

Resource Summary Report

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Motif Extractor

RRID:SCR_008628

Type: Tool

Proper Citation

Motif Extractor (RRID:SCR_008628)

Resource Information

URL: <http://motif-x.med.harvard.edu>

Proper Citation: Motif Extractor (RRID:SCR_008628)

Description: motif-x (short for motif extractor) is a software tool designed to extract overrepresented patterns from any sequence data set. The algorithm is an iterative strategy which builds successive motifs through comparison to a dynamic statistical background.

Synonyms: Motif-X

Resource Type: software resource

Resource Name: Motif Extractor

Resource ID: SCR_008628

Alternate IDs: nif-0000-32002

Record Creation Time: 20220129T080248+0000

Record Last Update: 20260829T182332+0000

Ratings and Alerts

No rating or validation information has been found for Motif Extractor.

No alerts have been found for Motif Extractor.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 159 mentions in open access literature.

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

Lai S, et al. (2026) PIPI-C: A Combinatorial Optimization Framework for Identifying Post-translational Modification Hot-spots in Mass Spectrometry Data. *Molecular & cellular proteomics : MCP*, 25(2), 101494.

Li T, et al. (2026) A Multi-omics PTM Atlas Reveals Key Insights into Metabolic Reprogramming in Colorectal Cancer. *Cancer genomics & proteomics*, 23(3), 448.

Zhang H, et al. (2026) Identification of protein lysine lactylation and potential targets in esophageal squamous cell carcinoma. *Translational cancer research*, 15(5), 404.

Liao X, et al. (2026) Dynamic lysine acetylation and succinylation of platelet proteins regulates platelet storage lesion: mechanistic insights from multi-omics. *Annals of medicine*, 58(1), 2635200.

Wang D, et al. (2026) Natural variation in PtoCPK3 governs drought tolerance by orchestrating xylem remodeling and lignin metabolism in *Populus*. *Science advances*, 12(23), eade2172.

Hu B, et al. (2025) Lysine succinylation precisely controls normal erythropoiesis. *Haematologica*, 110(2), 397.

Pan Z, et al. (2025) Integrative proteogenomic characterization reveals therapeutic targets in poorly differentiated and anaplastic thyroid cancers. *Nature communications*, 16(1), 3601.

Song J, et al. (2025) Comparative ubiquitinome analysis reveals the roles of protein ubiquitination in the heat stress response from *Metarhizium robertsii*. *Applied and environmental microbiology*, 91(12), e0146825.

Meng X, et al. (2025) Comprehensive analysis of the succinylome in Vero cells infected with peste des petits ruminants virus Nigeria 75/1 vaccine strain. *BMC veterinary research*, 21(1), 45.

Zhang N, et al. (2025) Integration of multi-omics data accelerates molecular analysis of common wheat traits. *Nature communications*, 16(1), 2200.

Han L, et al. (2024) Dapagliflozin Improves Angiogenesis after Hindlimb Ischemia through the PI3K-Akt-eNOS Pathway. *Biomolecules*, 14(5).

Ahsan N, et al. (2024) Decoding *Arabidopsis thaliana* CPK/SnRK Superfamily Kinase Client Signaling Networks Using Peptide Library and Mass Spectrometry. *Plants (Basel, Switzerland)*, 13(11).

Duan Y, et al. (2024) S-palmitoylation of MAP kinase is essential for fungal virulence. *mBio*, 15(12), e0270424.

Narula K, et al. (2024) Combining extracellular matrix proteome and phosphoproteome of chickpea and meta-analysis reveal novel proteoforms and evolutionary significance of clade-specific wall-associated events in plant. *Plant direct*, 8(3), e572.

Zhang L, et al. (2024) The crotonylated and succinylated proteins of jujube involved in phytoplasma-stress responses. *BMC biology*, 22(1), 113.

Chen X, et al. (2023) Comparative oxidation proteomics analyses suggest redox regulation of cytosolic translation in rice leaves upon *Magnaporthe oryzae* infection. *Plant communications*, 4(3), 100550.

Chen X, et al. (2023) Post-Translational Modification γ -Hydroxybutyrylation Regulates *Ustilagoidea virens* Virulence. *Molecular & cellular proteomics : MCP*, 22(8), 100616.

Esmaili F, et al. (2023) A Review of Machine Learning and Algorithmic Methods for Protein Phosphorylation Site Prediction. *Genomics, proteomics & bioinformatics*, 21(6), 1266.

Wang Y, et al. (2023) Lysine Succinylation of VBS Contributes to Sclerotia Development and Aflatoxin Biosynthesis in *Aspergillus flavus*. *Molecular & cellular proteomics : MCP*, 22(2), 100490.

Zhou M, et al. (2023) Proteome and phosphoproteome analysis of 2,4-epibrassinolide-mediated cold stress response in cucumber seedlings. *Frontiers in plant science*, 14, 1104036.