

序列比对3

复习 双序列比对及算法

如果两个序列长度相同:

一致度 (identity) = (一致字符的个数 / 全局比对长度) $\times 100\%$

相似度 (similarity) = (一致及相似的字符的个数 / 全局比对长度) $\times 100\%$

序列1: **CVHK-LA** identity = (4/7)*100% = 57%

序列2: **C-HKTIA** similarity = ((4+1)/7)*100% = 71%

如果两个序列长度不相同:

一致度 (identity) = (一致字符的个数 / 全局比对长度) $\times 100\%$

相似度 (similarity) = (一致及相似的字符的个数 / 全局比对长度) $\times 100\%$

序列1: **CVHKAT** identity = (4/6)*100% = 67%

序列2: **CIHK-T** similarity = ((4+1)/6)*100% = 83%

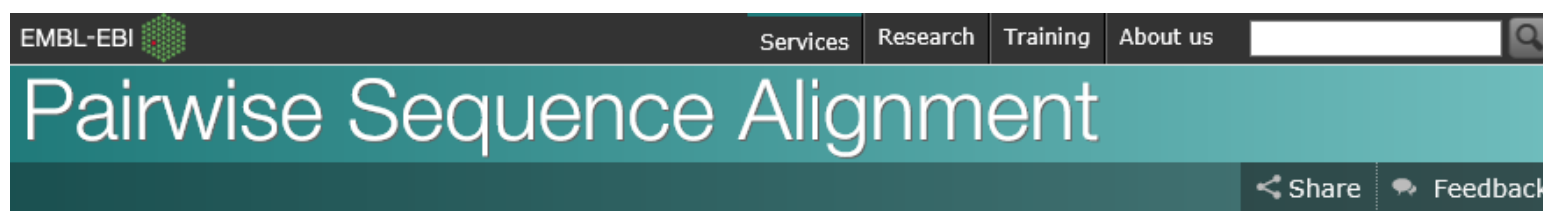
无论两个序列长度是否相同, 都要先做双序列全局比对, 然后根据比对结果及比对长度计算它们的一致度和相似度。



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EMBL双序列比对工具：全局比对工具

<http://www.ebi.ac.uk/Tools/psa>



[Tools](#) > Pairwise Sequence Alignment

Pairwise Sequence Alignment is used to identify regions of similarity that may indicate functional, structural and/or evolutionary relationships between two biological sequences (protein or nucleic acid).

By contrast, [Multiple Sequence Alignment \(MSA\)](#) is the alignment of three or more biological sequences of similar length. From the output of MSA applications, homology can be inferred and the evolutionary relationship between the sequences studied.

Global Alignment

Global alignment tools create an end-to-end alignment of the sequences to be aligned. There are separate forms for protein or nucleotide sequences.

Local Alignment

Local alignment tools find one, or more, alignments describing the most similar region(s) within the sequences to be aligned. There are separate forms for protein or nucleotide sequences.

Genomic Alignment

Genomic alignment tools concentrate on DNA (or to DNA) alignments while accounting for characteristics present in genomic data.



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EMBL双序列比对工具：全局比对工具

Global Alignment

Global alignment tools create an end-to-end alignment of the sequences to be aligned. There are separate forms for protein or nucleotide sequences.

Needle (EMBOSS)

EMBOSS Needle creates an optimal global alignment of two sequences using the Needleman-Wunsch algorithm.

 [Protein](#)  [Nucleotide](#)

Stretcher (EMBOSS)

EMBOSS Stretcher uses a modification of the Needleman-Wunsch algorithm that allows larger sequences to be globally aligned.

 [Protein](#)  [Nucleotide](#)

Genomic Alignment

Genomic alignment tools concentrate on DNA (or to DNA) alignments while accounting for characteristics present in genomic data.

Wise2DBA

Wise2DBA (DNA Block Aligner) aligns two sequences under the assumption that the sequences share a number of colinear blocks of conservation separated by potentially large and varied lengths of DNA in the two sequences.

 [Launch Wise2DBA](#)

GeneWise

GeneWise compares a protein sequence to a genomic DNA sequence, allowing for introns and frameshifting errors.

 [Launch GeneWise](#)

EMBL双序列比对工具：全局比对工具

Pairwise Sequence Alignment (PROTEIN)

EMBOSS Needle reads two input sequences and writes their optimal global sequence alignment to file.

This is the form for protein sequences. Please go to the [nucleotide](#) form if you wish to align DNA or RNA sequences.

STEP 1 - Enter your protein sequences

Enter or paste your first protein sequence in any supported format:

```
>seq1_for_global_alignment
MHHHHHHSSGVLDLTENLYFQSMKTTQEQLKRNVRFHAFISYSEHDSLWVKNELIPNLEK
EDGSILICLYESYFDPGKSISENIVSFIEKSYKSIFVLSPNFVQNEWCHYEFYFAHHNLF
HENS DHII LLEPIPFYCIPTRYHKLKALLEKKAYLEWPKDRRKCGLFWANLRAAIN
```

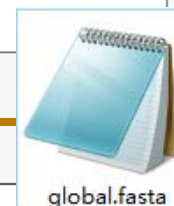
Or, upload a file: 浏览...

AND

Enter or paste your second protein sequence in any supported format:

```
>seq2_for_global_alignment
TTLD DPLGHMPERFDFAFICYCPSDIQFVQEMIRQLEQTNYRLKLCVSDRDVLPGTCVWSI
ASELIEKRCRRMVVVVSDDYLQSKCEDFQTKFALSLSPGAHQKRLIPIKYKAMKKEFPSI
LRFITVCDYTNPCTKSWFWTRLAKALSLP
```

Or, upload a file: 浏览...



STEP 2 - Set your pairwise alignment options

The default settings will fulfill the needs of most users and, for that reason, are not visible.

[More options...](#)

(Click here, if you want to view or change the default settings.)



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EMBL双序列比对工具：全局比对工具

BLOSUM-80	BLOSUM-62	BLOSUM-45
PAM-1	PAM-120	PAM-250
亲缘关系较近的 序列之间的比对	←→	亲缘关系较远的 序列之间的比对

Enter or paste your second protein sequence

>seq2 for global alignment
TTLDDPLGHMPERFDFAFICYCPSDIQFVQE
ASELIEKRCRRMWWWVSDDYLSKECDFQ
LRFITVCDYTNPCTKSWFWTRLAKALSLP

Or, upload a file: 浏览...

STEP 2 - Set your pairwise alignment options

MATRIX	GAP OPEN	GAP EXTEND	OUTPUT FORMAT
BLOSUM62	10	0.5	pair
END GAP PENALTY	END GAP OPEN	END GAP EXTEND	
false	10	0.5	

STEP 3 - Submit your job

☐ Be notified by email (Tick this box if you want to be notified by email when the results are available)



	上下一致
:	上下相似
.	上下不相似
空格	字母对空位



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KLKALLEKKAYLEWPKDRRL
.:|. |:.|...| |
AMKK-----EFPSILR-E

Gap的类型及分值设置

```
#=====
# Aligned_sequences: 2
# 1: seq1_for_global_alignment
# 2: seq2_for_global_alignment
# Matrix: EBLOSUM62
# Gap_penalty: 1.0
# Extend_penalty: 5.0
#
# Length: 201
# Identity:      46/201 (22.9%)
# Similarity:    78/201 (38.8%)
# Gaps:          75/201 (37.3%)
# Score: 210.0
#=====
```

gap open

gap extend

分散的空位

```
seq1_for_glob 1 MHHHHHSSGVDLGTENLYFQSMKIT-QEQLKR--NVRFHAFISYSEHDS 47
                        || .:.|.. . ||.|||.|...|
seq2_for_glob 1 -----TTLDDPLGHMPE-RFDAFICYCPSD- 24

seq1_for_glob 48 L-WVKNELIPNLEKEDGSI-L-ICLYE-SYFDPGKS-IS-ENIVS-FIEK 90
      :|: |:|..|| :. :. | :|:.. ... || : : :|.| .|||
seq2_for_glob 25 IQFVQ-EMIRQLE-QT-NYRLKLCVSDRDVL-PG-TCV-W-SIASELIEK 67

seq1_for_glob 91 -SYKSIFVLSPNFVQN-EWCHYEFYFAH-HNLFHENSDDHI-ILI-LLEPI 135
      .....|:|:|:|:|:| | |:|:|:| | :| :|:| | . |:| |
seq2_for_glob 68 RCRRMVVVSDDYLSKE-CDFQTKFA-L-SL-SPGA-H-Q-K-RLI-PI 108

seq1_for_glob 136 PFY-CIPTR-YHK-LKALLEKKA-YLEWPK-DRRKCGLFWANLRA-AIN- 178
      . | :. :. :.. |: :. :.. |.. | . | ..||..| | |:|
seq2_for_glob 109 K-YKAM-KKEFPSILR-FI-TVCDYTN-P-C-T-K-SWFWTRL-AKALSL 148

seq1_for_glob 179 - 178
seq2_for_glob 149 P 149
```



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gap open

gap extend

集中的空位

Gap的类型及分值设置

Enter or paste your second protein sequence in any supported format:

```
>seq2_for_global_alignment  
SEQUENCETTLDDPLGHMPERFDAFICYCPSDIQFVQEMIRQLEQTNYRLKLCVSDRDVL  
PGTCVWSIASSELIEKRCRRMVVVVSDDYLSKECDFQTKFALSLSPGAHQKRLIPIKYKA  
MKKEFPSILRFITVCDYTNPCTKSWFWTRLAKALSLP
```

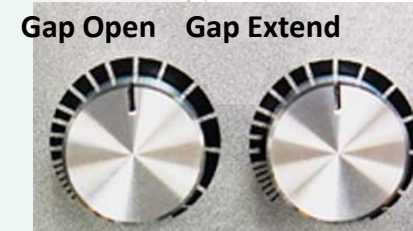
Or, upload a file:

浏览...

调整 gap open 和
gap extend 以达到
期望的比对结果

STEP 2 - Set your pairwise alignment options

MATRIX	GAP OPEN	GAP EXTEND	OUTPUT FORMAT
BLOSUM62	10	0.5	pair
END GAP PENALTY	100	0.0005	
END GAP OPEN	50	0.001	
false	25	0.05	
	20	0.1	
	15	0.2	
	10	0.4	
	5	0.5	
	1	0.6	
		0.8	
		1.0	
		5.0	
		10.0	



STEP 3 - Submit your job

☐ Be notified by email (Tick this)

email when the results are available)

If you plan to use these services please contact us.



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EMBL双序列比对工具：局部比对工具

Local Alignment

Local alignment tools find one, or more, alignments describing the most similar region(s) within the sequences to be aligned. There are separate forms for protein or nucleotide sequences.

Water (EMBOSS)

EMBOSS Water uses the Smith-Waterman algorithm (modified for speed enhancements) to calculate the local alignment of two sequences.

 [Protein](#)  [Nucleotide](#)

Matcher (EMBOSS)

EMBOSS Matcher identifies local similarities between two sequences using a rigorous algorithm based on the LALIGN application.

 [Protein](#)  [Nucleotide](#)

LALIGN

LALIGN finds internal duplications by calculating non-intersecting local alignments of protein or DNA sequences.

 [Protein](#)  [Nucleotide](#)

PromoterWise

PromoterWise compares two DNA sequences allowing for inversions and translocations, ideal for promoters.

 [Launch PromoterWise](#)

EMBL双序列比对工具：局部比对工具

STEP 1 - Enter your protein sequences

Enter or paste your first protein sequence in any supported format:

```
>Seq1
MHIIHHHHSSGVDLGTEENLYFQSMKTTQEQLKRNVRFHAFISYSEHDSLWVKNELIPNLEK
EDGSILICLYESYFDPGKSIENIVSFIEKSYKSIFVLSNPFVQNEWCHYEFYFAHHNLF
HENS DHII LLEPIPFYCIPTRYHKLKALLEKKAYLEWPKDRRKCGLFWANLRAAIN
```

Or, upload a file: 浏览...

AND

Enter or paste your second protein sequence in any supported format:

```
>Seq2
GTEENLYFQSMKTTQEQLKRNVRFHAFISYSEHDSLWVKNELIPNLEKEDGSILICLYESY
FDPGKEWCHYEFYFAHHNLFHENS DHII LLEPIPFYCIPTRAAAAAAAAAAAAA
```

Or, upload a file: 浏览...

local.fasta

STEP 2 - Set your pairwise alignment options

The default settings will fulfill the needs of most users and, for that reason, are not visible.

(Click here, if you want to view or change the default settings.)

STEP 3 - Submit your job

☐ Be notified by email (Tick this box if you want to be notified by email when the results are available)



EMBL双序列比对工具：局部比对工具

黑色是相似的部分，红色是不相似的部分

>Seq1

MHHHHHSSGVDLGTENLYFQSMKTTQEQLKRNVRFHAFISYSEHDSLWVKNELIPNLEKED
GSILICLYESYFDPGKSISENIVSFIEKSYKSIFVLSPNFVQNEWCHYEFYFAHHNLFHENS
DHIILILLEPIPFYCIPTRYHKLKALLEKKAYLEWPKDRRKCGLFWANLRAAIN

>Seq2

GTENLYFQSMKTTQEQLKRNVRFHAFISYSEHDSLWVKNELIPNLEKEDGSILICLYESYFD
PGKEWCHYEFYFAHHNLFHENS DHIILILLEPIPFYCIPTRAAAAAAAAAA

局部比对结果：

```
Seq1      22 GTENLYFQSMKTTQEQLKRNVRFHAFISYSEHDSLWVKNELIPNLEKEDG      71
          |||
Seq2      1  GTENLYFQSMKTTQEQLKRNVRFHAFISYSEHDSLWVKNELIPNLEKEDG      50

Seq1      72 SILICLYESYFDPGKSISENIVSFIEKSYKSIFVLSPNFVQNEWCHYEFY    121
          |||
Seq2      51 SILICLYESYFDPGK-----EWCHYEFY      73

Seq1     122 FAHHNLFHENS DHIILILLEPIPFYCIPTR      151
          |||
Seq2      74 FAHHNLFHENS DHIILILLEPIPFYCIPTR      103
```



全局比对与局部比对比较

局部比对

```
#####
# Aligned_sequences: 2
# 1: Seq1
# 2: Seq2
# Matrix: EBLOSUM62
# Gap_penalty: 10.0
# Extend_penalty: 0.5
#
# Length: 130
# Identity: 103/130 (79.2%)
# Similarity: 103/130 (79.2%)
# Gaps: 27/130 (20.8%)
# Score: 551.0

Seq1 14 GTENLYFQSMKTTQEQLKRNVRFHAFISYSEHDSLWVKNELIPNLEKEDG 63
      |||
Seq2 1 GTENLYFQSMKTTQEQLKRNVRFHAFISYSEHDSLWVKNELIPNLEKEDG 50
      |||
Seq1 64 SILICLYESYFDPGKSISENIVSFIEKSYKSIFVLSPNFVQNEWCHYEYF 113
      |||
Seq2 51 SILICLYESYFDPGK-----EWCHYEYF 73
      |||
Seq1 114 FAHHNLFHENS DHII LLEPIPFYCIPT R 143
      |||
Seq2 74 FAHHNLFHENS DHII LLEPIPFYCIPT R 103
```

全局比对

```

#####
# Aligned_sequences: 2
# 1: Seq1
# 2: Seq2
# Matrix: EBLOSUM62
# Gap_penalty: 10.0
# Extend_penalty: 0.5
#
# Length: 178
# Identity: 104/178 (58.4%)
# Similarity: 104/178 (58.4%)
# Gaps: 64/178 (36.0%)
# Score: 543.0
#####
Seq1 1 MHHHHHHSSGVDLGTENLYFQSMKTTQEQLKRNVRFHAFISYSEHDSLWV 50
      |||
Seq2 1 -----GTENLYFQSMKTTQEQLKRNVRFHAFISYSEHDSLWV 37
      |||
Seq1 51 KNELIPNLEKEDGSILICLYESYFDPGKSISENIVSFIEKSYKSIFVLSP 100
      |||
Seq2 38 KNELIPNLEKEDGSILICLYESYFDPGK----- 65
      |||
Seq1 101 NfVQNEwChYEFYfAHhNLFhENSdHIILILLEPIPFYCIPTryHKLKAL 150
      |||
Seq2 66 -----EWChYEFYfAHhNLFhENSdHIILILLEPIPFYCIPTRAAAAAAA 110
      |||
Seq1 151 LEKKAYLEWPKDRRKCGLFWANLRAAIN 178
      ....
Seq2 111 AAAA----- 114

```



EMBL双序列比对工具：局部比对工具

STEP 1 - Enter your protein sequences

Enter or paste your first protein sequence in any supported format:

```
>seq3  
TTLDDPLGHMPERFDAFICYCPSDIQFVQEMIRQLEQTNYRLKLCVSDRDVLPGTCVWSI  
ASELIEKRCRRMVVVVSDDSLSPGAHQKRLIPIKYKAMKKEFPSILRFITVCDYTNPCT  
KSWFWTRLAKALSLP
```

Or, upload a file: 浏览...

AND

Enter or paste your second protein sequence in any supported format:

```
>seq4  
MHSHHHHSSGVDLGTENLYFQSMKTTQEQLKRNVRFHAFISYSEHDSLWVKNELIPNLEK  
EDGSILICLYESYFDPGKSISENIVSTSNQNEWCHYEFYFAHHNLFHENS DHILILLEP  
IPFYCIPTRYHKLKALLEKKAYLEWPKDRRCGLFWANLRAAIN
```

Or, upload a file: 浏览...

STEP 2 - Set your pairwise alignment options

MATRIX	GAP OPEN	GAP EXTEND	OUTPUT FORMAT
BLOSUM62	10	5.0	pair

STEP 3 - Submit your job

☐ Be notified by email (Tick this box if you want to be notified by email when the results are available)



EMBL双序列比对工具：局部比对工具

黑色是相似的部分，红色是不相似的部分

>Seq3

TTLDDPLGHMPERFDAFICYCPSDIQFVQEMIRQLEQTNYRLKLCVSDRDVLPGTCVWSI
ASELIEKRCRMVVVVSDDSLSPGAHQKRLIPIKYKAMKKEFPSILRFITVCDYTNPCT
KSWFWTRLAKALSLP

>Seq4

MHHHHHSSGVDLGTENLYFQSMKTTQEQLKRNVRFHAFISYSEHDSLWVKNELIPNLEK
EDGSILICLYESYFDPGKSI SENIVSSNQNEWCHYEFYFAHHNLFHENS DHIILILLEPI
PFYCIPTRYHKLKALLEKKAYLEWPKDRRKCGLFWANLRAAIN

局部比对结果：

```
seq3   13 RFDAFICYCPSDIQFVQ-EMIRQLEQTNYRLKLCVSDRDVLPGTCV   57
      ||.|||.|...|...|: |:|..||:.....|:.....|...:
seq4   35 RFHAFISYSEHDSLWVKNELIPNLEKEDGSILICLYESYFDPGKSI   80
```



全局比对与局部比对比较

局部比对

```
seq3    13 RFDAFICYCPSDIQFVQ-EMIRQLQLTNYRLKLCVSDRDVLPGTCV 57  
      ||.|||.|...|.:.: |:|.|||:.....|:.....|...:  
seq4    35 RFHAFISYSEHDSLVNKNELIPNLEKEDGSILICLYESYFDPGKSI 80
```

全局比对

```

seq3      1 -----TTLDPLGHMPPERFDAFICYCPSDIQ      26
           ||:.....: ||:|||.|||.||.
seq4      1 MHHHHHHSSGVDLGTENLYFQSMKTTQEQLKRN--RFHAFISYSEHDSL 48
seq3     27 FVQ-EMIRQLEQTNRYRLKLCVSDRDVLPGICV-----WS---- 59
           |:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|.
seq4     49 WVKNELIPNLEKEDGSILICLYESYFDPGKSISENIVSTSNQNEWCHYEF 98
seq3     60 --IASELIEKRCRRMVVVVSDLSLSPGAHQKRLIPIKYAMKK----- 101
           ....|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|.
seq4     99 YFAHNNLFHENS DHIIILILLEPIPF-----YCIPTRYHKLKALLEKKA 141
seq3    102 --EFSILRFITVCDYTNPCTKSWFWIRLAKALSLP      135
           |:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|.
seq4    142 YLEWPKDRR-----KC--GLFWANLRAAIN--      164

```



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其他在线双序列比对工具

软件名	比对类型	网址链接
EMBL	Global/Local	http://www.ebi.ac.uk/Tools/psa
PIR	Global	http://pir.georgetown.edu/pirwww/search/pairwise.shtml
Lalign	Global/Local	http://www.ch.embnet.org/software/LALIGN_form.html
LAGAN	Global	http://lagan.stanford.edu/lagan_web/index.shtml
AlignMe	Alignment of Membrane Proteins	http://www.bioinfo.mpg.de/AlignMe/AlignMe.html
MCALIGN	Alignment of non-coding DNA sequences	http://homepages.ed.ac.uk/eang33/mcalign/mcinstructions.html
Biotoools	Global/Local	http://1.51.215.28/~gongj/biotoools

其他在线双序列比对工具

Biotoools双序列比对工具: <http://101.76.246.94/~gongj/biotoools>

Bioinformatical Tools

- Introduction
 - HOME
 - 0-2
- Subcellular Localization
 - What's subcellular localization?
 - About Database
 - Ensemble Prediction Method
 - Prediction by PDB Classification
 - Prediction by CATH Classification
 - Prediction by SCOP Classification
 - Insert New Entries
 - Delete Old Entries
- Sequence Alignment
 - **Pairwise Alignment**
 - Multiple Alignment
- Protein Secondary Structure
 - DSSP Converter
 - 3-2
- Protein Tertiary Structure
 - PDB Converter
 - 3-2
- ORF Detection
 - 4-1
 - 4-2
- Database Search
 - 5-1
 - 5-2

Pairwise Sequence Alignment (PROTEIN)

➡ STEP 1 - Set your pairwise alignment options :

sequence type :

alignment method :

gap penalty :

substitution matrix :

➡ STEP 2 - Enter your protein sequences :

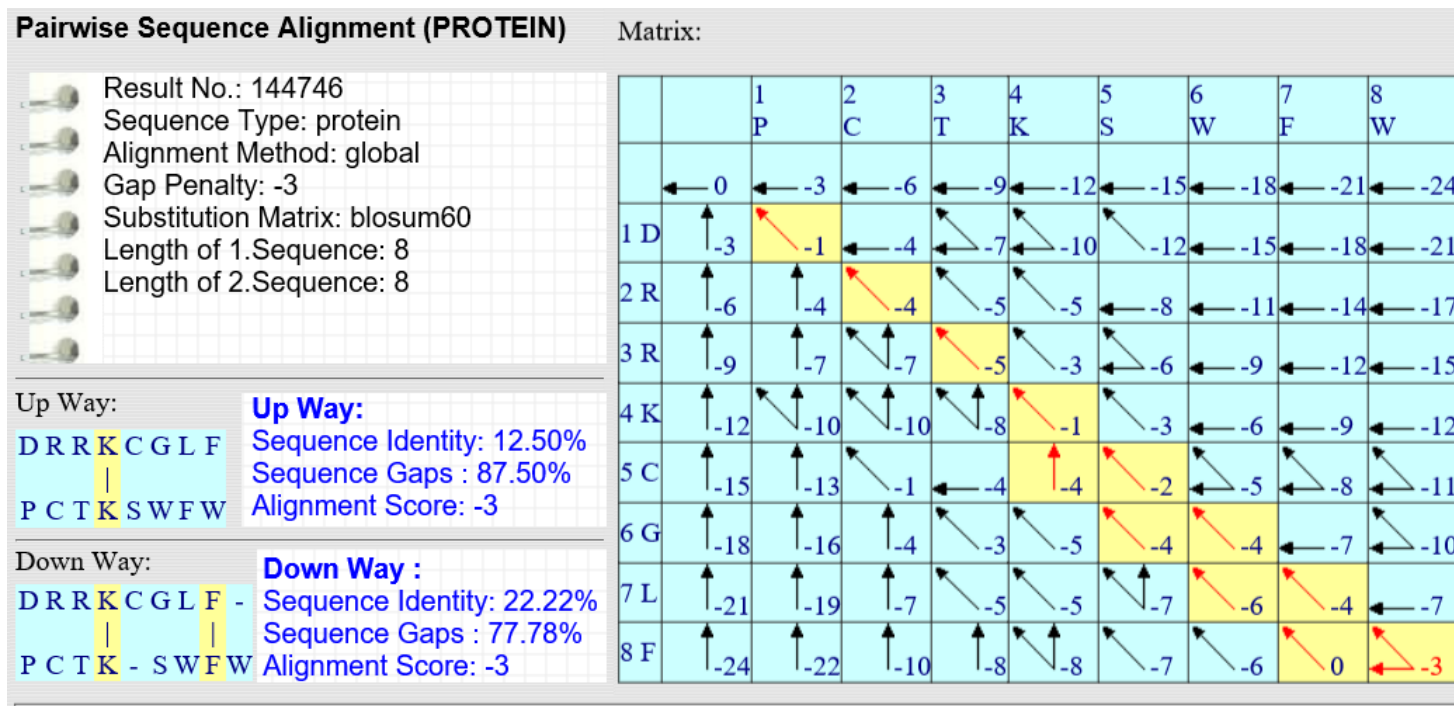
☒ enter or paste your sequences here :

1.seq

2.seq

☐ or upload a sequence file ([example](#)):

其他在线双序列比对工具



BLAST搜索

✓ 复习：数据库中的序列相似性搜索



在游戏麻将泰坦中，你需要用眼睛从一推麻将牌中找出一对相同的麻将牌。



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BLAST搜索

✓ 复习：数据库中的序列相似性搜索

对于一个蛋白质或核酸序列，你需要从序列数据库中找到与它相同或相似的序列。不可能再用眼睛去比较每一对序列，因为数据库中有太多序列，甚至用眼睛比较一对序列都是不可能做到的。

```
>TLR_433
MLEEVKLAELKKLDPENLSEYSLIYNAGYNIISKLPGLCKNPLQLQIKLEHNQHE
LPDGVFASCSNLTENLNGYNIIEVKNDPFKTELENLILDSHNLKSNLGLQQKLNLR
ELVLYSNQITELNKEDLKFLSNTSLNSLDLSSNPLKEFHTGCLHAIGNLFLILNNVGL
ENRTKKLCTELSDTAIQNLSLHVKLSHINRLTLQGLQNTLVNLKSNLSVIEDDSF
QWLSKLEYLNLEDNNIINVSSHLFYLSSITHNLINSLTGKIEDFSQWHLHLEYLMD
NNNFRITITNMFTGLKNLYSLYNCNTNLQRTNKTIVSLANSRLQVNLTKTRISTVE
SEAFSSLGQLKILDGLNEINQELTGHEFGLNIEYIYLYNKNTVLRSESFIFVPSLR
KLMRLKVGCCNNLAISPSFPHPLRLTLVDISNNNIANIREDLFNGHELDILNLQHNLA
RLWKCANPGGVLFLKDVNHLHNLKSNLGFDEIPVHVFKGLHQLKDLGSSNNLNLFA
TLFDDQTSNLNLNLQNLITISVEENVFGPAFKSLRTLEMDFNPFDCIESIAWFAWLNLD
TQAYIPGLQSQYICNTPKYHGTIVLHFDTSACKDSAPFKLLFLITTTAVMQFMFIVLLI
HFEGWRIAFYWNISINRILGFKELDRPLGVFDYDAYVIHARKDNTNVLNFTTLEENEQF
QVFKLEERDFEAGISEFEAIINCIRRSRKIIIVITEHLLQDPWCRKFKVHHAQQAEIQ
SRDSIILIFLHNIQDYKLNHALCLRRGMFRSCCINLWVQKERINAFHQQLMALKSNK
VFPVFNFLRAALRGVTLSSFRGSRGNQGLQGAQGVPSSEGSAAEIRRELPEPL
GEAQCIKRPVLVLLWFLVGLHEKHLKFLALCSAAHQQLKHPYVINTGFLKPKQHSIIPD
AMKGKSFPLSQLKPGHPCCHLTHSSGSDQCCTASFLGALGHKRLDTMQ
```

BLAST

```
>TLR_24
MKGRSSYLIYSFGGLLSLWLVVSTNQCTVRYNVADCSHLKLTIFDDLL
HHQLRGLPFPANFTRYSQLALLDAGFNSISKLEPELCQILPLLKVLNLQHN
APCTNLTLELHAGMTATKFTKSHREHNCSTLTELSSNNIISTVPTATGDD
KHN
>TLR_30
MSRPLPYHIYFFTGLLTCLWICTSAHKCTVRHEVADCSHLKLTQIE
LKV
HQLRLPFPANFTRYSLITLDDGFNSISKLEPELCQILPLLKVLNLQHN
LKV
>TLR_324
VFCM
>TLR_340
MLEEVKLAELKKLDPENLSEYSLIYNAGYNIISKLPGLCKNPLQLQIKLEHNQHE
LPDGVFASCSNLTENLNGYNIIEVKNDPFKTELENLILDSHNLKSNLGLQQKLNLR
ELVLYSNQITELNKEDLKFLSNTSLNSLDLSSNPLKEFHTGCLHAIGNLFLILNNVGL
ENRTKKLCTELSDTAIQNLSLHVKLSHINRLTLQGLQNTLVNLKSNLSVIEDDSF
QWLSKLEYLNLEDNNIINVSSHLFYLSSITHNLINSLTGKIEDFSQWHLHLEYLMD
NNNFRITITNMFTGLKNLYSLYNCNTNLQRTNKTIVSLANSRLQVNLTKTRISTVE
SEAFSSLGQLKILDGLNEINQELTGHEFGLNIEYIYLYNKNTVLRSESFIFVPSLR
KLMRLKVGCCNNLAISPSFPHPLRLTLVDISNNNIANIREDLFNGHELDILNLQHNLA
RLWKCANPGGVLFLKDVNHLHNLKSNLGFDEIPVHVFKGLHQLKDLGSSNNLNLFA
TLFDDQTSNLNLNLQNLITISVEENVFGPAFKSLRTLEMDFNPFDCIESIAWFAWLNLD
TQAYIPGLQSQYICNTPKYHGTIVLHFDTSACKDSAPFKLLFLITTTAVMQFMFIVLLI
HFEGWRIAFYWNISINRILGFKELDRPLGVFDYDAYVIHARKDNTNVLNFTTLEENEQF
QVFKLEERDFEAGISEFEAIINCIRRSRKIIIVITEHLLQDPWCRKFKVHHAQQAEIQ
SRDSIILIFLHNIQDYKLNHALCLRRGMFRSCCINLWVQKERINAFHQQLMALKSNK
VFPVFNFLRAALRGVTLSSFRGSRGNQGLQGAQGVPSSEGSAAEIRRELPEPL
GEAQCIKRPVLVLLWFLVGLHEKHLKFLALCSAAHQQLKHPYVINTGFLKPKQHSIIPD
AMKGKSFPLSQLKPGHPCCHLTHSSGSDQCCTASFLGALGHKRLDTMQ
```

UniProtKB

UniProt Knowledgebase

Swiss-Prot (550,552)



Manually annotated
and reviewed.

TrEMBL (60,971,489)

Automatically
annotated and not
reviewed.



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Advanced Search Interface

Sequence (BLAST/FASTA/PSI-BLAST)

Sequence search (BLAST or FASTA)

Structure Id

Chain Id

Sequence

BLAST Align Retrieve/ID mapping

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Swiss-Prot

UniRef

Sequence clusters

UniParc

Sequence archive

Proteomes

New

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BLAST是如何工作的?

BLAST (Basic Local Alignment Search Tool, 基本局部比对搜索工具) 是目前最常用的数据库搜索程序。

BLAST基本原理要点是片段对的概念。所谓片段对是指两个给定序列中的一对子序列, 它们的长度相等, 且可形成无空位的完全匹配。

KSD	FGETS	IV	ATGG	STE
NE	FGETS	LI	ATGG	NPA

BLAST首先找出探测序列和目标序列间所有的匹配程度超过一定阈值的序列片段对, 然后对片段对根据给定的相似性阈值进行延伸, 得到一定长度的相似性片段, 最后给出高分值片段对 (high-scoring pairs, HSPs)。改进后的BLAST允许空位的插入。

K	SD	FGETS	IV	ATGG	S	TE
	::		::		:	
	NE	FGETS	LI	ATGG	N	PA

高分值片段对



BLAST的种类

BLAST实际上是综合在一起的一组工具的统称，它不仅可用于直接对蛋白质序列数据库和核酸序列数据库进行搜索，而且可以将带搜索的核酸序列翻译成蛋白质序列后再进行搜索，或反之，以提高搜索效率。

Blastp：用蛋白质序列搜索蛋白质序列数据库

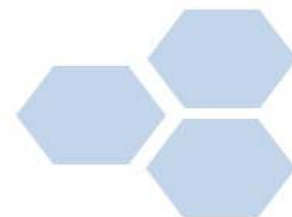
Blastn：用核酸序列搜索核酸序列数据库

Blastx：将核酸序列按6条链翻译成蛋白质序列后搜索蛋白质序列数据库

tblastn：用蛋白质序列搜索核酸序列数据库，数据库中的核酸序列要按6条链翻译成蛋白质序列后再搜索。

tblastx：将核酸序列按6条链翻译成蛋白质序列后搜索核酸序列数据库，数据库中的核酸序列要按6条链翻译成的蛋白质序列后再搜索。

根据搜索算法分：标准BLAST，PSI-BLAST，PHI-BLAST等。



BLAST的种类

BLAST实际上是综合在一起的一组工具的统称，它不仅可用于直接对蛋白质序列数据库和核酸序列数据库进行搜索，而且可以将带搜索的核酸序列翻译成蛋白质序列后再进行搜索，或反之，以提高搜索效率。

Blastn：用核酸序列搜索核酸序列数据库

Blastp：用蛋白质序列搜索蛋白质序列数据库

核酸序列



BLASTn

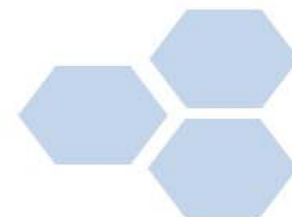
序列按6条链翻译成蛋白质序列后搜索蛋白质序列数据库
蛋白质序列搜索核酸序列数据库，数据库中的核酸序列要按6
蛋白质序列后再搜索。

序列按6条链翻译成蛋白质序列后搜索核酸序列数据库，
核酸序列要按6条链翻译成的蛋白质序列后再搜索。

BLAST：标准BLAST，PSI-BLAST，PHI-BLAST等。



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BLAST

BLAST实际上一组工具的统称，它不仅可用于直接对蛋白质序列数据库进行搜索，而且可以将带搜索的核酸序列翻译成蛋白质序列后再搜索，或反之，以提高搜索效率。

蛋白质序列

蛋白质数据库

BLAST是一组工具的统称，它不仅可用于直接对蛋白质数据库进行搜索，而且可以将带搜索的核酸序列翻译成蛋白质序列后再搜索，或反之，以提高搜索效率。

Blastn：用核酸序列数据库

BLASTp

Blastp：用蛋白质序列搜索蛋白质序列数据库

Blastx：将核酸序列按6条链翻译成蛋白质序列后搜索蛋白质序列数据库

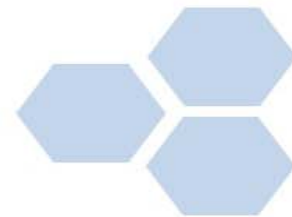
tblastn：用蛋白质序列搜索核酸序列数据库，数据库中的核酸序列要按6条链翻译成蛋白质序列后再搜索。

tblastx：将核酸序列按6条链翻译成蛋白质序列后搜索核酸序列数据库，数据库中的核酸序列要按6条链翻译成的蛋白质序列后再搜索。

根据搜索算法分：标准BLAST，PSI-BLAST，PHI-BLAST等。



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BLAST

BLAST实际
白质序列数
序列翻译成

Blastp: 用蛋

Blastn: 用核酸序列搜索核酸序列数据库

Blastx: 将核酸序列按6条链翻译成蛋白质序列后搜索蛋白质序列数据库

tblastn: 用蛋白质序列搜索核酸序列数据库, 数据库中的核酸序列要按6条链翻译成蛋白质序列后再搜索。

tblastx: 将核酸序列按6条链翻译成蛋白质序列后搜索核酸序列数据库, 数据库中的核酸序列要按6条链翻译成的蛋白质序列后再搜索。

根据搜索算法分: 标准BLAST, PSI-BLAST, PHI-BLAST等。

核酸序列

蛋白质序列

蛋白质
数据库

BLASTx

不仅可用于直接对蛋
可以将带搜索的核酸
提高搜索效率。

BLAST的

BLAST实际-
白质序列数
序列翻译成

Blastp: 用蛋白

Blastn: 用核酸序列搜索核酸序列数据库

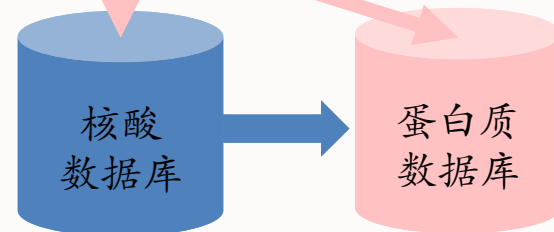
Blastx: 将核酸序列按6条链翻译成蛋白质序列后搜索蛋白质序列数据库

tblastn: 用蛋白质序列搜索核酸序列数据库, 数据库中的核酸序列要按6条链翻译成蛋白质序列后再被搜索。

tblastx: 将核酸序列按6条链翻译成蛋白质序列后搜索核酸序列数据库, 数据库中的核酸序列要按6条链翻译成的蛋白质序列后再被搜索。

根据搜索算法分: 标准BLAST, PSI-BLAST, PHI-BLAST等。

蛋白质序列



tBLASTn

它不仅可用于直接对蛋
且可以将带搜索的核酸
以提高搜索效率。

BLAST的

BLAST实际-
白质序列数
序列翻译成

Blastp: 用蛋

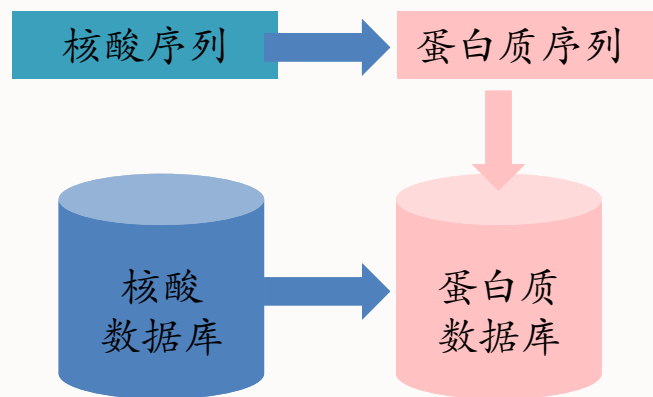
Blastn: 用核酸序列搜索核酸序列数据库

Blastx: 将核酸序列按6条链翻译成蛋白质序列后搜索蛋白质序列数据库

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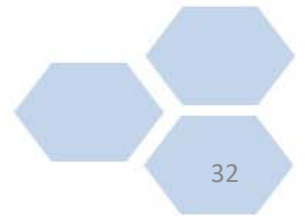
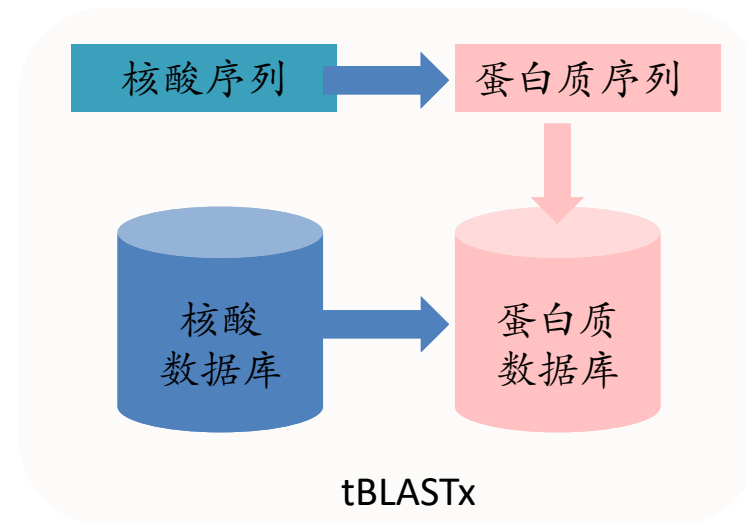
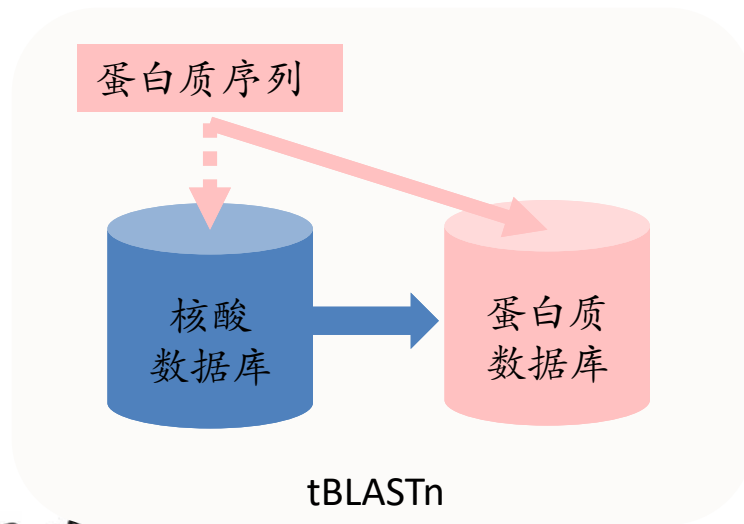
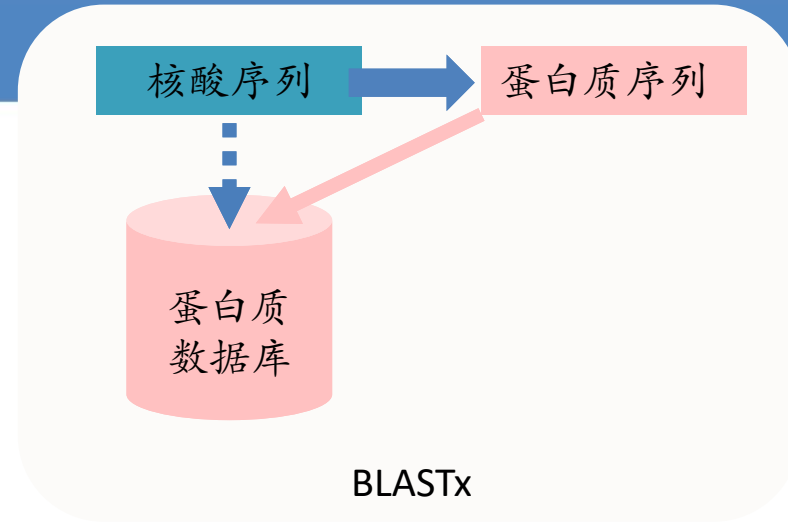
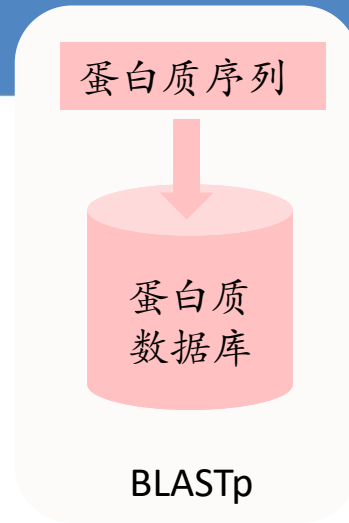
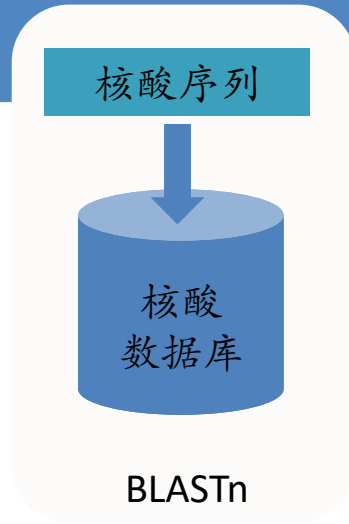
tblastx: 将核酸序列按6条链翻译成蛋白质序列后搜索核酸序列数据库, 数据库中的核酸序列要按6条链翻译成的蛋白质序列后再搜索。

根据搜索算法分: 标准BLAST, PSI-BLAST, PHI-BLAST等。



它不仅可用于直接对蛋
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BLAST的种类

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Blastp：用蛋白质序列搜索蛋白质序列数据库

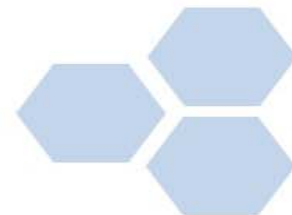
Blastn：用核酸序列搜索核酸序列数据库

Blastx：将核酸序列按6条链翻译成蛋白质序列后搜索蛋白质序列数据库

tblastn：用蛋白质序列搜索核酸序列数据库，数据库中的核酸序列要按6条链翻译成蛋白质序列后再搜索。

tblastx：将核酸序列按6条链翻译成蛋白质序列后搜索核酸序列数据库，数据库中的核酸序列要按6条链翻译成的蛋白质序列后再搜索。

根据搜索算法分：标准BLAST，PSI-BLAST，PHI-BLAST等。



NCBI: BLASTp



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Basic Local Alignment Search Tool

BLAST finds regions of similarity between biological sequences. The program compares nucleotide or protein sequences to sequence databases and calculates the statistical significance.

[Learn more](#)**BLAST+ 2.5.0 released****N
E
W
S**

The new version offers support for HTTPS, accession.version as the primary sequence identifier, support for composition-based statistics with RPS-BLASTN, and a new taxonomic organism report. Fri, 23 Sep 2016 17:00:00 EST [More BLAST news...](#)

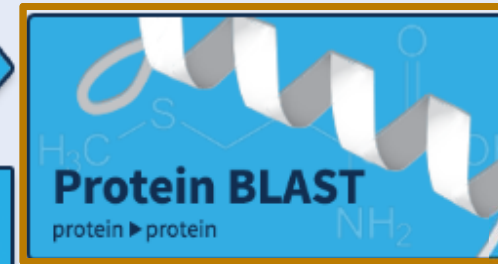
Web BLAST



Nucleotide BLAST
nucleotide ► nucleotide

blastx
translated nucleotide ► protein

tblastn
protein ► translated nucleotide



Protein BLAST
protein ► protein

BLAST Genomes

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Standard Protein BLAST

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Enter Query Sequence

Enter accession number(s), gi(s), or FASTA sequence(s) [Clear](#)

```
>my_protein_seq_for_NCBI_blast
VKCRLNVLLWYQDAYGEVEINDGKLYDAYVSYSDCPEDRKFEVNFILKPQLERRRGYKFL
DDRDLTPRAEPSADLLVNLSCRRLLIVVLSDAFLSRAWCSHSFREGLCRLLELTRPIFI
TFEGQRRDPAHPALRLLRQHRHLVTLVLRPGSVTPSSDFWKEVQLALPRKVQYRPVEGD
PQTQLQDDKDPMLILRGRVPEGRALDSEVDPDPEGDLGVRGPVFGEPSAPPHTSGVSLGE
```

Query subrange [?](#)From To

Or, upload file

浏览...

Job Title

my_protein_seq_for_NCBI_blast

Enter a descriptive title for your BLAST search [?](#)☐ Align two or more sequences [?](#)

Choose Search Set

Database

Orga

Option

Exclude

Optional

Entrez Query

Optional

☐ Models (XM/XP) ☐ Uncultured/environmental sample sequencesEnter an Entrez query to limit search [?](#)[YouTube](#) [Create custom database](#)同时提交多个
BLAST任务给搜索任
务起个名输入待搜
索的序列搜索输入序
列的子序列

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UniProtKB/Swiss-Prot(swissprot) ✓

Organism

Optional

Exclude

Optional

Entrez Query

Optional

Non-redundant protein sequences (nr)

Reference proteins (refseq_protein)

Model Organisms (landmark)

UniProtKB/Swiss-Prot(swissprot)

Patented protein sequences(pat)

Protein Data Bank proteins(pdb)

Metagenomic proteins(env_nr)

Transcriptome Shotgun Assembly proteins (tsa_nr)

Enter an Entrez query to limit search

☐ Exclude

taxa will be shown

sequences

YouTube



[Create custom database](#)

选择被搜索的数据库：
用NCBI的BLAST工具
搜索Swissprot数据库

Program Selection**Algorithm**☒ blastp (protein-protein BLAST)☐ PSI-BLAST (Position-Specific Iterated BLAST)☐ PHI-BLAST (Pattern Hit Initiated BLAST)☐ DELTA-BLAST (Domain Enhanced Lookup Time Accelerated BLAST)


Choose a BLAST algorithm

BLASTSearch using **Blastp (protein-protein BLAST)**☐ Show results in a new window

BLAST [®] >> blastp suite[Home](#)[Recent Results](#)[Saved Strategies](#)[Help](#)**Standard Protein BLAST**[blastn](#)**[blastp](#)**[blastx](#)[tblastn](#)[tblastx](#)BLASTP programs search protein databases using a protein query. [more...](#)[Reset page](#)**Choose Search Set****Database**UniProtKB/Swiss-Prot(swissprot) **Organism***Optional*☐ Exclude Enter organism common name, binomial, or tax id. Only 20 top taxa will be shown. **Exclude***Optional*☐ Models (XM/XP) ☐ Uncultured/environmental sample sequences**Entrez Query***Optional*[YouTube](#) [Create custom database](#)Enter an Entrez query to limit search 

把搜索范围限定在某一特定物种，或者排除某一物种。

Program Selection**Algorithm**

- ☒ **blastp (protein-protein BLAST)**
- ☐ PSI-BLAST (Position-Specific Iterated BLAST)
- ☐ PHI-BLAST (Pattern Hit Initiated BLAST)
- ☐ DELTA-BLAST (Domain Enhanced Lookup Time Accelerated BLAST)
- Choose a BLAST algorithm 

选择BLAST算法：标准算法

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

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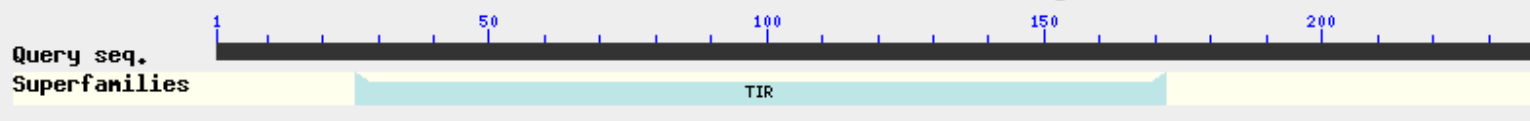
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**BLAST**® » **blastp suite** » RID-ZT2RRDU2014[Home](#)[Recent Results](#)[Saved Strategies](#)[Help](#)**BLAST Results**[Edit and Resubmit](#)[Save Search Strategies](#)[▶ Formatting options](#)[▶ Download](#)[YouTube](#) [How to read this page](#) [Blast re](#)**my_protein_seq_for_NCBI_blast**RID [ZT2RRDU2014](#) (Expires on 10-12 14:47 pm)Query ID [Id|Query_14945](#)Description [my_protein_seq_for_NCBI_blast](#)Molecule type [amino acid](#)Query Length [271](#)Database Name [swissprot](#)Description [Non-redundant UniProtKB/SwissProt s](#)Program [BLASTP 2.5.1+ ▶ Citation](#)Other reports: [▶ Search Summary](#) [\[Taxonomy reports\]](#) [\[Distance tree of results\]](#) [\[Multiple alignment\]](#)**New** Analyze your query

第一部分：搜索任务描述

Graphic Summary**Show Conserved Domains**

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

**Distribution of 50 Blast Hits on the Query Sequence**

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

Color key for ali

<40

40-50

50-

第二部分：图形化搜索结果



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Graphic Summary

Show Conserved Domains

输入序列所属的蛋白质家族

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

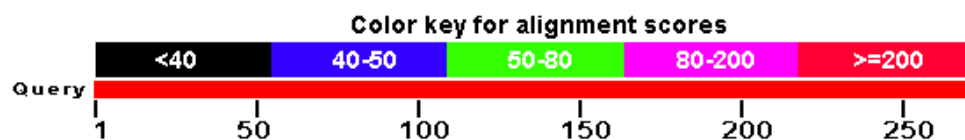
Query seq.
Superfamilies

TIR

找到50个
高分匹配
片段(Hits)

Distribution of 50 Blast Hits on the Query Sequence

Q9JLZ8 RecName: Full=Single Ig IL-1-related receptor; AltName:.. S=491 E=3.8e-175



所有搜索到的Hits
以不同颜色和长
短的线列出



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Descriptions

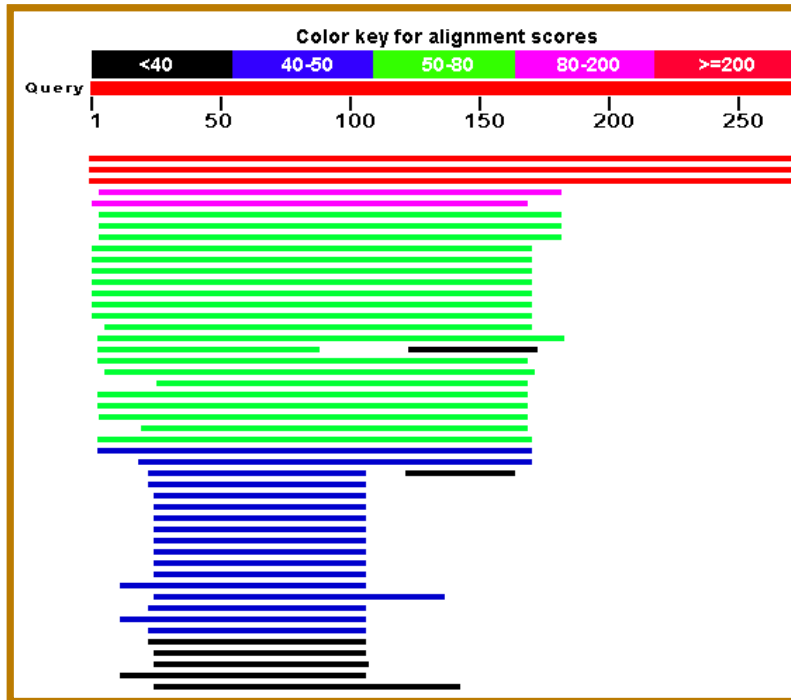
第三部分：序列信息列表

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"/>	RecName: Full=Single Iq IL-1-related receptor; AltName: Full=Single Iq IL-1R-related molecule; A	551	551	100%	0.0	100%	Q6IA17.3
<input type="checkbox"/>	RecName: Full=Single Iq IL-1-related receptor; AltName: Full=Single Iq IL-1R-related molecule; A	493	493	100%	7e-176	89%	Q4V892.1
<input type="checkbox"/>	RecName: Full=Single Iq IL-1-related receptor; AltName: Full=Single Iq IL-1R-related molecule; A	491	491	100%	4e-175	87%	Q9JLZ8.2
<input type="checkbox"/>	RecName: Full=Single Iq IL-1-related receptor; AltName: Full=Single Iq IL-1R-related molecule; A	81.3	81.3	65%	4e-16	32%	Q9NPH3.2
<input type="checkbox"/>	RecName: Full=Single Iq IL-1-related receptor; AltName: Full=Single Iq IL-1R-related molecule; A	80.5	80.5	61%	6e-16	31%	B6ZK77.1
<input type="checkbox"/>	RecName: Full=Single Iq IL-1-related receptor; AltName: Full=Single Iq IL-1R-related molecule; A	79.7	79.7	65%	1e-15	32%	Q61730.1
<input type="checkbox"/>	RecName: Full=Single Iq IL-1-related receptor; AltName: Full=Single Iq IL-1R-related molecule; A	79.7	79.7	65%	1e-15	31%	P59822.1
<input type="checkbox"/>	RecName: Full=Single Iq IL-1-related receptor; AltName: Full=Single Iq IL-1R-related molecule; A	78.6	78.6	65%	2e-15	31%	Q63621.1
<input type="checkbox"/>	RecName: Full=Single Iq IL-1-related receptor; AltName: Full=Single Iq IL-1R-related molecule; A	77.0	77.0	62%	1e-14	32%	Q9NP60.1
<input type="checkbox"/>	RecName: Full=Single Iq IL-1-related receptor; AltName: Full=Single Iq IL-1R-related molecule; A	76.3	76.3	62%	2e-14	29%	P59824.1
<input type="checkbox"/>	RecName: Full=Single Iq IL-1-related receptor; AltName: Full=Single Iq IL-1R-related molecule; A	75.9	75.9	62%	2e-14	29%	Q7YQL9.1
<input type="checkbox"/>	RecName: Full=Single Iq IL-1-related receptor; AltName: Full=Single Iq IL-1R-related molecule; A	75.9	75.9	62%	2e-14	29%	Q9NZN1.2
<input type="checkbox"/>	RecName: Full=Single Iq IL-1-related receptor; AltName: Full=Single Iq IL-1R-related molecule; A	75.5	75.5	62%	4e-14	32%	Q9ERS6.1
<input type="checkbox"/>	RecName: Full=Single Iq IL-1-related receptor; AltName: Full=Single Iq IL-1R-related molecule; A	72.8	72.8	62%	3e-13	31%	B6ZK76.1
<input type="checkbox"/>	RecName: Full=Single Iq IL-1-related receptor; AltName: Full=Single Iq IL-1R-related molecule; A	72.8	72.8	62%	3e-13	29%	P59823.1
<input type="checkbox"/>	RecName: Full=Single Iq IL-1-related receptor; AltName: Full=Single Iq IL-1R-related molecule; A	72.0	72.0	60%	5e-13	32%	Q61098.1
<input type="checkbox"/>	RecName: Full=Interleukin-1 receptor 1; Short=IL-1R-1; Short=IL-1R1; AltName: Full=CD218	68.2	68.2	66%	1e-11	31%	Q13478.1



颜色 | 长短



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Descriptions

Sequences producing significant alignments

Select: [All](#) [None](#) Selected: 0

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	Description	Max score	Total score	Query cover	E value	Ident	Accession
<input type="checkbox"/>	RecName: Full=Single Ig IL-1-related receptor; AltName: Full=Single Ig IL-1R-related molecule; A	551	551	100%	0.0	100%	Q6IA17.3
<input type="checkbox"/>	RecName: Full=Single Ig IL-1-related receptor; AltName: Full=Single Ig IL-1R-related molecule; A	493	493	100%	7e-176	89%	Q4V892.1
<input type="checkbox"/>	RecName: Full=Single Ig IL-1-related receptor; AltName: Full=Single Ig IL-1R-related molecule; A	491	491	100%	4e-175	87%	Q9JLZ8.2
<input type="checkbox"/>	RecName: Full=Interleukin-1 receptor accessory protein; Short=IL-1 receptor accessory protein; S	81.3	81.3	65%	4e-16	32%	Q9NPH3.2
<input type="checkbox"/>	RecName: Full=Interleukin-1 receptor accessory protein-like 1-B; Flags: Precursor	80.5	80.5	61%	6e-16	31%	B6ZK77.1
<input type="checkbox"/>	RecName: Full=Interleukin-1 receptor accessory protein; Short=IL-1 receptor accessory protein; S	79.7	79.7	65%	1e-15	32%	Q61730.1
<input type="checkbox"/>	RecName: Full=Interleukin-1 receptor accessory protein; Short=IL-1 receptor accessory protein; S	79.7	79.7	65%	1e-15	31%	P59822.1
<input type="checkbox"/>	RecName: Full=Interleukin-1 receptor accessory protein; Short=IL-1 receptor accessory protein; S	78.6	78.6	65%	2e-15	31%	Q63621.1
<input type="checkbox"/>	RecName: Full=X-linked interleukin-1 receptor accessory protein-like 2; Short=IL-1 receptor acce	77.0	77.0	62%	1e-14	32%	Q9NP60.1
<input type="checkbox"/>	RecName: Full=Interleukin-1 receptor accessory protein-like 1; Short=IL-1-RAPL-1; Short=IL-1R/	76.3	76.3	62%	2e-14	29%	P59824.1
<input type="checkbox"/>	RecName: Full=Interleukin-1 receptor accessory protein-like 1; Short=IL-1-RAPL-1; Short=IL-1R/	75.9	75.9	62%	2e-14	29%	Q7YQL9.1
<input type="checkbox"/>	RecName: Full=Interleukin-1 receptor accessory protein-like 1; Short=IL-1-RAPL-1; Short=IL-1R/	75.9	75.9	62%	2e-14	29%	Q9NZN1.2
<input type="checkbox"/>	RecName: Full=X-linked interleukin-1 receptor accessory protein-like 2; Short=IL-1 receptor acce	75.5	75.5	62%	4e-14	32%	Q9ERS6.1
<input type="checkbox"/>	RecName: Full=Interleukin-1 receptor accessory protein-like 1-A; Flags: Precursor	72.8	72.8	62%	3e-13	31%	B6ZK76.1
<input type="checkbox"/>	RecName: Full=Interleukin-1 receptor accessory protein-like 1; Short=IL-1-RAPL-1; Short=IL-1R/	72.8	72.8	62%	3e-13	29%	P59823.1
<input type="checkbox"/>	RecName: Full=Interleukin-18 receptor 1; Short=IL-18R-1; Short=IL-18R1; AltName: Full=CD218	72.0	72.0	60%	5e-13	32%	Q61098.1
<input type="checkbox"/>	RecName: Full=Interleukin-18 receptor 1; Short=IL-18R-1; Short=IL-18R1; AltName: Full=CD218	68.2	68.2	66%	1e-11	31%	Q13478.1

期望值E值越接近零，说明输入序列与当前这条序列为同一条序列的可能性越大

查看序列的详细注释

点击查看输入序列与当前这条序列的双序列比对



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NCBI: PSI-BLAST

有时基本的BLAST搜索还是不能满足需要。比如，你想通过一条蛋白质序列，搜罗出一个庞大的蛋白质家族。如果运行基本的BLAST搜索，你只能找到那些和探索序列十分相近的序列，而其他那些远亲就找不到了。换言之，你找到了你直接认识的朋友，而朋友的朋友都丢掉了。

PSI BLAST (Position-Specific Iterated BLAST, 位点特异性迭代BLAST)

PSI-BLAST的特色是每次用位置特异权重矩阵 (Position-Specific Scoring Matrix, PSSM) 搜索数据库后再利用搜索的结果重新构建PSSM，然后用新的PSSM再次搜索数据库，如此反复 (iteration) 直至没有新的结果产生为止。

Seq1: A B C D
Seq2: B B C D
Seq3: A C C D
Seq4: A B D D

	1	2	3	4
A	75%	0	0	0
B	25%	75%	0	0
C	0	25%	75%	0
D	0	0	25%	100%

假设：A的朋友只有B
B的朋友除A外还有C

BLAST® >> blastp suite

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Standard Protein BLAST

[blastn](#)**[blastp](#)**[blastx](#)[tblastn](#)[tblastx](#)

Enter Query Sequence

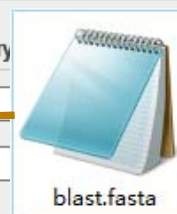
BLASTP programs search protein databases using a protein query. [more...](#)[Reset page](#)[Bookmark](#)Enter accession number(s), gi(s), or FASTA sequence(s) [Clear](#)

```
>my_protein_seq_for_NCBI_blast
VKCRLNVLLWYQDAYGEVEINDGKLYDAYVSYSDCPEDRKFNFIKLPQLERRRGYKLF
DDRDLTPRAEPSADLLVNLSCRLIVVLSDAFLSRAWCSHSFREGLCRLLELTRRPIFI
TFEGQRRDPAHPALRLLRQHRHLVTLILLWRPGSVTPSSDFWKEVQLALPRKVQYRPVEGD
PQTQLQDDKDPMLILGRVPEGRALDSEVDPDPEGLGVRGPFVGEPSAPPHTSGVSLGE
```

Query

From

To



Or, upload file

浏览...

Job Title

my_protein_seq_for_NCBI_blast

Enter a descriptive title for your BLAST search [?](#)☐ Align two or more sequences [?](#)

Choose Search Set

Database

UniProtKB/Swiss-Prot(swissprot) [?](#)

Program Selection

Algorithm

☐ blastp (protein-protein BLAST)☒ PSI-BLAST (Position-Specific Iterated BLAST)☐ PHI-BLAST (Pattern Hit Initiated BLAST)☐ DELTA-BLAST (Domain Enhanced Lookup Time Accelerated BLAST)Choose a BLAST algorithm [?](#)**BLAST**

Search database UniProtKB/Swiss-Prot(swissprot) using PSI-BLAST (Position-Specific Iterated BLAST)

☐ Show results in a new window

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Descriptions

Run PSI-Blast iteration 2 with max 500

Go

第一轮搜索结果（和标准BLAST是一样的）

Sequences producing significant alignments with E-value BETTER than threshold

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	Select for PSI blast	Used to build PSSM
<input type="checkbox"/>	RecName: Full=Single Iq IL-1-related receptor; AltName: Full=Single Iq IL-1	551	551	100%	0.0	100%	Q6IA17.3	<input checked="" type="checkbox"/>	<input type="checkbox"/>
<input type="checkbox"/>	RecName: Full=Single Iq IL-1-related receptor; AltName: Full=Single Iq IL-1	493	493	100%	7e-176	89%	Q4V892.1	<input checked="" type="checkbox"/>	<input type="checkbox"/>
<input type="checkbox"/>	RecName: Full=Single Iq IL-1-related receptor; AltName: Full=Single Iq IL-1	491	491	100%	4e-175	87%	Q9JLZ8.2	<input checked="" type="checkbox"/>	<input type="checkbox"/>
<input type="checkbox"/>	RecName: Full=Interleukin-1 receptor accessory protein; Short=IL-1 recept	81.3	81.3	65%	4e-16	32%	Q9NPH3.2	<input checked="" type="checkbox"/>	<input type="checkbox"/>
<input type="checkbox"/>	RecName: Full=Interleukin-1 receptor accessory protein-like 1-B; Flags: Pre	80.5	80.5	61%	6e-16	31%	B6ZK77.1	<input checked="" type="checkbox"/>	<input type="checkbox"/>
<input type="checkbox"/>	RecName: Full=Interleukin-1 receptor accessory protein; Short=IL-1 recept	79.7	79.7	65%	1e-15	32%	Q61730.1	<input checked="" type="checkbox"/>	<input type="checkbox"/>
<input type="checkbox"/>	RecName: Full=Interleukin-1 receptor accessory protein; Short=IL-1 recept						P59822.1	<input checked="" type="checkbox"/>	<input type="checkbox"/>
<input type="checkbox"/>	RecName: Full=Interleukin-1 receptor accessory protein; Short=IL-1 recept						Q63621.1	<input checked="" type="checkbox"/>	<input type="checkbox"/>
<input type="checkbox"/>	RecName: Full=X-linked interleukin-1 receptor accessory protein-like 2; Sho	77.0	77.0	62%	1e-14	32%	Q9NP60.1	<input checked="" type="checkbox"/>	<input type="checkbox"/>
<input type="checkbox"/>	RecName: Full=Interleukin-1 receptor accessory protein-like 1; Short=IL-1-F	76.3	76.3	62%	2e-14	29%	P59824.1	<input checked="" type="checkbox"/>	<input type="checkbox"/>
<input type="checkbox"/>	RecName: Full=Interleukin-1 receptor accessory protein-like 1; Short=IL-1-						Q7YQL9.1	<input checked="" type="checkbox"/>	<input type="checkbox"/>
<input type="checkbox"/>	RecName: Full=Interleukin-1 receptor accessory protein-like 1; Short=IL-1-						Q9NZN1.2	<input checked="" type="checkbox"/>	<input type="checkbox"/>
<input type="checkbox"/>	RecName: Full=X-linked interleukin-1 receptor accessory protein-like 2; Sho	75.5	75.5	62%	4e-14	32%	Q9ERS6.1	<input checked="" type="checkbox"/>	<input type="checkbox"/>
<input type="checkbox"/>	RecName: Full=Interleukin-1 receptor accessory protein-like 1-A; Flags: Pre	72.8	72.8	62%	3e-13	31%	B6ZK76.1	<input checked="" type="checkbox"/>	<input type="checkbox"/>

将在下一轮用来
建PSSM的序列

已在本轮中用来
建PSSM的序列



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Descriptions

Run PSI-Blast iteration 3 with max 500

Go

第二轮搜索结果（有新找到的序列）

Sequences producing significant alignments with E-value BETTER than threshold

Select: [All](#) [None](#) Selected:0

Yellow: sequences scoring below threshold on previous iteration

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

黄色序列是本轮新找到的序列

	Description	Max score	Total score	Query cover	E value	Ident	Accession	Select for PSI blast	Used to build PSSM
<input type="checkbox"/>	RecName: Full=Single Ig IL-1-related receptor; AltName: Full=Single Ig	427	427	100%	1e-149	100%	Q6IA17.3	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>
<input type="checkbox"/>	RecName: Full=Single Ig IL-1-related receptor; AltName: Full=Single Ig	424	424	100%	2e-148	89%	Q4V892.1	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>
<input type="checkbox"/>	RecName: Full=Single Ig IL-1-related receptor; AltName: Full=Single Ig	416	416	100%	2e-145	87%	Q9JLZ8.2	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>
<input type="checkbox"/>	RecName: Full=Interleukin-1 receptor accessory protein-like 1-B; Flags	214	214	70%	8e-64	29%	B6ZK77.1	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>
<input type="checkbox"/>	RecName: Full=Interleukin-1 receptor accessory protein-like 1; Short=I	213	213	63%	3e-63	29%	P59824.1	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>
<input type="checkbox"/>	RecName: Full=Interleukin-1 receptor accessory protein-like 1; Short=I	213	213	63%	3e-63	29%	Q9NZN1.2	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>
<input type="checkbox"/>	RecName: Full=Interleukin-1 receptor accessory protein-like 1; Short=I	213	213	63%	3e-63	29%	Q7YQL9.1	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>
<input type="checkbox"/>	RecName: Full=Interleukin-1 receptor accessory protein-like 1; Short=I	207	207	63%	4e-61	29%	P59823.1	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>
<input type="checkbox"/>	RecName: Full=X-linked interleukin-1 receptor accessory protein-like 2	205	205	63%	3e-60	29%	Q9ERS6.1	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>
<input type="checkbox"/>	RecName: Full=X-linked interleukin-1 receptor accessory protein-like 2	205	205	63%	3e-60	29%	Q9NP60.1	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>
<input type="checkbox"/>	RecName: Full=Interleukin-1 receptor accessory protein-like 1-A; Flags	205	205	63%	3e-60	29%	B6ZK76.1	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>
<input type="checkbox"/>	RecName: Full=Interleukin-18 receptor 1; Short=IL-18R-1; Short=IL-18	198	198	66%	2e-58	30%	Q13478.1	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>
<input type="checkbox"/>	RecName: Full=Interleukin-1 receptor accessory protein; Short=IL-1 re	195	195	65%	2e-57	31%	Q9NPH3.2	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>

将在下一轮用来
建PSSM的序列

已在本轮中用来
建PSSM的序列

46



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Descriptions

Run PSI-Blast iteration 3 with max

500

Go

第二轮搜索结果（有新找到的序列）

Sequences producing significant alignments with E-value BETTER than threshold

Select: [All](#) [None](#) Selected:0

Yellow: sequences scoring below threshold on previous iteration

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

黄色序列是本轮新找到的序列

	Description	Max score	Total score	Query cover	E value	Ident	Accession	Select for PSI blast	Used to build PSSM
<input type="checkbox"/>	RecName: Full=Toll-like receptor 2; AltName: CD antigen=CD282; Fla	168	168	52%	2e-46	28%	B2LT62.1	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>
<input type="checkbox"/>	RecName: Full=Toll-like receptor 2; AltName: CD antigen=CD282; Fla	168	168	52%	2e-46	28%	Q0GC71.1	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>
<input type="checkbox"/>	RecName: Full=Toll-like receptor 13; Flags: Precursor	167	167	61%	1e-45	24%	Q6R5N8.1	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>
<input type="checkbox"/>	RecName: Full=Toll-like receptor 2; AltName: CD antigen=CD282; Fla	166	166	52%	1e-45	28%	Q689D1.1	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>
<input type="checkbox"/>	RecName: Full=Toll-like receptor 2; AltName: CD antigen=CD282; Fla	164	164	52%	1e-44	28%	Q2V897.1	<input checked="" type="checkbox"/>	<input type="checkbox"/>
<input type="checkbox"/>	RecName: Full=Toll-like receptor 2; AltName: CD antigen=CD282; Fla	163	163	52%	1e-44	28%	B2LT65.1	<input checked="" type="checkbox"/>	<input type="checkbox"/>
<input type="checkbox"/>	RecName: Full=Toll-like receptor Tollo; AltName: Full=Toll-like recepto	164	164	61%	1e-44	29%	Q9V477.1	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>
<input type="checkbox"/>	RecName: Full=Toll-like receptor 2; AltName: CD antigen=CD282; Fla	163	163	52%	1e-44	27%	Q6T752.1	<input checked="" type="checkbox"/>	<input type="checkbox"/>
<input type="checkbox"/>	RecName: Full=Toll-like receptor 2; AltName: CD antigen=CD282; Fla	163	163	52%	2e-44	28%	Q2PZH4.1	<input checked="" type="checkbox"/>	<input type="checkbox"/>
<input type="checkbox"/>	RecName: Full=Toll-like receptor 2; AltName: CD antigen=CD282; Fla	162	162	52%	2e-44	28%	Q95LA9.1	<input checked="" type="checkbox"/>	<input type="checkbox"/>
<input type="checkbox"/>	RecName: Full=Toll-like receptor 2; AltName: CD antigen=CD282; Fla	162	162	52%	4e-44	28%	B5T267.1	<input checked="" type="checkbox"/>	<input type="checkbox"/>
<input type="checkbox"/>	RecName: Full=Toll-like receptor 2; AltName: CD antigen=CD282; Fla	162	162	52%	5e-44	28%	B2LT61.1	<input checked="" type="checkbox"/>	<input type="checkbox"/>



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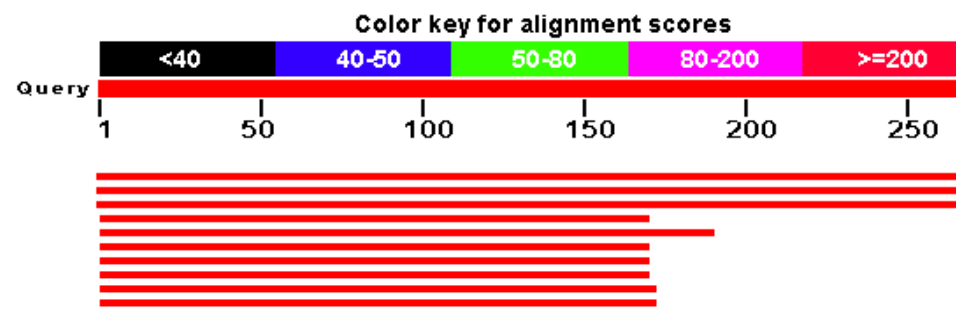
PSI blast Iteration 2

my_protein_seq_for_NCBI_blast

RID [ZWB37ATZ016](#) (Expires on 10-13 20:28 pm)Query ID [Id|Query_314303](#)Description [my_protein_seq_for_NCBI_blast](#)Molecule type [amino acid](#)Query Length [271](#)Database Name [swissprot](#)Description [Non-redundant UniProtKB/SwissProt sequences](#)Program [BLASTP 2.5.1+](#) [Citation](#)Other reports: [Search Summary](#) [Taxonomy reports](#) [Distance tree of results](#) [Multiple alignment](#)**New** Analyze your query with [SmartBLAST](#)**Graphic Summary**

Distribution of 100 Blast Hits on the Query Sequence

Mouse over to see the define, click to show alignments

[Skip to the first new sequence](#)

直接跳到
第一条新
找到的序
列，即第
一条标黄
的序列

NCBI: PHI-BLAST

PHI-BLAST (Pattern-Hit Initiated BLAST, 模式识别BLAST): 能找到与输入序列相似的并符合某种特定模式 (pattern) 的序列。

例如, N-糖基化位点基序 (N-glycosylation site motif) 总是符合以下特定模式: 以 *Asn* 开始, 然后紧跟除了 *Pro* 之外的任何一个氨基酸, 再紧跟 *Ser* 或者 *Thr*, 再紧跟除 *Pro* 外的任何一个氨基酸。N{P}[ST]{P}

用正则表达式书写的符合模式:

{L}GEx[GAS][LIVM]x(3,7)

VGEAAMPRI yes **VGEAAYPRI** no

MGEGLATA ? **FGETAIII** ?

这种序列特征模式可能代表某个翻译后修饰的发生位点, 也可以代表一个酶的活性位点, 或者一个蛋白质家族的结构域、功能域。



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```
>my_protein_seq_for_NCBI_blast
VKCRLNVLLWYQDAYGEVEINDGKLYDAYVSYSDCPEDRK FVNFILKPQLERRRGYKFL
DDRDLPRAEPSADLLVNL SRCRLIVVLSDAFLSRAWCSHSFREGLCRLLELTRPIFI
TFEGQRRDPAHPALRLLRQHRHLV TLLWRPGSVTPSSDFWKEVQLALPRKVQYRPVEGD
PQTQLQDDKDPMLILRGRVPEGRALDSEVDPDPEGDLGVRGPFVFGEPSAPPHTSGVSLGE
```

Query

From

To



blast.fasta

Or, upload file

浏览...

Job Title

my_protein_seq_for_NCBI_blast

Enter a descriptive title for your BLAST search [?](#)**Choose Search Set**

Database

UniProtKB/Swiss-Prot(swissprot) [?](#)**Program Selection**

Algorithm

☐ blastp (protein-protein BLAST)☐ PSI-BLAST (Position-Specific Iterated BLAST)☒ PHI-BLAST (Pattern Hit Initiated BLAST)

S[IVFL]TPS(2)

Enter a PHI pattern [?](#)☐ DELTA-BLAST (Domain Enhanced Lookup Time Accelerated BLAST)Choose a BLAST algorithm [?](#)**BLAST**

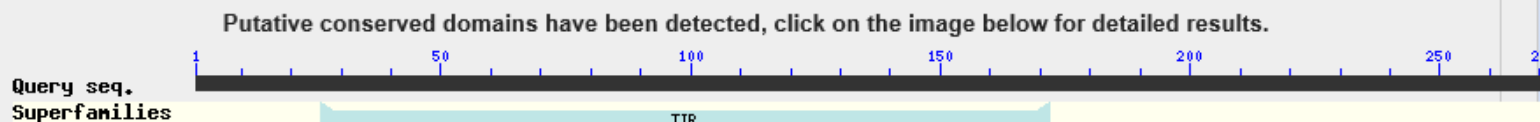
Search database UniProtKB/Swiss-Prot(swissprot) using PHI-BLAST (Pattern Hit Initiated BLAST)

☐ Show results in a new window

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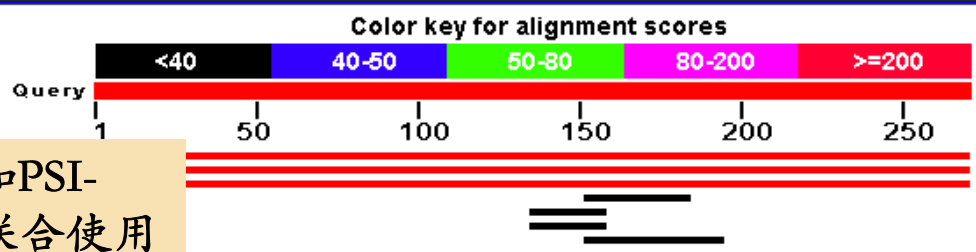
Graphic Summary

Show Conserved Domains



Distribution of 7 Blast Hits on the Query Sequence

Mouse over to see the define, click to show alignments



PHI-BLAST和PSI-BLAST可以联合使用

Descriptions

Run PSI-Blast iteration 2 with max 500

Go

Pattern at position: 153

Sequences producing significant alignments with E-value BETTER than threshold

Select: [All](#) [None](#) Selected:0

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

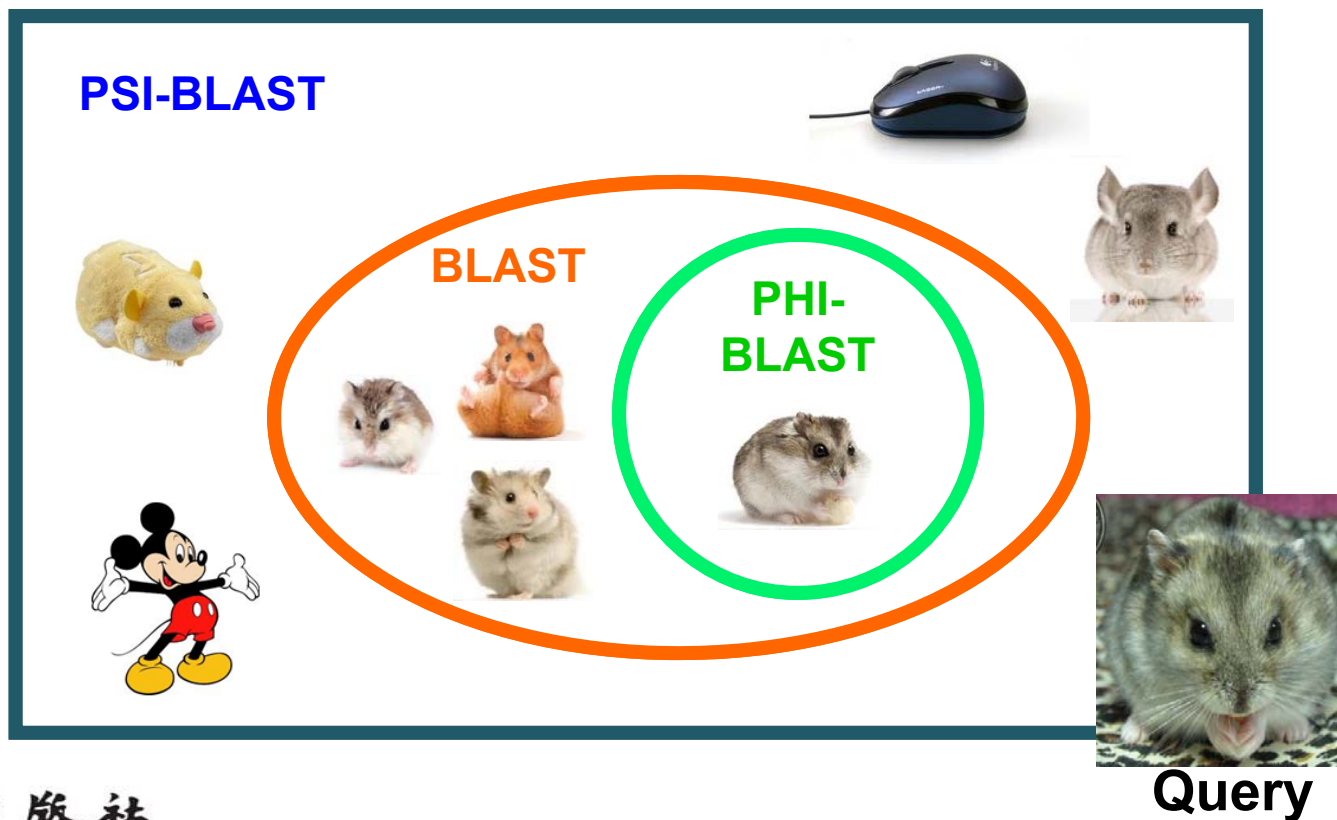
	Description	Max score	Total score	Query cover	E value	Ident	Accession	Select for PSI blast	Used to build PSSM
<input type="checkbox"/>	RecName: Full=Single Ig IL-1-related receptor; AltName: Full=Single Ig IL-1R	540	540	100%	3e-161	0%	Q6IA17.3	<input checked="" type="checkbox"/>	
<input type="checkbox"/>	RecName: Full=Single Ig IL-1-related receptor; AltName: Full=Single Ig IL-1R	483	483	100%	3e-144	0%	Q4V892.1	<input checked="" type="checkbox"/>	
<input type="checkbox"/>	RecName: Full=Single Ig IL-1-related receptor; AltName: Full=Single Ig IL-1R	481	481	100%	2e-143	0%	Q9JLZ8.2	<input checked="" type="checkbox"/>	



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NCBI: PHI-BLAST

三种BLAST的区别



其他BLAST

Standalone and API BLAST



Download BLAST

Get BLAST databases and executables



Use BLAST API

Call BLAST from your application



Use BLAST in the cloud

Start an instance at a cloud provider

Specialized searches

SmartBLAST



Find proteins highly similar to your query



Primer-BLAST



Design primers specific to your PCR template

Global Align



Compare two sequences across their entire span (Needleman-Wunsch)

CD-search



Find conserved domains in your sequence

GEO



Find matches to gene expression profiles

IgBLAST



Search immunoglobulins and T cell receptor sequences

VecScreen



Search sequences for vector contamination

CDART



Find sequences with similar conserved domain architecture

Targeted Loci



Search markers for phylogenetic analysis

Multiple Alignment



Align sequences using domain and protein constraints

BioAssay



Search protein or nucleotide targets in PubChem BioAssay

MOLE-BLAST



Establish taxonomy for uncultured or environmental sequences

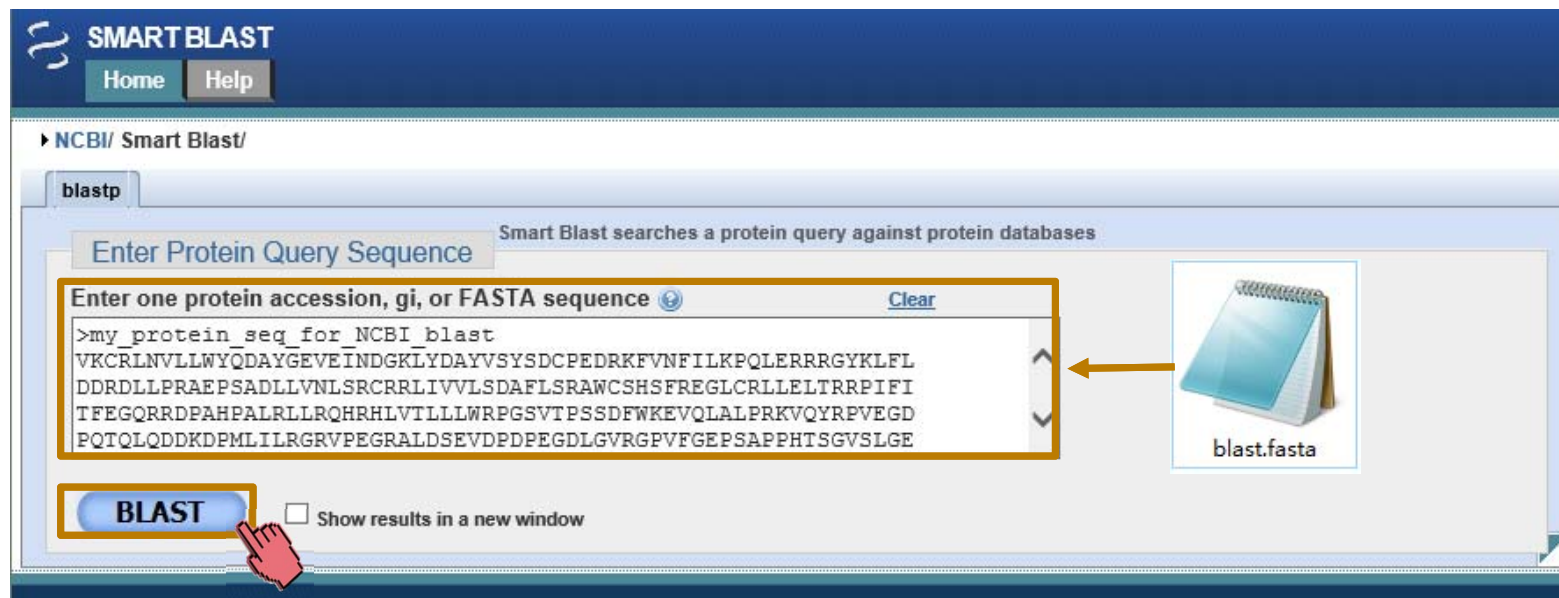


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其他BLAST



SMART BLAST

Home Help

NCBI/ Smart Blast/

blastp

Smart Blast searches a protein query against protein databases

Enter Protein Query Sequence

Enter one protein accession, gi, or FASTA sequence [Clear](#)

```
>my_protein_seq_for_NCBI_blast
VKCRLNVLLWYQDAYGEVEINDGKLYDAYVSYSDCPEDRK FVNFILKPQLERRRGYKFL
DDRDL LPRAEPSADLLVNL SRCRLIVVLSDAFLSRAWCSHSFREGLCRLLELTRPIFI
TFEGQRRDPAHPALRLLRQHRHLVITLLWRPGSVTPSSDFWKEVQLALPRKVQYRFVEGD
PQTQLQDDKDPMLILGRVPEGRALDSEVDPDFEGDLGVRGPVFGEPSAPPHTSGVSLGE
```

BLAST ☐ Show results in a new window

blast.fasta

超级简单明了的输入界面，
是BLASTp的简约强化版



SMART BLAST

[Home](#) [Help](#)

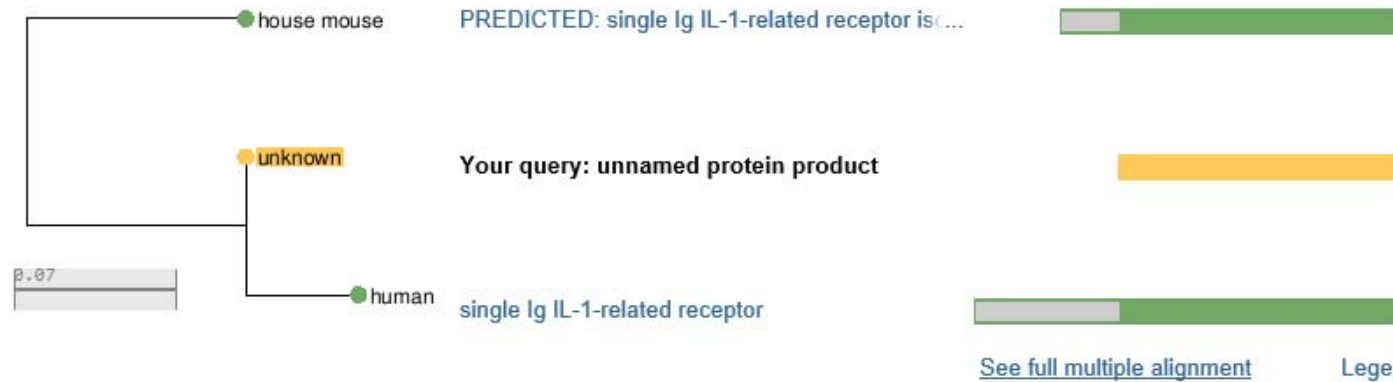
Query sequence Best matches Reference species
Not aligned to query Gap

NCBI/ Smart Blast/ Formatting Results - ZWESEH34011

Summary

[Report description](#) [Please, let us know what you think](#)

A concise summary of the three best matches in the sequence database together with the two best matches from well-studied reference species, showing phylogenetic relationships based on multiple sequence alignment and conserved protein domains.



Descriptions

Best hits

Select: [All](#) [None](#) Selected: 0

[Alignments](#) [GenPept](#)

	Description	Max score	Total score	Query cover	E value	Ident	Accession
<input checked="" type="checkbox"/>	single Ig IL-1-related receptor [Homo sapiens]	551	551	100%	0.0	100%	NP_068577.2
<input checked="" type="checkbox"/>	PREDICTED: single Ig IL-1-related receptor isoform X3 [Mus musculus]	490	490	100%	1e-175	87%	XP_011248144.1

精简的搜索结果包括数据库中与输入序列最相似的三条序列，以及研究的最透彻的物种中可以展现一定的进化关系的最相似的两条序列。



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其他BLAST

✓ 互联网上的免费搜索工具

位置	服务器	网址链接
USA	NCBI	http://www.ncbi.nlm.nih.gov/BLAST
Europe	ExPASy	http://web.expasy.org/blast
Europe	Uniprot	http://www.uniprot.org/blast/
Japan	DDBJ	http://blast.ddbj.nig.ac.jp

- ✓ WU-BLAST - WU 代表 Washington University. 比NCBI-BLAST更灵敏，在插入空位的算法上更灵活。
- ✓ Smith and Waterman (SSEARCH): 有点儿慢，但是比BLAST更准确。
- ✓ FASTA: 有点儿慢，但是对于DNA序列的比较比BLAST更准确。
- ✓ BLAT: 用于小的序列（如 cDNA 等）在大基因组中的搜索。

