

Supplemental TABLE 5. List of *Strongyloides* proteins found only in E/S products from free-living stages

N°	Cluster	BLAST Alignment	Species	Accession Number	E	SP	EST Lgt.	% Cov.	Pep. #	UPS
Protein digestion and folding										
1	SR00267	Carboxy-peptidase	<i>Streptomyces coelicolor</i>	NP_630237	0.89	yes	243	11.5	2	4.00
2	SR02550	Putative serine protease F56F10.1	<i>Caenorhabditis elegans</i>	P90893	2e ⁻³⁵	yes	239	11.7	2	5.22
3	SR05257	Putative serine protease F56F10.1	<i>C. elegans</i>	P90893	2e ⁻²⁴	yes	185	25.4	2	5.52
4	SR02579	Metallo-proteinase	<i>Necator americanus</i>	ACB13196	3e ⁻⁴⁶	yes	192	18.8	2	4.00
5	SR01063	Aspartyl protease precursor	<i>Caenorhabditis briggsae</i>	CAP30637	2e ⁻⁹⁸	yes	359	10.9	2	4.49
Carbohydrate metabolism										
6	SR00479	Hexosaminidase B	<i>Pan troglodytes</i>	XP_517705	2e ⁻⁴⁶	yes	167	16.8	2	7.13
Heat shock proteins										
7	SS01082	Hypothetical 86.9 kDa protein	<i>Brugia malayi</i>	XP_001896095	5e ⁻⁵¹	no	309	6.8	2	5.22
Developmental processes										
8	SR02018	Yeast Glc Seven-like Phosphatase	<i>C. elegans</i>	NP_491237	2e ⁻⁹⁴	no	184	13.0	2	4.74
Other functions										
9	SR00863	MFP2b	<i>Ascaris suum</i>	AAP94889	5e ⁻⁷¹	no	173	52.0	7	14.85
10	SR00750	Similar to mannose receptor	<i>Gallus gallus</i>	XP_418617	2e ⁻⁰⁷	yes	174	21.3	3	6.35
11	SR00671	Lysozyme family member (lys-5)	<i>C. elegans</i>	NP_502193	4e ⁻³⁷	yes	160	23.1	4	12.70
12	SR00576	MSP domain protein	<i>B. malayi</i>	XP_001899679	3e ⁻³²	no	97	47.4	4	8.02
13	SR01169	Aminotransferase	<i>Clostridium botulinum</i>	ZP_02614737	0.53	no	176	31.8	4	8.14
14	SS00790	NompA	<i>C. elegans</i>	NP_502699	5e ⁻⁶⁸	yes	160	12.5	2	4.00
15	SS01173	Enoyl-CoA reductase	<i>Ascaris suum</i>	AAC48316	1e ⁻¹⁰⁴	no	299	10.0	2	6.41
16	SR00354	Acid Sphingo-myelinase	<i>C. elegans</i>	NP_001040996	2e ⁻⁸⁹	yes	269	19.3	3	6.09
17	SR02017	26 kDa secreted antigen	<i>Toxocara canis</i>	P54190	5e ⁻⁰⁴	yes	139	21.6	2	4.00
18	SR02511	Acyl sphingosine amido hydro-lase	<i>C. briggsae</i>	CAP33700	2e ⁻⁴⁸	yes	184	27.2	4	8.35
19	SS00929	High mobility group protein	<i>C. elegans</i>	NP_496970	5e ⁻²¹	no	94	20.2	2	4.02
20	SR00172	60s acidic ribosomal protein P2	<i>B. malayi</i>	P90703	3e ⁻²¹	no	110	27.3	2	4.00
21	SR00821	Saposin-like protein	<i>C. elegans</i>	NP_491803	5.4	yes	86	54.7	3	6.39

N°	Cluster	BLASTAlignment	Species	Accession Number	E	SP	EST Lgt.	% Cov.	Pep. #	UPS
Not assigned										
22	SR00223	Hypothetical protein C50B6.7	<i>C. elegans</i>	NP_506303	6e ⁻⁵¹	yes	192	18.2	2	4.02
23	SR01917	Hypothetical protein F40F4.6	<i>C. elegans</i>	NP_508552	6e ⁻⁰³	yes	166	18.7	2	4.00
24	SR00294	Hypothetical protein R05F9.12	<i>C. elegans</i>	AAA83174	3e ⁻⁴⁹	yes	168	21.4	2	4.00
25	SR00380	Hypothetical protein EUBVEN_01944	<i>Eubacterium ventriosum</i>	ZP_02026680	7.9	yes	154	14.9	2	5.78
26	SR00282	Hypothetical protein F40F4.6	<i>C. elegans</i>	NP_508552	2e ⁻²⁸	yes	178	15.7	2	4.00
27	SR00716	F09C8.1	<i>C. elegans</i>	NP_510636	3e ⁻⁴⁵	yes	170	22.4	2	4.66
28	SR00375	Hypothetical protein CBG05949	<i>C. briggsae</i>	XP_001670383	5e ⁻⁰⁹	yes	148	31.1	5	13.91
29	SR00767	F25A2.1	<i>C. elegans</i>	NP_503390	6e ⁻²⁵	no	178	17.4	2	6.67
30	SR01936	Hypothetical protein CBG21853	<i>C. briggsae</i>	XP_001672742	1e ⁻²¹	yes	190	13.7	2	5.98
31	SR02994	Hypothetical protein Y49E10.18	<i>C. elegans</i>	NP_499623	2e ⁻²⁷	yes	143	51.0	7	19.13
32	SR00899	Hypothetical protein CBG09313	<i>C. briggsae</i>	XP_001674244	4e ⁻¹¹	no	231	13.9	2	4.01
33	SR02091	Hypothetical protein CBG22129	<i>C. briggsae</i>	XP_001667627	1e ⁻³⁵	yes	174	36.8	6	13.27

Novel Proteins that are not listed in one of the *Strongyloides ssp.* EST databases

N°	Acc. Number	BLASTAlignment	Species	SP	Fragment Length	% Cov.	Pep. #	UPS
34	gi 1480463	Cyclophilin Dicyp-2	<i>Dirofilaria immitis</i>	no	171	10.5	2	4.22
35	gi 17542416	Major sperm protein (msp-78)	<i>C. elegans</i>	no	127	25.2	2	4.70

E, expectation value; SP, signal peptide; EST Lgt., EST length; % Cov., percentage coverage; Pep. #, number of peptides (#); UPS, unused protein scores