







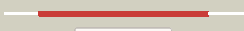












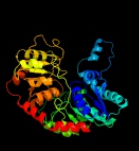











Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1526c_(-)_1720786_1722066
Date	Fri Aug 2 13:30:11 BST 2019
Unique Job ID	f7d9246056671d45

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1rrva_	 Alignment		100.0	25	Fold: UDP-Glycosyltransferase/glycogen phosphorylase Superfamily: UDP-Glycosyltransferase/glycogen phosphorylase Family: Gtf glycosyltransferase
2	c5gl5B_	 Alignment		100.0	20	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	d1iira_	 Alignment		100.0	29	Fold: UDP-Glycosyltransferase/glycogen phosphorylase Superfamily: UDP-Glycosyltransferase/glycogen phosphorylase Family: Gtf glycosyltransferase
4	d1pn3a_	 Alignment		100.0	26	Fold: UDP-Glycosyltransferase/glycogen phosphorylase Superfamily: UDP-Glycosyltransferase/glycogen phosphorylase Family: Gtf glycosyltransferase
5	c6jtdB_	 Alignment		100.0	12	PDB header: transferase Chain: B: PDB Molecule: c-glycosyltransferase; PDBTitle: crystal structure of tccgt1 in complex with udp
6	d2vcha1	 Alignment		100.0	13	Fold: UDP-Glycosyltransferase/glycogen phosphorylase Superfamily: UDP-Glycosyltransferase/glycogen phosphorylase Family: UDPGT-like
7	c5v2kA_	 Alignment		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
8	c6o86A_	 Alignment		100.0	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
9	c5tmdA_	 Alignment		100.0	12	PDB header: transferase Chain: A: PDB Molecule: glycosyltransferase, os79; PDBTitle: crystal structure of os79 from o. sativa in complex with u2f and2 trichothecene.
10	c3wc4A_	 Alignment		100.0	14	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
11	c3hbjA_	 Alignment		100.0	12	PDB header: transferase Chain: A: PDB Molecule: flavonoid 3-o-glucosyltransferase; PDBTitle: structure of ugt78g1 complexed with udp

12	d2acva1	Alignment		100.0	11	Fold: UDP-Glycosyltransferase/glycogen phosphorylase Superfamily: UDP-Glycosyltransferase/glycogen phosphorylase Family: UDPGT-like
13	c5nlmB_	Alignment		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
14	d2c1xa1	Alignment		100.0	10	Fold: UDP-Glycosyltransferase/glycogen phosphorylase Superfamily: UDP-Glycosyltransferase/glycogen phosphorylase Family: UDPGT-like
15	d2pq6a1	Alignment		100.0	17	Fold: UDP-Glycosyltransferase/glycogen phosphorylase Superfamily: UDP-Glycosyltransferase/glycogen phosphorylase Family: UDPGT-like
16	c5xvmB_	Alignment		100.0	21	PDB header: transferase Chain: B: PDB Molecule: sterol 3-beta-glucosyltransferase; PDBTitle: sterol 3-beta-glucosyltransferase (ugt51) from saccharomyces2 cerevisiae (strain atcc 204508 / s288c)
17	c5du2B_	Alignment		100.0	20	PDB header: transferase Chain: B: PDB Molecule: espg2 glycosyltransferase; PDBTitle: structural analysis of espg2 glycosyltransferase
18	c3iaaB_	Alignment		100.0	18	PDB header: transferase Chain: B: PDB Molecule: calg2; PDBTitle: crystal structure of calg2, calicheamicin glycosyltransferase, tdp2 bound form
19	c2p6pB_	Alignment		100.0	21	PDB header: transferase Chain: B: PDB Molecule: glycosyl transferase; PDBTitle: x-ray crystal structure of c-c bond-forming dtdp-d-olivose-transferase2 urdgt2
20	c4fzrA_	Alignment		100.0	21	PDB header: transferase Chain: A: PDB Molecule: ssfs6; PDBTitle: crystal structure of ssfs6, streptomyces sp. sf25752 glycosyltransferase
21	c3othB_	Alignment	not modelled	100.0	21	PDB header: transferase/antibiotic Chain: B: PDB Molecule: calg1; PDBTitle: crystal structure of calg1, calicheamicin glycosyltransferase, tdp2 and calicheamicin alpha3i bound form
22	c2iyfA_	Alignment	not modelled	100.0	20	PDB header: transferase Chain: A: PDB Molecule: oleandomycin glycosyltransferase; PDBTitle: the crystal structure of macrolide glycosyltransferases: a2 blueprint for antibiotic engineering
23	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 vicenistatin
24	c3ia7A_	Alignment	not modelled	100.0	18	PDB header: transferase Chain: A: PDB Molecule: calg4; PDBTitle: crystal structure of calg4, the calicheamicin glycosyltransferase
25	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
26	c2iyaB_	Alignment	not modelled	100.0	16	PDB header: transferase Chain: B: PDB Molecule: oleandomycin glycosyltransferase; PDBTitle: the crystal structure of macrolide glycosyltransferases: a blueprint2 for antibiotic engineering
27	c3tsaA_	Alignment	not modelled	100.0	17	PDB header: transferase Chain: A: PDB Molecule: ndp-rhamnosyltransferase; PDBTitle: spinosyn rhamnosyltransferase spng
28	c4ambB_	Alignment	not modelled	100.0	17	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	17	PDB header: transferase Chain: B: PDB Molecule: ndp-forosamyltransferase; PDBTitle: spinosyn forosaminytransferase spnp
31	c3s2uA_	Alignment	not modelled	100.0	16	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
32	d1f0ka_	Alignment	not modelled	100.0	17	Fold: UDP-Glycosyltransferase/glycogen phosphorylase Superfamily: UDP-Glycosyltransferase/glycogen phosphorylase Family: Peptidoglycan biosynthesis glycosyltransferase MurG
33	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
34	c3hbmA_	Alignment	not modelled	99.9	8	PDB header: hydrolase Chain: A: PDB Molecule: udp-sugar hydrolase; PDBTitle: crystal structure of pseg from campylobacter jejuni
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	c2r60A_	Alignment	not modelled	99.8	9	PDB header: transferase Chain: A: PDB Molecule: glycosyl transferase, group 1; PDBTitle: structure of apo sucrose phosphate synthase (sps) of2 halothermothrix orenii
37	d1f6da_	Alignment	not modelled	99.8	12	Fold: UDP-Glycosyltransferase/glycogen phosphorylase Superfamily: UDP-Glycosyltransferase/glycogen phosphorylase Family: UDP-N-acetylglucosamine 2-epimerase
38	c3c4vB_	Alignment	not modelled	99.8	12	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.
39	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
40	c5w8sA_	Alignment	not modelled	99.8	10	PDB header: transferase Chain: A: PDB Molecule: lipid-a-disaccharide synthase; PDBTitle: lipid a disaccharide synthase (lpxb)-7 solubilizing mutations
41	c3beoA_	Alignment	not modelled	99.8	11	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
42	c4hwgA_	Alignment	not modelled	99.8	12	PDB header: isomerase Chain: A: PDB Molecule: udp-n-acetylglucosamine 2-epimerase; PDBTitle: structure of udp-n-acetylglucosamine 2-epimerase from rickettsia2 bellii
43	c2qzsA_	Alignment	not modelled	99.8	13	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)
44	c5dldA_	Alignment	not modelled	99.8	13	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
45	d1o6ca_	Alignment	not modelled	99.7	13	Fold: UDP-Glycosyltransferase/glycogen phosphorylase Superfamily: UDP-Glycosyltransferase/glycogen phosphorylase Family: UDP-N-acetylglucosamine 2-epimerase
46	c5enzA_	Alignment	not modelled	99.7	11	PDB header: isomerase Chain: A: PDB Molecule: udp-glcna2 2-epimerase; PDBTitle: s. aureus mnaa-udp co-structure
47	c6d9tA_	Alignment	not modelled	99.7	10	PDB header: transferase Chain: A: PDB Molecule: glycosyl transferase; PDBTitle: bsha from staphylococcus aureus complexed with udp
48	c6gneB_	Alignment	not modelled	99.7	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
49	d1rzua_	Alignment	not modelled	99.7	13	Fold: UDP-Glycosyltransferase/glycogen phosphorylase Superfamily: UDP-Glycosyltransferase/glycogen phosphorylase Family: Glycosyl transferases group 1
50	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.
51	c2gejA_	Alignment	not modelled	99.7	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
52	d2bisa1	Alignment	not modelled	99.7	13	Fold: UDP-Glycosyltransferase/glycogen phosphorylase Superfamily: UDP-Glycosyltransferase/glycogen phosphorylase Family: Glycosyl transferases group 1
53	c2jimH_	Alignment	not modelled	99.7	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.
54	c5d00A	Alignment	not modelled	99.7	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	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
56	c6gnfC	Alignment	not modelled	99.7	10	PDB header: transferase Chain: C: PDB Molecule: glycogen synthase; PDBTitle: granule bound starch synthase from cyanobacterium sp. cig1 bound to2 acarbose and adp
57	c3oy2A	Alignment	not modelled	99.7	9	PDB header: viral protein,transferase Chain: A: PDB Molecule: glycosyltransferase b736l; PDBTitle: crystal structure of a putative glycosyltransferase from paramecium2 bursaria chlorella virus ny2a
58	c3okaA	Alignment	not modelled	99.7	13	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)
59	c4hlnA	Alignment	not modelled	99.7	10	PDB header: transferase Chain: A: PDB Molecule: starch synthase i; PDBTitle: structure of barley starch synthase i in complex with2 maltooligosaccharide
60	c4xsub	Alignment	not modelled	99.7	11	PDB header: transferase Chain: B: PDB Molecule: alr3699 protein; PDBTitle: crystal structure of anaebaena alr3699/hepe in complex with udp and2 glucose
61	c4nesA	Alignment	not modelled	99.7	12	PDB header: isomerase Chain: A: PDB Molecule: udp-n-acetylglucosamine 2-epimerase; PDBTitle: crystal structure of methanocaldococcus jannaschii udp-glcna2-2 epimerase in complex with udp-glcna2 and udp
62	c3s29C	Alignment	not modelled	99.6	13	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.
63	c6gngB	Alignment	not modelled	99.6	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
64	c2x6rA	Alignment	not modelled	99.6	16	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
65	c3vufA	Alignment	not modelled	99.6	11	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
66	c2xmpB	Alignment	not modelled	99.6	14	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
67	c6ejjA	Alignment	not modelled	99.5	12	PDB header: transferase Chain: A: PDB Molecule: wlac protein; PDBTitle: structure of a glycosyltransferase
68	c5xvsA	Alignment	not modelled	99.5	13	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
69	c2jzcA	Alignment	not modelled	99.5	19	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
70	d2iw1a1	Alignment	not modelled	99.4	12	Fold: UDP-Glycosyltransferase/glycogen phosphorylase Superfamily: UDP-Glycosyltransferase/glycogen phosphorylase Family: Glycosyl transferases group 1
71	c1uquB	Alignment	not modelled	99.4	10	PDB header: synthase Chain: B: PDB Molecule: alpha, alpha-trehalose-phosphate synthase; PDBTitle: trehalose-6-phosphate from e. coli bound with udp-glucose.
72	c5zesA	Alignment	not modelled	99.4	14	PDB header: transferase Chain: A: PDB Molecule: udp-glucose:tetrahydrobiopterin glucosyltransferase; PDBTitle: udp glucose alpha tetrahydrobiopterin glycosyltransferase from2 synechococcus species pcc 7942 - udp complex
73	c5v0tB	Alignment	not modelled	99.4	10	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
74	c2xcuC	Alignment	not modelled	99.4	12	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
75	c4zhtB	Alignment	not modelled	99.4	12	PDB header: isomerase Chain: B: PDB Molecule: bifunctional udp-n-acetylglucosamine 2-epimerase/n- PDBTitle: crystal structure of udp-glcna2-2 epimerase
76	c5hxaA	Alignment	not modelled	99.4	10	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
77	c2q6vA_	Alignment	not modelled	99.3	11	PDB header: transferase Chain: A: PDB Molecule: glucuronosyltransferase gumk; PDBTitle: crystal structure of gumk in complex with udp
78	c4rbnD_	Alignment	not modelled	99.3	12	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
79	c5jijA_	Alignment	not modelled	99.3	12	PDB header: transferase Chain: A: PDB Molecule: alpha,alpha-trehalose-phosphate synthase; PDBTitle: structure of mycobacterium thermoresistibile trehalose-6-phosphate2 synthase (apo form).
80	c4xywA_	Alignment	not modelled	99.2	11	PDB header: transferase Chain: A: PDB Molecule: o-antigen biosynthesis glycosyltransferase wbnh; PDBTitle: glycosyltransferases wbnh
81	c5djsA_	Alignment	not modelled	99.2	17	PDB header: transferase Chain: A: PDB Molecule: tetratricopeptide tpr_2 repeat protein; PDBTitle: thermobaculum terrenum o-glcna2 transferase mutant - k341m
82	c5n80A_	Alignment	not modelled	99.2	11	PDB header: transferase Chain: A: PDB Molecule: lipopolysaccharide 1,6-galactosyltransferase; PDBTitle: glycosyltransferase lps biosynthesis in complex with udp
83	c2vsnB_	Alignment	not modelled	99.1	13	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
84	c2x0dA_	Alignment	not modelled	99.1	9	PDB header: transferase Chain: A: PDB Molecule: wsaf; PDBTitle: apo structure of wsaf
85	c2iv3B_	Alignment	not modelled	99.1	18	PDB header: transferase Chain: B: PDB Molecule: glycosyltransferase; PDBTitle: crystal structure of avigt4, a glycosyltransferase involved2 in avilamycin a biosynthesis
86	d1uqta_	Alignment	not modelled	99.0	8	Fold: UDP-Glycosyltransferase/glycogen phosphorylase Superfamily: UDP-Glycosyltransferase/glycogen phosphorylase Family: Trehalose-6-phosphate synthase, OtsA
87	c5hutB_	Alignment	not modelled	99.0	7	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
88	c3pe3D_	Alignment	not modelled	99.0	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
89	c4x7pB_	Alignment	not modelled	99.0	10	PDB header: transferase Chain: B: PDB Molecule: tarm; PDBTitle: crystal structure of apo s. aureus tarm
90	c6fj3A_	Alignment	not modelled	99.0	10	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.
91	c4pqgB_	Alignment	not modelled	98.9	12	PDB header: transferase Chain: B: PDB Molecule: glycosyltransferase gtf1; PDBTitle: crystal structure of the pneumococcal o-glcna2 transferase gtfA in2 complex with udp and glcna2
92	c4bfcA_	Alignment	not modelled	98.8	10	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
93	c3rhzB_	Alignment	not modelled	98.8	9	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
94	c3t5tA_	Alignment	not modelled	98.8	12	PDB header: transferase Chain: A: PDB Molecule: putative glycosyltransferase; PDBTitle: vall from streptomyces hygroscopicus in apo form
95	c5dxfA_	Alignment	not modelled	98.7	12	PDB header: hydrolase Chain: A: PDB Molecule: trehalose-6-phosphate phosphatase; PDBTitle: structure of candida albicans trehalose-6-phosphate phosphatase n-2 terminal domain
96	c5e9tA_	Alignment	not modelled	98.7	11	PDB header: transferase/chaperone Chain: A: PDB Molecule: glycosyltransferase gtf1; PDBTitle: crystal structure of gtfA/b complex
97	c4w6qC_	Alignment	not modelled	98.7	11	PDB header: transferase Chain: C: PDB Molecule: glucosyltransferase; PDBTitle: glycosyltransferase c from streptococcus agalactiae
98	c3nb0A_	Alignment	not modelled	98.6	14	PDB header: transferase Chain: A: PDB Molecule: glycogen [starch] synthase isoform 2; PDBTitle: glucose-6-phosphate activated form of yeast glycogen synthase
99	c5lqdB_	Alignment	not modelled	98.6	11	PDB header: transferase Chain: B: PDB Molecule: alpha,alpha-trehalose-phosphate synthase; PDBTitle: trehalose-6-phosphate synthase, gdp-glucose-dependent otsA
100	d2f9fa1	Alignment	not modelled	98.5	14	Fold: UDP-Glycosyltransferase/glycogen phosphorylase Superfamily: UDP-Glycosyltransferase/glycogen phosphorylase Family: Glycosyl transferases group 1

101	c2h1fB	Alignment	not modelled	98.5	13	PDB header: transferase Chain: B: PDB Molecule: lipopolysaccharide heptosyltransferase-1; PDBTitle: e. coli heptosyltransferase waac with adp
102	c5hvoD	Alignment	not modelled	98.4	11	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
103	d1pswa	Alignment	not modelled	98.2	14	Fold: UDP-Glycosyltransferase/glycogen phosphorylase Superfamily: UDP-Glycosyltransferase/glycogen phosphorylase Family: ADP-heptose LPS heptosyltransferase II
104	c5i45A	Alignment	not modelled	98.1	9	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.
105	c3qhpB	Alignment	not modelled	98.0	15	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
106	c3tovB	Alignment	not modelled	98.0	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
107	d2bfwa1	Alignment	not modelled	98.0	11	Fold: UDP-Glycosyltransferase/glycogen phosphorylase Superfamily: UDP-Glycosyltransferase/glycogen phosphorylase Family: Glycosyl transferases group 1
108	c5vafD	Alignment	not modelled	98.0	14	PDB header: cell adhesion Chain: D: PDB Molecule: accessory sec system protein asp1; PDBTitle: crystal structure of accessory secretion protein 1
109	c5e9uB	Alignment	not modelled	97.6	9	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	c3o3cD	Alignment	not modelled	97.5	10	PDB header: transferase Chain: D: PDB Molecule: glycogen [starch] synthase isoform 2; PDBTitle: glycogen synthase basal state udp complex
111	c3q3hA	Alignment	not modelled	97.4	13	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	c4qlbD	Alignment	not modelled	97.1	13	PDB header: transferase Chain: D: PDB Molecule: probable glycogen [starch] synthase; PDBTitle: structural basis for the recruitment of glycogen synthase by2 glycogenin
113	c5ayvB	Alignment	not modelled	96.4	20	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	c3l7mC	Alignment	not modelled	96.3	12	PDB header: structural protein Chain: C: PDB Molecule: teichoic acid biosynthesis protein f; PDBTitle: structure of the wall teichoic acid polymerase tagf, h548a
115	c3ghyA	Alignment	not modelled	95.9	19	PDB header: oxidoreductase Chain: A: PDB Molecule: ketopantoate reductase protein; PDBTitle: crystal structure of a putative ketopantoate reductase from ralstonia2 solanacearum molk2
116	c5zikC	Alignment	not modelled	95.1	18	PDB header: oxidoreductase Chain: C: PDB Molecule: probable 2-dehydropantoate 2-reductase; PDBTitle: crystal structure of ketopantoate reductase from pseudomonas2 aeruginosa
117	c3wfiD	Alignment	not modelled	95.0	22	PDB header: oxidoreductase Chain: D: PDB Molecule: 2-dehydropantoate 2-reductase; PDBTitle: the complex structure of d-mandelate dehydrogenase with nadh
118	c5ig9H	Alignment	not modelled	94.5	11	PDB header: ligase Chain: H: PDB Molecule: atp grasp ligase; PDBTitle: crystal structure of macrocyclase mdnc bound with precursor peptide2 mdna from microcystis aeruginosa mrc
119	c5a9tA	Alignment	not modelled	94.4	24	PDB header: oxidoreductase Chain: A: PDB Molecule: putative dehydrogenase; PDBTitle: imine reductase from amycolatopsis orientalis in complex2 with (r)-methyltetrahydroisoquinoline
120	c3l4bG	Alignment	not modelled	94.4	16	PDB header: transport protein Chain: G: PDB Molecule: trka k+ channel protien tm1088b; PDBTitle: crystal structure of an octomeric two-subunit trka k+ channel ring2 gating assembly, tm1088a:tm1088b, from thermotoga maritima