Resource Summary Report

Generated by RRID on Apr 11, 2025

BAliBASE

RRID:SCR_001940
Type: Tool

Proper Citation

BAliBASE (RRID:SCR_001940)

Resource Information

URL: http://lbgi.fr/balibase/

Proper Citation: BAliBASE (RRID:SCR_001940)

Description: A collection of high quality multiple sequence alignments for objective, comparative studies of alignment algorithms. The alignments are constructed based on 3D structure superposition and manually refined to ensure alignment of important functional residues. A number of subsets are defined covering many of the most important problems encountered when aligning real sets of proteins. It is specifically designed to serve as an evaluation resource to address all the problems encountered when aligning complete sequences. The first release provided sets of reference alignments dealing with the problems of high variability, unequal repartition and large N/C-terminal extensions and internal insertions. Version 2.0 of the database incorporates three new reference sets of alignments containing structural repeats, trans-membrane sequences and circular permutations to evaluate the accuracy of detection/prediction and alignment of these complex sequences. Within the resource, users can look at a list of all the alignments, download the whole database by ftp, get the "c" program to compare a test alignment with the BAliBASE reference (The source code for the program is freely available), or look at the results of a comparison study of several multiple alignment programs, using BAliBASE reference sets.

Abbreviations: BAliBASE

Synonyms: Benchmark Alignment dataBASE

Resource Type: software resource, data set, data or information resource, source code

Defining Citation: PMID:16044462, PMID:11125126, PMID:10068696

Keywords: benchmark alignment, circular permutation, transmembrane sequence, multiple

sequence alignment, benchmark, reference alignment, sequence alignment, sequence, alignment

Funding:

Resource Name: BAliBASE

Resource ID: SCR_001940

Alternate IDs: nif-0000-02594, OMICS_00971

Old URLs: http://www-bio3d-igbmc.u-strasbg.fr/balibase/, http://www-igbmc.u-strasbg.fr/BioInfo/BAliBASE2/index.html

Record Creation Time: 20220129T080210+0000

Record Last Update: 20250411T054705+0000

Ratings and Alerts

No rating or validation information has been found for BAliBASE.

No alerts have been found for BAliBASE.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 23 mentions in open access literature.

Listed below are recent publications. The full list is available at RRID.

Iovino BG, et al. (2024) Protein embedding based alignment. BMC bioinformatics, 25(1), 85.

João M, et al. (2023) On closing the inopportune gap with consistency transformation and iterative refinement. PloS one, 18(7), e0287483.

Bastolla U, et al. (2023) PC_ali: a tool for improved multiple alignments and evolutionary inference based on a hybrid protein sequence and structure similarity score. Bioinformatics (Oxford, England), 39(11).

Benítez-Hidalgo A, et al. (2023) SALON ontology for the formal description of sequence alignments. BMC bioinformatics, 24(1), 69.

Seo TK, et al. (2022) Correlations between alignment gaps and nucleotide substitution or

amino acid replacement. Proceedings of the National Academy of Sciences of the United States of America, 119(34), e2204435119.

Penev PI, et al. (2021) TwinCons: Conservation score for uncovering deep sequence similarity and divergence. PLoS computational biology, 17(10), e1009541.

Sejour R, et al. (2020) Sirt4 Modulates Oxidative Metabolism and Sensitivity to Rapamycin Through Species-Dependent Phenotypes in Drosophila mtDNA Haplotypes. G3 (Bethesda, Md.), 10(5), 1599.

Sievers F, et al. (2020) QuanTest2: benchmarking multiple sequence alignments using secondary structure prediction. Bioinformatics (Oxford, England), 36(1), 90.

Ali RH, et al. (2019) Identifying Clusters of High Confidence Homologies in Multiple Sequence Alignments. Molecular biology and evolution, 36(10), 2340.

Kang Y, et al. (2019) PVTree: A Sequential Pattern Mining Method for Alignment Independent Phylogeny Reconstruction. Genes, 10(2).

Wang Y, et al. (2018) A benchmark study of sequence alignment methods for protein clustering. BMC bioinformatics, 19(Suppl 19), 529.

Li M, et al. (2018) Disease Sequences High-Accuracy Alignment Based on the Precision Medicine. BioMed research international, 2018, 1718046.

Dijkstra M, et al. (2018) Motif-Aware PRALINE: Improving the alignment of motif regions. PLoS computational biology, 14(11), e1006547.

Chen X, et al. (2017) CMSA: a heterogeneous CPU/GPU computing system for multiple similar RNA/DNA sequence alignment. BMC bioinformatics, 18(1), 315.

Chowdhury B, et al. (2017) A review on multiple sequence alignment from the perspective of genetic algorithm. Genomics, 109(5-6), 419.

Keul F, et al. (2017) PFASUM: a substitution matrix from Pfam structural alignments. BMC bioinformatics, 18(1), 293.

Gudy? A, et al. (2017) QuickProbs 2: Towards rapid construction of high-quality alignments of large protein families. Scientific reports, 7, 41553.

Long H, et al. (2016) Determination of optimal parameters of MAFFT program based on BAliBASE3.0 database. SpringerPlus, 5(1), 736.

Lange J, et al. (2016) KMAD: knowledge-based multiple sequence alignment for intrinsically disordered proteins. Bioinformatics (Oxford, England), 32(6), 932.

Ye Y, et al. (2016) PnpProbs: a better multiple sequence alignment tool by better handling of guide trees. BMC bioinformatics, 17 Suppl 8(Suppl 8), 285.