

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

Defining Citation: [PMID:18437229](https://pubmed.ncbi.nlm.nih.gov/18437229/)

Keywords: motif, analysis, sequence, find, amino acid, nucleotide, set, alignment, gapped, recurring, variable, length, 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: 20250329T061132+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 45 mentions in open access literature.

Listed below are recent publications. The full list is available at [FDI Lab - SciCrunch.org](#).

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).

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.

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).

Fu W, et al. (2024) Genome-wide identification and expression analysis of Ubiquitin-specific protease gene family in maize (*Zea mays* L.). *BMC plant biology*, 24(1), 404.

Zhang Y, et al. (2024) Genome-wide identification and expression analysis of ARF gene family in embryonic development of Korean pine (*Pinus koraiensis*). *BMC plant biology*, 24(1), 267.

Fu C, et al. (2024) Genome-wide identification and molecular evolution of elongation family of very long chain fatty acids proteins in *Cyrtotrachelus buqueti*. *BMC genomics*, 25(1), 758.

Guan Y, et al. (2024) Histone (de)acetylation in epigenetic regulation of Phytophthora pathobiology. *Molecular plant pathology*, 25(7), e13497.

Tang Y, et al. (2024) The structural and functional analysis of mycobacteria cysteine desulfurase-loaded encapsulin. *Communications biology*, 7(1), 1656.

Xia J, et al. (2024) Genome-Wide In Silico Analysis of 1-Aminocyclopropane-1-carboxylate oxidase (ACO) Gene Family in Rice (*Oryza sativa* L.). *Plants (Basel, Switzerland)*, 13(24).

Shah OU, et al. (2024) Genome-Wide Investigation of Class III Peroxidase Genes in *Brassica napus* Reveals Their Responsiveness to Abiotic Stresses. *Plants (Basel, Switzerland)*, 13(7).

Du Y, et al. (2024) Genome-wide identification and expression analysis of phosphate-sensing SPX proteins in oats. *Frontiers in genetics*, 15, 1469704.

Wang T, et al. (2024) SETD2 loss in renal epithelial cells drives epithelial-to-mesenchymal transition in a TGF- β -independent manner. *Molecular oncology*, 18(1), 44.

Mahapatra K, et al. (2024) Unveiling the structure and interactions of SOG1, a NAC domain transcription factor: An in-silico perspective. *Journal, genetic engineering & biotechnology*, 22(1), 100333.

Gao P, et al. (2024) Identification of MATE Family and Characterization of GmMATE13 and GmMATE75 in Soybean's Response to Aluminum Stress. *International journal of molecular sciences*, 25(7).

Zeng Q, et al. (2024) Genome-Wide Identification and Expression Analysis of TGA Family Genes Associated with Abiotic Stress in Sunflowers (*Helianthus annuus* L.). *International journal of molecular sciences*, 25(7).

Sun X, et al. (2024) A Comprehensive Analysis of the Peanut SQUAMOSA Promoter Binding Protein-like Gene Family and How AhSPL5 Enhances Salt Tolerance in Transgenic *Arabidopsis*. *Plants (Basel, Switzerland)*, 13(8).

Ulrich NJ, et al. (2024) Integration of horizontally acquired light-harvesting genes into an ancestral regulatory network in the cyanobacterium *Acaryochloris marina* MBIC11017. *mBio*, 15(12), e0242324.

Xun Z, et al. (2024) Identification of Hypoxia-ALCAM^{high} Macrophage- Exhausted T Cell Axis in Tumor Microenvironment Remodeling for Immunotherapy Resistance. *Advanced science (Weinheim, Baden-Wurttemberg, Germany)*, 11(33), e2309885.

Harvey A, et al. (2024) Describing and characterizing the WAK/WAKL gene family across plant species: a systematic review. *Frontiers in plant science*, 15, 1467148.