Resource Summary Report

Generated by NIF on May 15, 2025

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

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: Non-commercial, ELM Software License Agreement, Http://elm.eu.org/media/Elm_academic_license.pdf, Acknowledgement requested

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: 20250514T061239+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 282 mentions in open access literature.

Listed below are recent publications. The full list is available at NIF.

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

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

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

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

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

D'Incal C, et al. (2024) ADNP dysregulates methylation and mitochondrial gene expression in the cerebellum of a Helsmoortel-Van der Aa syndrome autopsy case. Acta neuropathologica communications, 12(1), 62.

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

Rashmi R, et al. (2024) Bioinformatic analysis of THAP9 transposase homolog: conserved regions, novel motifs. Current research in structural biology, 7, 100113.

Reys V, et al. (2024) SLiMAn 2.0: meaningful navigation through peptide-protein interaction networks. Nucleic acids research, 52(W1), W313.

Rubin AJ, et al. (2024) LAT encodes T cell activation pathway balance. bioRxiv : the preprint server for biology.

Foran G, et al. (2024) Notch1 Phase Separation Coupled Percolation facilitates target gene expression and enhancer looping. Scientific reports, 14(1), 21912.

Fu J, et al. (2024) Nardilysin-regulated scission mechanism activates polo-like kinase 3 to suppress the development of pancreatic cancer. Nature communications, 15(1), 3149.

Frank Y, et al. (2024) Statistical analysis of sequential motifs at biologically relevant protein-protein interfaces. Computational and structural biotechnology journal, 23, 1244.

Ali H, et al. (2024) The astrovirus N-terminal nonstructural protein anchors replication complexes to the perinuclear ER membranes. PLoS pathogens, 20(7), e1011959.

Luebbert L, et al. (2024) Fast and scalable querying of eukaryotic linear motifs with gget elm. Bioinformatics (Oxford, England), 40(3).

Reuter N, et al. (2024) The Autonomous Fusion Activity of Human Cytomegalovirus Glycoprotein B Is Regulated by Its Carboxy-Terminal Domain. Viruses, 16(9).

Franco-Romero A, et al. (2024) C16ORF70/MYTHO promotes healthy aging in C.elegans

and prevents cellular senescence in mammals. The Journal of clinical investigation, 134(15).

Luige J, et al. (2024) Predicting nuclear G-quadruplex RNA-binding proteins with roles in transcription and phase separation. Nature communications, 15(1), 2585.

Kohrt S, et al. (2024) Identification of a Nuclear Localization Signal (NLS) in Human Transcription Elongation Factor ELL2. Cell biochemistry and function, 42(8), e70019.

Klaus L, et al. (2023) Systematic identification and characterization of repressive domains in Drosophila transcription factors. The EMBO journal, 42(3), e112100.