

Similarities	FASTA	BLAST
	<ul style="list-style-type: none"> - Find local alignments - Not guaranteed to find the best alignment. - Use heuristics to speed up the search. 	
Differences	FASTA	BLAST
Speed	<p>BLAST is faster than FASTA.</p> <p><i>E.g.: The length of Query = 153; DB size: 5997 sequences; PC : Pentium 4</i> <i>→FASTA: 0.618 (s) and BLAST: 0.118 (s) (Takeshi Kawabata @ Nara Sentan Gijyutu University)</i></p>	
Sensitivity	<ul style="list-style-type: none"> - Protein searches: FASTA and BLAST are comparable - Nucleic acid searches: FASTA is more sensitive than BLAST; i.e. <i>k-tuple</i> 3-6 (FASTA) vs. <i>k-tuple</i> 7-11 (BLAST) 	
Method	<p>Step 1. Search all hot-spots (pairs of words of length k that exactly match)</p> <p>Step 2: Score the Hot-spot and locate the ten best diagonal run.</p> <p>Step 3: Combine sub-alignments into one alignment</p> <p>Step 4: Score Each alignment with gap penalty and pick up the best score alignment</p> <p>Step 5: Use the dynamic programming in restricted area around the best-score alignment to find out the alignment greater than the best-score alignment.</p>	<p>Step 1. Compile the short-hit scoring (neighborhood) word list from query.</p> <p>Step 2: For each words list, identify all exact matches with DB sequences.</p> <p>→ The purpose of step 1 and 2 is similar to FASTA.</p> <p>Step 3 (Search optimal alignment): Let S be a score of hit-word. For each hit-word, extend ungapped alignment in both directions.</p> <p>Step 4 (Evaluate the alignment statistically): Stop extension when E-value is less than threshold. The hit-word is called High Scoring Segment Pair (HSP).</p> <p>E-value = the number of HSPs having score S (or higher) expected to occur only by chance.</p> <p>→Smaller E-value, more significant in statistics</p>
Method (cont.)	Compare the query and a sequence one by one. Then compare the each result.	Compare the query and all sequences in database with the same threshold.