

# Resource Summary Report

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## 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](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:** computation service resource, software resource

**Defining Citation:** [PMID:17332019](#)

**Keywords:** gold standard

**Resource Name:** COBALT: Constraint-based Multiple Alignment Tool

**Resource ID:** SCR\_004152

**Alternate IDs:** nlx\_17358

**Record Creation Time:** 20220129T080223+0000

**Record Last Update:** 20260829T183057+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.

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## Data and Source Information

**Source:** [SciCrunch Registry](#)

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## Usage and Citation Metrics

We found 10 mentions in open access literature.

**Listed below are recent publications.** The full list is available at [NIF](#) .

Gunning V, et al. (2026) Mechanistic design of cell-penetrating disruptors for phospho-dependent TACC3-CHC interaction. Structure (London, England : 1993), 34(6), 915.

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.