

Resource Summary Report

Generated by [nidm-terms](#) on Jul 28, 2026

COALESCE

RRID:SCR_012005

Type: Tool

Proper Citation

COALESCE (RRID:SCR_012005)

Resource Information

URL: <http://quantbio-tools.princeton.edu/cgi-bin/COALESCE>

Proper Citation: COALESCE (RRID:SCR_012005)

Description: Software that can use large collections of genomic data and Bayesian integration to predict coregulated gene modules, the conditions of regulation, and the consensus binding motifs for regulation.

Abbreviations: COALESCE

Synonyms: Combinatorial Algorithm for Expression and Sequence-based Cluster Extraction

Resource Type: software resource

Resource Name: COALESCE

Resource ID: SCR_012005

Alternate IDs: OMICS_01804

Record Creation Time: 20220129T080307+0000

Record Last Update: 20260725T190724+0000

Ratings and Alerts

No rating or validation information has been found for COALESCE.

No alerts have been found for COALESCE.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 6 mentions in open access literature.

Listed below are recent publications. The full list is available at [nidm-terms](#) .

Baldwin E, et al. (2020) On fusion methods for knowledge discovery from multi-omics datasets. Computational and structural biotechnology journal, 18, 509.

Gundlach S, et al. (2019) Comparison of Markov Chain Monte Carlo Software for the Evolutionary Analysis of Y-Chromosomal Microsatellite Data. Computational and structural biotechnology journal, 17, 1082.

Padilha VA, et al. (2017) A systematic comparative evaluation of biclustering techniques. BMC bioinformatics, 18(1), 55.

Reiss DJ, et al. (2015) cMonkey2: Automated, systematic, integrated detection of co-regulated gene modules for any organism. Nucleic acids research, 43(13), e87.

Oliveira JV, et al. (2013) Modularity and evolutionary constraints in a baculovirus gene regulatory network. BMC systems biology, 7, 87.

Wellensiek BP, et al. (2006) Molecular characterization of the HIV-1 gag nucleocapsid gene associated with vertical transmission. Retrovirology, 3, 21.