

Resource Summary Report

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PrDOS

RRID:SCR_021886

Type: Tool

Proper Citation

PrDOS (RRID:SCR_021886)

Resource Information

URL: <https://prdos.hgc.jp/cgi-bin/top.cgi>

Proper Citation: PrDOS (RRID:SCR_021886)

Description: Web server to predict natively disordered regions of protein chain from its amino acid sequence. Returns disorder probability of each residue as prediction results.

Resource Type: software resource, data access protocol, web service

Keywords: predict natively disordered regions, protein chain, protein chain prediction, disordered regions, disorder probability

Resource Name: PrDOS

Resource ID: SCR_021886

Record Creation Time: 20220421T050137+0000

Record Last Update: 20260813T055246+0000

Ratings and Alerts

No rating or validation information has been found for PrDOS.

No alerts have been found for PrDOS.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 39 mentions in open access literature.

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

Adachi Y, et al. (2026) Chronic stress disrupts the network among stress granules, P-bodies, and motor proteins. *bioRxiv : the preprint server for biology*.

Gitman IFB, et al. (2026) OmicIntegrator: A Simple and Versatile Tool for Meta-Analysis. *Plants (Basel, Switzerland)*, 15(2).

Li Y, et al. (2026) 3D epigenome architecture orchestrates cis and trans regulation of flowering time in rice. *Genome biology*, 27(1).

Yang D, et al. (2026) Proximity proteomics reveals OTUD6B regulation of stress granule dynamics through coalescence with VCP/p97. *Cell death & disease*, 17(1), 206.

De Leon DO, et al. (2026) Immunoinformatics and molecular docking reveal potential multi-epitope vaccine against *Pseudomonas aeruginosa*. *Clinical and experimental vaccine research*, 15(1), 71.

Stong Tangan YA, et al. (2026) In-silico design of a multi-epitope vaccine candidate against *Strongyloides stercoralis*. *BMC infectious diseases*, 26(1).

Shumaker KA, et al. (2025) A screen for synthetic genetic interactions with the *Saccharomyces cerevisiae* hrq1^ΔN allele. *G3 (Bethesda, Md.)*, 15(12).

Shumaker KA, et al. (2025) A screen for synthetic genetic interactions with the *Saccharomyces cerevisiae* hrq1^ΔN allele. *bioRxiv : the preprint server for biology*.

Miyamura T, et al. (2025) Nuclear keratin 6A upregulates human papillomavirus oncogene expression through TEAD1 interaction. *Virology journal*, 22(1), 202.

Knutson BA, et al. (2025) Evolutionary and Structural Insights into the RNA Polymerase I A34 Protein Family: A Focus on Intrinsic Disorder and Phase Separation. *Genes*, 16(1).

Cao L, et al. (2025) Heat stress response factor ZmHSF10 positively regulates heat tolerance in maize. *BMC plant biology*, 25(1), 1473.

Teng L, et al. (2025) Genome-wide identification and analysis of expression of pathogenesis-related protein 1 (PR-1) gene family in brown algae. *Frontiers in plant science*, 16, 1754480.

Santjer S, et al. (2025) The activity of the EMT suppressor GRHL2 is regulated by SUMOylation. *The Journal of biological chemistry*, 301(10), 110662.

Singh S, et al. (2025) An efficient strategy for producing RNA-free Nucleocapsid protein of SARS-CoV-2 for biochemical and structural investigations. *FEBS open bio*, 15(11), 1762.

Mgbechidinma CL, et al. (2025) Phase separation and biomolecular condensate formation drive plant endomembrane and autophagy crosstalk. *Journal of experimental botany*, 77(1), 149.

Lal K, et al. (2025) Molecular identification and functional analysis of HrpZ2, a new member of the harpin superfamily from *Pseudomonas syringae*, inducing hypersensitive response in tobacco. *Frontiers in plant science*, 16, 1665817.

Harracksingh AN, et al. (2024) Functional characterization of optic photoreception in *Lymnaea stagnalis*. *PloS one*, 19(11), e0313407.

Watanabe T, et al. (2024) Conserved cysteine residues in Kaposi's sarcoma herpesvirus ORF34 are necessary for viral production and viral pre-initiation complex formation. *Journal of virology*, 98(8), e0100024.

Yang Y, et al. (2024) PCNA-binding activity separates RNF168 functions in DNA replication and DNA double-stranded break signaling. *Nucleic acids research*, 52(21), 13019.

Jang S, et al. (2024) HIV-1 usurps mixed-charge domain-dependent CPSF6 phase separation for higher-order capsid binding, nuclear entry and viral DNA integration. *Nucleic acids research*, 52(18), 11060.