

# Resource Summary Report

Generated by [PRECISE-TBI](#) on Aug 26, 2026

## DiMO

RRID:SCR\_001168

Type: Tool

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### Proper Citation

DiMO (RRID:SCR\_001168)

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### Resource Information

**URL:** <http://stormo.wustl.edu/DiMO/>

**Proper Citation:** DiMO (RRID:SCR\_001168)

**Description:** Software for discriminative motif optimization based on perceptron training. It takes a seed motif along with a positive and a negative database and improves the motif based on a discriminative strategy. They use the area under receiver-operating characteristic curve (AUC) as a measure of discriminating power of motifs and a strategy based on perceptron training that maximizes AUC rapidly in a discriminative manner.

**Abbreviations:** DiMO

**Synonyms:** Discriminative Motif Optimizer, DiMO: Discriminative Motif Optimizer

**Resource Type:** software resource

**Defining Citation:** [PMID:24369152](#)

**Keywords:** r, motif, perceptron

**Availability:** THIS RESOURCE IS NO LONGER IN SERVICE

**Resource Name:** DiMO

**Resource ID:** SCR\_001168

**Alternate IDs:** OMICS\_02190

**Record Creation Time:** 20220129T080206+0000

**Record Last Update:** 20260815T182153+0000

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### Ratings and Alerts

No rating or validation information has been found for DiMO.

No alerts have been found for DiMO.

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## Data and Source Information

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

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## Usage and Citation Metrics

We found 1 mentions in open access literature.

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

Mathelier A, et al. (2016) DNA Shape Features Improve Transcription Factor Binding Site Predictions In Vivo. Cell systems, 3(3), 278.