

multiple_alignment

Atributy

seq_number
seqs
seq01
seq02
main_seq
current_seq
seq_to_align_01
seq_to_align_02
distance
gap
gap_symbol
match_symbol
delete_symbol
insert_symbol
scoring_matrix
score_matrix
distance_matrix
orig_distance_matrix
direction_matrix
temporary_pair_align
consensus_seq
aligned_seq_flag_tab
seq_aligned_count
multiple_seq_alignment
log_table
score

Metody

multiple_alignment(seqs)
initialize_global(alignment)
pairwise(alignment)
initialize_pairwise(alignment)
pairwise_alignment(alignment)
initialize_constants(alignment)
pairwise_traceback(alignment)
calculate_distance(alignment)
get_align_order(alignment)
get_seq_to_align(alignment)
create_consensus_seq(alignment)
multiple_align(alignment)
adjust_mult_align(alignment)
sum_of_pairs(alignment)