DIALIGN

RRID:SCR_003041
Type: Tool

Proper Citation

DIALIGN (RRID:SCR_003041)

Resource Information

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

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/

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

Keywords: dna, protein, sequence alignment, sequence, alignment, fasta, genome, genomic sequence, homology

Resource ID: SCR_003041

Parent Organization: Bielefeld University; North Rhine-Westphalia; Germany

References: PMID: 15215344, PMID: 23620293

Availability: Acknowledgement requested
Website Status: Last checked up

Alternate IDs: nif-0000-30417, OMICS_00973

Alternate URLs: http://dialign.gobics.de/

Abbreviations: DIALIGN

Mentions Count: 30

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 30 mentions in open access literature.

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


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.


