

AIM - BLAST VERSION 1.0
EASY GUIDE

INDEX

	PAGE NO.
1. ABOUT AIM – BLAST.....	01
2. HOW TO USE AIM - BLAST.....	02
3. FREQUENTLY ASKED QUESTIONS.....	04
4. GLOSSARY.....	05

ABOUT AIM – BLAST:

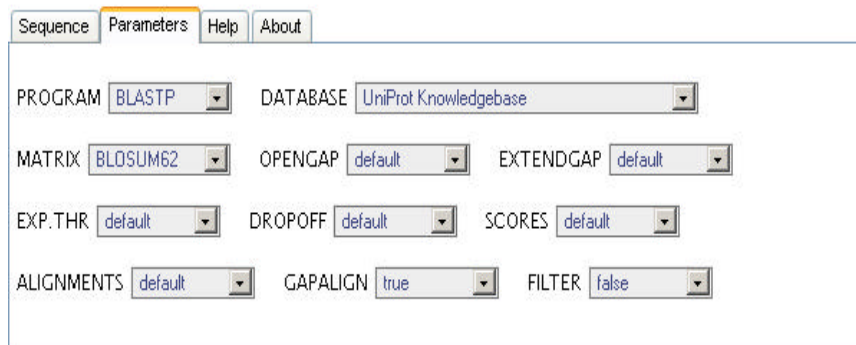
AIM-BLAST Version 1.0 is a system that has been developed to balance the limitations that exists in the other blast tools. This program is exclusively made to facilitate multiple sequences blast against all the genomes. Further AJAX is interfaced with the tool to reduce the loads of data transfer that will involve in any blast analysis. Above all AIM-BLAST will carryout the automatic parsing of the Blast results of the sequences submitted and produce the most appropriate hit. This facility will greatly reduce the burden of hectic human parsing and saves your time too.

FEATURES OF AIM – BLAST:

- ☞☞ Supports Multiple Sequences Blast at an instance.**
- ☞☞ Results displayed in an easily interpretable table.**
- ☞☞ Automatic parsing of Blast results and produces the most appropriate hit for each sequence separately.**
- ☞☞ Results can be saved in PDF format.**
- ☞☞ Blast results of each sequence can be viewed by a simple “click”**
- ☞☞ Consumes very low bandwidth and hence saves your time and money.**

How to use AIM-BLAST?

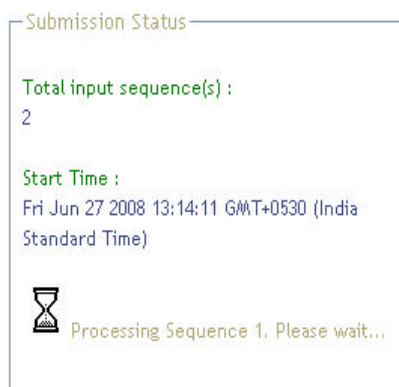
- ✍️ Submit your sequences (either protein sequences or nucleotide sequences) in fasta format. Presently AIM-BLAST restricts its users to submit only 15 sequences at an instance.
- ✍️ A list of parameters for conducting AIM-BLAST analysis such as Program, Database, Matrix, Scores, Alignments, GAPALIGN and Filter are present in the “Parameters” window. The options for each parameter are given in the drop down menu. Hence, the users can select the appropriate options for their analysis or they can be left as default.



Sequence	Parameters	Help	About		
PROGRAM	BLASTP	DATABASE	UniProt Knowledgebase		
MATRIX	BLOSUM62	OPENGAP	default	EXTENDGAP	default
EXP.THR	default	DROPOFF	default	SCORES	default
ALIGNMENTS	default	GAPALIGN	true	FILTER	false

Parameters Window


- ✍️ Once the sequences are pasted and the parameters are set, the users can run their blast analysis by clicking “**Run Blast**” button.
- ✍️ When the sequences are submitted to AIM-BLAST, the processing starts automatically. The status of your search will appear in the “Submission Status” window. This window will display the number of input sequences, Start time of the analysis, current process, End time of the analysis and the overall time taken for the analysis.



Submission Status

Total input sequence(s) :
2

Start Time :
Fri Jun 27 2008 13:14:11 GMT+0530 (India
Standard Time)

 Processing Sequence 1, Please wait...

Submission Status Window

Once your analysis is completed, a window informing the job completion will appear on your computer screen even in case you are involved in any other work or surfing through websites other than AIM-BLAST.



Job Completion Window

When the job is completed, the result table appears. The result table will show the sequence number, automatically parsed function for the sequence, E-value, Identity and similarity of the Hit and finally a link for the entire blast result. There are also options to save the result table in the PDF format.

Whereas, blast result of each sequence can be viewed by clicking the result icon in the result table. When this icon is clicked, the corresponding Blast result page will appear below the result table. This Blast result window will display the entire hits for each sequence.

When you click "Show annotation" Option, you will be diverted to the EBI page where you can view the annotation of all the blast hits.

Frequently Asked Questions:

1. Can I perform blast search for more than one sequence?

Yes. AIM-BLAST is exclusively meant for multiple sequences Blast.

2. Can I carryout blast search for an entire genome?

Unfortunately not now. Presently the search is restricted to only 15 sequences.

3. Is there any option to save the results in my computer?

Yes. The tool comes with an in-built option to save the result table in the PDF format.

4. Will AIM – BLAST help me in choosing a better hit from the blast results of my sequence?

Absolutely. AIM-BLAST performs an automated parsing over the blast results of all the sequences submitted and displays the most appropriate hits in the result table.

4. In what way AIM-BLAST is better than other Blast services?

Unlike other Blast services, AIM-BLAST has several advantages.

✍ It does automatic parsing of the Blast results and displays the user with one appropriate function for each sequence.

✍ AIM-BLAST is the only program that features multiple sequences blast against all the genomes.

✍ Above all, AIM-BLAST is interfaced with AJAX that will reduce the huge data transfer that is generally involved in the blast analysis.

Overall, AIM-BLAST saves your Internet bandwidth and time.

5. Can you give me one example to prove the efficiency of AIM-BLAST?

Yes. A sample set of sequences of varying length from *E.coli* were simultaneously run in AIM-BLAST and the EBI NCBI Blast with the HtpFox, a Firefox add-on, operating at the backend to measure the loads of bytes transfer. The results showed that AIM-BLAST consumed only 0.04 MB where EBI NCBI Blast consumed 6.1 MB. This shows the efficiency of AIM-BLAST.

GLOSSARY:

Annotation:

Annotation is the process of marking the genes and other biological features in a DNA sequence. Previously unknown sequence representation of genetic material is annotated with information relating position to intron-exon-boundaries, regulatory sequences, repeats, gene names and protein products, etc. This annotation is usually stored in predefined fields in biological databases, especially sequence databases.

Similarity:

The extent to which nucleotide or protein sequences are related. The extent of similarity between two sequences can be based on percent sequence identity and/or conservation. In BLAST similarity refers to a positive matrix score.

BLAST:

Basic Local Alignment Search Tool. (Altschul et al.) A sequence comparison algorithm optimized for speed used to search sequence databases for optimal local alignments to a query. The initial search is done for a word of length "W" that scores at least "T" when compared to the query using a substitution matrix. Word hits are then extended in either direction in an attempt to generate an alignment with a score exceeding the threshold of "S". The "T" parameter dictates the speed and sensitivity of the search. For additional details, see one of the BLAST tutorials (Query or BLAST) or the narrative guide to BLAST.

E-value:

Expectation value. The number of different alignments with scores equivalent to or better than S that are expected to occur in a database search by chance. The lower the E value, the more significant the score.

Homology:

Similarity attributed to descent from a common ancestor.

Identity:

The extent to which two (nucleotide or amino acid) sequences are invariant.

Homologous:

Homologous sequences in different species that arose from a common ancestral gene during speciation; may or may not be responsible for a similar function.

Accession number:

Accession number (bioinformatics), a unique identifier given to a biological polymer sequence (DNA, protein) when it is submitted to a sequence database.

Hypothetical proteins:

A **hypothetical protein** is a protein whose existence has been predicted, but for which there is no experimental evidence that it is expressed in vivo.

The usual scenario involving a hypothetical protein is in gene identification during genome analysis. When the bioinformatic tool used for the gene identification finds a large open reading frame without an analog in the protein database, it returns "hypothetical protein" as an annotation remark.

The function of a hypothetical protein can also be predicted by domain homology searches with various confidence levels.