

# Resource Summary Report

Generated by [T1D](#) on Aug 4, 2026

## 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:** 20260801T190334+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 148 mentions in open access literature.

**Listed below are recent publications.** The full list is available at [T1D](#) .

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

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

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.

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.

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).

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.

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

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  $\gamma$ -Hydroxybutyrylation Regulates *Ustilago violacea* 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.

Wang Z, et al. (2023) Global Proteome-Wide Analysis of Cysteine S-Nitrosylation in *Toxoplasma gondii*. *Molecules (Basel, Switzerland)*, 28(21).

Liu H, et al. (2023) Quantitative proteomic and phosphoproteomic analysis reveal the relationship between mitochondrial dysfunction and cytoskeletal remodeling in hiPSC-CMs deficient in PINK1. *Journal of translational medicine*, 21(1), 581.

Noordally ZB, et al. (2023) A phospho-dawn of protein modification anticipates light onset in the picoeukaryote *Ostreococcus tauri*. *Journal of experimental botany*, 74(18), 5514.

Lin HY, et al. (2022) Proteomic and Phosphoryproteomic Investigations Reveal that Autophagy-Related Protein 1, a Protein Kinase for Autophagy Initiation, Synchronously Deploys Phosphoregulation on the Ubiquitin-Like Conjugation System in the Mycopathogen *Beauveria bassiana*. *mSystems*, 7(1), e0146321.

Lan W, et al. (2022) Ubiquitome profiling reveals a regulatory pattern of UPL3 with UBP12 on metabolic-leaf senescence. *Life science alliance*, 5(12).

Jiang Y, et al. (2022) Phosphoproteomics Reveals the AMPK Substrate Network in Response to DNA Damage and Histone Acetylation. *Genomics, proteomics & bioinformatics*, 20(4), 597.

Zhang H, et al. (2022) Quantitative proteomic analysis of the lysine acetylome reveals diverse SIRT2 substrates. *Scientific reports*, 12(1), 3822.

Zhang N, et al. (2022) Global Profiling of 2-hydroxyisobutyrylome in Common Wheat. *Genomics, proteomics & bioinformatics*, 20(4), 688.