

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: data analysis software, data processing software, sequence analysis software, software application, software resource, 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: 20260905T132804+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 203 mentions in open access literature.

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

Ren Y, et al. (2026) Circular RNA Vv-circCOR27 modulates thermotolerance through attenuating VvHSP90.2b-VvHsfA7a interaction in grapevine. *The New phytologist*, 250(2), 988.

Li Z, et al. (2026) Genome-Wide Characterization of the wnt Gene Family Reveals a wnt5b-Mediated Regulatory Mechanism of Testicular Development in *Cynoglossus semilaevis*. *Animals : an open access journal from MDPI*, 16(3).

García-Telles V, et al. (2026) Chb and nag genes drive N,N'-diacetylchitobiose metabolism in probiotic *Lactobacillus paracasei*. *Applied microbiology and biotechnology*, 110(1), 7.

Xiao Q, et al. (2026) Insights into the Cytochrome P450 Monooxygenase Superfamily in *Kadsura heteroclita* (Xuetong). *Molecules (Basel, Switzerland)*, 31(12).

Kok JY, et al. (2026) Nucleosome positioning shapes cryptic antisense transcription. *PLoS genetics*, 22(3), e1012078.

Zhao WH, et al. (2026) AmXlnR, a transcription factor involved in xylan degradation and pentose catabolism, enhances pullulan production from xylose in *Aureobasidium melanogenum*. *Synthetic and systems biotechnology*, 12, 471.

Nakamura R, et al. (2026) YAP/TAZ inhibition refines TGF- β signaling to prevent laryngeal fibrosis. *bioRxiv : the preprint server for biology*.

Wang Y, et al. (2026) Genome-wide analysis of the EIN3/EIL family in rye and functional identification of ScEIL5 in stripe rust resistance. *Frontiers in plant science*, 17, 1791751.

Xing L, et al. (2026) Evolutionary Characteristics and Expression Patterns of the UGT Gene Family in *Epimedium* from Gansu, China. *Current issues in molecular biology*, 48(4).

Fan Y, et al. (2026) GhGLDH35A gene-mediated ROS homeostasis and stomatal movement via the ascorbic acid pathway confers alkaline stress tolerance. *Journal of advanced research*, 81, 75.

Xu X, et al. (2026) Identification of the RcbZIP gene family in *Rubus Chingii* and analysis of the regulation of flavonoid synthesis by RcbZIP1 and RcbZIP12. *Frontiers in plant science*, 17, 1769751.

Zhao X, et al. (2026) Machine and Deep Learning Reveal Sequence Determinants Encoding Bivalent Histone Modifications. *Communications biology*, 9(1).

Trotman JB, et al. (2026) Protocol for evaluating RNA-protein associations in mammalian cells with RIP-seq and RIP-qPCR. *STAR protocols*, 7(1), 104298.

Ramadan MA, et al. (2026) A protocol for computational design of mRNA vaccines with high functionality and specificity. *Biology direct*, 21(1).

Dao C, et al. (2026) Characterization of the Maize GASA Gene Family and Their Responses to Low-Phosphorus Stress. *Plants (Basel, Switzerland)*, 15(2).

Lv G, et al. (2026) Genome-wide characterization of the PHT gene family in *Uncaria rhynchophylla* identified UrPHT1;11 as a key regulator to low phosphorus response. *BMC plant biology*, 26(1).

Li J, et al. (2026) Comprehensive genomic identification and functional analysis of bHLH transcription factors in *Ganoderma lucidum*. *Chinese herbal medicines*, 18(1), 200.

Staab-Weijnitz CA, et al. (2026) Prolyl-3-hydroxylase 1 is a central regulator of collagen post-translational modifications and the collagen biosynthetic network. *The Journal of biological chemistry*, 302(5), 111422.

Lan G, et al. (2026) Genome-Wide Identification and Expression Profiling of the PYL Gene Family in Watermelon Under Abiotic Stresses. *Genes*, 17(4).

Li X, et al. (2026) Genome-wide analysis of leucine-rich repeat-only proteins gene family revealed FaLRROP26 responding *Colletotrichum Siamense* infection by regulated lignin synthesis in cultivated strawberry (*Fragaria × ananassa*). *BMC plant biology*, 26(1), 328.