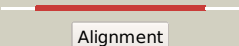



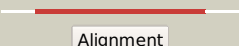


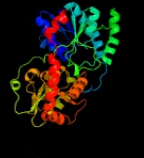

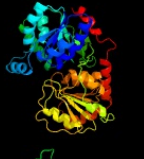
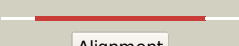


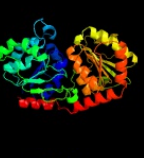










Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2739c (-)_3052033_3053199
Date	Wed Aug 7 12:50:39 BST 2019
Unique Job ID	a1a0d7c60be5a43c

Detailed template
information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c5gl5B_	 Alignment		100.0	15	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	c3iaaB_	 Alignment		100.0	16	PDB header: transferase Chain: B: PDB Molecule: calg2; PDBTitle: crystal structure of calg2, calicheamicin glycosyltransferase, tdp2 bound form
3	c5xvmB_	 Alignment		100.0	14	PDB header: transferase Chain: B: PDB Molecule: sterol 3-beta-glucosyltransferase; PDBTitle: sterol 3-beta-glucosyltransferase (ugt51) from saccharomyces2 cerevisiae (strain atcc 204508 / s288c)
4	c3tsaA_	 Alignment		100.0	18	PDB header: transferase Chain: A: PDB Molecule: ndp-rhamnosyltransferase; PDBTitle: spinosyn rhamnosyltransferase spng
5	c30thB_	 Alignment		100.0	21	PDB header: transferase/antibiotic Chain: B: PDB Molecule: calg1; PDBTitle: crystal structure of calg1, calicheamicin glycosyltransferase, tdp2 and calicheamicin alpha3l bound form
6	c3wadA_	 Alignment		100.0	15	PDB header: transferase Chain: A: PDB Molecule: glycosyltransferase; PDBTitle: crystal structure of glycosyltransferase vinc involved in the2 biosynthesis of vicenistatin
7	c2p6pB_	 Alignment		100.0	19	PDB header: transferase Chain: B: PDB Molecule: glycosyl transferase; PDBTitle: x-ray crystal structure of c-c bond-forming dtdp-d-olivose- transferase2 urdgt2
8	c2iyaB_	 Alignment		100.0	20	PDB header: transferase Chain: B: PDB Molecule: oleandomycin glycosyltransferase; PDBTitle: the crystal structure of macrolide glycosyltransferases: a blueprint2 for antibiotic engineering
9	d1rrva_	 Alignment		100.0	21	Fold: UDP-Glycosyltransferase/glycogen phosphorylase Superfamily: UDP-Glycosyltransferase/glycogen phosphorylase Family: Gtf glycosyltransferase
10	d1iira_	 Alignment		100.0	17	Fold: UDP-Glycosyltransferase/glycogen phosphorylase Superfamily: UDP-Glycosyltransferase/glycogen phosphorylase Family: Gtf glycosyltransferase
11	c4ambB_	 Alignment		100.0	23	PDB header: transferase Chain: B: PDB Molecule: snogd; PDBTitle: crystal structure of the glycosyltransferase snogd from streptomyces2 nogalater

12	c3ia7A_	Alignment		100.0	16	PDB header: transferase Chain: A: PDB Molecule: calg4; PDBTitle: crystal structure of calg4, the calicheamicin glycosyltransferase
13	c5du2B_	Alignment		100.0	18	PDB header: transferase Chain: B: PDB Molecule: espg2 glycosyltransferase; PDBTitle: structural analysis of espg2 glycosyltransferase
14	c4leiB_	Alignment		100.0	16	PDB header: transferase Chain: B: PDB Molecule: ndp-forosamyltransferase; PDBTitle: spinosyn forosaminyltransferase spnp
15	c2lyfA_	Alignment		100.0	19	PDB header: transferase Chain: A: PDB Molecule: oleandomycin glycosyltransferase; PDBTitle: the crystal structure of macrolide glycosyltransferases: a2 blueprint for antibiotic engineering
16	c4rieB_	Alignment		100.0	20	PDB header: transferase Chain: B: PDB Molecule: glycosyl transferase homolog; PDBTitle: landomycin glycosyltransferase langt2
17	c3d0qB_	Alignment		100.0	19	PDB header: transferase Chain: B: PDB Molecule: protein calg3; PDBTitle: crystal structure of calg3 from micromonospora echinospora determined2 in space group i222
18	d1pn3a_	Alignment		100.0	17	Fold: UDP-Glycosyltransferase/glycogen phosphorylase Superfamily: UDP-Glycosyltransferase/glycogen phosphorylase Family: Gtf glycosyltransferase
19	c4fzrA_	Alignment		100.0	24	PDB header: transferase Chain: A: PDB Molecule: ssfs6; PDBTitle: crystal structure of ssfs6, streptomyces sp. sf25752 glycosyltransferase
20	c6o86A_	Alignment		100.0	13	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
21	c5v2kA_	Alignment	not modelled	100.0	12	PDB header: transferase Chain: A: PDB Molecule: udp-glycosyltransferase 74f2; PDBTitle: crystal structure of udp-glucosyltransferase, ugt74f2 (t15a), with udp2 and 2-bromobenzoic acid
22	c5nlmB_	Alignment	not modelled	100.0	12	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
23	c3wc4A_	Alignment	not modelled	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
24	c5tmdA_	Alignment	not modelled	100.0	15	PDB header: transferase Chain: A: PDB Molecule: glycosyltransferase, os79; PDBTitle: crystal structure of os79 from o. sativa in complex with u2f and2 trichothecene.
25	c3s2uA_	Alignment	not modelled	100.0	21	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
26	c3hbjA_	Alignment	not modelled	100.0	14	PDB header: transferase Chain: A: PDB Molecule: flavonoid 3-o-glucosyltransferase; PDBTitle: structure of ugt78g1 complexed with udp
27	d2pq6a1	Alignment	not modelled	100.0	11	Fold: UDP-Glycosyltransferase/glycogen phosphorylase Superfamily: UDP-Glycosyltransferase/glycogen phosphorylase Family: UDPGT-like
						Fold: UDP-Glycosyltransferase/glycoqen phosphorylase

28	d2vcha1	Alignment	not modelled	100.0	15	Superfamily: UDP-Glycosyltransferase/glycogen phosphorylase Family: UDPGT-like
29	d2acva1	Alignment	not modelled	100.0	11	Fold: UDP-Glycosyltransferase/glycogen phosphorylase Superfamily: UDP-Glycosyltransferase/glycogen phosphorylase Family: UDPGT-like
30	d2c1xa1	Alignment	not modelled	100.0	17	Fold: UDP-Glycosyltransferase/glycogen phosphorylase Superfamily: UDP-Glycosyltransferase/glycogen phosphorylase Family: UDPGT-like
31	d1f0ka_	Alignment	not modelled	100.0	20	Fold: UDP-Glycosyltransferase/glycogen phosphorylase Superfamily: UDP-Glycosyltransferase/glycogen phosphorylase Family: Peptidoglycan biosynthesis glycosyltransferase MurG
32	c3s29C_	Alignment	not modelled	100.0	9	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.
33	c6jtdB_	Alignment	not modelled	100.0	16	PDB header: transferase Chain: B: PDB Molecule: c-glycosyltransferase; PDBTitle: crystal structure of tccgt1 in complex with udp
34	c3c4vB_	Alignment	not modelled	100.0	11	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.
35	c2r60A_	Alignment	not modelled	100.0	12	PDB header: transferase Chain: A: PDB Molecule: glycosyl transferase, group 1; PDBTitle: structure of apo sucrose phosphate synthase (sps) of2 halothermothrix orenii
36	c2qzsA_	Alignment	not modelled	99.9	14	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)
37	c6d9tA_	Alignment	not modelled	99.9	8	PDB header: transferase Chain: A: PDB Molecule: glycosyl transferase; PDBTitle: bsha from staphylococcus aureus complexed with udp
38	c4rbnD_	Alignment	not modelled	99.9	10	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
39	c2gejA_	Alignment	not modelled	99.9	13	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
40	c5d00A_	Alignment	not modelled	99.9	9	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
41	c2jjmH_	Alignment	not modelled	99.9	8	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.
42	c3vufA_	Alignment	not modelled	99.9	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
43	c6gneB_	Alignment	not modelled	99.9	9	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
44	d2bisa1	Alignment	not modelled	99.9	11	Fold: UDP-Glycosyltransferase/glycogen phosphorylase Superfamily: UDP-Glycosyltransferase/glycogen phosphorylase Family: Glycosyl transferases group 1
45	d1rzua_	Alignment	not modelled	99.9	15	Fold: UDP-Glycosyltransferase/glycogen phosphorylase Superfamily: UDP-Glycosyltransferase/glycogen phosphorylase Family: Glycosyl transferases group 1
46	c4hlnA_	Alignment	not modelled	99.9	11	PDB header: transferase Chain: A: PDB Molecule: starch synthase i; PDBTitle: structure of barley starch synthase i in complex with2 maltooligosaccharide
47	c3okaA_	Alignment	not modelled	99.9	14	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)
48	d2iw1a1	Alignment	not modelled	99.9	12	Fold: UDP-Glycosyltransferase/glycogen phosphorylase Superfamily: UDP-Glycosyltransferase/glycogen phosphorylase Family: Glycosyl transferases group 1
49	c6gnfC_	Alignment	not modelled	99.9	12	PDB header: transferase Chain: C: PDB Molecule: glycogen synthase; PDBTitle: granule bound starch synthase from cyanobacterium sp. clg1 bound to2 acarbose and adp
50	c6ejjA_	Alignment	not modelled	99.9	10	PDB header: transferase Chain: A: PDB Molecule: wlac protein; PDBTitle: structure of a glycosyltransferase
51	c2xmpB_	Alignment	not modelled	99.9	12	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
52	c2x6rA_	Alignment	not modelled	99.9	13	PDB header: isomerase Chain: A: PDB Molecule: trehalose-synthase tret;

52	c2x0tA	Alignment	not modelled	99.9	13	PDBTitle: crystal structure of trehalose synthase tret from p.2 horikoshi produced by soaking in trehalose PDB header: transferase
53	c4xsuB	Alignment	not modelled	99.9	15	Chain: B: PDB Molecule: alr3699 protein; PDBTitle: crystal structure of anabaena alr3699/hepe in complex with udp and2 glucose
54	c5zesA	Alignment	not modelled	99.9	13	PDB header: transferase Chain: A: PDB Molecule: udp-glucose:tetrahydrobiopterin glucosyltransferase; PDBTitle: udp glucose alpha tetrahydrobiopterin glucosyltransferase from2 synechococcus species pcc 7942 - udp complex
55	c3oy2A	Alignment	not modelled	99.9	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
56	c4xywA	Alignment	not modelled	99.9	11	PDB header: transferase Chain: A: PDB Molecule: o-antigen biosynthesis glycosyltransferase wbnh; PDBTitle: glycosyltransferases wbnh
57	c3beoA	Alignment	not modelled	99.9	10	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
58	d1v4va	Alignment	not modelled	99.9	14	Fold: UDP-Glycosyltransferase/glycogen phosphorylase Superfamily: UDP-Glycosyltransferase/glycogen phosphorylase Family: UDP-N-acetylglucosamine 2-epimerase
59	d1f6da	Alignment	not modelled	99.9	12	Fold: UDP-Glycosyltransferase/glycogen phosphorylase Superfamily: UDP-Glycosyltransferase/glycogen phosphorylase Family: UDP-N-acetylglucosamine 2-epimerase
60	c6gngB	Alignment	not modelled	99.9	10	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
61	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
62	c5dldA	Alignment	not modelled	99.9	10	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
63	c2iv3B	Alignment	not modelled	99.9	17	PDB header: transferase Chain: B: PDB Molecule: glycosyltransferase; PDBTitle: crystal structure of avigt4, a glycosyltransferase involved2 in avilamycin a biosynthesis
64	c5w8sA	Alignment	not modelled	99.9	15	PDB header: transferase Chain: A: PDB Molecule: lipid-a-disaccharide synthase; PDBTitle: lipid a disaccharide synthase (lpxb)-7 solubilizing mutations
65	c5n80A	Alignment	not modelled	99.9	10	PDB header: transferase Chain: A: PDB Molecule: lipopolysaccharide 1,6-galactosyltransferase; PDBTitle: glycosyltransferase lps biosynthesis in complex with udp
66	c3dzcA	Alignment	not modelled	99.9	10	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.
67	c5enzA	Alignment	not modelled	99.9	9	PDB header: isomerase Chain: A: PDB Molecule: udp-glcna2 2-epimerase; PDBTitle: s. aureus mnaa-udp co-structure
68	c5v0tB	Alignment	not modelled	99.9	12	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
69	c4hwgA	Alignment	not modelled	99.8	8	PDB header: isomerase Chain: A: PDB Molecule: udp-n-acetylglucosamine 2-epimerase; PDBTitle: structure of udp-n-acetylglucosamine 2-epimerase from rickettsia2 bellii
70	c1uquB	Alignment	not modelled	99.8	14	PDB header: synthase Chain: B: PDB Molecule: alpha, alpha-trehalose-phosphate synthase; PDBTitle: trehalose-6-phosphate from e. coli bound with udp-glucose.
71	c4nesA	Alignment	not modelled	99.8	10	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
72	c5hxaA	Alignment	not modelled	99.8	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
73	d1o6ca	Alignment	not modelled	99.8	9	Fold: UDP-Glycosyltransferase/glycogen phosphorylase Superfamily: UDP-Glycosyltransferase/glycogen phosphorylase Family: UDP-N-acetylglucosamine 2-epimerase
74	c2q6vA	Alignment	not modelled	99.8	14	PDB header: transferase Chain: A: PDB Molecule: glucuronosyltransferase gumk; PDBTitle: crystal structure of gumk in complex with udp
75	c2x0dA	Alignment	not modelled	99.8	8	PDB header: transferase Chain: A: PDB Molecule: wsaf; PDBTitle: apo structure of wsaf
76	d1uqta	Alignment	not modelled	99.8	13	Fold: UDP-Glycosyltransferase/glycogen phosphorylase Superfamily: UDP-Glycosyltransferase/glycogen phosphorylase Family: Trehalose-6-phosphate synthase, OtsA PDB header: transferase

77	c5jiiA_	Alignment	not modelled	99.8	13	Chain: A: PDB Molecule: alpha,alpha-trehalose-phosphate synthase; PDBTitle: structure of mycobacterium thermoresistibile trehalose-6-phosphate2 synthase (apo form).
78	c4x1tA_	Alignment	not modelled	99.7	17	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
79	c4x7pB_	Alignment	not modelled	99.7	10	PDB header: transferase Chain: B: PDB Molecule: starm; PDBTitle: crystal structure of apo s. aureus tarm
80	c5e9tA_	Alignment	not modelled	99.7	12	PDB header: transferase/chaperone Chain: A: PDB Molecule: glycosyltransferase gtf1; PDBTitle: crystal structure of gtfa/b complex
81	c3hbmA_	Alignment	not modelled	99.7	11	PDB header: hydrolase Chain: A: PDB Molecule: udp-sugar hydrolase; PDBTitle: crystal structure of pseg from campylobacter jejuni
82	c4pqgB_	Alignment	not modelled	99.7	12	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
83	c5hutB_	Alignment	not modelled	99.7	10	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
84	c3nb0A_	Alignment	not modelled	99.7	13	PDB header: transferase Chain: A: PDB Molecule: glycogen [starch] synthase isoform 2; PDBTitle: glucose-6-phosphate activated form of yeast glycogen synthase
85	c6fj3A_	Alignment	not modelled	99.6	11	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	c2xcuC_	Alignment	not modelled	99.6	11	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
87	c5xvsA_	Alignment	not modelled	99.6	13	PDB header: hydrolase Chain: A: PDB Molecule: gdp/udp-n,n'-diacetylbaCillosamine 2-epimerase PDBTitle: crystal structure of udp-glcnaC 2-epimerase neuc complexed with udp
88	c3o3cD_	Alignment	not modelled	99.6	12	PDB header: transferase Chain: D: PDB Molecule: glycogen [starch] synthase isoform 2; PDBTitle: glycogen synthase basal state udp complex
89	c2o6lA_	Alignment	not modelled	99.6	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
90	c3t5tA_	Alignment	not modelled	99.6	11	PDB header: transferase Chain: A: PDB Molecule: putative glycosyltransferase; PDBTitle: vall from streptomyces hygrosopicus in apo form
91	c3rhzB_	Alignment	not modelled	99.5	7	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
92	c2vsnB_	Alignment	not modelled	99.5	15	PDB header: transferase Chain: B: PDB Molecule: xcogt; PDBTitle: structure and topological arrangement of an o-glcnaC2 transferase homolog: insight into molecular control of3 intracellular glycosylation
93	c4w6qC_	Alignment	not modelled	99.5	9	PDB header: transferase Chain: C: PDB Molecule: glycosyltransferase; PDBTitle: glycosyltransferase c from streptococcus agalactiae
94	c5djsA_	Alignment	not modelled	99.4	12	PDB header: transferase Chain: A: PDB Molecule: tetratricopeptide tpr_2 repeat protein; PDBTitle: thermobaculum terrenum o-glcnaC transferase mutant -k341m
95	d2f9fa1	Alignment	not modelled	99.4	14	Fold: UDP-Glycosyltransferase/glycogen phosphorylase Superfamily: UDP-Glycosyltransferase/glycogen phosphorylase Family: Glycosyl transferases group 1
96	c5dxFA_	Alignment	not modelled	99.4	10	PDB header: hydrolase Chain: A: PDB Molecule: trehalose-6-phosphate phosphatase; PDBTitle: structure of candida albicans trehalose-6-phosphate phosphatase n-2 terminal domain
97	c5lqdB_	Alignment	not modelled	99.3	21	PDB header: transferase Chain: B: PDB Molecule: alpha,alpha-trehalose-phosphate synthase; PDBTitle: trehalose-6-phosphate synthase, gdp-glucose-dependent otsa
98	c5vafD_	Alignment	not modelled	99.3	12	PDB header: cell adhesion Chain: D: PDB Molecule: accessory sec system protein asp1; PDBTitle: crystal structure of accessory secretion protein 1
99	c4bfcA_	Alignment	not modelled	99.3	16	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
100	c4qlbD_	Alignment	not modelled	99.3	11	PDB header: transferase Chain: D: PDB Molecule: probable glycogen [starch] synthase; PDBTitle: structural basis for the recruitment of glycogen synthase

						by2 glycogenin
101	c5i45A	Alignment	not modelled	99.3	7	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.
102	c3pe3D	Alignment	not modelled	99.2	12	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
103	c5hvoD	Alignment	not modelled	99.2	13	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
104	c3qhpB	Alignment	not modelled	99.2	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
105	d2bfwa1	Alignment	not modelled	99.1	12	Fold: UDP-Glycosyltransferase/glycogen phosphorylase Superfamily: UDP-Glycosyltransferase/glycogen phosphorylase Family: Glycosyl transferases group 1
106	c5e9uB	Alignment	not modelled	99.1	13	PDB header: transferase/chaperone Chain: B: PDB Molecule: glycosyltransferase-stabilizing protein gtf2; PDBTitle: crystal structure of gtfA/b complex bound to udp and glcna2
107	c4zhtB	Alignment	not modelled	98.9	10	PDB header: isomerase Chain: B: PDB Molecule: bifunctional udp-n-acetylglucosamine 2-epimerase/n- PDBTitle: crystal structure of udp-glcna2 2-epimerase
108	c2jzcA	Alignment	not modelled	98.3	15	PDB header: transferase Chain: A: PDB Molecule: udp-n-acetylglucosamine transferase subunit PDBTitle: nmr solution structure of alg13: the sugar donor subunit of 2 a yeast n-acetylglucosamine transferase. northeast3 structural genomics consortium target yg1
109	c2h1fB	Alignment	not modelled	97.9	11	PDB header: transferase Chain: B: PDB Molecule: lipopolysaccharide heptosyltransferase-1; PDBTitle: e. coli heptosyltransferase waac with adp
110	d1pswa	Alignment	not modelled	97.9	11	Fold: UDP-Glycosyltransferase/glycogen phosphorylase Superfamily: UDP-Glycosyltransferase/glycogen phosphorylase Family: ADP-heptose LPS heptosyltransferase II
111	c3q3hA	Alignment	not modelled	97.3	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
112	c3tovB	Alignment	not modelled	96.9	12	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
113	c5ayvB	Alignment	not modelled	95.8	22	PDB header: oxidoreductase Chain: B: PDB Molecule: 2-dehydropantoate 2-reductase; PDBTitle: crystal structure of archaeal ketopantoate reductase complexed with2 coenzyme a and 2-oxopantoate
114	c2x4gA	Alignment	not modelled	95.5	18	PDB header: isomerase Chain: A: PDB Molecule: nucleoside-diphosphate-sugar epimerase; PDBTitle: crystal structure of pa4631, a nucleoside-diphosphate-sugar epimerase2 from pseudomonas aeruginosa
115	c3ghyA	Alignment	not modelled	95.4	23	PDB header: oxidoreductase Chain: A: PDB Molecule: ketopantoate reductase protein; PDBTitle: crystal structure of a putative ketopantoate reductase from ralstonia2 solanacearum molk2
116	c3icpA	Alignment	not modelled	95.1	14	PDB header: isomerase Chain: A: PDB Molecule: nad-dependent epimerase/dehydratase; PDBTitle: crystal structure of udp-galactose 4-epimerase
117	c4qeaG	Alignment	not modelled	95.0	15	PDB header: hydrolase Chain: G: PDB Molecule: 5'-nucleotidase sure; PDBTitle: crystal structure of stationary phase survival protein (sure) from2 brucella abortus
118	c5kstA	Alignment	not modelled	95.0	18	PDB header: hydrolase Chain: A: PDB Molecule: 5'-nucleotidase sure; PDBTitle: stationary phase survival protein e (sure) from xylella fastidiosa-2 xfsure-tsamp (tetramer smaller - crystallization with 3'amp).
119	c5zikC	Alignment	not modelled	95.0	22	PDB header: oxidoreductase Chain: C: PDB Molecule: probable 2-dehydropantoate 2-reductase; PDBTitle: crystal structure of ketopantoate reductase from pseudomonas2 aeruginosa
120	d1udca	Alignment	not modelled	94.8	24	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases