

# Resource Summary Report

Generated by [ASWG](#) on Aug 4, 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:** 20260801T190434+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](#)

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## Usage and Citation Metrics

We found 6 mentions in open access literature.

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

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.