

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 eukaryotic 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: Eukaryotic Linear Motif resource for Functional Sites in Proteins

Resource Type: production service resource, data analysis service, data or information resource, database, analysis 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: 20260804T043157+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 296 mentions in open access literature.

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

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

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.

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

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

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.

Faúndez-Acuña JY, et al. (2025) The mountain papaya may be a possible reservoir of the Kashmir bee virus. *PeerJ*, 13, e18634.

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.

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.

Baumgartner TJ, et al. (2025) Inhibition of the GSK3 β /Nav1.6 complex suppresses early-stage Alzheimer's hyperexcitability. *Alzheimer's & dementia : the journal of the Alzheimer's Association*, 21(7), e70507.

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

Ettaki I, et al. (2025) Missense variants weakening a SOX9 phosphodegron linked to odontogenesis defects, scoliosis, and other skeletal features. *HGG advances*, 6(2), 100404.

Belyantseva IA, et al. (2025) Taperin bundles F-actin at stereocilia pivot points enabling optimal lifelong mechanosensitivity. *The Journal of cell biology*, 224(8).

Murdocca M, et al. (2025) Structural and functional impact of the POLD1 Ser605del variant in MDPL syndrome: insights from protein-protein interactions. *Human genomics*, 19(1), 131.

Foran G, et al. (2024) Notch1 Phase Separation Coupled Percolation facilitates target gene expression and enhancer looping. *bioRxiv : the preprint server for biology*.

Du Y, et al. (2024) Multi-omics technologies and molecular biomarkers in brain tumor-related epilepsy. *CNS neuroscience & therapeutics*, 30(4), e14717.

Picarella ME, et al. (2024) Genetic and molecular mechanisms underlying the parthenocarpic fruit mutation in tomato. *Frontiers in plant science*, 15, 1329949.

Gong M, et al. (2024) MARK2 variants cause autism spectrum disorder via the downregulation of WNT/ β -catenin signaling pathway. *American journal of human genetics*, 111(11), 2392.

Kumar M, et al. (2024) ELM-the Eukaryotic Linear Motif resource-2024 update. *Nucleic acids research*, 52(D1), D442.

Idrees S, et al. (2024) Prediction of motif-mediated viral mimicry through the integration of host-pathogen interactions. Archives of microbiology, 206(3), 94.