Basic Local Alignment Search Tool

BLAST identifies similar regions among biological sequences by comparing nucleotide or protein sequences to sequence databases and calculating their statistical significance.

Usage:

1. Paste the sequence you want to query in the sequence box.

2. Select the database type.

3. Adjust the parameters if you need and click the button at the bottom right to submit.

Results:

1. First, there is a visual representation of the genomic positions where the sequences are aligned (box1).

2. Then, a list of all the aligned positions is provided (box2), users can click to obtain sequence alignment details (box3).

Download FASTA, XML, TSV
Alignment of all hits
Alignment of selected hit(s)

Standard tabular report

Full tabular report

Full XML report

SequenceServer 2.0.0 using **BLASTP 2.16.0+**, query submitted on 2024-11-28 14:36:02 UTC
Databases: 9311.Protein.databases (95066 sequences, 33607385 characters)
Parameters: matrix BLOSUM62, gap-open 11, gap-extend 1, filter F, evalue 10
Please cite: https://doi.org/10.1093/molbev/msz185

⊕ **Queries and their top hits: chord diagram**

1

Query= Test	length: 696

⊟ Graphical overview of hits   ⬇ SVG | ⬇ PNG

Stronger hits   Weaker hits

View More ⌄
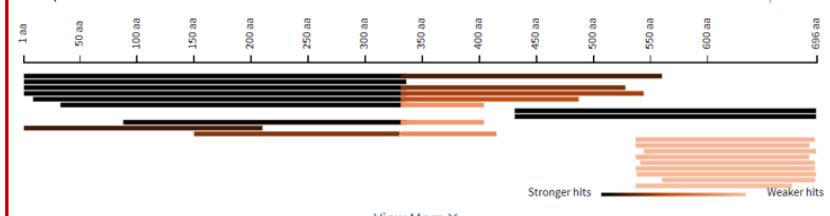
⊕ Length distribution of matching sequences

2 ⊟ Sequences producing significant alignments

#	Similar sequences	Query coverage (%)	Total score	E value	Identity (%)
1.	Os9311G0815563300.01.P01	80	2892	0	97%
2.	Os9311G0918024600.01.P01	48	1756	0	96.1%
3.	Os9311G0610951600.01.P01	76	2724	0	96.7%
4.	Os9311G1223892100.01.P02	78	2603	0	95.2%
5.	Os9311G0611376100.01.P01	69	2433	0	92.4%
6.	Os9311G0203173800.01.P02	53	1959	0	96.4%
7.	Os9311G0408504900.01.P04		1342	0	95.5%

Click to get

sequence

alignment details.

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⊟ **Os9311G0815563300.01.P01**	hit 1, length: 963

☐ Select | ⬇ Alignment
⊟ Graphical overview of aligning region(s)   ⬇ SVG | ⬇ PNG
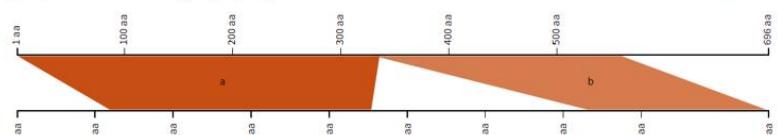
a. Score: 682.56 (1760), E value: 0, Identity: 326/336 (97%), Positives: 330/336 (98.2%), Gaps: 0/336 (0%)

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Query     1 MENIENEIDNAKQYNDFINTLDEVGLHNLDNAMEAMEVDLGIGKRKRYGEGTVKNEGERERPARAAGKWPPDREEFSYN 79
            MENIENEIDNA+QYNDFINTLDEVGLHNLDNAMEAMEVDLG GKRKRYGEGTVKNEGERERPARAAGKWPPDREEFSYN
Subject 119 MENIENEIDNAEQYNDFINTLDEVGLHNLDNAMEAMEVDLGTGKRKRYGEGTVKNEGERERPARAAGKWPPDREEFSYN 197

Query    80 YIPGQYRHMGTKRRDFEKPVKFQNQRSDGAILNLAAHDPIDWPNIISIWKCLIVQKYIQNQHNIGSKVEDMITYLETFL 158
            YIPGQYRH+GTKRRDFEKPVKFQNQRSDGAILNLAAHDPIDWPNIISIWK LIVQKYIQNQHNIGSKVEDMITYLETFL
Subject 198 YIPGQYRHIGTKRRDFEKPVKFQNQRSDGAILNLAAHDPIDWPNIISIWKGLIVQKYIQNQHNIGSKVEDMITYLETFL 276

Query   159 GESAKVLWEQWVEKNPNNYEELKRAGSNPHNFANVISNIIIAEDPELCYTTLQNERLKEIEKLTLTSWKGIKEFSQHYL 237
            GESAKVLWEQWVEKNPNNYEELKRAGSNPHNFANVISNIIIAEDPEL YTTLQNERLKEIEKLTLTSWKGIKEFSQHYL
Subject 277 GESAKVLWEQWVEKNPNNYEELKRAGSNPHNFANVISNIIIAEDPELGYTTLQNERLKEIEKLTLTSWKGIKEFSQHYL 355

Query   238 YNATTAKQGYNRGIVERYFNKLPDPLGSMIFEEYKKETEGAEINISQAITFVFKQLRKICTGIQAQRSMKHSDYNFCNK 316
            YNATTAKQGYNRGIVERYFNKLPDPLGSMIFEEYKKETEGAEINISQAITFVFKQLRKICTGIQAQRSMKHSDYNFCNK
Subject 356 YNATTAKQGYNRGIVERYFNKLPDPLGSMIFEEYKKETEGAEINISQAITFVFKQLRKICTGIQAQRSMKHSDYNFCNK 434

Query   317 IVQIPLSYGEDKPRIRLPFK 336
            IVQIPLSYGEDKPR + +K
Subject 435 IVQIPLSYGEDKPRSKRIYK 454
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b. Score: 440.65 (1132), E value: 5.50×10^{-142}, Identity: 216/230 (93.9%), Positives: 221/230 (96.1%), Gaps: 0/230 (0%)

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Query   331 IRLPFKEILGIRIPVKVKLTPKVSYKILALVDTGCTKNIIHDKYFTRCPEIVHTIDDNKAEVSTDMSGIKKIHNQLAYN 409
            +RLPFKEILGIRIPVK+KLTPKVSYKILALVDTGCTKNIIHDKYF RCPEIVHTIDDNKAEVSTDMS IKKIHNQLAYN
Subject 731 VRLPFKEILGIRIPVKIKLTPKVSYKILALVDTGCTKNIIHDKYFIRCPEIVHTIDDNKAEVSTDMSRIKKIHNQLAYN 809

Query   410 MEVYINATKYIIDEITIRDLSMINDDMIIGLRFLQQSVQTTVIHEQGITFIPYQNNVPYISEVRKRGGARIKPDNLEAL 488
            +EVYINATKYIIDEITIRDLSMINDDMIIGLRFLQQSVQTTVIHEQGITFIPYQNNVPYISEVRKRGG   K DNLE
Subject 810 IEVYINATKYIIDEITIRDLSMINDDMIIGLRFLQQSVQTTVIHEQGITFIPYQNNVPYISEVRKRGGISPKLDNLEVP 888

Query   489 NLESEERINEYELSENIDIYYISNSNIECIGLQAFAPNWYRDIKSKKDIEKIVQRLEDIQIIGEIPMKYWEK 560
            NLESEERINEYELSENID YYISNSNIECIGLQAFAPNWYRDIKSK+DIEKI+QRLEDIQIIGEIPMKYWEK
Subject 889 NLESEERINEYELSENIDNYYISNSNIECIGLQAFAPNWYRDIKSKRDIEKIIQRLEDIQIIGEIPMKYWEK 960
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