

Resource Summary Report

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RESID

RRID:SCR_003505

Type: Tool

Proper Citation

RESID (RRID:SCR_003505)

Resource Information

URL: <http://pir.georgetown.edu/resid/>

Proper Citation: RESID (RRID:SCR_003505)

Description: A comprehensive collection of annotations and structures for protein modifications including amino-terminal, carboxyl-terminal and peptide chain cross-link post-translational modifications. It provides: systematic and alternate names, atomic formulas and masses, enzyme activities generating the modifications, keywords, literature citations, Gene Ontology cross-references, Protein Information Resource (PIR) and SWISS-PROT protein sequence database feature table annotations, structure diagrams and molecular models. Each RESID Database entry presents a chemically unique modification and shows how that modification is currently annotated in the protein sequence databases, Swiss-Prot and the Protein Information Resource (PIR). The RESID Database provides a table of corresponding equivalent feature annotations that is used in the UniProt project, an international effort to combine the resources of the Swiss-Prot, TrEMBL and PIR. As an annotation tool, the RESID Database is used in standardizing and enhancing modification descriptions in the feature tables of Swiss-Prot entries.

Abbreviations: RESID

Synonyms: RESID Database at the EBI, RESID Database at PIR, RESID Database of Protein Modifications, RESID Database

Resource Type: data or information resource, database

Defining Citation: [PMID:15174122](#), [PMID:12520062](#)

Keywords: protein cross-link, protein modification, protein structure, protein, structure, annotation, amino-terminal, carboxyl-terminal, peptide chain cross-link, post-translational modification, gold standard, bio.tools

Resource Name: RESID

Resource ID: SCR_003505

Alternate IDs: nif-0000-03400, r3d100000023, biotools:resid

Alternate URLs: <https://bio.tools/resid>, <https://doi.org/10.17616/R3Z59M>

Old URLs: <http://www.ebi.ac.uk/RESID/>

Record Creation Time: 20220129T080219+0000

Record Last Update: 20260905T133121+0000

Ratings and Alerts

No rating or validation information has been found for RESID.

No alerts have been found for RESID.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 10 mentions in open access literature.

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

Suh D, et al. (2024) CHARMM-GUI QM/MM Interfacer for a Quantum Mechanical and Molecular Mechanical (QM/MM) Simulation Setup: 1. Semiempirical Methods. Journal of chemical theory and computation, 20(12), 5337.

Choi HP, et al. (2023) Differential Post-Translational Modifications of Proteins in Bladder Ischemia. Biomedicines, 12(1).

Manning SW, et al. (2023) Severe multi-year drought coincident with Hittite collapse around 1198-1196 BC. Nature, 614(7949), 719.

Yang JH, et al. (2021) Post-Translational Modification Networks of Contractile and Cellular Stress Response Proteins in Bladder Ischemia. Cells, 10(5).

Weterings S, et al. (2019) A resistance exercise set for a total body workout for adults with intellectual disabilities, a pilot study. Journal of applied research in intellectual disabilities : JARID, 32(3), 730.

Row JR, et al. (2017) Developing approaches for linear mixed modeling in landscape genetics through landscape-directed dispersal simulations. Ecology and evolution, 7(11), 3751.

Panigrahi P, et al. (2015) Engineering Proteins for Thermostability with iRDP Web Server. PloS one, 10(10), e0139486.

Mata-Gómez MA, et al. (2012) Accelerated identification of proteins by mass spectrometry by employing covalent pre-gel staining with Uniblue A. PloS one, 7(2), e31438.

Vertegaal AC, et al. (2011) Uncovering ubiquitin and ubiquitin-like signaling networks. Chemical reviews, 111(12), 7923.

Kleywegt GJ, et al. (2007) Crystallographic refinement of ligand complexes. Acta crystallographica. Section D, Biological crystallography, 63(Pt 1), 94.