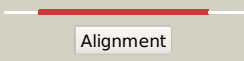

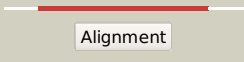

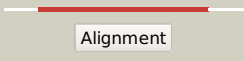

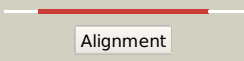

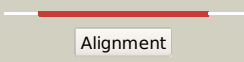

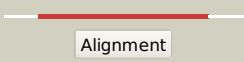

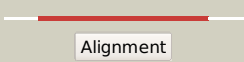

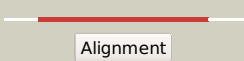

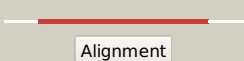

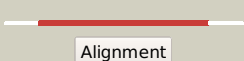

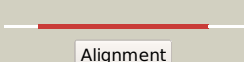

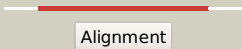

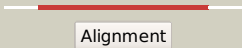



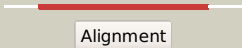

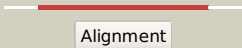





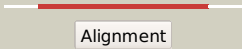


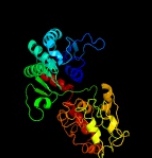
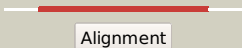

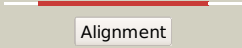
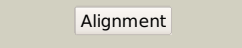


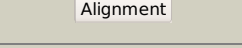



# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2610c_pimA_2937875_2939011
Date	Wed Aug 7 12:50:25 BST 2019
Unique Job ID	880553cf4d7bdda3

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c2gejA_</a>			100.0	83	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> phosphatidylinositol mannosyltransferase (pima); <b>PDBTitle:</b> crystal structure of phosphatidylinositol mannosyltransferase (pima)2 from mycobacterium smegmatis in complex with gdp-man
2	<a href="#">c3c4vB_</a>			100.0	22	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> predicted glycosyltransferases; <b>PDBTitle:</b> structure of the retaining glycosyltransferase msha:the2 first step in mycothiol biosynthesis. organism:3 corynebacterium glutamicum : complex with udp and 1l-ins-1-4 p.
3	<a href="#">c6d9tA_</a>			100.0	20	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> glycosyl transferase; <b>PDBTitle:</b> bsha from staphylococcus aureus complexed with udp
4	<a href="#">c2r60A_</a>			100.0	20	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> glycosyl transferase, group 1; <b>PDBTitle:</b> structure of apo sucrose phosphate synthase (sps) of2 halothermothrix orenii
5	<a href="#">c5d00A_</a>			100.0	16	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> n-acetyl-alpha-d-glucosaminyl l-malate synthase; <b>PDBTitle:</b> crystal structure of bsha from b. subtilis complexed with n-2 acetylglucosaminyl-malate and ump
6	<a href="#">d2bisa1</a>			100.0	22	<b>Fold:</b> UDP-Glycosyltransferase/glycogen phosphorylase <b>Superfamily:</b> UDP-Glycosyltransferase/glycogen phosphorylase <b>Family:</b> Glycosyl transferases group 1
7	<a href="#">c3okaA_</a>			100.0	17	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> gdp-mannose-dependent alpha-(1-6)-phosphatidylinositol <b>PDBTitle:</b> crystal structure of corynebacterium glutamicum pimB' in complex with2 gdp-man (triclinic crystal form)
8	<a href="#">c6ejjA_</a>			100.0	15	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> wlac protein; <b>PDBTitle:</b> structure of a glycosyltransferase
9	<a href="#">c6gneB_</a>			100.0	20	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> probable starch synthase 4, chloroplastic/amyloplastic; <b>PDBTitle:</b> catalytic domain of starch synthase iv from arabidopsis thaliana bound2 to adp and acarbose
10	<a href="#">c3s29C_</a>			100.0	14	<b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> sucrose synthase 1; <b>PDBTitle:</b> the crystal structure of sucrose synthase-1 from arabidopsis thaliana2 and its functional implications.
11	<a href="#">c2qzsA_</a>			100.0	19	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> glycogen synthase; <b>PDBTitle:</b> crystal structure of wild-type e.coli gs in complex with adp and2 glucose(wtgsb)

12	<a href="#">c6gnfC_</a>			100.0	16	<b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> glycogen synthase; <b>PDBTitle:</b> granule bound starch synthase from cyanobacterium sp. clg1 bound to2 acarbose and adp
13	<a href="#">c2jlmH_</a>			100.0	20	<b>PDB header:</b> transferase <b>Chain:</b> H: <b>PDB Molecule:</b> glycosyl transferase, group 1 family protein; <b>PDBTitle:</b> crystal structure of a family gt4 glycosyltransferase from bacillus2 anthracis orf ba1558.
14	<a href="#">d1rzua_</a>			100.0	17	<b>Fold:</b> UDP-Glycosyltransferase/glycogen phosphorylase <b>Superfamily:</b> UDP-Glycosyltransferase/glycogen phosphorylase <b>Family:</b> Glycosyl transferases group 1
15	<a href="#">c3vufA_</a>			100.0	16	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> granule-bound starch synthase 1, <b>PDBTitle:</b> crystal structure of rice granule bound starch synthase i catalytic2 domain in complex with adp
16	<a href="#">c4xsuB_</a>			100.0	17	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> alr3699 protein; <b>PDBTitle:</b> crystal structure of anabaena alr3699/hepe in complex with udp and2 glucose
17	<a href="#">c6gngB_</a>			100.0	15	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> granule-bound starch synthase; <b>PDBTitle:</b> granule bound starch synthase i from cyanophora paradoxa bound to2 acarbose and adp
18	<a href="#">c4hlnA_</a>			100.0	16	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> starch synthase i; <b>PDBTitle:</b> structure of barley starch synthase i in complex with2 maltooligosaccharide
19	<a href="#">c3oy2A_</a>			100.0	13	<b>PDB header:</b> viral protein,transferase <b>Chain:</b> A: <b>PDB Molecule:</b> glycosyltransferase b736i; <b>PDBTitle:</b> crystal structure of a putative glycosyltransferase from paramecium2 bursaria chlorella virus ny2a
20	<a href="#">c4rbdD_</a>			100.0	17	<b>PDB header:</b> transferase <b>Chain:</b> D: <b>PDB Molecule:</b> sucrose synthase:glycosyl transferases group 1; <b>PDBTitle:</b> the crystal structure of nitrosomonas europaea sucrose synthase:2 insights into the evolutionary origin of sucrose metabolism in3 prokaryotes
21	<a href="#">d2iw1a1</a>		not modelled	100.0	15	<b>Fold:</b> UDP-Glycosyltransferase/glycogen phosphorylase <b>Superfamily:</b> UDP-Glycosyltransferase/glycogen phosphorylase <b>Family:</b> Glycosyl transferases group 1
22	<a href="#">c5zesA_</a>		not modelled	100.0	18	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> udp-glucose:tetrahydrobiopterin glucosyltransferase; <b>PDBTitle:</b> udp glucose alpha tetrahydrobiopterin glycosyltransferase from2 synechococcus species pcc 7942 - udp complex
23	<a href="#">c5n80A_</a>		not modelled	100.0	11	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> lipopolysaccharide 1,6-galactosyltransferase; <b>PDBTitle:</b> glycosyltransferase lps biosynthesis in complex with udp
24	<a href="#">c2xmpB_</a>		not modelled	100.0	16	<b>PDB header:</b> sugar binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> trehalose-synthase tret; <b>PDBTitle:</b> crystal structure of trehalose synthase tret mutant e326a2 from p.horishiki in complex with udp
25	<a href="#">c2x6rA_</a>		not modelled	100.0	16	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> trehalose-synthase tret; <b>PDBTitle:</b> crystal structure of trehalose synthase tret from p.2 horikoshi produced by soaking in trehalose
26	<a href="#">c4xywA_</a>		not modelled	100.0	17	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> o-antigen biosynthesis glycosyltransferase wbnh; <b>PDBTitle:</b> glycosyltransferases wbnh
27	<a href="#">c4x7pB_</a>		not modelled	100.0	14	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> tarm; <b>PDBTitle:</b> crystal structure of apo s. aureus tarm
28	<a href="#">c5v0tB_</a>		not modelled	100.0	16	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> alpha,alpha-trehalose-phosphate synthase (udp-forming); <b>PDBTitle:</b> crystal structure of an alpha,alpha-trehalose-phosphate

						synthase (udp-2 forming) from burkholderia xenovorans in complex with glucose-6-3 phosphate
29	<a href="#">c1uquB_</a>	Alignment	not modelled	100.0	14	<b>PDB header:</b> synthase <b>Chain:</b> B: <b>PDB Molecule:</b> alpha, alpha-trehalose-phosphate synthase; <b>PDBTitle:</b> trehalose-6-phosphate from e. coli bound with udp-glucose.
30	<a href="#">c2iv3B_</a>	Alignment	not modelled	100.0	21	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> glycosyltransferase; <b>PDBTitle:</b> crystal structure of avigt4, a glycosyltransferase involved2 in avilamycin a biosynthesis
31	<a href="#">c5hxaA_</a>	Alignment	not modelled	100.0	15	<b>PDB header:</b> protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> alpha,alpha-trehalose-phosphate synthase (udp-forming); <b>PDBTitle:</b> crystal structure of an udp-forming alpha, alpha-trehalose-phosphate2 synthase from burkholderia xenovorans
32	<a href="#">c3nb0A_</a>	Alignment	not modelled	100.0	19	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> glycogen [starch] synthase isoform 2; <b>PDBTitle:</b> glucose-6-phosphate activated form of yeast glycogen synthase
33	<a href="#">c3o3cD_</a>	Alignment	not modelled	100.0	16	<b>PDB header:</b> transferase <b>Chain:</b> D: <b>PDB Molecule:</b> glycogen [starch] synthase isoform 2; <b>PDBTitle:</b> glycogen synthase basal state udp complex
34	<a href="#">d1uqta_</a>	Alignment	not modelled	100.0	14	<b>Fold:</b> UDP-Glycosyltransferase/glycogen phosphorylase <b>Superfamily:</b> UDP-Glycosyltransferase/glycogen phosphorylase <b>Family:</b> Trehalose-6-phosphate synthase, OtsA
35	<a href="#">c2x0dA_</a>	Alignment	not modelled	100.0	9	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> wsaf; <b>PDBTitle:</b> apo structure of wsaf
36	<a href="#">c4pqgB_</a>	Alignment	not modelled	100.0	19	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> glycosyltransferase gtf1; <b>PDBTitle:</b> crystal structure of the pneumococcal o-glcnac transferase gtfA in2 complex with udp and glcnac
37	<a href="#">c4qlbD_</a>	Alignment	not modelled	100.0	16	<b>PDB header:</b> transferase <b>Chain:</b> D: <b>PDB Molecule:</b> probable glycogen [starch] synthase; <b>PDBTitle:</b> structural basis for the recruitment of glycogen synthase by2 glycogenin
38	<a href="#">c5e9tA_</a>	Alignment	not modelled	100.0	17	<b>PDB header:</b> transferase/chaperone <b>Chain:</b> A: <b>PDB Molecule:</b> glycosyltransferase gtf1; <b>PDBTitle:</b> crystal structure of gtfA/b complex
39	<a href="#">c4w6qC_</a>	Alignment	not modelled	100.0	11	<b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> glucosyltransferase; <b>PDBTitle:</b> glycosyltransferase c from streptococcus agalactiae
40	<a href="#">c3rhzB_</a>	Alignment	not modelled	100.0	11	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> nucleotide sugar synthetase-like protein; <b>PDBTitle:</b> structure and functional analysis of a new subfamily of2 glycosyltransferases required for glycosylation of serine-rich3 streptococcal adhesions
41	<a href="#">c5jijA_</a>	Alignment	not modelled	100.0	14	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> alpha,alpha-trehalose-phosphate synthase; <b>PDBTitle:</b> structure of mycobacterium thermoresistibile trehalose-6-phosphate2 synthase (apo form).
42	<a href="#">c3s2uA_</a>	Alignment	not modelled	100.0	16	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> udp-n-acetylglucosamine--n-acetylmuramyl-(pentapeptide) <b>PDBTitle:</b> crystal structure of the pseudomonas aeruginosa murg:udp-glcna2 substrate complex
43	<a href="#">d1f6da_</a>	Alignment	not modelled	100.0	14	<b>Fold:</b> UDP-Glycosyltransferase/glycogen phosphorylase <b>Superfamily:</b> UDP-Glycosyltransferase/glycogen phosphorylase <b>Family:</b> UDP-N-acetylglucosamine 2-epimerase
44	<a href="#">c3ot5D_</a>	Alignment	not modelled	100.0	12	<b>PDB header:</b> isomerase <b>Chain:</b> D: <b>PDB Molecule:</b> udp-n-acetylglucosamine 2-epimerase; <b>PDBTitle:</b> 2.2 angstrom resolution crystal structure of putative udp-n-2 acetylglucosamine 2-epimerase from listeria monocytogenes
45	<a href="#">c4hwgA_</a>	Alignment	not modelled	100.0	11	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> udp-n-acetylglucosamine 2-epimerase; <b>PDBTitle:</b> structure of udp-n-acetylglucosamine 2-epimerase from rickettsia2 bellii
46	<a href="#">c5enzA_</a>	Alignment	not modelled	100.0	10	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> udp-glcna2 2-epimerase; <b>PDBTitle:</b> s. aureus mnaa-udp co-structure
47	<a href="#">c3beoA_</a>	Alignment	not modelled	100.0	11	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> udp-n-acetylglucosamine 2-epimerase; <b>PDBTitle:</b> a structural basis for the allosteric regulation of non-2 hydrolyzing udp-glcna2 2-epimerases
48	<a href="#">c5w8sA_</a>	Alignment	not modelled	100.0	15	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> lipid-a-disaccharide synthase; <b>PDBTitle:</b> lipid a disaccharide synthase (lpxb)-7 solubilizing mutations
49	<a href="#">c5hutB_</a>	Alignment	not modelled	100.0	15	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> alpha,alpha-trehalose-phosphate synthase [udp-forming]; <b>PDBTitle:</b> structure of candida albicans trehalose-6-phosphate synthase in2 complex with udp-glucose
50	<a href="#">c4nesA_</a>	Alignment	not modelled	100.0	10	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> udp-n-acetylglucosamine 2-epimerase; <b>PDBTitle:</b> crystal structure of methanocaldococcus jannaschii udp-glcna2 2-2 epimerase in complex with udp-glcna2 and udp
51	<a href="#">c5dldA_</a>	Alignment	not modelled	100.0	12	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> udp-n-acetylglucosamine 2-epimerase; <b>PDBTitle:</b> crystal structure of a udp-n-acetylglucosamine 2-epimerase from2 burkholderia vietnamiensis complexed with udp-glcna2 and udp
52	<a href="#">c3dzcA_</a>	Alignment	not modelled	100.0	13	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> udp-n-acetylglucosamine 2-epimerase; <b>PDBTitle:</b> 2.35 angstrom resolution structure of webc (vc0917), a udp-n-2 acetylglucosamine 2-epimerase from vibrio cholerae.

53	<a href="#">c2q6vA_</a>	Alignment	not modelled	100.0	12	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> glucuronosyltransferase gumk; <b>PDBTitle:</b> crystal structure of gumk in complex with udp
54	<a href="#">c3ia7A_</a>	Alignment	not modelled	100.0	13	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> calg4; <b>PDBTitle:</b> crystal structure of calg4, the calicheamicin glycosyltransferase
55	<a href="#">d1v4va_</a>	Alignment	not modelled	99.9	13	<b>Fold:</b> UDP-Glycosyltransferase/glycogen phosphorylase <b>Superfamily:</b> UDP-Glycosyltransferase/glycogen phosphorylase <b>Family:</b> UDP-N-acetylglucosamine 2-epimerase
56	<a href="#">c6fj3A_</a>	Alignment	not modelled	99.9	25	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> parathyroid hormone/parathyroid hormone-related peptide <b>PDBTitle:</b> high resolution crystal structure of parathyroid hormone 1 receptor in2 complex with a peptide agonist.
57	<a href="#">d1f0ka_</a>	Alignment	not modelled	99.9	16	<b>Fold:</b> UDP-Glycosyltransferase/glycogen phosphorylase <b>Superfamily:</b> UDP-Glycosyltransferase/glycogen phosphorylase <b>Family:</b> Peptidoglycan biosynthesis glycosyltransferase MurG
58	<a href="#">c3iaaB_</a>	Alignment	not modelled	99.9	15	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> calg2; <b>PDBTitle:</b> crystal structure of calg2, calicheamicin glycosyltransferase, tdp2 bound form
59	<a href="#">c5vafD_</a>	Alignment	not modelled	99.9	12	<b>PDB header:</b> cell adhesion <b>Chain:</b> D: <b>PDB Molecule:</b> accessory sec system protein asp1; <b>PDBTitle:</b> crystal structure of accessory secretion protein 1
60	<a href="#">c5xvsA_</a>	Alignment	not modelled	99.9	12	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> gdp/udp-n,n'-diacetyl bacillosamine 2-epimerase <b>PDBTitle:</b> crystal structure of udp-glcnae 2-epimerase neuc complexed with udp
61	<a href="#">d1o6ca_</a>	Alignment	not modelled	99.9	11	<b>Fold:</b> UDP-Glycosyltransferase/glycogen phosphorylase <b>Superfamily:</b> UDP-Glycosyltransferase/glycogen phosphorylase <b>Family:</b> UDP-N-acetylglucosamine 2-epimerase
62	<a href="#">c3tsaA_</a>	Alignment	not modelled	99.9	13	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> ndp-rhamnosyltransferase; <b>PDBTitle:</b> spinosyn rhamnosyltransferase spng
63	<a href="#">c2xcuC_</a>	Alignment	not modelled	99.9	11	<b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> 3-deoxy-d-manno-2-octulosonic acid transferase; <b>PDBTitle:</b> membrane-embedded monofunctional glycosyltransferase waaa of aquifex2 aeolicus, complex with cmp
64	<a href="#">c5xvmB_</a>	Alignment	not modelled	99.9	15	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> sterol 3-beta-glucosyltransferase; <b>PDBTitle:</b> sterol 3-beta-glucosyltransferase (ugt51) from saccharomyces2 cerevisiae (strain atcc 204508 / s288c)
65	<a href="#">c3t5tA_</a>	Alignment	not modelled	99.9	15	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> putative glycosyltransferase; <b>PDBTitle:</b> vall from streptomyces hygrosopicus in apo form
66	<a href="#">c5dxFA_</a>	Alignment	not modelled	99.9	13	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> trehalose-6-phosphate phosphatase; <b>PDBTitle:</b> structure of candida albicans trehalose-6-phosphate phosphatase n-2 terminal domain
67	<a href="#">c3wadA_</a>	Alignment	not modelled	99.9	14	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> glycosyltransferase; <b>PDBTitle:</b> crystal structure of glycosyltransferase vinc involved in the2 biosynthesis of vicenistatin
68	<a href="#">c3othB_</a>	Alignment	not modelled	99.9	14	<b>PDB header:</b> transferase/antibiotic <b>Chain:</b> B: <b>PDB Molecule:</b> calg1; <b>PDBTitle:</b> crystal structure of calg1, calicheamicin glycosyltransferase, tdp2 and calicheamicin alpha3i bound form
69	<a href="#">c4ambB_</a>	Alignment	not modelled	99.9	16	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> snogd; <b>PDBTitle:</b> crystal structure of the glycosyltransferase snogd from streptomyces2 nogalater
70	<a href="#">c4x1tA_</a>	Alignment	not modelled	99.9	13	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> monogalactosyldiacylglycerol synthase 1, chloroplastic; <b>PDBTitle:</b> the crystal structure of arabidopsis thaliana galactolipid synthase2 mgd1 in complex with udp
71	<a href="#">c5lqdB_</a>	Alignment	not modelled	99.9	16	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> alpha,alpha-trehalose-phosphate synthase; <b>PDBTitle:</b> trehalose-6-phosphate synthase, gdp-glucose-dependent otsa
72	<a href="#">c4rieB_</a>	Alignment	not modelled	99.9	15	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> glycosyl transferase homolog; <b>PDBTitle:</b> landomycin glycosyltransferase langt2
73	<a href="#">c4leiB_</a>	Alignment	not modelled	99.9	11	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> ndp-forosamyltransferase; <b>PDBTitle:</b> spinosyn forosaminyltransferase spnp
74	<a href="#">c5hvoD_</a>	Alignment	not modelled	99.9	15	<b>PDB header:</b> transferase <b>Chain:</b> D: <b>PDB Molecule:</b> alpha,alpha-trehalose-phosphate synthase (udp-forming); <b>PDBTitle:</b> structure of aspergillus fumigatus trehalose-6-phosphate synthase b in2 complex with udp and validoxylamine a
75	<a href="#">c2iyaB_</a>	Alignment	not modelled	99.9	13	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> oleandomycin glycosyltransferase; <b>PDBTitle:</b> the crystal structure of macrolide glycosyltransferases: a blueprint2 for antibiotic engineering
76	<a href="#">c2p6pB_</a>	Alignment	not modelled	99.9	14	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> glycosyl transferase; <b>PDBTitle:</b> x-ray crystal structure of c-c bond-forming dtdp-d-olivose-transferase2 urdgt2
77	<a href="#">c2vsnB_</a>	Alignment	not modelled	99.9	14	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> xcogt; <b>PDBTitle:</b> structure and topological arrangement of an o-glcnae2 transferase homolog: insight into molecular control of3 intracellular

						glycosylation
78	<a href="#">c2lyfA</a>	Alignment	not modelled	99.9	14	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> oleandomycin glycosyltransferase; <b>PDBTitle:</b> the crystal structure of macrolide glycosyltransferases: a2 blueprint for antibiotic engineering
79	<a href="#">c5djsA</a>	Alignment	not modelled	99.9	13	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> tetratricopeptide tpr_2 repeat protein; <b>PDBTitle:</b> thermobaculum terrenum o-glcnae transferase mutant - k341m
80	<a href="#">c5gl5B</a>	Alignment	not modelled	99.9	14	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> sterol 3-beta-glucosyltransferase; <b>PDBTitle:</b> sterol 3-beta-glucosyltransferase (ugt51) from saccharomyces2 cerevisiae (strain atcc 204508 / s288c): udpg complex
81	<a href="#">c5du2B</a>	Alignment	not modelled	99.8	14	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> espg2 glycosyltransferase; <b>PDBTitle:</b> structural analysis of espg2 glycosyltransferase
82	<a href="#">c5i45A</a>	Alignment	not modelled	99.8	21	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> glycosyl transferases group 1 family protein; <b>PDBTitle:</b> 1.35 angstrom crystal structure of c-terminal domain of glycosyl2 transferase group 1 family protein (lpc) from francisella3 tularensis.
83	<a href="#">c5e9uB</a>	Alignment	not modelled	99.8	11	<b>PDB header:</b> transferase/chaperone <b>Chain:</b> B: <b>PDB Molecule:</b> glycosyltransferase-stabilizing protein gtf2; <b>PDBTitle:</b> crystal structure of gtf2 complex bound to udp and glcnae
84	<a href="#">d2f9fa1</a>	Alignment	not modelled	99.8	17	<b>Fold:</b> UDP-Glycosyltransferase/glycogen phosphorylase <b>Superfamily:</b> UDP-Glycosyltransferase/glycogen phosphorylase <b>Family:</b> Glycosyl transferases group 1
85	<a href="#">c3pe3D</a>	Alignment	not modelled	99.8	12	<b>PDB header:</b> transferase <b>Chain:</b> D: <b>PDB Molecule:</b> udp-n-acetylglucosamine--peptide n- <b>PDBTitle:</b> structure of human o-glcnae transferase and its complex with a peptide2 substrate
86	<a href="#">c3d0qB</a>	Alignment	not modelled	99.8	13	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> protein calg3; <b>PDBTitle:</b> crystal structure of calg3 from micromonospora echinospora determined2 in space group i222
87	<a href="#">c4bfcA</a>	Alignment	not modelled	99.7	14	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> 3-deoxy-d-manno-octulosonic-acid transferase; <b>PDBTitle:</b> crystal structure of the c-terminal cmp-kdo binding domain of waaa2 from acinetobacter baumannii
88	<a href="#">d2bfwa1</a>	Alignment	not modelled	99.7	20	<b>Fold:</b> UDP-Glycosyltransferase/glycogen phosphorylase <b>Superfamily:</b> UDP-Glycosyltransferase/glycogen phosphorylase <b>Family:</b> Glycosyl transferases group 1
89	<a href="#">d1iira</a>	Alignment	not modelled	99.7	15	<b>Fold:</b> UDP-Glycosyltransferase/glycogen phosphorylase <b>Superfamily:</b> UDP-Glycosyltransferase/glycogen phosphorylase <b>Family:</b> Gtf glycosyltransferase
90	<a href="#">d1pn3a</a>	Alignment	not modelled	99.6	13	<b>Fold:</b> UDP-Glycosyltransferase/glycogen phosphorylase <b>Superfamily:</b> UDP-Glycosyltransferase/glycogen phosphorylase <b>Family:</b> Gtf glycosyltransferase
91	<a href="#">c4zhtB</a>	Alignment	not modelled	99.6	13	<b>PDB header:</b> isomerase <b>Chain:</b> B: <b>PDB Molecule:</b> bifunctional udp-n-acetylglucosamine 2-epimerase/n- <b>PDBTitle:</b> crystal structure of udp-glcnae 2-epimerase
92	<a href="#">c3qhpB</a>	Alignment	not modelled	99.6	21	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> type 1 capsular polysaccharide biosynthesis protein j <b>PDBTitle:</b> crystal structure of the catalytic domain of cholesterol-alpha-2 glucosyltransferase from helicobacter pylori
93	<a href="#">c4fzrA</a>	Alignment	not modelled	99.6	14	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> ssfs6; <b>PDBTitle:</b> crystal structure of ssfs6, streptomyces sp. sf25752 glycosyltransferase
94	<a href="#">d1rrva</a>	Alignment	not modelled	99.6	13	<b>Fold:</b> UDP-Glycosyltransferase/glycogen phosphorylase <b>Superfamily:</b> UDP-Glycosyltransferase/glycogen phosphorylase <b>Family:</b> Gtf glycosyltransferase
95	<a href="#">d2acva1</a>	Alignment	not modelled	99.3	12	<b>Fold:</b> UDP-Glycosyltransferase/glycogen phosphorylase <b>Superfamily:</b> UDP-Glycosyltransferase/glycogen phosphorylase <b>Family:</b> UDPGT-like
96	<a href="#">c6o86A</a>	Alignment	not modelled	99.2	12	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> udp-glycosyltransferase 76g1; <b>PDBTitle:</b> crystal structure of semet udp-dependent glucosyltransferases (ugt)2 from stevia rebaudiana in complex with udp
97	<a href="#">c3hbjA</a>	Alignment	not modelled	99.2	10	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> flavonoid 3-o-glucosyltransferase; <b>PDBTitle:</b> structure of ugt78g1 complexed with udp
98	<a href="#">c3wc4A</a>	Alignment	not modelled	99.2	10	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> udp-glucose:anthocyanidin 3-o-glucosyltransferase; <b>PDBTitle:</b> crystal structure of udp-glucose: anthocyanidin 3-o-2 glucosyltransferase from clitoria ternatea
99	<a href="#">d2c1xa1</a>	Alignment	not modelled	99.1	10	<b>Fold:</b> UDP-Glycosyltransferase/glycogen phosphorylase <b>Superfamily:</b> UDP-Glycosyltransferase/glycogen phosphorylase <b>Family:</b> UDPGT-like
100	<a href="#">c5nlmB</a>	Alignment	not modelled	99.1	11	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> indoxyl udp-glucosyltransferase; <b>PDBTitle:</b> complex between a udp-glucosyltransferase from polygonum tinctorium2 capable of glucosylating indoxyl and indoxyl sulfate
101	<a href="#">c5tmdA</a>	Alignment	not modelled	99.0	11	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> glycosyltransferase, os79; <b>PDBTitle:</b> crystal structure of os79 from o. sativa in complex with u2f and2 trichothecene. <b>PDB header:</b> transferase



102	<a href="#">c5v2kA_</a>	Alignment	not modelled	99.0	8	<b>Chain:</b> A: <b>PDB Molecule:</b> udp-glycosyltransferase 74f2; <b>PDBTitle:</b> crystal structure of udp-glucosyltransferase, ugt74f2 (t15a), with udp2 and 2-bromobenzoic acid
103	<a href="#">c3q3hA_</a>	Alignment	not modelled	98.9	9	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> hmw1c-like glycosyltransferase; <b>PDBTitle:</b> crystal structure of the actinobacillus pleuropneumoniae hmw1c2 glycosyltransferase in complex with udp-glc
104	<a href="#">c3hbmA_</a>	Alignment	not modelled	98.8	9	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> udp-sugar hydrolase; <b>PDBTitle:</b> crystal structure of pseg from campylobacter jejuni
105	<a href="#">d2pq6a1</a>	Alignment	not modelled	98.7	11	<b>Fold:</b> UDP-Glycosyltransferase/glycogen phosphorylase <b>Superfamily:</b> UDP-Glycosyltransferase/glycogen phosphorylase <b>Family:</b> UDPGT-like
106	<a href="#">c6jtdB_</a>	Alignment	not modelled	98.5	11	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> c-glycosyltransferase; <b>PDBTitle:</b> crystal structure of tccg1 in complex with udp
107	<a href="#">d2vcha1</a>	Alignment	not modelled	98.3	11	<b>Fold:</b> UDP-Glycosyltransferase/glycogen phosphorylase <b>Superfamily:</b> UDP-Glycosyltransferase/glycogen phosphorylase <b>Family:</b> UDPGT-like
108	<a href="#">c2h1fB_</a>	Alignment	not modelled	97.8	13	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> lipopolysaccharide heptosyltransferase-1; <b>PDBTitle:</b> e. coli heptosyltransferase waac with adp
109	<a href="#">c3l7mC_</a>	Alignment	not modelled	97.5	9	<b>PDB header:</b> structural protein <b>Chain:</b> C: <b>PDB Molecule:</b> teichoic acid biosynthesis protein f; <b>PDBTitle:</b> structure of the wall teichoic acid polymerase tagf, h548a
110	<a href="#">c3ddsB_</a>	Alignment	not modelled	97.3	17	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> glycogen phosphorylase, liver form; <b>PDBTitle:</b> crystal structure of glycogen phosphorylase complexed with an2 anthranilimide based inhibitor gsk261
111	<a href="#">c2c4mA_</a>	Alignment	not modelled	97.0	16	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> glycogen phosphorylase; <b>PDBTitle:</b> starch phosphorylase: structural studies explain oxyanion-dependent2 kinetic stability and regulatory control.
112	<a href="#">d2gj4a1</a>	Alignment	not modelled	97.0	17	<b>Fold:</b> UDP-Glycosyltransferase/glycogen phosphorylase <b>Superfamily:</b> UDP-Glycosyltransferase/glycogen phosphorylase <b>Family:</b> Oligosaccharide phosphorylase
113	<a href="#">d1ygpa_</a>	Alignment	not modelled	96.9	14	<b>Fold:</b> UDP-Glycosyltransferase/glycogen phosphorylase <b>Superfamily:</b> UDP-Glycosyltransferase/glycogen phosphorylase <b>Family:</b> Oligosaccharide phosphorylase
114	<a href="#">c2o6IA_</a>	Alignment	not modelled	96.8	13	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> udp-glucuronosyltransferase 2b7; <b>PDBTitle:</b> crystal structure of the udp-glucuronic acid binding domain2 of the human drug metabolizing udp-glucuronosyltransferase3 2b7
115	<a href="#">c4bqeA_</a>	Alignment	not modelled	96.8	12	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> alpha-glucan phosphorylase 2,4-glucan phosphorylase; <b>PDBTitle:</b> arabidopsis thaliana cytosolic alpha-1,4-glucan phosphorylase (phs2)
116	<a href="#">d2atia1</a>	Alignment	not modelled	96.7	17	<b>Fold:</b> UDP-Glycosyltransferase/glycogen phosphorylase <b>Superfamily:</b> UDP-Glycosyltransferase/glycogen phosphorylase <b>Family:</b> Oligosaccharide phosphorylase
117	<a href="#">c3tovB_</a>	Alignment	not modelled	96.6	9	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> glycosyl transferase family 9; <b>PDBTitle:</b> the crystal structure of the glycosyl transferase family 9 from2 veillonella parvula dsm 2008
118	<a href="#">d1pswa_</a>	Alignment	not modelled	96.5	13	<b>Fold:</b> UDP-Glycosyltransferase/glycogen phosphorylase <b>Superfamily:</b> UDP-Glycosyltransferase/glycogen phosphorylase <b>Family:</b> ADP-heptose LPS heptosyltransferase II
119	<a href="#">d1l5wa_</a>	Alignment	not modelled	96.5	16	<b>Fold:</b> UDP-Glycosyltransferase/glycogen phosphorylase <b>Superfamily:</b> UDP-Glycosyltransferase/glycogen phosphorylase <b>Family:</b> Oligosaccharide phosphorylase
120	<a href="#">c4l22A_</a>	Alignment	not modelled	95.9	14	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> phosphorylase; <b>PDBTitle:</b> crystal structure of putative glycogen phosphorylase from2 streptococcus mutans