Resource Summary Report

Generated by T1D on Aug 5, 2026

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: storage service resource, data repository, service resource, database, data or information 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: 20260805T044052+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 T1D .

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.