Resource Summary Report

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Eukaryotic Linear Motif

RRID:SCR_003085
Type: Tool

Proper Citation

Eukaryotic Linear Motif (RRID:SCR_003085)

Resource Information

URL: http://elm.eu.org

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Description: Computational biology resource for investigating candidate functional sites in eukarytic proteins. Functional sites which fit to the description linear motif are currently specified as patterns using Regular Expression rules. To improve the predictive power, context-based rules and logical filters are being developed and applied to reduce the amount of false positives. The current version of the ELM server provides core functionality including filtering by cell compartment, phylogeny, globular domain clash (using the SMART/Pfam databases) and structure. In addition, both the known ELM instances and any positionally conserved matches in sequences similar to ELM instance sequences are identified and displayed (see ELM instance mapper). Although the ELM resource contains a large collection of functional site motifs, the current set of motifs is not exhaustive.

Abbreviations: ELM

Synonyms: Eukarotic Linear Motif resource for Functional Sites in Proteins

Resource Type: analysis service resource, data analysis service, data or information resource, database, production service resource, service resource

Defining Citation: PMID:22110040

Keywords: linear motif, regulatory protein, motif, protein sequence, functional site, prediction, disease, virus, cell compartment, phylogeny, globular domain clash, structure, protein, bio.tools, FASEB list

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Availability: Free, Available for download, Freely available

Resource Name: Eukaryotic Linear Motif

Resource ID: SCR_003085

Alternate IDs: biotools:elm, nif-0000-30486

Alternate URLs: https://bio.tools/elm

Record Creation Time: 20220129T080217+0000

Record Last Update: 20260905T132457+0000

Ratings and Alerts

No rating or validation information has been found for Eukaryotic Linear Motif.

No alerts have been found for Eukaryotic Linear Motif.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 325 mentions in open access literature.

Listed below are recent publications. The full list is available at PRECISE-TBI .

Huang KW, et al. (2026) Disordered DNA-binding motif forms a modulation site for inhibiting the cancer immunotherapy target TREX1. Nucleic acids research, 54(2).

Hao Y, et al. (2026) SLiMs prediction method based on enhanced attention mechanism and feature fusion. Bioinformatics advances, 6(1), vbaf240.

Tang J, et al. (2026) An alternative reverse genetics system for PRRS virus and its application to define the role of endocytic sorting signal in GP3 protein intracellular trafficking. Frontiers in microbiology, 17, 1791468.

Abakarova M, et al. (2026) Proteome-wide prediction of the functional impact of missense variants with ProteoCast. Nature communications, 17(1).

D'Incal CP, et al. (2026) An Adnp frameshift variant disrupts Wnt signalling inducing chromatocytoskeletal defects and autism-related behaviour in male mice. EBioMedicine, 128, 106309.

Sedgwick AJ, et al. (2026) The NKp44-1 Isoform Is an Activating Receptor for PDGF-DD Expressed on Natural Killer Cells. Cancers, 18(7).

Qi Z, et al. (2026) A dileucine motif in TMEM163 is essential for its binding with both AP-3 and BLOC-1 complex. The Journal of biological chemistry, 302(6), 111451.

Wu H, et al. (2026) Characterization of viral diversity in wild marmot blood from the Qinghai-Tibet Plateau. Frontiers in microbiology, 17, 1668126.

Meng F, et al. (2025) Engineering yeast multicellular behaviors via synthetic adhesion and contact signaling. Cell, 188(18), 4936.

Yoshikawa R, et al. (2025) Crimean-Congo hemorrhagic fever virus NSm protein inhibits the type I interferon signaling by binding to STAT2. PLoS neglected tropical diseases, 19(11), e0013695.

Im JH, et al. (2025) MPK6-mediated phosphorylation destabilizes MYC2 and attenuates its transcriptional activity in jasmonate signaling. Plant communications, 6(11), 101465.

Brunello FG, et al. (2025) Integrating AlphaFold2 models and clinical data to improve the assessment of Short Linear Motifs (SLiMs) and their variants' pathogenicity. PLoS computational biology, 21(8), e1012829.

Hu D, et al. (2025) Transcription factor ELF4 in physiology and diseases: Molecular roles and clinical implications. Genes & diseases, 12(3), 101394.

Xu Y, et al. (2025) Modulation of tumor inflammatory signaling and drug sensitivity by CMTM4. The EMBO journal, 44(6), 1866.

Kalidass M, et al. (2025) Ubiquitin-dependent proteolysis of KNL2 driven by APC/CCDC20 is critical for centromere integrity and mitotic fidelity. The Plant cell, 37(7).

Goodwin HV, et al. (2025) PPI-ID: Streamlining protein-protein interaction prediction through domain and SLiM mapping. PLoS computational biology, 21(10), e1013062.

Fa??ndez-Acu??a JY, et al. (2025) The mountain papaya may be a possible reservoir of the Kashmir bee virus. PeerJ, 13, e18634.

Chow CFW, et al. (2025) SHARK-capture identifies functional motifs in intrinsically disordered protein regions. Protein science : a publication of the Protein Society, 34(4), e70091.

Kostareli M-M, et al. (2025) Diversification of DIX domain-containing proteins in the SAR supergroup. mBio, 16(5), e0396624.

Ahn J, et al. (2025) XAF1 is secreted from stressed tumor cells to activate T cell-mediated tumor surveillance via Lck-ERK signaling. Neoplasia (New York, N.Y.), 59, 101094.