

Resource Summary Report

Generated by [FDI Lab - SciCrunch.org](#) on Apr 29, 2025

Clustal 2

RRID:SCR_017055

Type: Tool

Proper Citation

Clustal 2 (RRID:SCR_017055)

Resource Information

URL: <http://www.clustal.org/clustal2/>

Proper Citation: Clustal 2 (RRID:SCR_017055)

Description: Software tool for nucleotide sequence alignment. Graphical version of multiple sequence alignment program for DNA and proteins. Windows interface for ClustalW multiple sequence alignment program. Provides integrated environment for performing multiple sequence and profile alignments and analyzing results. Available on Linux, Mac and Windows.

Synonyms: Clustalx, CLUSTAL_X, clustalx, clustal X, clustal2

Resource Type: data processing software, image analysis software, data visualization software, alignment software, software resource, software application

Defining Citation: [PMID:17846036](#), [PMID:9396791](#)

Keywords: graphical, multiple, sequence, alignment, DNA, protein

Funding: Science Foundation Ireland ;
INSERM ;
CNRS ;
Ministère de la Recherche et Technologie ;
EMBL

Availability: Free, Available for download, Freely available

Resource Name: Clustal 2

Resource ID: SCR_017055

Alternate IDs: biotools:clustal2

Alternate URLs: http://www.clustal.org/download/clustalx_help.html, <https://bio.tools/clustal2>

License: GNU Lesser GPL

Record Creation Time: 20220129T080333+0000

Record Last Update: 20250429T055904+0000

Ratings and Alerts

No rating or validation information has been found for Clustal 2.

No alerts have been found for Clustal 2.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 1456 mentions in open access literature.

Listed below are recent publications. The full list is available at [FDI Lab - SciCrunch.org](#).

Reshi HA, et al. (2024) EYA protein complex is required for Wntless retrograde trafficking from endosomes to Golgi. *Developmental cell*, 59(18), 2443.

Shao M, et al. (2024) Molecular evolution of Phytocyanin gene and analysis of expression at different coloring periods in apple (*Malus domestica*). *BMC plant biology*, 24(1), 374.

Han B, et al. (2024) Genome-wide identification and characterization of Calcium-Dependent Protein Kinase (CDPK) gene family in autotetraploid cultivated alfalfa (*Medicago sativa* subsp. *sativa*) and expression analysis under abiotic stresses. *BMC plant biology*, 24(1), 1241.

Kaur D, et al. (2024) Optimization of loop mediated isothermal amplification assay (LAMP) for detection of chloroquine resistance in *P. vivax* malaria. *Scientific reports*, 14(1), 25608.

Mao L, et al. (2024) Identification, function validation and haplotype analysis of salt-tolerant genes of lectin receptor kinase gene family in sorghum (*Sorghum bicolor* L.). *Frontiers in genetics*, 15, 1464537.

Riedhammer KM, et al. (2024) Implication of transcription factor FOXD2 dysfunction in syndromic congenital anomalies of the kidney and urinary tract (CAKUT). *Kidney international*, 105(4), 844.

Gharbi Z, et al. (2024) First Evidence of *Rickettsia conorii* Infection in Dogs in Northern Tunisia. *Veterinary sciences*, 11(9).

Tang R, et al. (2024) The FvABF3-FvALKBH10B-FvSEP3 cascade regulates fruit ripening in strawberry. *Nature communications*, 15(1), 10912.

Dmitrieva N, et al. (2024) Transport mechanism of DgoT, a bacterial homolog of SLC17 organic anion transporters. *The EMBO journal*, 43(24), 6740.

Qin S, et al. (2024) Predicting the sequence-dependent backbone dynamics of intrinsically disordered proteins. *eLife*, 12.

Wang YH, et al. (2024) Comprehensive analysis of B3 family genes in pearl millet (*Pennisetum glaucum*) and the negative regulator role of PgRAV-04 in drought tolerance. *Frontiers in plant science*, 15, 1400301.

Xu Y, et al. (2024) Genome-Wide Identification of NAC Family Genes in Oat and Functional Characterization of AsNAC109 in Abiotic Stress Tolerance. *Plants (Basel, Switzerland)*, 13(7).

Khalid MA, et al. (2024) GA-sensitive Rht13 gene improves root architecture and osmotic stress tolerance in bread wheat. *BMC genomic data*, 25(1), 90.

Kitazawa N, et al. (2024) Development of SNP genotyping assays for heading date in rice. *Breeding science*, 74(3), 274.

Loginova OA, et al. (2023) First report of *Orthostrongylus* sp. (Nematoda: Protostrongylidae) in wild reindeer (*Rangifer tarandus*) from the Taimyr, Russia: Nearctic parasites in a Palearctic host. *Parasitology research*, 122(2), 685.

Quijano-Barraza JM, et al. (2023) Evolution and functional role prediction of the CYP6DE and CYP6DJ subfamilies in *Dendroctonus* (Curculionidae: Scolytinae) bark beetles. *Frontiers in molecular biosciences*, 10, 1274838.

Siegl D, et al. (2023) A PCR protocol to establish standards for routine mycoplasma testing that by design detects over ninety percent of all known mycoplasma species. *iScience*, 26(5), 106724.

Bhandari M, et al. (2023) Toxigenic *Vibrio cholerae* strains in South-East Queensland, Australian river waterways. *Applied and environmental microbiology*, 89(10), e0047223.

Dong HJ, et al. (2023) Prevalence and genomic analysis of t203-like G9 (G9-VI) rotaviruses circulating in children with gastroenteritis in Beijing, China. Archives of virology, 168(10), 257.

Riedhammer KM, et al. (2023) Implication of FOXD2 dysfunction in syndromic congenital anomalies of the kidney and urinary tract (CAKUT). medRxiv : the preprint server for health sciences.