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Email	mdejesus@rockefeller.edu
Description	RVBD3490_otsA_3908415_3909917
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Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c5dxfA_	 Alignment		100.0	27	PDB header: hydrolase Chain: A: PDB Molecule: trehalose-6-phosphate phosphatase; PDBTitle: structure of candida albicans trehalose-6-phosphate phosphatase n-2 terminal domain
2	c5hvoD_	 Alignment		100.0	35	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
3	c3t5tA_	 Alignment		100.0	23	PDB header: transferase Chain: A: PDB Molecule: putative glycosyltransferase; PDBTitle: vall from streptomyces hygrosopicus in apo form
4	c5lqdB_	 Alignment		100.0	35	PDB header: transferase Chain: B: PDB Molecule: alpha,alpha-trehalose-phosphate synthase; PDBTitle: trehalose-6-phosphate synthase, gdp-glucose-dependent otsa
5	c5jijA_	 Alignment		100.0	82	PDB header: transferase Chain: A: PDB Molecule: alpha,alpha-trehalose-phosphate synthase; PDBTitle: structure of mycobacterium thermoresistibile trehalose-6-phosphate2 synthase (apo form).
6	c5hutB_	 Alignment		100.0	37	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
7	d1uqta_	 Alignment		100.0	33	Fold: UDP-Glycosyltransferase/glycogen phosphorylase Superfamily: UDP-Glycosyltransferase/glycogen phosphorylase Family: Trehalose-6-phosphate synthase, OtsA
8	c5hxaA_	 Alignment		100.0	36	PDB header: protein binding Chain: A: PDB Molecule: alpha,alpha-trehalose-phosphate synthase (udp-forming); PDBTitle: crystal structure of an udp-forming alpha, alpha-trehalose-phosphate2 synthase from burkholderia xenovorans
9	c1uquB_	 Alignment		100.0	33	PDB header: synthase Chain: B: PDB Molecule: alpha, alpha-trehalose-phosphate synthase; PDBTitle: trehalose-6-phosphate from e. coli bound with udp-glucose.
10	c5v0tB_	 Alignment		100.0	33	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
11	c3o3cD_	 Alignment		100.0	14	PDB header: transferase Chain: D: PDB Molecule: glycogen [starch] synthase isoform 2; PDBTitle: glycogen synthase basal state udp complex

12	c3nb0A_	Alignment		100.0	15	PDB header: transferase Chain: A: PDB Molecule: glycogen [starch] synthase isoform 2; PDBTitle: glucose-6-phosphate activated form of yeast glycogen synthase
13	c3s29C_	Alignment		100.0	14	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.
14	c2xmpB_	Alignment		100.0	17	PDB header: sugar binding protein Chain: B: PDB Molecule: trehalose-synthase tret; PDBTitle: crystal structure of trehalose synthase tret mutant e326a2 from Pichia horishiki in complex with UDP
15	c2x6rA_	Alignment		100.0	18	PDB header: isomerase Chain: A: PDB Molecule: trehalose-synthase tret; PDBTitle: crystal structure of trehalose synthase tret from Pichia horikoshi produced by soaking in trehalose
16	c4qlbD_	Alignment		100.0	14	PDB header: transferase Chain: D: PDB Molecule: probable glycogen [starch] synthase; PDBTitle: structural basis for the recruitment of glycogen synthase by2 glycogenin
17	c4hlnA_	Alignment		100.0	16	PDB header: transferase Chain: A: PDB Molecule: starch synthase i; PDBTitle: structure of barley starch synthase i in complex with maltotriose
18	c2r60A_	Alignment		100.0	16	PDB header: transferase Chain: A: PDB Molecule: glycosyl transferase, group 1; PDBTitle: structure of apo sucrose phosphate synthase (sps) of Haloferox volcanii
19	c4rbnD_	Alignment		100.0	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 in prokaryotes
20	c6gneB_	Alignment		100.0	14	PDB header: transferase Chain: B: PDB Molecule: probable starch synthase 4, chloroplastic/amyloplastic; PDBTitle: catalytic domain of starch synthase iv from Arabidopsis thaliana bound to ADP and acarbose
21	c6gngB_	Alignment	not modelled	100.0	15	PDB header: transferase Chain: B: PDB Molecule: granule-bound starch synthase; PDBTitle: granule bound starch synthase i from Cyanophora paradoxa bound to 2 acarbose and ADP
22	d2bisa1	Alignment	not modelled	100.0	15	Fold: UDP-Glycosyltransferase/glycogen phosphorylase Superfamily: UDP-Glycosyltransferase/glycogen phosphorylase Family: Glycosyl transferases group 1
23	c6gnfC_	Alignment	not modelled	100.0	13	PDB header: transferase Chain: C: PDB Molecule: glycogen synthase; PDBTitle: granule bound starch synthase from cyanobacterium sp. clg1 bound to 2 acarbose and ADP
24	c3c4vB_	Alignment	not modelled	100.0	17	PDB header: transferase Chain: B: PDB Molecule: predicted glycosyltransferases; PDBTitle: structure of the retaining glycosyltransferase MSHA:the 2 nd first step in mycothiol biosynthesis. organism:3 Corynebacterium glutamicum : complex with UDP and 1l-ins-1-4 p.
25	c2qzsA_	Alignment	not modelled	100.0	17	PDB header: transferase Chain: A: PDB Molecule: glycogen synthase; PDBTitle: crystal structure of wild-type E. coli GS in complex with ADP and 2 glucose (wtgsb)
26	c3vufA_	Alignment	not modelled	100.0	18	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
27	d1rzua_	Alignment	not modelled	100.0	14	Fold: UDP-Glycosyltransferase/glycogen phosphorylase Superfamily: UDP-Glycosyltransferase/glycogen phosphorylase Family: Glycosyl transferases group 1
28	c6fj3A_	Alignment	not modelled	100.0	18	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.
29	c4x7pB	Alignment	not modelled	100.0	12	PDB header: transferase Chain: B: PDB Molecule: tarm; PDBTitle: crystal structure of apo s. aureus tarm
30	c3oy2A	Alignment	not modelled	100.0	12	PDB header: viral protein,transferase Chain: A: PDB Molecule: glycosyltransferase b7361; PDBTitle: crystal structure of a putative glycosyltransferase from paramecium2 bursaria chlorella virus ny2a
31	c2x0dA	Alignment	not modelled	100.0	9	PDB header: transferase Chain: A: PDB Molecule: wsaf; PDBTitle: apo structure of wsaf
32	c3okaA	Alignment	not modelled	100.0	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)
33	c4xsuB	Alignment	not modelled	100.0	15	PDB header: transferase Chain: B: PDB Molecule: alr3699 protein; PDBTitle: crystal structure of anabaena alr3699/hepe in complex with udp and2 glucose
34	c5d00A	Alignment	not modelled	100.0	14	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
35	c2jimH	Alignment	not modelled	99.9	16	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.
36	c4pqgB	Alignment	not modelled	99.9	14	PDB header: transferase Chain: B: PDB Molecule: glycosyltransferase gtf1; PDBTitle: crystal structure of the pneumococcal o-glcnac transferase gtfA in2 complex with udp and glcnac
37	c6d9tA	Alignment	not modelled	99.9	11	PDB header: transferase Chain: A: PDB Molecule: glycosyl transferase; PDBTitle: bsha from staphylococcus aureus complexed with udp
38	c6ejiA	Alignment	not modelled	99.9	13	PDB header: transferase Chain: A: PDB Molecule: wlac protein; PDBTitle: structure of a glycosyltransferase
39	c5e9tA	Alignment	not modelled	99.9	13	PDB header: transferase/chaperone Chain: A: PDB Molecule: glycosyltransferase gtf1; PDBTitle: crystal structure of gtfA/b complex
40	c2q6vA	Alignment	not modelled	99.9	13	PDB header: transferase Chain: A: PDB Molecule: glucuronosyltransferase gumk; PDBTitle: crystal structure of gumk in complex with udp
41	d2iw1a1	Alignment	not modelled	99.9	12	Fold: UDP-Glycosyltransferase/glycogen phosphorylase Superfamily: UDP-Glycosyltransferase/glycogen phosphorylase Family: Glycosyl transferases group 1
42	c2gejA	Alignment	not modelled	99.9	14	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
43	d2bfwa1	Alignment	not modelled	99.9	17	Fold: UDP-Glycosyltransferase/glycogen phosphorylase Superfamily: UDP-Glycosyltransferase/glycogen phosphorylase Family: Glycosyl transferases group 1
44	c5vafD	Alignment	not modelled	99.9	10	PDB header: cell adhesion Chain: D: PDB Molecule: accessory sec system protein asp1; PDBTitle: crystal structure of accessory secretion protein 1
45	c3rhzB	Alignment	not modelled	99.9	14	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
46	c5j45A	Alignment	not modelled	99.9	15	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 (lpcc) from francisella3 tularensis.
47	c5zesA	Alignment	not modelled	99.9	16	PDB header: transferase Chain: A: PDB Molecule: udp-glucose:tetrahydrobiopterin glycosyltransferase; PDBTitle: udp glucose alpha tetrahydrobiopterin glycosyltransferase from2 synechococcus species pcc 7942 - udp complex
48	c4xywA	Alignment	not modelled	99.9	12	PDB header: transferase Chain: A: PDB Molecule: o-antigen biosynthesis glycosyltransferase wbnh; PDBTitle: glycosyltransferases wbnh
49	d1f6da	Alignment	not modelled	99.9	14	Fold: UDP-Glycosyltransferase/glycogen phosphorylase Superfamily: UDP-Glycosyltransferase/glycogen phosphorylase Family: UDP-N-acetylglucosamine 2-epimerase
50	c5enzA	Alignment	not modelled	99.9	12	PDB header: isomerase Chain: A: PDB Molecule: udp-glcnaC 2-epimerase; PDBTitle: s. aureus mnaa-udp co-structure
51	c4bfcA	Alignment	not modelled	99.9	13	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
52	c5lddA	Alignment	not modelled	99.9	15	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
53	c4w6qC_	Alignment	not modelled	99.9	14	PDB header: transferase Chain: C: PDB Molecule: glucosyltransferase; PDBTitle: glycosyltransferase c from streptococcus agalactiae
54	c3ot5D_	Alignment	not modelled	99.9	12	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
55	c2xcuC_	Alignment	not modelled	99.9	13	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
56	c3beoA_	Alignment	not modelled	99.8	15	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
57	d1v4va_	Alignment	not modelled	99.8	17	Fold: UDP-Glycosyltransferase/glycogen phosphorylase Superfamily: UDP-Glycosyltransferase/glycogen phosphorylase Family: UDP-N-acetylglucosamine 2-epimerase
58	c4nesA_	Alignment	not modelled	99.8	13	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
59	c5n80A_	Alignment	not modelled	99.8	14	PDB header: transferase Chain: A: PDB Molecule: lipopolysaccharide 1,6-galactosyltransferase; PDBTitle: glycosyltransferase lps biosynthesis in complex with udp
60	c3dzcA_	Alignment	not modelled	99.8	11	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.
61	d2f9fa1	Alignment	not modelled	99.8	19	Fold: UDP-Glycosyltransferase/glycogen phosphorylase Superfamily: UDP-Glycosyltransferase/glycogen phosphorylase Family: Glycosyl transferases group 1
62	c5w8sA_	Alignment	not modelled	99.8	13	PDB header: transferase Chain: A: PDB Molecule: lipid-a-disaccharide synthase; PDBTitle: lipid a disaccharide synthase (lpxb)-7 solubilizing mutations
63	c4hwgA_	Alignment	not modelled	99.8	10	PDB header: isomerase Chain: A: PDB Molecule: udp-n-acetylglucosamine 2-epimerase; PDBTitle: structure of udp-n-acetylglucosamine 2-epimerase from rickettsia2 bellii
64	c4x1tA_	Alignment	not modelled	99.8	9	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
65	d1o6ca_	Alignment	not modelled	99.7	13	Fold: UDP-Glycosyltransferase/glycogen phosphorylase Superfamily: UDP-Glycosyltransferase/glycogen phosphorylase Family: UDP-N-acetylglucosamine 2-epimerase
66	c2vsnB_	Alignment	not modelled	99.7	17	PDB header: transferase Chain: B: PDB Molecule: xcogt; PDBTitle: structure and topological arrangement of an o-glcna2 transferase homolog: insight into molecular control of3 intracellular glycosylation
67	c2iv3B_	Alignment	not modelled	99.7	17	PDB header: transferase Chain: B: PDB Molecule: glycosyltransferase; PDBTitle: crystal structure of avigt4, a glycosyltransferase involved2 in avilamycin a biosynthesis
68	c5xvsA_	Alignment	not modelled	99.7	9	PDB header: hydrolase Chain: A: PDB Molecule: gdp/udp-n,n'-diacetyl bacillosamine 2-epimerase PDBTitle: crystal structure of udp-glcna2 2-epimerase neuc complexed with udp
69	c3pe3D_	Alignment	not modelled	99.7	16	PDB header: transferase Chain: D: PDB Molecule: udp-n-acetylglucosamine--peptide n- PDBTitle: structure of human o-glcna2 transferase and its complex with a peptide2 substrate
70	c5djsA_	Alignment	not modelled	99.7	18	PDB header: transferase Chain: A: PDB Molecule: tetratricopeptide tpr_2 repeat protein; PDBTitle: thermobaculum terrenum o-glcna2 transferase mutant - k341m
71	c5e9uB_	Alignment	not modelled	99.7	12	PDB header: transferase/chaperone Chain: B: PDB Molecule: glycosyltransferase-stabilizing protein gt2; PDBTitle: crystal structure of gtfa/b complex bound to udp and glcna2
72	c3s2uA_	Alignment	not modelled	99.6	13	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
73	c3qhpB_	Alignment	not modelled	99.6	14	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
74	c3ia7A_	Alignment	not modelled	99.5	14	PDB header: transferase Chain: A: PDB Molecule: calg4; PDBTitle: crystal structure of calg4, the calicheamicin glycosyltransferase
75	c5xvmB_	Alignment	not modelled	99.4	9	PDB header: transferase Chain: B: PDB Molecule: sterol 3-beta-glucosyltransferase; PDBTitle: sterol 3-beta-glucosyltransferase (ugt51) from saccharomyces2 cerevisiae (strain atcc 204508 / s288c)
76	c3iaaB_	Alignment	not modelled	99.4	14	PDB header: transferase Chain: B: PDB Molecule: calg2; PDBTitle: crystal structure of calg2, calicheamicin glycosyltransferase, tdp2 bound form

77	c4rieB_	Alignment	not modelled	99.3	13	PDB header: transferase Chain: B: PDB Molecule: glycosyl transferase homolog; PDBTitle: landomycin glycosyltransferase langt2
78	c5gl5B_	Alignment	not modelled	99.2	9	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
79	c2iyfA_	Alignment	not modelled	99.2	12	PDB header: transferase Chain: A: PDB Molecule: oleandomycin glycosyltransferase; PDBTitle: the crystal structure of macrolide glycosyltransferases: a2 blueprint for antibiotic engineering
80	c30thB_	Alignment	not modelled	99.2	17	PDB header: transferase/antibiotic Chain: B: PDB Molecule: calg1; PDBTitle: crystal structure of calg1, calicheamicin glycosyltransferase, tdp2 and calicheamicin alpha3i bound form
81	d1f0ka_	Alignment	not modelled	99.2	11	Fold: UDP-Glycosyltransferase/glycogen phosphorylase Superfamily: UDP-Glycosyltransferase/glycogen phosphorylase Family: Peptidoglycan biosynthesis glycosyltransferase MurG
82	c2iyaB_	Alignment	not modelled	99.1	13	PDB header: transferase Chain: B: PDB Molecule: oleandomycin glycosyltransferase; PDBTitle: the crystal structure of macrolide glycosyltransferases: a blueprint2 for antibiotic engineering
83	c3tsaA_	Alignment	not modelled	99.1	13	PDB header: transferase Chain: A: PDB Molecule: ndp-rhamnosyltransferase; PDBTitle: spinosyn rhamnosyltransferase spng
84	c4zhtB_	Alignment	not modelled	99.0	10	PDB header: isomerase Chain: B: PDB Molecule: bifunctional udp-n-acetylglucosamine 2-epimerase/n- PDBTitle: crystal structure of udp-glcnac 2-epimerase
85	c2p6pB_	Alignment	not modelled	99.0	17	PDB header: transferase Chain: B: PDB Molecule: glycosyl transferase; PDBTitle: x-ray crystal structure of c-c bond-forming dtdp-d-olivose-transferase2 urdgt2
86	c3ddsB_	Alignment	not modelled	99.0	20	PDB header: transferase Chain: B: PDB Molecule: glycogen phosphorylase, liver form; PDBTitle: crystal structure of glycogen phosphorylase complexed with an2 anthranilimide based inhibitor gsk261
87	c4bqeA_	Alignment	not modelled	98.9	18	PDB header: transferase Chain: A: PDB Molecule: alpha-glucan phosphorylase 2,4-glucan phosphorylase; PDBTitle: arabidopsis thaliana cytosolic alpha-1,4-glucan phosphorylase (phs2)
88	c4leiB_	Alignment	not modelled	98.9	14	PDB header: transferase Chain: B: PDB Molecule: ndp-forosamyltransferase; PDBTitle: spinosyn forosaminyltransferase spnp
89	c4ambB_	Alignment	not modelled	98.8	13	PDB header: transferase Chain: B: PDB Molecule: snogd; PDBTitle: crystal structure of the glycosyltransferase snogd from streptomyces2 nogalater
90	c5lrbB_	Alignment	not modelled	98.8	19	PDB header: transferase Chain: B: PDB Molecule: alpha-1,4 glucan phosphorylase; PDBTitle: plastidial phosphorylase from barley in complex with acarbose
91	d2atia1	Alignment	not modelled	98.8	19	Fold: UDP-Glycosyltransferase/glycogen phosphorylase Superfamily: UDP-Glycosyltransferase/glycogen phosphorylase Family: Oligosaccharide phosphorylase
92	c3d0qB_	Alignment	not modelled	98.8	11	PDB header: transferase Chain: B: PDB Molecule: protein calg3; PDBTitle: crystal structure of calg3 from micromonospora echinospora determined2 in space group i222
93	c4l22A_	Alignment	not modelled	98.7	18	PDB header: transferase Chain: A: PDB Molecule: phosphorylase; PDBTitle: crystal structure of putative glycogen phosphorylase from2 streptococcus mutans
94	d1ygpa_	Alignment	not modelled	98.7	21	Fold: UDP-Glycosyltransferase/glycogen phosphorylase Superfamily: UDP-Glycosyltransferase/glycogen phosphorylase Family: Oligosaccharide phosphorylase
95	d2qj4a1	Alignment	not modelled	98.7	19	Fold: UDP-Glycosyltransferase/glycogen phosphorylase Superfamily: UDP-Glycosyltransferase/glycogen phosphorylase Family: Oligosaccharide phosphorylase
96	d1l5wa_	Alignment	not modelled	98.7	20	Fold: UDP-Glycosyltransferase/glycogen phosphorylase Superfamily: UDP-Glycosyltransferase/glycogen phosphorylase Family: Oligosaccharide phosphorylase
97	c3wadA_	Alignment	not modelled	98.6	10	PDB header: transferase Chain: A: PDB Molecule: glycosyltransferase; PDBTitle: crystal structure of glycosyltransferase vinc involved in the2 biosynthesis of vicanistatin
98	d1iira_	Alignment	not modelled	98.6	9	Fold: UDP-Glycosyltransferase/glycogen phosphorylase Superfamily: UDP-Glycosyltransferase/glycogen phosphorylase Family: Gtf glycosyltransferase
99	c5du2B_	Alignment	not modelled	98.4	15	PDB header: transferase Chain: B: PDB Molecule: espg2 glycosyltransferase; PDBTitle: structural analysis of espg2 glycosyltransferase
100	c2c4mA_	Alignment	not modelled	98.4	19	PDB header: transferase Chain: A: PDB Molecule: glycogen phosphorylase; PDBTitle: starch phosphorylase: structural studies explain oxyanion-dependent2 kinetic stability and regulatory control.
101	d1pn3a_	Alignment	not modelled	97.8	13	Fold: UDP-Glycosyltransferase/glycogen phosphorylase Superfamily: UDP-Glycosyltransferase/glycogen phosphorylase Family: Gtf glycosyltransferase
102	d1rrva_	Alignment	not modelled	97.5	14	Fold: UDP-Glycosyltransferase/glycogen phosphorylase Superfamily: UDP-Glycosyltransferase/glycogen phosphorylase Family: Gtf glycosyltransferase
						PDB header: transferase

103	c4fzrA	Alignment	not modelled	97.0	13	Chain: A: PDB Molecule: ssfs6; PDBTitle: crystal structure of ssfs6, streptomyces sp. sf25752 glycosyltransferase
104	c6o86A	Alignment	not modelled	97.0	14	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
105	d2c1xa1	Alignment	not modelled	96.9	17	Fold: UDP-Glycosyltransferase/glycogen phosphorylase Superfamily: UDP-Glycosyltransferase/glycogen phosphorylase Family: UDPGT-like
106	c3q3hA	Alignment	not modelled	96.3	14	PDB header: transferase Chain: A: PDB Molecule: hmw1c-like glycosyltransferase; PDBTitle: crystal structure of the actinobacillus pleuropneumoniae hmw1c2 glycosyltransferase in complex with udp-glc
107	c5nlmB	Alignment	not modelled	95.6	15	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
108	c3wc4A	Alignment	not modelled	94.5	12	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
109	c6jtdB	Alignment	not modelled	94.3	16	PDB header: transferase Chain: B: PDB Molecule: c-glycosyltransferase; PDBTitle: crystal structure of tccg1 in complex with udp
110	d2vcha1	Alignment	not modelled	94.1	15	Fold: UDP-Glycosyltransferase/glycogen phosphorylase Superfamily: UDP-Glycosyltransferase/glycogen phosphorylase Family: UDPGT-like
111	d2acva1	Alignment	not modelled	94.0	9	Fold: UDP-Glycosyltransferase/glycogen phosphorylase Superfamily: UDP-Glycosyltransferase/glycogen phosphorylase Family: UDPGT-like
112	c3hbjA	Alignment	not modelled	92.9	13	PDB header: transferase Chain: A: PDB Molecule: flavonoid 3-o-glucosyltransferase; PDBTitle: structure of ugt78g1 complexed with udp
113	c5tmdA	Alignment	not modelled	90.5	18	PDB header: transferase Chain: A: PDB Molecule: glycosyltransferase, os79; PDBTitle: crystal structure of os79 from o. sativa in complex with u2f and 2 trichothecene.
114	d2pq6a1	Alignment	not modelled	90.1	10	Fold: UDP-Glycosyltransferase/glycogen phosphorylase Superfamily: UDP-Glycosyltransferase/glycogen phosphorylase Family: UDPGT-like
115	c5v2kA	Alignment	not modelled	89.8	13	PDB header: transferase Chain: A: PDB Molecule: udp-glycosyltransferase 74f2; PDBTitle: crystal structure of udp-glucosyltransferase, ugt74f2 (t15a), with udp2 and 2-bromobenzoic acid
116	c3crnA	Alignment	not modelled	82.6	17	PDB header: signaling protein Chain: A: PDB Molecule: response regulator receiver domain protein, chey-like; PDBTitle: crystal structure of response regulator receiver domain protein (chey-2 like) from methanospirillum hungatei jf-1
117	d1peya	Alignment	not modelled	82.4	11	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
118	c3hbmA	Alignment	not modelled	65.6	6	PDB header: hydrolase Chain: A: PDB Molecule: udp-sugar hydrolase; PDBTitle: crystal structure of pseg from campylobacter jejuni
119	c2jk1A	Alignment	not modelled	63.1	15	PDB header: dna-binding Chain: A: PDB Molecule: hydrogenase transcriptional regulatory protein hupr1; PDBTitle: crystal structure of the wild-type hupr receiver domain
120	c2rjnA	Alignment	not modelled	56.2	21	PDB header: hydrolase Chain: A: PDB Molecule: response regulator receiver:metal-dependent PDBTitle: crystal structure of an uncharacterized protein q2bku2 from2 neptuniibacter caesariensis