Phyre2

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Description	RVBD2153c_(murG)_2412127_2413359
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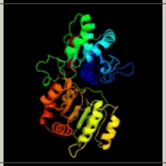
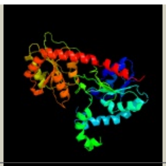
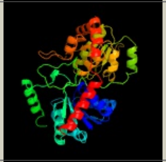
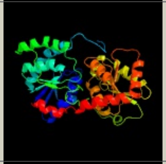
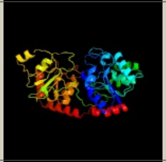
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1f0ka_	Alignment		100.0	36	**Fold:**UDP-Glycosyltransferase/glycogen phosphorylase **Superfamily:**UDP-Glycosyltransferase/glycogen phosphorylase **Family:**Peptidoglycan biosynthesis glycosyltransferase MurG
2	c3s2uA_	Alignment		100.0	38	**PDB header:**transferase **Chain:** A: **PDB Molecule:**udp-n-acetylglucosamine--n-acetylmuramyl-(pentapeptide) **PDBTitle:** crystal structure of the pseudomonas aeruginosa murg:udp-glcnac2 substrate complex
3	c3iaaB_	Alignment		100.0	17	**PDB header:**transferase **Chain:** B: **PDB Molecule:**calg2; **PDBTitle:** crystal structure of calg2, calicheamicin glycosyltransferase, tdp2 bound form
4	c5xvmB_	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)
5	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
6	c3ia7A_	Alignment		100.0	18	**PDB header:**transferase **Chain:** A: **PDB Molecule:**calg4; **PDBTitle:** crystal structure of calg4, the calicheamicin glycosyltransferase
7	c3othB_	Alignment		100.0	18	**PDB header:**transferase/antibiotic **Chain:** B: **PDB Molecule:**calg1; **PDBTitle:** crystal structure of calg1, calicheamicin glycostyltransferase, tdp2 and calicheamicin alpha3i bound form
8	c2iyaB_	Alignment		100.0	16	**PDB header:**transferase **Chain:** B: **PDB Molecule:**oleandomycin glycosyltransferase; **PDBTitle:** the crystal structure of macrolide glycosyltransferases: a blueprint2 for antibiotic engineering
9	c5du2B_	Alignment		100.0	19	**PDB header:**transferase **Chain:** B: **PDB Molecule:**espg2 glycosyltransferase; **PDBTitle:** structural analysis of espg2 glycosyltransferase
10	c2p6pB_	Alignment		100.0	16	**PDB header:**transferase **Chain:** B: **PDB Molecule:**glycosyl transferase; **PDBTitle:** x-ray crystal structure of c-c bond-forming dtdp-d-olivose-transferase2 urdgt2
11	d1iira_	Alignment		100.0	17	**Fold:**UDP-Glycosyltransferase/glycogen phosphorylase **Superfamily:**UDP-Glycosyltransferase/glycogen phosphorylase **Family:**Gtf glycosyltransferase

12	c2iyfA_	Alignment		100.0	18	**PDB header:**transferase **Chain:** A: **PDB Molecule:**oleandomycin glycosyltransferase; **PDBTitle:** the crystal structure of macrolide glycosyltransferases: a2 blueprint for antibiotic engineering
13	c3wadA_	Alignment		100.0	14	**PDB header:**transferase **Chain:** A: **PDB Molecule:**glycosyltransferase; **PDBTitle:** crystal structure of glycosyltransferase vinc involved in the2 biosynthesis of vicenistatin
14	d1rrva_	Alignment		100.0	21	**Fold:**UDP-Glycosyltransferase/glycogen phosphorylase **Superfamily:**UDP-Glycosyltransferase/glycogen phosphorylase **Family:**Gtf glycosyltransferase
15	d1pn3a_	Alignment		100.0	18	**Fold:**UDP-Glycosyltransferase/glycogen phosphorylase **Superfamily:**UDP-Glycosyltransferase/glycogen phosphorylase **Family:**Gtf glycosyltransferase
16	c4fzrA_	Alignment		100.0	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**ssfs6; **PDBTitle:** crystal structure of ssfs6, streptomyces sp. sf25752 glycosyltransferase
17	c4ambB_	Alignment		100.0	18	**PDB header:**transferase **Chain:** B: **PDB Molecule:**snogd; **PDBTitle:** crystal structure of the glycosyltransferase snogd from streptomyces2 nogalater
18	c3tsaA_	Alignment		100.0	16	**PDB header:**transferase **Chain:** A: **PDB Molecule:**ndp-rhamnosyltransferase; **PDBTitle:** spinosyn rhamnosyltransferase spng
19	c4leiB_	Alignment		100.0	13	**PDB header:**transferase **Chain:** B: **PDB Molecule:**ndp-forosamyltransferase; **PDBTitle:** spinosyn forosaminyltransferase spnp
20	c3d0qB_	Alignment		100.0	14	**PDB header:**transferase **Chain:** B: **PDB Molecule:**protein calg3; **PDBTitle:** crystal structure of calg3 from micromonospora echinospora determined2 in space group i222
21	c3c4vB_	Alignment	not modelled	100.0	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.
22	c5w8sA_	Alignment	not modelled	100.0	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**lipid-a-disaccharide synthase; **PDBTitle:** lipid a disaccharide synthase (lpxb)-7 solubilizing mutations
23	d2c1xa1	Alignment	not modelled	100.0	14	**Fold:**UDP-Glycosyltransferase/glycogen phosphorylase **Superfamily:**UDP-Glycosyltransferase/glycogen phosphorylase **Family:**UDPGT-like
24	c4rieB_	Alignment	not modelled	100.0	19	**PDB header:**transferase **Chain:** B: **PDB Molecule:**glycosyl transferase homolog; **PDBTitle:** landomycin glycosyltransferase langt2
25	d1v4va_	Alignment	not modelled	100.0	20	**Fold:**UDP-Glycosyltransferase/glycogen phosphorylase **Superfamily:**UDP-Glycosyltransferase/glycogen phosphorylase **Family:**UDP-N-acetylglucosamine 2-epimerase
26	c3hbjA_	Alignment	not modelled	100.0	12	**PDB header:**transferase **Chain:** A: **PDB Molecule:**flavonoid 3-o-glucosyltransferase; **PDBTitle:** structure of ugt78g1 complexed with udp
27	d2acva1	Alignment	not modelled	100.0	15	**Fold:**UDP-Glycosyltransferase/glycogen phosphorylase **Superfamily:**UDP-Glycosyltransferase/glycogen phosphorylase **Family:**UDPGT-like
28	c3s29C_	Alignment	not modelled	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.
						PDB header:transferase

29	c3wc4A_	Alignment	not modelled	100.0	14	**Chain:** A: **PDB Molecule:**udp-glucose:anthocyanidin 3-o-glucosyltransferase; **PDBTitle:** crystal structure of udp-glucose: anthocyanidin 3-o-2 glucosyltransferase from clitoria ternatea
30	c2r60A_	Alignment	not modelled	100.0	14	**PDB header:**transferase **Chain:** A: **PDB Molecule:**glycosyl transferase, group 1; **PDBTitle:** structure of apo sucrose phosphate synthase (sps) of2 halothermothrix orenii
31	c5v2kA_	Alignment	not modelled	99.9	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
32	c6o86A_	Alignment	not modelled	99.9	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
33	c5nlmB_	Alignment	not modelled	99.9	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
34	c4hlnA_	Alignment	not modelled	99.9	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**starch synthase i; **PDBTitle:** structure of barley starch synthase i in complex with2 maltooligosaccharide
35	d2vcha1	Alignment	not modelled	99.9	21	**Fold:**UDP-Glycosyltransferase/glycogen phosphorylase **Superfamily:**UDP-Glycosyltransferase/glycogen phosphorylase **Family:**UDPGT-like
36	d2pq6a1	Alignment	not modelled	99.9	12	**Fold:**UDP-Glycosyltransferase/glycogen phosphorylase **Superfamily:**UDP-Glycosyltransferase/glycogen phosphorylase **Family:**UDPGT-like
37	c5tmdA_	Alignment	not modelled	99.9	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**glycosyltransferase, os79; **PDBTitle:** crystal structure of os79 from o. sativa in complex with u2f and2 trichothecene.
38	d1o6ca_	Alignment	not modelled	99.9	12	**Fold:**UDP-Glycosyltransferase/glycogen phosphorylase **Superfamily:**UDP-Glycosyltransferase/glycogen phosphorylase **Family:**UDP-N-acetylglucosamine 2-epimerase
39	d1f6da_	Alignment	not modelled	99.9	15	**Fold:**UDP-Glycosyltransferase/glycogen phosphorylase **Superfamily:**UDP-Glycosyltransferase/glycogen phosphorylase **Family:**UDP-N-acetylglucosamine 2-epimerase
40	c5d00A_	Alignment	not modelled	99.9	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
41	c6jtdB_	Alignment	not modelled	99.9	15	**PDB header:**transferase **Chain:** B: **PDB Molecule:**c-glycosyltransferase; **PDBTitle:** crystal structure of tccgt1 in complex with udp
42	c3beoA_	Alignment	not modelled	99.9	12	**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-glcnac 2-epimerases
43	c6d9tA_	Alignment	not modelled	99.9	11	**PDB header:**transferase **Chain:** A: **PDB Molecule:**glycosyl transferase; **PDBTitle:** bsha from staphylococcus aureus complexed with udp
44	c2gejA_	Alignment	not modelled	99.9	12	**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
45	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
46	c4x1tA_	Alignment	not modelled	99.9	21	**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
47	c3okaA_	Alignment	not modelled	99.9	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)
48	c4rbnD_	Alignment	not modelled	99.9	14	**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
49	c6ejiA_	Alignment	not modelled	99.9	12	**PDB header:**transferase **Chain:** A: **PDB Molecule:**wlac protein; **PDBTitle:** structure of a glycosyltransferase
50	c5dldA_	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-glcnac and udp
51	c2jjmH_	Alignment	not modelled	99.9	11	**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.
						PDB header:transferase **Chain:** B: **PDB Molecule:**probable starch synthase 4,

52	c6gneB_	Alignment	not modelled	99.9	14	chloroplastic/amyloplastic; **PDBTitle:** catalytic domain of starch synthase iv from arabidopsis thaliana bound2 to adp and acarbose
53	c2x6rA_	Alignment	not modelled	99.9	11	**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
54	c3dzcA_	Alignment	not modelled	99.9	14	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**udp-n-acetylglucosamine 2-epimerase; **PDBTitle:** 2.35 angstrom resolution structure of wecb (vc0917), a udp-n-2 acetylglucosamine 2-epimerase from vibrio cholerae.
55	d2iw1a1	Alignment	not modelled	99.9	17	**Fold:**UDP-Glycosyltransferase/glycogen phosphorylase **Superfamily:**UDP-Glycosyltransferase/glycogen phosphorylase **Family:**Glycosyl transferases group 1
56	c3vufA_	Alignment	not modelled	99.9	17	**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
57	d2bisa1	Alignment	not modelled	99.9	15	**Fold:**UDP-Glycosyltransferase/glycogen phosphorylase **Superfamily:**UDP-Glycosyltransferase/glycogen phosphorylase **Family:**Glycosyl transferases group 1
58	c4hwgA_	Alignment	not modelled	99.9	10	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**udp-n-acetylglucosamine 2-epimerase; **PDBTitle:** structure of udp-n-acetylglucosamine 2-epimerase from rickettsia2 bellii
59	c5enzA_	Alignment	not modelled	99.9	11	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**udp-glcnac 2-epimerase; **PDBTitle:** s. aureus mnaa-udp co-structure
60	c2xmpB_	Alignment	not modelled	99.9	12	**PDB header:**sugar binding protein **Chain:** A: **PDB Molecule:**trehalose-synthase tret; **PDBTitle:** crystal structure of trehalose synthase tret mutant e326a2 from p.horishiki in complex with udp
61	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)
62	c4xsuB_	Alignment	not modelled	99.9	12	**PDB header:**transferase **Chain:** B: **PDB Molecule:**alr3699 protein; **PDBTitle:** crystal structure of anabaena alr3699/hepe in complex with udp and2 glucose
63	c6gnfC_	Alignment	not modelled	99.9	11	**PDB header:**transferase **Chain:** C: **PDB Molecule:**glycogen synthase; **PDBTitle:** granule bound starch synthase from cyanobacterium sp. clg1 bound to2 acarbose and adp
64	d1rzua_	Alignment	not modelled	99.9	16	**Fold:**UDP-Glycosyltransferase/glycogen phosphorylase **Superfamily:**UDP-Glycosyltransferase/glycogen phosphorylase **Family:**Glycosyl transferases group 1
65	c6gngB_	Alignment	not modelled	99.9	15	**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
66	c3hbmA_	Alignment	not modelled	99.9	10	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**udp-sugar hydrolase; **PDBTitle:** crystal structure of pseg from campylobacter jejuni
67	c4nesA_	Alignment	not modelled	99.8	11	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**udp-n-acetylglucosamine 2-epimerase; **PDBTitle:** crystal structure of methanocaldococcus jannaschii udp-glcnac 2-2 epimerase in complex with udp-glcnac and udp
68	c5xvsA_	Alignment	not modelled	99.8	12	**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
69	c1uquB_	Alignment	not modelled	99.8	13	**PDB header:**synthase **Chain:** B: **PDB Molecule:**alpha, alpha-trehalose-phosphate synthase; **PDBTitle:** trehalose-6-phosphate from e. coli bound with udp-glucose.
70	c5v0tB_	Alignment	not modelled	99.8	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
71	c3oy2A_	Alignment	not modelled	99.8	11	**PDB header:**viral protein,transferase **Chain:** A: **PDB Molecule:**glycosyltransferase b736l; **PDBTitle:** crystal structure of a putative glycosyltransferase from paramecium2 bursaria chlorella virus ny2a
72	c5hxaA_	Alignment	not modelled	99.8	14	**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	c5n80A_	Alignment	not modelled	99.8	8	**PDB header:**transferase **Chain:** A: **PDB Molecule:**lipopolysaccharide 1,6-galactosyltransferase; **PDBTitle:** glycosyltransferase lps biosynthesis in complex with udp
74	c5zesA_	Alignment	not modelled	99.8	13	**PDB header:**transferase **Chain:** A: **PDB Molecule:**udp-glucose:tetrahydrobiopterin glucosyltransferase; **PDBTitle:** udp glucose alpha tetrahydrobiopterin glycosyltransferase from2 synechococcus species pcc 7942 - udp complex
75	d1uqta_	Alignment	not modelled	99.8	13	**Fold:**UDP-Glycosyltransferase/glycogen phosphorylase **Superfamily:**UDP-Glycosyltransferase/glycogen phosphorylase **Family:**Trehalose-6-phosphate synthase, OtsA
76	c2q6vA_	Alignment	not modelled	99.8	13	**PDB header:**transferase **Chain:** A: **PDB Molecule:**glucuronosyltransferase gumk; **PDBTitle:** crystal structure of gumk in complex with udp

77	c4xywA_	Alignment	not modelled	99.7	10	**PDB header:**transferase **Chain:** A: **PDB Molecule:**o-antigen biosynthesis glycosyltransferase wbnh; **PDBTitle:** glycosyltransferases wbnh
78	c2xcuC_	Alignment	not modelled	99.7	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
79	c4zhtB_	Alignment	not modelled	99.7	14	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**bifunctional udp-n-acetylglucosamine 2-epimerase/n- **PDBTitle:** crystal structure of udp-glcnac 2-epimerase
80	c5jijA_	Alignment	not modelled	99.7	13	**PDB header:**transferase **Chain:** A: **PDB Molecule:**alpha,alpha-trehalose-phosphate synthase; **PDBTitle:** structure of mycobacterium thermoresistibile trehalose-6-phosphate2 synthase (apo form).
81	c2iv3B_	Alignment	not modelled	99.7	20	**PDB header:**transferase **Chain:** B: **PDB Molecule:**glycosyltransferase; **PDBTitle:** crystal structure of avigt4, a glycosyltransferase involved2 in avilamycin a biosynthesis
82	c4x7pB_	Alignment	not modelled	99.7	9	**PDB header:**transferase **Chain:** B: **PDB Molecule:**tarm; **PDBTitle:** crystal structure of apo s. aureus tarm
83	c2x0dA_	Alignment	not modelled	99.7	9	**PDB header:**transferase **Chain:** A: **PDB Molecule:**wsaf; **PDBTitle:** apo structure of wsaf
84	c5hutB_	Alignment	not modelled	99.7	12	**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
85	c2vsnB_	Alignment	not modelled	99.6	17	**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
86	c3nb0A_	Alignment	not modelled	99.6	14	**PDB header:**transferase **Chain:** A: **PDB Molecule:**glycogen [starch] synthase isoform 2; **PDBTitle:** glucose-6-phosphate activated form of yeast glycogen synthase
87	c6fj3A_	Alignment	not modelled	99.6	12	**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.
88	c2o6lA_	Alignment	not modelled	99.6	16	**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
89	c5e9tA_	Alignment	not modelled	99.5	10	**PDB header:**transferase/chaperone **Chain:** A: **PDB Molecule:**glycosyltransferase gtf1; **PDBTitle:** crystal structure of gtfa/b complex
90	c4pqgB_	Alignment	not modelled	99.5	11	**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
91	c3o3cD_	Alignment	not modelled	99.5	14	**PDB header:**transferase **Chain:** D: **PDB Molecule:**glycogen [starch] synthase isoform 2; **PDBTitle:** glycogen synthase basal state udp complex
92	c5dxfA_	Alignment	not modelled	99.5	11	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**trehalose-6-phosphate phosphatase; **PDBTitle:** structure of candida albicans trehalose-6-phosphate phosphatase n-2 terminal domain
93	c3t5tA_	Alignment	not modelled	99.5	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**putative glycosyltransferase; **PDBTitle:** vall from streptomyces hygroscopicus in apo form
94	c4w6qC_	Alignment	not modelled	99.5	10	**PDB header:**transferase **Chain:** C: **PDB Molecule:**glucosyltransferase; **PDBTitle:** glycosyltransferase c from streptococcus agalactiae
95	c5djsA_	Alignment	not modelled	99.5	12	**PDB header:**transferase **Chain:** A: **PDB Molecule:**tetratricopeptide tpr_2 repeat protein; **PDBTitle:** thermobaculum terrenum o-glcnac transferase mutant - k341m
96	c5lqdB_	Alignment	not modelled	99.4	14	**PDB header:**transferase **Chain:** B: **PDB Molecule:**alpha,alpha-trehalose-phosphate synthase; **PDBTitle:** trehalose-6-phosphate synthase, gdp-glucose-dependent otsa
97	c3rhzB_	Alignment	not modelled	99.4	13	**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
98	c5hvoD_	Alignment	not modelled	99.3	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
99	d2f9fa1	Alignment	not modelled	99.3	11	**Fold:**UDP-Glycosyltransferase/glycogen phosphorylase **Superfamily:**UDP-Glycosyltransferase/glycogen phosphorylase **Family:**Glycosyl transferases group 1
100	c4qlbD_	Alignment	not modelled	99.3	13	**PDB header:**transferase **Chain:** D: **PDB Molecule:**probable glycogen [starch] synthase; **PDBTitle:** structural basis for the recruitment of glycogen synthase by2 glycogenin

101	c4bfcA_	Alignment	not modelled	99.2	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
102	c3pe3D_	Alignment	not modelled	99.2	17	**PDB header:**transferase **Chain:** D: **PDB Molecule:**udp-n-acetylglucosamine--peptide n- **PDBTitle:** structure of human o-glcnac transferase and its complex with a peptide2 substrate
103	c5i45A_	Alignment	not modelled	99.1	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 (lpcc) from francisella3 tularensis.
104	c5vafD_	Alignment	not modelled	99.1	11	**PDB header:**cell adhesion **Chain:** D: **PDB Molecule:**accessory sec system protein asp1; **PDBTitle:** crystal structure of accessory secretion protein 1
105	d2bfwa1	Alignment	not modelled	99.1	14	**Fold:**UDP-Glycosyltransferase/glycogen phosphorylase **Superfamily:**UDP-Glycosyltransferase/glycogen phosphorylase **Family:**Glycosyl transferases group 1
106	c3qhpB_	Alignment	not modelled	99.0	10	**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
107	c5e9uB_	Alignment	not modelled	98.8	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
108	c2jzcA_	Alignment	not modelled	98.6	18	**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
109	d1pswa_	Alignment	not modelled	98.0	14	**Fold:**UDP-Glycosyltransferase/glycogen phosphorylase **Superfamily:**UDP-Glycosyltransferase/glycogen phosphorylase **Family:**ADP-heptose LPS heptosyltransferase II
110	c3q3hA_	Alignment	not modelled	98.0	8	**PDB header:**transferase **Chain:** A: **PDB Molecule:**hmw1c-like glycosyltransferase; **PDBTitle:** crystal structure of the actinobacillus pleuropneumoniae hmw1c2 glycosyltransferase in complex with udp-glc
111	c3tovB_	Alignment	not modelled	98.0	13	**PDB header:**transferase **Chain:** B: **PDB Molecule:**glycosyl transferase family 9; **PDBTitle:** the crystal structure of the glycosyl transferase family 9 from2 veillonella parvula dsm 2008
112	c2h1fB_	Alignment	not modelled	97.6	16	**PDB header:**transferase **Chain:** B: **PDB Molecule:**lipopolysaccharide heptosyltransferase-1; **PDBTitle:** e. coli heptosyltransferase waac with adp
113	c3l7mC_	Alignment	not modelled	97.1	12	**PDB header:**structural protein **Chain:** C: **PDB Molecule:**teichoic acid biosynthesis protein f; **PDBTitle:** structure of the wall teichoic acid polymerase tagf, h548a
114	d1fmta2	Alignment	not modelled	95.7	25	**Fold:**Formyltransferase **Superfamily:**Formyltransferase **Family:**Formyltransferase
115	c6qkgB_	Alignment	not modelled	95.4	23	**PDB header:**flavoprotein **Chain:** B: **PDB Molecule:**ncr a; **PDBTitle:** 2-naphthoyl-coa reductase(ncr)
116	c3dcjA_	Alignment	not modelled	95.3	16	**PDB header:**transferase **Chain:** A: **PDB Molecule:**probable 5'-phosphoribosylglycinamide formyltransferase **PDBTitle:** crystal structure of glycinamide formyltransferase (purn) from2 mycobacterium tuberculosis in complex with 5-methyl-5,6,7,8-3 tetrahydrofolic acid derivative
117	c2pzlB_	Alignment	not modelled	95.1	12	**PDB header:**sugar binding protein **Chain:** B: **PDB Molecule:**putative nucleotide sugar epimerase/ dehydratase; **PDBTitle:** crystal structure of the bordetella bronchiseptica enzyme wbmg in2 complex with nad and udp
118	c2x4gA_	Alignment	not modelled	94.9	15	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**nucleoside-diphosphate-sugar epimerase; **PDBTitle:** crystal structure of pa4631, a nucleoside-diphosphate-sugar epimerase2 from pseudomonas aeruginosa
119	c3ibgF_	Alignment	not modelled	94.8	15	**PDB header:**hydrolase **Chain:** F: **PDB Molecule:**atpase, subunit of the get complex; **PDBTitle:** crystal structure of aspergillus fumigatus get3 with bound2 adp
120	c3tqrA_	Alignment	not modelled	94.7	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**phosphoribosylglycinamide formyltransferase; **PDBTitle:** structure of the phosphoribosylglycinamide formyltransferase (purn) in2 complex with ches from coxiella burnetii