

Resource Summary Report

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Glam2

RRID:SCR_016129

Type: Tool

Proper Citation

Glam2 (RRID:SCR_016129)

Resource Information

URL: <http://acb.qfab.org/acb/glam2/>

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Description: Software package for finding novel, gapped (recurring, variable-length patterns) motifs in related groups of DNA or protein sequences (sample output from sequences). Used to perform motif based sequence discovery for gapped motifs on DNA or protein datasets.

Abbreviations: Glam2

Synonyms: Glam2: Gapped local alignment of motifs 2

Resource Type: software application, data analysis software, sequence analysis software, software resource, data processing software, software toolkit

Defining Citation: [PMID:18437229](#)

Keywords: motif, analysis, sequence, find, amino acid, nucleotide, set, alignment, gapped, recurring, variable, letnght, pattern, DNA, protein, output, discovery, dataset

Funding: NIGMS R01 GM103544

Availability: Free, Freely available for non-commercial use

Resource Name: Glam2

Resource ID: SCR_016129

Alternate URLs: <http://meme-suite.org/>

Record Creation Time: 20220129T080329+0000

Record Last Update: 20260729T044409+0000

Ratings and Alerts

No rating or validation information has been found for Glam2.

No alerts have been found for Glam2.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 72 mentions in open access literature.

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

Leib L, et al. (2025) The proximity-based protein interactome and regulatory logics of the transcription factor p65 NF- κ B/RELA. EMBO reports, 26(4), 1144.

Cao Y, et al. (2025) Polyadenylation Complex CFII Recognizes Downstream Cis-element for Pre-mRNA Polyadenylation Through Interaction with an RNA-Binding Protein in Arabidopsis. Advanced science (Weinheim, Baden-Wurttemberg, Germany), 12(41), e04562.

Bai F, et al. (2025) Genomic Insights into the Molecular Basis of Broad Host Adaptability of the Entomopathogenic Fungus *Conidiobolus coronatus* (Entomophthoromycotina). Journal of fungi (Basel, Switzerland), 11(8).

Huang D, et al. (2025) Genome-wide identification of sucrose synthase gene family from *Camellia sinensis* and regulatory role of CsSUS3 in sucrose metabolism in post-harvest tea leaves. BMC plant biology, 25(1), 1665.

Sun Y, et al. (2025) Identification and expression analysis of P-type ATPase IIIA subfamily in *Puccinia Striiformis* f. sp. *tritici*. BMC genomics, 26(1), 68.

Khaskhali S, et al. (2025) Expression profile and characterization of respiratory burst oxidase homolog genes in rice under MeJA, SA and Xoo treatments. Scientific reports, 15(1), 5936.

Hamid R, et al. (2025) Genome-wide identification of GhEDS1 gene family members in cotton and expression analysis in response to biotic and abiotic stresses. BMC plant biology, 25(1), 1229.

Wen X, et al. (2025) The ROS-FOXO pathway mediates broad-spectrum detoxification of acaricides in *Tetranychus cinnabarinus*. Communications biology, 8(1), 1274.

Li J, et al. (2025) Genome-Wide Identification and Expression Analysis of bHLH-MYC Family Genes from Mustard That May Be Important in Trichome Formation. Plants (Basel, Switzerland), 14(2).

Zhao G, et al. (2025) Genome-Wide Identification and Expression Analysis of the CaM Gene Family in Tree Peony (*Paeonia ostii*) During the Pistil Pollination Process. *Current issues in molecular biology*, 47(10).

Ben Romdhane W, et al. (2025) De novo, high-quality assembly and annotation of the halophyte grass *Aeluropus litoralis* draft genome and identification of A20/AN1 zinc finger protein family. *BMC plant biology*, 25(1), 556.

Luo Y, et al. (2025) Regulatory changes in the fatty acid elongase *eloF* underlie the evolution of sex-specific pheromone profiles in *Drosophila prolongata*. *BMC biology*, 23(1), 117.

Feng Y, et al. (2025) Serial innovations by Asgard archaea shaped the DNA replication machinery of the early eukaryotic ancestor. *Nature ecology & evolution*, 9(12), 2333.

Matthews ER, et al. (2025) Anthracyclines induce global changes in cardiomyocyte chromatin accessibility that overlap with cardiovascular disease loci. *PLoS genetics*, 21(10), e1011900.

Wang K, et al. (2025) LncLSTA: a versatile predictor unveiling subcellular localization of lncRNAs through long-short term attention. *Bioinformatics advances*, 5(1), vbae173.

Yu L, et al. (2025) Unraveling TEOSINTE BRANCHED1/CYCLOIDEA/PROLIFERATING CELL FACTOR Transcription Factors in Safflower: A Blueprint for Stress Resilience and Metabolic Regulation. *Molecules (Basel, Switzerland)*, 30(2).

Xue Y, et al. (2025) Identification of the BBX gene family in blueberry at different chromosome ploidy levels and fruit development and response under stress. *BMC genomics*, 26(1), 100.

Hu X, et al. (2025) Genome-wide identification of VOZ gene family in ten cotton species and the function analysis of GhVOZ2 involved in heat stress response. *BMC genomics*, 26(1), 753.

Xiao Y, et al. (2025) Cloning and function analysis of ZmICE1a, a contributor to the melioration of maize kernel traits. *Plant signaling & behavior*, 20(1), 2521320.

Wu Y, et al. (2025) Genome-wide identification and expression analysis of the GARP superfamily in response to abiotic stresses in alfalfa (*Medicago sativa* L.). *BMC plant biology*, 25(1), 1395.