

MSPcrunch - A BLAST post-processing filter.

Reference: Sonnhammer ELL & Durbin R (1994). A workbench for Large Scale Sequence Homology Analysis. Comput. Applic. Biosci. 10:301-307.

Usage: MSPcrunch [options] <blast output file>

Options:

-G Make gapped alignment of ungapped-MSP contigs.  
-P Big Picture output.  
-H Produce SFS output  
-q Produce seqbl output (for Blixem).  
-4 Produce .ace output (for ACEDB 4).  
-x Produce exblx output (for easy parsing).  
-d Produce exbladb output (as exblx with query names).  
-2 Produce fasta output (unaligned, for mult.alignm.)  
  
-C <#> <#> Set criteria for adjacency. "-C help" lists valid options.  
-l <#> Set coverage limit (Default=10, 0 -> No coverage rejection).  
-B <#> <#> Set bias-ratio limit and pseudocount factor.  
-O Use old step cutoffs for adjacency instead of the new continuous system.  
  
-N For seqbl output from Wublast, indicate query insertions with numbers  
(default: with a lower case residue after the insertion.)  
-w Don't reject any MSPs.  
-r Report only rejected MSPs.  
-I <#> Reject all matches with less than # % identity.  
-L <#> Reject all matches with length less than #.  
-e <#> Reject all matches with E-value higher than #.  
-m <file> Read in score matrix from file.  
-Q <file> Read in query seq (for rereading .seqbl files).  
-3 Print 3 frame translation (blastn only).  
-a Coverage limitation requires whole contig to be covered (always for Blastp).  
-F For -P output, force all matches to the same subject on one line.  
-s Accept hits to self.  
-A Ignore hits to earlier seqnames (for All-vs-All).  
-f Print footer with parameters and stats.  
-h Help and additional options.

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-M Don't mirror (i.e. print the subject object) in ACE4 format.  
-p Force Blastp mode (default Blastx).  
-n Force Blastn mode.  
-i Print percentage identity (seqbl output only).  
-j Recalculate percentage identity, ignoring X residues.  
-J Recalculate percentage identity, ignoring mismatches at ends.  
-o <file> Output coverage stats to file.  
-D Produce output for Domainer (trim overlaps).  
-S Do Statistics of Silent mutations (only cDNA!).  
-v Non-verbose mode.  
-E Print statistics on used matrices.  
-X Print all Expected scores (default only when positive).  
-W <#> Line length of Wrapped alignment (0 -> no wrapping).  
-0 List old archaic options (avoid).  
-g Print (debug) info.