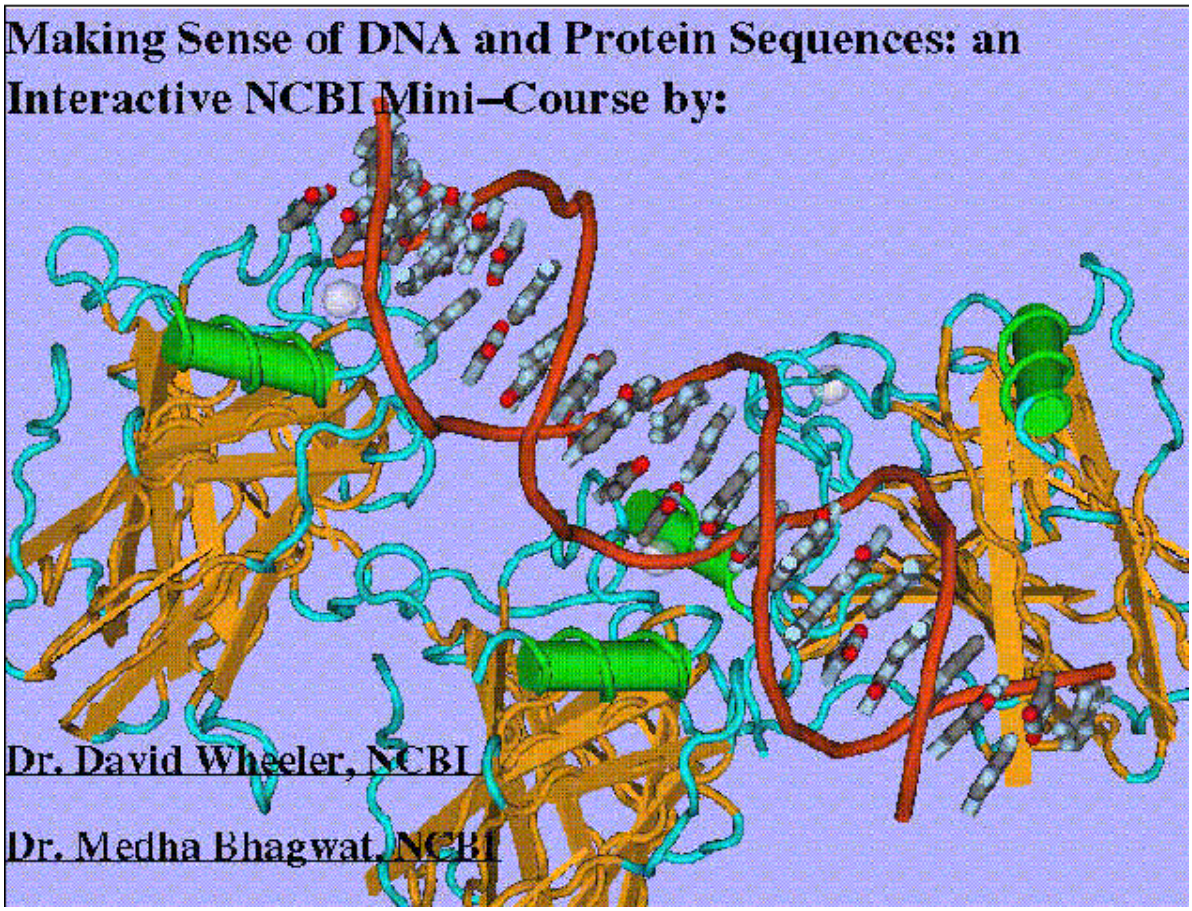
Making Sense of DNA and Protein Sequences: an Interactive NCBI Mini–Course by:



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Introduction:

In this course (http://www.ncbi.nlm.nih.gov/Class/minicourses/), we will first try to make sense of the DNA sequence by determining whether it codes for a protein. If it does, then we will use this protein sequence to search for the presence of any motifs or structural domains present in it and also to predict its function. Finally, we will map the protein sequence onto the structure of a protein with similar sequence.

We recommend beginning with the uncharacterized *Drosophila melanogaster* genomic sequence from the GenBank record AE003584 found in the first electronic notebook, however, you can use another uncharacterized *Drosophila melanogaster* genomic sequence by choosing another notebook from the list below.

Electronic Notebook for Protein Sequence Analysis

The electronic notebook is a tutorial and analysis web-form consisting of a set of links to protein analysis tools combined with areas into which results and personal notes can be recorded. All the analysis tools open into a second "tools" window from which the results of an analysis can be pasted into the electronic notebook. The "Cheat now!" links open a third window in which a complete set of results have already been recorded. The electronic notebook can also be used to analyze a new DNA sequence by substituting the new sequence the original sequence found in the DNA sequence text area. The electronic notebooks used in this course are publicly accessible over the internet.

URLs Used:

1. **Class Page:** http://www.ncbi.nlm.nih.gov/Class/minicourses/
2. **GenScan:** http://genes.mit.edu/GENSCAN.html
3. **ScanProsite:** http://www.expasy.org/tools/scanprosite/
4. **BLASTP:** http://www.ncbi.nlm.nih.gov/BLAST
5. **COGs:** http://www.ncbi.nlm.nih.gov/COG/old/
6. **MultAlin:** http://prodes.toulouse.inra.fr/multalin/multalin.html
7. **CDD:** http://www.ncbi.nlm.nih.gov/Structure/cdd/wrpsb.cgi

NoteBooks:

http://www.ncbi.nlm.nih.gov/Class/minicourses/x1a.html
http://www.ncbi.nlm.nih.gov/Class/minicourses/x2a.html

Outline

Making Sense of DNA and Protein Sequences
Eukaryotic DNA query (Drosophila genome)
Predict coding region/exons (GenScan)
Obtain protein product (GenScan)
Identify motif/site (ScanProsite)
Search for similar sequences (BLASTp)
Predict function (COG)
Perform multiple sequence alignment (Multalin)
Obtain 3-D structural template (CDD)

To identify any exons in the DNA sequence and generate a predicted protein sequence, click here:

GenScan

Paste your DNA sequence into the GenScan input window. Press the *"Run Genscan"* button. Select the protein translation with the highest exon P–values and paste this FASTA formatted output into your notebook.

Protein Sequence from Genscan

The New GENSCAN Web Server at MIT

Identification of complete gene structures in genomic DNA

```
                \\|//
                (o o)
-. .-.   .-oOOo~(_)~oOOo-.   .-. .-.   .-. .-.   .-. .-.   .-. .-.   .-. .-.   .-. .-.   .-. .-.   .-
||X|||\ /|||X|||\ /|||X|||\ /|||X|||\ /|||X|||\ /|||X|||\ /|||X|||\ /|||X|||\ /|||X|||\ /|||X|||\ /||
|/ \|||X|||/ \|||X|||/ \|||X|||/ \|||X|||/ \|||X|||/ \|||X|||/ \|||X|||/ \|||X|||/ \|||X|||/ \|||X|||/
'   `-' `-'   `-' `-'   `-' `-'   `-' `-'   `-' `-'   `-' `-'   `-' `-'   `-' `-'   `-' `-'   `-' `-'
```

For information about Genscan, click here

This server provides access to the program Genscan for predicting the locations and exon-intron structures of genes in genomic sequences from a variety of organisms.

This server can accept sequences up to 1 million base pairs (1 Mbp) in length. If you have trouble with the web server or if you have a large number of sequences to process, request a local copy of the program (see instructions at the bottom of this page) or use the GENSCAN email server. If your browser (*e.g.*, Lynx) does not support file upload or multipart forms, use the older version.

Organism: Vertebrate Suboptimal exon cutoff (optional): 1.00

Sequence name (optional):

Print options: Predicted peptides only

Upload your DNA sequence file (one-letter code, upper or lower case, spaces/numbers ignored):

Browse...

Or paste your DNA sequence here (one-letter code, upper or lower case, spaces/numbers ignored):

```
   239041 gctcctgtct gaacgatcca gcgcgatgtt gatcaccgcc ttgttgtcat
catccacaat
   239101 gatggtgacg ttgacatggg ttttgttgcc gtaattgagg cgcctgaagt
ggaagtccct
   239161 atgcagaaac ttcggatgga tgttgcactc cagatgctga ttgctaaaac
gaaagctgcc
   239221 aaagctcagg accatggctt ggatgactcc cgaagctccc gctcgaataa
gattgtggca
   239281 gccctgtttc tccaacgtta gcatccacga cgtaaccagg gagttaagct
gctgaagatt
   239341 agacatctcg cgccaaagat tctccgcctg cagagtgtga tacgaatcgt
agcagccttc
```

To have the results mailed to you, enter your email address here (optional):

Run GENSCAN Clear Input

GENSCAN 1.0 Date run: 3-May-107 Time: 10:10:48

Sequence 10:10:45 : 5100 bp : 46.29% C+G : Isochore 2 (43 - 51 C+G%)

Parameter matrix: HumanIso.smat

Predicted genes/exons:

Gn.Ex	Type	S	.Begin	...End	.Len	Fr	Ph	I/Ac	Do/T	CodRg	P....	Tscr..
1.01	Sngl	+	27	458	432	2	0	48	49	383	0.447	24.68
1.02	PlyA	+	489	494	6							1.05
2.00	Prom	+	830	869	40							-6.86
2.01	Init	+	1002	1069	68	2	2	53	89	83	0.970	3.88
2.02	Intr	+	2549	2708	160	2	1	72	105	284	0.980	28.49
2.03	Intr	+	2771	2872	102	1	0	10	86	251	0.999	17.47
2.04	Intr	+	2935	3183	249	0	0	73	100	586	0.999	55.93
2.05	Term	+	3253	3948	696	0	0	90	49	1324	0.999	122.25
2.06	PlyA	+	4120	4125	6							1.05
3.04	PlyA	-	4162	4157	6							-0.45
3.03	Term	-	4448	4261	188	0	2	37	42	95	0.922	-2.55
3.02	Intr	-	4635	4511	125	2	2	44	90	91	0.949	5.13
3.01	Init	-	5046	4694	353	0	2	66	43	485	0.897	38.43

Click here to view a PDF image of the predicted gene(s)

Click here for a PostScript image of the predicted gene(s)

Predicted peptide sequence(s):

```
>10:10:45|GENSCAN_predicted_peptide_1|143_aa
MPRTLPWTTVFTAVASSARAKSMEKLTVVFLLRMHSALVVSQPSMATRVNLPVFDPQSLN
SRAPAKTTSAAQAITAYLSIFFHLIELQGKRIGWLFRWLSPLSASSQRYESTKSGESPKT
TQSFRMNGKQLRAATQKKAFFDD

>10:10:45|GENSCAN_predicted_peptide_2|424_aa
MSQICKRGLLISNRLAPAALRCKSTWFSEVQMGPPDAILGVTEAFKKDTNPKKINLGAGA
YRDDNTQPFVLPSVREAEKRVVSRSLDKEYATIIGIPEFYNKAIELALGKGSKRLAAKHN
VTAQSISGTGALRIGAAFLAKFWQGNREIYIPSPSWGNHVAIFEHAGLPVNRYRYYDKDT
CALDFGGLIEDLKKIPEKSIVLLHACAHNPTGVDPTLEQWREISALVKKRNLYPFIDMAY
QGFATGDIDRDAQAVRTFEADGHDFCLAQSFAKNMGLYGERAGAFTVLCSDEEEAARVMS
QVKILIRGLYSNPPVHGARIAAEILNNEDLRAQWLKDVKLMADRIIDVRTKLKDNLIKLG
SSQNWDHIVNQIGMFCFTGLKPEQVQKLIKDHSVYLTNDGRVSMAGVTSKNVEYLAESIH
KVTK

>10:10:45|GENSCAN_predicted_peptide_3|221_aa
MSNLQQLNSLVTSWMLTLEKQGCHNLIRAGASGVIQAMVLSFGSFRFSNQHLECNIHPKF
LHRDFHFRRLNYGNKTHVNVTIIVDDDNKAVINIALDRSDRSYYACDGGCLDEPVLLTQN
RRQFPVKLTEPLTAILYITEDKQHMEELHHAIHVKEVVEAPAHEQHLIALHRHGHQLGGL
PTLFWVSVCAIIIVFHIFLCKLIIKEYCEPSDKLRYRYNKP
```

To scan the protein sequence for the occurrence of motifs/patterns found in the PROSITE database, use:

ScanProsite

Paste the raw (leave off the fasta defline) protein sequence from GenScan into the ScanProsite input box, choose to ***Exclude patterns with a high probability of occurrence***, and press the ***"Start the Scan"*** button. Paste the ScanProsite hit into your notebook. To see the Prosite summary for the hit, click on the PDOCxxxx number.

Hit from ScanProsite

Prosite pattern

Prosite Summary

Home | ScanProsite | ProRule | Documents | Downloads | Links

ScanProsite

The ScanProsite tool [Help / Commercial users] allows to scan protein sequence(s) (either from UniProt Knowledgebase (Swiss-Prot/TrEMBL) or PDB or provided by the user) for the occurrence of patterns, profiles and rules (motifs) stored in the PROSITE database, or to search protein database(s) for hits by specific motif(s) [Reference / Download ps_scan, the standalone version]. The program PRATT can be used to generate your own patterns. You may either:

- Enter one or more PROSITE accession numbers and/or patterns [1 by line] to search the UniProt Knowledgebase (Swiss-Prot/TrEMBL) and/or PDB databases, **OR**
- Enter one or more sequences [raw, Swiss-Prot or fasta format] and/or UniProt Knowledgebase (Swiss-Prot/TrEMBL) accession numbers and/or PDB accession numbers [1 by line] to be scanned with all patterns, profiles, rules in PROSITE, **OR**
- Fill in both fields to find all occurrences of specified motifs in specified sequences.

Protein(s) to be scanned:

Enter one or more Swiss-Prot/TrEMBL accession number(s) [AC] (e.g. **P00747**) and/or sequence identifier(s) [ID] (e.g. **ENTK_HUMAN**), and/or PDB identifier, and/or paste **your own protein sequence(s)** in the box below:
(leave this box blank to scan PROSITE entrie(s) against selected protein databases)

```
MSQICKRGLLISNRLAPAALRCKSTWFSEVQMGPPDAILGVT
YRDDNTQPFVLPSVREAEKRVVSRSLDKEYATIIGIPEFYNK
VTAQSISGTGALRIGAAFLAKFWQGNREIYIPSPSWGNHVAI
CALDFGGLIEDLKKIPEKSIVLLHACAHNPTGVDPTLEQWRE
QGFATGDIDRDAQAVRTFEADGHDFCLAQSFAKNMGLYGERA
QVKILIRGLYSNPPVHGARIAAEILNNEDLRAQWLKDVKLMA
SSQNWDHIVNQIGMFCFTGLKPEQVQKLIKDHSVYLTNDGRV
KVTK
```

Clear

General options:

- [x] Exclude motifs with a high probability of occurrence
- [ ] Show low level score
- [ ] Do not scan profiles [User Manual]

Show only sequences with at least [ ] hit(s)
Maximum of matched sequences [1000]
Output format [Graphic rich view]
[ ] Retrieve complete sequences
Your e-mail (optional): [ ] (will send results by e-mail)

START THE SCAN | reset

PROSITE pattern(s)/profile(s) to scan for:

Enter one or more PROSITE accession number(s) (e.g. **PS50240**), and/or identifier(s) (e.g. **CHEB**), and/or type **your pattern(s)** in PROSITE format in the box below:
(leave this box blank to scan sequence(s) against the entire PROSITE database)

and specify your search limits (only used if no protein data specified) **:**

- **Protein database(s):** [x] Swiss-Prot [ ] TrEMBL [ ] PDB databases
  [x] including splice variants
  randomize databases [no] (only with patterns, see help)
- Taxonomic lineage (OC) / species (OS) filter: [ ]
  (see NEWT Taxonomy ; separate multiple taxa/species with a semicolon, e.g. *Eukaryota; Escherichia coli;* . Does not work on PDB sequences.)
- Description (DE) filter: [ ] e.g. *protease*

pattern options:

Allow at most [1] X sequence characters to match a conserved position in the pattern
match mode [greedy, overlaps, no includes] (for patterns, see help)

Home ScanProsite ProRule Do

ScanProsite Results Viewer

This view shows ScanProsite results together with ProRule-based predicted intra-domain features (help).

Hits for all PROSITE (release 20.10) motifs on sequence 10-10-45-GENSCAN_predicted_peptide_2-424_aa :

found: 1 hit in 1 sequence

10-10-45-GENSCAN_predicted_peptide_2-424_aa (424 aa)

```
MSQICKRGLLISNRLAPAALRCKSTWFSEVQMGPPDAILGVTEAFKKDTNPKKINLGAGAYRDDNT
QPFVLPSVREAEKRVVSRSLDKEYATIIGIPEFYNKAIELALGKGSKRLAAKHNVTAQSISGTGAL
RIGAAFLAKFWQGNREIYIPSPSWGNHVAIFEHAGLPVNRYRYYDKDTCALDFGGLIEDLKKIPEK
SIVLLHACAHNPTGVDPTLEQWREISALVKKRNLYPFIDMAYQGFATGDIDRDAQAVRTFEADGHD
FCLAQSFAKNMGLYGERAGAFTVLCSDEEEAARVMSQVKILIRGLYSNPPVHGARIAAEILNNEDL
RAQWLKDVKLMADRIIDVRTKLKDNLIKLGSSQNWDHIVNQIGMFCFTGLKPEQVQKLIKDHSVYL
TNDGRVSMAGVTSKNVEYLAESIHKVTK
```

ruler: 1 100 200 300 400 500 600 700 800 900 10

hits by patterns: [1 hit (by 1 pattern) on 1 sequence]

Hits by PS00105 **AA_TRANSFER_CLASS_1** *Aminotransferases class-I pyridoxal-phosphate attachment site* :

10-10-45-GENS~ (424 aa)

270 - 283: SFAKnmGLyGERAG

Legend:

disulfide bridge active site other 'ranges' other sites

horizontal scaling: 0.6

do not show text labels:

do not show sites in hits:

do not show ranges in hits:

redisplay

Aminotransferases class-I pyridoxal-phosphate attachment site

Description:

Aminotransferases share certain mechanistic features with other pyridoxal-phosphate dependent enzymes, such as the covalent binding of the pyridoxal-phosphate group to a lysine residue. On the basis of sequence similarity, these various enzymes can be grouped [1,2] into subfamilies. One of these, called class-I, currently consists of the following enzymes:

- Aspartate aminotransferase (AAT) (EC 2.6.1.1). AAT catalyzes the reversible transfer of the amino group from L-aspartate to 2-oxoglutarate to form oxaloacetate and L-glutamate. In eukaryotes, there are two AAT isozymes: one is located in the mitochondrial matrix, the second is cytoplasmic. In prokaryotes, only one form of AAT is found (gene aspC).
- Tyrosine aminotransferase (EC 2.6.1.5) which catalyzes the first step in tyrosine catabolism by reversibly transferring its amino group to 2- oxoglutarate to form 4-hydroxyphenylpyruvate and L-glutamate.
- Aromatic aminotransferase (EC 2.6.1.57) involved in the synthesis of Phe, Tyr, Asp and Leu (gene tyrB).
- 1-aminocyclopropane-1-carboxylate synthase (EC 4.4.1.14) (ACC synthase) from plants. ACC synthase catalyzes the first step in ethylene biosynthesis.
- Pseudomonas denitrificans cobC, which is involved in cobalamin biosynthesis.
- Yeast hypothetical protein YJL060w.

The sequence around the pyridoxal-phosphate attachment site of this class of enzyme is sufficiently conserved to allow the creation of a specific pattern.

Last update:
April 2006 / Pattern and text revised.

Technical section:

PROSITE method (with tools and information) covered by this documentation:

AA_TRANSFER_CLASS_1, PS00105; **Aminotransferases class-I pyridoxal-phosphate attachment site** (PATTERN)

Consensus pattern:	**[GS] - [LIVMFYTAC] - [GSTA] - K - x(2) - [GSALVN] - [LIVMFA] - x - [GNAR] - {V} - R - [LIVMA] - [GA]** *K is the pyridoxal-P attachment site*
Sequences known to belong to this class detected by the pattern:	ALL
Other sequence(s) detected in Swiss-Prot:	1

BLAST

Home | Recent Results | Saved Strategies | Help

Basic Local Alignment Search Tool

NCBI/ BLAST/ blastp suite: BLASTP programs search protein databases using a protein query. more...

Enter Query Sequence

Enter accession number, gi, or FASTA sequence Clear

Query subrange

From

To

Or, upload file Browse...

Job Title

Enter a descriptive title for your BLAST search

Choose Search Set

Database Non-redundant protein sequences (nr)

Organism
Optional

Any Human *A.thaliana* Mouse Custom...

Search only sequences from selected organism

Entrez Query
Optional

Enter an Entrez query to limit search

Program Selection

Algorithm

blastp (protein-protein BLAST)

PSI-BLAST (Position-Specific Iterated BLAST)

PHI-BLAST (Pattern Hit Initiated BLAST)

Choose a BLAST algorithm

BLAST Search database nr using Blastp (protein-protein BLAST)

Show results in a new window

BLAST

Home | Recent Results | Saved Strategies | Help

Basic Local Alignment Search Tool

NCBI/ BLAST/ blastp suite: BLASTP programs search protein databases using a protein query. more...

Enter Query Sequence

Enter accession number, gi, or FASTA sequence — Clear

```
QGFATGDIDRDAQAVRTFEADGHDFCLAQSFAKNMGLYGERAGAFTVLCSDEEEAARVMS
QVKILIRGLYSNPPVHGARIAAEILNNEDLRAQWLKDVKLMADRIIDVRTKLKDNLIKLG
SSQNWDHIVNQIGMFCFTGLKPEQVQKLIKDHSVYLINDGRVSMAGVTSKNVEYLAESIH
KVTK
```

Query subrange — From — To

Or, upload file — Browse...

Job Title: 10:10:45|GENSCAN_predicted_peptide_2|424_aa

Enter a descriptive title for your BLAST search

Choose Search Set

Database: Swissprot protein sequences(swissprot)

Organism (Optional): Any | Human | *A.thaliana* | Mouse | Custom...

Search only sequences from selected organism

Entrez Query (Optional)

Enter an Entrez query to limit search

Program Selection

Algorithm:
- blastp (protein-protein BLAST)
- PSI-BLAST (Position-Specific Iterated BLAST)
- PHI-BLAST (Pattern Hit Initiated BLAST)

Choose a BLAST algorithm

BLAST — Search database swissprot using Blastp (protein-protein BLAST)

Show results in a new window

BLAST

Home | Recent Results | Saved Strategies | Help

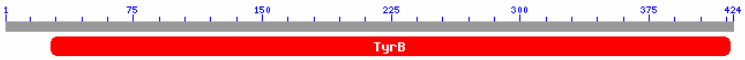
Basic Local Alignment Search Tool

My NCBI [Sign In] [Register]

NCBI/ BLAST/ Formatting Results - 43SPBAJ7012 [Formatting options]

Job Title: 10:59:58|GENSCAN_predicted_peptide_2|424_aa

Putative conserved domains have been detected, click on the image below for detailed results.



WAITING

Request ID	43SPBAJ7012
Status	Searching
Submitted at	Wed May 9 11:03:39 2007
Current time	Wed May 9 11:03:43 2007
Time since submission	00:00:04

This page will be automatically updated in **11** seconds until search is done

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NCBI | NLM | NIH | DHHS

BLAST

Home | Recent Results | Saved Strategies | Help

Basic Local Alignment Search Tool

NCBI/ BLAST/ Format Request

Query 10:10:45|GENSCAN_predicted_peptide_2|424_aa(424 letters)

Database swissprot

Job title 10:10:45|GENSCAN_predicted_peptide_2|424_aa

Request ID 2YTGEAWD015 View report Show results in a new window

Format

Show Alignment as HTML Advanced View Reset form to defaults

Alignment View Flat query-anchored with letters for identities

Display Graphical Overview Linkout Sequence Retrieval NCBI-gi

Masking Character: Lower Case Masking Color: Grey

Limit results Descriptions: 100 Graphical overview: 100 Alignments: 100

Entrez query:

Organism Type common name, binomial, taxid, or group name. Only 20 top taxa will be shown.

Expect Min: 0 Expect Max: 10

Format for PSI-BLAST with inclusion threshold: 0.001

Job Title: 10:59:58|GENSCAN_predicted_peptide_2|424_aa

▶ Show Conserved Domains

BLASTP 2.2.16 [Mar-25-2007]

Reference:
Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schäffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

RID: 43SPBAJ7012

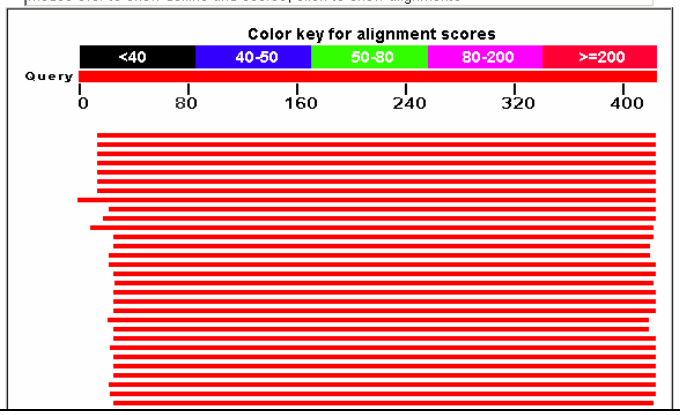
Database: Non-redundant SwissProt sequences
243,474 sequences; 91,728,505 total letters

If you have any problems or questions with the results of this search please refer to the **BLAST FAQs**
Taxonomy reports

Query= 10:59:58|GENSCAN_predicted_peptide_2|424_aa
Length=424

Distribution of 71 Blast Hits on the Query Sequence

Mouse-over to show defline and scores, click to show alignments



Distance tree of results NEW

Sequences producing significant alignments:	Score (Bits)	E Value	
gi|75042478|sp|Q5REB0|AATM PONPY Aspartate aminotransferase, ...	545	2e-154	
gi|112983|sp|P00505|AATM HUMAN Aspartate aminotransferase, mi...	543	4e-154	G
gi|112984|sp|P05202|AATM MOUSE Aspartate aminotransferase, mi...	543	5e-154	G
gi|112987|sp|P00507|AATM RAT Aspartate aminotransferase, mito...	543	6e-154	G
gi|75075926|sp|Q4R559|AATM MACFA Aspartate aminotransferase, ...	542	1e-153	
gi|112985|sp|P00506|AATM PIG Aspartate aminotransferase, mito...	538	2e-152	G
gi|1168261|sp|P12344|AATM BOVIN Aspartate aminotransferase, m...	536	5e-152	G
gi|112981|sp|P00508|AATM CHICK Aspartate aminotransferase, mi...	532	9e-151	G
gi|112982|sp|P08907|AATM HORSE Aspartate aminotransferase, mi...	532	1e-150	
gi|1168256|sp|P46643|AAT1 ARATH Aspartate aminotransferase, m...	429	1e-119	G
gi|2506178|sp|P28011|AAT1 MEDSA Aspartate aminotransferase 1 (Tr	418	2e-116	
gi|1168258|sp|P46644|AAT3 ARATH Aspartate aminotransferase, c...	405	2e-112	G
gi|21542386|sp|P46645|AAT2 ARATH Aspartate aminotransferase, ...	405	2e-112	G
gi|112972|sp|P28734|AATC DAUCA Aspartate aminotransferase, cytop	404	3e-112	
gi|584706|sp|P37833|AATC ORYSA Aspartate aminotransferase, cytop	401	3e-111	
gi|112971|sp|P00504|AATC CHICK Aspartate aminotransferase, cy...	390	7e-108	G
gi|21542387|sp|P46646|AAT4 ARATH Aspartate aminotransferase, ...	387	3e-107	G
gi|75041219|sp|Q5R691|AATC PONPY Aspartate aminotransferase, ...	387	4e-107	
gi|75076072|sp|Q4R5L1|AATC MACFA Aspartate aminotransferase, ...	386	1e-106	
gi|5902703|sp|P17174|AATC HUMAN Aspartate aminotransferase, c...	385	1e-106	G
gi|20532373|sp|P46248|AAT5 ARATH Aspartate aminotransferase, ...	381	2e-105	G
gi|112979|sp|P26563|AATM LUPAN Aspartate aminotransferase-P2,...	381	3e-105	
gi|112976|sp|P00503|AATC PIG Aspartate aminotransferase, cyto...	380	7e-105	G
gi|122065118|sp|P13221|AATC RAT Aspartate aminotransferase, c...	378	2e-104	G
gi|126302508|sp|P08906|AATC HORSE Aspartate aminotransferase,...	377	4e-104	
gi|122065117|sp|P33097|AATC BOVIN Aspartate aminotransferase,...	377	4e-104	G
gi|112975|sp|P05201|AATC MOUSE Aspartate aminotransferase, cy...	377	6e-104	G
gi|1703040|sp|P23542|AATC YEAST Aspartate aminotransferase, cyto	352	1e-96	G
gi|2492843|sp|Q22067|AATC CAEEL Probable aspartate aminotrans...	337	7e-92	G
gi|1168262|sp|P44425|AAT HAEIN Aspartate aminotransferase (Trans	333	1e-90	
gi|12230871|sp|P72173|AAT PSEAE Aspartate aminotransferase (Tran	325	2e-88	
gi|112989|sp|P00509|AAT ECOLI Aspartate aminotransferase (Transa	322	2e-87	
gi|17433702|sp|Q56114|AAT SALTI Aspartate aminotransferase (Tran	317	7e-86	
gi|20137200|sp|P58661|AAT SALTY Aspartate aminotransferase (Tran	316	1e-85	
gi|20141944|sp|P74861|TYRB SALTY Aromatic-amino-acid aminotransf	278	4e-74	
gi|12230956|sp|P43336|PHHC PSEAE Aromatic-amino-acid aminotransf	278	4e-74	
gi|136593|sp|P04693|TYRB ECOLI Aromatic-amino-acid aminotransfer	277	5e-74	
gi|83300284|sp|Q01802|AATM YEAST Aspartate aminotransferase, ...	264	4e-70	G
gi|6136085|sp|P95468|TYRB PARDE Aromatic-amino-acid aminotransfe	261	4e-69	
gi|399090|sp|Q02636|ATTY RHIME Tyrosine aminotransferase (L-t...	218	5e-56	
gi|112986|sp|P12345|AATM RABIT Aspartate aminotransferase, mi...	51.6	6e-06	
gi|6224986|sp|O67781|AAT AQUAE Aspartate aminotransferase (Trans	50.1	2e-05	
gi|3183545|sp|P16524|PATA BACSU Putative aminotransferase A	44.3	0.001	
gi|14285338|sp|Q9V0L2|AAT PYRAE Aspartate aminotransferase (Tran	43.9	0.001	
gi|74519992|sp|Q5V4K3|HIS8 HALMA Histidinol-phosphate aminotr...	41.2	0.008	
gi|14285336|sp|O58489|AAT PYRHO Aspartate aminotransferase (Tran	39.3	0.030	
gi|76364069|sp|Q4J8X2|AAT SULAC Aspartate aminotransferase (Tran	38.9	0.039	
gi|14285339|sp|Q9X0Y2|AAT THEMA Aspartate aminotransferase (Tran	37.0	0.15	
gi|112988|sp|P23034|AAT BACYZ Aspartate aminotransferase (Transa	36.6	0.19	
gi|21759150|sp|O28277|HIS81 ARCFU Histidinol-phosphate aminot...	35.4	0.43	
gi|32129920|sp|Q9JUQ8|PUR9 NEIMA Bifunctional purine biosynth...	35.4	0.43	
gi|112990|sp|P14909|AAT SULSO Aspartate aminotransferase (Transa	35.0	0.56	

```
Q92UL7   166   ------KWLIINSP-SNPIGASINLLLLNIARVLKK                          195
O14209   179   ------KMIVINTP-HNPLGKIFSEEELNEIADLVLKHNLLVVSDEVY              219
O27624   165   ------TRLVFLCTPNNPTG---GLIDKKDIRAVLESTDTLVVVDEAYTEFAGVDNT---  212
Q8PDW1   273   ------V                                                       273

Query    251   ----DAQAVR------TFE---ADGH----D-FCL-AQ--SFAKNMGLYGERAGAFTVLC  289
Q5REB0   257   ----DAWAVR------HFI---EQGI----N-VCL-CQ--SYAKNMGLYGERVGAFTMVC  295
P00505   257   ----DAWAVR------HFI---EQGI----N-VCL-CQ--SYAKNMGLYGERVGAFTMVC  295
P05202   257   ----DAWAVR------HFI---EQGI----N-VCL-CQ--SYAKNMGLYGERVGAFTVVC  295
P00507   257   ----DAWAVR------HFI---EQGI----N-VCL-CQ--SYAKNMGLYGERVGAFTVVC  295
Q4R559   257   ----DAWAVR------HFI---EQGI----N-VCL-CQ--SYAKNMGLYGERVGAFTMVC  295
P00506   257   ----DAWAVR------HFI---EQGI----N-VCL-CQ--SYAKNMGLYGERVGAFTVVC  295
P12344   257   ----DAWAVR------HFI---EQGI----N-VCL-CQ--SYAKNMGLYGERVGAFTVVC  295
P00508   250   ----DAWALR------HFI---EQGI----D-VVL-SQ--SYAKNMGLYGERAGAFTVIC  288
P08907   228   ----DAWAVR------YFI---EQGI----N-VCL-CQ--SYAKNMGLYGERVGAFTMVC  266
P46643   255   ----DAKSIR------IFL---EDGH----H-IGI-SQ--SYAKNMGLYGQRVGCLSVLC  293
P28011   242   ----DAQPVR------LFV---ADGG----E-LLV-AQ--SYAKNMGLYGERVGALSIVS  280
P46644   273   ----DAKPIR------MFV---ADGG----E-CLV-AQ--SYAKNMGLYGERVGALSIVC  311
P46645   229   ----DAQSVR------TFV---ADGG----E-CLI-AQ--SYAKNMGLYGERVGALSIVC  267
P28734   229   ----DAQSVR------IFV---ADGG----E-CLA-AQ--SYAKNMGLYGERVGALSIVC  267
P37833   231   ----DAQSVR------MFV---ADGG----E-LLM-AQ--SYAKNMGLYGERVGALSIVC  269
P00504   236   ----DAWAVR------YFV---SEGF----E-LFC-AQ--SFSKNFGLYNERVGNLSVVG  274
P46646   227   ----DAQAVR------MFV---ADGG----E-CLI-AQ--SYAKNMGLYGERIGSLTIVC  265
Q5R691   237   ----DAWAIR------YFV---SEGF----E-FFC-AQ--SFSKNFGLYNERVGNLTVVG  275
Q4R5L1   237   ----DAWAIR------YFV---SEGF----E-FFC-AQ--SFSKNFGLYNERVGNLTVVG  275
P17174   237   ----DAWAIR------YFV---SEGF----E-FFC-AQ--SFSKNFGLYNERVGNLTVVG  275
P46248   276   ----DAASVR------LFA---ERGM----E-FFV-AQ--SYSKNLGLYAERIGAINVVC  314
P26563   277   ----DAASVR------LFV---ARGL----E-VLV-AQ--SYSKNLGLYAERIGAINVIS  315
P00503   237   ----DAWAIR------YFV---SEGF----E-LFC-AQ--SFSKNFGLYNERVGNLTVVA  275
P13221   237   ----DAWAIR------YFV---SEGF----E-LFC-AQ--SFSKNFGLYNERVGNLTVVG  275
P08906   237   ----DAWAVR------YFV---SEGF----E-LFC-AQ--SFSKNFGLYNERVGNLTVVA  275
P33097   237   ----DAWAIR------YFV---SEGF----E-LFC-AQ--SFSKNFGLYNERVGNLTVVA  275
P05201   237   ----DAWAIR------YFV---SEGF----E-LFC-AQ--SFSKNFGLYNERVGNLTVVG  275
P23542   230   ----DAYAVR------LGVEKLSTVS----P-VFV-CQ--SFAKNAGMYGERVGCFHLAL  271
Q22067   229   ----DAWAIR------YFV---DQGM----E-MVV-SQ--SFAKNFGLYNERVGNLTVVV  267
P44425   224   ----DAYGLR------AFA---ANHK----E-LLV-AS--SFSKNFGLYNERVGAFTLVA  262
P72173   226   ----DAAAVR------LFA---QSGL----S-FFV-SS--SFSKSFSLYGERVGALSIVT  264
P00509   224   ----DAEGLR------AFA---AMHK----E-LIV-AS--SYSKNFGLYNERVGACTLVA  262
Q56114   224   ----DAEGLR------AFA---ALHK----E-LIV-AS--SYSKNFGLYNERVGACTLVA  262
P58661   224   ----DAEGLR------AFA---ALHK----E-LIV-AS--SYSKNFGLYNERVGACTLVA  262
P74861   225   ----DAYVIR------AIA---SAGL----P-ALV-SN--SFSKIFSLYGERVGGLSVVC  263
P43336   225   ----DAWAVR------LFA---GELP----E-VLV-TS--SCSKNFGLYRDRVGALIVCA  263
P04693   225   ----DAYAIR------AIA---SAGL----P-ALV-SN--SFSKIFSLYGERVGGLSVMC  263
Q01802   258   ----DAYLLRLCLNVNKYP---NWSN----G-IFL-CQ--SFAKNMGLYGERVGSLSVIT  302
P95468   221   ----DAAGTR------LIA---SRIP----E-VLI-AA--SCSKNFGIYRERTGCLLALC  259
Q02636   220   ----DVAGLR------HLL---GVVP----E-ALV-AV--SCSKSFGLYRERAGAIFART  258
O67781   218   ----VSPASF------SDE---VKNI----T-FTV--N--AFSKSYSMTGWRIG--YVAC  253
P16524   210   ----PHYSIA------TYL---RD------Q-TIV-IN--GLSKSHSMTGWRIG        240
Q9V0L2   215   IASLDGMFER------TIT---VNG----------------FSKTFAMTGWRLG        243
Q5V4K3   200   ----EKPSKR------PLL---SDRD----D-VAL-LR--TFSKAYGLAGIRLG-YAVVP  237
O58489   214   ----DAKHYP------MIK---FAPE----N-TIL-AN--SFSKTFAMTGWRLG        246
Q4J8X2   222   ----SVLE----------D---PDWK----N-FSIYVN--GFSKTFSMTGWRLGYVVA--  255
Q9X0Y2   215   ----SILDV-------------SEGF----DRIVY-IN--GFSKSHSMTGWRVG---YLI  247
O28277   166   ----------------SFS---VDAE----N-VVI-AR--TFSKAFGLANLRIG        192
P14909   223   ----STLE----------D---SDWR----D-FLIYVN--GFSKTFSMTGWRLGYIVA--  256
P39643   215   ----DQKPAS------FLE---AEDA----K-TVG-AELYSFSKTFNMAGWRM-AFAV    252
Q9HQS0   202   ----TPSAVT------LFDGQPAGGHAPRDD-IAV-LR--TFSKAYGLAGIRLGYAVVPD  247
O28255   188   ----KIEMVR-------------DYN----N-LIV-LR--SFSKFFGLAGMRVG--YAVC  220
P72817   104   ----EGMA                                                      107
O27624   213   ----------------DLL---PDHE----N-LFI-LR--TFSKVMGLAGMRIG        239
Q8XLH3   156                                                   LFGDGAGA-TVLT  167

Query    290   SDEEE----AAR-------------VMSQVK--------ILIRGLYSNPPVHGARIAAEI  324
Q5REB0   296   KDADE----AKR-------------VESQLK--------ILIRPMYSNPPLNGARIAAAI  330
P00505   296   KDADE----AKR-------------VESQLK--------ILIRPMYSNPPLNGARIAAAI  330
P05202   296   KDADE----AKR-------------VESQLK--------ILIRPLYSNPPLNGARIAATI  330
```

COGs

Phylogenetic classification of proteins encoded in complete genomes

NCBI

Clusters of Orthologous Groups of proteins (COGs) were delineated by comparing protein sequences encoded in 43 complete
G consists of individual proteins or groups of paralogs from at least 3

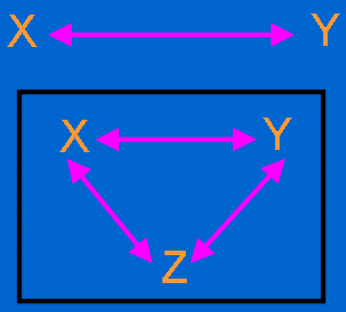
Code	Name	Proteins	in COGs
A	*Archaeoglobus fulgidus*	2420	1872
O	*Halobacterium sp. NRC-1*	2605	1701
M	*Methanococcus jannaschii*	1786	1330
	Methanobacterium thermoautotrophicum	1873	1388
P	*Thermoplasma acidophilum*	1482	1230
	Thermoplasma volcanium	1499	1243
K	*Pyrococcus horikoshii*	1800	1378
	Pyrococcus abyssi	1768	1456
Z	*Aeropyrum pernix*	1841	1178
Y	*Saccharomyces cerevisiae*	5955	2290
Q	*Aquifex aeolicus*	1560	1329
V	*Thermotoga maritima*	1858	1527
D	*Deinococcus radiodurans*	3187	2226
R	*Mycobacterium tuberculosis*	3927	2584
	Mycobacterium leprae	1605	1134
L	*Lactococcus lactis*	2267	1618
	Streptococcus pyogenes	1697	1211
B	*Bacillus subtilis*	4118	2870
	Bacillus halodurans	4066	2878
C	*Synechocystis*	3167	2159
E	*Escherichia coli K12*	4275	3414
	Escherichia coli O157	5315	3662
	Buchnera sp. APS	575	568
F	*Pseudomonas aeruginosa*	5567	4392
G	*Vibrio cholerae*	3835	2820
H	*Haemophilus influenzae*	1714	1542
	Pasteurella multocida	2015	1751

Help

COGnitor

Genome A
All proteins

Genome O
All proteins



NCBI

To search against the COGs database, click here:

COGs

Clusters of Orthologous Groups of proteins (COGs) were delineated by comparing protein sequences encoded in 43 complete genomes, representing 30 major phylogenetic lineages. Each COG consists of individual proteins or groups of paralogs from at least 3 lineages and thus corresponds to an ancient conserved domain. Use the COGnitor to compare the protein sequence to the COGs database.

Paste the FASTA formatted protein sequence from GenScan into the COGnitor input box and press the ***"compare to COGs"*** button. Click on the link to the highest-scoring COG and click on the disk icon to save the sequences in the COG to a local file on your desktop to be used as input to Multalin below. Drag this file from your desktop onto your "tools" browser window to display the sequences. Then copy and paste these into your notebook under "COGs FASTA Sequences".

COGs FASTA Sequences

Updated version

COGs

Phylogenetic classification of proteins encoded in complete genomes

Clusters of Orthologous Groups of proteins (COGs) were delineated by comparing protein sequences encoded in 43 complete gen
representing 30 major phylogenetic lineages. Each COG consists of individual proteins or groups of paralogs from at least 3 lineages
corresponds to an ancient conserved domain.

Science 1997 Oct 24;278(5338):631-7,
Nucleic Acids Res 2001 Jan 1; 29(1):22-28.

Help

COGnitor

Protein/Gene name:

Text search:

Code	Name	Proteins	in COGs
A	*Archaeoglobus fulgidus*	2420	1872
O	*Halobacterium sp. NRC-1*	2605	1701
M	*Methanococcus jannaschii*	1786	1330
	Methanobacterium thermoautotrophicum	1873	1388
P	*Thermoplasma acidophilum*	1482	1230
	Thermoplasma volcanium	1499	1243
K	*Pyrococcus horikoshii*	1800	1378
	Pyrococcus abyssi	1768	1456
Z	*Aeropyrum pernix*	1841	1178
Y	*Saccharomyces cerevisiae*	5955	2290
Q	*Aquifex aeolicus*	1560	1329
V	*Thermotoga maritima*	1858	1527
D	*Deinococcus radiodurans*	3187	2226
R	*Mycobacterium tuberculosis*	3927	2585
	Mycobacterium leprae	1605	1134
L	*Lactococcus lactis*	2267	1618
	Streptococcus pyogenes	1697	1211
B	*Bacillus subtilis*	4118	2870
	Bacillus halodurans	4066	2878
C	*Synechocystis*	3167	2159

Principal component analysis of genomes

List of COGs

Distribution

Co-occurrences

Phylogenetic patterns

Phylogenetic patterns search

Functional categories

J K L

D O M N P T

G C E F H I Q

R S

Pathways and functional systems

FTP

COGnitor

Compare your sequence to COG database

NCBI

compare to COGs | Clear | BeTs to 3 clades

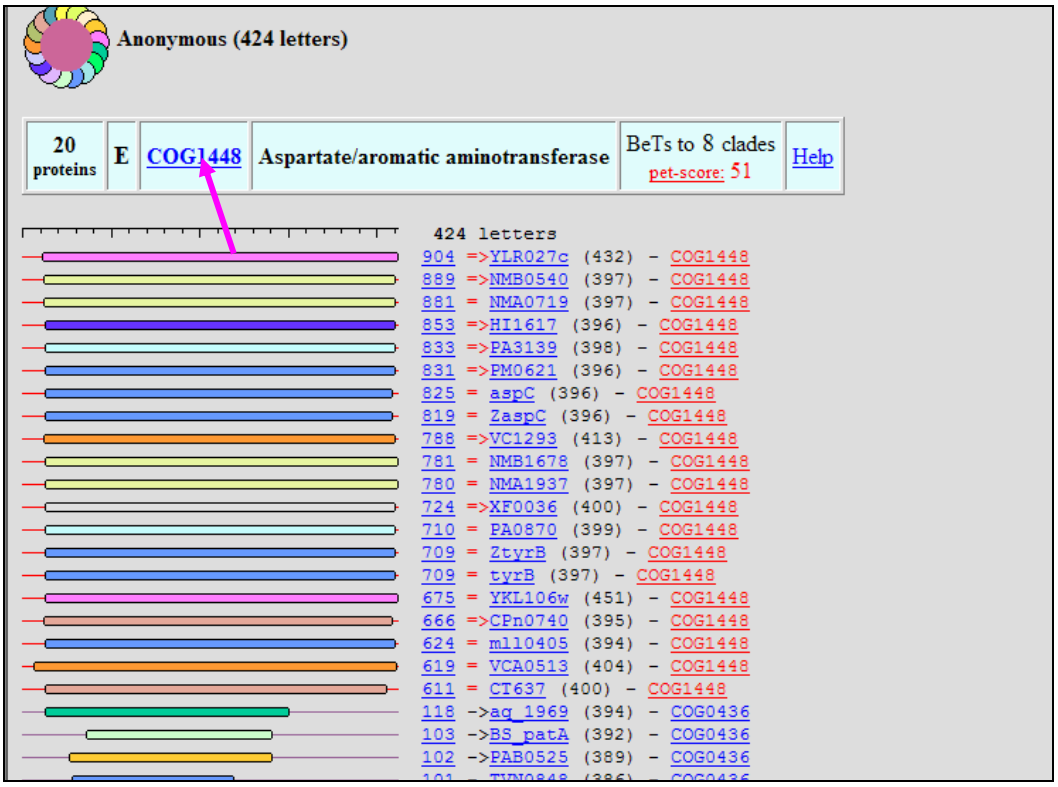
Help

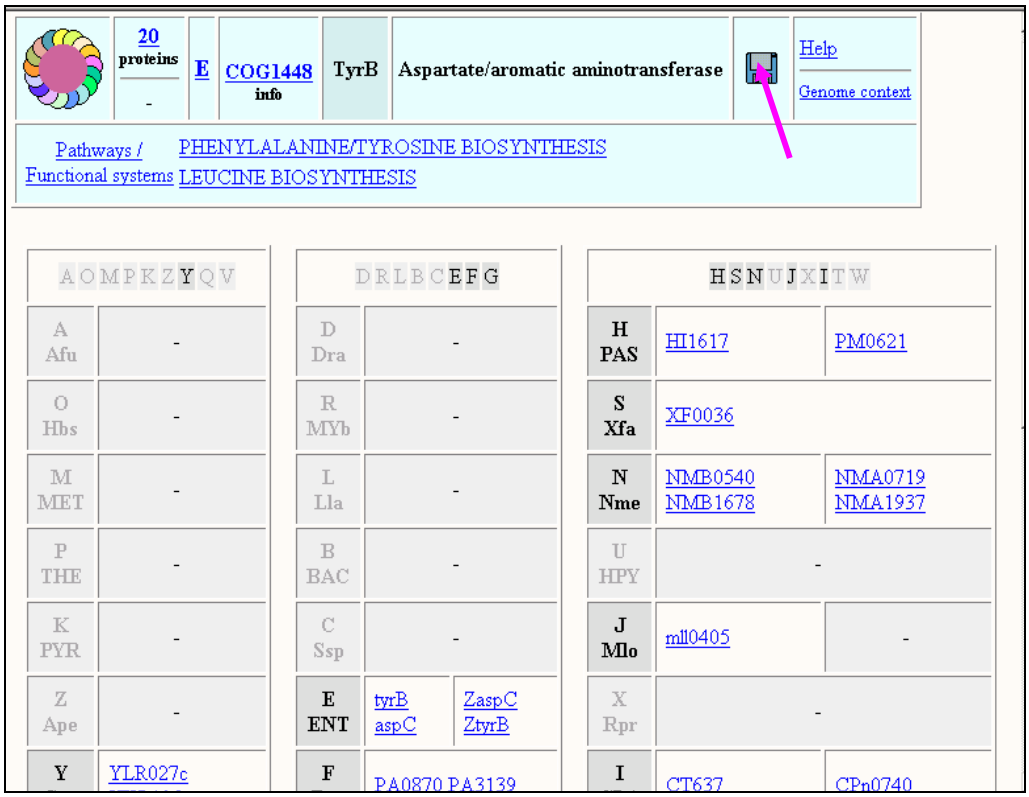
Example

Paste your sequence and press the button above.

```
MSQICKRGLLISNRLAPAALRCKSTWFSEVQMGPPDAILGVTEAFKKDTNPKKINLGAGA
YRDDNTQPFVLPSVREAEKRVVSRSLDKEYATIIGIPEFYNKAIELALGKGSKRLAAKHN
VTAQSISGTGALRIGAAFLAKFWQGNREIYIPSPSWGNHVAIFEHAGLPVNRYRYYDKDT
CALDFGGLIEDLKKIPEKSIVLLHACAHNPTGVDPTLEQWREISALVKKRNLYPFIDMAY
QGFATGDIDRDAQAVRTFEADGHDFCLAQSFAKNMGLYGERAGAFTVLCSDEEEAARVMS
QVKILIRGLYSNPPVHGARIAAEILNNEDLRAQWLKDVKLMADRIIDVRTKLKDNLIKLG
SSQNWDHIVNQIGMFCFTGLKPEQVQKLIKDHSVYLTNDGRVSMAGVTSKNVEYLAESIH
KVTK
```

Skip low-complexity filtering


Anonymous (424 letters)
20 proteins
E
COG1448
Aspartate/aromatic aminotransferase
BeTs to 8 clades
pet-score: 51
Help
424 letters
904 =>YLR027c (432) - COG1448
889 =>NMB0540 (397) - COG1448
881 = NMA0719 (397) - COG1448
853 =>HI1617 (396) - COG1448
833 =>PA3139 (398) - COG1448
831 =>PM0621 (396) - COG1448
825 = aspC (396) - COG1448
819 = ZaspC (396) - COG1448
788 =>VC1293 (413) - COG1448
781 = NMB1678 (397) - COG1448
780 = NMA1937 (397) - COG1448
724 =>XF0036 (400) - COG1448
710 = PA0870 (399) - COG1448
709 = ZtyrB (397) - COG1448
709 = tyrB (397) - COG1448
675 = YKL106w (451) - COG1448
666 =>CPn0740 (395) - COG1448
624 = mll0405 (394) - COG1448
619 = VCA0513 (404) - COG1448
611 = CT637 (400) - COG1448
118 ->aq_1969 (394) - COG0436
103 ->BS_patA (392) - COG0436
102 ->PAB0525 (389) - COG0436


20 proteins
E
COG1448
info
TyrB
Aspartate/aromatic aminotransferase
Help
Genome context
Pathways / Functional systems
PHENYLALANINE/TYROSINE BIOSYNTHESIS
LEUCINE BIOSYNTHESIS
A O M P K Z Y Q V
A Afu -
O Hbs -
M MET -
P THE -
K PYR -
Z Ape -
Y YLR027c
D R L B C E F G
D Dra -
R MYb -
L Lla -
B BAC -
C Ssp -
E ENT tyrB aspC ZaspC ZtyrB
F PA0870 PA3139
H S N U J X I T W
H PAS HI1617 PM0621
S Xfa XF0036
N Nme NMB0540 NMB1678 NMA0719 NMA1937
U HPY -
J Mlo mll0405 -
X Rpr -
I CT637 CPn0740

To generate a multiple sequence alignment, use:

MultAlin

Paste the sequences from your best–hit COG, saved in your "COGs FASTA Sequences" notebook area, into the input box of Multalin. Also paste in the protein sequence derived from GenScan to include your unknown sequence in this alignment and press the ***"Start Multalin!"*** button. Display these results in text form by clicking on the "–Results as a text page (msf) " link. Paste this Multalin display into your notebook.

Multalin Alignment

MultAlin

Multiple sequence alignment by Florence Corpet

Published research using this software should cite:
"Multiple sequence alignment with hierarchical clustering"
F. CORPET, 1988, Nucl. Acids Res., 16 (22), 10881-10890

INRA Home page | INRA L.G.C.-Auzeville | MultAlin

Sequence data

Cut and paste your sequences here below.

```
>08:28:21|GENSCAN_predicted_peptide_2|424_aa
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YRDDNTQPFVLPSVREAEKRVVSRSLDKEYATIIGIPEFYNKAIELALGKGSKRLAAKHN
VTAQSISGTGALRIGAAFLAKFWQGNREIYIPSPSWGNHVAIFEHAGLPVNRYRYYDKDT
CALDFGGLIEDLKKIPEKSIVLLHACAHNPTGVDPTLEQWREISALVKKRNLYPFIDMAY
QGFATGDIDRDAQAVRTFEADGHDFCLAQSFAKNMGLYGERAGAFTVLCSDEEEAARVMS
QVKILIRGLYSNPPVHGARIAAEILNNEDLRAQWLKDVKLMADRIIDVRTKLKDNLIKLG
SSQNWDHIVNQIGMFCFTGLKPEQVQKLIKDHSVYLTNDGRVSMAGVTSKNVEYLAESIH
KVTK
>tyrB
MFQKVDAYAGDPILTLMERFKEDPRSDKVNLSIGLYYNEDGIIPQLQAVAEAEARLNAQPHGASLYLPME
```

(sample sequences)

or select a file: Browse... new

Sequence input format: Auto

```
                    1       10        20        30        40        50        60        70        80        90       100       110       120       130
                    |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
14:10:32|GENSCAN_pre MSQICKRGLLISNRLAPAALRCKSTWFSEVQMGPPDAILGVTEAFKKDTNPKKINLGAGAYRDDNTQPFVLPSVREAEKRVVS-RSLDKE--YATIIGIPEFYNKAIELALGKGSKR-----LAAKHNVT
          YLR027c     MNKRTQEYKNTRAIMS----ATLFNNIELLPPDALFGIKQRYGQDQRATKVDLGIGAYRDDNGKPWVLPSVKAAEKLIHNDSSYNHE--YLGITGLPSLTSNAAKIIFGTQSDA-----FQEDRVIS
                aspC                         MFENITAAPADPILGLADLFRADERPGKINLGIGVYKDETGKTPVLTSVKKAEQYL-LENETTKN--YLGIDGIPEFGRCTQELLFGKGSAL-----INDKRART
             HI1617                          MFEHIKAAPADPILGLGEAFKSETRENKINLGIGVYKDAQGTTPIMHAVKEAEKRL-FDKEKTKN--YLTIDGIADYNEQTKALLFGKDSEV-----IQSNRART
               tyrB                          MFQKVDAYAGDPILTLMERFKEDPRSDKVNLSIGLYYNEDGIIPQLQAVAEAEARLNAQPHGASL--YLPMEGLNCYRHAIAPLLFGADHPV-----LKQQRVAT
               CT637                       MSLFEQLPSFSPDSILGLAQAFQEDPREDKINLLLGTYEREKKRYGGFSSVRKAQS-VFFDDEKDKN--YLPIKGSSTFLEEMAALCFGE---------VDASRWVG
             CPn0740                       MSFFNHIPTFSPDAILGLQNVFFADKRPEKVNLVIGVYEHPQKRYGGLSCIRKAQT-VILEEEQNKS--YLPISGLQIFLDEMRELVFGA---------VDPSAIVG
              YKL106w          MLRTRLTNCSLWRPYYTSSLSRVPRAPPDKVLGLSEHFKKVKNVNKIDLTVGIYKDGWGKVTTFPSVAKAQKLIESHLELNKNLSYLPITGSKEFQENVMKFLFKESCPQFGPFYLAHDRISF
             Consensus .........................f..v...ppD.ilgl.#.%k.d.r..K!#L.iG.Y.d..g....l.s!.kA#k......e..k...Ylpi.G...f.......llfg..........l...r...

                    131     140       150       160       170       180       190       200       210       220       230       240       250       260
                    |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
14:10:32|GENSCAN_pre AQSISGTGALRIGAAFLAKFWQGNREIYIPSPSWGNHVAIFEHAGLPVNRYRYYDKDTCALDFGGLIEDLKKIPEKS---------IVLLHACAHNPTGVDPTLEQWREISALVKKRNLYPFIDMAYQGF
          YLR027c VQSLSGTGALHISAKFFSKFFP-DKLVYLSKPTWANNMAIFENQGLKTATYPYWANETKSLDLNGFLNAIQKAPEGS---------IFVLHSCAHNPTGLDPTSEQWVQIVDAIASKNHIALFDTAYQGF
                aspC AQTPGGTGALRVAADFLAKNTS-VKRVWVSNPSWPNHKSVFNSAGLEVREYAYYDAENHTLDFDALINSLNEAQAGD---------VVLFHGCCHNPTGIDPTLEQWQTLAQLSVEKGWLPLFDFAYQGF
             HI1617 VQSLGGTGALRIAAEFIKRQTK-AQNVWISTPTWPNHNAIFNAYGMTIREYRYYDAERKALDWEHLLEDLSQASEGD---------VVLLHGCCHNPTGIDPTPEQWQELAALSAKNGWLPLFDFAYQGL
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              YKL106w VQTLSGTGALAVAAKFLALFI--SRDIWIPDPSWANHKNIFQNNGFE-NIYRYSYYKDGQIDIDGWIEQLKTFAYNNQQENNKNPPCIILHACCHNPTGLDPTKEQWEKIIDTIYELKMYPIVDMAYQGL
             Consensus vQ.lgGtGAL...A.fla........!wip.ptW.NH..IF...Gle...Y.ygd..t..ld..gli..lk..p..s..........vlLH.CcHNPTG.Dpt.eqW..i.....e....p..D.AYqGf

                    261     270       280       290       300       310       320       330       340       350       360       370       380       390
                    |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
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                aspC ARG-LEEDAEGLRAFA---AM---HKELIVASSYSKNFGLYNERVGACTLYAADS---------ET----VDRAFSQMKAAIRANYSNPPAHGASVVATILSNDALRAIWEQELTDMRQRIQRMRQLFVN
             HI1617 ANG-LDEDAYGLRAFA---AN---HKELLVASSFSKNFGLYNERVGAFTLVAENA---------EI----ASTSLTQVKSIIRTLYSNPASHGGATVATVLNDAQLRQEWENELTEMRERIKKMRHLFVQ
               tyrB GAG-MEEDAYAIRAIA---SA---GLPALVSNSFSKIFSLYGERVGGLSVMCEDA---------ER----AGRVLGQLKATVRRNYSSPPNFGAQVVAAVLNDEALKASWLAEVEEMRTRILAMRQELVK
               CT637 ASG-IEEDRRPVRLCI---EA---GVTTFVAGGASKIFSLYGSRVGFFGAIHQDK---------LD----LNRILSFLEEQIRGEYSSPAREGYAIVTSILSNPYLRQEWELELNGIRQSLEEIRSSFVI
             CPn0740 AHG-IELDRKPIEIFI---SE---GNTVLVAASSSKNFALYGERVGYFAVHSTFT---------DE----LVKIHSFLEEKIRGEYSSPQRWGVEIVSTILSNPYLKEEWQSELNFIRESLGKMRTRFVQ
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             Consensus a.G.l..Day..r................v..sfsKnfg$YgeRvG.f.v.........................sqlk..!Rg.ySsPp..G..!va..Ls...L...W..#v..mr.ri..mR...v.

                    391     400       410       420       430       440       450       460       468
                    |--------+---------+---------+---------+---------+---------+---------+-------|
14:10:32|GENSCAN_pre NLIKLGSSQNWDHIVNQIGMFCFTGLKPEQVQKLIKDHSVYLTNDGRVSMAGVTSKNVEYLAESIHKVTK
          YLR027c HLVKLGTPGNWDHIVNQCGMFSFTGLTPQMVKRLEETHRVYLVASGRASIAGLNQGNVEYVAKAIDEVVRFYTIEAKL
                aspC TLQEKGANRDFSFIIKQNGMFSFSGLTKEQVLRLREEFGVYAVASGRVNVAGMTPDNMAPLCEAIVAYL
             HI1617 LLKEYGAEQDFSFIIEQNGMFSFSGLTGEQVDRLKNEFAIYAVRSGRINVAGITEDNIRYLCESIVKVL
               tyrB VLSTEMPERNFDYLLNQRGMFSYTGLSAAQVDRLREEFGVYLIASGRMCVAGLNTANVQRVAKAFAAVM
               CT637 AMRNV-AGHSFDFIASQKGFFGYPGFSKEQVLFLREELGIYTTAGGRFNLNGITDKNINRVTHGFAQAYEYPRSVS
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             Consensus .$........fd.i..Q.GmF.%tgls..qV..Lre...!Ylta.GR...aG.n..N!.yl.es...v..........
```

```
      Consensus levels: high=90% low=50%
Consensus symbols:
 ! is anyone of IV
 $ is anyone of LM
 % is anyone of FY
 # is anyone of NDQEBZ//
```

```
                        251                                                300
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                tyrB  PFLDIAYQGF GAG.MEEDAY AIRAIA...S ..AGLP.ALV SNSFSKIFSL
               ZtyrB  PFLDIAYQGF GAG.MEEDAY AIRAIA...S ..AGLP.ALV SNSFSKIFSL
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               ZaspC  PLFDFAYQGF ARG.LEEDAE GLRAFA...A ..M.HKELIV ASSYSKNFGL
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              HI1617  PLFDFAYQGL ANG.LDEDAY GLRAFA...A ..N.HKELLV ASSFSKNFGL
              PM0621  PLFDFAYQGF ANG.LEEDAF GLRTFA...K ..N.HKELLV ASSYSKNFGL
             NMB0540  PLFDFAYQGF GNG.LEEDAY GLRVFL...K ..H.NTELLI ASSYSKNFGM
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           Consensus  Pf.D.AYQGf ..G.le.Da. ..Rl.a.... .........v a.S.sKnfg$

                      301                                                350
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                tyrB  YGERVGGLSV MCEDA..... ....EA.... AGRVLGQLKA TVRRNYSSPP
               ZtyrB  YGERVGGLSV LCEDA..... ....EA.... AGRVLGQLKA TVRRNYSSPP
             NMB1678  YGERVGGLSV VCPNK..... ....EE.... ADLVFGQLKF TVRRIYSSPP
             NMA1937  YGERVGGLSV VCPNK..... ....EE.... ADLVFGQLKF TVRRIYSSPP
              PA3139  YGERVGALSI VTESR..... ....DE.... SARVLSQVKR VIRTNYSNPP
              XF0036  YGERVGGLSI VASNT..... ....EQ.... AQAIQSQVKR IIRTIYSSPS
                aspC  YNERVGACTL VAADS..... ....ET.... VDRAFSQMKA AIRANYSNPP
               ZaspC  YNERVGACTL VAADS..... ....ET.... VDRAFSQMKA AIRANYSNPP
              VC1293  YNERVGAFTL VAPST..... ....TV.... AETAFSQVKA IIRSIYSNPP
              HI1617  YNERVGAFTL VAENA..... ....EI.... ASTSLTQVKS IIRTLYSNPA
              PM0621  YSERVGAFTL VAETE..... ....QI.... AATALTQVKT IIRTLYSNPA
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               CT637  YGSRVGFFGA IHQDK..... ....LD.... LNRILSFLEE QIRGEYSSPA
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           Consensus  Yg#RvGa..v .......... .......... .....sqlk. .iR..yS.Pp
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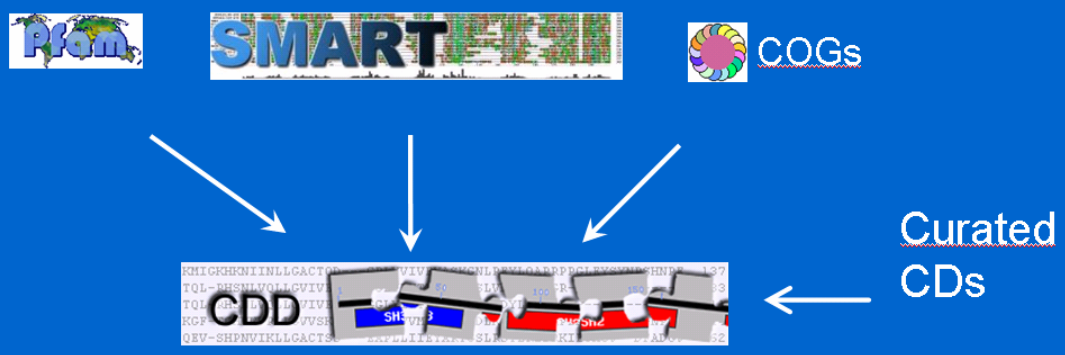
http://www.ncbi.nlm.nih.gov/Structure/cdd/cdd.shtml

Conserved Domain

- recurring unit in molecular evolution, whose extents can be determined by sequence and structure analysis
- performs a particular function
- represented as a multiple local sequence alignment of proteins containing the domain

NCBI

Conserved Domain Database



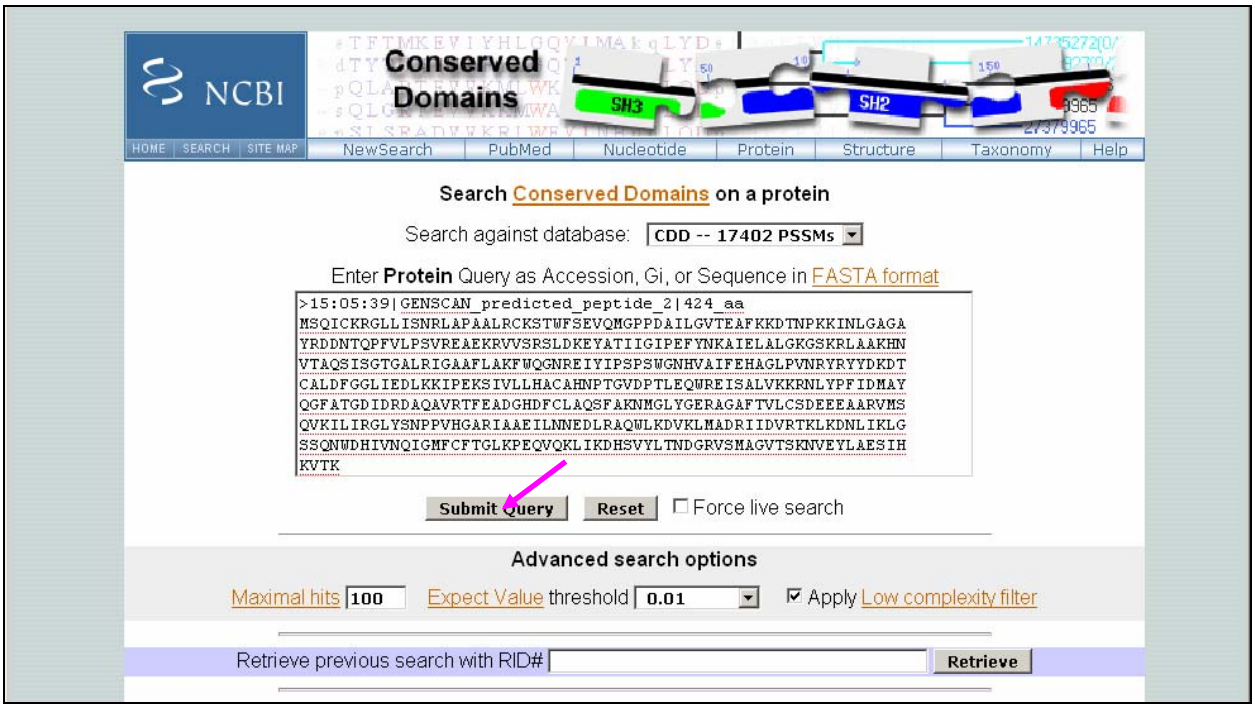
- A position-specific scoring matrix (PSSM) is calculated
- CD-Search can be used to search against the PSSMs
- Manual curation of CDs has begun

NCBI

To search for protein domains and view a model structure for your protein, click here:

NCBI's Conserved Domain Search allows you to match your protein sequence to a library of conserved protein domains, generate a multiple sequence alignment based on this match, and explore 3D modeling templates for your sequence.

Paste your protein sequence from GenScan into the CD–Search query box and run the search. From the search results page, generate a multiple sequence alignment for the top 10 sequences representitive of the conserved domain hit by clicking on the cartoon of the domain. Paste this alignment into your notebook. Before viewing a structure with Cn3D, use the listbox to specify "up to 5" sequences and "All Atoms". Invoke Cn3D with a display of a 3D modeling template, and a multiple sequence alignment including your query sequence, by pressing the "View 3D Structure" button. Residues identical in your sequence and the structura template are shown in red. Locate the Prosite Motif you found earlier within the Cn3D alignment window by using View––Find Pattern. Use Style––Annotate from the Cn3D window to color the highlighted residues and show their side chains.


NCBI
Conserved Domains
SH3
SH2
HOME | SEARCH | SITE MAP
NewSearch | PubMed | Nucleotide | Protein | Structure | Taxonomy | Help
Search Conserved Domains on a protein
Search against database: CDD -- 17402 PSSMs
Enter Protein Query as Accession, Gi, or Sequence in FASTA format
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Force live search
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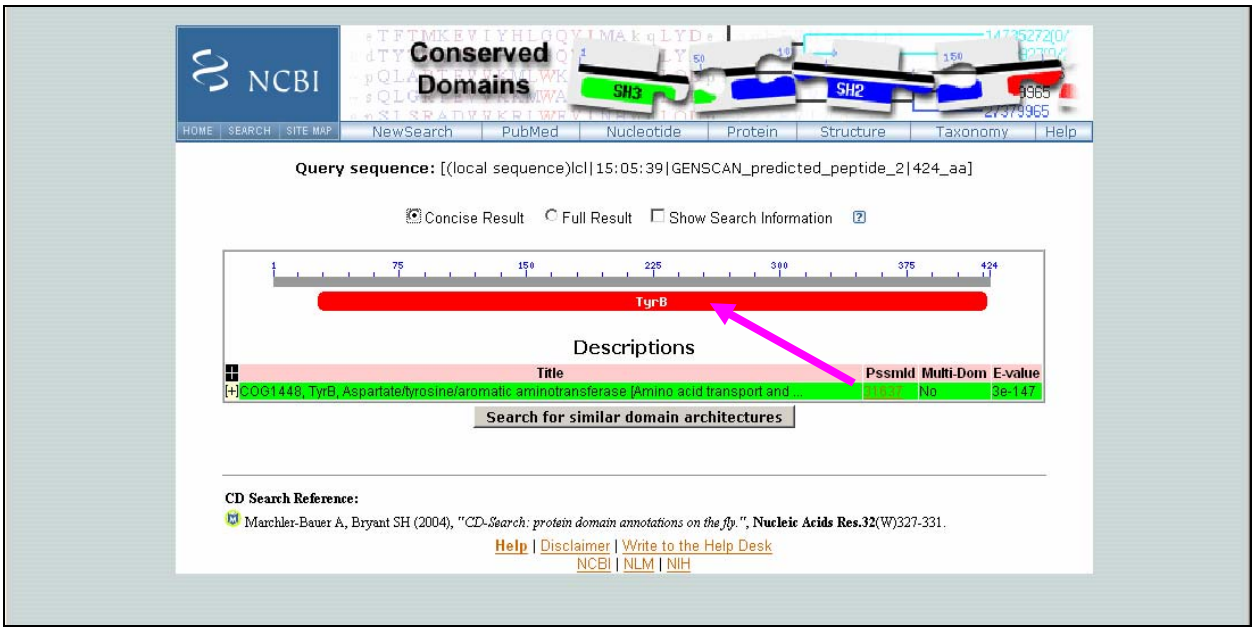
Apply Low complexity filter
Retrieve previous search with RID#
Retrieve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SH3
SH2
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Concise Result
Full Result
Show Search Information
1
75
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225
300
375
424
TyrB
Descriptions
Title
PssmId
Multi-Dom
E-value
[+]COG1448, TyrB, Aspartate/tyrosine/aromatic aminotransferase [Amino acid transport and ...
No
3e-147
Search for similar domain architectures
CD Search Reference:
Marchler-Bauer A, Bryant SH (2004), "CD-Search: protein domain annotations on the fly.", Nucleic Acids Res.32(W)327-331.
Help | Disclaimer | Write to the Help Desk
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Conserved Domains

SH3 SH2

Entrez | CDD | Structure | Protein | Help

COG1448.2

TyrB, with user query added

Aspartate/tyrosine/aromatic aminotransferase [Amino acid transport and metabolism]

[+] Links:

[+] Statistics:

[−] Structure:

Show Structure

Program: Cn3D

Drawing: All Atoms

Aligned Rows: up to 10

[Download Cn3D]

Other Related Conserved Domains: COG0075 COG0079 COG0156 COG0399 COG0436 COG0520 COG0626 COG2008 COG3977 pfam00155 pfam00266 pfam01041 pfam04864

Reformat Sequence Alignment | Format: Compact Hypertext | Row Display: up to 10 | Color Bits: 2.0 bits | Type Selection: the most similar members

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1ART          1 .[1].F     ENITAAPADPILGLADLFRADERPGKINLGIGVYKDETGKTPVLTSVKKAEQYLLENE     TTKNYL 66
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3TAT_A       68 PMEGLNCYRHAIAPLLFG.[1].DHPVLKQQRVATIQTLGGSGALKVGADFLKRY     FPESGVWVSDPTWENHVAIF 138
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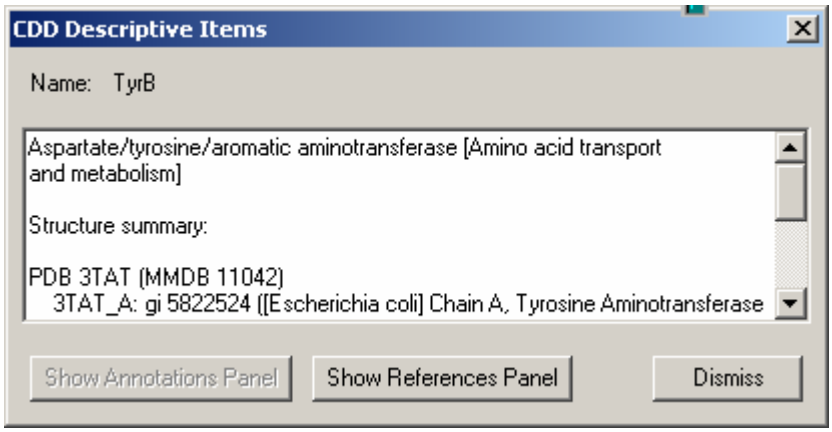

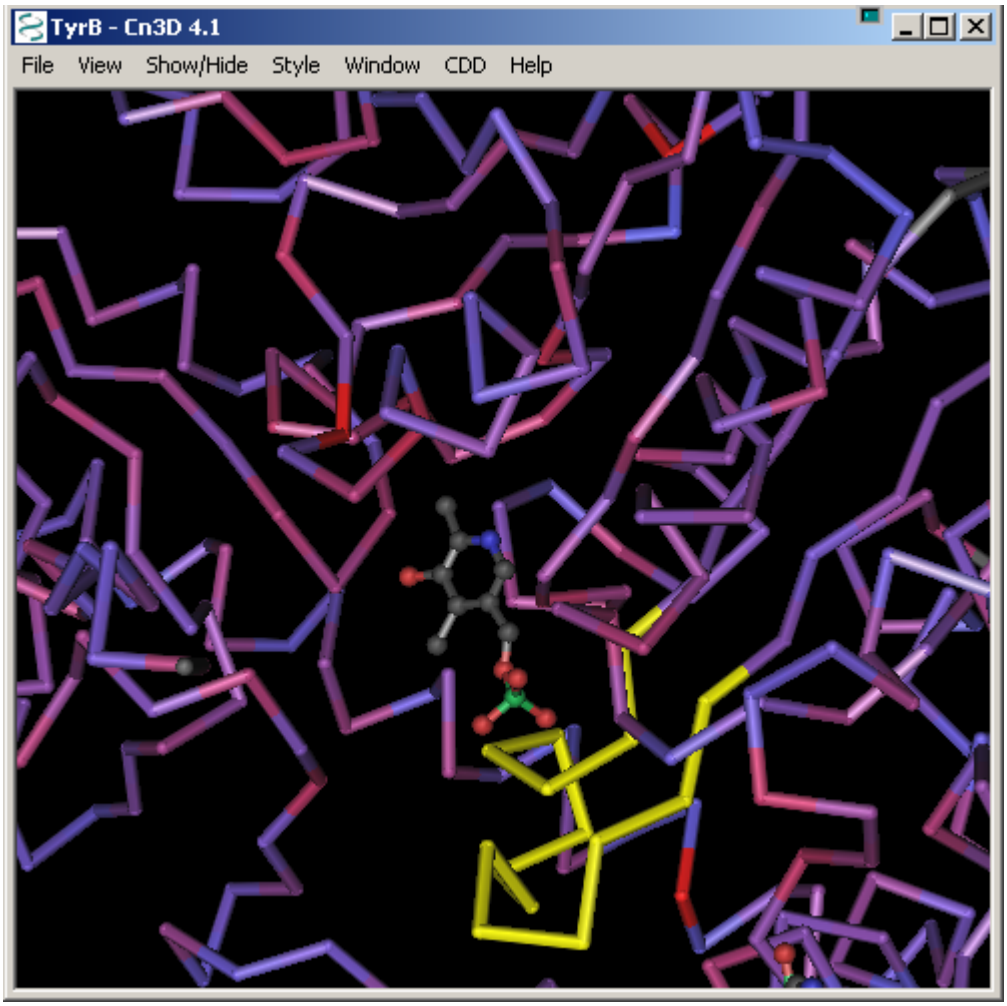
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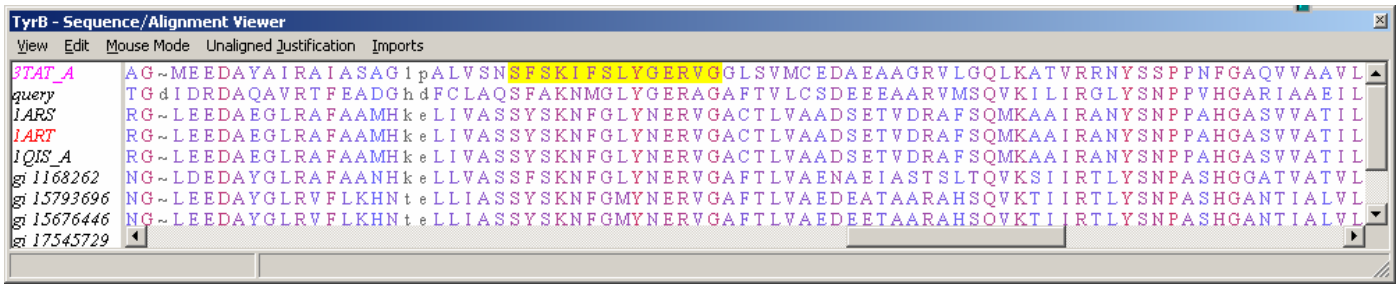
TyrB - Sequence/Alignment Viewer
View Edit Mouse Mode Unaligned Justification Imports
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1QIS_A RG~LEEDAEGLRAFAAMHkeLIVASSYSKNFGLYNERVGACTLVAADSETVDRAFSQMKAAIRANYSNPPAHGASVVATIL
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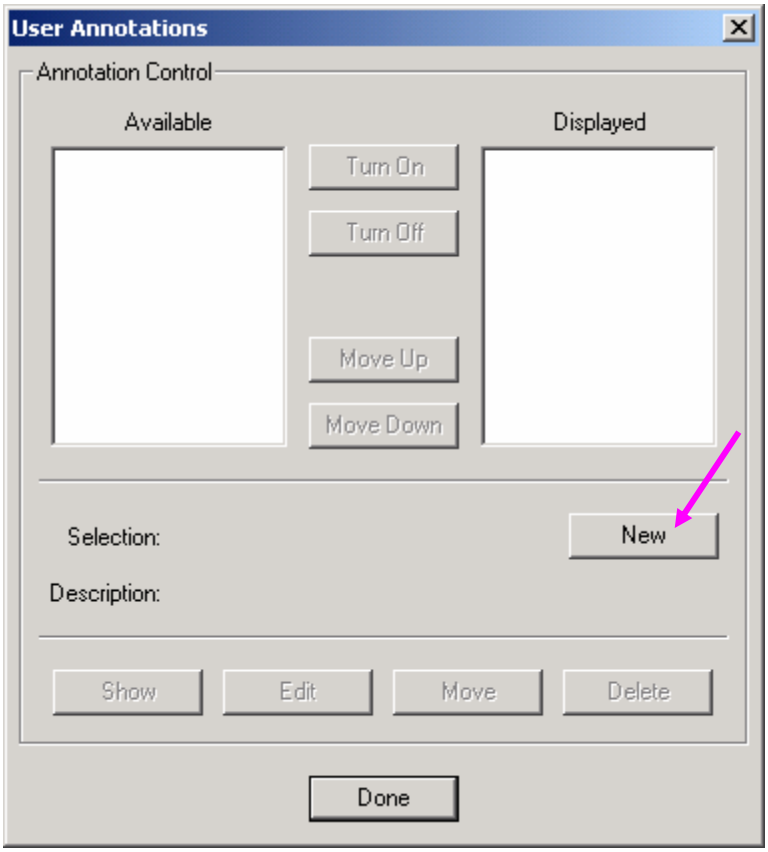
gi 17545729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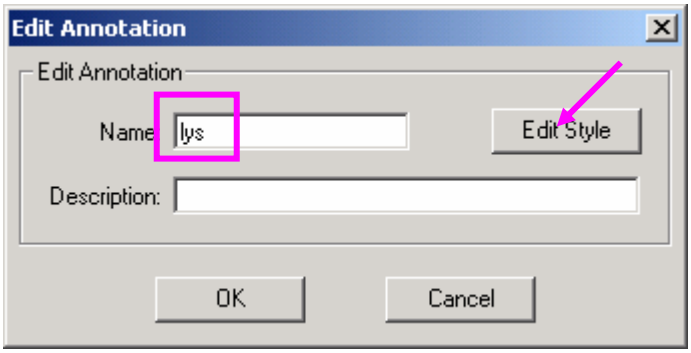
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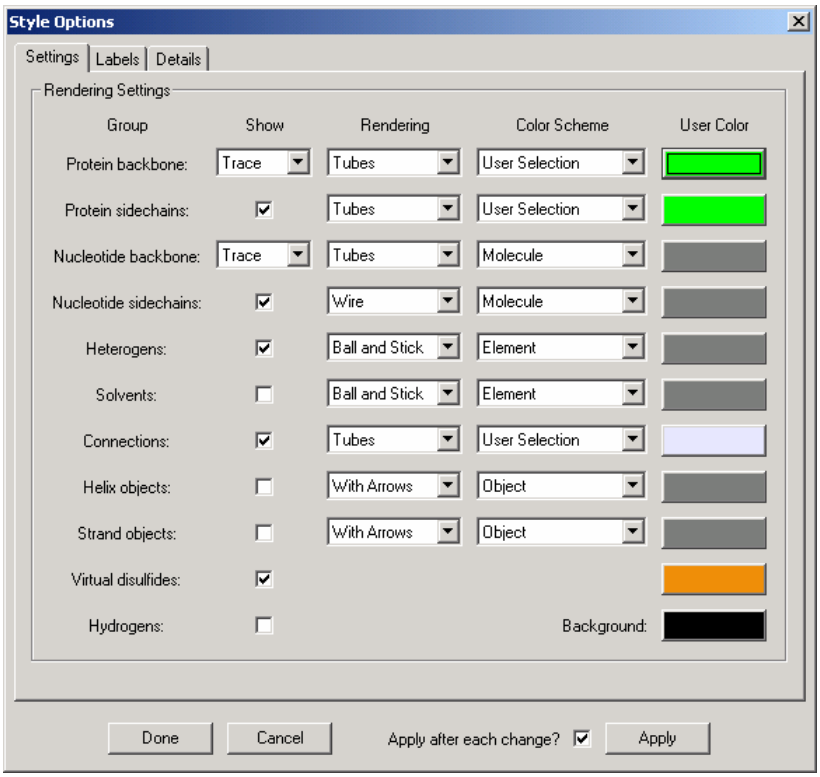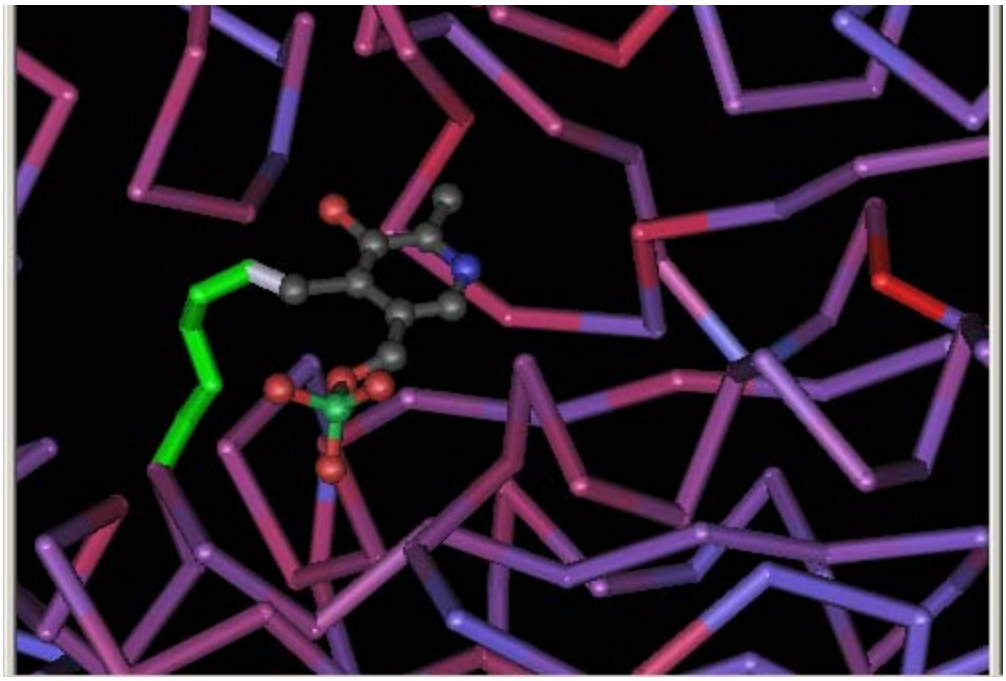
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Nucleotide backbone:
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Tubes
Molecule
Nucleotide sidechains:
Wire
Molecule
Heterogens:
Ball and Stick
Element
Solvents:
Ball and Stick
Element
Connections:
Tubes
User Selection
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Strand objects:
With Arrows
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Background:
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Cancel
Apply after each change?
Apply