

# BLAST

**Slides adapted & edited from a set by  
Cheryl A. Kerfeld (UC Berkeley/JGI) &  
Kathleen M. Scott (U South Florida)**

Kerfeld CA, Scott KM (2011) Using BLAST to Teach “E-value-tionary” Concepts.  
*PLoS Biology* 9(2):e1001014

## Starts with a Query Sequence in FASTA Format

Amino acid sequence:

```
>ribosomal protein L7/L12 [Thiomicrospira crunogena XCL-2]
MAITKDDILEAVANMSVMEVVELVEAMEEKFGVSAAVAVAGPAGDAGAA
GEEQTEFDVVLTGAGDNKVAAIKAVRGATGLGLKEAKSAVESAPFTLKEG
VSKEEAETLANELKEAGIEVEVK
```

Nucleotide sequence:

```
>gi|118139508:333094-333465 Thiomicrospira crunogena XCL-2
ATGGCAATTACAAAAGACGATATTTTAGAAGCAGTTGCTAACATGTCAGTAATGGAAG
TTGTTGAACCTGTTGAAGCAATGGAAGAGAAGTTTGGTGTCTTCTGCAGCAGCAGTTGC
GGTTGCAGGTCCTGCAGGTGATGCTGGCGCTGCTGGTGAAGAACAAACAGAGTTTGAC
GTTGTCTTGACTGGTGCTGGTGACAACAAAGTTGCAGCAATCAAAGCCGTTTCGTGGCG
CAACTGGTCTTGGGCTTAAAGAAGCGAAAAGTGCAGTTGAAAGTGCACCATTTACGCT
TAAAGAGGGTGTTTCTAAAGAAGAAGCAGAAACTCTTGCAAATGAGCTTAAAGAAGCA
GGTATTGAAGTCGAAGTTAAATAA
```

Note the description line

Starts with “>”, ends with carriage return

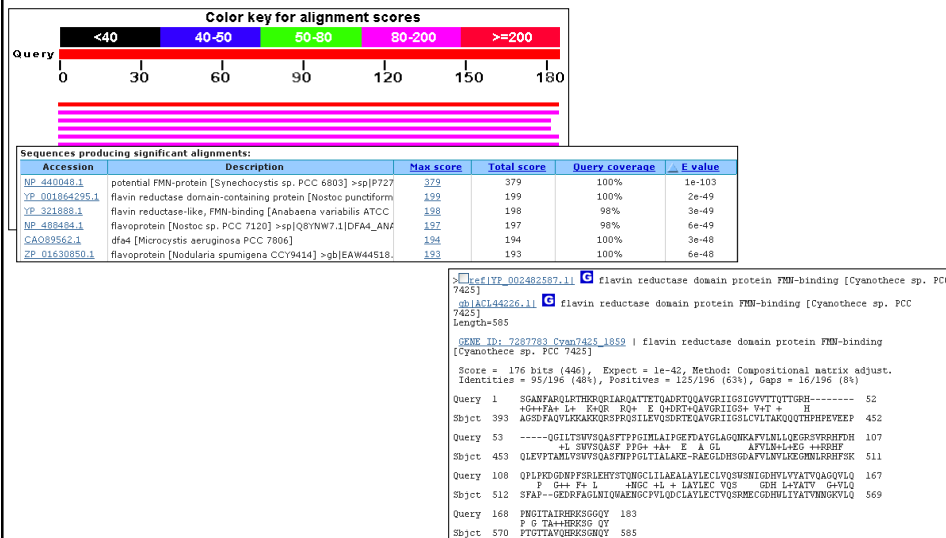
Not read as sequence data

# NCBI BLAST Interface (blastp: for protein-protein alignments)

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## NCBI BLAST Results Page: Potential homologs retrieved from database



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# Overview of BLAST

1. Segment the query sequence into short “words”
2. Use the query sequence segments to scan the database for matching sequences
3. Extend the matched segments in either direction to find local alignments.
4. Create a list of hits & alignments, with best matches first

## BLAST Phase 1: Segment the query sequence and identify words that could form potential alignments

Query Sequence:

```
>gi|16329320 (residues 412 to 594)
SGANFARQLRTHKRQRIARQATTETQADRTQQAVGRIIGSIGVVTQTG
RHQGILTSWVSQASFTPPGIMLAIPGEFDAYGLAGQNKAFVNLNLLQEGRS
VRRHFDHQPLPKDGDNPFSRLEHYSTQNGCLILAEALAYLECLVQSWNSI
GDHVLVYATVQAGQVLQPNGITAIRHRKSGGQY
```

Fragmentation into words:

SWVSQASFTPPGIM → SWV WVS VSQ SQA QAS ASF SFT ...

Selection of words scoring above threshold (for word SWV):

Substitution Matrix*									
	R	G	I	K	F	S	T	W	V
R	5	0	-1	-1	-2	1	0	-3	0
G	6	4	-2	-3	0	-2	-2	-3	-3
I			4	-3	0	-2	-1	-3	-3
K				5	-3	0	-1	-3	-2
F					6	-2	-2	1	-1
S						4	1	-3	-2
T							5	-2	0
W								11	-3
V									4

\*A portion of the BLOSUM 62 matrix

Selection of words scoring above threshold (for word SWV):

- SWV (4+11+4 = 19)
- SWI (4+11+3 = 18)
- TWV (1+11+4 = 16)
- GWV (0+11+4 = 15)
- KWV (0+11+4 = 15)
- SWS (4+11-2 = 13)
- SEV (4+1+4 = 9)
- SRV (4-3+4 = 5)

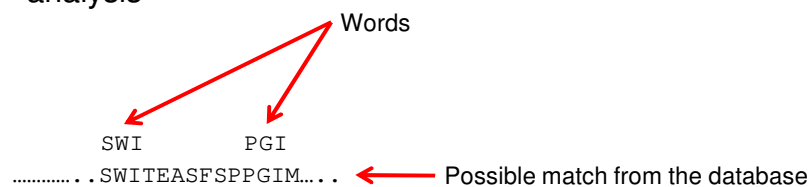
Synonyms above threshold 11... (others not shown)

Synonyms below threshold 11... (others not shown)

- Segment the query sequence into pieces (“words”)
  - Default word length: 3 amino acids or 11 nucleic acids
- Create a list of synonyms and their scores for comparing query words to target words
  - Uses scoring matrix to calculate scores for synonyms that might be found in the database
- Save the scores (and synonyms) exceeding a given threshold T

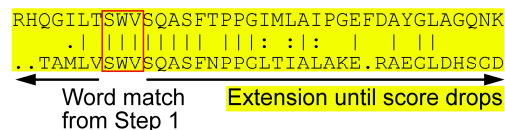
## BLAST Phase 2: Using the query sequence word list, scan the database for synonyms (hits)

- Scan the database for matches to the word list with acceptable T values
- Require two matches (“hits”) within the target sequence
- Set aside sequences with matches above T for further analysis



## BLAST Phase 3: Extending the hits

- Search 5' and 3' of the word hit on both the query and target sequence
- Add up the score for sequence identity or similarity until value exceeds S
- Alignment is dropped from subsequent analyses if value never exceeds S

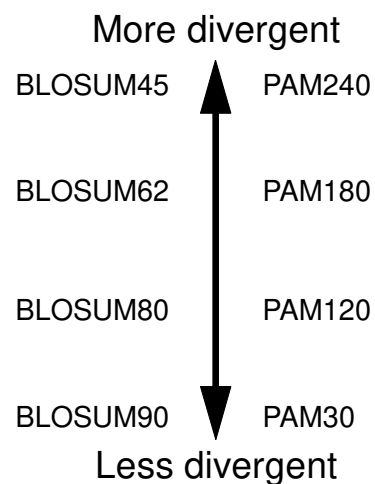


## So, to summarize:

- BLAST segments query sequence into “words” and scores potential word matches
- Scans this list for alignments that meet a threshold score T
  - uses a scoring matrix to calculate this (e.g., **BLOSUM62**)
- Uses this list of ‘synonyms’ to scan the database
- Extends the alignments to see if they meet a cutoff score S
  - uses a scoring matrix to calculate this
- Reports the alignments that exceed S

## PAM and BLOSUM Matrices

- Scoring matrices are calibrated to capture different degrees of sequence similarity
- In practice, this means choosing a matrix appropriate to the suspected degree of sequence identity between the query and its hits
- PAM: empirically derived for close relatives
- BLOSUM: empirically derived for distant relatives



## Raw Scores ( $S$ values) from an Alignment

$$S = (\sum M_{ij}) - cO - dG,$$

where

$M$  = score from a similarity matrix  
for a particular pair of amino acids ( $ij$ )

$c$  = number of gaps

$O$  = penalty for the existence of a gap

$d$  = total length of gaps

$G$  = per-residue penalty for extending  
the gap

## Limitations of Raw Scores

- $S$  values depend on the substitution matrix, gap penalties
- Impossible to compare  $S$  values from hits retrieved from BLAST searches when different matrices and gap penalties are used

## Going from Raw Scores to Bit Scores

$$S' = [\lambda S - \ln(K)] / \ln(2)$$

where

$S'$  = bit score

$\lambda$  and  $K$  = normalizing parameters of the specific matrices and search spaces

(as in 0 vs 1)

- Larger raw scores result in larger bit scores
- Allows user to compare scores obtained by using different matrices and search spaces

## Limitations of Bit Scores

- How high does a bit score have to be to suggest common ancestry?
  - Hard to evaluate hits as homologs or not, based solely on bit scores

## E-value

- Number of distinct alignments with scores greater than or equal to a given value expected to occur in a search against a database of known size, based solely on chance, not homology.
  - Large E-values suggest that the query sequence and retrieved sequence similarities are due to chance
  - Small E-values suggest that the sequence similarities are due to shared ancestry (or potentially convergent evolution)

## Calculating E-values

$$E = (n \times m) / 2^S$$

where

- $m$  = effective length of the query sequence
  - = length of query sequence – average length of alignments  
(Controls for fewer alignments occurring at the ends of the query sequence)
- $n$  = effective length of the database sequence  
(total number of bases)

The value of  $E$  decreases exponentially with increasing  $S$



## BLAST Parameters

- Expect
- Word size
- Matrix
- Gap costs
- Filter
- Mask

**Algorithm parameters**

**General Parameters**

Max target sequences: 100  
Select the maximum number of aligned sequences to display

Short queries: ☒ Automatically adjust parameters for short input sequences

Expect threshold: 10

Word size: 3

**Scoring Parameters**

Matrix: BLOSUM62

Gap Costs: Existence: 11 Extension: 1

Compositional adjustments: Conditional compositional score matrix adjustment

**Filters and Masking**

Filter: ☐ Low complexity regions

Mask: ☐ Mask for lookup table only  
☐ Mask lower case letters

**BLAST** Search database nr using Blastp (protein-protein BLAST)  
☐ Show results in a new window

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## E value Threshold

- Alignments will be reported with E-values less than or equal to the expect values threshold
  - Setting a larger E threshold will result in more reported hits
  - Setting a smaller E threshold will result in fewer reported hits

**Algorithm parameters**

**General Parameters**

Max target sequences: 100  
Select the maximum number of aligned sequences to display

Short queries: ☒ Automatically adjust parameters for short input sequences

Expect threshold: 10

Word size: 3

**Scoring Parameters**

Matrix: BLOSUM62

Gap Costs: Existence: 11 Extension: 1

Compositional adjustments: Conditional compositional score matrix adjustment

**Filters and Masking**

Filter: ☐ Low complexity regions

Mask: ☐ Mask for lookup table only  
☐ Mask lower case letters

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## Filter and Mask

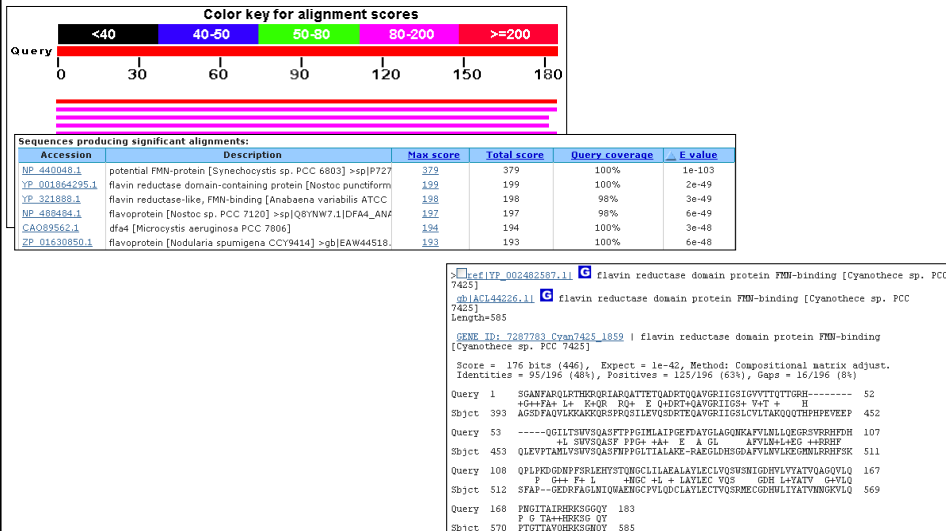
- **Filter: Low complexity**
  - Replaces the following with N (nucleotides) or X (amino acids)
    - Dinucleotide repeats
    - Amino acid repeats
    - Leader sequences
    - Stretches of hydrophobic residues
- **Mask: Lower case**
  - Replaces lowercase letters in sequence with N or X
    - Lowercase letters typically indicate base or amino acid not known with certainty

The screenshot shows the 'Algorithm parameters' section of the NCBI BLAST interface. Under the 'Filters and Masking' sub-section, the 'Filter' checkbox is checked, and the 'Mask' checkbox is also checked. Red arrows point to these checkboxes. The 'BLAST' button is visible at the bottom of the section.

## Parameter Summary is Found at the Bottom of the Output.....

Search Parameters		
Program	blastp	
Word size	3	
Expect value	10	
Hitlist size	100	
Gapcosts	11,1	
Matrix	BLOSUM62	
Filter string	F	
Genetic Code	1	
Window Size	40	
Threshold	11	
Composition-based stats	2	
Database		
Posted date	Sep 6, 2010 4:42 AM	
Number of letters	4,014,994,744	
Number of sequences	11,756,863	
Entrez query	none	
Karlin-Altschul statistics		
Lambda	0.319424	0.267
K	0.13352	0.041
H	0.397413	0.14
Results Statistics		
Length adjustment	129	
Effective length of query	54	
Effective length of database	2498359417	
Effective search space	134911408518	
Effective search space used	134911408518	

# Evaluating BLAST Results



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## Examine the BLAST Alignment

```
>ref|YP_002482587.1| G flavin reductase domain protein FMN-binding [Cyanotheca sp. PCC 7425]
gb|ACL44226.1| G flavin reductase domain protein FMN-binding [Cyanotheca sp. PCC 7425]
Length=585
GENE ID: 7287783 Cyan7425_1859 | flavin reductase domain protein FMN-binding [Cyanotheca sp. PCC 7425]
Score = 176 bits (446), Expect = 1e-42, Method: Compositional matrix adjust.
Identities = 95/196 (48%), Positives = 125/196 (63%), Gaps = 16/196 (8%)
Query 1 SGANFARQLRTHKRQRIARQATTETQADRTQAVGRIIGSIGVTTTQTTGRH----- 52
+G++FA+ L+ K+QR RQ+ E Q+DRT+QAVGRIIGS+ V+T + H
Sbjct 393 AGSDFAQVLKKAQRSPRQSILEVQSDRTEQAVGRIIGSLCVLTAKQQQTHPHEVEEP 452
Query 53 -----QGILTSUVVSQASFTPPGIMLAIPGEFDAYGLAGQNKAFVNLNLQEGRSVRRHFDH 107
+L SUVSQASF PPG+ +A+ E A GL AFVLM+L+EG ++RRHF
Sbjct 453 QLEVPMTAMLVSVVSQASFTNPPGLTIALAKE-RAEGLDHSQDAFVNLNLKEGMNLRHFFSK 511
Query 108 QPLPKDGNPFPSRLEHYSTQNGCLILAEALAYLECLVQSUSNIGDHVLYATVQAGQVLQ 167
P G++ F+ L +NGC +L + LAYLEC VQS GDH L+YATV G+VLQ
Sbjct 512 SFAP--GEDRFAGLNIQWANGCPVLQDCLAYLECTVQSRMECGDHVLIYATVYNNKVLQ 569
Query 168 PNGITAIRHRKSGGQY 183
P G TA++HRKSG QY
Sbjct 570 PTGTTAVQHRKSGNQY 585
```

Does it cover the whole length of both the query and subject sequences?

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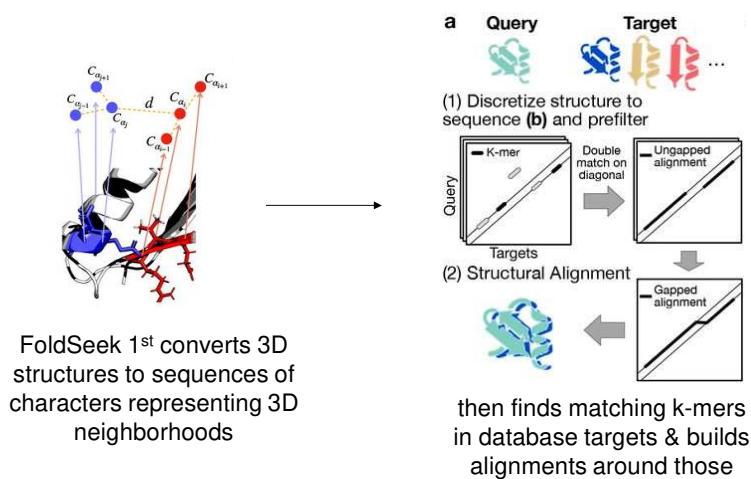
## High E-value: Discovery of a Distant Homolog or Garbage?

- Take another look at the target (subject) sequence(s) that have high E-values
  - Similar length?
  - Recurring motifs?
  - Similar biological functions?
- Use target sequences as query sequences for another BLAST search
  - Does the original query sequence come up in report?

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**Currently the best algorithm to compare a protein's 3D structure to a large database of structures is also very BLAST-like in the way it operates:**



<https://www.biorxiv.org/content/10.1101/2022.02.07.479398v4.full>

You can try it out at <https://search.foldseek.com>  
& search >200M protein structures

Foldseek Search

[GITHUB](#) [SÖDING LAB](#) [STEINEGGER LAB](#)

Queries

HEADER

PROTEIN BINDING

13-APR-21

707Q

TITLE

(H-ALPHA2M)4 TRYPSIN-ACTIVATED STATE

COMPND

MOL\_ID: 1;

COMPND

2 MOLECULE: ALPHA-2-MACROGLOBULIN;

COMPND

3 CHAIN: A, B, C, D;

COMPND

4 SYNONYM: ALPHA-2-M, C3 AND PZP-LIKE ALPHA-2-MACROGLOBULIN DOMAIN-

COMPND

5 CONTAINING PROTEIN 5

SOURCE

MOL\_ID: 1;

SOURCE

2 ORGANISM\_SCIENTIFIC: HOMO SAPIENS;

SOURCE

3 ORGANISM\_COMMON: HUMAN;

SOURCE

4 ORGANISM\_TAXID: 9606

KEYWDS

ALPHA2-MACROGLOBULIN, PROTEINASE, SERUM PROTEOSTASIS, HYDROLASE

KEYWDS

2 INHIBITOR, PROTEIN BINDING

EXPDTA

ELECTRON MICROSCOPY

AUTHOR

D..LUQUE,T..GOULAS,C..P..MATA,S..R..MENDES,F..X..GOMIS-RUTH,J..R..CASTON

CURL COMMAND

LOAD ACCESSION

UPLOAD PDB

PREDICT STRUCTURE

Search Settings

Databases

☒ AlphaFold/UniProt50 v4

☒ AlphaFold/Swiss-Prot v4

☒ AlphaFold/Proteome v4

☒ MGnify-ESM30 v1

☒ PDB100 2201222

☒ GMGCL 2204

Mode

☒ 3Di/AA

☐ TM-align

Taxonomic filter

SEARCH

(courtesy of the Steinegger lab @ [steineggerlab.com](https://steineggerlab.com),  
who also make great illustrations for all their programs)

