Resource Summary Report

Generated by FDI Lab - SciCrunch.org on May 8, 2024

DIALIGN

RRID:SCR_003041
Type: Tool

Proper Citation

DIALIGN (RRID:SCR_003041)

Resource Information

URL: http://bibiserv.techfak.uni-bielefeld.de/dialign/

Proper Citation: DIALIGN (RRID:SCR_003041)

Description: Tool for multiple sequence alignment using various sources of external information that is particularly useful to detect local homologies in sequences with low overall similarity. While standard alignment methods rely on comparing single residues and imposing gap penalties, DIALIGN constructs pairwise and multiple alignments by comparing entire segments of the sequences. No gap penalty is used. This approach can be used for both global and local alignment, but it is particularly successful in situations where sequences share only local homologies. Several versions of DIALIGN are available online at GOBICS, http://dialign.gobics.de/

Abbreviations: DIALIGN

Synonyms: DIALIGN at GOBICS

Resource Type: production service resource, analysis service resource, web service, software resource, service resource, data access protocol, data analysis service

Defining Citation: PMID:15215344, PMID:23620293, DOI:10.1186/1748-7188-3-6

Keywords: dna, protein, sequence alignment, sequence, alignment, fasta, genome, genomic sequence, homology, bio.tools

Availability: Acknowledgement requested

Resource Name: DIALIGN

Resource ID: SCR_003041

Alternate IDs: nif-0000-30417, OMICS_24606, OMICS_00973, biotools:dialign-tx

Alternate URLs: http://dialign.gobics.de/, https://bio.tools/dialign-tx

Old URLs: https://sources.debian.org/src/dialign-tx/

Ratings and Alerts

No rating or validation information has been found for DIALIGN.

No alerts have been found for DIALIGN.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 40 mentions in open access literature.

Listed below are recent publications. The full list is available at FDI Lab - SciCrunch.org.

Bartelt-Kirbach B, et al. (2023) Regulation of rat HspB5/alphaB-Crystallin by microRNAs miR-101a-3p, miR-140-5p, miR-330-5p, and miR-376b-3p. Cell stress & chaperones, 28(6), 787.

Shnyreva AV, et al. (2023) Structure Analysis of the MatA Locus of Sexual Compatibility in the Edible Mushroom Pleurotus ostreatus. Doklady. Biochemistry and biophysics, 511(1), 203.

Grotz S, et al. (2022) Early disruption of photoreceptor cell architecture and loss of vision in a humanized pig model of usher syndromes. EMBO molecular medicine, 14(4), e14817.

Tossavainen H, et al. (2022) Structure of SNX9 SH3 in complex with a viral ligand reveals the molecular basis of its unique specificity for alanine-containing class I SH3 motifs. Structure (London, England : 1993), 30(6), 828.

Marciniak K, et al. (2021) Anther dehiscence is regulated by gibberellic acid in yellow lupine (Lupinus luteus L.). BMC plant biology, 21(1), 314.

Akand EH, et al. (2020) Mutational networks of escape from transmitted HIV-1 infection. PloS one, 15(12), e0243391.

Marciniak K, et al. (2020) Gibberellin Signaling Repressor LlDELLA1 Controls the Flower and Pod Development of Yellow Lupine (Lupinus luteus L.). International journal of molecular

sciences, 21(5).

Ejigu GF, et al. (2020) Review on the Computational Genome Annotation of Sequences Obtained by Next-Generation Sequencing. Biology, 9(9).

Ravi V, et al. (2019) SIRT6 transcriptionally regulates global protein synthesis through transcription factor Sp1 independent of its deacetylase activity. Nucleic acids research, 47(17), 9115.

Monte I, et al. (2019) A Single JAZ Repressor Controls the Jasmonate Pathway in Marchantia polymorpha. Molecular plant, 12(2), 185.

Mehennaoui S, et al. (2019) Selection of high affinity aptamer-ligand for dexamethasone and its electrochemical biosensor. Scientific reports, 9(1), 6600.

Roeske MJ, et al. (2018) Cis-regulatory evolution integrated the Bric-à-brac transcription factors into a novel fruit fly gene regulatory network. eLife, 7.

Waldron FM, et al. (2018) Metagenomic sequencing suggests a diversity of RNA interference-like responses to viruses across multicellular eukaryotes. PLoS genetics, 14(7), e1007533.

He C, et al. (2017) A hydrophobic residue in the TALE homeodomain of PBX1 promotes epithelial-to-mesenchymal transition of gastric carcinoma. Oncotarget, 8(29), 46818.

Lanfray D, et al. (2016) Involvement of the Acyl-CoA binding domain containing 7 in the control of food intake and energy expenditure in mice. eLife, 5.

Appel E, et al. (2016) An ensemble of regulatory elements controls Runx3 spatiotemporal expression in subsets of dorsal root ganglia proprioceptive neurons. Genes & development, 30(23), 2607.

Fan L, et al. (2015) Identification and Characterization of a PRDM14 Homolog in Japanese Flounder (Paralichthys olivaceus). International journal of molecular sciences, 16(5), 9097.

Chang Q, et al. (2015) HOXB9 induction of mesenchymal-to-epithelial transition in gastric carcinoma is negatively regulated by its hexapeptide motif. Oncotarget, 6(40), 42838.

Forsberg SK, et al. (2015) The Multi-allelic Genetic Architecture of a Variance-Heterogeneity Locus for Molybdenum Concentration in Leaves Acts as a Source of Unexplained Additive Genetic Variance. PLoS genetics, 11(11), e1005648.

Cao PB, et al. (2015) Genome-wide analysis of the AP2/ERF family in Eucalyptus grandis: an intriguing over-representation of stress-responsive DREB1/CBF genes. PloS one, 10(4), e0121041.