

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).

1. **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**

EDI_244000 phosphatidylcholine-sterol acyltransferase precursor, putative

Type: protein coding
Chromosome: Not Assigned
Location: DS548829:7,885..9,171(-)
Species: Entamoeba dispar
Strain: SAW760
Status: Reference Strain

Add the first user comment

Shortcuts
Synteny BLAT Alignments SNPs Protein Features
Also see EDI_244000 in the Genome Browser or Protein Browser

Expand All | Collapse All

Contents
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Search section names...
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15 Pathways and interactions

1 Gene models

Exons in Gene 1
Transcripts 1

Gene Models

View in genome browser

7,7k 7,8k 8k 8,1k 8,2k 8,3k 8,4k 8,5k 8,6k 8,7k 8,8k 8,9k 9k 9,1k 9,2k 9,3k

Annotated Transcripts (UTRs in gray when available)

EDI_244000

View in genome browser

Transcripts Download Data sets



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13 Protein features and properties

- ▶ BLASTP (protein-protein BLAST)
- ▶ InterPro Domains Download Data sets
- ▶ MitoProt
- ▶ Proteins Properties and Features Download Data sets
- ▶ WolfPSORT

14 Function prediction

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

13 Protein features and properties

▼ BLASTP (protein-protein BLAST)

Select the Database:

- ☒ Non-redundant protein sequences (nr)
- ☐ Reference proteins (refseq_protein)
- ☐ UniProtKB/Swiss-Prot (swissprot)
- ☐ Model Organisms (landmark)
- ☐ Patented protein sequences (pat)
- ☐ Protein Data Bank proteins (pdb)
- ☐ Metagenomic proteins (env_nr)
- ☐ Transcriptome Shotgun Assembly proteins (tsa_nr)

For more information about BLAST programs [click here](#)

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:

Job title: Protein Sequence (428 letters)

RID: VERH2M3Z014 (Expires on 10-06 20:51 pm)

Query ID: lcl|Query_110981

Description: None

Molecule type: amino acid

Query Length: 428

Database Name: nr

Description: All non-redundant GenBank CDS translations+PDB+SwissProt+PIR+PRF excluding environmental samples from WGS projects

Program: BLASTP 2.8.1+ > [Citation](#)

Other reports: > [Search Summary](#) [Taxonomy reports](#) [Distance tree of results](#) [Multiple alignment](#) [MSA viewer](#)

[New](#) Analyze your query with [SmartBLAST](#)

Graphic Summary

Distribution of the top 100 Blast Hits on 100 subject sequences

Mouse over to see the title, click to show alignments

Color key for alignment scores

- <40
- 40-50
- 50-80
- 80-200
- >=200

Query

1 80 160 240 320 400

Descriptions

Sequences producing significant alignments:

Select: All None Selected:0

Alignments [Download](#) [GenPept](#) [Graphics](#) [Distance tree of results](#) [Multiple alignment](#)

Description	Max score	Total score	Query cover	E value	Ident	Accession
<input type="checkbox"/> phosphatidylcholine-sterol acyltransferase precursor [Entamoeba dispar SAW760]	881	881	100%	0.0	100%	XP_001738413.1
<input type="checkbox"/> phosphatidylcholine-sterol acyltransferase precursor, putative [Entamoeba histolytica KU27]	784	784	96%	0.0	91%	EMD46408.1
<input type="checkbox"/> lecithin:cholesterol acyltransferase, putative [Entamoeba histolytica HM-1:IMSS]	781	781	96%	0.0	91%	XP_654285.1
<input type="checkbox"/> phosphatidylcholine-sterol acyltransferase precursor [Entamoeba dispar SAW760]	758	758	94%	0.0	88%	XP_001739607.1
<input type="checkbox"/> Lecithin:cholesterol acyltransferase, putative [Entamoeba histolytica HM-1:IMSS]	723	723	94%	0.0	83%	XP_652402.1
<input type="checkbox"/> phosphatidylcholine-sterol acyltransferase precursor, putative [Entamoeba histolytica KU27]	720	720	87%	0.0	90%	EMD46516.1
<input type="checkbox"/> 1-o-acylceramide synthase precursor, putative [Entamoeba histolytica]	692	692	84%	0.0	92%	GAT97589.1
<input type="checkbox"/> 1-O-acylceramide synthase precursor, putative [Entamoeba histolytica HM-1:IMSS]	681	681	82%	0.0	92%	XP_001913972.1
<input type="checkbox"/> Lecithin:cholesterol acyltransferase, putative [Entamoeba nutalli P19]	549	549	72%	0.0	81%	XP_00860555.1