InfoBoxes

1. Input one gene name from one of the 17 species (i.e. 2L52)
2. Clicking on one or more species will output all the genes that meet the criteria specified in the boxes chosen below.
3. The database can be searched by entering a specific GO ID (i.e. GO:0005737)
4. The database can be searched by entering a specific KO number (i.e. K06233)
5. The database can be search by entering a specific InterPro ID (i.e. IPR06570)
6. Choose whether to parse based on essentiality (based on C. elegans RNAi phenotype data). If “Do not filter on this” is picked, genes will be output regardless of essentiality. If “Severe” is picked only RNAi phenotypes
7. Search based on PDB ID (i.e. 1U39).
8. Choose “Yes” to search for genes that have a signal peptide and “No” to search for genes with no signal peptide. If the option “Do not filter on this” is chosen, the presence of a signal peptide will not be used as a filter.
9. Enter a DrugBank ID (i.e. DB01103) and only genes that have homology to the target DB01103 binds will be displayed.
10. Hopkins druggable targets are targets that bind small molecules that follow Lipinski’s Rule of 5. The search is based on a list of InterPro ID’s found in Hopkins study (see FAQ).
11. This option will list the orthologous group in which the gene resides.
12. The GO ID will be listed with the gene name output.
13. The KO number will be listed with the gene name output.
14. The EC number will be listed with the gene name in the output.
15. The InterPro ID will be listed with the gene name in the output.
16. Any nematode specific insertion or deletion relative to mammals (check) will be listed. See FAQ for more information.
17. The associated RNAi phenotype (based on C. elegans data) will be listed with the gene name in the output.
18. If the gene has homology to a protein in the PDB, the associated PDB structure name (i.e. 1U39) will be listed with the gene name in the output.
19. If the gene has homology to a protein target in DrugBank, the target name and DrugBank ID will be output along with cheminformatic information regarding the drugs. [I think we split this into two boxes in the output]
20. If a gene is involved in a protein-protein interaction (PPI), the uniprot ID of both protein partners in the interaction will be listed along with the gene of interest.
21. If the gene of interest has a signal peptide or transmembrane region, the information will be listed in the output with the gene name. The signal peptide and transmembrane domain were determined using Phobius.
22. A link to Paircoil2 output will be listed along with the associated gene in the output. Regions that have a pscore less than 0.1 are considered coiled coil regions.
23. Links to the output of several secondary structure programs (JUFO, PsiPred, IUPred, PHDPROF) [one of these didn’t work, I think]
24. A link will be provided to an EPS file with data plotted from RONN, a disorder prediction program. A probability above 0.5 indicates the region is disordered.
25. Genes can be search for epitopes that may be potential vaccine candidates. The user can choose a linear motif (obtained from regions of disorder between 25-100 amino acids determine by RONN) or structural motifs: coiled coil of 4-10 heptad repeats (determined by Paircoil2) [check], Zinc-fingers, knottins, animal toxins, EGF modules, and collagens (determined by InterProID).

[Note this section can be split up among the various checked boxes]