
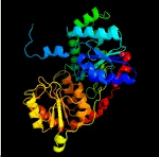
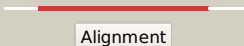

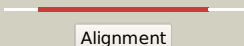







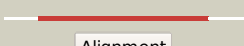











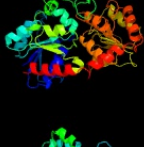
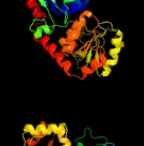
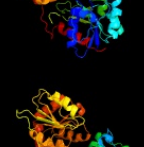

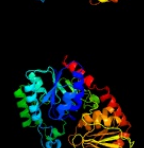

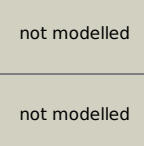


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2962c_(-)_3313783_3315132
Date	Thu Aug 8 16:20:12 BST 2019
Unique Job ID	0debac9cd2794fac

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c5gl5B_	 Alignment		100.0	17	PDB header: transferase Chain: B: PDB Molecule: sterol 3-beta-glucosyltransferase; PDBTitle: sterol 3-beta-glucosyltransferase (ugt51) from saccharomyces2 cerevisiae (strain atcc 204508 / s288c): udpg complex
2	d1rrva_	 Alignment		100.0	20	Fold: UDP-Glycosyltransferase/glycogen phosphorylase Superfamily: UDP-Glycosyltransferase/glycogen phosphorylase Family: Gtf glycosyltransferase
3	d1pn3a_	 Alignment		100.0	18	Fold: UDP-Glycosyltransferase/glycogen phosphorylase Superfamily: UDP-Glycosyltransferase/glycogen phosphorylase Family: Gtf glycosyltransferase
4	c6o86A_	 Alignment		100.0	15	PDB header: transferase Chain: A: PDB Molecule: udp-glycosyltransferase 76g1; PDBTitle: crystal structure of semet udp-dependent glucosyltransferases (ugt)2 from stevia rebaudiana in complex with udp
5	d1iira_	 Alignment		100.0	18	Fold: UDP-Glycosyltransferase/glycogen phosphorylase Superfamily: UDP-Glycosyltransferase/glycogen phosphorylase Family: Gtf glycosyltransferase
6	c5v2kA_	 Alignment		100.0	14	PDB header: transferase Chain: A: PDB Molecule: udp-glycosyltransferase 74f2; PDBTitle: crystal structure of udp-glucosyltransferase, ugt74f2 (t15a), with udp2 and 2-bromobenzoic acid
7	c3wc4A_	 Alignment		100.0	13	PDB header: transferase Chain: A: PDB Molecule: udp-glucose:anthocyanidin 3-o-glucosyltransferase; PDBTitle: crystal structure of udp-glucose: anthocyanidin 3-o-2 glucosyltransferase from clitoria ternatea
8	d2vcha1	 Alignment		100.0	12	Fold: UDP-Glycosyltransferase/glycogen phosphorylase Superfamily: UDP-Glycosyltransferase/glycogen phosphorylase Family: UDPGT-like
9	c5nlmB_	 Alignment		100.0	10	PDB header: transferase Chain: B: PDB Molecule: indoxyl udp-glucosyltransferase; PDBTitle: complex between a udp-glucosyltransferase from polygonum tinctorium2 capable of glucosylating indoxyl and indoxyl sulfate
10	d2pq6a1	 Alignment		100.0	12	Fold: UDP-Glycosyltransferase/glycogen phosphorylase Superfamily: UDP-Glycosyltransferase/glycogen phosphorylase Family: UDPGT-like
11	c5tmdA_	 Alignment		100.0	14	PDB header: transferase Chain: A: PDB Molecule: glycosyltransferase, os79; PDBTitle: crystal structure of os79 from o. sativa in complex with u2f and 2 trichothecene.

12	d2acva1	Alignment		100.0	13	Fold: UDP-Glycosyltransferase/glycogen phosphorylase Superfamily: UDP-Glycosyltransferase/glycogen phosphorylase Family: UDPGT-like
13	c6jtdB_	Alignment		100.0	14	PDB header: transferase Chain: B: PDB Molecule: c-glycosyltransferase; PDBTitle: crystal structure of tccgt1 in complex with udp
14	c3hbjA_	Alignment		100.0	13	PDB header: transferase Chain: A: PDB Molecule: flavonoid 3-o-glycosyltransferase; PDBTitle: structure of ugt78g1 complexed with udp
15	c4fzrA_	Alignment		100.0	22	PDB header: transferase Chain: A: PDB Molecule: ssfs6; PDBTitle: crystal structure of ssfs6, streptomyces sp. sf25752 glycosyltransferase
16	d2c1xa1	Alignment		100.0	14	Fold: UDP-Glycosyltransferase/glycogen phosphorylase Superfamily: UDP-Glycosyltransferase/glycogen phosphorylase Family: UDPGT-like
17	c5du2B_	Alignment		100.0	17	PDB header: transferase Chain: B: PDB Molecule: espg2 glycosyltransferase; PDBTitle: structural analysis of espg2 glycosyltransferase
18	c5xvmB_	Alignment		100.0	15	PDB header: transferase Chain: B: PDB Molecule: sterol 3-beta-glycosyltransferase; PDBTitle: sterol 3-beta-glycosyltransferase (ugt51) from saccharomyces2 cerevisiae (strain atcc 204508 / s288c)
19	c3iaaB_	Alignment		100.0	18	PDB header: transferase Chain: B: PDB Molecule: calg2; PDBTitle: crystal structure of calg2, calicheamicin glycosyltransferase, tdp2 bound form
20	c3othB_	Alignment		100.0	29	PDB header: transferase/antibiotic Chain: B: PDB Molecule: calg1; PDBTitle: crystal structure of calg1, calicheamicin glycosyltransferase, tdp2 and calicheamicin alpha3i bound form
21	c2p6pB_	Alignment	not modelled	100.0	20	PDB header: transferase Chain: B: PDB Molecule: glycosyl transferase; PDBTitle: x-ray crystal structure of c-c bond-forming dtdp-d-olivose-transferase2 urdgt2
22	c3d0qB_	Alignment	not modelled	100.0	21	PDB header: transferase Chain: B: PDB Molecule: protein calg3; PDBTitle: crystal structure of calg3 from micromonospora echinospora determined2 in space group i222
23	c3ia7A_	Alignment	not modelled	100.0	19	PDB header: transferase Chain: A: PDB Molecule: calg4; PDBTitle: crystal structure of calg4, the calicheamicin glycosyltransferase
24	c2iyfA_	Alignment	not modelled	100.0	15	PDB header: transferase Chain: A: PDB Molecule: oleandomycin glycosyltransferase; PDBTitle: the crystal structure of macrolide glycosyltransferases: a2 blueprint for antibiotic engineering
25	c3wadA_	Alignment	not modelled	100.0	21	PDB header: transferase Chain: A: PDB Molecule: glycosyltransferase; PDBTitle: crystal structure of glycosyltransferase vinc involved in the2 biosynthesis of vicienistatin
26	c3tsaA_	Alignment	not modelled	100.0	22	PDB header: transferase Chain: A: PDB Molecule: ndp-rhamnosyltransferase; PDBTitle: spinosyn rhamnosyltransferase spng
27	c2iyaB_	Alignment	not modelled	100.0	17	PDB header: transferase Chain: B: PDB Molecule: oleandomycin glycosyltransferase; PDBTitle: the crystal structure of macrolide glycosyltransferases: a blueprint2 for antibiotic engineering
28	c4ambB_	Alignment	not modelled	100.0	21	PDB header: transferase Chain: B: PDB Molecule: snogd; PDBTitle: crystal structure of the glycosyltransferase snogd from streptomyces2 nogalater

29	c4rieB_	Alignment	not modelled	100.0	24	PDB header: transferase Chain: B: PDB Molecule: glycosyl transferase homolog; PDBTitle: landomycin glycosyltransferase langt2
30	c4leiB_	Alignment	not modelled	100.0	20	PDB header: transferase Chain: B: PDB Molecule: ndp-forosamyltransferase; PDBTitle: spinosyn forosaminytransferase spnp
31	c3hbmA_	Alignment	not modelled	100.0	15	PDB header: hydrolase Chain: A: PDB Molecule: udp-sugar hydrolase; PDBTitle: crystal structure of pseg from campylobacter jejuni
32	c2o6lA_	Alignment	not modelled	100.0	20	PDB header: transferase Chain: A: PDB Molecule: udp-glucuronosyltransferase 2b7; PDBTitle: crystal structure of the udp-glucuronic acid binding domain2 of the human drug metabolizing udp-glucuronosyltransferase3 2b7
33	c3s2uA_	Alignment	not modelled	100.0	25	PDB header: transferase Chain: A: PDB Molecule: udp-n-acetylglucosamine--n-acetylmuramyl-(pentapeptide) PDBTitle: crystal structure of the pseudomonas aeruginosa murg:udp-glcna2 substrate complex
34	d1f0ka_	Alignment	not modelled	100.0	22	Fold: UDP-Glycosyltransferase/glycogen phosphorylase Superfamily: UDP-Glycosyltransferase/glycogen phosphorylase Family: Peptidoglycan biosynthesis glycosyltransferase MurG
35	d1v4va_	Alignment	not modelled	99.9	17	Fold: UDP-Glycosyltransferase/glycogen phosphorylase Superfamily: UDP-Glycosyltransferase/glycogen phosphorylase Family: UDP-N-acetylglucosamine 2-epimerase
36	d1f6da_	Alignment	not modelled	99.8	15	Fold: UDP-Glycosyltransferase/glycogen phosphorylase Superfamily: UDP-Glycosyltransferase/glycogen phosphorylase Family: UDP-N-acetylglucosamine 2-epimerase
37	c2r60A_	Alignment	not modelled	99.8	13	PDB header: transferase Chain: A: PDB Molecule: glycosyl transferase, group 1; PDBTitle: structure of apo sucrose phosphate synthase (sps) of2 halothermothrix orenii
38	c3beoA_	Alignment	not modelled	99.8	14	PDB header: isomerase Chain: A: PDB Molecule: udp-n-acetylglucosamine 2-epimerase; PDBTitle: a structural basis for the allosteric regulation of non-2 hydrolyzing udp-glcna2 2-epimerases
39	c5dldA_	Alignment	not modelled	99.8	14	PDB header: isomerase Chain: A: PDB Molecule: udp-n-acetylglucosamine 2-epimerase; PDBTitle: crystal structure of a udp-n-acetylglucosamine 2-epimerase from2 burkholderia vietnamiensis complexed with udp-glcna2 and udp
40	c3ot5D_	Alignment	not modelled	99.8	14	PDB header: isomerase Chain: D: PDB Molecule: udp-n-acetylglucosamine 2-epimerase; PDBTitle: 2.2 angstrom resolution crystal structure of putative udp-n-2 acetylglucosamine 2-epimerase from listeria monocytogenes
41	d1o6ca_	Alignment	not modelled	99.8	14	Fold: UDP-Glycosyltransferase/glycogen phosphorylase Superfamily: UDP-Glycosyltransferase/glycogen phosphorylase Family: UDP-N-acetylglucosamine 2-epimerase
42	c4hwgA_	Alignment	not modelled	99.8	13	PDB header: isomerase Chain: A: PDB Molecule: udp-n-acetylglucosamine 2-epimerase; PDBTitle: structure of udp-n-acetylglucosamine 2-epimerase from rickettsia2 bellii
43	c3dzcA_	Alignment	not modelled	99.8	15	PDB header: isomerase Chain: A: PDB Molecule: udp-n-acetylglucosamine 2-epimerase; PDBTitle: 2.35 angstrom resolution structure of webc (vc0917), a udp-n-2 acetylglucosamine 2-epimerase from vibrio cholerae.
44	c5enzA_	Alignment	not modelled	99.8	13	PDB header: isomerase Chain: A: PDB Molecule: udp-glcna2 2-epimerase; PDBTitle: s. aureus mnaa-udp co-structure
45	c5w8sA_	Alignment	not modelled	99.8	18	PDB header: transferase Chain: A: PDB Molecule: lipid-a-disaccharide synthase; PDBTitle: lipid a disaccharide synthase (lpxb)-7 solubilizing mutations
46	c3c4vB_	Alignment	not modelled	99.7	15	PDB header: transferase Chain: B: PDB Molecule: predicted glycosyltransferases; PDBTitle: 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.
47	c4nesA_	Alignment	not modelled	99.7	15	PDB header: isomerase Chain: A: PDB Molecule: udp-n-acetylglucosamine 2-epimerase; PDBTitle: crystal structure of methanocaldococcus jannaschii udp-glcna2 2-2 epimerase in complex with udp-glcna2 and udp
48	c2x6rA_	Alignment	not modelled	99.7	15	PDB header: isomerase Chain: A: PDB Molecule: trehalose-synthase tret; PDBTitle: crystal structure of trehalose synthase tret from p.2 horikoshi produced by soaking in trehalose
49	c4x1tA_	Alignment	not modelled	99.7	15	PDB header: transferase Chain: A: PDB Molecule: monogalactosyldiacylglycerol synthase 1, chloroplastic; PDBTitle: the crystal structure of arabidopsis thaliana galactolipid synthase2 mgd1 in complex with udp
50	c2xmpB_	Alignment	not modelled	99.7	16	PDB header: sugar binding protein Chain: B: PDB Molecule: trehalose-synthase tret; PDBTitle: crystal structure of trehalose synthase tret mutant e326a2 from p.horishiki in complex with udp
51	c3okaA_	Alignment	not modelled	99.7	16	PDB header: transferase Chain: A: PDB Molecule: gdp-mannose-dependent alpha-(1-6)-phosphatidylinositol PDBTitle: crystal structure of corynebacterium glutamicum pimb' in complex with2 gdp-man (triclinic crystal form)
52	c6d9tA_	Alignment	not modelled	99.6	13	PDB header: transferase Chain: A: PDB Molecule: glycosyl transferase; PDBTitle: bsha from staphylococcus aureus complexed with udp
53	c2qeIA_	Alignment	not modelled	99.6	16	PDB header: transferase Chain: A: PDB Molecule: phosphatidylinositol mannosyltransferase (pima); PDBTitle: crystal structure of phosphatidylinositol

						mannosyltransferase (pima)2 from mycobacterium smegmatis in complex with gdp-man
54	c5d00A_	Alignment	not modelled	99.6	12	PDB header: transferase Chain: A: PDB Molecule: n-acetyl-alpha-d-glucosaminyl l-malate synthase; PDBTitle: crystal structure of bsha from b. subtilis complexed with n-2 acetylglucosaminyl-malate and ump
55	c2qzsA_	Alignment	not modelled	99.6	12	PDB header: transferase Chain: A: PDB Molecule: glycogen synthase; PDBTitle: crystal structure of wild-type e.coli gs in complex with adp and2 glucose(wtgsb)
56	c2jzcA_	Alignment	not modelled	99.6	14	PDB header: transferase Chain: A: PDB Molecule: udp-n-acetylglucosamine transferase subunit PDBTitle: nmr solution structure of alg13: the sugar donor subunit of2 a yeast n-acetylglucosamine transferase. northeast3 structural genomics consortium target yg1
57	c2jjmH_	Alignment	not modelled	99.6	12	PDB header: transferase Chain: H: PDB Molecule: glycosyl transferase, group 1 family protein; PDBTitle: crystal structure of a family gt4 glycosyltransferase from bacillus2 anthracis orf ba1558.
58	c4xsuB_	Alignment	not modelled	99.6	16	PDB header: transferase Chain: B: PDB Molecule: alr3699 protein; PDBTitle: crystal structure of anaebaena alr3699/hepe in complex with udp and2 glucose
59	c3s29C_	Alignment	not modelled	99.6	11	PDB header: transferase Chain: C: PDB Molecule: sucrose synthase 1; PDBTitle: the crystal structure of sucrose synthase-1 from arabidopsis thaliana2 and its functional implications.
60	c6ejjA_	Alignment	not modelled	99.6	15	PDB header: transferase Chain: A: PDB Molecule: wlac protein; PDBTitle: structure of a glycosyltransferase
61	c5xvsA_	Alignment	not modelled	99.6	12	PDB header: hydrolase Chain: A: PDB Molecule: gdp/udp-n,n'-diacetylbaucillosamine 2-epimerase PDBTitle: crystal structure of udp-glcna 2-epimerase neuc complexed with udp
62	c5zesA_	Alignment	not modelled	99.5	12	PDB header: transferase Chain: A: PDB Molecule: udp-glucose:tetrahydrobiopterin glycosyltransferase; PDBTitle: udp glucose alpha tetrahydrobiopterin glycosyltransferase from2 synechococcus species pcc 7942 - udp complex
63	d2iw1a1	Alignment	not modelled	99.5	14	Fold: UDP-Glycosyltransferase/glycogen phosphorylase Superfamily: UDP-Glycosyltransferase/glycogen phosphorylase Family: Glycosyl transferases group 1
64	c4hlnA_	Alignment	not modelled	99.5	12	PDB header: transferase Chain: A: PDB Molecule: starch synthase i; PDBTitle: structure of barley starch synthase i in complex with2 maltooligosaccharide
65	c2xcuC_	Alignment	not modelled	99.5	14	PDB header: transferase Chain: C: PDB Molecule: 3-deoxy-d-manno-2-octulosonic acid transferase; PDBTitle: membrane-embedded monofunctional glycosyltransferase waaa of aquifex2 aeolicus, complex with cmp
66	d1rzua_	Alignment	not modelled	99.5	13	Fold: UDP-Glycosyltransferase/glycogen phosphorylase Superfamily: UDP-Glycosyltransferase/glycogen phosphorylase Family: Glycosyl transferases group 1
67	c6gneB_	Alignment	not modelled	99.5	14	PDB header: transferase Chain: B: PDB Molecule: probable starch synthase 4, chloroplastic/amyloplastic; PDBTitle: catalytic domain of starch synthase iv from arabidopsis thaliana bound2 to adp and acarbose
68	c4xywA_	Alignment	not modelled	99.5	9	PDB header: transferase Chain: A: PDB Molecule: o-antigen biosynthesis glycosyltransferase wbnh; PDBTitle: glycosyltransferases wbnh
69	c3oy2A_	Alignment	not modelled	99.5	15	PDB header: viral protein,transferase Chain: A: PDB Molecule: glycosyltransferase b736); PDBTitle: crystal structure of a putative glycosyltransferase from paramecium2 bursaria chlorella virus ny2a
70	c6gnfC_	Alignment	not modelled	99.4	10	PDB header: transferase Chain: C: PDB Molecule: glycogen synthase; PDBTitle: granule bound starch synthase from cyanobacterium sp. clg1 bound to2 acarbose and adp
71	d2bisa1	Alignment	not modelled	99.4	12	Fold: UDP-Glycosyltransferase/glycogen phosphorylase Superfamily: UDP-Glycosyltransferase/glycogen phosphorylase Family: Glycosyl transferases group 1
72	c4rbdD_	Alignment	not modelled	99.4	13	PDB header: transferase Chain: D: PDB Molecule: sucrose synthase:glycosyl transferases group 1; PDBTitle: the crystal structure of nitrosomonas europaea sucrose synthase:2 insights into the evolutionary origin of sucrose metabolism in3 prokaryotes
73	c3vufA_	Alignment	not modelled	99.4	12	PDB header: transferase Chain: A: PDB Molecule: granule-bound starch synthase 1, PDBTitle: crystal structure of rice granule bound starch synthase i catalytic2 domain in complex with adp
74	c2x0dA_	Alignment	not modelled	99.4	13	PDB header: transferase Chain: A: PDB Molecule: wsaf; PDBTitle: apo structure of wsaf
75	c4zhtB_	Alignment	not modelled	99.4	14	PDB header: isomerase Chain: B: PDB Molecule: bifunctional udp-n-acetylglucosamine 2-epimerase/n- PDBTitle: crystal structure of udp-glcna 2-epimerase
76	c2vsnB_	Alignment	not modelled	99.3	14	PDB header: transferase Chain: B: PDB Molecule: xcogt; PDBTitle: structure and topological arrangement of an o-glcna 2 transferase homolog: insight into molecular control of3 intracellular glycosylation

77	c2iv3B_	Alignment	not modelled	99.2	16	PDB header: transferase Chain: B: PDB Molecule: glycosyltransferase; PDBTitle: crystal structure of avigt4, a glycosyltransferase involved2 in avilamycin a biosynthesis
78	c6gngB_	Alignment	not modelled	99.1	14	PDB header: transferase Chain: B: PDB Molecule: granule-bound starch synthase; PDBTitle: granule bound starch synthase i from cyanophora paradoxa bound to2 acarbose and adp
79	c1uquB_	Alignment	not modelled	99.1	11	PDB header: synthase Chain: B: PDB Molecule: alpha, alpha-trehalose-phosphate synthase; PDBTitle: trehalose-6-phosphate from e. coli bound with udp-glucose.
80	c5v0tB_	Alignment	not modelled	99.1	11	PDB header: transferase Chain: B: PDB Molecule: alpha,alpha-trehalose-phosphate synthase (udp-forming); PDBTitle: crystal structure of an alpha,alpha-trehalose-phosphate synthase (udp-2 forming) from burkholderia xenovorans in complex with glucose-6-3 phosphate
81	c5djsA_	Alignment	not modelled	99.1	19	PDB header: transferase Chain: A: PDB Molecule: tetratricopeptide tpr_2 repeat protein; PDBTitle: thermobaculum terrenum o-glcnae transferase mutant - k341m
82	c5n80A_	Alignment	not modelled	99.1	15	PDB header: transferase Chain: A: PDB Molecule: lipopolysaccharide 1,6-galactosyltransferase; PDBTitle: glycosyltransferase lps biosynthesis in complex with udp
83	c2q6vA_	Alignment	not modelled	99.1	9	PDB header: transferase Chain: A: PDB Molecule: glucuronosyltransferase gumk; PDBTitle: crystal structure of gumk in complex with udp
84	c5hxaA_	Alignment	not modelled	99.0	11	PDB header: protein binding Chain: A: PDB Molecule: alpha,alpha-trehalose-phosphate synthase (udp-forming); PDBTitle: crystal structure of an udp-forming alpha, alpha-terhalose-phosphate2 synthase from burkholderia xenovorans
85	c6fj3A_	Alignment	not modelled	98.9	20	PDB header: membrane protein Chain: A: PDB Molecule: parathyroid hormone/parathyroid hormone-related peptide PDBTitle: high resolution crystal structure of parathyroid hormone 1 receptor in2 complex with a peptide agonist.
86	c3pe3D_	Alignment	not modelled	98.8	17	PDB header: transferase Chain: D: PDB Molecule: udp-n-acetylglucosamine--peptide n- PDBTitle: structure of human o-glcnae transferase and its complex with a peptide2 substrate
87	c4x7pB_	Alignment	not modelled	98.8	16	PDB header: transferase Chain: B: PDB Molecule: tarm; PDBTitle: crystal structure of apo s. aureus tarm
88	c3tovB_	Alignment	not modelled	98.7	13	PDB header: transferase Chain: B: PDB Molecule: glycosyl transferase family 9; PDBTitle: the crystal structure of the glycosyl transferase family 9 from2 veillonella parvula dsm 2008
89	c5jijA_	Alignment	not modelled	98.7	12	PDB header: transferase Chain: A: PDB Molecule: alpha,alpha-trehalose-phosphate synthase; PDBTitle: structure of mycobacterium thermoresistibile trehalose-6-phosphate2 synthase (apo form).
90	c4bfcA_	Alignment	not modelled	98.7	14	PDB header: transferase Chain: A: PDB Molecule: 3-deoxy-d-manno-octulosonic-acid transferase; PDBTitle: crystal structure of the c-terminal cmp-kdo binding domain of waaa2 from acinetobacter baumannii
91	c5e9tA_	Alignment	not modelled	98.6	16	PDB header: transferase/chaperone Chain: A: PDB Molecule: glycosyltransferase gtf1; PDBTitle: crystal structure of gtfa/b complex
92	c3rhzB_	Alignment	not modelled	98.6	20	PDB header: transferase Chain: B: PDB Molecule: nucleotide sugar synthetase-like protein; PDBTitle: structure and functional analysis of a new subfamily of2 glycosyltransferases required for glycosylation of serine-rich3 streptococcal adhesions
93	c4pqgB_	Alignment	not modelled	98.6	19	PDB header: transferase Chain: B: PDB Molecule: glycosyltransferase gtf1; PDBTitle: crystal structure of the pneumococcal o-glcnae transferase gtfa in2 complex with udp and glcnae
94	d2f9fa1	Alignment	not modelled	98.5	19	Fold: UDP-Glycosyltransferase/glycogen phosphorylase Superfamily: UDP-Glycosyltransferase/glycogen phosphorylase Family: Glycosyl transferases group 1
95	d1pswa_	Alignment	not modelled	98.5	15	Fold: UDP-Glycosyltransferase/glycogen phosphorylase Superfamily: UDP-Glycosyltransferase/glycogen phosphorylase Family: ADP-heptose LPS heptosyltransferase II
96	d1uqta_	Alignment	not modelled	98.5	11	Fold: UDP-Glycosyltransferase/glycogen phosphorylase Superfamily: UDP-Glycosyltransferase/glycogen phosphorylase Family: Trehalose-6-phosphate synthase, OtsA
97	c4w6qC_	Alignment	not modelled	98.3	14	PDB header: transferase Chain: C: PDB Molecule: glucosyltransferase; PDBTitle: glycosyltransferase c from streptococcus agalactiae
98	c5i45A_	Alignment	not modelled	98.1	18	PDB header: transferase Chain: A: PDB Molecule: glycosyl transferases group 1 family protein; PDBTitle: 1.35 angstrom crystal structure of c-terminal domain of glycosyl2 transferase group 1 family protein (lpc) from francisella3 tularensis.
99	c3q3hA_	Alignment	not modelled	98.1	12	PDB header: transferase Chain: A: PDB Molecule: hmw1c-like glycosyltransferase; PDBTitle: crystal structure of the actinobacillus pleuropneumoniae hmw1c2 glycosyltransferase in complex with udp-glc
100	c5hutB_	Alignment	not modelled	98.1	9	PDB header: transferase Chain: B: PDB Molecule: alpha,alpha-trehalose-phosphate synthase [udp-forming];

						PDBTitle: structure of candida albicans trehalose-6-phosphate synthase in2 complex with udp-glucose
101	c3qhpB_	Alignment	not modelled	98.0	12	PDB header: transferase Chain: B: PDB Molecule: type 1 capsular polysaccharide biosynthesis protein j PDBTitle: crystal structure of the catalytic domain of cholesterol-alpha-2 glucosyltransferase from helicobacter pylori
102	c3t5tA_	Alignment	not modelled	97.8	14	PDB header: transferase Chain: A: PDB Molecule: putative glycosyltransferase; PDBTitle: vall from streptomyces hygroscopicus in apo form
103	c2h1fB_	Alignment	not modelled	97.7	13	PDB header: transferase Chain: B: PDB Molecule: lipopolysaccharide heptosyltransferase-1; PDBTitle: e. coli heptosyltransferase waac with adp
104	c5dxfA_	Alignment	not modelled	97.6	9	PDB header: hydrolase Chain: A: PDB Molecule: trehalose-6-phosphate phosphatase; PDBTitle: structure of candida albicans trehalose-6-phosphate phosphatase n-2 terminal domain
105	c5vafD_	Alignment	not modelled	97.6	16	PDB header: cell adhesion Chain: D: PDB Molecule: accessory sec system protein asp1; PDBTitle: crystal structure of accessory secretion protein 1
106	c5hvoD_	Alignment	not modelled	97.4	14	PDB header: transferase Chain: D: PDB Molecule: alpha,alpha-trehalose-phosphate synthase (udp-forming); PDBTitle: structure of aspergillus fumigatus trehalose-6-phosphate synthase b in2 complex with udp and validoxylamine a
107	d2bfwa1	Alignment	not modelled	97.4	16	Fold: UDP-Glycosyltransferase/glycogen phosphorylase Superfamily: UDP-Glycosyltransferase/glycogen phosphorylase Family: Glycosyl transferases group 1
108	c5e9uB_	Alignment	not modelled	97.4	14	PDB header: transferase/chaperone Chain: B: PDB Molecule: glycosyltransferase-stabilizing protein gtf2; PDBTitle: crystal structure of gtfA/b complex bound to udp and glcnac
109	c3nb0A_	Alignment	not modelled	97.2	15	PDB header: transferase Chain: A: PDB Molecule: glycogen [starch] synthase isoform 2; PDBTitle: glucose-6-phosphate activated form of yeast glycogen synthase
110	c3o3cD_	Alignment	not modelled	96.9	10	PDB header: transferase Chain: D: PDB Molecule: glycogen [starch] synthase isoform 2; PDBTitle: glycogen synthase basal state udp complex
111	c5lqdB_	Alignment	not modelled	96.8	18	PDB header: transferase Chain: B: PDB Molecule: alpha,alpha-trehalose-phosphate synthase; PDBTitle: trehalose-6-phosphate synthase, gdp-glucose-dependent otsa
112	c4qlbD_	Alignment	not modelled	96.3	11	PDB header: transferase Chain: D: PDB Molecule: probable glycogen [starch] synthase; PDBTitle: structural basis for the recruitment of glycogen synthase by2 glycogenin
113	c3l7mC_	Alignment	not modelled	96.0	13	PDB header: structural protein Chain: C: PDB Molecule: teichoic acid biosynthesis protein f; PDBTitle: structure of the wall teichoic acid polymerase tagf, h548a
114	c5xr2D_	Alignment	not modelled	95.4	18	PDB header: chaperone Chain: D: PDB Molecule: protein/nucleic acid deglycase hcha; PDBTitle: sav0551
115	c4i2nC_	Alignment	not modelled	94.3	20	PDB header: hydrolase Chain: C: PDB Molecule: intracellular protease/amidase; PDBTitle: crystal structure of 31kd heat shock protein, vchsp31 from vibrio2 cholerae
116	c6qlgD_	Alignment	not modelled	94.2	18	PDB header: transferase Chain: D: PDB Molecule: flavin prenyltransferase pad1, mitochondrial; PDBTitle: crystal structure of anubix (pada1) in complex with fm and2 dimethylallyl pyrophosphate
117	c5bmoB_	Alignment	not modelled	94.0	17	PDB header: hydrolase Chain: B: PDB Molecule: putative uncharacterized protein lnmx; PDBTitle: lnmx protein, a putative glcnac-pi de-n-acetylase from streptomyces2 atroolivaceus
118	d1n57a_	Alignment	not modelled	94.0	20	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: DJ-1/Pfpl
119	c3dfiA_	Alignment	not modelled	94.0	18	PDB header: hydrolase Chain: A: PDB Molecule: pseudoaglycone deacetylase dbv21; PDBTitle: the crystal structure of antimicrobial reagent a40926 pseudoaglycone2 deacetylase dbv21
120	c4qeaG_	Alignment	not modelled	94.0	20	PDB header: hydrolase Chain: G: PDB Molecule: 5'-nucleotidase sure; PDBTitle: crystal structure of stationary phase survival protein (sure) from2 brucella abortus