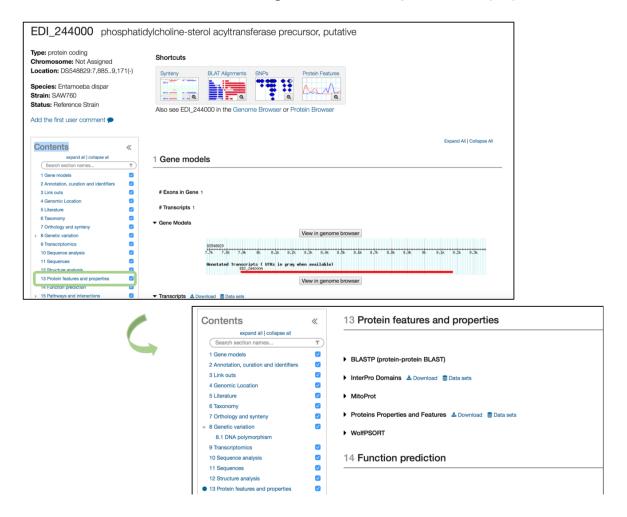
Running BLASTP (protein-protein BLAST) from gene record pages.

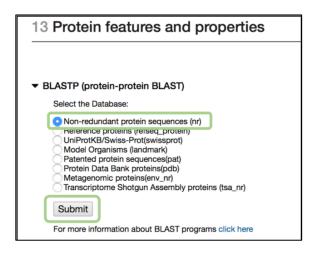
BlastP finds regions of similarity between protein sequences by comparing sequences in FASTA to various sequence databases and then calculating the statistical significance (E value).

NCBI BlastP can be accessed directly from the gene record pages. Below is a short overview of the how to perform protein-protein BLAST using non-redundant protein sequence database (nr).

- Navigate to a gene record page of your choice (e.g. EDI_244000 gene of Entamoeba dispar: http://amoebadb.org/amoeba/app/record/gene/EDI_244000)
- 2. Use the Contents menu to navigate to the Protein features and properties menu



3. Select one of the eight databases available (e.g. the non-redundant protein sequences (nr)) and click on the Submit button



A new tab will be opened automatically, and you will be redirected to the NCBI BlastP query page that will refresh automatically until the results are ready for display:

