

Resource Summary Report

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O-GLYCBASE

RRID:SCR_003288

Type: Tool

Proper Citation

O-GLYCBASE (RRID:SCR_003288)

Resource Information

URL: <https://services.healthtech.dtu.dk/datasets/OglycBase/>

Proper Citation: O-GLYCBASE (RRID:SCR_003288)

Description: Revised database of O- and C-glycosylated proteins. The criteria for inclusion are at least one experimentally verified O- or C-glycosylation site. Each entry contains information about the glycan involved, the species, sequence, a literature reference and http-linked cross-references to other databases. Version 6.00 has 242 glycoprotein entries. The terminal sugar linked to serine or threonine is cited when known. The database is non-redundant in the sense that it contains no identical sequences, unless there is conflicting glycosylation data. Mucins have tandem repeat sequences, which are O-glycosylated. This result in some redundancy of the O-glycosylation sites. For prediction purposes they have also included a version of the database which contains no identical O-glycosylation sites (window=9) called O-Unique.seq. Data can no longer be retrieved by anonymous ftp. Only http is supported. New data, comments and suggestions are welcome.

Abbreviations: O-GlycBase

Resource Type: data or information resource, data repository, database, service resource, storage service resource

Defining Citation: [PMID:9847232](#)

Keywords: glycosylated protein, glycoprotein, serine, threonine, o-glycosylation site, c-glycosylation site, carbohydrate, o-glycan, asparagine, glycosylation, glycan

Availability: Free, Freely available

Resource Name: O-GLYCBASE

Resource ID: SCR_003288

Alternate IDs: nif-0000-03209

Old URLs: <http://www.cbs.dtu.dk/databases/OGLYCBASE/>

Record Creation Time: 20220129T080218+0000

Record Last Update: 20260829T182150+0000

Ratings and Alerts

No rating or validation information has been found for O-GLYCBASE.

No alerts have been found for O-GLYCBASE.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 12 mentions in open access literature.

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

Vellosillo P, et al. (2021) A global map of associations between types of protein posttranslational modifications and human genetic diseases. *iScience*, 24(8), 102917.

Gianazza E, et al. (2016) In silico prediction and characterization of protein post-translational modifications. *Journal of proteomics*, 134, 65.

DePriest AD, et al. (2016) Regulators of Androgen Action Resource: a one-stop shop for the comprehensive study of androgen receptor action. *Database : the journal of biological databases and curation*, 2016.

Li F, et al. (2016) GlycoMinestruct: a new bioinformatics tool for highly accurate mapping of the human N-linked and O-linked glycoproteomes by incorporating structural features. *Scientific reports*, 6, 34595.

Kao HJ, et al. (2015) A two-layered machine learning method to identify protein O-GlcNAcylation sites with O-GlcNAc transferase substrate motifs. *BMC bioinformatics*, 16 Suppl 18(Suppl 18), S10.

Baycin Hizal D, et al. (2014) Glycoproteomic and glycomic databases. *Clinical proteomics*, 11(1), 15.

Frank M, et al. (2010) Bioinformatics and molecular modeling in glycobiology. *Cellular and molecular life sciences : CMLS*, 67(16), 2749.

Hamby SE, et al. (2008) Prediction of glycosylation sites using random forests. *BMC bioinformatics*, 9, 500.

Vadaie N, et al. (2008) Cleavage of the signaling mucin Msb2 by the aspartyl protease Yps1 is required for MAPK activation in yeast. *The Journal of cell biology*, 181(7), 1073.

Hiller M, et al. (2005) Creation and disruption of protein features by alternative splicing -- a novel mechanism to modulate function. *Genome biology*, 6(7), R58.

Galperin MY, et al. (2005) The Molecular Biology Database Collection: 2005 update. *Nucleic acids research*, 33(Database issue), D5.

Perrier AL, et al. (2002) PRiMA: the membrane anchor of acetylcholinesterase in the brain. *Neuron*, 33(2), 275.