Resource Summary Report

Generated by NIF on May 14, 2025

COBALT: Constraint-based Multiple Alignment Tool

RRID:SCR_004152
Type: Tool

Proper Citation

COBALT: Constraint-based Multiple Alignment Tool (RRID:SCR_004152)

Resource Information

URL: http://www.ncbi.nlm.nih.gov/tools/cobalt/cobalt.cgi?link_loc=BlastHomeAd

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Description: COBALT is a multiple sequence alignment tool that finds a collection of pairwise constraints derived from conserved domain database, protein motif database, and sequence similarity, using RPS-BLAST, BLASTP, and PHI-BLAST. Pairwise constraints are then incorporated into a progressive multiple alignment. A Linux executable for COBALT, and CDD and PROSITE data used is available at ftp://ftp.ncbi.nlm.nih.gov/pub/agarwala/cobalt/ COBALT has reasonable runtime performance and alignment accuracy comparable to or exceeding that of other tools for a broad range of problems.

Synonyms: NCBI COBALT, NCBI Constraint-based Multiple Alignment Tool, Constraint-based Multiple Alignment Tool

Resource Type: software resource, computation service resource

Defining Citation: PMID:17332019

Keywords: gold standard

Funding:

Resource Name: COBALT: Constraint-based Multiple Alignment Tool

Resource ID: SCR_004152

Alternate IDs: nlx_17358

Record Creation Time: 20220129T080223+0000

Record Last Update: 20250509T055640+0000

Ratings and Alerts

No rating or validation information has been found for COBALT: Constraint-based Multiple Alignment Tool.

No alerts have been found for COBALT: Constraint-based Multiple Alignment Tool.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 9 mentions in open access literature.

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

Schott CR, et al. (2024) Osteosarcoma PDX-Derived Cell Line Models for Preclinical Drug Evaluation Demonstrate Metastasis Inhibition by Dinaciclib through a Genome-Targeted Approach. Clinical cancer research : an official journal of the American Association for Cancer Research, 30(4), 849.

Lyu Y, et al. (2024) A rare inherited homozygous missense variant in PLA2G6 influences susceptibility to infantile neuroaxonal dystrophy: a case report. Translational pediatrics, 13(3), 484.

Yu M, et al. (2022) Computational analysis on two putative mitochondrial protein-coding genes from the Emydura subglobosa genome: A functional annotation approach. PloS one, 17(8), e0268031.

Sette-DE-Souza PH, et al. (2021) Dental workers in front-line of COVID-19: an in silico evaluation targeting their prevention. Journal of applied oral science : revista FOB, 29, e20200678.

Wegscheid ML, et al. (2021) Patient-derived iPSC-cerebral organoid modeling of the 17q11.2 microdeletion syndrome establishes CRLF3 as a critical regulator of neurogenesis. Cell reports, 36(1), 109315.

Chen RZ, et al. (2020) An ENU-induced mutation in Twist1 transactivation domain causes hindlimb polydactyly with complete penetrance and dominant-negatively impairs E2A-dependent transcription. Scientific reports, 10(1), 2501.

Lyu X, et al. (2015) A "footprint" of plant carbon fixation cycle functions during the development of a heterotrophic fungus. Scientific reports, 5, 12952.

Huang Z, et al. (2013) Roles of JnRAP2.6-like from the transition zone of black walnut in hormone signaling. PloS one, 8(11), e75857.

Liu H, et al. (2011) Widespread horizontal gene transfer from circular single-stranded DNA viruses to eukaryotic genomes. BMC evolutionary biology, 11, 276.