

# Resource Summary Report

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## IDEAL - Intrinsically Disordered proteins with Extensive Annotations and Literature

RRID:SCR\_006027

Type: Tool

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### Proper Citation

IDEAL - Intrinsically Disordered proteins with Extensive Annotations and Literature  
(RRID:SCR\_006027)

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### Resource Information

**URL:** <http://www.ideal.force.cs.is.nagoya-u.ac.jp/IDEAL/>

**Proper Citation:** IDEAL - Intrinsically Disordered proteins with Extensive Annotations and Literature (RRID:SCR\_006027)

**Description:** IDEAL, Intrinsically Disordered proteins with Extensive Annotations and Literature, is a collection of knowledge on experimentally verified intrinsically disordered proteins (IDPs) or intrinsically disordered regions (IDRs). IDEAL contains manually curated annotations on IDPs in locations, structures, and functional sites such as protein binding regions and posttranslational modification sites together with references and structural domain assignments. Protean segment One of the unique phenomena seen in IDPs is so-called the coupled folding and binding, where a short flexible segment can bind to its binding partner with forming a specific structure to act as a molecular recognition element. IDEAL explicitly annotates these regions as protean segment (ProS) when unstructured and structured information are both available in the region. Access to the data All the entries are tabulated in the list and individual entries can be retrieved by using the search tool at the upper-right corner in this page. IDEAL also provides the BLAST search, which can find homologs in IDEAL. All the information in IDEAL can be downloaded in the XML file.

**Abbreviations:** IDEAL

**Synonyms:** IDEAL - Intrinsically Disordered proteins with Extensive Annotations Literature, Intrinsically Disordered proteins with Extensive Annotations and Literature

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

**Defining Citation:** [PMID:22067451](#)

**Keywords:** intrinsically disordered protein, protein, intrinsically disordered region, region, location, structure, functional site, protein binding region, binding region, posttranslational modification site, reference, structural domain assignment, blast, homolog, simian virus 40, epstein-barr virus, human herpesvirus 1, residue, protean segment, bio.tools

**Funding:** Japanese Ministry of Education Culture Sports Science and Technology MEXT

**Resource Name:** IDEAL - Intrinsically Disordered proteins with Extensive Annotations and Literature

**Resource ID:** SCR\_006027

**Alternate IDs:** biotools:ideal, nlx\_151427

**Alternate URLs:** <https://bio.tools/ideal>

**Record Creation Time:** 20220129T080233+0000

**Record Last Update:** 20260905T132959+0000

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## Ratings and Alerts

No rating or validation information has been found for IDEAL - Intrinsically Disordered proteins with Extensive Annotations and Literature.

No alerts have been found for IDEAL - Intrinsically Disordered proteins with Extensive Annotations and Literature.

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## Data and Source Information

**Source:** [SciCrunch Registry](#)

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## Usage and Citation Metrics

We found 11 mentions in open access literature.

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

Chen R, et al. (2022) Prediction of protein-protein interaction sites in intrinsically disordered proteins. *Frontiers in molecular biosciences*, 9, 985022.

Dong Y, et al. (2021) Regularized joint water-fat separation with B0 map estimation in image space for 2D-navigated interleaved EPI based diffusion MRI. *Magnetic resonance in medicine*, 86(6), 3034.

Perry DC, et al. (2020) A protocol for a nationwide multicentre, prospective surveillance cohort and nested-consented cohort to determine the incidence and clinical outcomes of slipped capital femoral epiphysis. *Bone & joint open*, 1(3), 35.

Piovesan D, et al. (2018) MobiDB 3.0: more annotations for intrinsic disorder, conformational diversity and interactions in proteins. *Nucleic acids research*, 46(D1), D471.

Ota H, et al. (2017) Sequence conservation of protein binding segments in intrinsically disordered regions. *Biochemical and biophysical research communications*, 494(3-4), 602.

Taneyhill LA, et al. (2016) The society for craniofacial genetics and developmental biology 38th annual meeting. *American journal of medical genetics. Part A*, 170(7), 1732.

van der Lee R, et al. (2014) Classification of intrinsically disordered regions and proteins. *Chemical reviews*, 114(13), 6589.

Takasu M, et al. (2014) Magnetic resonance evaluation of multiple myeloma at 3.0 Tesla: how do bone marrow plasma cell percentage and selection of protocols affect lesion conspicuity? *PloS one*, 9(1), e85931.

Fukuchi S, et al. (2014) IDEAL in 2014 illustrates interaction networks composed of intrinsically disordered proteins and their binding partners. *Nucleic acids research*, 42(Database issue), D320.

Galperin MY, et al. (2012) The 2012 Nucleic Acids Research Database Issue and the online Molecular Biology Database Collection. *Nucleic acids research*, 40(Database issue), D1.

Fukuchi S, et al. (2012) IDEAL: Intrinsically Disordered proteins with Extensive Annotations and Literature. *Nucleic acids research*, 40(Database issue), D507.