

WEBLEM 12**Comparison between BLAST and FASTA**

BLAST	FASTA
Basic local alignment search tool available in NCBI website that facilitates comparison of biological sequence similarities	A program available at European Bioinformatics Institute that provides facility to search similar sequences to one's query sequence.
Less sensitive as compared to FASTA	FASTA scans smaller window sizes. Thus, it gives more sensitive
BLAST uses a substitution matrix to find matching words.	FASTA identifies identical matching words using the hashing procedure.
Uses local sequence alignment.	Uses local sequence alignment first, then extends to global alignment..
BLAST sometimes gives best-scoring alignments from the same sequence.	FASTA returns only one final alignment
Better for similarity searching in closely related sequences.	Better for similarity searching in less similar sequences
Low-complexity masking in the BLAST procedure means that it may have higher specificity than FASTA because potential false positives are reduced	Less accurate as compared to BLAST
Faster than FASTA	Comparatively slow.

References:

1. <https://www.differencebetween.com/difference-between-blast-and-vs-fast/>
2. <https://pediaa.com/difference-between-blast-and-fast/>