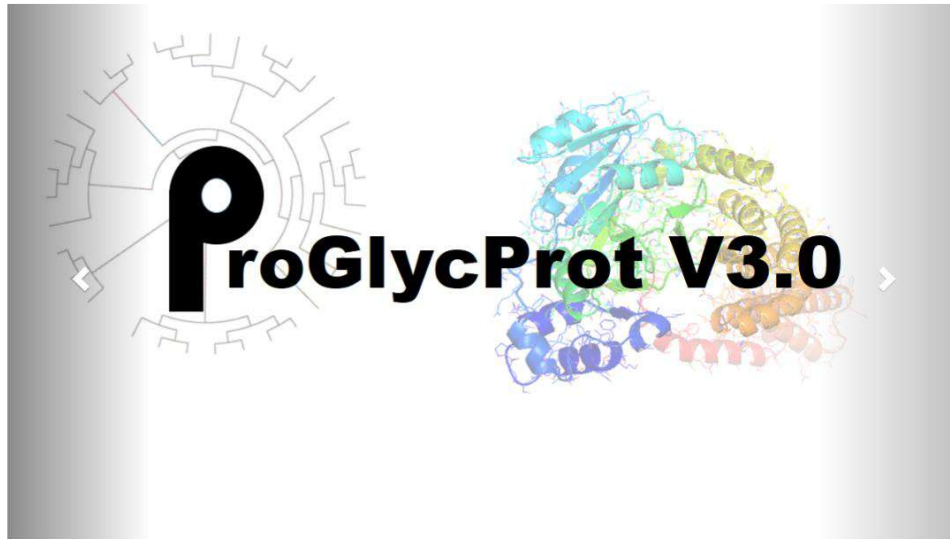


# ProGlycProt Tutorial

Third release

A Manually Curated Repository of Experimentally Characterized Glycoproteins and Protein Glycosyltransferases of Prokaryotes

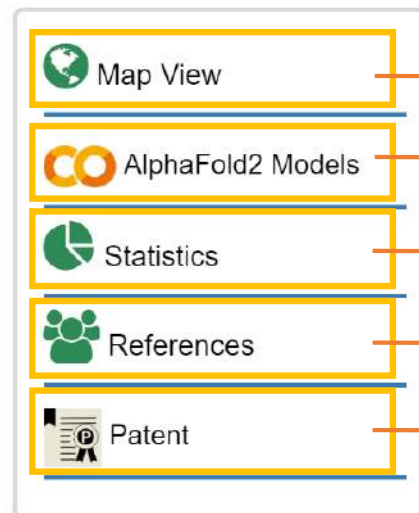


- Information can be retrieved by clicking on any of the desired links appearing as pull-down menus under six headings – ProGPdb, ProGTdb, Search by Feature, Structure Gallery, Tools, Links
- Clicking on the Home icon lands on the home page at any point of time.

## ProGlycProt Third Release (2022)

ProGlycProt is a manually curated, comprehensive web repository of experimentally characterized glycoproteins and glycosyltransferases that are involved in protein glycosylation, in prokaryotes, exclusively. The website is a focused effort to provide concise and relevant information derived from rapidly expanding literature on prokaryotic glycoproteins, attached glycans, their glycosylating enzyme(s), their specificities, mutants, glycosylation linked genes, and genomic content thereof, in a cross-referenced, interactive manner.

ProGlycProt database has two main sections namely, ProGPdb and ProGTdb that are cross-referenced to each other and searchable through specified criteria, by selecting Feature or by Interactive Map-view of cited Glyco-Research Groups. ProGPdb provides extensive experimentally verified information on glycosites and glycoproteins of the prokaryotes, wherein each entry has a unique ProGP ID. ProGPdb has two catalogues: ProCGP and ProUGP. While ProCGP is a catalogue of characterized prokaryotic glycoproteins, defined as entries with at least one experimentally known "glycosylated residue (glycosite)", ProUGP is a catalogue of uncharacterized prokaryotic glycoproteins, defined as entries where glycosylation is known but not the glycosite(s). .. [More>>>](#)



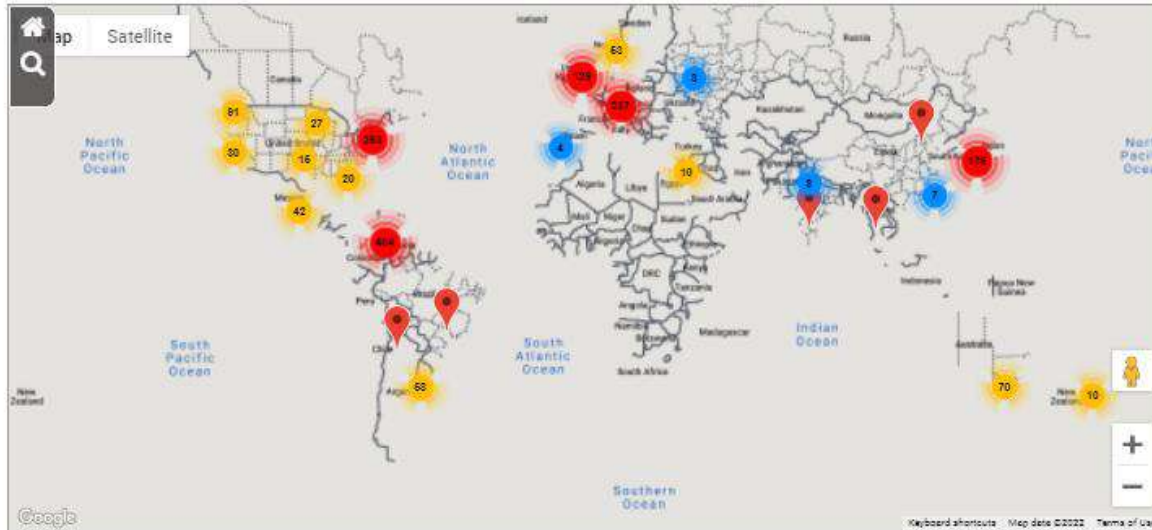
Click on any of the five links to go to –

1. Map view – to view the location of the research group on the world map
2. Alpha Fold2 Structures – Structures of the GTs and GPs predicted using ColabPro
3. Statistics – Displays statistics of particular subcategory within each section of database
4. References – Shows the papers published on this database
5. Patent – Contains a list of patents of prokaryotic glycosylation

## Map View of Prokaryotic Glyco-Groups

Facilitates an interactive database search using search feature displayed on the left side of the map.

**Map View of Prokaryotic Glyco-Groups:** Allows user to obtain a map view of the research groups cited in ProGlycProt. This interface further facilitates an interactive database search using select features and simultaneous display of map view of the associated research group as well as database statistics against the selected features.



### ProGlycProt Third Release (2022)

ProGlycProt is a manually curated, comprehensive web repository of experimentally characterized glycoproteins and glycosyltransferases that are involved in protein glycosylation, in prokaryotes, exclusively. The website is a focused effort to provide concise and relevant information derived from rapidly expanding literature on prokaryotic glycoproteins, attached glycans, their glycosylating enzyme(s), their specificities, mutants, glycosylation linked genes, and genomic content thereof, in a cross-referenced, interactive manner.

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 Map View

 AlphaFold2 Models

 Statistics

 References

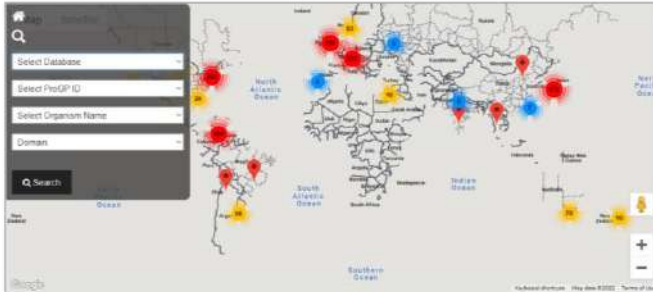
 Patent

Map view can be directly opened by clicking on the Map View here.

# 1. Click on the search icon.

Map View of Prokaryotic Glyco-Groups

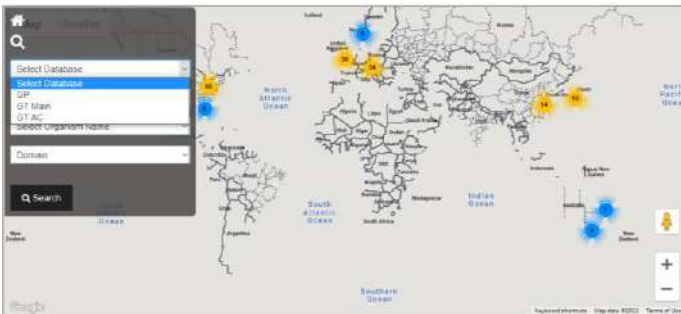
Map View of Prokaryotic Glyco-Groups: Allows user to obtain a map view of the research groups cited in ProGlycProt. This interface further facilitates an interactive database search using select features and simultaneous display of map view of the associated research group as well as database statistics against the selected features.



# 2. Click on 'Select Database'.

Map View of Prokaryotic Glyco-Groups

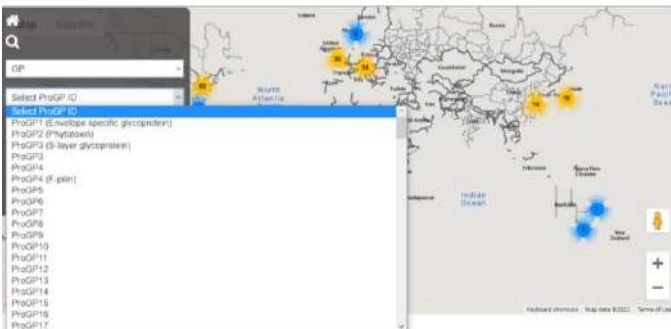
Map View of Prokaryotic Glyco-Groups: Allows user to obtain a map view of the research groups cited in ProGlycProt. This interface further facilitates an interactive database search using select features and simultaneous display of map view of the associated research group as well as database statistics against the selected features.



# 3. Choose desired ProGP or ProGT ID.

Map View of Prokaryotic Glyco-Groups

Map View of Prokaryotic Glyco-Groups: Allows user to obtain a map view of the research groups cited in ProGlycProt. This interface further facilitates an interactive database search using select features and simultaneous display of map view of the associated research group as well as database statistics against the selected features.



# 4. Result of the search for ProGP.

Map View of Prokaryotic Glyco-Groups

Map View of Prokaryotic Glyco-Groups: Allows user to obtain a map view of the research groups cited in ProGlycProt. This interface further facilitates an interactive database search using select features and simultaneous display of map view of the associated research group as well as database statistics against the selected features.



# 5. Ctrl+Z+scroll to zoom in the map view.

Map View of Prokaryotic Glyco-Groups

Map View of Prokaryotic Glyco-Groups: Allows user to obtain a map view of the research groups cited in ProGlycProt. This interface further facilitates an interactive database search using select features and simultaneous display of map view of the associated research group as well as database statistics against the selected features.

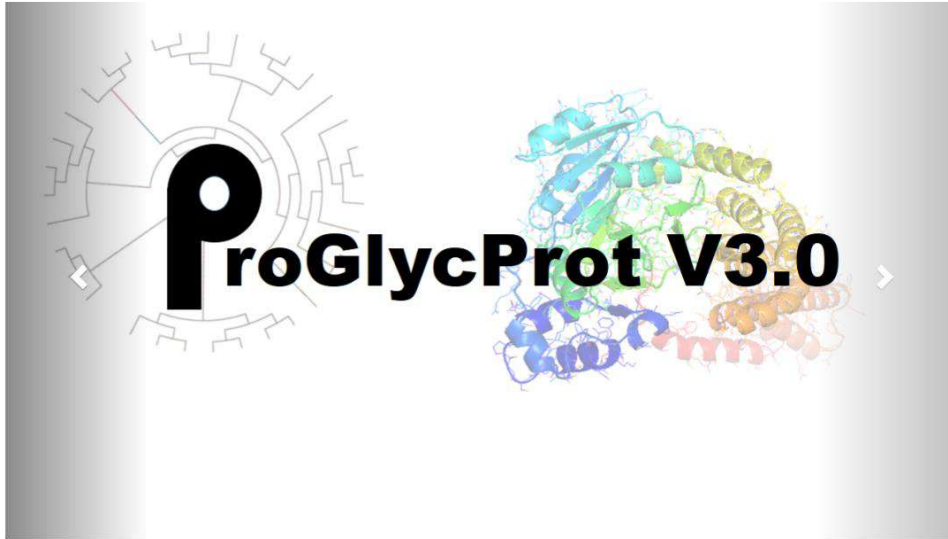


- Similarly, search can be made for ProGT Main and ProGT Accessory.
- One can search by name of organism as well as domain (refer to point 1) after selecting the database.



# How to search glycoproteins in ProGPdb?

A Manually Curated Repository of Experimentally Characterized Glycoproteins and Protein Glycosyltransferases of Prokaryotes



1. Click on the search icon.

Search

Example Display Page

Upd

2. Choose either ProCGP or ProUGP for characterized and uncharacterized glycoproteins, respectively.

ProCGP (Characterized Glycoproteins)  
 ProUGP (Uncharacterized Glycoproteins)

Choose Search Criteria  
Choose

Select Value  
[Empty]

Choose Display Criteria  
All

Search

Example display page will give you an idea of the type of information existing for a given entry.

3. Choose from different search criteria.

- ProCGP (Characterized Glycoproteins)  
 ProUGP (Uncharacterized Glycoproteins)

Choose Search Criteria

Choose

Choose  
ProGP ID  
Organism  
Protein Name  
UniProtKB/SwissProt ID  
Glyco-group  
Choose Display Criteria

All

Search

4. Select value and click on search.

- ProCGP (Characterized Glycoproteins)  
 ProUGP (Uncharacterized Glycoproteins)

Choose Search Criteria

ProGP ID

Select Value  
ProGP3 (S-layer glycoprotein)

Choose Display Criteria

All

Search

## ProGP3 (S-layer glycoprotein)

Home -> ProGPdb -> Search ProGP -> Display data

Compare ID

ProGP3 (S- ▾)

Compare ID

Choose Co: ▾

Compare ID

Choose Co: ▾

Compare ID

Choose Co: ▾

Search Display Criteria

all ▾

Display

Compare

Download  
the excel of  
the result.

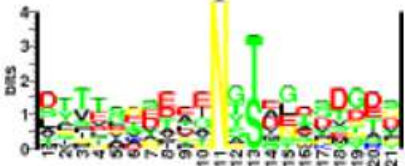


Print  
result  
save it  
as  
PDF.

ProGP ID	ProGP3 (S-layer glycoprotein)
Validation Status	Characterized
Organism Information	
Organism Name	<i>Halobacterium salinarum</i> (Halobium) R1M1/NRC-1
Domain	Archaea
Classification	Phylum : Euryarchaeota Class : Halobacteria Orders : Halobacteriales Family : Halobacteriaceae Genus : <i>Halobacterium</i> Species : <i>salinarum</i> Strain : R1M1/NRC-1
Taxonomic ID (NCBI)	64091
Genome Information	
GenBank	AE004437.1
EMBL	AE004437
Gene Information	
Gene Name	csg (VNG_2679G)
NCBI Gene ID	1449008
GenBank Gene Sequence	NC_002607
Protein Information	
Protein Name	S-layer glycoprotein

Protein Information	
Protein Name	S-layer glycoprotein
UniProtKB/SwissProt ID	P0DME1
NCBI RefSeq	WP_012289536.1
EMBL-CDS	AE004437.1
UniProtKB Sequence	>sp P0DME1 CSG_HALSA Cell surface glycoprotein OS=Halobacterium salinarum (strain ATCC 700922 / JCM 11081 / NRC-1) GN=csg PE=3 SV=1 MTDTTGKLRVLLTALMVGSVIGAGVAFTGGAAAANASDLNDYQRFNENTNYTYSTASED GKTEGSVASGATIFQGEEDVTFRKLNDNEKEVSPATLSRTGGSDGEGVPLQMPIPEDQSTGS YDSNGPDNDEADFGVTVQSPSVTMEVRRNADNDVTGGVLTNTQQDESSIAVDYNYAAED LETLVEDEDGLDVTDEILAADQSGGAYEDGTGNGNPNTLRFDIDPNNVDAGDYTVSVEGV EDLDFGDATESASVTISSNKAASLNLAEDVVQGANLKYTIENSPEGNYHAVTIDSSDFR DSSSGADAAKVMRSVGDVDTGLVVDNDSTTEIVDDYENTSISDSDYAYAVEIDDGNGV GSIETQYLDSSADIDLYPASDTEADPYVNSNEELTNGSALDGVSTDDDTDFDVTQGDITLDNPTGAYVVGSEVDINGTANEGTDDVLYARDNDFELVTVGKEKSIEVSDDDTFEEE DITLSDGDKGGDILGLPGTYRLGIIAKSDAVNSSGGVKNIDTSDFNQGVSSSTSSIRVT DTELTSFETYNGQVADDNQIDVEGTAPGKDNVAIIIIGSRGKVKFQISVSDDDTFDE EDIDISELRQGSASAHILSSGRDGKFGEDTANSISDLEDEVGNYTSGSPTGDQIRDRILS NTVDDTASDDLIVTQQFRLVDGLTTIEATEGGEAGGSLTVMGTTNRKADDNTITVELLQG DASIEINSTDEWNSDGQWSVDVPLSNVEPGNYTVEADDGNDTDRQNVEIVEELEEPDQTT VDQPENNQTMTTMTTETTTETTTETTTQENTTENGSEGTSDGESGGSSIPFGVGVALVALGAALLALRQN
Sequence length	852 AA
Subcellular Location	Surface
Function	In Archaea, which do not possess other cell wall components, the S-layer has been implicated in the maintenance of the cell integrity and stabilize as well as to protect the cell against mechanical and osmotic stresses or extreme pH conditions. It is also predicted that the S-layer has to maintain or even determine the cell shape.
Glycosylation Status	
Glycosylation Type	N- (Asn) linked, (O- (Thr) linked residues not known)
Experimentally Validated Glycosite(s) in Full Length Protein	(Signal peptide: 1-34) N36, N339, N398, N438, N513, N643, N727, N751, N787, N811, N815 (N36, N513 and N643 were confirmed glycosylated directly by glycopeptide sequence analysis, the reference no. 2 mentions that ten sulfated saccharides are N-linked to the protein implying that most or all sites are glycosylated.)
Experimentally Validated Glycosite(s) in Mature Protein	N2, N305, N364, N404, N479, N609, N693, N717, N753, N777, N781
	>sp P0DME1 CSG_HALSA Cell surface glycoprotein OS=Halobacterium salinarum (strain ATCC 700922 / JCM 11081 / NRC-1) GN=csg PE=3 SV=1 MTDTTGKLRVLLTALMVGSVIGAGVAFTGGAAAAN <sup>(36)</sup> ASDLNDYQRFNENTNYTYSTASED GKTEGSVASGATIFQGEEDVTFRKLNDNEKEVSPATLSRTGGSDGEGVPLQMPIPEDQSTGS YDSNGPDNDEADFGVTVQSPSVTMEVRRNADNDVTGGVLTNTQQDESSIAVDYNYAAED LETLVEDEDGLDVTDEILAADQSGGAYEDGTGNGNPNTLRFDIDPNNVDAGDYTVSVEGV EDLDFGDATESASVTISSNKAASLNLAEDVVQGANLKYTIENSPEGNYHAVTIDSSDFR DSSSGADAAKVMRSVGDVDTGLVVDNDSTTEIVDDYEN <sup>(339)</sup> TSISDSDYAYAVEIDDGNGV



<p><b>Glycosite(s) Annotated Protein Sequence</b></p>	<p>DSSSGADAAKVMRSVGDVTDTGLVVDNDSTTEIVDDYEN*(339)TSISDVDYAYAIIVEIDDGNGV          GSIETQYLLDSSADIDLYPASDTEADPDYVNSNEELTN*(398)GSALDGVSTDDDDTDFDVTQGDITLDNPTGAYVVGSEVDIN*(438)          GTANEGTDDVVLYARDNNDFFELVTVDGEKSIEVDSDDTFEEEDITLSDGDKGGDDILGLPGTYRLGIIAKSDAVN*(513)          SSGGVKDNIDTSDFNQGVSSSTSSIRVT          DTELTASFETYNGQVADDDNQIDVEGTAPGKDNVAIIIIGSRGKVKFQSSISVSDSDDTFDE          EDIDISELRQGSASAHILSSGRDGKFGEDTANSISDLEDEVGN*(643)YTSGSPTGDQIRDRILS          NTVDDTASDDLIVTQQFRLVDGLTTIEATEEGEAGGSLTVMGTTNRKADDNTITVELLQG DASIEIN*(727)          STDEWNSDGGQWSVDVPLSNVEPGN*(751)YTV EADDGNTDRQNVEIVEELEEPDQTT VDQPENN*(787)          QTMTTTTMTETTTETTTETMTTQEN*(811)TTEN*(815)GSEGTS DGESGG SIPGFGVGVALVA VLGAALLALRQN</p>
<p><b>Sequence Around Glycosites (21 AA)</b></p>	<p>VAFTGGAAAANASDLNDYQRF          STTEIVDDYENTSISDVDYAY          DYVNSNEELTNGSALDGVSTD          AYYVGSEVDINGTANEGTDDV          LGIIAKSDAVNSSGGVKDNID          SISDLEDEVGNYSPTGDQ          LLQGDASIEINSTDEWNSDGG          DVPLSNVEPGNYTVEADDGDN          DQTTVDQPENNTMTTMTET          TTETMTTQENTTENGSEGT          MTTQENTTENGSEGTSDGES</p>
<p><b>ProGP Web Logo</b></p>	
<p><b>Technique(s) used for Glycosylation Detection</b></p>	<p>Periodate-arsenite-Schiff reagent staining and carbohydrate analysis using GC. LC ESI MS, MS/MS</p>
<p><b>Technique(s) used for Glycosylated Residue(s) Detection</b></p>	<p>Glycopeptide sequencing</p>
<p><b>Protein Glycosylation-Implication</b></p>	<p>It is the pattern and the chemical nature of the N-linked saccharides which exhibits a drastic change at the transition from moderate to extreme halophily. This different pattern of glycosylation (sulfated glucuronic acids and a repeating unit saccharide) introduces at least 120 additional negative charges into the glycoprotein. The protruding highly negatively charged loops are required for stabilization in high salt concentrations. Thus, the sulfated repeating unit saccharide is required for stabilization of the rod shaped morphology.</p>

**Glycan Information**

Linkages:  $\beta$  GalNAc-Asn, Glc-Asn, Gal-Thr.  
 Total carbohydrate content is approximately 10 to 12% of 200kDa S layer glycoprotein.  
 N glycosylated (at position N2) with GlcNAc-linked repeating (10-15 repeats) sulfated pentasaccharide and with sulphated oligosaccharides: (GlcA(OSO<sub>3</sub>-)-[ $\beta$ 1 $\rightarrow$ 4GlcA(OSO<sub>3</sub>-)]<sub>2</sub>- $\beta$ 1 $\rightarrow$ 4Glc-Asn) at ten other positions.



<b>Glycan Annotation</b>	Abut 20 neutral di/ tri- saccharides $\beta$ -D-Glc-(1 $\rightarrow$ 2)-Gal-(1 $\rightarrow$ or (uronic acid, glucose)-galactose are O-glycosidically attached to clustered threonine residues (14) adjacent to the TM domain at the C terminus but precise position of O glycosylated residues is not known. A tetrasaccharide comprising a hexose as the linking sugar, a sulfated hexuronic acid at position 2, a hexuronic acid at position 3 and a second sulfated hexuronic acid at position 4
<b>BCSDB ID</b>	<a href="#">136320</a>
<b>GlyYouCan</b>	<a href="#">G81788YA</a>
<b>Technique(s) used for Glycan Identification</b>	GC-MS (gas chromatography-mass spectrometry) analysis of peracetylated alditols.
<b>Protein Glycosylation linked (PGL) gene(s)</b>	
<b>OST Gene Name</b>	AgIB/STT3 subunit
<b>OST ProGT ID</b>	<a href="#">ProGT80</a>
<b>Additional Comment</b>	First prokaryotic glycoprotein that was characterized experimentally for the site of glycosylation as well as glycan attached. The features unique to N glycosylation in <i>H. salinarium</i> are: the majority of glycans are linked via glucose instead of GlcNAc or GalNAc to the Asn in protein. Presence of sulfated oligosaccharides that bind to a C60-dolichol monophosphate carrier lipid. Protein associated glycans differ mainly in terminal sugars. S layer proteins of <i>H. salinarium</i> and <i>H. volcanii</i> are the examples of a lesser understood and rare type of glycosylation namely O glycosylation in Archaea. A cluster of 14 threonine residues (yet uncharacterized) present at hydrophobic C terminus membrane anchor has also been reported glycosylated with glucosylgalactose disaccharides in S layer glycoprotein of <i>H. salinarium</i> . Bacitracin inhibits growth of Halobacteria. Sequon features: excluding the only unique Asn-GalNAc site, all sequon sequences are preceded by 1 or even 2 negatively charged amino acid residues.
<b>Literature</b>	
<b>Year of Identification</b>	1974
<b>Year of Identification Month Wise</b>	1974
<b>Year of Validation</b>	1987
<b>Reference</b>	<a href="#">Mengele, R. and Sumper, M., 1992. Drastic differences in glycosylation of related S-layer glycoproteins from moderate and extreme halophiles. Journal of Biological Chemistry, 267(12), pp.8182-8185.</a>
<b>Corresponding Author</b>	Manfred Sumper
<b>Contact</b>	Chair of Biochemistry I, University of Regensburg, Federal Republic of Germany
<b>Reference</b>	<a href="#">Lechner, J. and Sumper, M., 1987. The primary structure of a procaryotic glycoprotein. Cloning and sequencing of the cell surface glycoprotein gene of halobacteria. Journal of Biological Chemistry, 262(20), pp.9724-9729.</a>
<b>Corresponding Author</b>	Manfred Sumper
<b>Contact</b>	Chair of Biochemistry I, University of Regensburg, Federal Republic of Germany
<b>Reference</b>	<a href="#">Lechner, J., Wieland, F. and Sumper, M., 1985. Transient methylation of dolichyl oligosaccharides is an obligatory step in halobacterial sulfated glycoprotein biosynthesis. Journal of Biological Chemistry, 260(15), pp.8984-8989.</a>
<b>Corresponding Author</b>	Felix Wieland
<b>Contact</b>	Dept. of Biochemistry, Stanford University School of Medicine, Stanford University Medical Center, Stanford, CA 94305.

Reference	<a href="#">Paul, G., Lottspeich, F. and Wieland, F., 1986. Asparaginyln-N-acetylgalactosamine. Linkage unit of halobacterial glycosaminoglycan. Journal of Biological Chemistry, 261(3), pp.1020-1024.</a>
Corresponding Author	Felix Wieland
Contact	Dept. of Biochemistry, Stanford University School of Medicine, Stanford University Medical Center, Stanford, CA 94305.
Reference	<a href="#">Wieland, F., Paul, G. and Sumper, M., 1985. Halobacterial flagellins are sulfated glycoproteins. Journal of Biological Chemistry, 260(28), pp.15180-15185.</a>
Corresponding Author	Felix Wieland
Contact	Dept. of Biochemistry, Stanford University School of Medicine, Stanford University Medical Center, Stanford, CA 94305.
Reference	<a href="#">Wieland, F., Heitzer, R. and Schaefer, W., 1983. Asparaginylgucose: novel type of carbohydrate linkage. Proceedings of the National Academy of Sciences, 80(18), pp.5470-5474.</a>
Corresponding Author	Felix Wieland
Contact	Dept. of Biochemistry, Stanford University School of Medicine, Stanford University Medical Center, Stanford, CA 94305.
Reference	<a href="#">Mescher, M.F. and Strominger, J.L., 1976. Purification and characterization of a prokaryotic glycoprotein from the cell envelope of Halobacterium salinarium. Journal of Biological Chemistry, 251(7), pp.2005-2014.</a>
Corresponding Author	Jack L Strominger
Contact	Biological Laboratories, Harvard University, Cambridge, Massachusetts 02138
Reference	<a href="#">Mescher, M.F., Strominger, J.L. and Watson, S.W., 1974. Protein and carbohydrate composition of the cell envelope of Halobacterium salinarium. Journal of Bacteriology, 120(2), pp.945-954.</a>
Corresponding Author	Jack L Strominger
Contact	Biological Laboratories, Harvard University, Cambridge, Massachusetts 02138
Reference	<a href="#">Wieland, F., Dompert, W., Bernhardt, G. and Sumper, M., 1980. Halobacterial glycoprotein saccharides contain covalently linked sulphate. FEBS letters, 120(1), pp.110-114.</a>
Corresponding Author	Felix Wieland
Contact	Dept. of Biochemistry, Stanford University School of Medicine, Stanford University Medical Center, Stanford, CA 94305.
Reference	<a href="#">Vershinin, Z., Zaretsky, M., Guan, Z. and Eichler, J., 2021. Revisiting N-glycosylation in Halobacterium salinarum: Characterizing a dolichol phosphate-and glycoprotein-bound tetrasaccharide. Glycobiology.</a>



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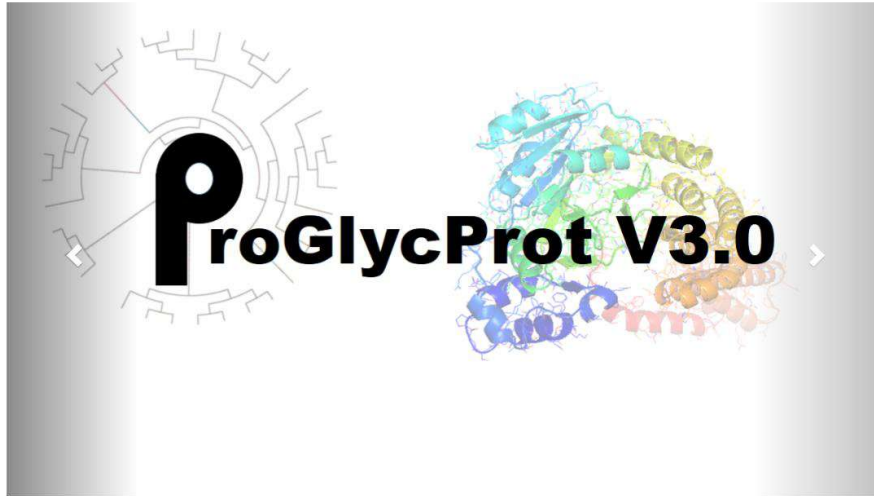
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 E-mail: raoalka@imtech.res.in

ProGlycProt Visitor Counter



# How to search glycosyltransferases in ProGTdb?

A Manually Curated Repository of Experimentally Characterized Glycoproteins and Protein Glycosyltransferases of Prokaryotes



1. Click on the search icon.



2. Choose either ProGT\_Main or ProGT\_Accessory for characterized and uncharacterized glycoproteins, respectively.

ProGT\_Main (Prokaryotic Protein Glycosyl Transferases):  
 ProGT\_Accessory (Accessory Protein or enzyme to Prokaryotic Protein Glycosyl Transferases):

Choose Search Criteria  
Choose

Select Value  
[Empty dropdown]

Search Display Criteria  
All

Search

Example display page will give you an idea of the type of information existing for a given entry.

3. Choose from different search criteria.

ProGT\_Main (Prokaryotic Protein Glycosyl Transferases):  
 ProGT\_Accessory (Accessory Protein or enzyme to Prokaryotic Protein Glycosyl Transferases):

Choose Search Criteria  
Choose  
ProGT ID  
Organism  
Protein Name  
UniProtKB/SwissProt ID  
Glyco-group

Search Display Criteria  
All

Search

4. Select value and click on search.

ProGT\_Main (Prokaryotic Protein Glycosyl Transferases):  
 ProGT\_Accessory (Accessory Protein or enzyme to Prokaryotic Protein Glycosyl Transferases):

Choose Search Criteria  
ProGT ID

Select Value  
ProGT143 (SvGT)

Search Display Criteria  
All

Search



# Result Page:

## ProGT143 (SvGT)

Home -> ProGTdb -> Search ProGT\_Main -> Display data

Selected ID ProGT143	Compare ID	Compare ID	Compare ID	Search Display Criteria all
Display				

Compare



ProGT ID	ProGT143 (SvGT)
Organism Information	
Organism Name	<i>Streptomyces venezulae</i>
Clinical Implication	Non-pathogenic
Domain	Bacteria
Classification	<b>Phylum</b> : Actinobacteria <b>Class</b> : Actinomycetia <b>Orders</b> : Streptomycetales <b>Family</b> : Streptomycetaceae <b>Genus</b> : <i>Streptomyces</i> <b>Species</b> : <i>venezulae</i>
Taxonomic ID (NCBI)	<a href="#">54571</a>
Genome Information	
Gene Bank	<a href="#">CP013129.1</a>



Gene Information	
Gene Name	<i>SvGT</i>
Protein information	
Protein Name	SvGT
NCBI Ref Seq	<a href="#">ALO08693.1</a>
Function in Native Organism	SvGT define the distinct donor specificity, acceptor specificity, regioselectivity, chemoselectivity, and Y(G/A/K/Q/E≠ΔG)(C/S/T≠Y/N)(G/A≠P/Q)G as the minimum acceptor sequon of SvGT. Although UDP-GlcNAc served as the donor in the cellular milieui, SvGT could also utilize UDP-Glc and UDP-GalNAc as donors in vitro
Additional Information	Also used as glycoengineering tool for modification of neo glycoicin
Glycosyltransferase Information	
Glycosylation Type	S- (Cys) and O- (Ser/Thr) linked
CAZY Family	<a href="#">GT2</a>
Mechanism of Glycan Transfer	Sequential
Donor Type	UDP-GlcNAc, UDP-Glc, UDP-GalNAc
Donor Specificity	Nucleotide activated sugars
Glycan Information	
Glycan transferred	Monosaccharide (GlcNAc, Glc, GalNAc)
Method of Glycan Indentification	mass spectrometry and western blotting
Experimental_strategies	In vivo and In vitro
Acceptor Substrate Information	
Acceptor Substrate name	SvC
ProGPdb ID	<a href="#">ProGP1215 (SvC)</a>

## Litrature

Year Of Validation	2021
Reference	<a href="#">Sharma, Y., Ahlawat, S. and Rao, A., 2021. Biochemical characterization of an inverting S/O-HexNAc-transferase and evidence of S-linked glycosylation in Actinobacteria. Glycobiology.</a>
Corresponding Author	Rao, A.
Contacts	2 CSIR-Institute of Microbial Technology, Sector 39A, Chandigarh 160036, India



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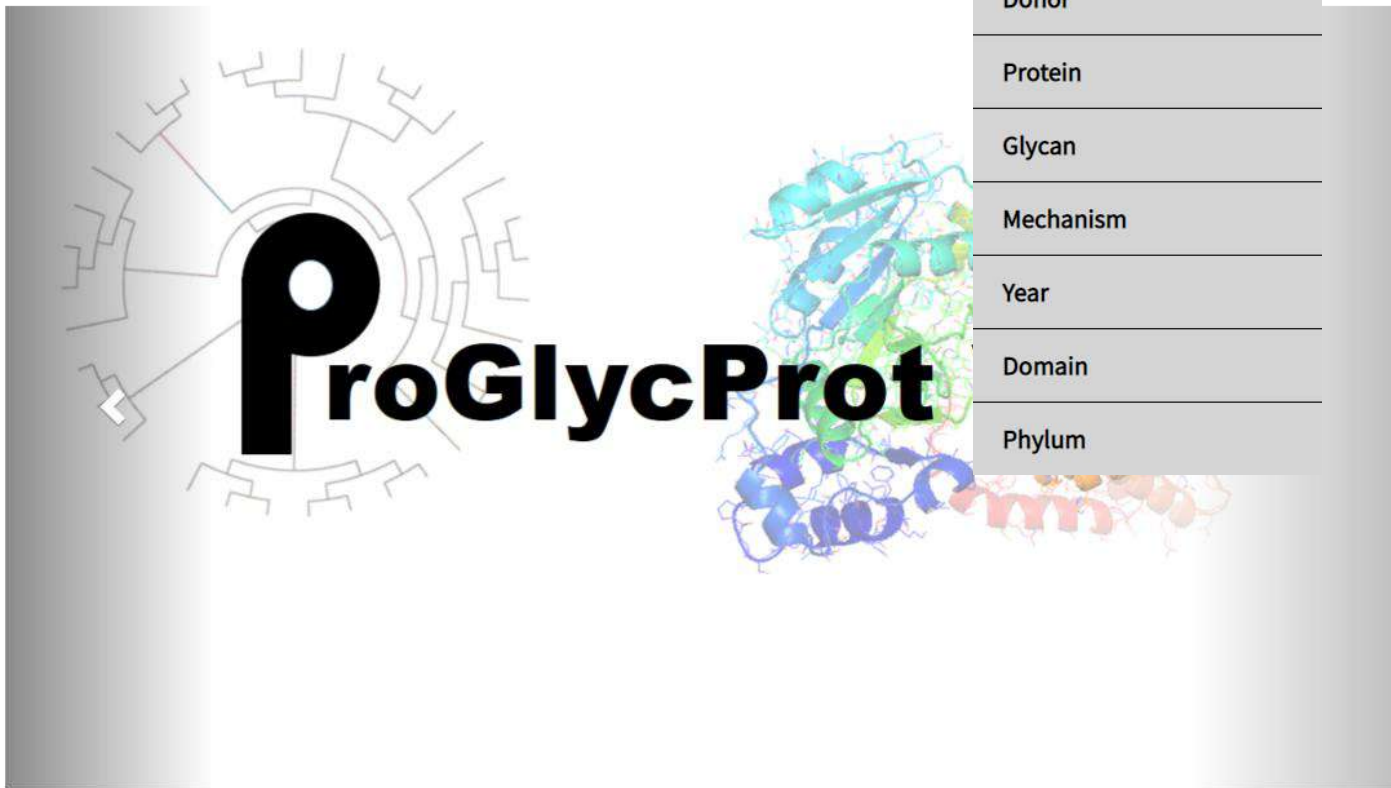


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This site is best viewed in Chrome, Mozilla Firefox at screen resolution of 1024 × 768 and above

# How to search all the section by Features?

A Manually Curated Repository of Experimentally Characterized Glycoproteins and [ases of Prokaryotes](#)



## Organism

Donor

ProGPdb ProGT\_Main ProGT\_Accessory

Organism	ProGPdb
<i>Acetogenium kivui</i> ( <i>Thermoanaerobacter kivui</i> )	ProGP55 (Cell surface protein/S-layer protein)
<i>Acidovorax</i> ( <i>Pseudomonas</i> ) <i>avenae</i> K1 (#8301)	ProGP198 (Flagellin)
<i>Acidovorax avenae</i> N1141	ProGP199 (Flagellin)
<i>Acinetobacter baumannii</i> ATCC 17978	ProGP412 (OmpA/MotB), ProGP413 (Putative Uncharacterized Protein), ProGP414 (Putative Uncharacterized Protein), ProGP415 (Putative Uncharacterized Protein), ProGP416 (Putative Uncharacterized Protein), ProGP417 (Putative Uncharacterized Protein), ProGP418 (Putative Uncharacterized Protein)
<i>Acinetobacter baylyi</i>	ProGP196 (ComP)
<i>Acinetobacter nosocomialis</i>	ProGP496 (PIIA), ProGP497 (Putative secretion protein), ProGP498 (Uncharacterized protein), ProGP499 (Uncharacterized protein), ProGP500 (Uncharacterized protein), ProGP501 (Uncharacterized protein), ProGP502 (Uncharacterized protein), ProGP503 (Uncharacterized protein), ProGP504 (Uncharacterized protein)
<i>Acinetobacter nosocomialis</i> M2	ProGP419 (PIIA)
<i>Actinobacillus actinomycetemcomitans</i> Y4 (serotype b)	ProGP135 (37-kDa protein)
<i>Actinobacillus pleuropneumoniae</i>	ProGP450 (AtaC), ProGP451 (COK_1394)
<i>Actinomyces naeslundii</i> KWS 81	ProGP156 (AnAF)
<i>Aeribacillus pallidus</i> 8	ProGP703 (PaIA)
<i>Aeromonas caviae</i> ( <i>punctata</i> ) UU 51	ProGP247 (Flagellin A), ProGP248 (Flagellin B)
<i>Aeromonas caviae</i> Sch3N strain	ProGP296 (FlaA (Flagellin)), ProGP297 (FlaB (Flagellin))
<i>Aeromonas hydrophila</i> AH-3 (serotype O34)	ProGP420 (FlaA (Polar flagellin)), ProGP421 (FlaB (Polar flagellin))

ProGT\_Main ProGT\_Accessory

Donor	ProGTdb
ADP-Heptose	ProGT8 (Aah), ProGT11 (TibC), ProGT79 (BAHTCr)
CMP-KDO	ProGT141 (Maf)
CMP-Leg	ProGT144 (Maf4)
CMP-Neu5Ac	ProGT140 (Maf)
CMP-Pse5Ac7Ac	ProGT54 (Maf1)
Dol-PP-Pentasaccharide	ProGT80 (AglB)
DolP-GlcNAc-Glc-2,3-diNAcA	ProGT16 (AglB)
DolP-Pentasaccharide	ProGT15 (AglB)
	ProGT13 (AglB)
	ProGT23 (AglB)
	ProGT102 (SO_2329 (EarP)/ Efp-associated protein of unknown function DUF2331), ProGT103 (EarP), ProGT109 (EarP), ProGT118 (EarP), ProGT121 (EarP)
	ProGT35 (Pmt)
	ProGT125 (GtfE/F)
	ProGT33 (GtfA), ProGT34 (GtfB)
	ProGT49 (PglA), ProGT50 (PglA)
	ProGT12 (Rv1002c), ProGT14 (Pmt)
	ProGT24 (PglL)
	ProGT145 (GccA)
	ProGT3 (Toxin A), ProGT4 (Toxin B), ProGT5 (Tcsl), ProGT19 (Lgt1), ProGT27 (Lgt2), ProGT28 (Lgt3), ProGT128 (Nss), ProGT129 (Gly), ProGT130 (GT), ProGT131 (GT), ProGT132 (GT), ProGT133 (GT), ProGT134 (GT), ProGT135 (GtfA), ProGT136 (GtfB)

Search by Feature Structure

Organism



Gene



Donor



Protein



Glycan

Mechanism

Year

Domain

Phylum

Protein

ProGPdb ProGT\_Main ProGT\_Accessory

Gene Name	ProGPdb
(Rv3491)	ProGP263 (Rv3491)
A0K9U9	ProGP472 (Putative signal peptide)
A15_0556	ProGP413 (Putative Uncharacterized Protein)
A15_1193	ProGP412 (OmpA/MotB)
A15_2371	ProGP414 (Putative Uncharacterized Protein)
A15_3580	ProGP415 (Putative Uncharacterized Protein)
A15_3626	ProGP416 (Putative Uncharacterized Protein)
A15_3658	ProGP417 (Putative Uncharacterized Protein)
A15_3744	ProGP418 (Putative Uncharacterized Protein)
aatA	ProGP714 (Aminotransferase)
acm2	ProGP436 (AcM2), ProGP1219 (GkFlaA1)
acnA	ProGP715 (Aconitate hydratase)
acpP	ProGP716 (Acyl carrier protein)
acrA	ProGP529 (AcrA)
adk	ProGP717 (Adenylate kinase)
afpA	ProGP142 (Antifreeze protein)
aidA	ProGP1212 (SLP-5818)
aidA (plasmid encoded)	ProGP201 (Diffuse Adherence Adhesion (AIDA-I))
alaS	ProGP718 (Alanine-tRNA ligase)
aniA (NMB_1623)	ProGP423 (AniA)
apa (BCG_1896)	ProGP110 (45 to 47-kDa protein)
Apa (Rv1860) or modD	ProGP51 (Alanine and proline-rich secreted protein Apa (50/55-kDa or 45

ProGT\_Accessory

Protein	ProGPdb
(MAC)	ProGP701 (CleA), ProGP1216 (BTL2)
(DIM)	ProGP70 ((1,3-1,4)-beta-glucanase (MAC))
(DIMethylallyl)adenosine tRNA methylthiotransferase	ProGP746 ((Dimethylallyl)adenosine tRNA methylthiotransferase)
12 kDa antigen	ProGP12 (12 kDa antigen)
15 kDa-phosphate containing glycoprotein	ProGP64 (15 kDa-phosphate containing glycoprotein)
152 kDa membrane glycoprotein	ProGP8 (Membrane glycoprotein 152 kDa)
18 kDa and 32 kDa lectin binding proteins	ProGP62 (18 kDa and 32 kDa lectin binding proteins)
2,3,4,5-tetrahydropyridine-2,6-dicarboxylate N-succinyltransferase	ProGP1019 (2,3,4,5-tetrahydropyridine-2,6-dicarboxylate N-succinyltransferase)
2,3-bisphosphoglycerate-independent phosphoglycerate mutase	ProGP847 (2,3-bisphosphoglycerate-independent phosphoglycerate mutase)
2-amino-4-hydroxy-6-hydroxymethylidihydropteridine pyrophosphokinase	ProGP1041 (2-amino-4-hydroxy-6-hydroxymethylidihydropteridine pyrophosphokinase)
2-oxoglutarate dehydrogenase E1 component	ProGP1073 (2-oxoglutarate dehydrogenase E1 component)
24 kDa flagellin	ProGP65 (24 kDa flagellin)
25 kDa flagellin	ProGP66 (25 kDa flagellin)
27kDa flagellin	ProGP97 (27kDa flagellin)
3,4-dihydroxy-2-butanone 4-phosphate synthase	ProGP1064 (3,4-dihydroxy-2-butanone 4-phosphate synthase)
3-hydroxyacyl-[acyl-carrier-protein] dehydratase FabZ	ProGP826 (3-hydroxyacyl-[acyl-carrier-protein] dehydratase FabZ)
3-oxoacyl-[acyl-carrier-protein] synthase 2	ProGP825 (3-oxoacyl-[acyl-carrier-protein] synthase 2)
30S ribosomal protein S1	ProGP936 (30S ribosomal protein S1)
30S ribosomal protein S10	ProGP940 (30S ribosomal protein S10)



**Glycan**

**Year**

ProGPdb ProGT\_Main

ProGPdb ProGT\_Main ProGT\_Accessory

Glycan :	ProGP ID:
Pentasaccharide (HexNAc - HexNAc -HexNAc-HexNAc-HexNAc)	ProGP196 (ComP), ProGP497 (Putative secretion protein), ProGP498 (Uncharacterized protein), ProGP499 (Uncharacterized protein), ProGP500 (Uncharacterized protein), ProGP501 (Uncharacterized protein), ProGP502 (Uncharacterized protein), ProGP503 (Uncharacterized protein), ProGP504 (Uncharacterized protein)
single and double glucosylated ( glucose and galactose)	ProGP552 (Hypothetical protein but identical to enterocin95 of Enterococcus faecalis WHE96)
X-P-HexNAc-HexNAc-Hex-Hex-HexNAc, where X denotes the unknown monosaccharide containing a phosphate group	ProGP340 (FTH_1071)
(398-Da glycan) O-linked HexNAc residue, to which a methylated aspartic acid is linked via a phosphate bond. Flagellins from a number of C. difficile isolates from more recent outbreaks are modified in O linkage with a heterogeneous glycan containing up to five monosaccharide residues with masses of 204 (HexNAc), 146 (deoxyhexose), 160 (methylated deoxyhexose), and 192 (heptose).	ProGP298 (FliC (Flagellin subunit))
(GlcNAc-135)2-Hex-HexA	ProGP1157 (Mpsy_1486)
(HexNAc)2-(Hex)3-[HexNAc]2-[Hex]2	ProGP1212 (SLP-5818)
0.69–1.81% carbohydrates	ProGP39 (Acidic glycoproteins (133-155 kDa))
0.7 pg of hexose per 100 pg of protein. Rhamnose (1.2 mol%), galactose (92.6 mol%), and glucose (6.2 mol%) as hexose, but no pentose.	ProGP156 (AnAF)
0.8% carbohydrate content.	ProGP9 (8 kDa fimbriae)
0.8% galactose, 0.3% glucose, and 0.1% mannose.	ProGP104 (S-layer glycoprotein (138 kDa))

Year	ProGPdb
1968	ProGP1 (Envelope specific glycoprotein)
1971	ProGP2 (Phytotoxin)
1974	ProGP3 (S-layer glycoprotein)
1975	ProGP4 (F-pilin)
1976	ProGP5 (Factor PG-1)
1978	ProGP6 (Cellulase CA), ProGP7 (Cellulase CB)
1979	ProGP8 (Membrane glycoprotein 152 kDa ), ProGP9 (8 kDa fimbriae)
	ProGP10 (Flagellin)
	ProGP11 (Autolysin (28 kDa))
	ProGP12 (12 kDa antigen), ProGP13 (33 kDa antigen), ProGP14 (Membrane glycoprotein)
	ProGP15 (N-acetylmuramoylhydrolase (Muramidase-2)), ProGP16 (50 kDa antigen), ProGP17 (Flagellin)
	ProGP18 (S-layer glycoprotein SgsE), ProGP19 (Outer membrane protein (26.5 kDa)), ProGP20 (Outer membrane protein (50 kDa)), ProGP21 (Outer membrane protein (75 kDa)), ProGP22 (Flagellin FlaB1), ProGP23 (Flagellin FlaB2), ProGP24 (Flagellin FlaB3), ProGP25 (33 and 34 kDa antigens), ProGP26 (CenA (Endoglucanase A)), ProGP27 (Cex (Exoglucanase or xylanase))
	ProGP28 (Flagellin A1), ProGP29 (Flagellin A2), ProGP30 (Flagellin B1), ProGP31 (Flagellin B2), ProGP32 (Flagellin B3), ProGP33 (Streptococcal acid glycoprotein SAGP), ProGP34 (S-layer glycoprotein), ProGP35 (β-1,4-

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**Mechanism**

**Domain**

ProGT\_Main

ProGT\_Accessory

Mechanism of Catalysis: Mechanism of Glycan Transfer

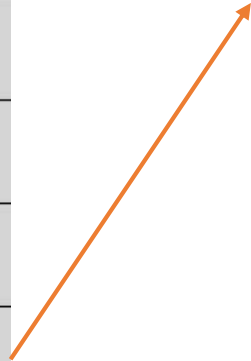
Mechanism of Glycan Transfer	En bloc	Sequential	Sequential disaccharide	
<b>ProGPdb ID</b>	ProGT1 (PILO), ProGT9 (PglB), ProGT10 (PglB), ProGT13 (AglB), ProGT15 (AglB), ProGT16 (AglB), ProGT17 (PglL), ProGT21 (PglO), ProGT23 (AglB), ProGT24 (PglL), ProGT25 (PglL), ProGT26 (TfpW), ProGT36 (PglB), ProGT40 (PglB1), ProGT47 (ClpPglB), ProGT48 (DdPglB), ProGT49 (PglA), ProGT50 (PglA), ProGT51 (AglB), ProGT52 (PglLb), ProGT53 (AglB), ProGT55 (PglLAb), ProGT56 (PglB), ProGT57 (PglLvc), ProGT59 (WsfB), ProGT60 (AglB), ProGT71 (PglLbc), ProGT72 (Tot/AglB), ProGT73 (STT3), ProGT80 (AglB), ProGT83 (PglLADP1), ProGT84 (PglLComP), ProGT85 (TfpOM2), ProGT86 (PglLM2), ProGT89 (CcpPglB), ProGT90 (PglB), ProGT91 (PglB), ProGT92 (PglB), ProGT93 (PglB),	ProGT2 (Alpha-toxin), ProGT3 (Toxin A), ProGT4 (Toxin B), ProGT5 (TcsL), ProGT6 (TcsL 82), ProGT7 (TcsL 9048), ProGT8 (Aah), ProGT11 (TibC), ProGT18 (PseD), ProGT19 (Lgt1), ProGT20 (GmaR), ProGT22 (TcdBF/TcdB1470), ProGT27 (Lgt2), ProGT28 (Lgt3), ProGT29 (Gap1), ProGT30 (Gap3), ProGT31 (XcOGT), ProGT32 (GT), ProGT33 (GtfA), ProGT34 (GtfB), ProGT35 (Pmt), ProGT37 (Gtf1), ProGT38 (Gtf2), ProGT39 (HMW1C), ProGT41 (NGT), ProGT42 (ApNGT), ProGT43 (NGT), ProGT44 (NGT), ProGT45 (TpeL), ProGT46 (SunS), ProGT63 (NleB1), ProGT64 (TcsH), ProGT65 (ThuS), ProGT66 (SdgA), ProGT67 (SdgB), ProGT68 (PaTox), ProGT69 (GtfA), ProGT70 (GtfB), ProGT74 (FilmQ), ProGT75 (GtfA), ProGT76 (GtfB),	ProGT116 (En)	

	Archaea	Bacteria
	ProGP3 (S-layer glycoprotein), ProGP8 (Membrane glycoprotein 152 kDa ), ProGP10 (Flagellin), ProGP17 (Flagellin), ProGP28 (Flagellin A1), ProGP29 (Flagellin A2), ProGP30 (Flagellin B1), ProGP31 (Flagellin B2), ProGP32 (Flagellin B3), ProGP34 (S-layer glycoprotein), ProGP36 (S-layer glycoprotein), ProGP43 (SigA (cell surface glycoprotein)), ProGP44 (S-layer glycoprotein), ProGP45 (S-layer glycoprotein (94 kDa)), ProGP46 (S-layer glycoprotein (90 kDa)), ProGP47 (S-layer glycoprotein (92 kDa)), ProGP48 (S-layer glycoprotein), ProGP49 (S-layer glycoprotein), ProGP52 (Hypothetical protein), ProGP58 (Thermopsin), ProGP60 (S-layer glycoprotein (118 kDa)), ProGP61 (S-layer glycoprotein (132 kDa)), ProGP65 (24 kDa flagellin), ProGP66 (25 kDa flagellin), ProGP67 (35 kDa flagellin), ProGP69 (S-layer glycoprotein), ProGP71 (S-layer glycoprotein), ProGP72 (Alkaline Phosphatase D), ProGP78 (Cell surface glycoprotein (SigA)), ProGP79 (S-layer glycoprotein), ProGP80 (S-layer	ProGP1 (Envelope specific glycoprotein), ProGP2 (Phytotoxin), ProGP4 (F-pilin), ProGP5 (Factor PG-1), ProGP6 (Cellulase CA), ProGP7 (Cellulase CB), ProGP9 (8 kDa fimbriae), ProGP11 (Autolysin (28 kDa)), ProGP12 (12 kDa antigen), ProGP13 (33 kDa antigen), ProGP14 (Membrane glycoprotein), ProGP15 (N-acetylmuramoylhydrolase (Muramidase-2)), ProGP16 (50 kDa antigen), ProGP18 (S-layer glycoprotein SgsE), ProGP19 (Outer membrane protein (26.5 kDa)), ProGP20 (Outer membrane protein (50 kDa)), ProGP21 (Outer membrane protein (75 kDa)), ProGP22 (Flagellin FlaB1), ProGP23 (Flagellin FlaB2), ProGP24 (Flagellin FlaB3), ProGP25 (33 and 34 kDa antigens), ProGP27 (Cex (Exoglucanase or xylanase)), ProGP33 (Streptococcal acid glycoprotein SAGP), ProGP35 (β-1,4-Endoglucanases), ProGP37 (S-layer glycoprotein), ProGP38 (VGP (74 kDa)), ProGP39 (Acidic glycoproteins (133-155 kDa)), ProGP40 (Long-fibril protein (LFP)), ProGP41

ProGPdb ProGT\_Main ProGT\_Accessory

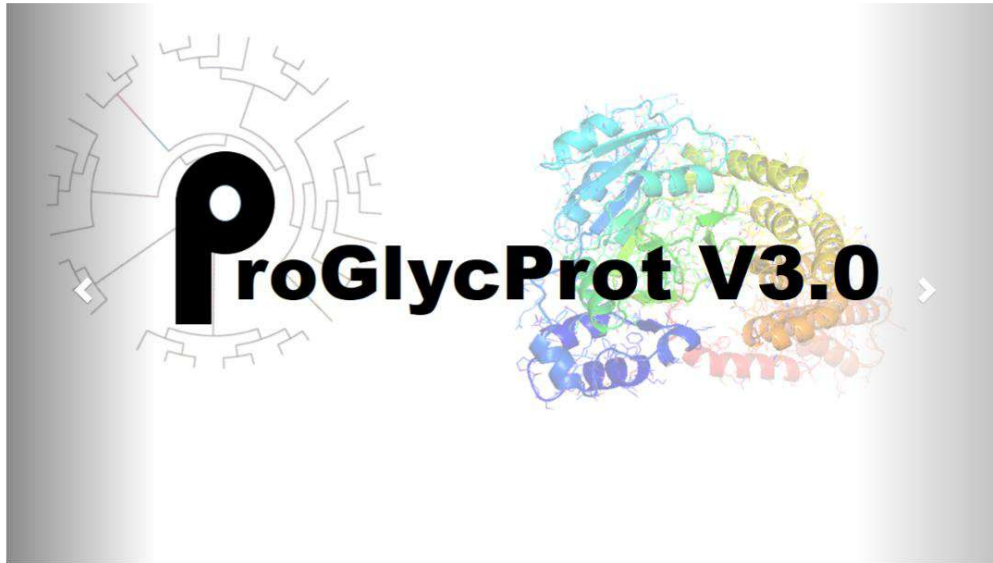
Search by Feature ▼ Structure

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phylum	ProGPdb
	ProGP79 (S-layer glycoprotein), ProGP180 (S-layer glycoprotein (27 kDa)), ProGP705 (Hyp2)
<i>Actinobacteria</i>	ProGP2 (Phytotoxin), ProGP6 (Cellulase CA), ProGP7 (Cellulase CB), ProGP12 (12 kDa antigen), ProGP13 (33 kDa antigen), ProGP14 (Membrane glycoprotein), ProGP16 (50 kDa antigen), ProGP26 (CenA (Endoglucanase A)), ProGP27 (Cex (Exoglucanase or xylanase)), ProGP35 (β <sup>2</sup> -1,4-Endoglucanases), ProGP44 (S-layer glycoprotein), ProGP51 (Alanine and proline-rich secreted protein Apa (50/55-kDa or 45 kDa MPT 32)), ProGP57 (38 kDa antigen), ProGP59 (β-1, 4-D-glucosidase (51 kDa)), ProGP63 (Xylanase B (Endo-1,4-beta-xylanase B)), ProGP76 (Cell surface lipoprotein MPB83 (25/23-kDa antigen)), ProGP96 (PS2 (S-layer glycoprotein)), ProGP110 (45 to 47-kDa protein), ProGP138 (Cell surface glycoprotein), ProGP156 (AnAF), ProGP157 (HBHA (Heparinase II)), ProGP171 (MucA), ProGP172 (MucB), ProGP173 (MucC), ProGP174 (MucD), ProGP175 (MucE), ProGP176 (MucF), ProGP177 (MucG), ProGP178 (MucH), ProGP179 (MucI), ProGP181 (MucJ), ProGP182 (MucK), ProGP183 (MucL), ProGP184 (MucM), ProGP185 (MucN), ProGP186 (MucO), ProGP187 (MucP), ProGP188 (MucQ), ProGP189 (MucR), ProGP190 (MucS), ProGP191 (MucT), ProGP192 (MucU), ProGP193 (MucV), ProGP194 (MucW), ProGP195 (MucX), ProGP196 (MucY), ProGP197 (MucZ), ProGP198 (MucAA), ProGP199 (MucAB), ProGP200 (MucAC), ProGP201 (MucAD), ProGP202 (MucAE), ProGP203 (MucAF), ProGP204 (MucAG), ProGP205 (MucAH), ProGP206 (MucAI), ProGP207 (MucAJ), ProGP208 (MucAK), ProGP209 (MucAL), ProGP210 (MucAM), ProGP211 (MucAN), ProGP212 (MucAO), ProGP213 (MucAP), ProGP214 (MucAQ), ProGP215 (MucAR), ProGP216 (MucAS), ProGP217 (MucAT), ProGP218 (MucAU), ProGP219 (MucAV), ProGP220 (MucAW), ProGP221 (MucAX), ProGP222 (MucAY), ProGP223 (MucAZ), ProGP224 (MucBA), ProGP225 (MucBB), ProGP226 (MucBC), ProGP227 (MucBD), ProGP228 (MucBE), ProGP229 (MucBF), ProGP230 (MucBG), ProGP231 (MucBH), ProGP232 (MucBI), ProGP233 (MucBJ), ProGP234 (MucBK), ProGP235 (MucBL), ProGP236 (MucBM), ProGP237 (MucBN), ProGP238 (MucBO), ProGP239 (MucBP), ProGP240 (MucBQ), ProGP241 (MucBR), ProGP242 (MucBS), ProGP243 (MucBT), ProGP244 (MucBU), ProGP245 (MucBV), ProGP246 (MucBW), ProGP247 (MucBX), ProGP248 (MucBY), ProGP249 (MucBZ), ProGP250 (MucCA), ProGP251 (MucCB), ProGP252 (MucCC), ProGP253 (MucCD), ProGP254 (MucCE), ProGP255 (MucCF), ProGP256 (MucCG), ProGP257 (MucCH), ProGP258 (MucCI), ProGP259 (MucCJ), ProGP260 (MucCK), ProGP261 (MucCL), ProGP262 (MucCM), ProGP263 (MucCN), ProGP264 (MucCO), ProGP265 (MucCP), ProGP266 (MucCQ), ProGP267 (MucCR), ProGP268 (MucCS), ProGP269 (MucCT), ProGP270 (MucCU), ProGP271 (MucCV), ProGP272 (MucCW), ProGP273 (MucCX), ProGP274 (MucCY), ProGP275 (MucCZ), ProGP276 (MucDA), ProGP277 (MucDB), ProGP278 (MucDC), ProGP279 (MucDD), ProGP280 (MucDE), ProGP281 (MucDF), ProGP282 (MucDG), ProGP283 (MucDH), ProGP284 (MucDI), ProGP285 (MucDJ), ProGP286 (MucDK), ProGP287 (MucDL), ProGP288 (MucDM), ProGP289 (MucDN), ProGP290 (MucDO), ProGP291 (MucDP), ProGP292 (MucDQ), ProGP293 (MucDR), ProGP294 (MucDS), ProGP295 (MucDT), ProGP296 (MucDU), ProGP297 (MucDV), ProGP298 (MucDW), ProGP299 (MucDX), ProGP300 (MucDY), ProGP301 (MucDZ), ProGP302 (MucEA), ProGP303 (MucEB), ProGP304 (MucEC), ProGP305 (MucED), ProGP306 (MucEE), ProGP307 (MucEF), ProGP308 (MucEG), ProGP309 (MucEH), ProGP310 (MucEI), ProGP311 (MucEJ), ProGP312 (MucEK), ProGP313 (MucEL), ProGP314 (MucEM), ProGP315 (MucEN), ProGP316 (MucEO), ProGP317 (MucEP), ProGP318 (MucEQ), ProGP319 (MucER), ProGP320 (MucES), ProGP321 (MucET), ProGP322 (MucEU), ProGP323 (MucEV), ProGP324 (MucEW), ProGP325 (MucEX), ProGP326 (MucEY), ProGP327 (MucEZ), ProGP328 (MucFA), ProGP329 (MucFB), ProGP330 (MucFC), ProGP331 (MucFD), ProGP332 (MucFE), ProGP333 (MucFF), ProGP334 (MucFG), ProGP335 (MucFH), ProGP336 (MucFI), ProGP337 (MucFJ), ProGP338 (MucFK), ProGP339 (MucFL), ProGP340 (MucFM), ProGP341 (MucFN), ProGP342 (MucFO), ProGP343 (MucFP), ProGP344 (MucFQ), ProGP345 (MucFR), ProGP346 (MucFS), ProGP347 (MucFT), ProGP348 (MucFU), ProGP349 (MucFV), ProGP350 (MucFW), ProGP351 (MucFX), 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(MucIB), ProGP408 (MucIC), ProGP409 (MucID), ProGP410 (MucIE), ProGP411 (MucIF), ProGP412 (MucIG), ProGP413 (MucIH), ProGP414 (MucII), ProGP415 (MucIJ), ProGP416 (MucIK), ProGP417 (MucIL), ProGP418 (MucIM), ProGP419 (MucIN), ProGP420 (MucIO), ProGP421 (MucIP), ProGP422 (MucIQ), ProGP423 (MucIR), ProGP424 (MucIS), ProGP425 (MucIT), ProGP426 (MucIU), ProGP427 (MucIV), ProGP428 (MucIW), ProGP429 (MucIX), ProGP430 (MucIY), ProGP431 (MucIZ), ProGP432 (MucJA), ProGP433 (MucJB), ProGP434 (MucJC), ProGP435 (MucJD), ProGP436 (MucJE), ProGP437 (MucJF), ProGP438 (MucJG), ProGP439 (MucJH), ProGP440 (MucJI), ProGP441 (MucJJ), ProGP442 (MucJK), ProGP443 (MucJL), ProGP444 (MucJM), ProGP445 (MucJN), ProGP446 (MucJO), ProGP447 (MucJP), ProGP448 (MucJQ), ProGP449 (MucJR), ProGP450 (MucJS), ProGP451 (MucJT), ProGP452 (MucJU), ProGP453 (MucJV), ProGP454 (MucJW), ProGP455 (MucJX), ProGP456 (MucJY), ProGP457 (MucJZ), ProGP458 (MucKA), ProGP459 (MucKB), ProGP460 (MucKC), ProGP461 (MucKD), ProGP462 (MucKE), ProGP463 (MucKF), ProGP464 (MucKG), ProGP465 (MucKH), ProGP466 (MucKI), ProGP467 (MucKJ), ProGP468 (MucKL), ProGP469 (MucKM), ProGP470 (MucKN), ProGP471 (MucKO), ProGP472 (MucKP), ProGP473 (MucKQ), ProGP474 (MucKR), ProGP475 (MucKS), ProGP476 (MucKT), ProGP477 (MucKU), ProGP478 (MucKV), ProGP479 (MucKW), ProGP480 (MucKX), ProGP481 (MucKY), ProGP482 (MucKZ), ProGP483 (MucLA), ProGP484 (MucLB), ProGP485 (MucLC), ProGP486 (MucLD), ProGP487 (MucLE), ProGP488 (MucLF), ProGP489 (MucLG), ProGP490 (MucLH), ProGP491 (MucLI), ProGP492 (MucLJ), ProGP493 (MucLK), ProGP494 (MucLL), ProGP495 (MucLM), ProGP496 (MucLN), ProGP497 (MucLO), ProGP498 (MucLP), ProGP499 (MucLQ), ProGP500 (MucLR), ProGP501 (MucLS), ProGP502 (MucLT), ProGP503 (MucLU), ProGP504 (MucLV), ProGP505 (MucLW), ProGP506 (MucLX), ProGP507 (MucLY), ProGP508 (MucLZ), ProGP509 (MucMA), ProGP510 (MucMB), ProGP511 (MucMC), ProGP512 (MucMD), ProGP513 (MucME), ProGP514 (MucMF), ProGP515 (MucMG), ProGP516 (MucMH), ProGP517 (MucMI), ProGP518 (MucMJ), ProGP519 (MucMK), ProGP520 (MucML), ProGP521 (MucMN), ProGP522 (MucMO), ProGP523 (MucMP), ProGP524 (MucMQ), ProGP525 (MucMR), ProGP526 (MucMS), ProGP527 (MucMT), ProGP528 (MucMU), ProGP529 (MucMV), ProGP530 (MucMW), ProGP531 (MucMX), ProGP532 (MucMY), ProGP533 (MucMZ), ProGP534 (MucNA), ProGP535 (MucNB), ProGP536 (MucNC), ProGP537 (MucND), ProGP538 (MucNE), ProGP539 (MucNF), ProGP540 (MucNG), ProGP541 (MucNH), ProGP542 (MucNI), ProGP543 (MucNJ), ProGP544 (MucNK), ProGP545 (MucNL), ProGP546 (MucNM), ProGP547 (MucNN), ProGP548 (MucNO), ProGP549 (MucNP), ProGP550 (MucNQ), ProGP551 (MucNR), ProGP552 (MucNS), ProGP553 (MucNT), ProGP554 (MucNU), ProGP555 (MucNV), ProGP556 (MucNW), ProGP557 (MucNX), ProGP558 (MucNY), ProGP559 (MucNZ), ProGP560 (MucOA), ProGP561 (MucOB), ProGP562 (MucOC), ProGP563 (MucOD), ProGP564 (MucOE), ProGP565 (MucOF), ProGP566 (MucOG), ProGP567 (MucOH), ProGP568 (MucOI), ProGP569 (MucOJ), ProGP570 (MucOK), ProGP571 (MucOL), ProGP572 (MucOM), ProGP573 (MucON), ProGP574 (MucOO), ProGP575 (MucOP), ProGP576 (MucOQ), ProGP577 (MucOR), ProGP578 (MucOS), ProGP579 (MucOT), ProGP580 (MucOU), ProGP581 (MucOV), ProGP582 (MucOW), ProGP583 (MucOX), ProGP584 (MucOY), ProGP585 (MucOZ), ProGP586 (MucPA), ProGP587 (MucPB), ProGP588 (MucPC), ProGP589 (MucPD), ProGP590 (MucPE), ProGP591 (MucPF), ProGP592 (MucPG), ProGP593 (MucPH), ProGP594 (MucPI), ProGP595 (MucPJ), ProGP596 (MucPK), ProGP597 (MucPL), ProGP598 (MucPM), ProGP599 (MucPN), ProGP600 (MucPO), ProGP601 (MucPP), ProGP602 (MucPQ), ProGP603 (MucPR), ProGP604 (MucPS), ProGP605 (MucPT), ProGP606 (MucPU), ProGP607 (MucPV), ProGP608 (MucPW), ProGP609 (MucPX), ProGP610 (MucPY), ProGP611 (MucPZ), ProGP612 (MucQA), ProGP613 (MucQB), ProGP614 (MucQC), ProGP615 (MucQD), ProGP616 (MucQE), ProGP617 (MucQF), ProGP618 (MucQG), ProGP619 (MucQH), ProGP620 (MucQI), ProGP621 (MucQJ), ProGP622 (MucQK), ProGP623 (MucQL), ProGP624 (MucQM), ProGP625 (MucQN), ProGP626 (MucQO), ProGP627 (MucQP), ProGP628 (MucQQ), ProGP629 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ProGP685 (MucSV), ProGP686 (MucSW), ProGP687 (MucSX), ProGP688 (MucSY), ProGP689 (MucSZ), ProGP690 (MucTA), ProGP691 (MucTB), ProGP692 (MucTC), ProGP693 (MucTD), ProGP694 (MucTE), ProGP695 (MucTF), ProGP696 (MucTG), ProGP697 (MucTH), ProGP698 (MucTI), ProGP699 (MucTJ), ProGP700 (MucTK), ProGP701 (MucTL), ProGP702 (MucTM), ProGP703 (MucTN), ProGP704 (MucTO), ProGP705 (MucTP), ProGP706 (MucTQ), ProGP707 (MucTR), ProGP708 (MucTS), ProGP709 (MucTT), ProGP710 (MucTU), ProGP711 (MucTV), ProGP712 (MucTW), ProGP713 (MucTX), ProGP714 (MucTY), ProGP715 (MucTZ), ProGP716 (MucUA), ProGP717 (MucUB), ProGP718 (MucUC), ProGP719 (MucUD), ProGP720 (MucUE), ProGP721 (MucUF), ProGP722 (MucUG), ProGP723 (MucUH), ProGP724 (MucUI), ProGP725 (MucUJ), ProGP726 (MucUK), ProGP727 (MucUL), ProGP728 (MucUM), ProGP729 (MucUN), ProGP730 (MucUO), ProGP731 (MucUP), ProGP732 (MucUQ), ProGP733 (MucUR), ProGP734 (MucUS), ProGP735 (MucUT), ProGP736 (MucUU), ProGP737 (MucUV), ProGP738 (MucUW), ProGP739 (MucUX), ProGP740 (MucUY), ProGP741 (MucUZ), ProGP742 (MucVA), ProGP743 (MucVB), ProGP744 (MucVC), ProGP745 (MucVD), ProGP746 (MucVE), ProGP747 (MucVF), ProGP748 (MucVG), ProGP749 (MucVH), ProGP750 (MucVI), ProGP751 (MucVJ), ProGP752 (MucVK), ProGP753 (MucVL), ProGP754 (MucVM), ProGP755 (MucVN), ProGP756 (MucVO), ProGP757 (MucVP), ProGP758 (MucVQ), ProGP759 (MucVR), ProGP760 (MucVS), ProGP761 (MucVT), ProGP762 (MucVU), ProGP763 (MucVV), ProGP764 (MucVW), ProGP765 (MucVX), ProGP766 (MucVY), ProGP767 (MucVZ), ProGP768 (MucWA), ProGP769 (MucWB), ProGP770 (MucWC), ProGP771 (MucWD), ProGP772 (MucWE), ProGP773 (MucWF), ProGP774 (MucWG), ProGP775 (MucWH), ProGP776 (MucWI), ProGP777 (MucWJ), ProGP778 (MucWK), ProGP779 (MucWL), ProGP780 (MucWM), ProGP781 (MucWN), ProGP782 (MucWO), ProGP783 (MucWP), ProGP784 (MucWQ), ProGP785 (MucWR), ProGP786 (MucWS), ProGP787 (MucWT), ProGP788 (MucWU), ProGP789 (MucWV), ProGP790 (MucWW), ProGP791 (MucWX), ProGP792 (MucWY), ProGP793 (MucWZ), ProGP794 (MucXA), ProGP795 (MucXB), ProGP796 (MucXC), ProGP797 (MucXD), ProGP798 (MucXE), ProGP799 (MucXF), ProGP800 (MucXG), ProGP801 (MucXH), ProGP802 (MucXI), ProGP803 (MucXJ), ProGP804 (MucXK), ProGP805 (MucXL), ProGP806 (MucXM), ProGP807 (MucXN), ProGP808 (MucXO), ProGP809 (MucXP), ProGP810 (MucXQ), ProGP811 (MucXR), ProGP812 (MucXS), ProGP813 (MucXT), ProGP814 (MucXU), ProGP815 (MucXV), ProGP816 (MucXW), ProGP817 (MucXX), ProGP818 (MucXY), ProGP819 (MucXZ), ProGP820 (MucYA), ProGP821 (MucYB), ProGP822 (MucYC), ProGP823 (MucYD), ProGP824 (MucYE), ProGP825 (MucYF), ProGP826 (MucYG), ProGP827 (MucYH), ProGP828 (MucYI), ProGP829 (MucYJ), ProGP830 (MucYK), ProGP831 (MucYL), ProGP832 (MucYM), ProGP833 (MucYN), ProGP834 (MucYO), ProGP835 (MucYP), ProGP836 (MucYQ), ProGP837 (MucYR), ProGP838 (MucYS), ProGP839 (MucYT), ProGP840 (MucYU), ProGP841 (MucYV), ProGP842 (MucYW), ProGP843 (MucYX), ProGP844 (MucYY), ProGP845 (MucYZ), ProGP846 (MucZA), ProGP847 (MucZB), ProGP848 (MucZC), ProGP849 (MucZD), ProGP850 (MucZE), ProGP851 (MucZF), ProGP852 (MucZG), ProGP853 (MucZH), ProGP854 (MucZI), ProGP855 (MucZJ), ProGP856 (MucZK), ProGP857 (MucZL), ProGP858 (MucZM), ProGP859 (MucZN), ProGP860 (MucZO), ProGP861 (MucZP), ProGP862 (MucZQ), ProGP863 (MucZR), ProGP864 (MucZS), ProGP865 (MucZT), ProGP866 (MucZU), ProGP867 (MucZV), ProGP868 (MucZW), ProGP869 (MucZX), ProGP870 (MucZY), ProGP871 (MucZZ), ProGP872 (MucAA), ProGP873 (MucAB), ProGP874 (MucAC), ProGP875 (MucAD), ProGP876 (MucAE), ProGP877 (MucAF), ProGP878 (MucAG), ProGP879 (MucAH), ProGP880 (MucAI), ProGP881 (MucAJ), ProGP882 (MucAK), ProGP883 (MucAL), ProGP884 (MucAM), ProGP885 (MucAN), ProGP886 (MucAO), ProGP887 (MucAP), ProGP888 (MucAQ), ProGP889 (MucAR), ProGP890 (MucAS), ProGP891 (MucAT), ProGP892 (MucAU), ProGP893 (MucAV), ProGP894 (MucAW), ProGP895 (MucAX), ProGP896 (MucAY), ProGP897 (MucAZ), ProGP898 (MucBA), ProGP899 (MucBB), ProGP900 (MucBC), ProGP901 (MucBD), ProGP902 (MucBE), ProGP903 (MucBF), ProGP904 (MucBG), ProGP905 (MucBH), ProGP906 (MucBI), ProGP907 (MucBJ), ProGP908 (MucBK), ProGP909 (MucBL), ProGP910 (MucBM), ProGP911 (MucBN), ProGP912 (MucBO), ProGP913 (MucBP), ProGP914 (MucBQ), ProGP915 (MucBR), ProGP916 (MucBS), ProGP917 (MucBT), ProGP918 (MucBU), ProGP919 (MucBV), ProGP920 (MucBW), ProGP921 (MucBX), ProGP922 (MucBY), ProGP923 (MucBZ), ProGP924 (MucCA), ProGP925 (MucCB), ProGP926 (MucCC), ProGP927 (MucCD), ProGP928 (MucCE), ProGP929 (MucCF), ProGP930 (MucCG), ProGP931 (MucCH), ProGP932 (MucCI), ProGP933 (MucCJ), ProGP934 (MucCK), ProGP935 (MucCL), ProGP936 (MucCM), ProGP937 (MucCN), ProGP938 (MucCO), ProGP939 (MucCP), ProGP940 (MucCQ), ProGP941 (MucCR), ProGP942 (MucCS), ProGP943 (MucCT), ProGP944 (MucCU), ProGP945 (MucCV), ProGP946 (MucCW), ProGP947 (MucCX), ProGP948 (MucCY), ProGP949 (MucCZ), ProGP950 (MucDA), ProGP951 (MucDB), ProGP952 (MucDC), ProGP953 (MucDD), ProGP954 (MucDE), ProGP955 (MucDF), ProGP956 (MucDG), ProGP957 (MucDH), ProGP958 (MucDI), ProGP959 (MucDJ), ProGP960 (MucDK), ProGP961 (MucDL), ProGP962 (MucDM), ProGP963 (MucDN), ProGP964 (MucDO), ProGP965 (MucDP), ProGP966 (MucDQ), ProGP967 (MucDR), ProGP968 (MucDS), ProGP969 (MucDT), ProGP970 (MucDU), ProGP971 (MucDV), ProGP972 (MucDW), ProGP973 (MucDX), ProGP974 (MucDY), ProGP975 (MucDZ), ProGP976 (MucEA), ProGP977 (MucEB), ProGP978 (MucEC), ProGP979 (MucED), ProGP980 (MucEE), ProGP981 (MucEF), ProGP982 (MucEG), ProGP983 (MucEH), ProGP984 (MucEI), ProGP985 (MucEJ), ProGP986 (MucEK), ProGP987 (MucEL), ProGP988 (MucEM), ProGP989 (MucEN), ProGP990 (MucEO), ProGP991 (MucEP), ProGP992 (MucEQ), ProGP993 (MucER), ProGP994 (MucES), ProGP995 (MucET), ProGP996 (MucEU), ProGP997 (MucEV), ProGP998 (MucEW), ProGP999 (MucEX), ProGP1000 (MucEY)
<i>Bacteroidata</i>	ProGP114 (Endo-β-N-acetylglucosaminidase F2), ProGP115 (Flavastacin (P40)), ProGP116 (Endo-β-N-acetylglucosaminidase F3)
<i>Bacteroides</i>	ProGP106 (Heparin lyase I or Heparinase I)
<i>Bacteroidetes</i>	ProGP132 (Chondroitinase-AC), ProGP133 (Heparinase II), ProGP136 (Antigen (60 kDa)), ProGP141 (PGP), ProGP145 (Adhesion inhibitor), ProGP166 (Chondroitinase-B), ProGP170 (Cysteine proteases (extracellular) Arg-gingipains (RgpA)), ProGP177 (HRgpA), ProGP178 (mtRgpA), ProGP228 (Short glycopeptides), ProGP252 (DgpA), ProGP253 (DgpC), ProGP311 (BF2494), ProGP312 (Hypothetical protein), ProGP313 (Hypothetical protein), ProGP314 (Putative exported protein), ProGP315 (Putative outer membrane protein), ProGP317 (BF3567), ProGP318 (BF3918), ProGP319 (BF0935), ProGP345 (Mfa1 (67 kDa minor fimbriillin)), ProGP348 (TfsB (S-layer protein)), ProGP349 (TF1259), ProGP350 (TF2339), ProGP351 (BF0810), ProGP352 (Putative cell division protein), ProGP353 (Putative exported protein), ProGP399 (TfsA (S-layer protein)), ProGP405 (TF0091), ProGP406 (TF1056)
<i>Candidatus Thermoplasmatota</i>	ProGP8 (Membrane glycoprotein 152 kDa ), ProGP127 (Flagellin B1 (41 kDa))
<i>Chlamydiae</i>	ProGP62 (18 kDa and 32 kDa lectin binding proteins), ProGP77 (Major outer membrane protein (MOMP, 40 kD))
<i>Chloroflexi</i>	ProGP84 (Auracyanin-B1 (22 kDa)), ProGP85 (Auracyanin-B2 (18 kDa))
<i>Crenarchaeota</i>	ProGP17 (Flagellin), ProGP52 (Hypothetical protein), ProGP58

# How to search Crystal Structure in Structure gallery?



Crystal Structure

AlphaFold2 Models

1. Put the cursor on Crystal Structure.

Crystal Structure

ProGP

AlphaFold2 Models

ProGT

ProGT Accessory

2. Click on ProGP for glycoproteins' crystal structures, ProGT for glycosyltransferase' crystal structures, and ProGT Accessory for Accessory GTs' crystal structures.



# Result page of Crystal Structure of ProGP:

## Crystal Structure ProGP




Home -> Structure Gallery -> Crystal Structure

Allows user to search for known crystal structures (retrieved from PDB) of prokaryotic glycoproteins compiled under ProGP.

Search can be made by selecting organisms name.

Search can be made by selecting ProGP ID.

Select words(s)

ProGP ID	Organism Name	Protein Name	UniProtKB/SwissProt ID	PDB ID	Crystal Structure(PDB)
<a href="#">ProGP197 (Subtilisin (SBL)-Cys mutant)</a>	Bacillus lentus	Subtilisin (SBL)- Cys mutant	<a href="#">P29600</a>	<a href="#">1JEA</a>	
<a href="#">ProGP542 (Translation elongation factor P (EF-P))</a>	Neisseria meningitidis HT1125	Translation elongation factor P(EF-P)	<a href="#">E6MWW0</a>	<a href="#">5WXX</a>	
<a href="#">ProGP402 (Glycocin F)</a>	Lactobacillus plantarum KW30	Glycocin F	<a href="#">E9K9Z1</a>	<a href="#">2KUY</a>	

Select

- Select
- Bacillus lentus
- Neisseria meningitidis HT1125
- Lactobacillus plantarum KW30
- Pyrococcus furiosus DSM 3638
- Neisseria gonorrhoeae N400 /MS11
- Escherichia coli K12
- Pseudomonas syringae strain S203
- Mycobacterium tuberculosis
- Escherichia coli K12/DH5alpha
- Paenibacillus (Bacillus) macerans and Bacillus amyloliquefaciens (velezensis)
- Chloroflexus aurantiacus
- Chloroflexus aurantiacus
- Flavobacterium meningosepticum (Elizabethkingia meningoseptica)
- Pyrococcus furiosus DSM 3638
- Proteus vulgaris
- Bacillus subtilis 168
- Mycobacterium tuberculosis H37Rv
- Mycobacterium tuberculosis
- Mycobacterium tuberculosis

Select

- Select
- ProGP101 (H(A16-M) (1,3-1,4)-beta-glucanase)
- ProGP108 (Tetrabrachion (S layer glycoprotein))
- ProGP116 (Endo-?-N-acetylglucosaminidase F3)
- ProGP119 (Fimbrial protein (pilin))
- ProGP132 (Chondroitinase-AC)
- ProGP133 (Heparinase II)
- ProGP166 (Chondroitinase-B)
- ProGP171 (Man26A (b-mannosidase 26A))
- ProGP189 (Superoxide dismutase [Cu-Zn])
- ProGP197 (Subtilisin (SBL)-Cys mutant)
- ProGP209 (FapI (Fimbrial adhesin))
- ProGP211 (TMBP (Trehalose/maltose binding protein))
- ProGP212 (MDBP (Maltodextrin binding protein))
- ProGP216 (BclA (collagen-like protein))
- ProGP222 (PEB3)
- ProGP227 (HMW1 (Adhesin))
- ProGP255 (HmcA)
- ProGP270 (BlaC)
- ProGP273 (LppX (Putative lipoprotein))



# Result page of Crystal Structure of ProGT:



## Crystal Structure ProGT

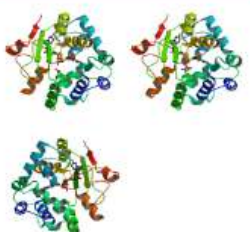

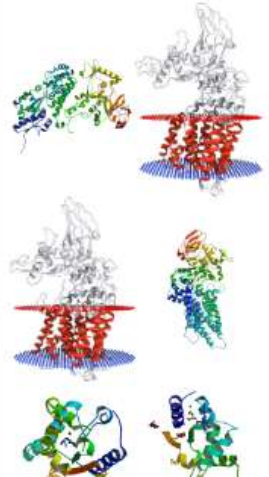
Home -> Structure Gallery -> Crystal Structure

Allows user to search for known crystal structures (retrieved from PDB) of prokaryotic protein glycosyltransferases compiled under ProGT\_Main.

Search can be made by selecting organisms name.

Search can be made by selecting ProGT ID.

Select words(s)     

ProGT ID	Organism Name	Protein Name	PDB ID	Crystal Structure(PDB)
<a href="#">ProGT75 (GtfA)</a>	Streptococcus pneumoniae serotype 4 (strain ATCC BAA-334 / TIGR4)	GtfA	4PQG	
<a href="#">ProGT60 (AglB)</a>	Pyrococcus horikoshii	AglB	3VU1	
<a href="#">ProGT53 (AglB)</a>	Archaeoglobus fulgidus (strain ATCC 49558 / VC-16 / DSM 4304 / JCM 9628 / NBRC 100126)	AglB	3VGP 3VU0 3WAI 3WAJ 3WAK 5GMY	

# Result page of Crystal Structure of ProGT Accessory:

## Crystal Structure ProGT Accessory

Home -> Structure Gallery -> Crystal Structure

Allows user to search for known crystal structures (retrieved from PDB) of prokaryotic enzymes/proteins that are involved in protein glycosylation compiled under ProGT\_Accessory

Search can be made by selecting organisms name.

Select words(s)

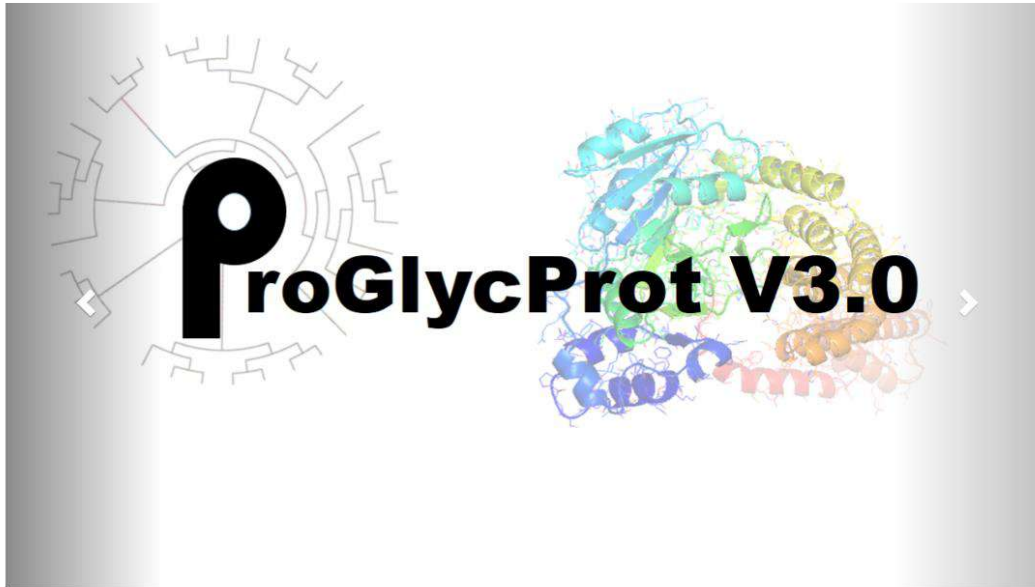
Search Now

Search can be made by selecting ProGT ID.



ProGT ID	Organism Name	Protein Name	PDB ID	Crystal Structure(PDB)
<a href="#">ProGTNC9 (WbpE)</a>	Pseudomonas aeruginosa (strain ATCC 15692 / DSM 22644 / CIP 104116 / JCM 14847 / LMG 12228 / 1C / PRS 101 / PAO1)	WbpE	<a href="#">3NU7</a> <a href="#">3NU8</a> <a href="#">3NUB</a> <a href="#">3NYS</a> <a href="#">3NYT</a> <a href="#">3NYU</a>	
<a href="#">ProGTNC8 (WbpB)</a>	Pseudomonas aeruginosa (strain ATCC 15692 / DSM 22644 / CIP 104116 / JCM 14847 / LMG 12228 / 1C / PRS 101 / PAO1)	WbpB	<a href="#">3OA2</a>	
<a href="#">ProGTNC6 (PseH)</a>	Helicobacter pylori 26695	PseH	<a href="#">4RI1</a>	
<a href="#">ProGTNC5 (PseC)</a>	Helicobacter pylori 26695	PseC (HP_0366)	<a href="#">2FN6</a> <a href="#">2FNI</a> <a href="#">2FNU</a>	

# How to search AlphaFold2 Models in Structure Gallery?



Crystal Structure

AlphaFold2 Models

1. Put the cursor on AlphaFold2 Models.

Crystal Structure

AlphaFold2 Models

ProGP

ProGT

rotein Glycosyltransferases

2. Click on ProGP or ProGT for AlphaFold2 models of glycoproteins or glycosyltransferases, respectively.



# Result page of AlphaFold2 models of ProGT:

## AlphaFold2 models ProGT

Home -> Structure Gallery -> AlphaFold2 models

AlphaFold is an original AI approach that consolidates physical and natural information about protein structure, utilizing multi-sequence alignments, into the plan of the deep learning algorithm.

Search can be made by selecting organisms name.


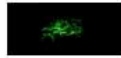
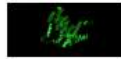

Search can be made by selecting ProGP ID.

Select words(s)

Select

Select

Search Now

ProGP ID	Organism Name	Protein Name	UniProtKB/SwissProt ID	AlphaFold2 Models
<a href="#">ProGT1 (PiI0)</a>	<i>Pseudomonas aeruginosa</i> 1244	PiI0	<a href="#">A0A1U9XPN7</a>	
<a href="#">ProGT8 (Aah)</a>	<i>Escherichia coli</i> K12	Aah	<a href="#">Q93K96</a>	
<a href="#">ProGT9 (PglB)</a>	<i>Campylobacter Jejuni</i> 81-176	PglB	<a href="#">A0A0H3P9U9</a>	
<a href="#">ProGT10 (PglB)</a>	<i>Campylobacter jejuni</i> subsp. <i>jejuni</i> serotype O:2 (strain ATCC 700819 / NCTC 11168)	PglB	<a href="#">Q0P9C8</a>	

Click on the structure, PDB file of the structure will get downloaded.

Select Select Search Now

- Select
- Pseudomonas aeruginosa 1244
- Escherichia coli K12
- Campylobacter Jejuni 81-176
- Campylobacter jejuni subsp. jejuni serotype O:2 (strain ATCC 700819 / NCTC 11168)
- Escherichia coli ETEC
- Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv)
- Methanococcus maripaludis (strain S2 / LL)
- Corynebacterium glutamicum (strain ATCC 13032 / DSM 20300 / JCM 1318 / LMG 3730 / NCIMB 10025)
- Haloflex volcanii (strain ATCC 29605 / DSM 3757 / JCM 8879 / NBRC 14742 / NCIMB 2012 / VKM B-1768 / DS2) (Halobacterium volcanii)
- Methanococcus voltae PS
- Neisseria meningitidis C311#3
- Campylobacter jejuni subsp. jejuni serotype O:23/36 (strain 81-176)
- Legionella pneumophila subsp. pneumophila (strain Philadelphia 1 / ATCC 33152 / DSM 7513)
- Listeria monocytogenes serovar 1/2a (strain ATCC BAA-679 / EGD-e)
- Neisseria gonorrhoeae N400
- Neisseria meningitidis MC58
- Pseudomonas aeruginosa Pa5196
- Legionella pneumophila subsp. pneumophila (strain Philadelphia 1 / ATCC 33152 / DSM 7513)
- Legionella pneumophila subsp. pneumophila (strain Philadelphia 1 / ATCC 33152 / DSM 7513)

Select Search Now

- Select
- ProGT1 (PiI0)
- ProGT8 (Aah)
- ProGT9 (PglB)
- ProGT10 (PglB)
- ProGT11 (TibC)
- ProGT12 (Rv1002c)
- ProGT13 (AglB)
- ProGT14 (Pmt)
- ProGT15 (AglB)
- ProGT16 (AglB)
- ProGT17 (PglL)
- ProGT18 (PseD)
- ProGT19 (Lgt1)
- ProGT20 (GmaR)
- ProGT21 (PglO)
- ProGT25 (PglL)
- ProGT26 (TfpW)

AlphaFold2 models can be retrieved from this option

Map View

AlphaFold2 Models

Statistics

References

Patent

AlphaFold2 models can be retrieved from here as well.

Result page will be displayed on the homepage.

Click on Search Now

AlphaFold2 Models

AlphaFold is an original AI approach that consolidates physical and natural information about protein structure, utilizing multi-sequence alignments, into the plan of the deep learning algorithm.

Select ProGT ID

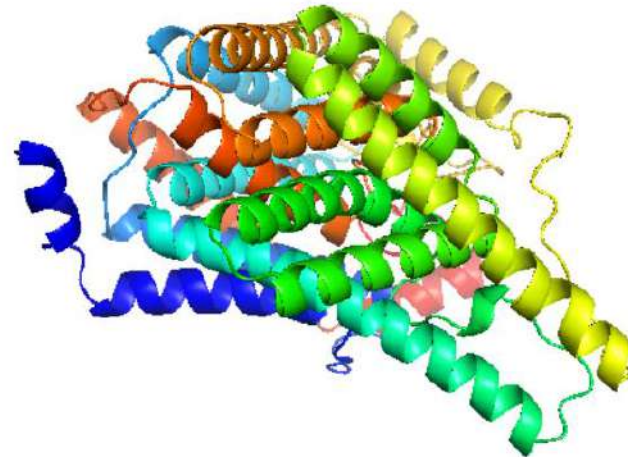
Select ProGP ID

ProGT1 (P/I/O)

File - For Evaluation Only (0 days remaining)

Select ProGT/ProGP ID from the list

Click on the image, PDB file will get downloaded.



Pseudomonas aeruginosa 1244

# How to find Related reviews, related tools and databases, and bibliography?

Click on the links drop down menu.

Links



Update: ProGlycF

Related Reviews

Related Tools & Databases

Bibliography ProGlycProt

A Manually Curated Repository of Experimentally Characterized Glycoproteins

Transferases of Prokaryotes

## Related Review

Home-> Links -> Related Review

List of selected reviews on the theme "Prokaryotic glycoproteins and protein glycosyltransferases". May serve as primer for curious minds.

Enter review title or year

Enter Key words(s)

Enter Key words

Review Title

(e.g. bacterial glycoproteins)

Year of Publication

(e.g. 2006)



S.No	Review Title	PMID	Comments	Year Of Publication
1	Structure and Biosynthesis of Prokaryotic Glycoproteins	<a href="#">2673008</a>	It could be the first ever compilation of prokaryotic glycoproteins known until 1989.	1989
2	Non-S-layer glycoproteins in eubacteria	<a href="#">8013865</a>	Exclusive review of bacterial S-layer glycoproteins. Authors coined term "S layer glycoprotein".	1994
3	Bacterial Glycoproteins	<a href="#">9076508</a>	A total of 22 archaeal and 46 bacterial glycoproteins are enlisted together with some of the sugar linkages. Subcellular locations of these glycoproteins are also given.	1997

Click to see review in the PubMed



## Related Tools & Database

Home -> Links -> Related Tools & Database

List the other available tools and databases related to glycoproteins and glycosyltransferases.

Database	Description
Databases and Tools	
<a href="#">Aglgenes</a>	Database containing all available information on archaeal N-glycosylation
<a href="#">Animal Lectins</a>	A genomic resource of animal lectins
<a href="#">Bacterial Carbohydrate Structure DataBase</a>	Carbohydrate databases
<a href="#">BCSDB</a>	Structural, bibliographic, taxonomic and related information on bacterial carbohydrate structures (Encoding BCSDB linear code)
<a href="#">BRENDA</a>	Repository of Enzyme Information

Links



Related Reviews

Related Tools & Databases

Bibliography ProGlycProt

## Bibliography

Home -> Links -> Bibliography

Enter Key words(s)

Enter Key words

Submit

(e.g. 19379697)

Click to open databases and tools

Search references by entering the PubMed ID

S.No	Reference	PubmedID
1	Zellner, G., Stackebrandt, E., Messner, P., Tindall, B.J., Conway de Macario, E., Kneifel, H., Sleytr, U.B. and Winter, J., 1989. Methanocorpusculaceae fam. nov., represented by Methanocorpusculum parvum, Methanocorpusculum sinense spec. nov. and Methanocorpusculum bavaricum spec. nov. Archives of microbiology, 151(5), pp.381-390.	<a href="#">2742452</a>
2	ZELLNER, G., MESSNER, P., KNEIFEL, H., TINDALL, B.J., WINTER, J. and STACKEBRANDT, E., 1989. Methanolacinia gen. nov., incorporating Methanomicrobium paynteri as Methanolacinia paynteri comb. nov. The Journal of General and Applied Microbiology, 35(3), pp.185-202.	
3	Logan, S.M., Hui, J.P., Vinogradov, E., Aubry, A.J., Melanson, J.E., Kelly, J.F., Nothaft, H. and Soo, E.C., 2009. Identification of novel carbohydrate modifications on Campylobacter jejuni 11168 flagellin using metabolomics-based approaches. The FEBS Journal, 276(4), pp.1014-1023.	<a href="#">19154343</a>
4	McNally, D.J., Aubry, A.J., Hui, J.P., Khieu, N.H., Whitfield, D., Ewing, C.P., Guerry, P., Brisson, J.R., Logan, S.M. and Soo, E.C., 2007. Targeted metabolomics analysis of Campylobacter coli VC167 reveals legionaminic acid derivatives as novel flagellar glycans. Journal of Biological Chemistry, 282(19), pp.14463-14475.	<a href="#">17371878</a>

Click to see reference in the PubMed

# How to find different tools on ProGlycProt?



A Manually Curated Repository of Experimentally Characterized Glycoproteins and Protein Glycosyltransferases

## How to use MapSequon Tool?

- MapSequon
- GlySeq Extractor
- Predict Glycosite
- Compare
- BLAST
- Patent

Map Sequon

Home ->Tools -> Map Sequon

Allows user the linear mapping of specified glycosite sequon (s) for the visual display of sequon positions, frequency, clustering or complete absence in the input sequence (s). The sequons specified below represent the major patterns identified at/ around the glycosylated residue in the characterized prokaryotic glycoproteins.

Paste protein sequence in FASTA format

Input Protein Sequence(s)(FASTA Format) For Example File [Click Here](#)

```
>Myseq
MKRLIPILLAVYFAACEKDPDMKIDLNISLVYNTYTKGADFKQFSTYI
PDSVLLVIGDKKDSFYWKGEAAEAIIINAYKENLNSKGFYTDNKDAADLGI
QVSYVQSTYYFTVYGGQPEWNNWNYPGYWDAPYWGNGWGWYYPVWVNSITT
NSFLTEIMNLLKAPERGEKQKLPVLWESNLSQPASVSGKVINQTLVVRAINQS
FAQSPVLTNK
```

Clear Submit

Click Submit

Note: Please click on "Example Glycoprotein" as given above to retrieve results for one sequon (selected) at a time. This tool is based on literature-derived information on prokaryotic sequon features and result output may not be statistically significant.

Result page: Visual display of specified glycosite sequons in the protein sequence



S. No. 1 Input Sequence ID	Input Sequence Length	Specified Glycosite Sequon	Mapped Sequence(s)	Residue No.
>Myseq	210 AA	NX(S/T), X ≠ P	MKRLIPILLAVYAFAACEKDPD MDKDLN <sup>N</sup> ISLVYTN <sup>N</sup> YTKKADFK QFSTYYIPDSVLVIGDKKDSEY WKGEEAEIINAYKENLNSKG FTYTDNKDAADLGIQVSYVQS TYYFTVYGQPEWWWNYPGY WDAPYWGNGWGGWYYPYVW <sup>N</sup> YSITTNSFLTEIMNLKAPEGEK QKLPVLWES <sup>N</sup> LSGPASYS <sup>N</sup> SGKV N <sup>N</sup> QTLVRAIN <sup>N</sup> QSF <sup>N</sup> AQSPYL <sup>N</sup> TN K	N28 N35 N145 N177 N189 N198
>Myseq	210 AA	(D/E)X1NX(S/T),X1 and X ≠ P	MKRLIPILLAVYAFAACEKDPD MDKDLN <sup>N</sup> ISLVYTN <sup>N</sup> YTKKADFK QFSTYYIPDSVLVIGDKKDSEY WKGEEAEIINAYKENLNSKG FTYTDNKDAADLGIQVSYVQS TYYFTVYGO <sup>N</sup> PFWWWNYPGY	N28 N177



# How to use GlySeq Extractor Tool?

Tools ▾ Links ▾ 

MapSequon

GlySeq Extractor

Predict Glycosite

Compare

BLAST

Patent

Glyseq Extractor

Home ->Tools -> Glyseq Extractor

Allows user the extraction of sequence of selected length around a selected glycosite pattern from given sequence (s). The output is suitable for weblogo generation.

## Select Glycosite Pattern

(Where X1 & X ≠ P)

- N-X-(S/T)-
- N-X-(S/T)-
- (D/E)-X1-N-X-(S/T)-
- D-(S/T)-
- D(S/T)(A/I/L/N/M/T)-
- S/T
- S
- T
- N
- V-Y

## Input Protein Sequence(s)(FASTA Format) For Example File [Click Here](#)

```
>Myseq
MKRLIPILLAVYFAACEKDPDMDKDLNISLVYTNYYKKADFKQFSTYYI
PDSVLVIGDKKDSSEYWKGEAAEAIINAYKENLNSKGFTYTDNKDAADLGI
QVSYVQSTYYFTVYGGQPEWWWNYPGYWDAPYWGNNWGGWYYPVWVNSITT
NSPLTEIMNLLKAPERGEKQKLPVLWESNLSGRASYSYSGKVNQTLVVRAINQS
FAQSPYLTNK
```

## Select Glycosite Pattern

(Where X1 & X ≠ P)

-N-X-(S/T)-

## Select Sequence Window

-5 to +5

Clear Submit

## Select Sequence Window

- 5 to +5
- 5 to +5
- 10 to +10
- 15 to +15
- 20 to +20
- 30 to +30
- 50 to +50

Clear

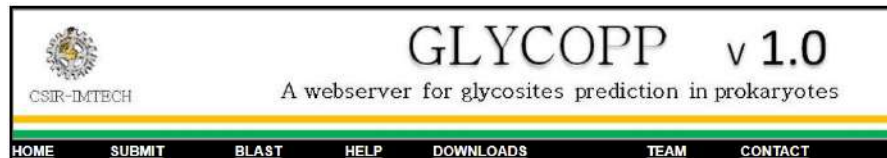
Result page:

Sequence No.	Input Sequence ID	Input Sequence Length	Input Glycosite Pattern	Input Sequence Window	Extracted Sequences	Residue No.
1	>Myseq	210	NX(S/T)	11	MDKDLNISLVY SLVYTNVTKKA YPYVVNYSITT VLWESNLSGPA YSGKVNQTLW VRAINQSFAQ	N28 N35 N145 N177 N189 N198

# How to use Predict Glycosite Tool?

Tools ▾ Links ▾ 

- MapSequon
- GlySeq Extractor
- Predict Glycosite**
- Compare
- BLAST
- Patent



An Introduction to GlycoPP

[OSDDlinux for Standalone, Galaxy & Local version](#)

GlycoPP is a webservice for predicting potential N-and O-glycosites in prokaryotic protein sequence(s), where N-glycosite is an Asn residue and O-glycosite could be a serine or threonine residue having a glycan attached covalently and enzymatically at amide or hydroxyl group respectively.

[HOME](#)

[SUBMIT](#)

[BLAST](#)

[HELP](#)



Sequence Name: [optional]

E-mail Address: [optional]

Type/paste protein sequence in FASTA format:

[Use Example Sequence](#)

## N-linked Glycosylation Prediction

For more information click here 

- Prediction based on Binary Profile of Patterns (BPP)
- Prediction based on Composition Profile of Patterns (CPP)
- Prediction based on PSSM Profile of patterns (PPP)
- Prediction based on Average Surface Accessibility (ASA+BPP)

## O-linked Glycosylation Prediction

- Prediction based on Binary Profile of Patterns (BPP)
- Prediction based on Composition Profile of Patterns (CPP)
- Prediction based on PSSM Profile of patterns (PPP)
- Prediction based on Average Surface Accessibility (ASA+PPP)

Selection prediction programme either for N-linked or O-linked glycosylation prediction

Select threshold by pull down menu.

SVM threshold:

Click on SUBMIT to go the result page



# How to use Compare Tool?

- MapSequon
- GlySeq Extractor
- Predict Glycosite
- Compare**
- BLAST
- Patent

## Compare

Home -> Tools -> Compare

Allows to compare upto four prokaryotic glycoproteins or protein glycosyltransferases compiled under ProGPdb and ProGTdb database, respectively.

1. Select a section from which entries are to be compared

Compare ProGPdb
  Compare ProGTdb\_Main
  Compare ProGTdb\_Accessory

ProGP ID I: 
 ProGP ID II: 
 ProGP ID III: 
 ProGP ID IV: 
 Search Display Criteria:

Compare

4. Click on Compare

2. Choose the entries to be compared.

3. Select a display criteria. All is set as default.

Result Page:

ProGP ID	ProGP101	ProGP105	ProGP110	ProGP115
Validation Status	Characterized	Uncharacterized	Uncharacterized	Characterized
Organism Information				
Organism	Paenibacillus (Bacillus) macerans and Bacillus amyloliquefaciens (velezensis)	Thermoanaerobacter thermohydrosulfuricus L111-69 and L110-69	Mycobacterium bovis BCG	Flavobacterium meningosepticum (Elizabethkingia meningoseptica)
Domain	Bacteria	Bacteria	Bacteria	Bacteria
Classification	Family: Bacillaceae Order: Bacillales Class: Bacilli (or	Family: Thermoanaerobacteracea e	Family: Mycobacteriaceae Suborder: Corynebacterineae	Family: Flavobacteriaceae Order: "Flavobacteriales" Class: Flavobacteria

# How to use BLAST Tool?

Tools ▾ Links ▾ 

- MapSequon
- GlySeq Extractor
- Predict Glycosite
- Compare
- BLAST**
- Patent

Home -> BLAST

Allows user to run BLAST against protein sequences in ProGlycProtodb

BLAST

1. Paste a protein sequence in fasta format

Input Protein Sequence(s) in (FASTA format) For Example file [Click here](#)

```
>protein_bl09
MKIKEFLKTKKGASGDFEFSOSSGIGTLIVFIAMVLVAVAASVLINTSGFLQQKASTTG
KESTEQVASGLLLNGITGSVGTSDVKLLAIYLC
PNAGSSAIDLQTKIMLDYDGKSVDFGDTWEDAEQSLGYGGNQDMSSGNSSVFSND
TGATATTFQVNIQLQDYDDSAVDNAVINKGDAVALIVD
VSDWSRESDTWDSDRDDREENASFGGEIPERTAISGKVQPEFGAPGVISFTTPASYTTA
LVELQ
```

2. Select weight matrix.

3. Select Expect Value. 1 is set by default

Choice for BLAST

Expect Value

Weight Matrix

BLAST Against

- ProGP
- ProGT(Main)
- ProGT(Accessory)

4. Select the option against which BLAST to be run

Clear All

RUN BLAST

5. Run BLAST

```
Database: ../../1/ProGP_combined.fasta
551 sequences; 259,649 total letters

Query= protein_bl09

Length=252

Sequences producing significant alignments:
```

	Score (Bits)	E Value
tr Q9C4R3 Q9C4R3_METMI Flagellin OS=Methanococcus maripaludis G...	367	2e-130
sp P27803 FLAB1_METVO Flagellin B1 OS=Methanococcus voltae GN=F...	191	3e-61
sp P27804 FLAB2_METVO Flagellin B2 OS=Methanococcus voltae GN=F...	180	3e-57
tr Q9C4R2 Q9C4R2_METMI Flagellin OS=Methanococcus maripaludis G...	156	6e-48
tr Q6LWP1 Q6LWP1_METMP Flagellin OS=Methanococcus maripaludis (...)	125	2e-36
sp P27805 FLAB3_METVO Flagellin B3 OS=Methanococcus voltae GN=F...	116	2e-32
sp P27802 FLAA_METVO Flagellin A OS=Methanococcus voltae GN=Fla...	107	3e-29
sp P57719 FLA1_THEVO Flagellin B1 OS=Thermoplasma volcanium (st...	98.6	8e-26
sp Q9P913 FLAB1_NATMM Flagellin B1 OS=Natrialba magadii (strain...	78.6	3e-19
sp P13075 FLAA2_HALSA Flagellin A2 OS=Halobacterium salinarum (...)	77.8	6e-19
sp P13078 FLAB3_HALSA Flagellin B3 OS=Halobacterium salinarum (...)	75.5	3e-18
sp P61116 FLAB1_HALSA Flagellin B1 OS=Halobacterium salinarum (...)	75.1	4e-18
sp P61118 FLAA1_HALSA Flagellin A1 OS=Halobacterium salinarum (...)	74.7	7e-18
sp P13077 FLAB2_HALSA Flagellin B2 OS=Halobacterium salinarum (...)	72.8	3e-17
sp O93718 FLAB2_NATMM Flagellin B2 OS=Natrialba magadii (strain...	71.6	2e-16

```
> tr|Q9C4R3|Q9C4R3_METMI Flagellin OS=Methanococcus maripaludis
GN=flaB1 PE=3 SV=1
Length=211

Score = 367 bits (942), Expect = 2e-130, Method: Compositional matrix adjust.
Identities = 211/252 (84%), Positives = 211/252 (84%), Gaps = 41/252 (16%)






Query 1 MKIKEFLKTKKGASGDFEFSOSSGIGTLIVFIAMVLVAVAASVLINTSGFLQQKASTT 60
        MKIKEFLKTKKGASG          IGTLIVFIAMVLVAVAASVLINTSGFLQQKASTT
Sbjct 1 MKIKEFLKTKKGASG-----IGTLIVFIAMVLVAVAASVLINTSGFLQQKASTT 50
```

# How to use Patent Tool?

A list of Patent is made available on the website which is related to the glycosylation and its application.

patent

- MapSequon
- GlySeq Extractor
- Predict Glycosite
- Compare
- BLAST
- Patent

-  Map View
-  AlphaFold2 Models
-  Statistics
-  References
-  Patent

Home -> Links -> patent

Select words(s)

Select GT/GP name ▾

Select Organism ▾

**Search Now**



S.No	ProGT/Pro GP ID	GT/GP name	Organism Name	GT family	Patent Number	PCT No	CPC Classification No	Priority date	Date of publication	Legal Status
<b>Title : Conjugate vaccine against gram-negative bacterial infections</b> <b>Inventors : Castric Peter, Cross Alan S, Sadoff Jerald C</b>										
1	ProGT1 (PilO)	PilO	Pseudomonas aeruginosa 1244	GTNC	<a href="#">US 6872398 B2</a>		G01N33/56911	22-12-1995	29-05-2005	Expired
<b>Title : A Novel Pilin Glycoprotein From A Group 4 Pseudomonas Aeruginosa Strain</b> <b>Inventors : Burrows Lori L , Kus Julianne V , Kelly John , Voisin Sebastien , Houliston Scott</b>										
2	ProGT26 (TfpW)	TfpW	Pseudomonas aeruginosa	GTNC	<a href="#">WO2007/128136A1</a>	PCT/CA2007/000849	C07K14/21	09-05-2006	15-11-2005	Pending
<b>Title : Glycoproteins as well As vaccines, antibodies and antibody fragments useful for Combating campylobacter bacteria.</b> <b>Inventors : Young Noel M, Brisson Jean-Robert , Kelly John F, Watson David C, Szymanski Christine M , Jarrell Harold C</b>										
3	ProGT10 (PglB)	PglB	Campylobacter jejuni NCTC 11168	GT66	<a href="#">US 20060165728A1 / US 7598354 B2</a>	PCT/CA03/01156	G01N33/56922	01-08-2002	27-07-2006	Active

Click on the Patent Number to see the patent

# patent

Home-> Links -> patent

1. Click on drop down menu to the Select GT/GP name to search a patent by GT/GP name

2. Click on 'Search Now' to get the result

Select words(s)

Select GT/GP name

S.No	ProGT/Pro GP ID	GT/GP name	C	Priority date	Date of publication	Legal Status				
<p>Title : Conjugate vaccine against gram</p> <p>Inventors : Castric Peter, Cross Alan S,</p>										
1	ProGT1 (PiLO)	PiLO	Pse aeri	3/5	22-12-1995	29-05-2005	Expired			
<p>Title : A Novel Pilin Glycoprotein From</p> <p>Inventors : Burrows Lori L , Kus Julian</p>										
2	ProGT26 (TfpW)	TfpW	Pse aeri	4/21	09-05-2006	15-11-2005	Pending			
<p>Title : Glycoproteins as well As vaccin</p> <p>Inventors : Young Noel M, Brisson Jean-Robert , Kelly John F, Watson David C, Szymanski Christine M , Jarrell Harold C</p>										
3	ProGT10 (PglB)	PglB	Campylobacter jejuni NCTC 11168	GT66	US 200601657 28A1 / US 7598354 B2	PCT/CA03/01156	G01N33/56922	01-08-2002	27-07-2006	Active

Result page:

S.No	GT/GP name	Organism Name	GT family	Patent Number	PCT No	CPC Classification No	Priority date	Date of publication	Legal Status
<p>Title : N glycosyl transferase AaNGT and application thereof</p>									
1	AaNGT	Aggregatibacter aphrophilus	GT41	CN10703420 2A		C07K1/1077	26-06-2017	11-08-2017	Discontinued



# patent

Home-> Links -> patent

1. Click on drop down menu to search a patent by organisms' name

Select words(s)  Select GT/GP name  Select Organism

2. Click on 'Search Now' to get the result

Acinetobacter baylyi (strain ATCC 33305 / BD413 / ADP1)

S.No	ProGT/Pro GP ID	GT/GP name	Organism Name
<b>Title : Conjugate vaccine against gram-negative bacteria</b> <b>Inventors : Castric Peter, Cross Alan S, Sadoff Jera</b>			
1	ProGT1 (PiLO)	PiLO	Pseudomonas aeruginosa 124
<b>Title : A Novel Pilin Glycoprotein From A Group 4 F</b> <b>Inventors : Burrows Lori L, Kus Julianne V, Kelly J</b>			
2	ProGT26 (TfpW)	TfpW	Pseudomonas aeruginosa
<b>Title : Glycoproteins as well As vaccines, antibodies</b> <b>Inventors : Young Noel M, Brisson Jean-Robert, Kelly John F, Watson David C, Szymanski Christine M, Jarrell Harold C</b>			
3	ProGT10 (PgIB)	PgIB	Campylobacter jejuni NCTC 11168

Result page:



S.No	GT/GP name	Organism Name	GT family	Patent Number	PCT No	CPC Classification No	Priority date	Date of publication	Legal Status
<b>Title : Acinetobacter O-oligosaccharyltransferases And Uses Thereof</b>									
1	PgLLComP	Acinetobacter baylyi (strain ATCC 33305 / BD413 / ADP1)		US 2018/00501 01 A1/ WO2016134 485A1	PCT/CA2016 /050208	A61K39/09	26-02-2015	22-02-2011	Active

Map View

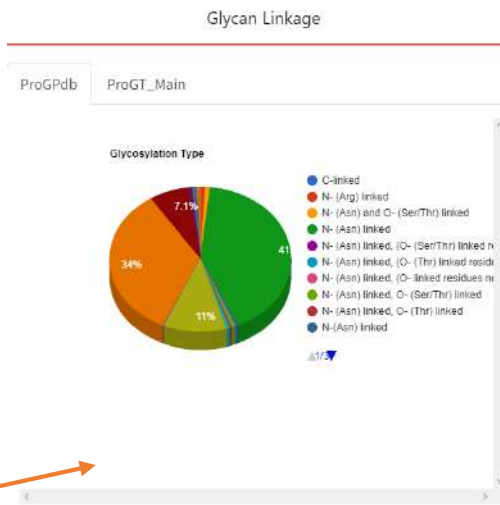
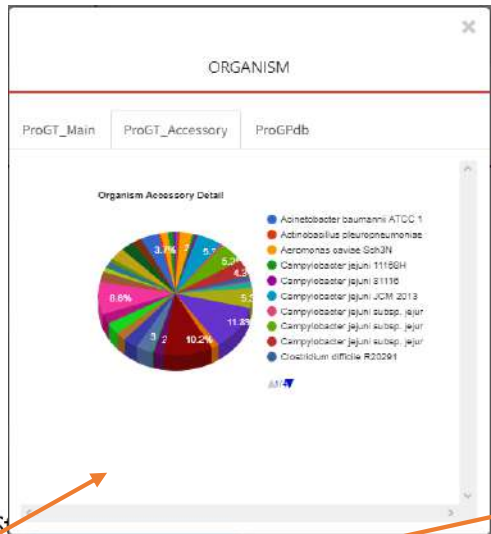
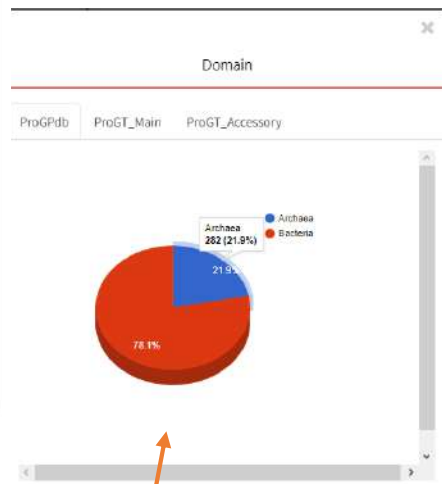
AlphaFold2 Models

Statistics

References

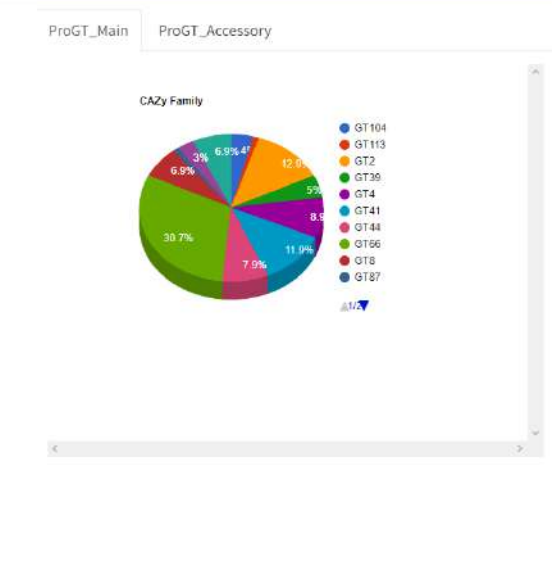
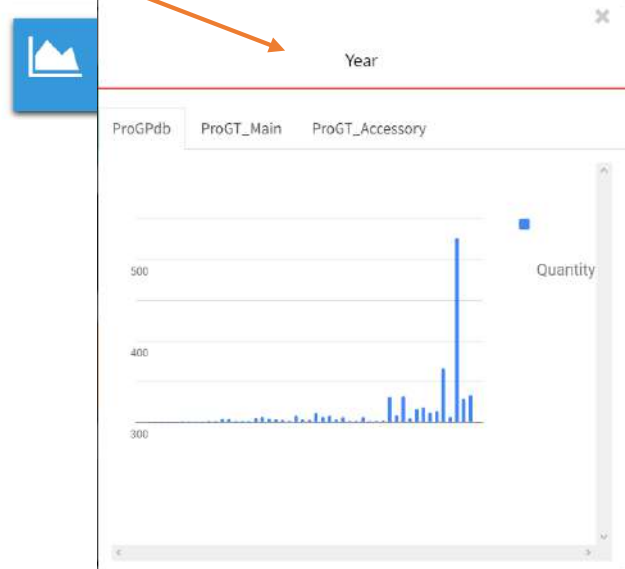
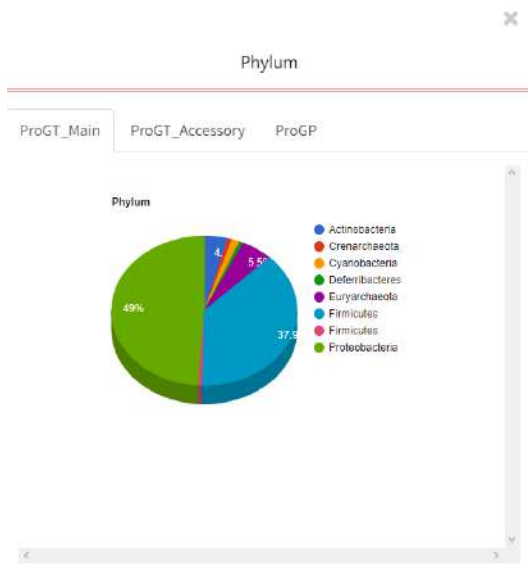
Patent

# Look for Statistics



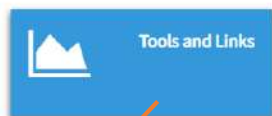
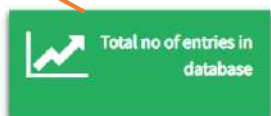
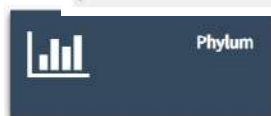
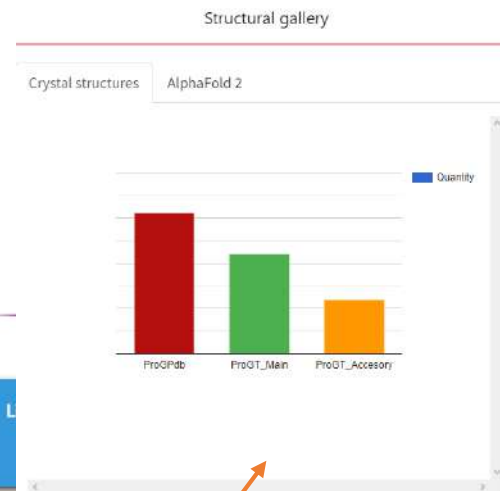
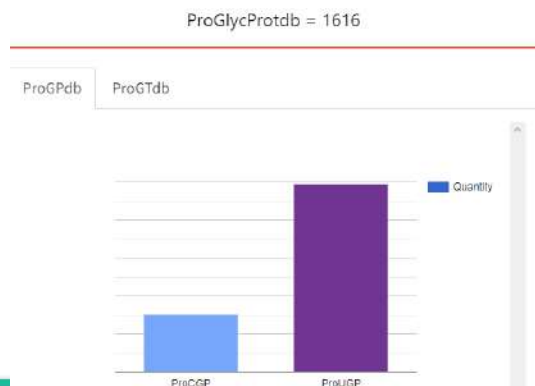
Navigation menu with icons and labels:

- Domain (Pie chart icon)
- Organism (Line graph icon)
- Linkage (Line graph icon)
- CAZy Family (Bar chart icon)
- Phylum (Bar chart icon)
- Year (Pie chart icon)
- Total no of entries in database (Line graph icon)
- Structural (Bar chart icon)

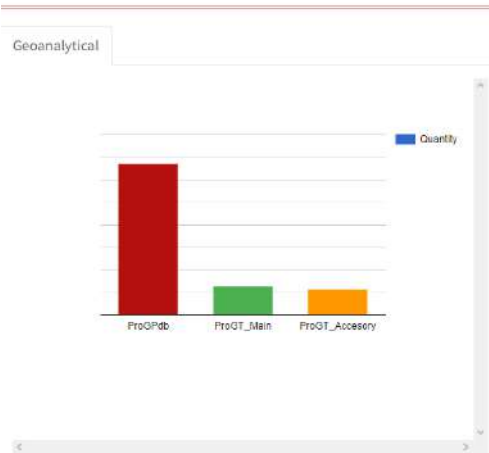


# Look for Statistics

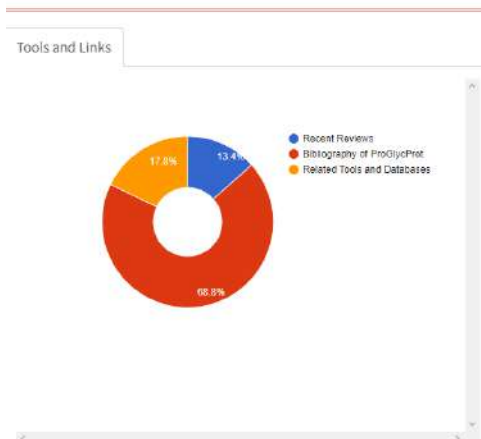
- Map View
- AlphaFold2 Models
- Statistics**
- References
- Patent



Geoanalytical (Mapview) entries



Tools and Links



Patent



## Look for References

 Map View

 AlphaFold2 Models

 Statistics

 References

 Patent

1. Click on References to see the paper published on this database.

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Aadil H. Bhat; Homchoru Mondal; Jagat S. Chauhan; Gajendra P. S. Raghava; Amrish Methi and **Alka Rao** (2012) [ProGlycProt: a repository of experimentally characterized prokaryotic glycoproteins](#). *Nucleic Acids Res.* 2012 Jan;40(Database issue):D388-93. Epub 2011 Oct 28.

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## Our Team

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### ProGlycProt Visitor Counter



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<a href="#">Does ProGlycProt represent all known prokaryotic glycoproteins?</a>
<a href="#">What is the Scope of ProGlycProt?</a>
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<p>Upload File (Detail of Glycoprotein/Glycoenzyme)</p> <p><input type="button" value="Choose File"/> No file chosen</p>	<p>Enter Your Email ID*</p> <input type="text" value="Enter Your Email"/>
<p><input type="button" value="Submit"/> <input type="button" value="Clear"/></p>	

### Glossary of Terms used in ProGlycProt

S.No.	Term/Acronym	Definition
1.	AAL	Alouria Aurantia Lectin
2.	ABEE	p-Aminobenzoic acid ethyl ester

Click on the questions about the database to see their answers