



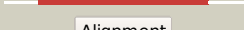

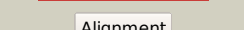







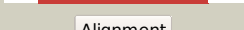

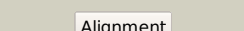

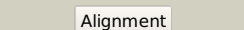










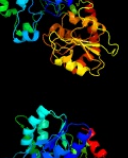



Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2958c (-) _3310724_3312010
Date	Thu Aug 8 16:20:11 BST 2019
Unique Job ID	244bf1ef9bf6193f

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1rrva_	 Alignment		100.0	22	Fold: UDP-Glycosyltransferase/glycogen phosphorylase Superfamily: UDP-Glycosyltransferase/glycogen phosphorylase Family: Gtf glycosyltransferase
2	c5gl5B_	 Alignment		100.0	16	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
3	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
4	c3wc4A_	 Alignment		100.0	15	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
5	d2vcha1	 Alignment		100.0	13	Fold: UDP-Glycosyltransferase/glycogen phosphorylase Superfamily: UDP-Glycosyltransferase/glycogen phosphorylase Family: UDPGT-like
6	d2pq6a1	 Alignment		100.0	13	Fold: UDP-Glycosyltransferase/glycogen phosphorylase Superfamily: UDP-Glycosyltransferase/glycogen phosphorylase Family: UDPGT-like
7	c5nlmB_	 Alignment		100.0	13	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
8	d1pn3a_	 Alignment		100.0	17	Fold: UDP-Glycosyltransferase/glycogen phosphorylase Superfamily: UDP-Glycosyltransferase/glycogen phosphorylase Family: Gtf glycosyltransferase
9	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
10	d1iira_	 Alignment		100.0	20	Fold: UDP-Glycosyltransferase/glycogen phosphorylase Superfamily: UDP-Glycosyltransferase/glycogen phosphorylase Family: Gtf glycosyltransferase
11	c5tmdA_	 Alignment		100.0	16	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	d2c1xa1	Alignment		100.0	14	Fold: UDP-Glycosyltransferase/glycogen phosphorylase Superfamily: UDP-Glycosyltransferase/glycogen phosphorylase Family: UDPGT-like
13	d2acva1	Alignment		100.0	15	Fold: UDP-Glycosyltransferase/glycogen phosphorylase Superfamily: UDP-Glycosyltransferase/glycogen phosphorylase Family: UDPGT-like
14	c6jtdB_	Alignment		100.0	15	PDB header: transferase Chain: B: PDB Molecule: c-glycosyltransferase; PDBTitle: crystal structure of tccgt1 in complex with udp
15	c3hbjA_	Alignment		100.0	15	PDB header: transferase Chain: A: PDB Molecule: flavonoid 3-o-glycosyltransferase; PDBTitle: structure of ugt78g1 complexed with udp
16	c4fzrA_	Alignment		100.0	22	PDB header: transferase Chain: A: PDB Molecule: ssfs6; PDBTitle: crystal structure of ssfs6, streptomyces sp. sf25752 glycosyltransferase
17	c5xvmB_	Alignment		100.0	14	PDB header: transferase Chain: B: PDB Molecule: sterol 3-beta-glycosyltransferase; PDBTitle: sterol 3-beta-glycosyltransferase (ugt51) from saccharomyces2 cerevisiae (strain atcc 204508 / s288c)
18	c5du2B_	Alignment		100.0	16	PDB header: transferase Chain: B: PDB Molecule: espg2 glycosyltransferase; PDBTitle: structural analysis of espg2 glycosyltransferase
19	c3iaaB_	Alignment		100.0	17	PDB header: transferase Chain: B: PDB Molecule: calg2; PDBTitle: crystal structure of calg2, calicheamicin glycosyltransferase, tdp2 bound form
20	c3othB_	Alignment		100.0	27	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	18	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	18	PDB header: transferase Chain: B: PDB Molecule: protein calg3; PDBTitle: crystal structure of calg3 from micromonospora echinospora determined2 in space group i222
23	c2iyfA_	Alignment	not modelled	100.0	16	PDB header: transferase Chain: A: PDB Molecule: oleandomycin glycosyltransferase; PDBTitle: the crystal structure of macrolide glycosyltransferases: a2 blueprint for antibiotic engineering
24	c3wadA_	Alignment	not modelled	100.0	20	PDB header: transferase Chain: A: PDB Molecule: glycosyltransferase; PDBTitle: crystal structure of glycosyltransferase vinc involved in the2 biosynthesis of vicanistatin
25	c3tsaA_	Alignment	not modelled	100.0	22	PDB header: transferase Chain: A: PDB Molecule: ndp-rhamnosyltransferase; PDBTitle: spinosyn rhamnosyltransferase spng
26	c2iyaB_	Alignment	not modelled	100.0	15	PDB header: transferase Chain: B: PDB Molecule: oleandomycin glycosyltransferase; PDBTitle: the crystal structure of macrolide glycosyltransferases: a blueprint2 for antibiotic engineering
27	c3ia7A_	Alignment	not modelled	100.0	17	PDB header: transferase Chain: A: PDB Molecule: calg4; PDBTitle: crystal structure of calg4, the calicheamicin glycosyltransferase
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	23	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	18	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	19	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	23	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	19	Fold: UDP-Glycosyltransferase/glycogen phosphorylase Superfamily: UDP-Glycosyltransferase/glycogen phosphorylase Family: Peptidoglycan biosynthesis glycosyltransferase MurG
35	d1v4va_	Alignment	not modelled	99.9	19	Fold: UDP-Glycosyltransferase/glycogen phosphorylase Superfamily: UDP-Glycosyltransferase/glycogen phosphorylase Family: UDP-N-acetylglucosamine 2-epimerase
36	d1f6da_	Alignment	not modelled	99.8	16	Fold: UDP-Glycosyltransferase/glycogen phosphorylase Superfamily: UDP-Glycosyltransferase/glycogen phosphorylase Family: UDP-N-acetylglucosamine 2-epimerase
37	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
38	c5dldA_	Alignment	not modelled	99.7	16	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
39	d1o6ca_	Alignment	not modelled	99.7	15	Fold: UDP-Glycosyltransferase/glycogen phosphorylase Superfamily: UDP-Glycosyltransferase/glycogen phosphorylase Family: UDP-N-acetylglucosamine 2-epimerase
40	c3ot5D_	Alignment	not modelled	99.7	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	c5w8sA_	Alignment	not modelled	99.7	17	PDB header: transferase Chain: A: PDB Molecule: lipid-a-disaccharide synthase; PDBTitle: lipid a disaccharide synthase (lpxb)-7 solubilizing mutations
42	c5enzA_	Alignment	not modelled	99.7	16	PDB header: isomerase Chain: A: PDB Molecule: udp-glcna2 2-epimerase; PDBTitle: s. aureus mnaa-udp co-structure
43	c2r60A_	Alignment	not modelled	99.7	13	PDB header: transferase Chain: A: PDB Molecule: glycosyl transferase, group 1; PDBTitle: structure of apo sucrose phosphate synthase (sps) of2 halothermothrix orenii
44	c3dzcA_	Alignment	not modelled	99.7	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.
45	c4hwgA_	Alignment	not modelled	99.7	13	PDB header: isomerase Chain: A: PDB Molecule: udp-n-acetylglucosamine 2-epimerase; PDBTitle: structure of udp-n-acetylglucosamine 2-epimerase from rickettsia2 bellii
46	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
47	c2jzcA_	Alignment	not modelled	99.6	16	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
48	c4x1tA_	Alignment	not modelled	99.6	14	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
49	c3c4vB_	Alignment	not modelled	99.5	14	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.
50	c5xvsA_	Alignment	not modelled	99.5	12	PDB header: hydrolase Chain: A: PDB Molecule: gdp/udp-n,n'-diacetylbaucillosamine 2-epimerase PDBTitle: crystal structure of udp-glcna2 2-epimerase neuc complexed with udp
51	c2xcuC_	Alignment	not modelled	99.4	15	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
52	c2x6rA_	Alignment	not modelled	99.4	13	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

53	c6d9tA_	Alignment	not modelled	99.4	13	PDB header: transferase Chain: A: PDB Molecule: glycosyl transferase; PDBTitle: bsha from staphylococcus aureus complexed with udp
54	c5d00A_	Alignment	not modelled	99.4	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	c3s29C_	Alignment	not modelled	99.4	15	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.
56	c2xmpB_	Alignment	not modelled	99.4	15	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
57	c3okaA_	Alignment	not modelled	99.4	15	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)
58	c2gejA_	Alignment	not modelled	99.4	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
59	c2jmhH_	Alignment	not modelled	99.3	13	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.
60	c6ejjA_	Alignment	not modelled	99.3	16	PDB header: transferase Chain: A: PDB Molecule: wlac protein; PDBTitle: structure of a glycosyltransferase
61	c4zhtB_	Alignment	not modelled	99.3	13	PDB header: isomerase Chain: B: PDB Molecule: bifunctional udp-n-acetylglucosamine 2-epimerase/n- PDBTitle: crystal structure of udp-glcna2 2-epimerase
62	c2qzsA_	Alignment	not modelled	99.3	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)
63	c3oy2A_	Alignment	not modelled	99.2	11	PDB header: viral protein,transferase Chain: A: PDB Molecule: glycosyltransferase b736i; PDBTitle: crystal structure of a putative glycosyltransferase from paramecium2 bursaria chlorella virus ny2a
64	c2x0dA_	Alignment	not modelled	99.2	13	PDB header: transferase Chain: A: PDB Molecule: wsaf; PDBTitle: apo structure of wsaf
65	c4hlnA_	Alignment	not modelled	99.2	12	PDB header: transferase Chain: A: PDB Molecule: starch synthase i; PDBTitle: structure of barley starch synthase i in complex with2 maltooligosaccharide
66	c5zesA_	Alignment	not modelled	99.2	10	PDB header: transferase Chain: A: PDB Molecule: udp-glucose:tetrahydrobiopterin glycosyltransferase; PDBTitle: udp glucose alpha tetrahydrobiopterin glycosyltransferase from2 synechococcus species pcc 7942 - udp complex
67	d2iw1a1	Alignment	not modelled	99.2	14	Fold: UDP-Glycosyltransferase/glycogen phosphorylase Superfamily: UDP-Glycosyltransferase/glycogen phosphorylase Family: Glycosyl transferases group 1
68	d1rzua_	Alignment	not modelled	99.1	11	Fold: UDP-Glycosyltransferase/glycogen phosphorylase Superfamily: UDP-Glycosyltransferase/glycogen phosphorylase Family: Glycosyl transferases group 1
69	c5djsA_	Alignment	not modelled	99.1	22	PDB header: transferase Chain: A: PDB Molecule: tetratricopeptide tpr_2 repeat protein; PDBTitle: thermobaculum terrenum o-glcna2 transferase mutant - k341m
70	c4xsuB_	Alignment	not modelled	99.1	12	PDB header: transferase Chain: B: PDB Molecule: alr3699 protein; PDBTitle: crystal structure of anabaena alr3699/hepe in complex with udp and2 glucose
71	c6gneB_	Alignment	not modelled	99.1	12	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
72	c4xywA_	Alignment	not modelled	99.1	10	PDB header: transferase Chain: A: PDB Molecule: o-antigen biosynthesis glycosyltransferase wbnh; PDBTitle: glycosyltransferases wbnh
73	d2bisa1	Alignment	not modelled	99.1	13	Fold: UDP-Glycosyltransferase/glycogen phosphorylase Superfamily: UDP-Glycosyltransferase/glycogen phosphorylase Family: Glycosyl transferases group 1
74	c4rbdD_	Alignment	not modelled	99.0	15	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
75	c3vufA_	Alignment	not modelled	99.0	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
76	c2vsnb_	Alignment	not modelled	99.0	15	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
77	c6gnfC_	Alignment	not modelled	99.0	9	PDB header: transferase Chain: C: PDB Molecule: glycogen synthase; PDBTitle: granule bound starch synthase from cyanobacterium sp. clg1 bound to2 acarbose and adp
78	c2q6vA_	Alignment	not modelled	98.9	13	PDB header: transferase Chain: A: PDB Molecule: glucuronosyltransferase gumk; PDBTitle: crystal structure of gumk in complex with udp
79	c3pe3D_	Alignment	not modelled	98.8	19	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
80	c2iv3B_	Alignment	not modelled	98.8	17	PDB header: transferase Chain: B: PDB Molecule: glycosyltransferase; PDBTitle: crystal structure of avigt4, a glycosyltransferase involved2 in avilamycin a biosynthesis
81	c3rhzB_	Alignment	not modelled	98.7	25	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
82	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
83	c6fj3A_	Alignment	not modelled	98.6	19	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.
84	c5v0tB_	Alignment	not modelled	98.5	15	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
85	c5n80A_	Alignment	not modelled	98.5	13	PDB header: transferase Chain: A: PDB Molecule: lipopolysaccharide 1,6-galactosyltransferase; PDBTitle: glycosyltransferase lps biosynthesis in complex with udp
86	d2f9fa1	Alignment	not modelled	98.5	19	Fold: UDP-Glycosyltransferase/glycogen phosphorylase Superfamily: UDP-Glycosyltransferase/glycogen phosphorylase Family: Glycosyl transferases group 1
87	c4pqgB_	Alignment	not modelled	98.4	15	PDB header: transferase Chain: B: PDB Molecule: glycosyltransferase gtf1; PDBTitle: crystal structure of the pneumococcal o-glcna2 transferase gtf1 in2 complex with udp and glcna2
88	c5hxaA_	Alignment	not modelled	98.4	16	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
89	c3tovB_	Alignment	not modelled	98.4	14	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
90	d1pswa_	Alignment	not modelled	98.4	18	Fold: UDP-Glycosyltransferase/glycogen phosphorylase Superfamily: UDP-Glycosyltransferase/glycogen phosphorylase Family: ADP-heptose LPS heptosyltransferase II
91	c5e9tA_	Alignment	not modelled	98.4	14	PDB header: transferase/chaperone Chain: A: PDB Molecule: glycosyltransferase gtf1; PDBTitle: crystal structure of gtf1/b complex
92	c1uquB_	Alignment	not modelled	98.3	14	PDB header: synthase Chain: B: PDB Molecule: alpha, alpha-trehalose-phosphate synthase; PDBTitle: trehalose-6-phosphate from e. coli bound with udp-glucose.
93	c4w6qC_	Alignment	not modelled	98.2	18	PDB header: transferase Chain: C: PDB Molecule: glucosyltransferase; PDBTitle: glycosyltransferase c from streptococcus agalactiae
94	c4x7pB_	Alignment	not modelled	98.1	13	PDB header: transferase Chain: B: PDB Molecule: tarm; PDBTitle: crystal structure of apo s. aureus tarm
95	d1uqta_	Alignment	not modelled	98.1	14	Fold: UDP-Glycosyltransferase/glycogen phosphorylase Superfamily: UDP-Glycosyltransferase/glycogen phosphorylase Family: Trehalose-6-phosphate synthase, OtsA
96	c5jijA_	Alignment	not modelled	98.1	16	PDB header: transferase Chain: A: PDB Molecule: alpha,alpha-trehalose-phosphate synthase; PDBTitle: structure of mycobacterium thermoresistibile trehalose-6-phosphate2 synthase (apo form).
97	c2h1fB_	Alignment	not modelled	98.0	17	PDB header: transferase Chain: B: PDB Molecule: lipopolysaccharide heptosyltransferase-1; PDBTitle: e. coli heptosyltransferase waac with adp
98	c3t5tA_	Alignment	not modelled	98.0	14	PDB header: transferase Chain: A: PDB Molecule: putative glycosyltransferase; PDBTitle: vall from streptomyces hygroscopicus in apo form
99	c3qhpB_	Alignment	not modelled	97.9	13	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
100	c5i45A_	Alignment	not modelled	97.8	12	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 (lpsc) from francisella3 tularensis.
101	c6nggB	Alignment	not modelled	97.7	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
102	c5hutB	Alignment	not modelled	97.7	14	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
103	c5dxfA	Alignment	not modelled	97.6	14	PDB header: hydrolase Chain: A: PDB Molecule: trehalose-6-phosphate phosphatase; PDBTitle: structure of candida albicans trehalose-6-phosphate phosphatase n-2 terminal domain
104	c5hvoD	Alignment	not modelled	97.3	16	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
105	c5vafD	Alignment	not modelled	97.2	15	PDB header: cell adhesion Chain: D: PDB Molecule: accessory sec system protein asp1; PDBTitle: crystal structure of accessory secretion protein 1
106	c3q3hA	Alignment	not modelled	97.1	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
107	d2bfwa1	Alignment	not modelled	97.0	16	Fold: UDP-Glycosyltransferase/glycogen phosphorylase Superfamily: UDP-Glycosyltransferase/glycogen phosphorylase Family: Glycosyl transferases group 1
108	c5lqdB	Alignment	not modelled	96.9	16	PDB header: transferase Chain: B: PDB Molecule: alpha,alpha-trehalose-phosphate synthase; PDBTitle: trehalose-6-phosphate synthase, gdp-glucose-dependent otsa
109	c5e9uB	Alignment	not modelled	96.9	13	PDB header: transferase/chaperone Chain: B: PDB Molecule: glycosyltransferase-stabilizing protein gtf2; PDBTitle: crystal structure of gtfa/b complex bound to udp and glcnac
110	c3zquA	Alignment	not modelled	94.6	19	PDB header: lyase Chain: A: PDB Molecule: probable aromatic acid decarboxylase; PDBTitle: structure of a probable aromatic acid decarboxylase
111	c3nb0A	Alignment	not modelled	94.5	16	PDB header: transferase Chain: A: PDB Molecule: glycogen [starch] synthase isoform 2; PDBTitle: glucose-6-phosphate activated form of yeast glycogen synthase
112	c3l7mC	Alignment	not modelled	93.8	13	PDB header: structural protein Chain: C: PDB Molecule: teichoic acid biosynthesis protein f; PDBTitle: structure of the wall teichoic acid polymerase tagf, h548a
113	c6qlgD	Alignment	not modelled	93.6	18	PDB header: transferase Chain: D: PDB Molecule: flavin prenyltransferase pad1, mitochondrial; PDBTitle: crystal structure of anubix (pada1) in complex with fmn and2 dimethylallyl pyrophosphate
114	d1n57a	Alignment	not modelled	93.3	14	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: DJ-1/Pfp1
115	c4rheB	Alignment	not modelled	93.0	16	PDB header: lyase Chain: B: PDB Molecule: 3-octaprenyl-4-hydroxybenzoate carboxylase; PDBTitle: crystal structure of ubix, an aromatic acid decarboxylase from the2 colwellia psychrerythraea 34h
116	c3qjgD	Alignment	not modelled	92.3	11	PDB header: oxidoreductase Chain: D: PDB Molecule: epidermin biosynthesis protein epid; PDBTitle: epidermin biosynthesis protein epid from staphylococcus aureus
117	c1mvIA	Alignment	not modelled	92.1	17	PDB header: lyase Chain: A: PDB Molecule: ppc decarboxylase athal3a; PDBTitle: ppc decarboxylase mutant c175s
118	d1mvla	Alignment	not modelled	92.1	17	Fold: Homo-oligomeric flavin-containing Cys decarboxylases, HFCD Superfamily: Homo-oligomeric flavin-containing Cys decarboxylases, HFCD Family: Homo-oligomeric flavin-containing Cys decarboxylases, HFCD
119	c3rggD	Alignment	not modelled	91.8	17	PDB header: lyase Chain: D: PDB Molecule: phosphoribosylaminoimidazole carboxylase, pure protein; PDBTitle: crystal structure of treponema denticola pure bound to air
120	c2ejbA	Alignment	not modelled	91.8	17	PDB header: lyase Chain: A: PDB Molecule: probable aromatic acid decarboxylase; PDBTitle: crystal structure of phenylacrylic acid decarboxylase from2 aquifex aeolicus