

Resource Summary Report

Generated by [NIF](#) on Sep 1, 2026

Minimotif Miner

RRID:SCR_007788

Type: Tool

Proper Citation

Minimotif Miner (RRID:SCR_007788)

Resource Information

URL: <http://mnm.engr.uconn.edu>

Proper Citation: Minimotif Miner (RRID:SCR_007788)

Description: It analyzes protein queries for the presence of short functional motifs that, in at least one protein, has been demonstrated to be involved in posttranslational modifications (PTM), binding to other proteins, nucleic acids, or small molecules, or proteins trafficking. The low sequence complexity of motifs, suggest that "false positive" motifs may occur and any prediction made by MnM should be experimentally tested. To aid in the selection of motifs, MnM ranks motifs based on frequencies in proteomes, protein surface prediction, and evolutionary conservation. Using annotation of motifs in the Swiss-Prot database, we have found that higher scores are globally correlated with experimentally validated motifs when compared to a similar analysis using randomized motifs with the same amino acid composition. We suggest that the known biology of the protein of interest and of motifs be used in selecting motifs for experimental study.

Abbreviations: MnM

Synonyms: Minimotif Miner

Resource Type: data or information resource, database

Resource Name: Minimotif Miner

Resource ID: SCR_007788

Alternate IDs: nif-0000-03129

Record Creation Time: 20220129T080243+0000

Record Last Update: 20260829T183005+0000

Ratings and Alerts

No rating or validation information has been found for Minimotif Miner.

No alerts have been found for Minimotif Miner.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 8 mentions in open access literature.

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

Zhu R, et al. (2025) Decoding allosteric landscapes: computational methodologies for enzyme modulation and drug discovery. RSC chemical biology, 6(4), 539.

Kleene R, et al. (2022) Cell adhesion molecule L1 interacts with the chromo shadow domain of heterochromatin protein 1 isoforms ?, ?, and ? via its intracellular domain. FASEB journal : official publication of the Federation of American Societies for Experimental Biology, 36(1), e22074.

Franco-Serrano L, et al. (2021) Pathogen Moonlighting Proteins: From Ancestral Key Metabolic Enzymes to Virulence Factors. Microorganisms, 9(6).

Lyon KF, et al. (2018) Minimotif Miner 4: a million peptide minimotifs and counting. Nucleic acids research, 46(D1), D465.

Gibson TJ, et al. (2015) Experimental detection of short regulatory motifs in eukaryotic proteins: tips for good practice as well as for bad. Cell communication and signaling : CCS, 13, 42.

van der Lee R, et al. (2014) Classification of intrinsically disordered regions and proteins. Chemical reviews, 114(13), 6589.

Mi T, et al. (2012) Achieving high accuracy prediction of minimotifs. PloS one, 7(9), e45589.

Demirkan G, et al. (2011) Phosphoproteomic profiling of in vivo signaling in liver by the mammalian target of rapamycin complex 1 (mTORC1). PloS one, 6(6), e21729.