2463 | 576.2413 | **HPEDPF** | 695.3148 | 723.3097 | **PE** | 199.1077 | 227.1026 |
| **PED** | 314.1347 | 342.1296 | **PEDP** | 411.1874 | 439.1823 | **PEDPF** | 558.2558 | 586.2508 |
| **PEDPFA** | 629.2930 | 657.2879 | **ED** | 217.0819 | 245.0768 | **EDP** | 314.1347 | 342.1296 |
| **EDPF** | 461.2031 | 489.1980 | **EDPFA** | 532.2402 | 560.2351 | **EDPFAA** | 603.2773 | 631.2722 |
| **DP** | 185.0921 | 213.0870 | **DPF** | 332.1605 | 360.1554 | **DPFA** | 403.1976 | 431.1925 |
| **DPFAA** | 474.2347 | 502.2296 | **DPFAAE** | 603.2773 | 631.2722 | **PF** | 217.1335 | 245.1285 |
| **PFA** | 288.1707 | 316.1656 | **PFAA** | 359.2078 | 387.2027 | **PFAAE** | 488.2504 | 516.2453 |
| **FA** | 191.1179 | 219.1128 | **FAA** | 262.1550 | 290.1499 | **FAAE** | 391.1976 | 419.1925 |
| **AA** | 115.0866 | 143.0815 | **AAE** | 244.1292 | 272.1241 | **AE** | 173.0921 | 201.0870 |

**Band 6:**

**http://msmsms/mascot/images/88x31_logo_white.gifMascot Search Results**

**User :**

**Email :**

**Search title : SampleSetID: 683, AnalysisID: 1071, MaldiWellID: 82750, SpectrumID: 217115, Path=\Jimmy\Cooperia 3\Co ES Conc 3 Frac 13012012 (strict)**

**Database : cooperia\_oncophora oncophora\_20110405 (34373 sequences; 5289600 residues)**

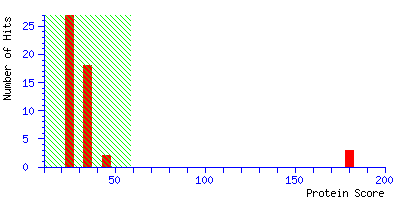
**Timestamp : 13 Jan 2012 at 14:33:25 GMT**

**Warning : A Peptide summary report will usually give a much clearer picture of MS/MS search results.**

**Top Score : 180 for isotig13456, putative nuclear encoded protein Method: similarity and extension**

**Mascot Score Histogram**

Protein score is -10\*Log(P), where P is the probability that the observed match is a random event.  
Protein scores greater than 58 are significant (p<0.05).  
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



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**Protein Summary Report**

|  |  |  |  |
| --- | --- | --- | --- |
|  |  |  | [Help](http://msmsms/mascot/help/msms_summaries_help.html" \t "_blank) |
|  | Significance threshold p< | Max. number of hits |  |

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Bottom of Form

**Index**

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
|  | **Accession** | **Mass** | **Score** | **Description** |
| **1.** | [**isotig13456**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20120113/F018134.dat#Hit1) | 17575 | 180 | putative nuclear encoded protein Method: similarity and extension |
| **2.** | [**contig55746**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20120113/F018134.dat#Hit2) | 17086 | 180 | putative nuclear encoded protein Method: similarity and extension |
| **3.** | [**isotig13457**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20120113/F018134.dat#Hit3) | 17585 | 180 | putative nuclear encoded protein Method: similarity and extension |
| **4.** | [**isotig04669**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20120113/F018134.dat#Hit4) | 19076 | 42 | putative nuclear encoded protein Method: similarity and extension |
| **5.** | [**isotig28702**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20120113/F018134.dat#Hit5) | 6282 | 40 | putative nuclear encoded protein Method: Longest ORF |
| **6.** | [**isotig25596**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20120113/F018134.dat#Hit6) | 8134 | 40 | putative nuclear encoded protein Method: Longest ORF |
| **7.** | [**isotig19871**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20120113/F018134.dat#Hit7) | 8224 | 37 | putative nuclear encoded protein Method: Longest ORF |
| **8.** | [**isotig24688**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20120113/F018134.dat#Hit8) | 25850 | 36 | putative nuclear encoded protein Method: similarity and extension |
| **9.** | [**isotig11802**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20120113/F018134.dat#Hit9) | 20387 | 35 | putative nuclear encoded protein Method: similarity and extension |
| **10.** | [**isotig25980**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20120113/F018134.dat#Hit10) | 15476 | 34 | putative nuclear encoded protein Method: similarity and extension |
| **11.** | [**isotig04667**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20120113/F018134.dat#Hit11) | 19060 | 33 | putative nuclear encoded protein Method: similarity and extension |
| **12.** | [**isotig04666**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20120113/F018134.dat#Hit12) | 19060 | 33 | putative nuclear encoded protein Method: similarity and extension |
| **13.** | [**isotig04665**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20120113/F018134.dat#Hit13) | 19060 | 33 | putative nuclear encoded protein Method: similarity and extension |
| **14.** | [**isotig04668**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20120113/F018134.dat#Hit14) | 19060 | 33 | putative nuclear encoded protein Method: similarity and extension |
| **15.** | [**isotig06171**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20120113/F018134.dat#Hit15) | 28463 | 33 | putative nuclear encoded protein Method: similarity and extension |
| **16.** | [**isotig06173**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20120113/F018134.dat#Hit16) | 28463 | 33 | putative nuclear encoded protein Method: similarity and extension |
| **17.** | [**isotig15126**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20120113/F018134.dat#Hit17) | 14297 | 32 | putative nuclear encoded protein Method: similarity and extension |
| **18.** | [**isotig31538**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20120113/F018134.dat#Hit18) | 18068 | 32 | putative nuclear encoded protein Method: similarity and extension |
| **19.** | [**isotig22202**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20120113/F018134.dat#Hit19) | 9035 | 32 | putative nuclear encoded protein Method: Longest ORF |
| **20.** | [**isotig14500**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20120113/F018134.dat#Hit20) | 32548 | 31 | putative nuclear encoded protein Method: similarity and extension |

**Results List**

|  |  |
| --- | --- |
| **1.** | [isotig13456](http://msmsms/mascot/cgi/protein_view.pl?file=../data/20120113/F018134.dat&hit=1" \t "_blank)    **Mass:** 17575    **Score:** 180    **Expect:** 3.4e-014  **Matches:** 2 |
|  | putative nuclear encoded protein Method: similarity and extension |

|  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | **Observed** | **Mr(expt)** | **Mr(calc)** | **ppm** | **Start** |  | **End** | **Miss** | **Ions** | **Peptide** |
|  | 2208.0708 | 2207.0635 | 2207.0858 | -10.11 | 8 | - | 26 | 0 | --- | K.NVYHDIVPEPVTENPSELR.M |
|  | 2208.0708 | 2207.0635 | 2207.0858 | -10.11 | 8 | - | 26 | 0 | 180 | K.NVYHDIVPEPVTENPSELR.M |

|  |  |
| --- | --- |
|  | **No match to:** 900.4832, 1055.6084, 1056.6086, 1072.5629, 1102.5759, 1144.5884, 1149.6083, 1151.5963, 1163.6310, 1163.6310, 1184.6912, 1189.6516, 1280.6090, 1284.6603, 1300.6605, 1314.6099, 1318.6664, 1332.6473, 1356.6650, 1363.7089, 1364.6975, 1393.7203, 1408.6951, 1430.7308, 1440.6825, 1442.7367, 1454.7703, 1454.7703, 1638.7915, 1732.6772, 1743.7064, 1757.7041, 2002.0405, 2059.0625, 2069.0720, 2075.0544, 2075.0544, 2148.1162, 2148.1162, 2150.4014, 2160.1497, 2180.0657, 2182.0891, 2276.2063, 2276.2063, 2288.2410, 2337.1973, 2337.1973, 2349.2312, 2465.2910, 2496.2922, 2508.3250, 2518.1885, 2851.3174, 2851.3174, 3365.6033, 3365.6033 |

|  |  |
| --- | --- |
| **2.** | [contig55746](http://msmsms/mascot/cgi/protein_view.pl?file=../data/20120113/F018134.dat&hit=2" \t "_blank)    **Mass:** 17086    **Score:** 180    **Expect:** 3.4e-014  **Matches:** 2 |
|  | putative nuclear encoded protein Method: similarity and extension |

|  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | **Observed** | **Mr(expt)** | **Mr(calc)** | **ppm** | **Start** |  | **End** | **Miss** | **Ions** | **Peptide** |
|  | 2208.0708 | 2207.0635 | 2207.0858 | -10.11 | 4 | - | 22 | 0 | --- | K.NVYHDIVPEPVTENPSELR.M |
|  | 2208.0708 | 2207.0635 | 2207.0858 | -10.11 | 4 | - | 22 | 0 | 180 | K.NVYHDIVPEPVTENPSELR.M |

|  |  |
| --- | --- |
|  | **No match to:** 900.4832, 1055.6084, 1056.6086, 1072.5629, 1102.5759, 1144.5884, 1149.6083, 1151.5963, 1163.6310, 1163.6310, 1184.6912, 1189.6516, 1280.6090, 1284.6603, 1300.6605, 1314.6099, 1318.6664, 1332.6473, 1356.6650, 1363.7089, 1364.6975, 1393.7203, 1408.6951, 1430.7308, 1440.6825, 1442.7367, 1454.7703, 1454.7703, 1638.7915, 1732.6772, 1743.7064, 1757.7041, 2002.0405, 2059.0625, 2069.0720, 2075.0544, 2075.0544, 2148.1162, 2148.1162, 2150.4014, 2160.1497, 2180.0657, 2182.0891, 2276.2063, 2276.2063, 2288.2410, 2337.1973, 2337.1973, 2349.2312, 2465.2910, 2496.2922, 2508.3250, 2518.1885, 2851.3174, 2851.3174, 3365.6033, 3365.6033 |

|  |  |
| --- | --- |
| **3.** | [isotig13457](http://msmsms/mascot/cgi/protein_view.pl?file=../data/20120113/F018134.dat&hit=3" \t "_blank)    **Mass:** 17585    **Score:** 180    **Expect:** 3.4e-014  **Matches:** 2 |
|  | putative nuclear encoded protein Method: similarity and extension |

|  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | **Observed** | **Mr(expt)** | **Mr(calc)** | **ppm** | **Start** |  | **End** | **Miss** | **Ions** | **Peptide** |
|  | 2208.0708 | 2207.0635 | 2207.0858 | -10.11 | 8 | - | 26 | 0 | --- | K.NVYHDIVPEPVTENPSELR.M |
|  | 2208.0708 | 2207.0635 | 2207.0858 | -10.11 | 8 | - | 26 | 0 | 180 | K.NVYHDIVPEPVTENPSELR.M |

|  |  |
| --- | --- |
|  | **No match to:** 900.4832, 1055.6084, 1056.6086, 1072.5629, 1102.5759, 1144.5884, 1149.6083, 1151.5963, 1163.6310, 1163.6310, 1184.6912, 1189.6516, 1280.6090, 1284.6603, 1300.6605, 1314.6099, 1318.6664, 1332.6473, 1356.6650, 1363.7089, 1364.6975, 1393.7203, 1408.6951, 1430.7308, 1440.6825, 1442.7367, 1454.7703, 1454.7703, 1638.7915, 1732.6772, 1743.7064, 1757.7041, 2002.0405, 2059.0625, 2069.0720, 2075.0544, 2075.0544, 2148.1162, 2148.1162, 2150.4014, 2160.1497, 2180.0657, 2182.0891, 2276.2063, 2276.2063, 2288.2410, 2337.1973, 2337.1973, 2349.2312, 2465.2910, 2496.2922, 2508.3250, 2518.1885, 2851.3174, 2851.3174, 3365.6033, 3365.6033 |

**http://msmsms/mascot/images/88x31_logo_white.gifMascot Search Results**

**Protein View**

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Match to: **isotig13456** Score: **180** Expect: **3.4e-014**

**putative nuclear encoded protein Method: similarity and extension**

Nominal mass (Mr): **17575**; Calculated pI value: **4.55**

NCBI BLAST search of [isotig13456](http://www.ncbi.nlm.nih.gov/blast/Blast.cgi?ALIGNMENTS=50&ALIGNMENT_VIEW=Pairwise&AUTO_FORMAT=Semiauto&CDD_SEARCH=on&CLIENT=web&COMPOSITION_BASED_STATISTICS=on&DATABASE=nr&DESCRIPTIONS=100&ENTREZ_QUERY=(none)&EXPECT=10&FILTER=L&FORMAT_BLOCK_ON_RESPAGE=None&FORMAT_OBJECT=Alignment&FORMAT_TYPE=HTML&GAPCOSTS=11+1&I_THRESH=0.001&LAYOUT=TwoWindows&MATRIX_NAME=BLOSUM62&NCBI_GI=on&PAGE=Proteins&PROGRAM=blastp&QUERY=QLQDLGKNVYHDIVPEPVTENPSELRMRKYNFISAAIDDWLMPTETYPIEGDVRYKESLYSDSNLYTFANMAYDKIYEVGCNYEECSKGDETQASLICIYNTKVPDHTQLYQVGSKDPDHAGCNKDKTVCQFLGKADATCDDLLCKLPNVVSSFL&SERVICE=plain&SET_DEFAULTS.x=9&SET_DEFAULTS.y=5&SHOW_OVERVIEW=on&WORD_SIZE=3&END_OF_HTTPGET=Yes" \t "_blank) against nr

Unformatted [sequence string](http://msmsms/mascot/cgi/getseq.pl?cooperia_oncophora+isotig13456+seq" \t "_blank) for pasting into other applications

Variable modifications: Oxidation (HW),Oxidation (M)

Cleavage by Trypsin/P: cuts C-term side of KR

Sequence Coverage: **12%**

Matched peptides shown in **Bold Red**

**1** QLQDLGK**NVY HDIVPEPVTE NPSELR**MRKY NFISAAIDDW LMPTETYPIE

**51** GDVRYKESLY SDSNLYTFAN MAYDKIYEVG CNYEECSKGD ETQASLICIY

**101** NTKVPDHTQL YQVGSKDPDH AGCNKDKTVC QFLGKADATC DDLLCKLPNV

**151** VSSFL

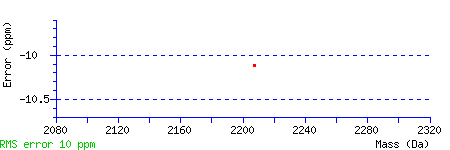


  Residue Number  Increasing Mass  Decreasing Mass

**Start - End Observed Mr(expt) Mr(calc) ppm Miss Sequence**

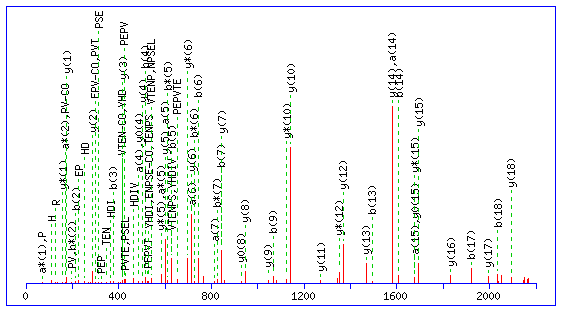
**8 - 26 2208.0708 2207.0635 2207.0858 -10 0 K.NVYHDIVPEPVTENPSELR.M**  ([No match](http://msmsms/mascot/cgi/peptide_view.pl?file=../data/20120113/F018134.dat&query=44&hit=1" \t "_blank))

**8 - 26 2208.0708 2207.0635 2207.0858 -10 0 K.NVYHDIVPEPVTENPSELR.M**  ([Ions score 180](http://msmsms/mascot/cgi/peptide_view.pl?file=../data/20120113/F018134.dat&query=45&hit=1" \t "_blank))



**Bottom of Form**

🡪 Annotated MS2 spectrum for peptide NVYHDIVPEPVTENPSELR



**Monoisotopic mass of neutral peptide Mr(calc):** 2207.0858

**Ions Score:** 180 **Expect:** 7.9e-017

**Matches :** 89/346 fragment ions using 76 most intense peaks   ([help](http://msmsms/mascot/help/results_help.html" \l "PEP" \t "_blank))

|  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **#** | **Immon.** | **a** | **a\*** | **a0** | **b** | **b\*** | **b0** | **Seq.** | **v** | **w** | **w'** | **y** | **y\*** | **y0** | **#** |
| **1** | 87.0553 | 87.0553 | 70.0287 |  | 115.0502 | 98.0237 |  | **N** |  |  |  |  |  |  | **19** |
| **2** | 72.0808 | 186.1237 | 169.0972 |  | **214.1186** | 197.0921 |  | **V** | 2049.9876 | 2063.0080 |  | ***2094.0502*** | 2077.0237 | 2076.0396 | **18** |
| **3** | 136.0757 | 349.1870 | 332.1605 |  | **377.1819** | 360.1554 |  | **Y** | 1886.9243 |  |  | ***1994.9818*** | 1977.9552 | 1976.9712 | **17** |
| **4** | 110.0713 | **486.2459** | 469.2194 |  | **514.2409** | 497.2143 |  | **H** | 1749.8654 |  |  | ***1831.9185*** | 1814.8919 | 1813.9079 | **16** |
| **5** | 88.0393 | **601.2729** | 584.2463 | 583.2623 | **629.2678** | 612.2413 | 611.2572 | **D** | 1634.8384 | 1633.8432 |  | ***1694.8596*** | 1677.8330 | 1676.8490 | **15** |
| **6** | 86.0964 | **714.3569** | 697.3304 | 696.3464 | **742.3519** | 725.3253 | 724.3413 | **I** | 1521.7544 | 1534.7748 | 1548.7904 | ***1579.8326*** | 1562.8061 | 1561.8220 | **14** |
| **7** | 72.0808 | **813.4254** | 796.3988 | 795.4148 | **841.4203** | 824.3937 | 823.4097 | **V** | 1422.6859 | 1435.7064 |  | ***1466.7485*** | 1449.7220 | 1448.7380 | **13** |
| **8** | 70.0651 | 910.4781 | 893.4516 | 892.4676 | 938.4730 | 921.4465 | 920.4625 | **P** | 1325.6332 | 1324.6379 |  | ***1367.6801*** | 1350.6536 | 1349.6696 | **12** |
| **9** | 102.0550 | 1039.5207 | 1022.4942 | 1021.5102 | **1067.5156** | 1050.4891 | 1049.5051 | **E** | 1196.5906 | 1195.5953 |  | ***1270.6274*** | 1253.6008 | 1252.6168 | **11** |
| **10** | 70.0651 | 1136.5735 | 1119.5469 | 1118.5629 | 1164.5684 | 1147.5419 | 1146.5578 | **P** | 1099.5378 | 1098.5426 |  | ***1141.5848*** | 1124.5582 | 1123.5742 | **10** |
| **11** | 72.0808 | 1235.6419 | 1218.6154 | 1217.6313 | 1263.6368 | 1246.6103 | 1245.6262 | **V** | 1000.4694 | 1013.4898 |  | ***1044.5320*** | 1027.5055 | 1026.5214 | **9** |
| **12** | 74.0600 | 1336.6896 | 1319.6630 | 1318.6790 | 1364.6845 | 1347.6579 | 1346.6739 | **T** | 899.4217 | 912.4421 | 914.4214 | ***945.4636*** | 928.4371 | 927.4530 | **8** |
| **13** | 102.0550 | 1465.7322 | 1448.7056 | 1447.7216 | **1493.7271** | 1476.7005 | 1475.7165 | **E** | 770.3791 | 769.3839 |  | ***844.4159*** | 827.3894 | 826.4054 | **7** |
| **14** | 87.0553 | **1579.7751** | 1562.7485 | 1561.7645 | **1607.7700** | 1590.7435 | 1589.7594 | **N** | 656.3362 | 655.3410 |  | ***715.3733*** | 698.3468 | 697.3628 | **6** |
| **15** | 70.0651 | **1676.8279** | 1659.8013 | 1658.8173 | 1704.8228 | 1687.7962 | 1686.8122 | **P** | 559.2835 | 558.2882 |  | ***601.3304*** | 584.3039 | 583.3198 | **5** |
| **16** | 60.0444 | 1763.8599 | 1746.8333 | 1745.8493 | 1791.8548 | 1774.8283 | 1773.8442 | **S** | 472.2514 | 471.2562 |  | ***504.2776*** | 487.2511 | 486.2671 | **4** |
| **17** | 102.0550 | 1892.9025 | 1875.8759 | 1874.8919 | **1920.8974** | 1903.8708 | 1902.8868 | **E** | 343.2088 | 342.2136 |  | ***417.2456*** | 400.2191 | 399.2350 | **3** |
| **18** | 86.0964 | 2005.9865 | 1988.9600 | 1987.9760 | **2033.9815** | 2016.9549 | 2015.9709 | **L** | 230.1248 | 229.1295 |  | ***288.2030*** | 271.1765 |  | **2** |
| **19** | 129.1135 |  |  |  |  |  |  | **R** | 74.0237 | 73.0284 |  | ***175.1190*** | 158.0924 |  | **1** |

|  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **Seq** | **ya** | **yb** | **Seq** | **ya** | **yb** | **Seq** | **ya** | **yb** |
| **VY** | 235.1441 | 263.1390 | **VYH** | 372.2030 | 400.1979 | **VYHD** | 487.2300 | 515.2249 |
| **VYHDI** | 600.3140 | 628.3089 | **VYHDIV** | 699.3824 | 727.3774 | **YH** | 273.1346 | 301.1295 |
| **YHD** | 388.1615 | 416.1565 | **YHDI** | 501.2456 | 529.2405 | **YHDIV** | 600.3140 | 628.3089 |
| **YHDIVP** | 697.3668 | 725.3617 | **HD** | 225.0982 | 253.0931 | **HDI** | 338.1823 | 366.1772 |
| **HDIV** | 437.2507 | 465.2456 | **HDIVP** | 534.3035 | 562.2984 | **HDIVPE** | 663.3461 | 691.3410 |
| **DI** | 201.1234 | 229.1183 | **DIV** | 300.1918 | 328.1867 | **DIVP** | 397.2445 | 425.2395 |
| **DIVPE** | 526.2871 | 554.2821 | **DIVPEP** | 623.3399 | 651.3348 | **IV** | 185.1648 | 213.1598 |
| **IVP** | 282.2176 | 310.2125 | **IVPE** | 411.2602 | 439.2551 | **IVPEP** | 508.3130 | 536.3079 |
| **IVPEPV** | 607.3814 | 635.3763 | **VP** | 169.1335 | 197.1285 | **VPE** | 298.1761 | 326.1710 |
| **VPEP** | 395.2289 | 423.2238 | **VPEPV** | 494.2973 | 522.2922 | **VPEPVT** | 595.3450 | 623.3399 |
| **PE** | 199.1077 | 227.1026 | **PEP** | 296.1605 | 324.1554 | **PEPV** | 395.2289 | 423.2238 |
| **PEPVT** | 496.2766 | 524.2715 | **PEPVTE** | 625.3192 | 653.3141 | **EP** | 199.1077 | 227.1026 |
| **EPV** | 298.1761 | 326.1710 | **EPVT** | 399.2238 | 427.2187 | **EPVTE** | 528.2664 | 556.2613 |
| **EPVTEN** | 642.3093 | 670.3042 | **PV** | 169.1335 | 197.1285 | **PVT** | 270.1812 | 298.1761 |
| **PVTE** | 399.2238 | 427.2187 | **PVTEN** | 513.2667 | 541.2617 | **PVTENP** | 610.3195 | 638.3144 |
| **PVTENPS** | 697.3515 | 725.3464 | **VT** | 173.1285 | 201.1234 | **VTE** | 302.1710 | 330.1660 |
| **VTEN** | 416.2140 | 444.2089 | **VTENP** | 513.2667 | 541.2617 | **VTENPS** | 600.2988 | 628.2937 |
| **TE** | 203.1026 | 231.0975 | **TEN** | 317.1456 | 345.1405 | **TENP** | 414.1983 | 442.1932 |
| **TENPS** | 501.2304 | 529.2253 | **TENPSE** | 630.2729 | 658.2679 | **EN** | 216.0979 | 244.0928 |
| **ENP** | 313.1506 | 341.1456 | **ENPS** | 400.1827 | 428.1776 | **ENPSE** | 529.2253 | 557.2202 |
| **ENPSEL** | 642.3093 | 670.3042 | **NP** | 184.1081 | 212.1030 | **NPS** | 271.1401 | 299.1350 |
| **NPSE** | 400.1827 | 428.1776 | **NPSEL** | 513.2667 | 541.2617 | **PS** | 157.0972 | 185.0921 |
| **PSE** | 286.1397 | 314.1347 | **PSEL** | 399.2238 | 427.2187 | **SE** | 189.0870 | 217.0819 |
| **SEL** | 302.1710 | 330.1660 | **EL** | 215.1390 | 243.1339 |  |  |  |

**Band 7:**

**http://msmsms/mascot/images/88x31_logo_white.gifMascot Search Results**

**User :**

**Email :**

**Search title : SampleSetID: 683, AnalysisID: 1071, MaldiWellID: 82751, SpectrumID: 217125, Path=\Jimmy\Cooperia 3\Co ES Conc 3 Frac 13012012 (strict)**

**Database : cooperia\_oncophora oncophora\_20110405 (34373 sequences; 5289600 residues)**

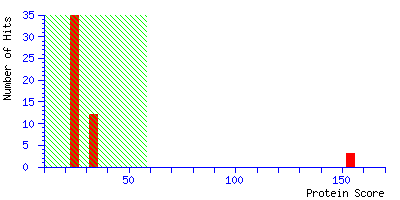
**Timestamp : 13 Jan 2012 at 14:33:40 GMT**

**Warning : A Peptide summary report will usually give a much clearer picture of MS/MS search results.**

**Top Score : 154 for isotig13456, putative nuclear encoded protein Method: similarity and extension**

**Mascot Score Histogram**

Protein score is -10\*Log(P), where P is the probability that the observed match is a random event.  
Protein scores greater than 58 are significant (p<0.05).  
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



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**Protein Summary Report**

|  |  |  |  |
| --- | --- | --- | --- |
|  |  |  | [Help](http://msmsms/mascot/help/msms_summaries_help.html" \t "_blank) |
|  | Significance threshold p< | Max. number of hits |  |

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**Index**

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
|  | **Accession** | **Mass** | **Score** | **Description** |
| **1.** | [**isotig13456**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20120113/F018135.dat#Hit1) | 17575 | 154 | putative nuclear encoded protein Method: similarity and extension |
| **2.** | [**contig55746**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20120113/F018135.dat#Hit2) | 17086 | 154 | putative nuclear encoded protein Method: similarity and extension |
| **3.** | [**isotig13457**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20120113/F018135.dat#Hit3) | 17585 | 154 | putative nuclear encoded protein Method: similarity and extension |
| **4.** | [**isotig19871**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20120113/F018135.dat#Hit4) | 8224 | 37 | putative nuclear encoded protein Method: Longest ORF |
| **5.** | [**isotig19137**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20120113/F018135.dat#Hit5) | 17632 | 35 | putative nuclear encoded protein Method: similarity and extension |
| **6.** | [**isotig25980**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20120113/F018135.dat#Hit6) | 15476 | 33 | putative nuclear encoded protein Method: similarity and extension |
| **7.** | [**isotig32650**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20120113/F018135.dat#Hit7) | 10244 | 32 | putative nuclear encoded protein Method: similarity and extension |
| **8.** | [**isotig28347**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20120113/F018135.dat#Hit8) | 15702 | 32 | putative nuclear encoded protein Method: similarity and extension |
| **9.** | [**isotig32079**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20120113/F018135.dat#Hit9) | 9321 | 31 | putative nuclear encoded protein Method: ESTScan |
| **10.** | [**isotig12445**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20120113/F018135.dat#Hit10) | 48729 | 30 | putative nuclear encoded protein Method: similarity and extension |
| **11.** | [**isotig12444**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20120113/F018135.dat#Hit11) | 48731 | 30 | putative nuclear encoded protein Method: similarity and extension |
| **12.** | [**isotig25071**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20120113/F018135.dat#Hit12) | 14223 | 30 | putative nuclear encoded protein Method: similarity and extension |
| **13.** | [**isotig20450**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20120113/F018135.dat#Hit13) | 13893 | 30 | putative nuclear encoded protein Method: similarity and extension |
| **14.** | [**isotig28702**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20120113/F018135.dat#Hit14) | 6282 | 30 | putative nuclear encoded protein Method: Longest ORF |
| **15.** | [**isotig31538**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20120113/F018135.dat#Hit15) | 18068 | 29 | putative nuclear encoded protein Method: similarity and extension |
| **16.** | [**isotig27153**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20120113/F018135.dat#Hit16) | 10658 | 29 | putative nuclear encoded protein Method: similarity and extension |
| **17.** | [**isotig21603**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20120113/F018135.dat#Hit17) | 19176 | 29 | putative nuclear encoded protein Method: Longest ORF |
| **18.** | [**isotig20305**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20120113/F018135.dat#Hit18) | 16534 | 28 | putative nuclear encoded protein Method: similarity and extension |
| **19.** | [**isotig27563**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20120113/F018135.dat#Hit19) | 12381 | 28 | putative nuclear encoded protein Method: Longest ORF |
| **20.** | [**isotig11802**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20120113/F018135.dat#Hit20) | 20387 | 28 | putative nuclear encoded protein Method: similarity and extension |

**Results List**

|  |  |
| --- | --- |
| **1.** | [isotig13456](http://msmsms/mascot/cgi/protein_view.pl?file=../data/20120113/F018135.dat&hit=1" \t "_blank)    **Mass:** 17575    **Score:** 154    **Expect:** 1.4e-011  **Matches:** 2 |
|  | putative nuclear encoded protein Method: similarity and extension |

|  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | **Observed** | **Mr(expt)** | **Mr(calc)** | **ppm** | **Start** |  | **End** | **Miss** | **Ions** | **Peptide** |
|  | 2208.0781 | 2207.0708 | 2207.0858 | -6.81 | 8 | - | 26 | 0 | --- | K.NVYHDIVPEPVTENPSELR.M |
|  | 2208.0781 | 2207.0708 | 2207.0858 | -6.81 | 8 | - | 26 | 0 | 154 | K.NVYHDIVPEPVTENPSELR.M |

|  |  |
| --- | --- |
|  | **No match to:** 900.4819, 1056.5884, 1056.5884, 1061.5049, 1072.5562, 1102.5726, 1102.5726, 1151.5844, 1163.6268, 1163.6268, 1179.6278, 1184.6736, 1189.5985, 1205.5212, 1257.6237, 1280.5981, 1284.5896, 1300.6443, 1356.6499, 1363.7112, 1370.5972, 1380.6415, 1393.7161, 1393.7161, 1408.6913, 1430.8137, 1434.7466, 1439.7509, 1440.6829, 1442.7350, 1454.7704, 1454.7704, 1541.8116, 1668.8651, 1746.8872, 1757.7065, 1762.6736, 1777.8439, 1990.8376, 2002.0454, 2011.0691, 2059.0667, 2069.0771, 2069.0771, 2075.0645, 2105.0330, 2148.1218, 2148.1218, 2160.1538, 2276.2126, 2276.2126, 2288.2454, 2337.2051, 2349.2393, 2465.3003, 2480.3096, 2851.3264, 2851.3264 |

|  |  |
| --- | --- |
| **2.** | [contig55746](http://msmsms/mascot/cgi/protein_view.pl?file=../data/20120113/F018135.dat&hit=2" \t "_blank)    **Mass:** 17086    **Score:** 154    **Expect:** 1.4e-011  **Matches:** 2 |
|  | putative nuclear encoded protein Method: similarity and extension |

|  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | **Observed** | **Mr(expt)** | **Mr(calc)** | **ppm** | **Start** |  | **End** | **Miss** | **Ions** | **Peptide** |
|  | 2208.0781 | 2207.0708 | 2207.0858 | -6.81 | 4 | - | 22 | 0 | --- | K.NVYHDIVPEPVTENPSELR.M |
|  | 2208.0781 | 2207.0708 | 2207.0858 | -6.81 | 4 | - | 22 | 0 | 154 | K.NVYHDIVPEPVTENPSELR.M |

|  |  |
| --- | --- |
|  | **No match to:** 900.4819, 1056.5884, 1056.5884, 1061.5049, 1072.5562, 1102.5726, 1102.5726, 1151.5844, 1163.6268, 1163.6268, 1179.6278, 1184.6736, 1189.5985, 1205.5212, 1257.6237, 1280.5981, 1284.5896, 1300.6443, 1356.6499, 1363.7112, 1370.5972, 1380.6415, 1393.7161, 1393.7161, 1408.6913, 1430.8137, 1434.7466, 1439.7509, 1440.6829, 1442.7350, 1454.7704, 1454.7704, 1541.8116, 1668.8651, 1746.8872, 1757.7065, 1762.6736, 1777.8439, 1990.8376, 2002.0454, 2011.0691, 2059.0667, 2069.0771, 2069.0771, 2075.0645, 2105.0330, 2148.1218, 2148.1218, 2160.1538, 2276.2126, 2276.2126, 2288.2454, 2337.2051, 2349.2393, 2465.3003, 2480.3096, 2851.3264, 2851.3264 |

|  |  |
| --- | --- |
| **3.** | [isotig13457](http://msmsms/mascot/cgi/protein_view.pl?file=../data/20120113/F018135.dat&hit=3" \t "_blank)    **Mass:** 17585    **Score:** 154    **Expect:** 1.4e-011  **Matches:** 2 |
|  | putative nuclear encoded protein Method: similarity and extension |

|  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | **Observed** | **Mr(expt)** | **Mr(calc)** | **ppm** | **Start** |  | **End** | **Miss** | **Ions** | **Peptide** |
|  | 2208.0781 | 2207.0708 | 2207.0858 | -6.81 | 8 | - | 26 | 0 | --- | K.NVYHDIVPEPVTENPSELR.M |
|  | 2208.0781 | 2207.0708 | 2207.0858 | -6.81 | 8 | - | 26 | 0 | 154 | K.NVYHDIVPEPVTENPSELR.M |

|  |  |
| --- | --- |
|  | **No match to:** 900.4819, 1056.5884, 1056.5884, 1061.5049, 1072.5562, 1102.5726, 1102.5726, 1151.5844, 1163.6268, 1163.6268, 1179.6278, 1184.6736, 1189.5985, 1205.5212, 1257.6237, 1280.5981, 1284.5896, 1300.6443, 1356.6499, 1363.7112, 1370.5972, 1380.6415, 1393.7161, 1393.7161, 1408.6913, 1430.8137, 1434.7466, 1439.7509, 1440.6829, 1442.7350, 1454.7704, 1454.7704, 1541.8116, 1668.8651, 1746.8872, 1757.7065, 1762.6736, 1777.8439, 1990.8376, 2002.0454, 2011.0691, 2059.0667, 2069.0771, 2069.0771, 2075.0645, 2105.0330, 2148.1218, 2148.1218, 2160.1538, 2276.2126, 2276.2126, 2288.2454, 2337.2051, 2349.2393, 2465.3003, 2480.3096, 2851.3264, 2851.3264 |

**http://msmsms/mascot/images/88x31_logo_white.gifMascot Search Results**

**Protein View**

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Match to: **isotig13456** Score: **154** Expect: **1.4e-011**

**putative nuclear encoded protein Method: similarity and extension**

Nominal mass (Mr): **17575**; Calculated pI value: **4.55**

NCBI BLAST search of [isotig13456](http://www.ncbi.nlm.nih.gov/blast/Blast.cgi?ALIGNMENTS=50&ALIGNMENT_VIEW=Pairwise&AUTO_FORMAT=Semiauto&CDD_SEARCH=on&CLIENT=web&COMPOSITION_BASED_STATISTICS=on&DATABASE=nr&DESCRIPTIONS=100&ENTREZ_QUERY=(none)&EXPECT=10&FILTER=L&FORMAT_BLOCK_ON_RESPAGE=None&FORMAT_OBJECT=Alignment&FORMAT_TYPE=HTML&GAPCOSTS=11+1&I_THRESH=0.001&LAYOUT=TwoWindows&MATRIX_NAME=BLOSUM62&NCBI_GI=on&PAGE=Proteins&PROGRAM=blastp&QUERY=QLQDLGKNVYHDIVPEPVTENPSELRMRKYNFISAAIDDWLMPTETYPIEGDVRYKESLYSDSNLYTFANMAYDKIYEVGCNYEECSKGDETQASLICIYNTKVPDHTQLYQVGSKDPDHAGCNKDKTVCQFLGKADATCDDLLCKLPNVVSSFL&SERVICE=plain&SET_DEFAULTS.x=9&SET_DEFAULTS.y=5&SHOW_OVERVIEW=on&WORD_SIZE=3&END_OF_HTTPGET=Yes" \t "_blank) against nr

Unformatted [sequence string](http://msmsms/mascot/cgi/getseq.pl?cooperia_oncophora+isotig13456+seq" \t "_blank) for pasting into other applications

Variable modifications: Oxidation (HW),Oxidation (M)

Cleavage by Trypsin/P: cuts C-term side of KR

Sequence Coverage: **12%**

Matched peptides shown in **Bold Red**

**1** QLQDLGK**NVY HDIVPEPVTE NPSELR**MRKY NFISAAIDDW LMPTETYPIE

**51** GDVRYKESLY SDSNLYTFAN MAYDKIYEVG CNYEECSKGD ETQASLICIY

**101** NTKVPDHTQL YQVGSKDPDH AGCNKDKTVC QFLGKADATC DDLLCKLPNV

**151** VSSFL

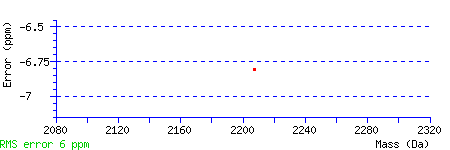


  Residue Number  Increasing Mass  Decreasing Mass

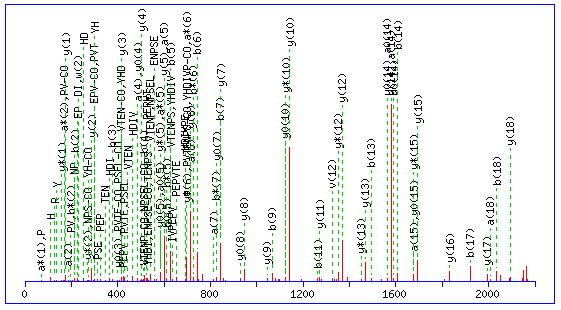
**Start - End Observed Mr(expt) Mr(calc) ppm Miss Sequence**

**8 - 26 2208.0781 2207.0708 2207.0858 -7 0 K.NVYHDIVPEPVTENPSELR.M**  ([No match](http://msmsms/mascot/cgi/peptide_view.pl?file=../data/20120113/F018135.dat&query=50&hit=1" \t "_blank))

**8 - 26 2208.0781 2207.0708 2207.0858 -7 0 K.NVYHDIVPEPVTENPSELR.M**  ([Ions score 154](http://msmsms/mascot/cgi/peptide_view.pl?file=../data/20120113/F018135.dat&query=51&hit=1" \t "_blank))



🡪 Annotated MS2 spectrum for peptide NVYHDIVPEPVTENPSELR



**Monoisotopic mass of neutral peptide Mr(calc):** 2207.0858

**Ions Score:** 154 **Expect:** 3e-014

**Matches :** 125/346 fragment ions using 114 most intense peaks   ([help](http://msmsms/mascot/help/results_help.html" \l "PEP" \t "_blank))

|  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **#** | **Immon.** | **a** | **a\*** | **a0** | **b** | **b\*** | **b0** | **Seq.** | **v** | **w** | **w'** | **y** | **y\*** | **y0** | **#** |
| **1** | 87.0553 | 87.0553 | 70.0287 |  | 115.0502 | 98.0237 |  | **N** |  |  |  |  |  |  | **19** |
| **2** | 72.0808 | **186.1237** | 169.0972 |  | **214.1186** | 197.0921 |  | **V** | 2049.9876 | 2063.0080 |  | ***2094.0502*** | 2077.0237 | 2076.0396 | **18** |
| **3** | 136.0757 | 349.1870 | 332.1605 |  | **377.1819** | 360.1554 |  | **Y** | 1886.9243 |  |  | ***1994.9818*** | 1977.9552 | 1976.9712 | **17** |
| **4** | 110.0713 | **486.2459** | 469.2194 |  | **514.2409** | 497.2143 |  | **H** | 1749.8654 |  |  | ***1831.9185*** | 1814.8919 | 1813.9079 | **16** |
| **5** | 88.0393 | **601.2729** | 584.2463 | 583.2623 | **629.2678** | 612.2413 | 611.2572 | **D** | 1634.8384 | 1633.8432 |  | ***1694.8596*** | 1677.8330 | 1676.8490 | **15** |
| **6** | 86.0964 | **714.3569** | 697.3304 | 696.3464 | **742.3519** | 725.3253 | 724.3413 | **I** | 1521.7544 | 1534.7748 | 1548.7904 | ***1579.8326*** | 1562.8061 | 1561.8220 | **14** |
| **7** | 72.0808 | **813.4254** | 796.3988 | 795.4148 | **841.4203** | 824.3937 | 823.4097 | **V** | 1422.6859 | 1435.7064 |  | ***1466.7485*** | 1449.7220 | 1448.7380 | **13** |
| **8** | 70.0651 | 910.4781 | 893.4516 | 892.4676 | 938.4730 | 921.4465 | 920.4625 | **P** | 1325.6332 | 1324.6379 |  | ***1367.6801*** | 1350.6536 | 1349.6696 | **12** |
| **9** | 102.0550 | 1039.5207 | 1022.4942 | 1021.5102 | **1067.5156** | 1050.4891 | 1049.5051 | **E** | 1196.5906 | 1195.5953 |  | ***1270.6274*** | 1253.6008 | 1252.6168 | **11** |
| **10** | 70.0651 | 1136.5735 | 1119.5469 | 1118.5629 | 1164.5684 | 1147.5419 | 1146.5578 | **P** | 1099.5378 | 1098.5426 |  | ***1141.5848*** | 1124.5582 | 1123.5742 | **10** |
| **11** | 72.0808 | 1235.6419 | 1218.6154 | 1217.6313 | **1263.6368** | 1246.6103 | 1245.6262 | **V** | 1000.4694 | 1013.4898 |  | ***1044.5320*** | 1027.5055 | 1026.5214 | **9** |
| **12** | 74.0600 | 1336.6896 | 1319.6630 | 1318.6790 | 1364.6845 | 1347.6579 | 1346.6739 | **T** | 899.4217 | 912.4421 | 914.4214 | ***945.4636*** | 928.4371 | 927.4530 | **8** |
| **13** | 102.0550 | 1465.7322 | 1448.7056 | 1447.7216 | **1493.7271** | 1476.7005 | 1475.7165 | **E** | 770.3791 | 769.3839 |  | ***844.4159*** | 827.3894 | 826.4054 | **7** |
| **14** | 87.0553 | **1579.7751** | 1562.7485 | 1561.7645 | **1607.7700** | 1590.7435 | 1589.7594 | **N** | 656.3362 | 655.3410 |  | ***715.3733*** | 698.3468 | 697.3628 | **6** |
| **15** | 70.0651 | **1676.8279** | 1659.8013 | 1658.8173 | 1704.8228 | 1687.7962 | 1686.8122 | **P** | 559.2835 | 558.2882 |  | ***601.3304*** | 584.3039 | 583.3198 | **5** |
| **16** | 60.0444 | 1763.8599 | 1746.8333 | 1745.8493 | 1791.8548 | 1774.8283 | 1773.8442 | **S** | 472.2514 | 471.2562 |  | ***504.2776*** | 487.2511 | 486.2671 | **4** |
| **17** | 102.0550 | 1892.9025 | 1875.8759 | 1874.8919 | **1920.8974** | 1903.8708 | 1902.8868 | **E** | 343.2088 | 342.2136 |  | ***417.2456*** | 400.2191 | 399.2350 | **3** |
| **18** | 86.0964 | **2005.9865** | 1988.9600 | 1987.9760 | **2033.9815** | 2016.9549 | 2015.9709 | **L** | 230.1248 | 229.1295 |  | ***288.2030*** | 271.1765 |  | **2** |
| **19** | 129.1135 |  |  |  |  |  |  | **R** | 74.0237 | 73.0284 |  | ***175.1190*** | 158.0924 |  | **1** |

|  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **Seq** | **ya** | **yb** | **Seq** | **ya** | **yb** | **Seq** | **ya** | **yb** |
| **VY** | 235.1441 | 263.1390 | **VYH** | 372.2030 | 400.1979 | **VYHD** | 487.2300 | 515.2249 |
| **VYHDI** | 600.3140 | 628.3089 | **VYHDIV** | 699.3824 | 727.3774 | **YH** | 273.1346 | 301.1295 |
| **YHD** | 388.1615 | 416.1565 | **YHDI** | 501.2456 | 529.2405 | **YHDIV** | 600.3140 | 628.3089 |
| **YHDIVP** | 697.3668 | 725.3617 | **HD** | 225.0982 | 253.0931 | **HDI** | 338.1823 | 366.1772 |
| **HDIV** | 437.2507 | 465.2456 | **HDIVP** | 534.3035 | 562.2984 | **HDIVPE** | 663.3461 | 691.3410 |
| **DI** | 201.1234 | 229.1183 | **DIV** | 300.1918 | 328.1867 | **DIVP** | 397.2445 | 425.2395 |
| **DIVPE** | 526.2871 | 554.2821 | **DIVPEP** | 623.3399 | 651.3348 | **IV** | 185.1648 | 213.1598 |
| **IVP** | 282.2176 | 310.2125 | **IVPE** | 411.2602 | 439.2551 | **IVPEP** | 508.3130 | 536.3079 |
| **IVPEPV** | 607.3814 | 635.3763 | **VP** | 169.1335 | 197.1285 | **VPE** | 298.1761 | 326.1710 |
| **VPEP** | 395.2289 | 423.2238 | **VPEPV** | 494.2973 | 522.2922 | **VPEPVT** | 595.3450 | 623.3399 |
| **PE** | 199.1077 | 227.1026 | **PEP** | 296.1605 | 324.1554 | **PEPV** | 395.2289 | 423.2238 |
| **PEPVT** | 496.2766 | 524.2715 | **PEPVTE** | 625.3192 | 653.3141 | **EP** | 199.1077 | 227.1026 |
| **EPV** | 298.1761 | 326.1710 | **EPVT** | 399.2238 | 427.2187 | **EPVTE** | 528.2664 | 556.2613 |
| **EPVTEN** | 642.3093 | 670.3042 | **PV** | 169.1335 | 197.1285 | **PVT** | 270.1812 | 298.1761 |
| **PVTE** | 399.2238 | 427.2187 | **PVTEN** | 513.2667 | 541.2617 | **PVTENP** | 610.3195 | 638.3144 |
| **PVTENPS** | 697.3515 | 725.3464 | **VT** | 173.1285 | 201.1234 | **VTE** | 302.1710 | 330.1660 |
| **VTEN** | 416.2140 | 444.2089 | **VTENP** | 513.2667 | 541.2617 | **VTENPS** | 600.2988 | 628.2937 |
| **TE** | 203.1026 | 231.0975 | **TEN** | 317.1456 | 345.1405 | **TENP** | 414.1983 | 442.1932 |
| **TENPS** | 501.2304 | 529.2253 | **TENPSE** | 630.2729 | 658.2679 | **EN** | 216.0979 | 244.0928 |
| **ENP** | 313.1506 | 341.1456 | **ENPS** | 400.1827 | 428.1776 | **ENPSE** | 529.2253 | 557.2202 |
| **ENPSEL** | 642.3093 | 670.3042 | **NP** | 184.1081 | 212.1030 | **NPS** | 271.1401 | 299.1350 |
| **NPSE** | 400.1827 | 428.1776 | **NPSEL** | 513.2667 | 541.2617 | **PS** | 157.0972 | 185.0921 |
| **PSE** | 286.1397 | 314.1347 | **PSEL** | 399.2238 | 427.2187 | **SE** | 189.0870 | 217.0819 |
| **SEL** | 302.1710 | 330.1660 | **EL** | 215.1390 | 243.1339 |  |  |  |

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**Band 8:**

**http://msmsms/mascot/images/88x31_logo_white.gifMascot Search Results**

**User :**

**Email :**

**Search title : SampleSetID: 683, AnalysisID: 1071, MaldiWellID: 82752, SpectrumID: 217136, Path=\Jimmy\Cooperia 3\Co ES Conc 3 Frac 13012012 (strict)**

**Database : cooperia\_oncophora oncophora\_20110405 (34373 sequences; 5289600 residues)**

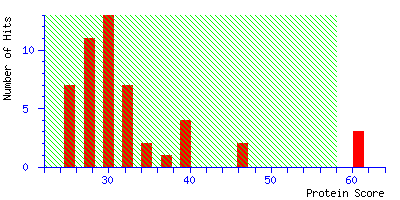
**Timestamp : 13 Jan 2012 at 14:33:53 GMT**

**Warning : A Peptide summary report will usually give a much clearer picture of MS/MS search results.**

**Top Score : 61 for isotig00466, putative nuclear encoded protein Method: similarity and extension**

**Mascot Score Histogram**

Protein score is -10\*Log(P), where P is the probability that the observed match is a random event.  
Protein scores greater than 58 are significant (p<0.05).  
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



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**Protein Summary Report**

|  |  |  |  |
| --- | --- | --- | --- |
|  |  |  | [Help](http://msmsms/mascot/help/msms_summaries_help.html" \t "_blank) |
|  | Significance threshold p< | Max. number of hits |  |

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**Index**

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
|  | **Accession** | **Mass** | **Score** | **Description** |
| **1.** | [**isotig00466**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20120113/F018136.dat#Hit1) | 14324 | 61 | putative nuclear encoded protein Method: similarity and extension |
| **2.** | [**isotig00467**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20120113/F018136.dat#Hit2) | 14324 | 61 | putative nuclear encoded protein Method: similarity and extension |
| **3.** | [**isotig00468**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20120113/F018136.dat#Hit3) | 14324 | 61 | putative nuclear encoded protein Method: similarity and extension |
| **4.** | [**isotig06171**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20120113/F018136.dat#Hit4) | 28463 | 46 | putative nuclear encoded protein Method: similarity and extension |
| **5.** | [**isotig06173**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20120113/F018136.dat#Hit5) | 28463 | 46 | putative nuclear encoded protein Method: similarity and extension |
| **6.** | [**isotig12445**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20120113/F018136.dat#Hit6) | 48729 | 39 | putative nuclear encoded protein Method: similarity and extension |
| **7.** | [**isotig12444**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20120113/F018136.dat#Hit7) | 48731 | 39 | putative nuclear encoded protein Method: similarity and extension |
| **8.** | [**isotig19871**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20120113/F018136.dat#Hit8) | 8224 | 38 | putative nuclear encoded protein Method: Longest ORF |
| **9.** | [**isotig19822**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20120113/F018136.dat#Hit9) | 36809 | 38 | putative nuclear encoded protein Method: similarity and extension |
| **10.** | [**isotig06172**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20120113/F018136.dat#Hit10) | 28208 | 38 | putative nuclear encoded protein Method: similarity and extension |
| **11.** | [**isotig13507**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20120113/F018136.dat#Hit11) | 9281 | 34 | putative nuclear encoded protein Method: Longest ORF |
| **12.** | [**isotig10914**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20120113/F018136.dat#Hit12) | 6803 | 34 | putative nuclear encoded protein Method: Longest ORF |
| **13.** | [**isotig23047**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20120113/F018136.dat#Hit13) | 15747 | 33 | putative nuclear encoded protein Method: similarity and extension |
| **14.** | [**isotig14500**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20120113/F018136.dat#Hit14) | 32548 | 33 | putative nuclear encoded protein Method: similarity and extension |
| **15.** | [**isotig14931**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20120113/F018136.dat#Hit15) | 31854 | 33 | putative nuclear encoded protein Method: similarity and extension |
| **16.** | [**isotig21678**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20120113/F018136.dat#Hit16) | 15249 | 33 | putative nuclear encoded protein Method: Longest ORF |
| **17.** | [**isotig23872**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20120113/F018136.dat#Hit17) | 9335 | 31 | putative nuclear encoded protein Method: Longest ORF |
| **18.** | [**isotig27188**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20120113/F018136.dat#Hit18) | 21031 | 31 | putative nuclear encoded protein Method: similarity and extension |
| **19.** | [**isotig14224**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20120113/F018136.dat#Hit19) | 33786 | 31 | putative nuclear encoded protein Method: similarity and extension |
| **20.** | [**isotig27038**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20120113/F018136.dat#Hit20) | 30963 | 31 | putative nuclear encoded protein Method: similarity and extension |

**Results List**

|  |  |
| --- | --- |
| **1.** | [isotig00466](http://msmsms/mascot/cgi/protein_view.pl?file=../data/20120113/F018136.dat&hit=1" \t "_blank)    **Mass:** 14324    **Score:** 61     **Expect:** 0.029  **Matches:** 14 |
|  | putative nuclear encoded protein Method: similarity and extension |

|  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | **Observed** | **Mr(expt)** | **Mr(calc)** | **ppm** | **Start** |  | **End** | **Miss** | **Ions** | **Peptide** |
|  | 1054.5273 | 1053.5200 | 1053.5243 | -4.09 | 100 | - | 107 | 0 | --- | K.VDEHQIWK.K |
|  | 1061.4967 | 1060.4894 | 1060.4978 | -7.89 | 60 | - | 67 | 0 | --- | K.FFEEHQPK.N |
|  | 1189.5488 | 1188.5415 | 1188.5927 | -43.09 | 59 | - | 67 | 1 | --- | K.KFFEEHQPK.N |
|  | 1205.5109 | 1204.5036 | 1204.5877 | -69.76 | 59 | - | 67 | 1 | --- | K.KFFEEHQPK.N + Oxidation (HW) |
|  | 1265.6339 | 1264.6266 | 1264.6387 | -9.53 | 32 | - | 42 | 0 | --- | K.FLHPECVGVHK.G |
|  | 1268.5476 | 1267.5403 | 1267.5543 | -11.03 | 115 | - | 124 | 0 | --- | K.LYHMEYDVQA.- |
|  | 1284.5387 | 1283.5314 | 1283.5492 | -13.87 | 115 | - | 124 | 0 | --- | K.LYHMEYDVQA.- + Oxidation (M) |
|  | 1285.6924 | 1284.6851 | 1284.7037 | -14.47 | 20 | - | 31 | 1 | --- | K.NIAAGKLEENVK.F |
|  | 1430.8088 | 1429.8015 | 1429.8180 | -11.54 | 8 | - | 19 | 1 | --- | K.AILKPLYDEIQK.N |
|  | 1439.7477 | 1438.7404 | 1438.7569 | -11.42 | 96 | - | 107 | 1 | --- | K.GSLKVDEHQIWK.K |
|  | 1567.8358 | 1566.8285 | 1566.8518 | -14.86 | 96 | - | 108 | 2 | --- | K.GSLKVDEHQIWKK.I |
|  | 1602.8064 | 1601.7991 | 1601.8123 | -8.22 | 45 | - | 58 | 1 | --- | K.AAYYGKEQILTSMK.K |
|  | 1730.8920 | 1729.8847 | 1729.9072 | -13.02 | 45 | - | 59 | 2 | --- | K.AAYYGKEQILTSMKK.F |
|  | 1746.8850 | 1745.8777 | 1745.9022 | -14.00 | 45 | - | 59 | 2 | --- | K.AAYYGKEQILTSMKK.F + Oxidation (M) |

|  |  |
| --- | --- |
|  | **No match to:** 900.4697, 914.3483, 917.4649, 1043.5529, 1056.5776, 1056.5776, 1072.5463, 1102.5571, 1146.6042, 1151.5815, 1162.5952, 1163.6207, 1163.6207, 1179.6031, 1184.6626, 1318.6542, 1341.6317, 1447.7317, 1454.7653, 1454.7653, 1611.6730, 1767.7791, 1785.8806, 1807.9165, 1828.7050, 1895.8650, 2034.0640, 2075.0596, 2075.0596, 2130.1016, 2131.1106, 2147.1077, 2148.1162, 2148.1162, 2160.1147, 2162.1245, 2276.2012, 2276.2012, 2467.1743, 2480.2903, 2480.2903, 2608.3831, 3346.5842, 3346.5842 |

|  |  |
| --- | --- |
| **2.** | [isotig00467](http://msmsms/mascot/cgi/protein_view.pl?file=../data/20120113/F018136.dat&hit=2" \t "_blank)    **Mass:** 14324    **Score:** 61     **Expect:** 0.029  **Matches:** 14 |
|  | putative nuclear encoded protein Method: similarity and extension |

|  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | **Observed** | **Mr(expt)** | **Mr(calc)** | **ppm** | **Start** |  | **End** | **Miss** | **Ions** | **Peptide** |
|  | 1054.5273 | 1053.5200 | 1053.5243 | -4.09 | 100 | - | 107 | 0 | --- | K.VDEHQIWK.K |
|  | 1061.4967 | 1060.4894 | 1060.4978 | -7.89 | 60 | - | 67 | 0 | --- | K.FFEEHQPK.N |
|  | 1189.5488 | 1188.5415 | 1188.5927 | -43.09 | 59 | - | 67 | 1 | --- | K.KFFEEHQPK.N |
|  | 1205.5109 | 1204.5036 | 1204.5877 | -69.76 | 59 | - | 67 | 1 | --- | K.KFFEEHQPK.N + Oxidation (HW) |
|  | 1265.6339 | 1264.6266 | 1264.6387 | -9.53 | 32 | - | 42 | 0 | --- | K.FLHPECVGVHK.G |
|  | 1268.5476 | 1267.5403 | 1267.5543 | -11.03 | 115 | - | 124 | 0 | --- | K.LYHMEYDVQA.- |
|  | 1284.5387 | 1283.5314 | 1283.5492 | -13.87 | 115 | - | 124 | 0 | --- | K.LYHMEYDVQA.- + Oxidation (M) |
|  | 1285.6924 | 1284.6851 | 1284.7037 | -14.47 | 20 | - | 31 | 1 | --- | K.NIAAGKLEENVK.F |
|  | 1430.8088 | 1429.8015 | 1429.8180 | -11.54 | 8 | - | 19 | 1 | --- | K.AILKPLYDEIQK.N |
|  | 1439.7477 | 1438.7404 | 1438.7569 | -11.42 | 96 | - | 107 | 1 | --- | K.GSLKVDEHQIWK.K |
|  | 1567.8358 | 1566.8285 | 1566.8518 | -14.86 | 96 | - | 108 | 2 | --- | K.GSLKVDEHQIWKK.I |
|  | 1602.8064 | 1601.7991 | 1601.8123 | -8.22 | 45 | - | 58 | 1 | --- | K.AAYYGKEQILTSMK.K |
|  | 1730.8920 | 1729.8847 | 1729.9072 | -13.02 | 45 | - | 59 | 2 | --- | K.AAYYGKEQILTSMKK.F |
|  | 1746.8850 | 1745.8777 | 1745.9022 | -14.00 | 45 | - | 59 | 2 | --- | K.AAYYGKEQILTSMKK.F + Oxidation (M) |

|  |  |
| --- | --- |
|  | **No match to:** 900.4697, 914.3483, 917.4649, 1043.5529, 1056.5776, 1056.5776, 1072.5463, 1102.5571, 1146.6042, 1151.5815, 1162.5952, 1163.6207, 1163.6207, 1179.6031, 1184.6626, 1318.6542, 1341.6317, 1447.7317, 1454.7653, 1454.7653, 1611.6730, 1767.7791, 1785.8806, 1807.9165, 1828.7050, 1895.8650, 2034.0640, 2075.0596, 2075.0596, 2130.1016, 2131.1106, 2147.1077, 2148.1162, 2148.1162, 2160.1147, 2162.1245, 2276.2012, 2276.2012, 2467.1743, 2480.2903, 2480.2903, 2608.3831, 3346.5842, 3346.5842 |

|  |  |
| --- | --- |
| **3.** | [isotig00468](http://msmsms/mascot/cgi/protein_view.pl?file=../data/20120113/F018136.dat&hit=3" \t "_blank)    **Mass:** 14324    **Score:** 61     **Expect:** 0.029  **Matches:** 14 |
|  | putative nuclear encoded protein Method: similarity and extension |

|  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | **Observed** | **Mr(expt)** | **Mr(calc)** | **ppm** | **Start** |  | **End** | **Miss** | **Ions** | **Peptide** |
|  | 1054.5273 | 1053.5200 | 1053.5243 | -4.09 | 100 | - | 107 | 0 | --- | K.VDEHQIWK.K |
|  | 1061.4967 | 1060.4894 | 1060.4978 | -7.89 | 60 | - | 67 | 0 | --- | K.FFEEHQPK.N |
|  | 1189.5488 | 1188.5415 | 1188.5927 | -43.09 | 59 | - | 67 | 1 | --- | K.KFFEEHQPK.N |
|  | 1205.5109 | 1204.5036 | 1204.5877 | -69.76 | 59 | - | 67 | 1 | --- | K.KFFEEHQPK.N + Oxidation (HW) |
|  | 1265.6339 | 1264.6266 | 1264.6387 | -9.53 | 32 | - | 42 | 0 | --- | K.FLHPECVGVHK.G |
|  | 1268.5476 | 1267.5403 | 1267.5543 | -11.03 | 115 | - | 124 | 0 | --- | K.LYHMEYDVQA.- |
|  | 1284.5387 | 1283.5314 | 1283.5492 | -13.87 | 115 | - | 124 | 0 | --- | K.LYHMEYDVQA.- + Oxidation (M) |
|  | 1285.6924 | 1284.6851 | 1284.7037 | -14.47 | 20 | - | 31 | 1 | --- | K.NIAAGKLEENVK.F |
|  | 1430.8088 | 1429.8015 | 1429.8180 | -11.54 | 8 | - | 19 | 1 | --- | K.AILKPLYDEIQK.N |
|  | 1439.7477 | 1438.7404 | 1438.7569 | -11.42 | 96 | - | 107 | 1 | --- | K.GSLKVDEHQIWK.K |
|  | 1567.8358 | 1566.8285 | 1566.8518 | -14.86 | 96 | - | 108 | 2 | --- | K.GSLKVDEHQIWKK.I |
|  | 1602.8064 | 1601.7991 | 1601.8123 | -8.22 | 45 | - | 58 | 1 | --- | K.AAYYGKEQILTSMK.K |
|  | 1730.8920 | 1729.8847 | 1729.9072 | -13.02 | 45 | - | 59 | 2 | --- | K.AAYYGKEQILTSMKK.F |
|  | 1746.8850 | 1745.8777 | 1745.9022 | -14.00 | 45 | - | 59 | 2 | --- | K.AAYYGKEQILTSMKK.F + Oxidation (M) |

|  |  |
| --- | --- |
|  | **No match to:** 900.4697, 914.3483, 917.4649, 1043.5529, 1056.5776, 1056.5776, 1072.5463, 1102.5571, 1146.6042, 1151.5815, 1162.5952, 1163.6207, 1163.6207, 1179.6031, 1184.6626, 1318.6542, 1341.6317, 1447.7317, 1454.7653, 1454.7653, 1611.6730, 1767.7791, 1785.8806, 1807.9165, 1828.7050, 1895.8650, 2034.0640, 2075.0596, 2075.0596, 2130.1016, 2131.1106, 2147.1077, 2148.1162, 2148.1162, 2160.1147, 2162.1245, 2276.2012, 2276.2012, 2467.1743, 2480.2903, 2480.2903, 2608.3831, 3346.5842, 3346.5842 |

**http://msmsms/mascot/images/88x31_logo_white.gifMascot Search Results**

**Protein View**

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Match to: **isotig00466** Score: **61** Expect: **0.029**

**putative nuclear encoded protein Method: similarity and extension**

Nominal mass (Mr): **14324**; Calculated pI value: **7.60**

NCBI BLAST search of [isotig00466](http://www.ncbi.nlm.nih.gov/blast/Blast.cgi?ALIGNMENTS=50&ALIGNMENT_VIEW=Pairwise&AUTO_FORMAT=Semiauto&CDD_SEARCH=on&CLIENT=web&COMPOSITION_BASED_STATISTICS=on&DATABASE=nr&DESCRIPTIONS=100&ENTREZ_QUERY=(none)&EXPECT=10&FILTER=L&FORMAT_BLOCK_ON_RESPAGE=None&FORMAT_OBJECT=Alignment&FORMAT_TYPE=HTML&GAPCOSTS=11+1&I_THRESH=0.001&LAYOUT=TwoWindows&MATRIX_NAME=BLOSUM62&NCBI_GI=on&PAGE=Proteins&PROGRAM=blastp&QUERY=MKPDEAKAILKPLYDEIQKNIAAGKLEENVKFLHPECVGVHKGKAAYYGKEQILTSMKKFFEEHQPKNIKRSNEVYCGCDCCICVSYVATFDTTKGSLKVDEHQIWKKIDGQWKLYHMEYDVQA&SERVICE=plain&SET_DEFAULTS.x=9&SET_DEFAULTS.y=5&SHOW_OVERVIEW=on&WORD_SIZE=3&END_OF_HTTPGET=Yes" \t "_blank) against nr

Unformatted [sequence string](http://msmsms/mascot/cgi/getseq.pl?cooperia_oncophora+isotig00466+seq" \t "_blank) for pasting into other applications

Variable modifications: Oxidation (HW),Oxidation (M)

Cleavage by Trypsin/P: cuts C-term side of KR

Sequence Coverage: **65%**

Matched peptides shown in **Bold Red**

**1** MKPDEAK**AIL KPLYDEIQKN IAAGKLEENV KFLHPECVGV HK**GK**AAYYGK**

**51 EQILTSMKKF FEEHQPK**NIK RSNEVYCGCD CCICVSYVAT FDTTK**GSLKV**

**101 DEHQIWKK**ID GQWK**LYHMEY DVQA**



  Residue Number  Increasing Mass  Decreasing Mass

**Start - End Observed Mr(expt) Mr(calc) ppm Miss Sequence**

**8 - 19 1430.8088 1429.8015 1429.8180 -12 1 K.AILKPLYDEIQK.N**  ([No match](http://msmsms/mascot/cgi/peptide_view.pl?file=../data/20120113/F018136.dat&query=26&hit=1" \t "_blank))

**20 - 31 1285.6924 1284.6851 1284.7037 -14 1 K.NIAAGKLEENVK.F**  ([No match](http://msmsms/mascot/cgi/peptide_view.pl?file=../data/20120113/F018136.dat&query=23&hit=1" \t "_blank))

**32 - 42 1265.6339 1264.6266 1264.6387 -10 0 K.FLHPECVGVHK.G**  ([No match](http://msmsms/mascot/cgi/peptide_view.pl?file=../data/20120113/F018136.dat&query=20&hit=1" \t "_blank))

**45 - 58 1602.8064 1601.7991 1601.8123 -8 1 K.AAYYGKEQILTSMK.K**  ([No match](http://msmsms/mascot/cgi/peptide_view.pl?file=../data/20120113/F018136.dat&query=32&hit=1" \t "_blank))

**45 - 59 1730.8920 1729.8847 1729.9072 -13 2 K.AAYYGKEQILTSMKK.F**  ([No match](http://msmsms/mascot/cgi/peptide_view.pl?file=../data/20120113/F018136.dat&query=34&hit=1" \t "_blank))

**45 - 59 1746.8850 1745.8777 1745.9022 -14 2 K.AAYYGKEQILTSMKK.F**  Oxidation (M) ([No match](http://msmsms/mascot/cgi/peptide_view.pl?file=../data/20120113/F018136.dat&query=35&hit=1" \t "_blank))

**59 - 67 1189.5488 1188.5415 1188.5927 -43 1 K.KFFEEHQPK.N**  ([No match](http://msmsms/mascot/cgi/peptide_view.pl?file=../data/20120113/F018136.dat&query=18&hit=1" \t "_blank))

**59 - 67 1205.5109 1204.5036 1204.5877 -70 1 K.KFFEEHQPK.N**  Oxidation (HW) ([No match](http://msmsms/mascot/cgi/peptide_view.pl?file=../data/20120113/F018136.dat&query=19&hit=1" \t "_blank))

**60 - 67 1061.4967 1060.4894 1060.4978 -8 0 K.FFEEHQPK.N**  ([No match](http://msmsms/mascot/cgi/peptide_view.pl?file=../data/20120113/F018136.dat&query=8&hit=1" \t "_blank))

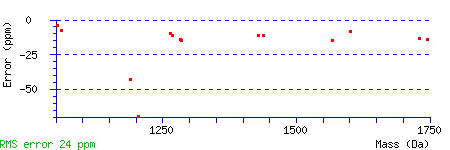
**96 - 107 1439.7477 1438.7404 1438.7569 -11 1 K.GSLKVDEHQIWK.K**  ([No match](http://msmsms/mascot/cgi/peptide_view.pl?file=../data/20120113/F018136.dat&query=27&hit=1" \t "_blank))

**96 - 108 1567.8358 1566.8285 1566.8518 -15 2 K.GSLKVDEHQIWKK.I**  ([No match](http://msmsms/mascot/cgi/peptide_view.pl?file=../data/20120113/F018136.dat&query=31&hit=1" \t "_blank))

**100 - 107 1054.5273 1053.5200 1053.5243 -4 0 K.VDEHQIWK.K**  ([No match](http://msmsms/mascot/cgi/peptide_view.pl?file=../data/20120113/F018136.dat&query=5&hit=1" \t "_blank))

**115 - 124 1268.5476 1267.5403 1267.5543 -11 0 K.LYHMEYDVQA.-**  ([No match](http://msmsms/mascot/cgi/peptide_view.pl?file=../data/20120113/F018136.dat&query=21&hit=1" \t "_blank))

**115 - 124 1284.5387 1283.5314 1283.5492 -14 0 K.LYHMEYDVQA.-**  Oxidation (M) ([No match](http://msmsms/mascot/cgi/peptide_view.pl?file=../data/20120113/F018136.dat&query=22&hit=1" \t "_blank))



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**Band 9:**

**http://msmsms/mascot/images/88x31_logo_white.gifMascot Search Results**

**User :**

**Email :**

**Search title : SampleSetID: 683, AnalysisID: 1071, MaldiWellID: 82753, SpectrumID: 217145, Path=\Jimmy\Cooperia 3\Co ES Conc 3 Frac 13012012 (strict)**

**Database : cooperia\_oncophora oncophora\_20110405 (34373 sequences; 5289600 residues)**

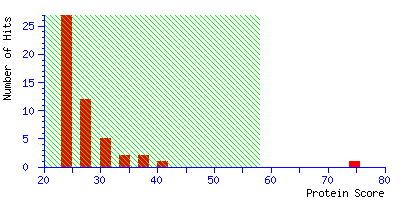
**Timestamp : 13 Jan 2012 at 14:34:06 GMT**

**Warning : A Peptide summary report will usually give a much clearer picture of MS/MS search results.**

**Top Score : 75 for isotig32303, putative nuclear encoded protein Method: Longest ORF**

**Mascot Score Histogram**

Protein score is -10\*Log(P), where P is the probability that the observed match is a random event.  
Protein scores greater than 58 are significant (p<0.05).  
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



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**Protein Summary Report**

|  |  |  |  |
| --- | --- | --- | --- |
|  |  |  | [Help](http://msmsms/mascot/help/msms_summaries_help.html" \t "_blank) |
|  | Significance threshold p< | Max. number of hits |  |

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**Index**

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
|  | **Accession** | **Mass** | **Score** | **Description** |
| **1.** | [**isotig32303**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20120113/F018137.dat#Hit1) | 12330 | 75 | putative nuclear encoded protein Method: Longest ORF |
| **2.** | [**isotig06539**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20120113/F018137.dat#Hit2) | 21639 | 40 | putative nuclear encoded protein Method: ESTScan |
| **3.** | [**isotig24906**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20120113/F018137.dat#Hit3) | 10958 | 38 | putative nuclear encoded protein Method: Longest ORF |
| **4.** | [**isotig26954**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20120113/F018137.dat#Hit4) | 15407 | 37 | putative nuclear encoded protein Method: similarity and extension |
| **5.** | [**isotig15839**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20120113/F018137.dat#Hit5) | 14965 | 35 | putative nuclear encoded protein Method: Longest ORF |
| **6.** | [**contig02082**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20120113/F018137.dat#Hit6) | 46378 | 34 | putative nuclear encoded protein Method: similarity and extension |
| **7.** | [**isotig10616**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20120113/F018137.dat#Hit7) | 24153 | 32 | putative nuclear encoded protein Method: similarity and extension |
| **8.** | [**isotig10615**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20120113/F018137.dat#Hit8) | 24153 | 32 | putative nuclear encoded protein Method: similarity and extension |
| **9.** | [**isotig16917**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20120113/F018137.dat#Hit9) | 25518 | 32 | putative mitochondrial protein Method: similarity and extension |
| **10.** | [**isotig18389**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20120113/F018137.dat#Hit10) | 33997 | 30 | putative nuclear encoded protein Method: similarity and extension |
| **11.** | [**isotig16457**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20120113/F018137.dat#Hit11) | 8553 | 30 | putative nuclear encoded protein Method: Longest ORF |
| **12.** | [**isotig13437**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20120113/F018137.dat#Hit12) | 27414 | 29 | putative nuclear encoded protein Method: similarity and extension |
| **13.** | [**contig09094**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20120113/F018137.dat#Hit13) | 33134 | 29 | putative nuclear encoded protein Method: similarity and extension |
| **14.** | [**isotig27547**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20120113/F018137.dat#Hit14) | 63882 | 29 | putative nuclear encoded protein Method: similarity and extension |
| **15.** | [**isotig18802**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20120113/F018137.dat#Hit15) | 23758 | 29 | putative nuclear encoded protein Method: similarity and extension |
| **16.** | [**isotig25174**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20120113/F018137.dat#Hit16) | 11860 | 28 | putative nuclear encoded protein Method: Longest ORF |
| **17.** | [**isotig18643**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20120113/F018137.dat#Hit17) | 32787 | 27 | putative nuclear encoded protein Method: similarity and extension |
| **18.** | [**contig50358**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20120113/F018137.dat#Hit18) | 46598 | 27 | putative nuclear encoded protein Method: similarity and extension |
| **19.** | [**isotig31699**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20120113/F018137.dat#Hit19) | 15484 | 27 | putative nuclear encoded protein Method: similarity and extension |
| **20.** | [**isotig10305**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20120113/F018137.dat#Hit20) | 10144 | 27 | putative nuclear encoded protein Method: similarity and extension |

**Results List**

|  |  |
| --- | --- |
| **1.** | [isotig32303](http://msmsms/mascot/cgi/protein_view.pl?file=../data/20120113/F018137.dat&hit=1" \t "_blank)    **Mass:** 12330    **Score:** 75     **Expect:** 0.0012  **Matches:** 3 |
|  | putative nuclear encoded protein Method: Longest ORF |

|  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | **Observed** | **Mr(expt)** | **Mr(calc)** | **ppm** | **Start** |  | **End** | **Miss** | **Ions** | **Peptide** |
|  | 995.5327 | 994.5254 | 994.5236 | 1.83 | 33 | - | 40 | 1 | --- | K.VYKGEFPR.N |
|  | 995.5327 | 994.5254 | 994.5236 | 1.83 | 33 | - | 40 | 1 | 63 | K.VYKGEFPR.N |
|  | 1225.6630 | 1224.6557 | 1224.6462 | 7.74 | 81 | - | 92 | 0 | --- | K.IGSDAVAHQISK.E |

|  |  |
| --- | --- |
|  | **No match to:** 913.5322, 931.4977, 1005.5302, 1045.5701, 1065.6130, 1113.5592, 1121.5593, 1169.5728, 1179.6002, 1181.5515, 1203.5643, 1203.5643, 1228.5538, 1235.5729, 1260.5487, 1274.5909, 1277.6383, 1279.5535, 1422.7220, 1475.7474, 1493.7482, 1543.7859, 1590.8463, 1590.8463, 1608.7977, 1624.7966, 1707.7679, 1791.7614, 1974.9226, 2211.0654, 2383.9204, 2414.0562, 2414.0562, 2431.0789, 2432.0635, 2538.1111, 3029.2983 |

**http://msmsms/mascot/images/88x31_logo_white.gifMascot Search Results**

**Protein View**

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Match to: **isotig32303** Score: **75** Expect: **0.0012**

**putative nuclear encoded protein Method: Longest ORF**

Nominal mass (Mr): **12330**; Calculated pI value: **4.69**

NCBI BLAST search of [isotig32303](http://www.ncbi.nlm.nih.gov/blast/Blast.cgi?ALIGNMENTS=50&ALIGNMENT_VIEW=Pairwise&AUTO_FORMAT=Semiauto&CDD_SEARCH=on&CLIENT=web&COMPOSITION_BASED_STATISTICS=on&DATABASE=nr&DESCRIPTIONS=100&ENTREZ_QUERY=(none)&EXPECT=10&FILTER=L&FORMAT_BLOCK_ON_RESPAGE=None&FORMAT_OBJECT=Alignment&FORMAT_TYPE=HTML&GAPCOSTS=11+1&I_THRESH=0.001&LAYOUT=TwoWindows&MATRIX_NAME=BLOSUM62&NCBI_GI=on&PAGE=Proteins&PROGRAM=blastp&QUERY=HRRKMKLVTLAFLLYIAHSVMGDCQLLYSSFKVYKGEFPRNPFTVEYKDDDLVTLLWVQNEDSSLDVVDIQTDDGNVYYKIGSDAVAHQISKEEYDSFYYDTCGLF&SERVICE=plain&SET_DEFAULTS.x=9&SET_DEFAULTS.y=5&SHOW_OVERVIEW=on&WORD_SIZE=3&END_OF_HTTPGET=Yes" \t "_blank) against nr

Unformatted [sequence string](http://msmsms/mascot/cgi/getseq.pl?cooperia_oncophora+isotig32303+seq" \t "_blank) for pasting into other applications

Variable modifications: Oxidation (HW),Oxidation (M)

Cleavage by Trypsin/P: cuts C-term side of KR

Sequence Coverage: **18%**

Matched peptides shown in **Bold Red**

**1** HRRKMKLVTL AFLLYIAHSV MGDCQLLYSS FK**VYKGEFPR** NPFTVEYKDD

**51** DLVTLLWVQN EDSSLDVVDI QTDDGNVYYK **IGSDAVAHQI SK**EEYDSFYY

**101** DTCGLF



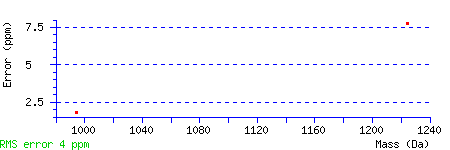
  Residue Number  Increasing Mass  Decreasing Mass

**Start - End Observed Mr(expt) Mr(calc) ppm Miss Sequence**

**33 - 40 995.5327 994.5254 994.5236 2 1 K.VYKGEFPR.N**  ([No match](http://msmsms/mascot/cgi/peptide_view.pl?file=../data/20120113/F018137.dat&query=3&hit=1" \t "_blank))

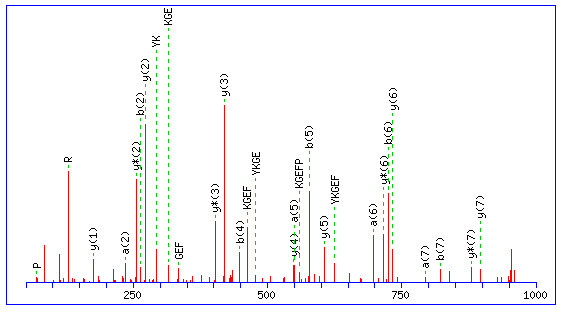
**33 - 40 995.5327 994.5254 994.5236 2 1 K.VYKGEFPR.N**  ([Ions score 63](http://msmsms/mascot/cgi/peptide_view.pl?file=../data/20120113/F018137.dat&query=4&hit=1" \t "_blank))

**81 - 92 1225.6630 1224.6557 1224.6462 8 0 K.IGSDAVAHQISK.E**  ([No match](http://msmsms/mascot/cgi/peptide_view.pl?file=../data/20120113/F018137.dat&query=15&hit=1" \t "_blank))



**Bottom of Form**

🡪 Annotated MS2 spectrum for peptide VYKGEFPR



**Monoisotopic mass of neutral peptide Mr(calc):** 994.5236

**Ions Score:** 63 **Expect:** 3.1e-005

**Matches :** 30/95 fragment ions using 36 most intense peaks   ([help](http://msmsms/mascot/help/results_help.html" \l "PEP" \t "_blank))

|  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **#** | **Immon.** | **a** | **a\*** | **a0** | **b** | **b\*** | **b0** | **Seq.** | **v** | **w** | **y** | **y\*** | **y0** | **#** |
| **1** | 72.0808 | 72.0808 |  |  | 100.0757 |  |  | **V** |  |  |  |  |  | **8** |
| **2** | 136.0757 | **235.1441** |  |  | **263.1390** |  |  | **Y** | 788.4050 |  | ***896.4625*** | 879.4359 | 878.4519 | **7** |
| **3** | 101.1073 | 363.2391 | 346.2125 |  | 391.2340 | 374.2074 |  | **K** | 660.3100 | 659.3148 | ***733.3992*** | 716.3726 | 715.3886 | **6** |
| **4** | 30.0338 | 420.2605 | 403.2340 |  | **448.2554** | 431.2289 |  | **G** |  |  | ***605.3042*** | 588.2776 | 587.2936 | **5** |
| **5** | 102.0550 | **549.3031** | 532.2766 | 531.2926 | **577.2980** | 560.2715 | 559.2875 | **E** | 474.2459 | 473.2507 | ***548.2827*** | 531.2562 | 530.2722 | **4** |
| **6** | 120.0808 | **696.3715** | 679.3450 | 678.3610 | **724.3665** | 707.3399 | 706.3559 | **F** | 327.1775 |  | ***419.2401*** | 402.2136 |  | **3** |
| **7** | 70.0651 | **793.4243** | 776.3978 | 775.4137 | **821.4192** | 804.3927 | 803.4087 | **P** | 230.1248 | 229.1295 | ***272.1717*** | 255.1452 |  | **2** |
| **8** | 129.1135 |  |  |  |  |  |  | **R** | 74.0237 | 73.0284 | ***175.1190*** | 158.0924 |  | **1** |

|  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **Seq** | **ya** | **yb** | **Seq** | **ya** | **yb** | **Seq** | **ya** | **yb** |
| **YK** | 264.1707 | 292.1656 | **YKG** | 321.1921 | 349.1870 | **YKGE** | 450.2347 | 478.2296 |
| **YKGEF** | 597.3031 | 625.2980 | **YKGEFP** | 694.3559 | 722.3508 | **KG** | 158.1288 | 186.1237 |
| **KGE** | 287.1714 | 315.1663 | **KGEF** | 434.2398 | 462.2347 | **KGEFP** | 531.2926 | 559.2875 |
| **GE** | 159.0764 | 187.0713 | **GEF** | 306.1448 | 334.1397 | **GEFP** | 403.1976 | 431.1925 |
| **EF** | 249.1234 | 277.1183 | **EFP** | 346.1761 | 374.1710 | **FP** | 217.1335 | 245.1285 |

**Band 10:**

**http://msmsms/mascot/images/88x31_logo_white.gifMascot Search Results**

**User :**

**Email :**

**Search title : SampleSetID: 683, AnalysisID: 1071, MaldiWellID: 82754, SpectrumID: 217150, Path=\Jimmy\Cooperia 3\Co ES Conc 3 Frac 13012012 (strict)**

**Database : cooperia\_oncophora oncophora\_20110405 (34373 sequences; 5289600 residues)**

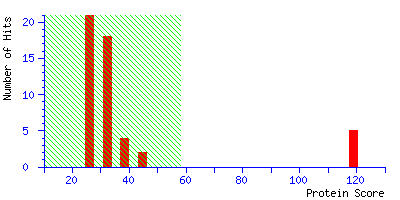
**Timestamp : 13 Jan 2012 at 14:34:18 GMT**

**Warning : A Peptide summary report will usually give a much clearer picture of MS/MS search results.**

**Top Score : 119 for isotig11584, putative nuclear encoded protein Method: similarity and extension**

**Mascot Score Histogram**

Protein score is -10\*Log(P), where P is the probability that the observed match is a random event.  
Protein scores greater than 58 are significant (p<0.05).  
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



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**Protein Summary Report**

|  |  |  |  |
| --- | --- | --- | --- |
|  |  |  | [Help](http://msmsms/mascot/help/msms_summaries_help.html" \t "_blank) |
|  | Significance threshold p< | Max. number of hits |  |

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Bottom of Form

**Index**

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
|  | **Accession** | **Mass** | **Score** | **Description** |
| **1.** | [**isotig11584**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20120113/F018138.dat#Hit1) | 14584 | 119 | putative nuclear encoded protein Method: similarity and extension |
| **2.** | [**isotig25277**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20120113/F018138.dat#Hit2) | 14624 | 119 | putative nuclear encoded protein Method: similarity and extension |
| **3.** | [**isotig26116**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20120113/F018138.dat#Hit3) | 14692 | 119 | putative nuclear encoded protein Method: similarity and extension |
| **4.** | [**isotig11583**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20120113/F018138.dat#Hit4) | 14759 | 119 | putative nuclear encoded protein Method: similarity and extension |
| **5.** | [**isotig11585**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20120113/F018138.dat#Hit5) | 14759 | 119 | putative nuclear encoded protein Method: similarity and extension |
| **6.** | [**isotig21742**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20120113/F018138.dat#Hit6) | 11576 | 46 | putative nuclear encoded protein Method: Longest ORF |
| **7.** | [**isotig19498**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20120113/F018138.dat#Hit7) | 22886 | 43 | putative nuclear encoded protein Method: similarity and extension |
| **8.** | [**isotig17496**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20120113/F018138.dat#Hit8) | 10613 | 36 | putative nuclear encoded protein Method: similarity and extension |
| **9.** | [**isotig13277**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20120113/F018138.dat#Hit9) | 35891 | 36 | putative nuclear encoded protein Method: similarity and extension |
| **10.** | [**isotig13276**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20120113/F018138.dat#Hit10) | 35891 | 36 | putative nuclear encoded protein Method: similarity and extension |
| **11.** | [**isotig17078**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20120113/F018138.dat#Hit11) | 11211 | 36 | putative nuclear encoded protein Method: similarity and extension |
| **12.** | [**isotig14337**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20120113/F018138.dat#Hit12) | 14387 | 35 | putative nuclear encoded protein Method: similarity and extension |
| **13.** | [**isotig31779**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20120113/F018138.dat#Hit13) | 6879 | 33 | putative nuclear encoded protein Method: Longest ORF |
| **14.** | [**isotig21870**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20120113/F018138.dat#Hit14) | 32088 | 33 | putative nuclear encoded protein Method: Longest ORF |
| **15.** | [**isotig19912**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20120113/F018138.dat#Hit15) | 24835 | 32 | putative nuclear encoded protein Method: similarity and extension |
| **16.** | [**isotig31288**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20120113/F018138.dat#Hit16) | 14054 | 32 | putative nuclear encoded protein Method: similarity and extension |
| **17.** | [**isotig06027**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20120113/F018138.dat#Hit17) | 48296 | 32 | putative nuclear encoded protein Method: similarity and extension |
| **18.** | [**isotig06028**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20120113/F018138.dat#Hit18) | 48296 | 32 | putative nuclear encoded protein Method: similarity and extension |
| **19.** | [**isotig06029**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20120113/F018138.dat#Hit19) | 48296 | 32 | putative nuclear encoded protein Method: similarity and extension |
| **20.** | [**isotig32612**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20120113/F018138.dat#Hit20) | 15100 | 31 | putative nuclear encoded protein Method: Longest ORF |

**Results List**

|  |  |
| --- | --- |
| **1.** | [isotig11584](http://msmsms/mascot/cgi/protein_view.pl?file=../data/20120113/F018138.dat&hit=1" \t "_blank)    **Mass:** 14584    **Score:** 119    **Expect:** 4.3e-008  **Matches:** 4 |
|  | putative nuclear encoded protein Method: similarity and extension |

|  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | **Observed** | **Mr(expt)** | **Mr(calc)** | **ppm** | **Start** |  | **End** | **Miss** | **Ions** | **Peptide** |
|  | 914.4983 | 913.4910 | 913.4981 | -7.77 | 93 | - | 100 | 0 | --- | K.EAQVNVVR.N |
|  | 1125.5247 | 1124.5174 | 1124.6012 | -74.48 | 84 | - | 92 | 2 | --- | R.TLMRAYKDK.E |
|  | 1519.8030 | 1518.7957 | 1518.8154 | -12.96 | 88 | - | 100 | 2 | --- | R.AYKDKEAQVNVVR.N |
|  | 1519.8030 | 1518.7957 | 1518.8154 | -12.96 | 88 | - | 100 | 2 | 104 | R.AYKDKEAQVNVVR.N |

|  |  |
| --- | --- |
|  | **No match to:** 915.4942, 931.4911, 947.5018, 948.4457, 982.4308, 995.5223, 1013.4594, 1014.4489, 1023.5059, 1041.4943, 1052.4482, 1057.4343, 1064.5565, 1089.6228, 1094.5530, 1131.5505, 1156.5281, 1162.5831, 1174.5835, 1232.5940, 1235.5186, 1311.5471, 1320.5725, 1328.6375, 1350.6694, 1412.6882, 1463.7767, 1468.6788, 1475.7159, 1493.7111, 1533.8210, 1575.7871, 1575.7871, 1598.8032, 1632.8075, 1791.7026, 1804.8514, 1956.8993, 1974.9122, 1974.9122, 1976.5770, 1996.8802, 2002.9349, 2102.9949, 2217.0115, 2322.0437, 2326.9988, 2383.9102, 2383.9102, 2705.1084 |

|  |  |
| --- | --- |
| **2.** | [isotig25277](http://msmsms/mascot/cgi/protein_view.pl?file=../data/20120113/F018138.dat&hit=2" \t "_blank)    **Mass:** 14624    **Score:** 119    **Expect:** 4.3e-008  **Matches:** 4 |
|  | putative nuclear encoded protein Method: similarity and extension |

|  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | **Observed** | **Mr(expt)** | **Mr(calc)** | **ppm** | **Start** |  | **End** | **Miss** | **Ions** | **Peptide** |
|  | 914.4983 | 913.4910 | 913.4981 | -7.77 | 94 | - | 101 | 0 | --- | K.EAQVNVVR.N |
|  | 1125.5247 | 1124.5174 | 1124.6012 | -74.48 | 85 | - | 93 | 2 | --- | R.TLMRAYKDK.E |
|  | 1519.8030 | 1518.7957 | 1518.8154 | -12.96 | 89 | - | 101 | 2 | --- | R.AYKDKEAQVNVVR.N |
|  | 1519.8030 | 1518.7957 | 1518.8154 | -12.96 | 89 | - | 101 | 2 | 104 | R.AYKDKEAQVNVVR.N |

|  |  |
| --- | --- |
|  | **No match to:** 915.4942, 931.4911, 947.5018, 948.4457, 982.4308, 995.5223, 1013.4594, 1014.4489, 1023.5059, 1041.4943, 1052.4482, 1057.4343, 1064.5565, 1089.6228, 1094.5530, 1131.5505, 1156.5281, 1162.5831, 1174.5835, 1232.5940, 1235.5186, 1311.5471, 1320.5725, 1328.6375, 1350.6694, 1412.6882, 1463.7767, 1468.6788, 1475.7159, 1493.7111, 1533.8210, 1575.7871, 1575.7871, 1598.8032, 1632.8075, 1791.7026, 1804.8514, 1956.8993, 1974.9122, 1974.9122, 1976.5770, 1996.8802, 2002.9349, 2102.9949, 2217.0115, 2322.0437, 2326.9988, 2383.9102, 2383.9102, 2705.1084 |

|  |  |
| --- | --- |
| **3.** | [isotig26116](http://msmsms/mascot/cgi/protein_view.pl?file=../data/20120113/F018138.dat&hit=3" \t "_blank)    **Mass:** 14692    **Score:** 119    **Expect:** 4.3e-008  **Matches:** 4 |
|  | putative nuclear encoded protein Method: similarity and extension |

|  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | **Observed** | **Mr(expt)** | **Mr(calc)** | **ppm** | **Start** |  | **End** | **Miss** | **Ions** | **Peptide** |
|  | 914.4983 | 913.4910 | 913.4981 | -7.77 | 94 | - | 101 | 0 | --- | K.EAQVNVVR.N |
|  | 1125.5247 | 1124.5174 | 1124.6012 | -74.48 | 85 | - | 93 | 2 | --- | R.TLMRAYKDK.E |
|  | 1519.8030 | 1518.7957 | 1518.8154 | -12.96 | 89 | - | 101 | 2 | --- | R.AYKDKEAQVNVVR.N |
|  | 1519.8030 | 1518.7957 | 1518.8154 | -12.96 | 89 | - | 101 | 2 | 104 | R.AYKDKEAQVNVVR.N |

|  |  |
| --- | --- |
|  | **No match to:** 915.4942, 931.4911, 947.5018, 948.4457, 982.4308, 995.5223, 1013.4594, 1014.4489, 1023.5059, 1041.4943, 1052.4482, 1057.4343, 1064.5565, 1089.6228, 1094.5530, 1131.5505, 1156.5281, 1162.5831, 1174.5835, 1232.5940, 1235.5186, 1311.5471, 1320.5725, 1328.6375, 1350.6694, 1412.6882, 1463.7767, 1468.6788, 1475.7159, 1493.7111, 1533.8210, 1575.7871, 1575.7871, 1598.8032, 1632.8075, 1791.7026, 1804.8514, 1956.8993, 1974.9122, 1974.9122, 1976.5770, 1996.8802, 2002.9349, 2102.9949, 2217.0115, 2322.0437, 2326.9988, 2383.9102, 2383.9102, 2705.1084 |

|  |  |
| --- | --- |
| **4.** | [isotig11583](http://msmsms/mascot/cgi/protein_view.pl?file=../data/20120113/F018138.dat&hit=4" \t "_blank)    **Mass:** 14759    **Score:** 119    **Expect:** 4.3e-008  **Matches:** 4 |
|  | putative nuclear encoded protein Method: similarity and extension |

|  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | **Observed** | **Mr(expt)** | **Mr(calc)** | **ppm** | **Start** |  | **End** | **Miss** | **Ions** | **Peptide** |
|  | 914.4983 | 913.4910 | 913.4981 | -7.77 | 95 | - | 102 | 0 | --- | K.EAQVNVVR.N |
|  | 1125.5247 | 1124.5174 | 1124.6012 | -74.48 | 86 | - | 94 | 2 | --- | R.TLMRAYKDK.E |
|  | 1519.8030 | 1518.7957 | 1518.8154 | -12.96 | 90 | - | 102 | 2 | --- | R.AYKDKEAQVNVVR.N |
|  | 1519.8030 | 1518.7957 | 1518.8154 | -12.96 | 90 | - | 102 | 2 | 104 | R.AYKDKEAQVNVVR.N |

|  |  |
| --- | --- |
|  | **No match to:** 915.4942, 931.4911, 947.5018, 948.4457, 982.4308, 995.5223, 1013.4594, 1014.4489, 1023.5059, 1041.4943, 1052.4482, 1057.4343, 1064.5565, 1089.6228, 1094.5530, 1131.5505, 1156.5281, 1162.5831, 1174.5835, 1232.5940, 1235.5186, 1311.5471, 1320.5725, 1328.6375, 1350.6694, 1412.6882, 1463.7767, 1468.6788, 1475.7159, 1493.7111, 1533.8210, 1575.7871, 1575.7871, 1598.8032, 1632.8075, 1791.7026, 1804.8514, 1956.8993, 1974.9122, 1974.9122, 1976.5770, 1996.8802, 2002.9349, 2102.9949, 2217.0115, 2322.0437, 2326.9988, 2383.9102, 2383.9102, 2705.1084 |

|  |  |
| --- | --- |
| **5.** | [isotig11585](http://msmsms/mascot/cgi/protein_view.pl?file=../data/20120113/F018138.dat&hit=5" \t "_blank)    **Mass:** 14759    **Score:** 119    **Expect:** 4.3e-008  **Matches:** 4 |
|  | putative nuclear encoded protein Method: similarity and extension |

|  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | **Observed** | **Mr(expt)** | **Mr(calc)** | **ppm** | **Start** |  | **End** | **Miss** | **Ions** | **Peptide** |
|  | 914.4983 | 913.4910 | 913.4981 | -7.77 | 95 | - | 102 | 0 | --- | K.EAQVNVVR.N |
|  | 1125.5247 | 1124.5174 | 1124.6012 | -74.48 | 86 | - | 94 | 2 | --- | R.TLMRAYKDK.E |
|  | 1519.8030 | 1518.7957 | 1518.8154 | -12.96 | 90 | - | 102 | 2 | --- | R.AYKDKEAQVNVVR.N |
|  | 1519.8030 | 1518.7957 | 1518.8154 | -12.96 | 90 | - | 102 | 2 | 104 | R.AYKDKEAQVNVVR.N |

|  |  |
| --- | --- |
|  | **No match to:** 915.4942, 931.4911, 947.5018, 948.4457, 982.4308, 995.5223, 1013.4594, 1014.4489, 1023.5059, 1041.4943, 1052.4482, 1057.4343, 1064.5565, 1089.6228, 1094.5530, 1131.5505, 1156.5281, 1162.5831, 1174.5835, 1232.5940, 1235.5186, 1311.5471, 1320.5725, 1328.6375, 1350.6694, 1412.6882, 1463.7767, 1468.6788, 1475.7159, 1493.7111, 1533.8210, 1575.7871, 1575.7871, 1598.8032, 1632.8075, 1791.7026, 1804.8514, 1956.8993, 1974.9122, 1974.9122, 1976.5770, 1996.8802, 2002.9349, 2102.9949, 2217.0115, 2322.0437, 2326.9988, 2383.9102, 2383.9102, 2705.1084 |

**http://msmsms/mascot/images/88x31_logo_white.gifMascot Search Results**

**Protein View**

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Match to: **isotig11584** Score: **119** Expect: **4.3e-008**

**putative nuclear encoded protein Method: similarity and extension**

Nominal mass (Mr): **14584**; Calculated pI value: **6.47**

NCBI BLAST search of [isotig11584](http://www.ncbi.nlm.nih.gov/blast/Blast.cgi?ALIGNMENTS=50&ALIGNMENT_VIEW=Pairwise&AUTO_FORMAT=Semiauto&CDD_SEARCH=on&CLIENT=web&COMPOSITION_BASED_STATISTICS=on&DATABASE=nr&DESCRIPTIONS=100&ENTREZ_QUERY=(none)&EXPECT=10&FILTER=L&FORMAT_BLOCK_ON_RESPAGE=None&FORMAT_OBJECT=Alignment&FORMAT_TYPE=HTML&GAPCOSTS=11+1&I_THRESH=0.001&LAYOUT=TwoWindows&MATRIX_NAME=BLOSUM62&NCBI_GI=on&PAGE=Proteins&PROGRAM=blastp&QUERY=LALTILCIFVMNAYANDCVPDFHQKHLYAKFHNGINNNLVWDEDLSERACEEAYGELGSHGFDKLEVEREVPKSLVRSSRIQRTLMRAYKDKEAQVNVVRNLPAGTKYGCNAVEIGDKTKVVCLYEKQ&SERVICE=plain&SET_DEFAULTS.x=9&SET_DEFAULTS.y=5&SHOW_OVERVIEW=on&WORD_SIZE=3&END_OF_HTTPGET=Yes" \t "_blank) against nr

Unformatted [sequence string](http://msmsms/mascot/cgi/getseq.pl?cooperia_oncophora+isotig11584+seq" \t "_blank) for pasting into other applications

Variable modifications: Oxidation (HW),Oxidation (M)

Cleavage by Trypsin/P: cuts C-term side of KR

Sequence Coverage: **13%**

Matched peptides shown in **Bold Red**

**1** LALTILCIFV MNAYANDCVP DFHQKHLYAK FHNGINNNLV WDEDLSERAC

**51** EEAYGELGSH GFDKLEVERE VPKSLVRSSR IQR**TLMRAYK DKEAQVNVVR**

**101** NLPAGTKYGC NAVEIGDKTK VVCLYEKQ



  Residue Number  Increasing Mass  Decreasing Mass

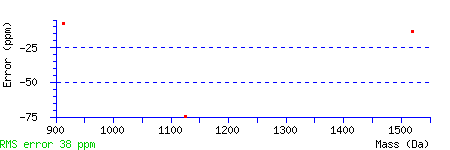
**Start - End Observed Mr(expt) Mr(calc) ppm Miss Sequence**

**84 - 92 1125.5247 1124.5174 1124.6012 -74 2 R.TLMRAYKDK.E**  ([No match](http://msmsms/mascot/cgi/peptide_view.pl?file=../data/20120113/F018138.dat&query=17&hit=1" \t "_blank))

**88 - 100 1519.8030 1518.7957 1518.8154 -13 2 R.AYKDKEAQVNVVR.N**  ([No match](http://msmsms/mascot/cgi/peptide_view.pl?file=../data/20120113/F018138.dat&query=33&hit=1" \t "_blank))

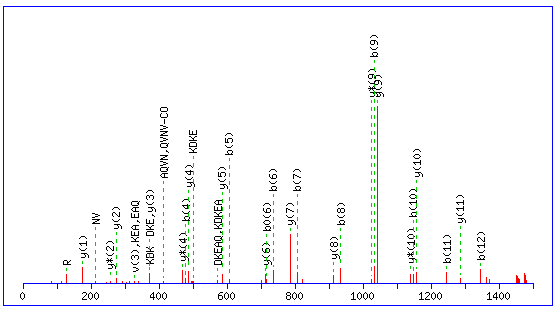
**88 - 100 1519.8030 1518.7957 1518.8154 -13 2 R.AYKDKEAQVNVVR.N**  ([Ions score 104](http://msmsms/mascot/cgi/peptide_view.pl?file=../data/20120113/F018138.dat&query=34&hit=1" \t "_blank))

**93 - 100 914.4983 913.4910 913.4981 -8 0 K.EAQVNVVR.N**  ([No match](http://msmsms/mascot/cgi/peptide_view.pl?file=../data/20120113/F018138.dat&query=1&hit=1" \t "_blank))



Bottom of Form

🡪 Annotated MS2 spectrum for peptide AYKDKEAQVNVVR



**Monoisotopic mass of neutral peptide Mr(calc):** 1518.8154

**Ions Score:** 104 **Expect:** 3e-009

**Matches :** 38/203 fragment ions using 38 most intense peaks   ([help](http://msmsms/mascot/help/results_help.html" \l "PEP" \t "_blank))

|  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **#** | **Immon.** | **a** | **a\*** | **a0** | **b** | **b\*** | **b0** | **Seq.** | **v** | **w** | **y** | **y\*** | **y0** | **#** |
| **1** | 44.0495 | 44.0495 |  |  | 72.0444 |  |  | **A** |  |  |  |  |  | **13** |
| **2** | 136.0757 | 207.1128 |  |  | 235.1077 |  |  | **Y** | 1340.7281 |  | 1448.7856 | 1431.7591 | 1430.7750 | **12** |
| **3** | 101.1073 | 335.2078 | 318.1812 |  | 363.2027 | 346.1761 |  | **K** | 1212.6331 | 1211.6379 | ***1285.7223*** | 1268.6957 | 1267.7117 | **11** |
| **4** | 88.0393 | 450.2347 | 433.2082 | 432.2241 | **478.2296** | 461.2031 | 460.2191 | **D** | 1097.6062 | 1096.6109 | ***1157.6273*** | 1140.6008 | 1139.6167 | **10** |
| **5** | 101.1073 | 578.3297 | 561.3031 | 560.3191 | **606.3246** | 589.2980 | 588.3140 | **K** | 969.5112 | 968.5160 | ***1042.6004*** | 1025.5738 | 1024.5898 | **9** |
| **6** | 102.0550 | 707.3723 | 690.3457 | 689.3617 | **735.3672** | 718.3406 | 717.3566 | **E** | 840.4686 | 839.4734 | ***914.5054*** | 897.4789 | 896.4948 | **8** |
| **7** | 44.0495 | 778.4094 | 761.3828 | 760.3988 | **806.4043** | 789.3777 | 788.3937 | **A** | 769.4315 |  | ***785.4628*** | 768.4363 |  | **7** |
| **8** | 101.0709 | 906.4680 | 889.4414 | 888.4574 | **934.4629** | 917.4363 | 916.4523 | **Q** | 641.3729 | 640.3777 | ***714.4257*** | 697.3992 |  | **6** |
| **9** | 72.0808 | 1005.5364 | 988.5098 | 987.5258 | **1033.5313** | 1016.5047 | 1015.5207 | **V** | 542.3045 | 555.3249 | ***586.3671*** | 569.3406 |  | **5** |
| **10** | 87.0553 | 1119.5793 | 1102.5528 | 1101.5687 | **1147.5742** | 1130.5477 | 1129.5636 | **N** | 428.2616 | 427.2663 | ***487.2987*** | 470.2722 |  | **4** |
| **11** | 72.0808 | 1218.6477 | 1201.6212 | 1200.6371 | **1246.6426** | 1229.6161 | 1228.6321 | **V** | 329.1932 | 342.2136 | ***373.2558*** | 356.2292 |  | **3** |
| **12** | 72.0808 | 1317.7161 | 1300.6896 | 1299.7056 | **1345.7110** | 1328.6845 | 1327.7005 | **V** | 230.1248 | 243.1452 | ***274.1874*** | 257.1608 |  | **2** |
| **13** | 129.1135 |  |  |  |  |  |  | **R** | 74.0237 | 73.0284 | ***175.1190*** | 158.0924 |  | **1** |

|  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **Seq** | **ya** | **yb** | **Seq** | **ya** | **yb** | **Seq** | **ya** | **yb** |
| **YK** | 264.1707 | 292.1656 | **YKD** | 379.1976 | 407.1925 | **YKDK** | 507.2926 | 535.2875 |
| **YKDKE** | 636.3352 | 664.3301 | **KD** | 216.1343 | 244.1292 | **KDK** | 344.2292 | 372.2241 |
| **KDKE** | 473.2718 | 501.2667 | **KDKEA** | 544.3089 | 572.3039 | **KDKEAQ** | 672.3675 | 700.3624 |
| **DK** | 216.1343 | 244.1292 | **DKE** | 345.1769 | 373.1718 | **DKEA** | 416.2140 | 444.2089 |
| **DKEAQ** | 544.2726 | 572.2675 | **DKEAQV** | 643.3410 | 671.3359 | **KE** | 230.1499 | 258.1448 |
| **KEA** | 301.1870 | 329.1819 | **KEAQ** | 429.2456 | 457.2405 | **KEAQV** | 528.3140 | 556.3089 |
| **KEAQVN** | 642.3570 | 670.3519 | **EA** | 173.0921 | 201.0870 | **EAQ** | 301.1506 | 329.1456 |
| **EAQV** | 400.2191 | 428.2140 | **EAQVN** | 514.2620 | 542.2569 | **EAQVNV** | 613.3304 | 641.3253 |
| **AQ** | 172.1081 | 200.1030 | **AQV** | 271.1765 | 299.1714 | **AQVN** | 385.2194 | 413.2143 |
| **AQVNV** | 484.2878 | 512.2827 | **AQVNVV** | 583.3562 | 611.3511 | **QV** | 200.1394 | 228.1343 |
| **QVN** | 314.1823 | 342.1772 | **QVNV** | 413.2507 | 441.2456 | **QVNVV** | 512.3191 | 540.3140 |
| **VN** | 186.1237 | 214.1186 | **VNV** | 285.1921 | 313.1870 | **VNVV** | 384.2605 | 412.2554 |
| **NV** | 186.1237 | 214.1186 | **NVV** | 285.1921 | 313.1870 | **VV** | 171.1492 | 199.1441 |

**Band 11:**

**http://msmsms/mascot/images/88x31_logo_white.gifMascot Search Results**

**User :**

**Email :**

**Search title : SampleSetID: 683, AnalysisID: 1071, MaldiWellID: 82755, SpectrumID: 217155, Path=\Jimmy\Cooperia 3\Co ES Conc 3 Frac 13012012 (strict)**

**Database : cooperia\_oncophora oncophora\_20110405 (34373 sequences; 5289600 residues)**

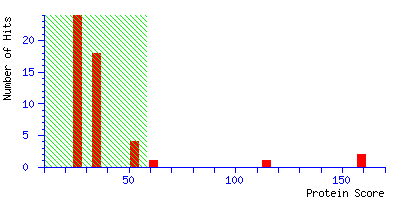
**Timestamp : 13 Jan 2012 at 14:34:33 GMT**

**Warning : A Peptide summary report will usually give a much clearer picture of MS/MS search results.**

**Top Score : 159 for isotig21044, putative nuclear encoded protein Method: similarity and extension**

**Mascot Score Histogram**

Protein score is -10\*Log(P), where P is the probability that the observed match is a random event.  
Protein scores greater than 58 are significant (p<0.05).  
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



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**Protein Summary Report**

|  |  |  |  |
| --- | --- | --- | --- |
|  |  |  | [Help](http://msmsms/mascot/help/msms_summaries_help.html" \t "_blank) |
|  | Significance threshold p< | Max. number of hits |  |

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**Index**

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
|  | **Accession** | **Mass** | **Score** | **Description** |
| **1.** | [**isotig21044**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20120113/F018139.dat#Hit1) | 15109 | 159 | putative nuclear encoded protein Method: similarity and extension |
| **2.** | [**isotig29536**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20120113/F018139.dat#Hit2) | 15107 | 158 | putative nuclear encoded protein Method: similarity and extension |
| **3.** | [**contig45229**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20120113/F018139.dat#Hit3) | 14139 | 112 | putative nuclear encoded protein Method: similarity and extension |
| **4.** | [**isotig09197**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20120113/F018139.dat#Hit4) | 14129 | 62 | putative nuclear encoded protein Method: similarity and extension |
| **5.** | [**isotig19733**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20120113/F018139.dat#Hit5) | 14161 | 54 | putative nuclear encoded protein Method: similarity and extension |
| **6.** | [**isotig21928**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20120113/F018139.dat#Hit6) | 14159 | 54 | putative nuclear encoded protein Method: similarity and extension |
| **7.** | [**isotig09196**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20120113/F018139.dat#Hit7) | 13826 | 54 | putative nuclear encoded protein Method: similarity and extension |
| **8.** | [**isotig14336**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20120113/F018139.dat#Hit8) | 14407 | 54 | putative nuclear encoded protein Method: similarity and extension |
| **9.** | [**isotig17384**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20120113/F018139.dat#Hit9) | 7444 | 38 | putative nuclear encoded protein Method: Longest ORF |
| **10.** | [**isotig21970**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20120113/F018139.dat#Hit10) | 20044 | 37 | putative nuclear encoded protein Method: Longest ORF |
| **11.** | [**isotig03510**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20120113/F018139.dat#Hit11) | 36619 | 35 | putative nuclear encoded protein Method: similarity and extension |
| **12.** | [**isotig03509**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20120113/F018139.dat#Hit12) | 36619 | 35 | putative nuclear encoded protein Method: similarity and extension |
| **13.** | [**isotig03511**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20120113/F018139.dat#Hit13) | 36619 | 35 | putative nuclear encoded protein Method: similarity and extension |
| **14.** | [**isotig02262**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20120113/F018139.dat#Hit14) | 15469 | 34 | putative nuclear encoded protein Method: similarity and extension |
| **15.** | [**contig64654**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20120113/F018139.dat#Hit15) | 12053 | 33 | putative nuclear encoded protein Method: Longest ORF |
| **16.** | [**isotig10745**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20120113/F018139.dat#Hit16) | 17708 | 33 | putative nuclear encoded protein Method: Longest ORF |
| **17.** | [**isotig13322**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20120113/F018139.dat#Hit17) | 27234 | 32 | putative nuclear encoded protein Method: similarity and extension |
| **18.** | [**isotig13323**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20120113/F018139.dat#Hit18) | 27234 | 32 | putative nuclear encoded protein Method: similarity and extension |
| **19.** | [**isotig19833**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20120113/F018139.dat#Hit19) | 30936 | 32 | putative nuclear encoded protein Method: similarity and extension |
| **20.** | [**isotig07200**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20120113/F018139.dat#Hit20) | 8434 | 32 | putative nuclear encoded protein Method: similarity and extension |

**Results List**

|  |  |
| --- | --- |
| **1.** | [isotig21044](http://msmsms/mascot/cgi/protein_view.pl?file=../data/20120113/F018139.dat&hit=1" \t "_blank)    **Mass:** 15109    **Score:** 159    **Expect:** 4.3e-012  **Matches:** 9 |
|  | putative nuclear encoded protein Method: similarity and extension |

|  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | **Observed** | **Mr(expt)** | **Mr(calc)** | **ppm** | **Start** |  | **End** | **Miss** | **Ions** | **Peptide** |
|  | 940.5433 | 939.5360 | 939.5542 | -19.31 | 89 | - | 95 | 1 | --- | R.RTIFYLK.D |
|  | 1345.6954 | 1344.6881 | 1344.7190 | -22.97 | 35 | - | 45 | 0 | --- | R.NLQFNPSLVWK.N |
|  | 1501.7532 | 1500.7459 | 1500.8201 | -49.43 | 34 | - | 45 | 1 | --- | R.RNLQFNPSLVWK.N |
|  | 1667.7834 | 1666.7761 | 1666.8315 | -33.20 | 58 | - | 72 | 1 | --- | K.GANIFTGDFKLEAER.R |
|  | 1667.7834 | 1666.7761 | 1666.8315 | -33.20 | 58 | - | 72 | 1 | 57 | K.GANIFTGDFKLEAER.R |
|  | 1823.9012 | 1822.8939 | 1822.9326 | -21.20 | 58 | - | 73 | 2 | --- | K.GANIFTGDFKLEAERR.F |
|  | 1823.9012 | 1822.8939 | 1822.9326 | -21.20 | 58 | - | 73 | 2 | 72 | K.GANIFTGDFKLEAERR.F |
|  | 1932.9163 | 1931.9090 | 1931.9563 | -24.49 | 90 | - | 105 | 1 | --- | R.TIFYLKDNAYNVANMR.S |
|  | 1948.9067 | 1947.8994 | 1947.9512 | -26.60 | 90 | - | 105 | 1 | --- | R.TIFYLKDNAYNVANMR.S + Oxidation (M) |

|  |  |
| --- | --- |
|  | **No match to:** 941.4846, 947.5524, 982.4292, 999.4522, 1005.4380, 1013.4515, 1014.4409, 1022.4707, 1064.4894, 1081.4723, 1081.4723, 1088.6039, 1097.5671, 1122.5115, 1127.5645, 1131.5376, 1136.5867, 1140.5129, 1150.5669, 1156.5237, 1162.5654, 1162.5654, 1197.5367, 1232.6401, 1280.5977, 1296.5890, 1296.5890, 1360.7290, 1453.6608, 1499.6467, 1548.7196, 1550.7024, 1550.7024, 1565.8199, 1608.7123, 1630.7996, 1632.8007, 1632.8007, 1649.7594, 1666.7286, 1764.8990, 1805.9031, 1904.8408, 1921.8184, 1921.8184, 2003.8491, 2003.8491, 2011.9176, 2107.8901, 2176.0808, 2176.0808, 2574.1155, 2727.2361 |

|  |  |
| --- | --- |
| **2.** | [isotig29536](http://msmsms/mascot/cgi/protein_view.pl?file=../data/20120113/F018139.dat&hit=2" \t "_blank)    **Mass:** 15107    **Score:** 158    **Expect:** 5.4e-012  **Matches:** 9 |
|  | putative nuclear encoded protein Method: similarity and extension |

|  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | **Observed** | **Mr(expt)** | **Mr(calc)** | **ppm** | **Start** |  | **End** | **Miss** | **Ions** | **Peptide** |
|  | 940.5433 | 939.5360 | 939.5542 | -19.31 | 89 | - | 95 | 1 | --- | R.RTIFYLK.D |
|  | 1345.6954 | 1344.6881 | 1344.7190 | -22.97 | 35 | - | 45 | 0 | --- | R.NLQFNPSLVWK.N |
|  | 1501.7532 | 1500.7459 | 1500.8201 | -49.43 | 34 | - | 45 | 1 | --- | R.RNLQFNPSLVWK.N |
|  | 1667.7834 | 1666.7761 | 1666.8315 | -33.20 | 58 | - | 72 | 1 | --- | K.GANIFTGDFKLEAER.R |
|  | 1667.7834 | 1666.7761 | 1666.8315 | -33.20 | 58 | - | 72 | 1 | 57 | K.GANIFTGDFKLEAER.R |
|  | 1823.9012 | 1822.8939 | 1822.9326 | -21.20 | 58 | - | 73 | 2 | --- | K.GANIFTGDFKLEAERR.F |
|  | 1823.9012 | 1822.8939 | 1822.9326 | -21.20 | 58 | - | 73 | 2 | 72 | K.GANIFTGDFKLEAERR.F |
|  | 1932.9163 | 1931.9090 | 1931.9563 | -24.49 | 90 | - | 105 | 1 | --- | R.TIFYLKDNAYNVANMR.S |
|  | 1948.9067 | 1947.8994 | 1947.9512 | -26.60 | 90 | - | 105 | 1 | --- | R.TIFYLKDNAYNVANMR.S + Oxidation (M) |

|  |  |
| --- | --- |
|  | **No match to:** 941.4846, 947.5524, 982.4292, 999.4522, 1005.4380, 1013.4515, 1014.4409, 1022.4707, 1064.4894, 1081.4723, 1081.4723, 1088.6039, 1097.5671, 1122.5115, 1127.5645, 1131.5376, 1136.5867, 1140.5129, 1150.5669, 1156.5237, 1162.5654, 1162.5654, 1197.5367, 1232.6401, 1280.5977, 1296.5890, 1296.5890, 1360.7290, 1453.6608, 1499.6467, 1548.7196, 1550.7024, 1550.7024, 1565.8199, 1608.7123, 1630.7996, 1632.8007, 1632.8007, 1649.7594, 1666.7286, 1764.8990, 1805.9031, 1904.8408, 1921.8184, 1921.8184, 2003.8491, 2003.8491, 2011.9176, 2107.8901, 2176.0808, 2176.0808, 2574.1155, 2727.2361 |

|  |  |
| --- | --- |
| **3.** | [contig45229](http://msmsms/mascot/cgi/protein_view.pl?file=../data/20120113/F018139.dat&hit=3" \t "_blank)    **Mass:** 14139    **Score:** 112    **Expect:** 2.2e-007  **Matches:** 4 |
|  | putative nuclear encoded protein Method: similarity and extension |

|  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | **Observed** | **Mr(expt)** | **Mr(calc)** | **ppm** | **Start** |  | **End** | **Miss** | **Ions** | **Peptide** |
|  | 1162.5654 | 1161.5581 | 1161.5778 | -16.98 | 74 | - | 84 | 0 | --- | R.TFPSGSSQPVR.S |
|  | 1162.5654 | 1161.5581 | 1161.5778 | -16.98 | 74 | - | 84 | 0 | 53 | R.TFPSGSSQPVR.S |
|  | 1632.8007 | 1631.7934 | 1631.8267 | -20.41 | 59 | - | 73 | 1 | --- | K.NPGTTTIPNKFTGER.T |
|  | 1632.8007 | 1631.7934 | 1631.8267 | -20.41 | 59 | - | 73 | 1 | 54 | K.NPGTTTIPNKFTGER.T |

|  |  |
| --- | --- |
|  | **No match to:** 940.5433, 941.4846, 947.5524, 982.4292, 999.4522, 1005.4380, 1013.4515, 1014.4409, 1022.4707, 1064.4894, 1081.4723, 1081.4723, 1088.6039, 1097.5671, 1122.5115, 1127.5645, 1131.5376, 1136.5867, 1140.5129, 1150.5669, 1156.5237, 1197.5367, 1232.6401, 1280.5977, 1296.5890, 1296.5890, 1345.6954, 1360.7290, 1453.6608, 1499.6467, 1501.7532, 1548.7196, 1550.7024, 1550.7024, 1565.8199, 1608.7123, 1630.7996, 1649.7594, 1666.7286, 1667.7834, 1667.7834, 1764.8990, 1805.9031, 1823.9012, 1823.9012, 1904.8408, 1921.8184, 1921.8184, 1932.9163, 1948.9067, 2003.8491, 2003.8491, 2011.9176, 2107.8901, 2176.0808, 2176.0808, 2574.1155, 2727.2361 |

|  |  |
| --- | --- |
| **4.** | [isotig09197](http://msmsms/mascot/cgi/protein_view.pl?file=../data/20120113/F018139.dat&hit=4" \t "_blank)    **Mass:** 14129    **Score:** 62     **Expect:** 0.024  **Matches:** 3 |
|  | putative nuclear encoded protein Method: similarity and extension |

|  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | **Observed** | **Mr(expt)** | **Mr(calc)** | **ppm** | **Start** |  | **End** | **Miss** | **Ions** | **Peptide** |
|  | 941.4846 | 940.4773 | 940.5454 | -72.39 | 81 | - | 88 | 1 | --- | R.QPVQSKVR.S |
|  | 1632.8007 | 1631.7934 | 1631.8267 | -20.41 | 59 | - | 73 | 1 | --- | K.NPGTTTIPNKFTGER.T |
|  | 1632.8007 | 1631.7934 | 1631.8267 | -20.41 | 59 | - | 73 | 1 | 54 | K.NPGTTTIPNKFTGER.T |

|  |  |
| --- | --- |
|  | **No match to:** 940.5433, 947.5524, 982.4292, 999.4522, 1005.4380, 1013.4515, 1014.4409, 1022.4707, 1064.4894, 1081.4723, 1081.4723, 1088.6039, 1097.5671, 1122.5115, 1127.5645, 1131.5376, 1136.5867, 1140.5129, 1150.5669, 1156.5237, 1162.5654, 1162.5654, 1197.5367, 1232.6401, 1280.5977, 1296.5890, 1296.5890, 1345.6954, 1360.7290, 1453.6608, 1499.6467, 1501.7532, 1548.7196, 1550.7024, 1550.7024, 1565.8199, 1608.7123, 1630.7996, 1649.7594, 1666.7286, 1667.7834, 1667.7834, 1764.8990, 1805.9031, 1823.9012, 1823.9012, 1904.8408, 1921.8184, 1921.8184, 1932.9163, 1948.9067, 2003.8491, 2003.8491, 2011.9176, 2107.8901, 2176.0808, 2176.0808, 2574.1155, 2727.2361 |

**http://msmsms/mascot/images/88x31_logo_white.gifMascot Search Results**

**Protein View**

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Match to: **isotig21044** Score: **159** Expect: **4.3e-012**

**putative nuclear encoded protein Method: similarity and extension**

Nominal mass (Mr): **15109**; Calculated pI value: **7.62**

NCBI BLAST search of [isotig21044](http://www.ncbi.nlm.nih.gov/blast/Blast.cgi?ALIGNMENTS=50&ALIGNMENT_VIEW=Pairwise&AUTO_FORMAT=Semiauto&CDD_SEARCH=on&CLIENT=web&COMPOSITION_BASED_STATISTICS=on&DATABASE=nr&DESCRIPTIONS=100&ENTREZ_QUERY=(none)&EXPECT=10&FILTER=L&FORMAT_BLOCK_ON_RESPAGE=None&FORMAT_OBJECT=Alignment&FORMAT_TYPE=HTML&GAPCOSTS=11+1&I_THRESH=0.001&LAYOUT=TwoWindows&MATRIX_NAME=BLOSUM62&NCBI_GI=on&PAGE=Proteins&PROGRAM=blastp&QUERY=MLFTLTVLCLFLVNANADSGCVDYHGLSEHYIRRNLQFNPSLVWKNDLASEACDVAKGANIFTGDFKLEAERRFKAGQAPSTVKEKARRTIFYLKDNAYNVANMRSVRPEFGCNSFFQGDVMKVVCLYRESDE&SERVICE=plain&SET_DEFAULTS.x=9&SET_DEFAULTS.y=5&SHOW_OVERVIEW=on&WORD_SIZE=3&END_OF_HTTPGET=Yes" \t "_blank) against nr

Unformatted [sequence string](http://msmsms/mascot/cgi/getseq.pl?cooperia_oncophora+isotig21044+seq" \t "_blank) for pasting into other applications

Variable modifications: Oxidation (HW),Oxidation (M)

Cleavage by Trypsin/P: cuts C-term side of KR

Sequence Coverage: **33%**

Matched peptides shown in **Bold Red**

**1** MLFTLTVLCL FLVNANADSG CVDYHGLSEH YIR**RNLQFNP SLVWK**NDLAS

**51** EACDVAK**GAN IFTGDFKLEA ERR**FKAGQAP STVKEKAR**RT IFYLKDNAYN**

**101 VANMR**SVRPE FGCNSFFQGD VMKVVCLYRE SDE



  Residue Number  Increasing Mass  Decreasing Mass

**Start - End Observed Mr(expt) Mr(calc) ppm Miss Sequence**

**34 - 45 1501.7532 1500.7459 1500.8201 -49 1 R.RNLQFNPSLVWK.N**  ([No match](http://msmsms/mascot/cgi/peptide_view.pl?file=../data/20120113/F018139.dat&query=33&hit=1" \t "_blank))

**35 - 45 1345.6954 1344.6881 1344.7190 -23 0 R.NLQFNPSLVWK.N**  ([No match](http://msmsms/mascot/cgi/peptide_view.pl?file=../data/20120113/F018139.dat&query=29&hit=1" \t "_blank))

**58 - 72 1667.7834 1666.7761 1666.8315 -33 1 K.GANIFTGDFKLEAER.R**  ([No match](http://msmsms/mascot/cgi/peptide_view.pl?file=../data/20120113/F018139.dat&query=44&hit=1" \t "_blank))

**58 - 72 1667.7834 1666.7761 1666.8315 -33 1 K.GANIFTGDFKLEAER.R**  ([Ions score 57](http://msmsms/mascot/cgi/peptide_view.pl?file=../data/20120113/F018139.dat&query=45&hit=1" \t "_blank))

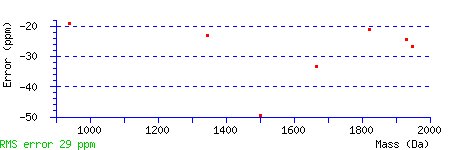
**58 - 73 1823.9012 1822.8939 1822.9326 -21 2 K.GANIFTGDFKLEAERR.F**  ([No match](http://msmsms/mascot/cgi/peptide_view.pl?file=../data/20120113/F018139.dat&query=48&hit=1" \t "_blank))

**58 - 73 1823.9012 1822.8939 1822.9326 -21 2 K.GANIFTGDFKLEAERR.F**  ([Ions score 72](http://msmsms/mascot/cgi/peptide_view.pl?file=../data/20120113/F018139.dat&query=49&hit=1" \t "_blank))

**89 - 95 940.5433 939.5360 939.5542 -19 1 R.RTIFYLK.D**  ([No match](http://msmsms/mascot/cgi/peptide_view.pl?file=../data/20120113/F018139.dat&query=1&hit=1" \t "_blank))

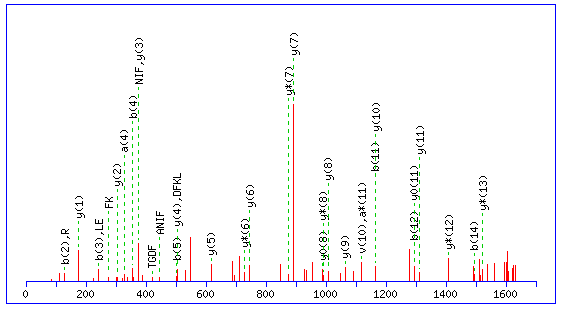
**90 - 105 1932.9163 1931.9090 1931.9563 -24 1 R.TIFYLKDNAYNVANMR.S**  ([No match](http://msmsms/mascot/cgi/peptide_view.pl?file=../data/20120113/F018139.dat&query=53&hit=1" \t "_blank))

**90 - 105 1948.9067 1947.8994 1947.9512 -27 1 R.TIFYLKDNAYNVANMR.S**  Oxidation (M) ([No match](http://msmsms/mascot/cgi/peptide_view.pl?file=../data/20120113/F018139.dat&query=54&hit=1" \t "_blank))



Bottom of Form

🡪 Annotated MS2 spectrum for peptide GANIFTGDFKLEAER



**Monoisotopic mass of neutral peptide Mr(calc):** 1666.8315

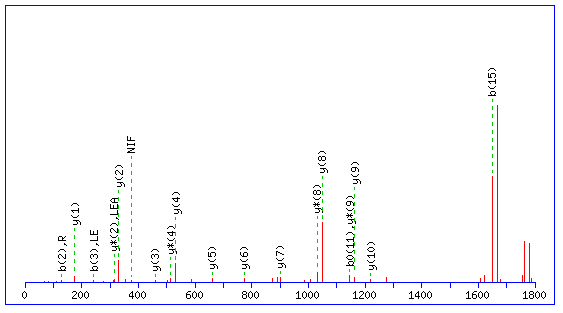
**Ions Score:** 57 **Expect:** 0.00017

**Matches :** 36/249 fragment ions using 63 most intense peaks   ([help](http://msmsms/mascot/help/results_help.html" \l "PEP" \t "_blank))

|  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **#** | **Immon.** | **a** | **a\*** | **a0** | **b** | **b\*** | **b0** | **Seq.** | **v** | **w** | **w'** | **y** | **y\*** | **y0** | **#** |
| **1** | 30.0338 | 30.0338 |  |  | 58.0287 |  |  | **G** |  |  |  |  |  |  | **15** |
| **2** | 44.0495 | 101.0709 |  |  | **129.0659** |  |  | **A** | 1594.7860 |  |  | 1610.8173 | 1593.7907 | 1592.8067 | **14** |
| **3** | 87.0553 | 215.1139 | 198.0873 |  | **243.1088** | 226.0822 |  | **N** | 1480.7431 | 1479.7478 |  | 1539.7802 | 1522.7536 | 1521.7696 | **13** |
| **4** | 86.0964 | 328.1979 | 311.1714 |  | **356.1928** | 339.1663 |  | **I** | 1367.6590 | 1380.6794 | 1394.6951 | 1425.7373 | 1408.7107 | 1407.7267 | **12** |
| **5** | 120.0808 | 475.2663 | 458.2398 |  | **503.2613** | 486.2347 |  | **F** | 1220.5906 |  |  | ***1312.6532*** | 1295.6266 | 1294.6426 | **11** |
| **6** | 74.0600 | 576.3140 | 559.2875 | 558.3035 | 604.3089 | 587.2824 | 586.2984 | **T** | 1119.5429 | 1132.5633 | 1134.5426 | ***1165.5848*** | 1148.5582 | 1147.5742 | **10** |
| **7** | 30.0338 | 633.3355 | 616.3089 | 615.3249 | 661.3304 | 644.3039 | 643.3198 | **G** |  |  |  | ***1064.5371*** | 1047.5106 | 1046.5265 | **9** |
| **8** | 88.0393 | 748.3624 | 731.3359 | 730.3519 | 776.3573 | 759.3308 | 758.3468 | **D** | 947.4945 | 946.4993 |  | ***1007.5156*** | 990.4891 | 989.5051 | **8** |
| **9** | 120.0808 | 895.4308 | 878.4043 | 877.4203 | 923.4258 | 906.3992 | 905.4152 | **F** | 800.4261 |  |  | ***892.4887*** | 875.4621 | 874.4781 | **7** |
| **10** | 101.1073 | 1023.5258 | 1006.4993 | 1005.5152 | 1051.5207 | 1034.4942 | 1033.5102 | **K** | 672.3311 | 671.3359 |  | ***745.4203*** | 728.3937 | 727.4097 | **6** |
| **11** | 86.0964 | 1136.6099 | 1119.5833 | 1118.5993 | **1164.6048** | 1147.5782 | 1146.5942 | **L** | 559.2471 | 558.2518 |  | ***617.3253*** | 600.2988 | 599.3148 | **5** |
| **12** | 102.0550 | 1265.6525 | 1248.6259 | 1247.6419 | **1293.6474** | 1276.6208 | 1275.6368 | **E** | 430.2045 | 429.2092 |  | ***504.2413*** | 487.2147 | 486.2307 | **4** |
| **13** | 44.0495 | 1336.6896 | 1319.6630 | 1318.6790 | 1364.6845 | 1347.6579 | 1346.6739 | **A** | 359.1674 |  |  | ***375.1987*** | 358.1721 | 357.1881 | **3** |
| **14** | 102.0550 | 1465.7322 | 1448.7056 | 1447.7216 | **1493.7271** | 1476.7005 | 1475.7165 | **E** | 230.1248 | 229.1295 |  | ***304.1615*** | 287.1350 | 286.1510 | **2** |
| **15** | 129.1135 |  |  |  |  |  |  | **R** | 74.0237 | 73.0284 |  | ***175.1190*** | 158.0924 |  | **1** |

|  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **Seq** | **ya** | **yb** | **Seq** | **ya** | **yb** | **Seq** | **ya** | **yb** |
| **AN** | 158.0924 | 186.0873 | **ANI** | 271.1765 | 299.1714 | **ANIF** | 418.2449 | 446.2398 |
| **ANIFT** | 519.2926 | 547.2875 | **ANIFTG** | 576.3140 | 604.3089 | **ANIFTGD** | 691.3410 | 719.3359 |
| **NI** | 200.1394 | 228.1343 | **NIF** | 347.2078 | 375.2027 | **NIFT** | 448.2554 | 476.2504 |
| **NIFTG** | 505.2769 | 533.2718 | **NIFTGD** | 620.3039 | 648.2988 | **IF** | 233.1648 | 261.1598 |
| **IFT** | 334.2125 | 362.2074 | **IFTG** | 391.2340 | 419.2289 | **IFTGD** | 506.2609 | 534.2558 |
| **IFTGDF** | 653.3293 | 681.3243 | **FT** | 221.1285 | 249.1234 | **FTG** | 278.1499 | 306.1448 |
| **FTGD** | 393.1769 | 421.1718 | **FTGDF** | 540.2453 | 568.2402 | **FTGDFK** | 668.3402 | 696.3352 |
| **TG** | 131.0815 | 159.0764 | **TGD** | 246.1084 | 274.1034 | **TGDF** | 393.1769 | 421.1718 |
| **TGDFK** | 521.2718 | 549.2667 | **TGDFKL** | 634.3559 | 662.3508 | **GD** | 145.0608 | 173.0557 |
| **GDF** | 292.1292 | 320.1241 | **GDFK** | 420.2241 | 448.2191 | **GDFKL** | 533.3082 | 561.3031 |
| **GDFKLE** | 662.3508 | 690.3457 | **DF** | 235.1077 | 263.1026 | **DFK** | 363.2027 | 391.1976 |
| **DFKL** | 476.2867 | 504.2817 | **DFKLE** | 605.3293 | 633.3243 | **DFKLEA** | 676.3665 | 704.3614 |
| **FK** | 248.1757 | 276.1707 | **FKL** | 361.2598 | 389.2547 | **FKLE** | 490.3024 | 518.2973 |
| **FKLEA** | 561.3395 | 589.3344 | **FKLEAE** | 690.3821 | 718.3770 | **KL** | 214.1914 | 242.1863 |
| **KLE** | 343.2340 | 371.2289 | **KLEA** | 414.2711 | 442.2660 | **KLEAE** | 543.3137 | 571.3086 |
| **LE** | 215.1390 | 243.1339 | **LEA** | 286.1761 | 314.1710 | **LEAE** | 415.2187 | 443.2136 |
| **EA** | 173.0921 | 201.0870 | **EAE** | 302.1347 | 330.1296 | **AE** | 173.0921 | 201.0870 |

🡪 Annotated MS2 spectrum for peptide GANIFTGDFKLEAERR



**Monoisotopic mass of neutral peptide Mr(calc):** 1822.9326

**Ions Score:** 72 **Expect:** 5.3e-006

**Matches :** 23/270 fragment ions using 27 most intense peaks   ([help](http://msmsms/mascot/help/results_help.html" \l "PEP" \t "_blank))

|  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **#** | **Immon.** | **a** | **a\*** | **a0** | **b** | **b\*** | **b0** | **d** | **Seq.** | **v** | **w** | **w'** | **y** | **y\*** | **y0** | **#** |
| **1** | 30.0338 | 30.0338 |  |  | 58.0287 |  |  |  | **G** |  |  |  |  |  |  | **16** |
| **2** | 44.0495 | 101.0709 |  |  | **129.0659** |  |  |  | **A** | 1750.8871 |  |  | 1766.9184 | 1749.8919 | 1748.9078 | **15** |
| **3** | 87.0553 | 215.1139 | 198.0873 |  | **243.1088** | 226.0822 |  |  | **N** | 1636.8442 | 1635.8489 |  | 1695.8813 | 1678.8547 | 1677.8707 | **14** |
| **4** | 86.0964 | 328.1979 | 311.1714 |  | 356.1928 | 339.1663 |  |  | **I** | 1523.7601 | 1536.7805 | 1550.7962 | 1581.8384 | 1564.8118 | 1563.8278 | **13** |
| **5** | 120.0808 | 475.2663 | 458.2398 |  | 503.2613 | 486.2347 |  |  | **F** | 1376.6917 |  |  | 1468.7543 | 1451.7278 | 1450.7437 | **12** |
| **6** | 74.0600 | 576.3140 | 559.2875 | 558.3035 | 604.3089 | 587.2824 | 586.2984 |  | **T** | 1275.6440 | 1288.6644 | 1290.6437 | 1321.6859 | 1304.6593 | 1303.6753 | **11** |
| **7** | 30.0338 | 633.3355 | 616.3089 | 615.3249 | 661.3304 | 644.3039 | 643.3198 |  | **G** |  |  |  | ***1220.6382*** | 1203.6117 | 1202.6276 | **10** |
| **8** | 88.0393 | 748.3624 | 731.3359 | 730.3519 | 776.3573 | 759.3308 | 758.3468 |  | **D** | 1103.5956 | 1102.6004 |  | ***1163.6167*** | 1146.5902 | 1145.6062 | **9** |
| **9** | 120.0808 | 895.4308 | 878.4043 | 877.4203 | 923.4258 | 906.3992 | 905.4152 |  | **F** | 956.5272 |  |  | ***1048.5898*** | 1031.5633 | 1030.5792 | **8** |
| **10** | 101.1073 | 1023.5258 | 1006.4993 | 1005.5152 | 1051.5207 | 1034.4942 | 1033.5102 |  | **K** | 828.4322 | 827.4370 |  | ***901.5214*** | 884.4948 | 883.5108 | **7** |
| **11** | 86.0964 | 1136.6099 | 1119.5833 | 1118.5993 | 1164.6048 | 1147.5782 | 1146.5942 |  | **L** | 715.3482 | 714.3529 |  | ***773.4264*** | 756.3999 | 755.4159 | **6** |
| **12** | 102.0550 | 1265.6525 | 1248.6259 | 1247.6419 | 1293.6474 | 1276.6208 | 1275.6368 |  | **E** | 586.3056 | 585.3103 |  | ***660.3424*** | 643.3158 | 642.3318 | **5** |
| **13** | 44.0495 | 1336.6896 | 1319.6630 | 1318.6790 | 1364.6845 | 1347.6579 | 1346.6739 |  | **A** | 515.2685 |  |  | ***531.2998*** | 514.2732 | 513.2892 | **4** |
| **14** | 102.0550 | 1465.7322 | 1448.7056 | 1447.7216 | 1493.7271 | 1476.7005 | 1475.7165 |  | **E** | 386.2259 | 385.2306 |  | ***460.2627*** | 443.2361 | 442.2521 | **3** |
| **15** | 129.1135 | 1621.8333 | 1604.8067 | 1603.8227 | **1649.8282** | 1632.8016 | 1631.8176 | 1536.7693 | **R** | 230.1248 | 229.1295 |  | ***331.2201*** | 314.1935 |  | **2** |
| **16** | 129.1135 |  |  |  |  |  |  |  | **R** | 74.0237 | 73.0284 |  | ***175.1190*** | 158.0924 |  | **1** |

|  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **Seq** | **ya** | **yb** | **Seq** | **ya** | **yb** | **Seq** | **ya** | **yb** |
| **AN** | 158.0924 | 186.0873 | **ANI** | 271.1765 | 299.1714 | **ANIF** | 418.2449 | 446.2398 |
| **ANIFT** | 519.2926 | 547.2875 | **ANIFTG** | 576.3140 | 604.3089 | **ANIFTGD** | 691.3410 | 719.3359 |
| **NI** | 200.1394 | 228.1343 | **NIF** | 347.2078 | 375.2027 | **NIFT** | 448.2554 | 476.2504 |
| **NIFTG** | 505.2769 | 533.2718 | **NIFTGD** | 620.3039 | 648.2988 | **IF** | 233.1648 | 261.1598 |
| **IFT** | 334.2125 | 362.2074 | **IFTG** | 391.2340 | 419.2289 | **IFTGD** | 506.2609 | 534.2558 |
| **IFTGDF** | 653.3293 | 681.3243 | **FT** | 221.1285 | 249.1234 | **FTG** | 278.1499 | 306.1448 |
| **FTGD** | 393.1769 | 421.1718 | **FTGDF** | 540.2453 | 568.2402 | **FTGDFK** | 668.3402 | 696.3352 |
| **TG** | 131.0815 | 159.0764 | **TGD** | 246.1084 | 274.1034 | **TGDF** | 393.1769 | 421.1718 |
| **TGDFK** | 521.2718 | 549.2667 | **TGDFKL** | 634.3559 | 662.3508 | **GD** | 145.0608 | 173.0557 |
| **GDF** | 292.1292 | 320.1241 | **GDFK** | 420.2241 | 448.2191 | **GDFKL** | 533.3082 | 561.3031 |
| **GDFKLE** | 662.3508 | 690.3457 | **DF** | 235.1077 | 263.1026 | **DFK** | 363.2027 | 391.1976 |
| **DFKL** | 476.2867 | 504.2817 | **DFKLE** | 605.3293 | 633.3243 | **DFKLEA** | 676.3665 | 704.3614 |
| **FK** | 248.1757 | 276.1707 | **FKL** | 361.2598 | 389.2547 | **FKLE** | 490.3024 | 518.2973 |
| **FKLEA** | 561.3395 | 589.3344 | **FKLEAE** | 690.3821 | 718.3770 | **KL** | 214.1914 | 242.1863 |
| **KLE** | 343.2340 | 371.2289 | **KLEA** | 414.2711 | 442.2660 | **KLEAE** | 543.3137 | 571.3086 |
| **KLEAER** | 699.4148 | 727.4097 | **LE** | 215.1390 | 243.1339 | **LEA** | 286.1761 | 314.1710 |
| **LEAE** | 415.2187 | 443.2136 | **LEAER** | 571.3198 | 599.3148 | **EA** | 173.0921 | 201.0870 |
| **EAE** | 302.1347 | 330.1296 | **EAER** | 458.2358 | 486.2307 | **AE** | 173.0921 | 201.0870 |
| **AER** | 329.1932 | 357.1881 | **ER** | 258.1561 | 286.1510 |  |  |  |

**Band 12:**

**http://msmsms/mascot/images/88x31_logo_white.gifMascot Search Results**

**User :**

**Email :**

**Search title : SampleSetID: 683, AnalysisID: 1071, MaldiWellID: 82756, SpectrumID: 217168, Path=\Jimmy\Cooperia 3\Co ES Conc 3 Frac 13012012 (strict)**

**Database : cooperia\_oncophora oncophora\_20110405 (34373 sequences; 5289600 residues)**

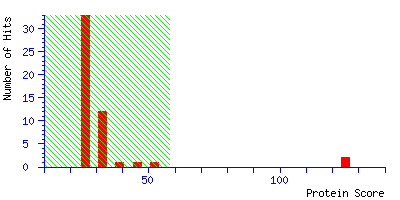
**Timestamp : 13 Jan 2012 at 14:34:47 GMT**

**Warning : A Peptide summary report will usually give a much clearer picture of MS/MS search results.**

**Top Score : 125 for gi|14140089|emb|CAC38986.1|, ES antigen 1 [Cooperia oncophora]**

**Mascot Score Histogram**

Protein score is -10\*Log(P), where P is the probability that the observed match is a random event.  
Protein scores greater than 58 are significant (p<0.05).  
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



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**Protein Summary Report**

|  |  |  |  |
| --- | --- | --- | --- |
|  |  |  | [Help](http://msmsms/mascot/help/msms_summaries_help.html" \t "_blank) |
|  | Significance threshold p< | Max. number of hits |  |

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Bottom of Form

**Index**

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
|  | **Accession** | **Mass** | **Score** | **Description** |
| **1.** | [**gi|14140089|emb|CAC38986.1|**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20120113/F018140.dat#Hit1) | 13887 | 125 | ES antigen 1 [Cooperia oncophora] |
| **2.** | [**isotig26364**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20120113/F018140.dat#Hit2) | 14131 | 125 | putative nuclear encoded protein Method: similarity and extension |
| **3.** | [**isotig27927**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20120113/F018140.dat#Hit3) | 38685 | 54 | putative nuclear encoded protein Method: similarity and extension |
| **4.** | [**isotig29234**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20120113/F018140.dat#Hit4) | 12421 | 44 | putative nuclear encoded protein Method: similarity and extension |
| **5.** | [**isotig22321**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20120113/F018140.dat#Hit5) | 8559 | 36 | putative nuclear encoded protein Method: Longest ORF |
| **6.** | [**isotig25113**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20120113/F018140.dat#Hit6) | 20456 | 32 | putative nuclear encoded protein Method: similarity and extension |
| **7.** | [**isotig00884**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20120113/F018140.dat#Hit7) | 48075 | 31 | putative nuclear encoded protein Method: similarity and extension |
| **8.** | [**isotig00883**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20120113/F018140.dat#Hit8) | 48075 | 31 | putative nuclear encoded protein Method: similarity and extension |
| **9.** | [**isotig13352**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20120113/F018140.dat#Hit9) | 36997 | 31 | putative nuclear encoded protein Method: similarity and extension |
| **10.** | [**isotig26319**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20120113/F018140.dat#Hit10) | 11269 | 31 | putative nuclear encoded protein Method: similarity and extension |
| **11.** | [**isotig17250**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20120113/F018140.dat#Hit11) | 13453 | 31 | putative nuclear encoded protein Method: similarity and extension |
| **12.** | [**isotig16936**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20120113/F018140.dat#Hit12) | 12339 | 30 | putative nuclear encoded protein Method: Longest ORF |
| **13.** | [**contig17118**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20120113/F018140.dat#Hit13) | 26388 | 30 | putative nuclear encoded protein Method: similarity and extension |
| **14.** | [**isotig07318**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20120113/F018140.dat#Hit14) | 11677 | 30 | putative nuclear encoded protein Method: Longest ORF |
| **15.** | [**isotig22001**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20120113/F018140.dat#Hit15) | 22330 | 30 | putative nuclear encoded protein Method: similarity and extension |
| **16.** | [**isotig28918**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20120113/F018140.dat#Hit16) | 13641 | 30 | putative nuclear encoded protein Method: Longest ORF |
| **17.** | [**isotig01032**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20120113/F018140.dat#Hit17) | 12179 | 30 | putative nuclear encoded protein Method: Longest ORF |
| **18.** | [**isotig28699**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20120113/F018140.dat#Hit18) | 21729 | 29 | putative nuclear encoded protein Method: similarity and extension |
| **19.** | [**isotig00737**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20120113/F018140.dat#Hit19) | 14790 | 28 | putative nuclear encoded protein Method: similarity and extension |
| **20.** | [**isotig12636**](http://msmsms/mascot/cgi/master_results.pl?REPTYPE=Protein&file=../data/20120113/F018140.dat#Hit20) | 14579 | 28 | putative nuclear encoded protein Method: similarity and extension |

**Results List**

|  |  |
| --- | --- |
| **1.** | [gi|14140089|emb|CAC38986.1|](http://msmsms/mascot/cgi/protein_view.pl?file=../data/20120113/F018140.dat&hit=1" \t "_blank)    **Mass:** 13887    **Score:** 125    **Expect:** 1.1e-008  **Matches:** 1 |
|  | ES antigen 1 [Cooperia oncophora] |

|  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | **Observed** | **Mr(expt)** | **Mr(calc)** | **ppm** | **Start** |  | **End** | **Miss** | **Ions** | **Peptide** |
|  | 3214.4309 | 3213.4236 | 3213.4806 | -17.73 | 71 | - | 100 | 0 | 122 | K.TFASGGSVPVMIGETLMDGLQDETQTENVR.N + 2 Oxidation (M) |

|  |  |
| --- | --- |
|  | **No match to:** 906.4820, 909.4041, 924.4171, 925.4001, 940.5432, 942.5428, 976.5508, 980.4566, 994.4777, 995.4977, 1014.4626, 1015.4807, 1047.5900, 1052.5449, 1054.6315, 1059.5737, 1074.5470, 1075.5115, 1081.5134, 1114.5217, 1129.5273, 1131.5450, 1131.5450, 1136.5881, 1147.5315, 1152.5447, 1161.5968, 1163.5341, 1167.5065, 1171.5736, 1183.4919, 1213.6635, 1216.6055, 1350.6853, 1359.6407, 1512.6694, 1520.7821, 1528.6650, 1593.7621, 1635.7416, 1667.7982, 1681.7515, 1708.7562, 1713.6978, 1745.8204, 1823.8956, 1876.9468, 1876.9468, 1947.8035, 2622.1021, 2622.1021, 2679.1245, 2679.1245, 2924.3943, 2924.3943 |

|  |  |
| --- | --- |
| **2.** | [isotig26364](http://msmsms/mascot/cgi/protein_view.pl?file=../data/20120113/F018140.dat&hit=2" \t "_blank)    **Mass:** 14131    **Score:** 125    **Expect:** 1.1e-008  **Matches:** 1 |
|  | putative nuclear encoded protein Method: similarity and extension |

|  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | **Observed** | **Mr(expt)** | **Mr(calc)** | **ppm** | **Start** |  | **End** | **Miss** | **Ions** | **Peptide** |
|  | 3214.4309 | 3213.4236 | 3213.4806 | -17.73 | 73 | - | 102 | 0 | 122 | K.TFASGGSVPVMIGETLMDGLQDETQTENVR.N + 2 Oxidation (M) |

|  |  |
| --- | --- |
|  | **No match to:** 906.4820, 909.4041, 924.4171, 925.4001, 940.5432, 942.5428, 976.5508, 980.4566, 994.4777, 995.4977, 1014.4626, 1015.4807, 1047.5900, 1052.5449, 1054.6315, 1059.5737, 1074.5470, 1075.5115, 1081.5134, 1114.5217, 1129.5273, 1131.5450, 1131.5450, 1136.5881, 1147.5315, 1152.5447, 1161.5968, 1163.5341, 1167.5065, 1171.5736, 1183.4919, 1213.6635, 1216.6055, 1350.6853, 1359.6407, 1512.6694, 1520.7821, 1528.6650, 1593.7621, 1635.7416, 1667.7982, 1681.7515, 1708.7562, 1713.6978, 1745.8204, 1823.8956, 1876.9468, 1876.9468, 1947.8035, 2622.1021, 2622.1021, 2679.1245, 2679.1245, 2924.3943, 2924.3943 |

**http://msmsms/mascot/images/88x31_logo_white.gifMascot Search Results**

**Protein View**

Top of Form



Match to: **gi|14140089|emb|CAC38986.1|** Score: **125** Expect: **1.1e-008**

**ES antigen 1 [Cooperia oncophora]**

Nominal mass (Mr): **13887**; Calculated pI value: **5.30**

NCBI BLAST search of [gi|14140089|emb|CAC38986.1|](http://www.ncbi.nlm.nih.gov/blast/Blast.cgi?ALIGNMENTS=50&ALIGNMENT_VIEW=Pairwise&AUTO_FORMAT=Semiauto&CDD_SEARCH=on&CLIENT=web&COMPOSITION_BASED_STATISTICS=on&DATABASE=nr&DESCRIPTIONS=100&ENTREZ_QUERY=(none)&EXPECT=10&FILTER=L&FORMAT_BLOCK_ON_RESPAGE=None&FORMAT_OBJECT=Alignment&FORMAT_TYPE=HTML&GAPCOSTS=11+1&I_THRESH=0.001&LAYOUT=TwoWindows&MATRIX_NAME=BLOSUM62&NCBI_GI=on&PAGE=Proteins&PROGRAM=blastp&QUERY=FVLVPLCFLLINVAAGNRCPTYTARKEWYSSFNEFLNPALEWDPGLSSDACNEARGIVASNAPHKFIAEKTFASGGSVPVMIGETLMDGLQDETQTENVRNLPPHTKYGCNSYFEGNLVKVVCVYK&SERVICE=plain&SET_DEFAULTS.x=9&SET_DEFAULTS.y=5&SHOW_OVERVIEW=on&WORD_SIZE=3&END_OF_HTTPGET=Yes" \t "_blank) against nr

Unformatted [sequence string](http://msmsms/mascot/cgi/getseq.pl?cooperia_oncophora+gi%7c14140089%7cemb%7cCAC38986%2e1%7c+seq" \t "_blank) for pasting into other applications

Variable modifications: Oxidation (HW),Oxidation (M)

Cleavage by Trypsin/P: cuts C-term side of KR

Sequence Coverage: **23%**

Matched peptides shown in **Bold Red**

**1** FVLVPLCFLL INVAAGNRCP TYTARKEWYS SFNEFLNPAL EWDPGLSSDA

**51** CNEARGIVAS NAPHKFIAEK **TFASGGSVPV MIGETLMDGL QDETQTENVR**

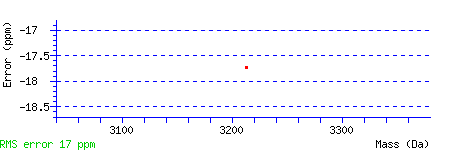
**101** NLPPHTKYGC NSYFEGNLVK VVCVYK



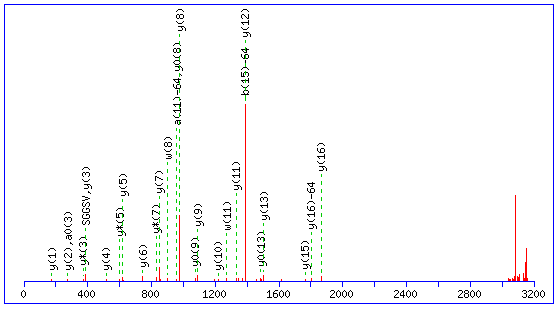
  Residue Number  Increasing Mass  Decreasing Mass

**Start - End Observed Mr(expt) Mr(calc) ppm Miss Sequence**

**71 - 100 3214.4309 3213.4236 3213.4806 -18 0 K.TFASGGSVPVMIGETLMDGLQDETQTENVR.N**  2 Oxidation (M) ([Ions score 122](http://msmsms/mascot/cgi/peptide_view.pl?file=../data/20120113/F018140.dat&query=56&hit=1" \t "_blank))



🡪 Annotated MS2 spectrum for peptide TFASGGSVPVMIGETLMDGLQDETQTENVR Bottom of Form



**Monoisotopic mass of neutral peptide Mr(calc):** 3213.4806

**Variable modifications:**

**M11 :** Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983

**M17 :** Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983

**Ions Score:** 122 **Expect:** 4.2e-011

**Matches :** 28/813 fragment ions using 31 most intense peaks   ([help](http://msmsms/mascot/help/results_help.html" \l "PEP" \t "_blank))

|  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **#** | **Immon.** | **a** | **a\*** | **a0** | **b** | **b\*** | **b0** | **Seq.** | **v** | **w** | **w'** | **y** | **y\*** | **y0** | **#** |
| **1** | 74.0600 | 74.0600 |  | 56.0495 | 102.0550 |  | 84.0444 | **T** |  |  |  |  |  |  | **30** |
| **2** | 120.0808 | 221.1285 |  | 203.1179 | 249.1234 |  | 231.1128 | **F** | 3021.3776 |  |  | 3113.4402 | 3096.4136 | 3095.4296 | **29** |
| **3** | 44.0495 | 292.1656 |  | 274.1550 | 320.1605 |  | 302.1499 | **A** | 2950.3405 |  |  | 2966.3718 | 2949.3452 | 2948.3612 | **28** |
| **4** | 60.0444 | 379.1976 |  | 361.1870 | 407.1925 |  | 389.1819 | **S** | 2863.3084 | 2862.3132 |  | 2895.3346 | 2878.3081 | 2877.3241 | **27** |
| **5** | 30.0338 | 436.2191 |  | 418.2085 | 464.2140 |  | 446.2034 | **G** |  |  |  | 2808.3026 | 2791.2761 | 2790.2921 | **26** |
| **6** | 30.0338 | 493.2405 |  | 475.2300 | 521.2354 |  | 503.2249 | **G** |  |  |  | 2751.2812 | 2734.2546 | 2733.2706 | **25** |
| **7** | 60.0444 | 580.2726 |  | 562.2620 | 608.2675 |  | 590.2569 | **S** | 2662.2335 | 2661.2382 |  | 2694.2597 | 2677.2331 | 2676.2491 | **24** |
| **8** | 72.0808 | 679.3410 |  | 661.3304 | 707.3359 |  | 689.3253 | **V** | 2563.1651 | 2576.1855 |  | 2607.2277 | 2590.2011 | 2589.2171 | **23** |
| **9** | 70.0651 | 776.3937 |  | 758.3832 | 804.3886 |  | 786.3781 | **P** | 2466.1123 | 2465.1170 |  | 2508.1592 | 2491.1327 | 2490.1487 | **22** |
| **10** | 72.0808 | 875.4621 |  | 857.4516 | 903.4571 |  | 885.4465 | **V** | 2367.0439 | 2380.0643 |  | 2411.1065 | 2394.0799 | 2393.0959 | **21** |
| **11** | 120.0478 | 1022.4975 |  | 1004.4870 | 1050.4925 |  | 1032.4819 | **M** | 2220.0085 | 2219.0132 |  | 2312.0381 | 2295.0115 | 2294.0275 | **20** |
| **12** | 86.0964 | 1135.5816 |  | 1117.5710 | 1163.5765 |  | 1145.5660 | **I** | 2106.9244 | 2119.9448 | 2133.9605 | 2165.0027 | 2147.9761 | 2146.9921 | **19** |
| **13** | 30.0338 | 1192.6031 |  | 1174.5925 | 1220.5980 |  | 1202.5874 | **G** |  |  |  | 2051.9186 | 2034.8921 | 2033.9080 | **18** |
| **14** | 102.0550 | 1321.6457 |  | 1303.6351 | 1349.6406 |  | 1331.6300 | **E** | 1920.8604 | 1919.8651 |  | 1994.8971 | 1977.8706 | 1976.8866 | **17** |
| **15** | 74.0600 | 1422.6933 |  | 1404.6828 | 1450.6883 |  | 1432.6777 | **T** | 1819.8127 | 1832.8331 | 1834.8124 | ***1865.8545*** | 1848.8280 | 1847.8440 | **16** |
| **16** | 86.0964 | 1535.7774 |  | 1517.7668 | 1563.7723 |  | 1545.7618 | **L** | 1706.7286 | 1705.7334 |  | ***1764.8069*** | 1747.7803 | 1746.7963 | **15** |
| **17** | 120.0478 | 1682.8128 |  | 1664.8022 | 1710.8077 |  | 1692.7972 | **M** | 1559.6932 | 1558.6980 |  | 1651.7228 | 1634.6963 | 1633.7122 | **14** |
| **18** | 88.0393 | 1797.8398 |  | 1779.8292 | 1825.8347 |  | 1807.8241 | **D** | 1444.6663 | 1443.6710 |  | ***1504.6874*** | 1487.6609 | 1486.6768 | **13** |
| **19** | 30.0338 | 1854.8612 |  | 1836.8506 | 1882.8561 |  | 1864.8456 | **G** |  |  |  | ***1389.6605*** | 1372.6339 | 1371.6499 | **12** |
| **20** | 86.0964 | 1967.9453 |  | 1949.9347 | 1995.9402 |  | 1977.9296 | **L** | 1274.5607 | 1273.5655 |  | ***1332.6390*** | 1315.6125 | 1314.6284 | **11** |
| **21** | 101.0709 | 2096.0039 | 2078.9773 | 2077.9933 | 2123.9988 | 2106.9722 | 2105.9882 | **Q** | 1146.5022 | 1145.5069 |  | ***1219.5549*** | 1202.5284 | 1201.5444 | **10** |
| **22** | 88.0393 | 2211.0308 | 2194.0043 | 2193.0202 | 2239.0257 | 2221.9992 | 2221.0151 | **D** | 1031.4752 | 1030.4800 |  | ***1091.4964*** | 1074.4698 | 1073.4858 | **9** |
| **23** | 102.0550 | 2340.0734 | 2323.0468 | 2322.0628 | 2368.0683 | 2351.0418 | 2350.0577 | **E** | 902.4326 | 901.4374 |  | ***976.4694*** | 959.4429 | 958.4588 | **8** |
| **24** | 74.0600 | 2441.1211 | 2424.0945 | 2423.1105 | 2469.1160 | 2452.0894 | 2451.1054 | **T** | 801.3850 | 814.4054 | 816.3846 | ***847.4268*** | 830.4003 | 829.4163 | **7** |
| **25** | 101.0709 | 2569.1796 | 2552.1531 | 2551.1691 | 2597.1746 | 2580.1480 | 2579.1640 | **Q** | 673.3264 | 672.3311 |  | ***746.3791*** | 729.3526 | 728.3686 | **6** |
| **26** | 74.0600 | 2670.2273 | 2653.2008 | 2652.2168 | 2698.2222 | 2681.1957 | 2680.2117 | **T** | 572.2787 | 585.2991 | 587.2784 | ***618.3206*** | 601.2940 | 600.3100 | **5** |
| **27** | 102.0550 | 2799.2699 | 2782.2434 | 2781.2594 | 2827.2648 | 2810.2383 | 2809.2543 | **E** | 443.2361 | 442.2409 |  | ***517.2729*** | 500.2463 | 499.2623 | **4** |
| **28** | 87.0553 | 2913.3128 | 2896.2863 | 2895.3023 | 2941.3078 | 2924.2812 | 2923.2972 | **N** | 329.1932 | 328.1979 |  | ***388.2303*** | 371.2037 |  | **3** |
| **29** | 72.0808 | 3012.3813 | 2995.3547 | 2994.3707 | 3040.3762 | 3023.3496 | 3022.3656 | **V** | 230.1248 | 243.1452 |  | ***274.1874*** | 257.1608 |  | **2** |
| **30** | 129.1135 |  |  |  |  |  |  | **R** | 74.0237 | 73.0284 |  | ***175.1190*** | 158.0924 |  | **1** |

|  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **Seq** | **ya** | **yb** | **Seq** | **ya** | **yb** | **Seq** | **ya** | **yb** |
| **FA** | 191.1179 | 219.1128 | **FAS** | 278.1499 | 306.1448 | **FASG** | 335.1714 | 363.1663 |
| **FASGG** | 392.1928 | 420.1878 | **FASGGS** | 479.2249 | 507.2198 | **FASGGSV** | 578.2933 | 606.2882 |
| **FASGGSVP** | 675.3461 | 703.3410 | **AS** | 131.0815 | 159.0764 | **ASG** | 188.1030 | 216.0979 |
| **ASGG** | 245.1244 | 273.1193 | **ASGGS** | 332.1565 | 360.1514 | **ASGGSV** | 431.2249 | 459.2198 |
| **ASGGSVP** | 528.2776 | 556.2726 | **ASGGSVPV** | 627.3461 | 655.3410 | **SG** | 117.0659 | 145.0608 |
| **SGG** | 174.0873 | 202.0822 | **SGGS** | 261.1193 | 289.1143 | **SGGSV** | 360.1878 | 388.1827 |
| **SGGSVP** | 457.2405 | 485.2354 | **SGGSVPV** | 556.3089 | 584.3039 | **GG** | 87.0553 | 115.0502 |
| **GGS** | 174.0873 | 202.0822 | **GGSV** | 273.1557 | 301.1506 | **GGSVP** | 370.2085 | 398.2034 |
| **GGSVPV** | 469.2769 | 497.2718 | **GGSVPVM** | 616.3123 | 644.3072 | **GS** | 117.0659 | 145.0608 |
| **GSV** | 216.1343 | 244.1292 | **GSVP** | 313.1870 | 341.1819 | **GSVPV** | 412.2554 | 440.2504 |
| **GSVPVM** | 559.2908 | 587.2858 | **GSVPVMI** | 672.3749 | 700.3698 | **SV** | 159.1128 | 187.1077 |
| **SVP** | 256.1656 | 284.1605 | **SVPV** | 355.2340 | 383.2289 | **SVPVM** | 502.2694 | 530.2643 |
| **SVPVMI** | 615.3534 | 643.3484 | **SVPVMIG** | 672.3749 | 700.3698 | **VP** | 169.1335 | 197.1285 |
| **VPV** | 268.2020 | 296.1969 | **VPVM** | 415.2374 | 443.2323 | **VPVMI** | 528.3214 | 556.3163 |
| **VPVMIG** | 585.3429 | 613.3378 | **PV** | 169.1335 | 197.1285 | **PVM** | 316.1689 | 344.1639 |
| **PVMI** | 429.2530 | 457.2479 | **PVMIG** | 486.2745 | 514.2694 | **PVMIGE** | 615.3171 | 643.3120 |
| **VM** | 219.1162 | 247.1111 | **VMI** | 332.2002 | 360.1952 | **VMIG** | 389.2217 | 417.2166 |
| **VMIGE** | 518.2643 | 546.2592 | **VMIGET** | 619.3120 | 647.3069 | **MI** | 233.1318 | 261.1267 |
| **MIG** | 290.1533 | 318.1482 | **MIGE** | 419.1959 | 447.1908 | **MIGET** | 520.2436 | 548.2385 |
| **MIGETL** | 633.3276 | 661.3225 | **IG** | 143.1179 | 171.1128 | **IGE** | 272.1605 | 300.1554 |
| **IGET** | 373.2082 | 401.2031 | **IGETL** | 486.2922 | 514.2871 | **IGETLM** | 633.3276 | 661.3225 |
| **GE** | 159.0764 | 187.0713 | **GET** | 260.1241 | 288.1190 | **GETL** | 373.2082 | 401.2031 |
| **GETLM** | 520.2436 | 548.2385 | **GETLMD** | 635.2705 | 663.2654 | **GETLMDG** | 692.2920 | 720.2869 |
| **ET** | 203.1026 | 231.0975 | **ETL** | 316.1867 | 344.1816 | **ETLM** | 463.2221 | 491.2170 |
| **ETLMD** | 578.2490 | 606.2440 | **ETLMDG** | 635.2705 | 663.2654 | **TL** | 187.1441 | 215.1390 |
| **TLM** | 334.1795 | 362.1744 | **TLMD** | 449.2064 | 477.2014 | **TLMDG** | 506.2279 | 534.2228 |
| **TLMDGL** | 619.3120 | 647.3069 | **LM** | 233.1318 | 261.1267 | **LMD** | 348.1588 | 376.1537 |
| **LMDG** | 405.1802 | 433.1751 | **LMDGL** | 518.2643 | 546.2592 | **LMDGLQ** | 646.3229 | 674.3178 |
| **MD** | 235.0747 | 263.0696 | **MDG** | 292.0962 | 320.0911 | **MDGL** | 405.1802 | 433.1751 |
| **MDGLQ** | 533.2388 | 561.2337 | **MDGLQD** | 648.2658 | 676.2607 | **DG** | 145.0608 | 173.0557 |
| **DGL** | 258.1448 | 286.1397 | **DGLQ** | 386.2034 | 414.1983 | **DGLQD** | 501.2304 | 529.2253 |
| **DGLQDE** | 630.2729 | 658.2679 | **GL** | 143.1179 | 171.1128 | **GLQ** | 271.1765 | 299.1714 |
| **GLQD** | 386.2034 | 414.1983 | **GLQDE** | 515.2460 | 543.2409 | **GLQDET** | 616.2937 | 644.2886 |
| **LQ** | 214.1550 | 242.1499 | **LQD** | 329.1819 | 357.1769 | **LQDE** | 458.2245 | 486.2195 |
| **LQDET** | 559.2722 | 587.2671 | **LQDETQ** | 687.3308 | 715.3257 | **QD** | 216.0979 | 244.0928 |
| **QDE** | 345.1405 | 373.1354 | **QDET** | 446.1882 | 474.1831 | **QDETQ** | 574.2467 | 602.2416 |
| **QDETQT** | 675.2944 | 703.2893 | **DE** | 217.0819 | 245.0768 | **DET** | 318.1296 | 346.1245 |
| **DETQ** | 446.1882 | 474.1831 | **DETQT** | 547.2358 | 575.2307 | **DETQTE** | 676.2784 | 704.2733 |
| **ET** | 203.1026 | 231.0975 | **ETQ** | 331.1612 | 359.1561 | **ETQT** | 432.2089 | 460.2038 |
| **ETQTE** | 561.2515 | 589.2464 | **ETQTEN** | 675.2944 | 703.2893 | **TQ** | 202.1186 | 230.1135 |
| **TQT** | 303.1663 | 331.1612 | **TQTE** | 432.2089 | 460.2038 | **TQTEN** | 546.2518 | 574.2467 |
| **TQTENV** | 645.3202 | 673.3151 | **QT** | 202.1186 | 230.1135 | **QTE** | 331.1612 | 359.1561 |
| **QTEN** | 445.2041 | 473.1991 | **QTENV** | 544.2726 | 572.2675 | **TE** | 203.1026 | 231.0975 |
| **TEN** | 317.1456 | 345.1405 | **TENV** | 416.2140 | 444.2089 | **EN** | 216.0979 | 244.0928 |
| **ENV** | 315.1663 | 343.1612 | **NV** | 186.1237 | 214.1186 |  |  |  |

**Table.** Overview of all significant isotigs/contigs identified during MALDI-MS analyses (of both 2D- and 1D-PAGE) employing the *C. oncophora* transcriptome database (Suppl. Information File 1). Underlined isotigs/contigs represent top-hits and are found back in the Tables on pages 3 and 210 of this file. The top-hits’ corresponding isotig codes from <http://www.nematode.net>, which are displayed in Table 1 in the manuscript, are also provided here. Isotig/contig numbers in italics were used for full-length amino acid sequence determination (for GenBank accession numbers, see Table 1 in the manuscript).

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Homology-based ID MS-identified contigs/isotigs <http://www.nematode.net> corresponding isotig #

of top-hits (underlined)

\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_

Double-domain ASP contig05709, contig63173, isotig31886, isotig00099 contig31766

Hypothetical protein isotig24792 isotig27828

Aldose reductase isotigs01074 - 01089, *isotig01086*, isotig20646, isotig31867 isotig02668

Single-domain ASP *contig55746*, isotig13456, isotig13457 isotig02366

Innexin isotig14500 isotig12080

Thioredoxin peroxidase *isotig09291*, isotig09292 isotig10347

Parasitic stage specific protein 2 *isotig00466*, isotig00467, isotig00468 isotig02429

14 kDa ES protein isotig25459, contig45229, isotig19733, isotig21928, isotig09197, isotig14336, N/A

isotig09196, isotig14337, isotig17113, isotig17160, isotig21044, isotig29536

ES antigen 2 protein isotig09711, isotig09712 N/A

ES antigen 1 isotig11584, isotig25277, isotig26116, isotig11583, isotig11585, isotig26364 N/A

Unknown 1 *isotig32303* isotig01702

Unknown 2 *isotig10739*, isotig10740 isotig10695

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