



Target Genomic Sequence (FASTA Format)

Query Protein Sequence (FASTA Format)

blat_score

blat_tlesize

blat_oneoff

blat_identity

blat_identity = 90*min_identity unless defined blat_identity

min_identity

max_mismatch

exhaust_gap_size

exhaust_align_size

nw_insert_penalty

nw_gap_penalty

nw_intron_penalty

nw_stop_penalty

nw_frameshift_penalty

min_intron_len

gap_to_close

max_move_exon

accepted_intron_penalty

min_coverage

min_score

single_target_hits

max_assemble_size

min_dna_coverage

multiple_results

BLAT Run

Significance Filtering (for every single hit)

[gap_length > exhaust_gap_size OR gap_length * 3 > intron_length]

[else]

[intron_length > exhaust_align_size]

[else]

Gap Closing by Needleman-Wunsch Alignment

Gap Closing by Exon Extension with Exact Pattern Matching

Intron Border Refinement (for every single hit)

Significance Filtering (for every single hit)

Sorting Hits by Score

[highest score < min_score]

[else]

[single_target_hits on]

[else]

Hit Assembling

Intron Border Refinement (for assembled hits)

[multiple_results on]

[else]

Return Multiple Hit Assemblies

Return Best Hit Assembly

Return No Hit