

Resource Summary Report

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NetNGlyc

RRID:SCR_001570

Type: Tool

Proper Citation

NetNGlyc (RRID:SCR_001570)

Resource Information

URL: <https://services.healthtech.dtu.dk/services/NetNGlyc-1.0/>

Proper Citation: NetNGlyc (RRID:SCR_001570)

Description: Server that predicts N-Glycosylation sites in human proteins using artificial neural networks that examine the sequence context of Asn-Xaa-Ser/Thr sequons. NetNGlyc 1.0 is also available as a stand-alone software package, with the same functionality as the service above. Ready-to-ship packages exist for the most common UNIX platforms.

Abbreviations: NetNGlyc

Synonyms: NetNGlyc Server

Resource Type: data analysis service, service resource, software application, production service resource, software resource, analysis service resource

Keywords: predict, n-glycosylation site, human, protein, neural network, sequence, asn-xaa-ser/thr sequon, glycoprotein, bio.tools

Availability: Free, Freely available

Resource Name: NetNGlyc

Resource ID: SCR_001570

Alternate IDs: nlx_153863, biotools:netnglyc

Alternate URLs: <https://bio.tools/netnglyc>

Record Creation Time: 20220129T080208+0000

Record Last Update: 20260801T042512+0000

Ratings and Alerts

No rating or validation information has been found for NetNGlyc.

No alerts have been found for NetNGlyc.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 1753 mentions in open access literature.

Listed below are recent publications. The full list is available at [kravitz2](#).

De Coninck T, et al. (2025) OsAPSE modulates non-covalent interactions between arabinogalactan protein O-glycans and pectin in rice cell walls. *Frontiers in plant science*, 16, 1588802.

Hu Y, et al. (2025) Functional Divergence of Plant-Derived Thaumatin-Like Protein Genes in Two Closely Related Whitefly Species. *Advanced science (Weinheim, Baden-Wurttemberg, Germany)*, 12(16), e2502193.

Recalde A, et al. (2025) New components of the community-based DNA-repair mechanism in Sulfolobales. *microLife*, 6, uqaf002.

Tariq TB, et al. (2025) Molecular modelling and gene expression analysis to probe the GT-? trihelix transcription factors in *Solanum tuberosum* under drought stress. *Scientific reports*, 15(1), 12471.

Espinheira RP, et al. (2025) Discovery and Characterization of Mannan-Specialized GH5 Endo-1,4-?-mannanases: a Strategy for Açai (*Euterpe oleracea* Mart.) Seeds Upgrading. *Journal of agricultural and food chemistry*, 73(1), 625.

Sun P, et al. (2025) The Regulatory Mechanisms of *Treponema pallidum* Enolase on Macrophages: From Enzymatic Activity to Signal Transduction. *FASEB journal : official publication of the Federation of American Societies for Experimental Biology*, 39(13), e70801.

Quaranta M, et al. (2025) Structural Analysis of the SARS-CoV-2 Spike N-Terminal Domain Across Wild-Type and Recent Variants: A Comparative Study. *Proteins*, 93(11), 1891.

Yao X-Y, et al. (2025) Epidemiological, virological, and pathogenic insights into Nairobi sheep disease virus infection in sheep and goats in China. *Journal of virology*, 99(6), e0000625.

Suneesh NS, et al. (2025) Reverse vaccinology-based design of multivalent multiepitope mRNA vaccines targeting key viral proteins of Herpes Simplex Virus type-2. *Frontiers in immunology*, 16, 1586271.

Xu R, et al. (2025) Cryptosporidium exports a mucin glycoprotein into the microvilli of intestinal epithelium. *Virulence*, 16(1), 2553780.

Singh G, et al. (2025) Characterization of the glycoproteins of fish and amphibian influenza B-like viruses. *Science advances*, 11(34), eady8610.

Guo X, et al. (2025) Dominance of the GI-19 genotype and genomic characterization of the S1 gene in avian infectious bronchitis virus from 2020 to 2024. *Frontiers in cellular and infection microbiology*, 15, 1640152.

Dong X, et al. (2025) Genome-wide identification, expression analysis of taars (trace amine-associated receptors) and response to cadaverine and putrescine in Mandarin fish (*Siniperca chuatsi*). *BMC genomics*, 26(1), 962.

Lei H, et al. (2025) Chronology of H3N2 human influenza virus surface glycoprotein adaptation from 1968 to 2019 reveals a surge of adaptation between 1997 and 2002. *Journal of virology*, 99(11), e0132925.

Shahid S, et al. (2025) First detection and genetic characterization of atypical Porcine pestivirus in pigs, Thailand. *Scientific reports*, 15(1), 33384.

Alkubaisi NA, et al. (2025) Evolution and Vaccine Strain Match of HA and NA Genes of Influenza A/H3N2 Subtype in Riyadh, Saudi Arabia, 2020-2023. *Vaccines*, 13(12).

Steck MR, et al. (2025) Hiding in plain sight: Genomic and phenotypic characterization of mosquito-borne Bussuquara virus. *PLoS neglected tropical diseases*, 19(12), e0013774.

Oh SH, et al. (2025) Novel HIV-1 fusion peptide immunogens using glycan-engineered alphavirus-like particles. *NPJ vaccines*, 10(1), 232.

Li Z, et al. (2025) The glycosylation variant at residue 381 of the spike protein contributes to virulence shifts in porcine epidemic diarrhea virus during both natural field transmission and laboratory cell passaging with poor cross-protection. *Journal of virology*, 99(12), e0156125.

Aloryi KD, et al. (2025) Genome landscape of the universal stress protein gene family in lettuce and expression profile in response to heat stress. *BMC plant biology*, 25(1), 1636.