

# Resource Summary Report

Generated by [NIF](#) on Aug 7, 2026

## [MRFSEQ](#)

RRID:SCR\_002972

Type: Tool

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### Proper Citation

MRFSEQ (RRID:SCR\_002972)

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### Resource Information

**URL:** <http://www.cs.ucr.edu/~yyang027/mrfseq.htm>

**Proper Citation:** MRFSEQ (RRID:SCR\_002972)

**Description:** Algorithm based on a Markov random field (MRF) model that uses additional gene coexpression data to enhance differential gene expression prediction power. It is able to call differentially expressed (DE) genes but also assign confidence scores to each inferred DE gene.

**Resource Type:** software resource, algorithm resource

**Defining Citation:** [PMID:23793751](#)

**Keywords:** markov, algorithm, gene expression, prediction algorithm, bio.tools

**Availability:** Free, Available for download, Freely available

**Resource Name:** MRFSEQ

**Resource ID:** SCR\_002972

**Alternate IDs:** biotools:mrfseq, OMICS\_01309

**Alternate URLs:** <https://bio.tools/mrfseq>

**Record Creation Time:** 20220129T080216+0000

**Record Last Update:** 20260807T042546+0000

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### Ratings and Alerts

No rating or validation information has been found for MRFSEQ.

No alerts have been found for MRFSEQ.

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## Data and Source Information

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

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## Usage and Citation Metrics

We have not found any literature mentions for this resource.