







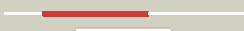















# Phyre2

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Description	RVBD0696 (-) _795522_796934
Date	Fri Jul 26 01:50:26 BST 2019
Unique Job ID	7a164b9441e784f5

Detailed template information
























#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c4hg6A_</a>	 Alignment		100.0	17	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> cellulose synthase subunit a; <b>PDBTitle:</b> structure of a cellulose synthase - cellulose translocation2 intermediate
2	<a href="#">c5nqaA_</a>	 Alignment		100.0	23	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> polypeptide n-acetylgalactosaminyltransferase 4; <b>PDBTitle:</b> crystal structure of galnac-t4 in complex with the monoglycopeptide 3
3	<a href="#">c6e4rB_</a>	 Alignment		100.0	21	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> polypeptide n-acetylgalactosaminyltransferase 9; <b>PDBTitle:</b> crystal structure of the drosophila melanogaster polypeptide n-2 acetylgalactosaminyl transferase pgant9b
4	<a href="#">c1xhbA_</a>	 Alignment		100.0	21	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> polypeptide n-acetylgalactosaminyltransferase 1; <b>PDBTitle:</b> the crystal structure of udp-galnac: polypeptide alpha-n-2 acetylgalactosaminyltransferase-t1
5	<a href="#">c2d7iA_</a>	 Alignment		100.0	21	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> polypeptide n-acetylgalactosaminyltransferase 10; <b>PDBTitle:</b> crystal structure of pp-galnac-t10 with udp, galnac and mn2+
6	<a href="#">c2ffuA_</a>	 Alignment		100.0	24	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> polypeptide n-acetylgalactosaminyltransferase 2; <b>PDBTitle:</b> crystal structure of human ppgalnac-2 complexed with udp and ea2
7	<a href="#">c6iwiqE_</a>	 Alignment		100.0	18	<b>PDB header:</b> transferase <b>Chain:</b> E: <b>PDB Molecule:</b> n-acetylgalactosaminyltransferase 7; <b>PDBTitle:</b> crystal structure of galnac-t7 with mn2+
8	<a href="#">d1xhba2</a>	 Alignment		100.0	21	<b>Fold:</b> Nucleotide-diphospho-sugar transferases <b>Superfamily:</b> Nucleotide-diphospho-sugar transferases <b>Family:</b> Polypeptide N-acetylgalactosaminyltransferase 1, N-terminal domain
9	<a href="#">c4fixA_</a>	 Alignment		100.0	17	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> udp-galactofuranosyl transferase glft2; <b>PDBTitle:</b> crystal structure of glft2
10	<a href="#">c2z86D_</a>	 Alignment		100.0	24	<b>PDB header:</b> transferase <b>Chain:</b> D: <b>PDB Molecule:</b> chondroitin synthase; <b>PDBTitle:</b> crystal structure of chondroitin polymerase from escherichia coli2 strain k4 (k4cp) complexed with udp-glcua and udp
11	<a href="#">c5mm1A_</a>	 Alignment		100.0	14	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> dolichol monophosphate mannose synthase; <b>PDBTitle:</b> dolichyl phosphate mannose synthase in complex with gdp and dolichyl2 phosphate mannose

12	<a href="#">c5tz8C_</a>	Alignment		100.0	19	<b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> glycosyl transferase; <b>PDBTitle:</b> crystal structure of s. aureus tars
13	<a href="#">c6h4mA_</a>	Alignment		100.0	19	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> probable ss-1,3-n-acetylglucosaminyltransferase; <b>PDBTitle:</b> tarp-udp-glcnac-3rbop
14	<a href="#">c3f1yC_</a>	Alignment		100.0	16	<b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> mannosyl-3-phosphoglycerate synthase; <b>PDBTitle:</b> mannosyl-3-phosphoglycerate synthase from rubrobacter xylanophilus
15	<a href="#">c3zf8A_</a>	Alignment		100.0	15	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> mannan polymerase complexes subunit mnn9; <b>PDBTitle:</b> crystal structure of saccharomyces cerevisiae mnn9 in2 complex with gdp and mn.
16	<a href="#">c3ckvA_</a>	Alignment		100.0	20	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> putative uncharacterized protein; <b>PDBTitle:</b> crystal structure of a mycobacterial protein
17	<a href="#">c5ekeB_</a>	Alignment		100.0	15	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> uncharacterized glycosyltransferase sli0501; <b>PDBTitle:</b> structure of the polyisoprenyl-phosphate glycosyltransferase gtrb2 (f215a mutant)
18	<a href="#">c5heaA_</a>	Alignment		99.9	17	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> putative glycosyltransferase (galt1); <b>PDBTitle:</b> cgt structure in hexamer
19	<a href="#">c3bcvA_</a>	Alignment		99.9	21	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> putative glycosyltransferase protein; <b>PDBTitle:</b> crystal structure of a putative glycosyltransferase from bacteroides2 fragilis
20	<a href="#">d1qg8a_</a>	Alignment		99.9	12	<b>Fold:</b> Nucleotide-diphospho-sugar transferases <b>Superfamily:</b> Nucleotide-diphospho-sugar transferases <b>Family:</b> Spore coat polysaccharide biosynthesis protein SpsA
21	<a href="#">c2qgiA_</a>	Alignment	not modelled	99.9	11	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> atp synthase subunits region orf 6; <b>PDBTitle:</b> the udp complex structure of the sixth gene product of the f1-atpase2 operon of rhodobacter blasticus
22	<a href="#">c6p61D_</a>	Alignment	not modelled	99.9	21	<b>PDB header:</b> transferase <b>Chain:</b> D: <b>PDB Molecule:</b> glycosyltransferase; <b>PDBTitle:</b> structure of a glycosyltransferase from leptospira borgpetersenii2 serovar hardjo-bovis (strain jb197)
23	<a href="#">c1omxB_</a>	Alignment	not modelled	99.9	12	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> alpha-1,4-n-acetylhexosaminyltransferase extl2; <b>PDBTitle:</b> crystal structure of mouse alpha-1,4-n-acetylhexosaminyltransferase2 (extl2)
24	<a href="#">d1omza_</a>	Alignment	not modelled	99.9	11	<b>Fold:</b> Nucleotide-diphospho-sugar transferases <b>Superfamily:</b> Nucleotide-diphospho-sugar transferases <b>Family:</b> Exostosin
25	<a href="#">c5z8bB_</a>	Alignment	not modelled	99.8	9	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> kfia protein; <b>PDBTitle:</b> truncated n-acetylglucosaminyl transferase kfia from e. coli k5 strain2 apo form
26	<a href="#">c5ggfC_</a>	Alignment	not modelled	99.7	18	<b>PDB header:</b> transferase, sugar binding protein <b>Chain:</b> C: <b>PDB Molecule:</b> protein o-linked-mannose beta-1,2-n- <b>PDBTitle:</b> crystal structure of human protein o-mannose beta-1,2-n-2 acetylglucosaminyltransferase form ii
27	<a href="#">d2bo4a1</a>	Alignment	not modelled	99.5	14	<b>Fold:</b> Nucleotide-diphospho-sugar transferases <b>Superfamily:</b> Nucleotide-diphospho-sugar transferases <b>Family:</b> MGS-like
28	<a href="#">c4irqB_</a>	Alignment	not modelled	99.5	16	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> beta-1,4-galactosyltransferase 7; <b>PDBTitle:</b> crystal structure of catalytic domain of human beta1,2 4galactosyltransferase 7 in closed conformation in complex with3

						manganese and udp
29	<a href="#">d1pzta_</a>	Alignment	not modelled	99.3	20	<b>Fold:</b> Nucleotide-diphospho-sugar transferases <b>Superfamily:</b> Nucleotide-diphospho-sugar transferases <b>Family:</b> beta 1,4 galactosyltransferase (b4GalT1)
30	<a href="#">c3lw6A_</a>	Alignment	not modelled	98.8	23	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> beta-4-galactosyltransferase 7; <b>PDBTitle:</b> crystal structure of drosophila beta1,4-galactosyltransferase-7
31	<a href="#">d1fo8a_</a>	Alignment	not modelled	98.5	10	<b>Fold:</b> Nucleotide-diphospho-sugar transferases <b>Superfamily:</b> Nucleotide-diphospho-sugar transferases <b>Family:</b> N-acetylglucosaminyltransferase I
32	<a href="#">c5vcmA_</a>	Alignment	not modelled	98.1	19	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> alpha-1,6-mannosyl-glycoprotein 2-beta-n- <b>PDBTitle:</b> alpha-1,6-mannosyl-glycoprotein 2-beta-n-acetylglucosaminyltransferase2 with bound udp and manganese
33	<a href="#">c6fxyA_</a>	Alignment	not modelled	98.0	18	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> procollagen-lysine,2-oxoglutarate 5-dioxygenase 3; <b>PDBTitle:</b> crystal structure of full-length human lysyl hydroxylase lh3 -2 cocrystal with fe2+, mn2+, udp-gal - structure from long-wavelength3 s-sad
34	<a href="#">c2wvmA_</a>	Alignment	not modelled	97.3	18	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> mannosyl-3-phosphoglycerate synthase; <b>PDBTitle:</b> h309a mutant of mannosyl-3-phosphoglycerate synthase from2 thermus thermophilus hb27 in complex with3 gdp-alpha-d-mannose and mg(ii)
35	<a href="#">c2zu8A_</a>	Alignment	not modelled	97.1	17	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> mannosyl-3-phosphoglycerate synthase; <b>PDBTitle:</b> crystal structure of mannosyl-3-phosphoglycerate synthase2 from pyrococcus horikoshii
36	<a href="#">d1vh3a_</a>	Alignment	not modelled	96.8	13	<b>Fold:</b> Nucleotide-diphospho-sugar transferases <b>Superfamily:</b> Nucleotide-diphospho-sugar transferases <b>Family:</b> Cytidylyltransferase
37	<a href="#">c2d0jD_</a>	Alignment	not modelled	96.3	23	<b>PDB header:</b> transferase <b>Chain:</b> D: <b>PDB Molecule:</b> galactosylgalactosylxylosylprotein 3-beta- <b>PDBTitle:</b> crystal structure of human gcat-s apo form
38	<a href="#">d1v82a_</a>	Alignment	not modelled	96.1	23	<b>Fold:</b> Nucleotide-diphospho-sugar transferases <b>Superfamily:</b> Nucleotide-diphospho-sugar transferases <b>Family:</b> 1,3-glucuronyltransferase
39	<a href="#">d3cu0a1</a>	Alignment	not modelled	96.1	23	<b>Fold:</b> Nucleotide-diphospho-sugar transferases <b>Superfamily:</b> Nucleotide-diphospho-sugar transferases <b>Family:</b> 1,3-glucuronyltransferase
40	<a href="#">c5vcsB_</a>	Alignment	not modelled	96.0	20	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> alpha-1,6-mannosyl-glycoprotein 2-beta-n- <b>PDBTitle:</b> alpha-1,6-mannosyl-glycoprotein 2-beta-n-acetylglucosaminyltransferase2 with bound acceptor
41	<a href="#">c4xwiA_</a>	Alignment	not modelled	95.1	16	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> 3-deoxy-manno-octulosonate cytidylyltransferase; <b>PDBTitle:</b> x-ray crystal structure of cmp-kdo synthase from pseudomonas2 aeruginosa
42	<a href="#">d1fxoa_</a>	Alignment	not modelled	94.6	13	<b>Fold:</b> Nucleotide-diphospho-sugar transferases <b>Superfamily:</b> Nucleotide-diphospho-sugar transferases <b>Family:</b> glucose-1-phosphate thymidylyltransferase
43	<a href="#">c4kt7A_</a>	Alignment	not modelled	94.5	12	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> 2-c-methyl-d-erythritol 4-phosphate cytidylyltransferase; <b>PDBTitle:</b> the crystal structure of 4-diphosphocytidyl-2c-methyl-d-2 erythritolsynthase from anaerococcus prevotii dsm 20548
44	<a href="#">d1mc3a_</a>	Alignment	not modelled	94.4	10	<b>Fold:</b> Nucleotide-diphospho-sugar transferases <b>Superfamily:</b> Nucleotide-diphospho-sugar transferases <b>Family:</b> glucose-1-phosphate thymidylyltransferase
45	<a href="#">c6b5kA_</a>	Alignment	not modelled	94.3	14	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> glucose-1-phosphate thymidylyltransferase; <b>PDBTitle:</b> mycobacterium tuberculosis rmla in complex with mg/dttp
46	<a href="#">c2px7A_</a>	Alignment	not modelled	94.2	18	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> 2-c-methyl-d-erythritol 4-phosphate cytidylyltransferase; <b>PDBTitle:</b> crystal structure of 2-c-methyl-d-erythritol 4-phosphate2 cytidylyltransferase from thermus thermophilus hb8
47	<a href="#">d1iina_</a>	Alignment	not modelled	94.0	12	<b>Fold:</b> Nucleotide-diphospho-sugar transferases <b>Superfamily:</b> Nucleotide-diphospho-sugar transferases <b>Family:</b> glucose-1-phosphate thymidylyltransferase
48	<a href="#">d1h5ra_</a>	Alignment	not modelled	93.8	12	<b>Fold:</b> Nucleotide-diphospho-sugar transferases <b>Superfamily:</b> Nucleotide-diphospho-sugar transferases <b>Family:</b> glucose-1-phosphate thymidylyltransferase
49	<a href="#">c2pa4B_</a>	Alignment	not modelled	93.1	13	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> utp-glucose-1-phosphate uridylyltransferase; <b>PDBTitle:</b> crystal structure of udp-glucose pyrophosphorylase from corynebacteria2 glutamicum in complex with magnesium and udp-glucose
50	<a href="#">c3tqdA_</a>	Alignment	not modelled	93.1	12	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> 3-deoxy-manno-octulosonate cytidylyltransferase; <b>PDBTitle:</b> structure of the 3-deoxy-d-manno-octulosonate cytidylyltransferase2 (kdsb) from coxiella burnetii
51	<a href="#">c6bwhB_</a>	Alignment	not modelled	91.6	24	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> 2-phospho-l-lactate guanylyltransferase; <b>PDBTitle:</b> crystal structure of mycobacterium tuberculosis rv2983 in complex2 with pep
52	<a href="#">d1h7ea_</a>	Alignment	not modelled	91.3	16	<b>Fold:</b> Nucleotide-diphospho-sugar transferases <b>Superfamily:</b> Nucleotide-diphospho-sugar transferases <b>Family:</b> Cytidylyltransferase

53	<a href="#">d1vh1a_</a>	Alignment	not modelled	91.2	14	<b>Fold:</b> Nucleotide-diphospho-sugar transferases <b>Superfamily:</b> Nucleotide-diphospho-sugar transferases <b>Family:</b> Cytidylyltransferase
54	<a href="#">c4ys8B_</a>	Alignment	not modelled	91.1	19	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> 2-c-methyl-d-erythritol 4-phosphate cytidylyltransferase; <b>PDBTitle:</b> crystal structure of 2-c-methyl-d-erythritol 4-phosphate2 cytidylyltransferase (ispd) from burkholderia thailandensis
55	<a href="#">c3d5nB_</a>	Alignment	not modelled	90.7	13	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> q97w15_sulso; <b>PDBTitle:</b> crystal structure of the q97w15_sulso protein from sulfolobus2 solfataricus. nesg target ssr125.
56	<a href="#">c3polA_</a>	Alignment	not modelled	90.6	10	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> 3-deoxy-manno-octulosonate cytidylyltransferase; <b>PDBTitle:</b> 2.3 angstrom crystal structure of 3-deoxy-manno-octulosonate2 cytidylyltransferase (kdsb) from acinetobacter baumannii.
57	<a href="#">c4jd0A_</a>	Alignment	not modelled	90.0	10	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> nucleotidyl transferase; <b>PDBTitle:</b> structure of the inositol-1-phosphate ctp transferase from t.2 maritima.
58	<a href="#">c4mybA_</a>	Alignment	not modelled	89.8	8	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> 2-c-methyl-d-erythritol 4-phosphate cytidylyltransferase; <b>PDBTitle:</b> crystal structure of francisella tularensis 2-c-methyl-d-erythritol 4-2 phosphate cytidylyltransferase (ispd)
59	<a href="#">c3oamD_</a>	Alignment	not modelled	89.7	11	<b>PDB header:</b> transferase <b>Chain:</b> D: <b>PDB Molecule:</b> 3-deoxy-manno-octulosonate cytidylyltransferase; <b>PDBTitle:</b> crystal structure of cytidylyltransferase from vibrio cholerae
60	<a href="#">c5ddtA_</a>	Alignment	not modelled	89.5	10	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> 2-c-methyl-d-erythritol 4-phosphate cytidylyltransferase; <b>PDBTitle:</b> crystal structure of ispd from bacillus subtilis at 1.80 angstroms2 resolution, crystal form i
61	<a href="#">c2wawA_</a>	Alignment	not modelled	86.8	12	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> moba relate protein; <b>PDBTitle:</b> crystal structure of mycobacterium tuberculosis rv0371c2 homolog from mycobacterium sp. strain jc1
62	<a href="#">c3okrA_</a>	Alignment	not modelled	86.5	16	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> 2-c-methyl-d-erythritol 4-phosphate cytidylyltransferase; <b>PDBTitle:</b> structure of mtb apo 2-c-methyl-d-erythritol 4-phosphate2 cytidyltransferase (ispd)
63	<a href="#">d1lwva_</a>	Alignment	not modelled	86.2	10	<b>Fold:</b> Nucleotide-diphospho-sugar transferases <b>Superfamily:</b> Nucleotide-diphospho-sugar transferases <b>Family:</b> glucose-1-phosphate thymidylyltransferase
64	<a href="#">d1vica_</a>	Alignment	not modelled	86.0	14	<b>Fold:</b> Nucleotide-diphospho-sugar transferases <b>Superfamily:</b> Nucleotide-diphospho-sugar transferases <b>Family:</b> Cytidylyltransferase
65	<a href="#">d1i52a_</a>	Alignment	not modelled	83.9	17	<b>Fold:</b> Nucleotide-diphospho-sugar transferases <b>Superfamily:</b> Nucleotide-diphospho-sugar transferases <b>Family:</b> Cytidylyltransferase
66	<a href="#">c2j0bA_</a>	Alignment	not modelled	82.5	16	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> beta-1,3-n-acetylglucosaminyltransferase manic fringe; <b>PDBTitle:</b> structure of the catalytic domain of mouse manic fringe in2 complex with udp and manganese
67	<a href="#">c2xmhB_</a>	Alignment	not modelled	82.3	14	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> ctp-inositol-1-phosphate cytidylyltransferase; <b>PDBTitle:</b> the x-ray structure of ctp:inositol-1-phosphate cytidylyltransferase2 from archaeoglobus fulgidus
68	<a href="#">d2oi6a2</a>	Alignment	not modelled	82.1	10	<b>Fold:</b> Nucleotide-diphospho-sugar transferases <b>Superfamily:</b> Nucleotide-diphospho-sugar transferases <b>Family:</b> UDP-glucose pyrophosphorylase
69	<a href="#">c5xhwA_</a>	Alignment	not modelled	82.0	14	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> putative 6-deoxy-d-mannoheptose pathway protein; <b>PDBTitle:</b> crystal structure of hddc from yersinia pseudotuberculosis
70	<a href="#">c4mndA_</a>	Alignment	not modelled	81.4	9	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> ctp l-myo-inositol-1-phosphate cytidylyltransferase/cdp-l- <b>PDBTitle:</b> crystal structure of archaeoglobus fulgidus ipct-dipps bifunctional2 membrane protein
71	<a href="#">c3d8vA_</a>	Alignment	not modelled	80.8	15	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> bifunctional protein glmu; <b>PDBTitle:</b> crystal structure of glmu from mycobacterium tuberculosis2 in complex with uridine-diphosphate-n-acetylglucosamine
72	<a href="#">c2e8bA_</a>	Alignment	not modelled	80.7	15	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> A: <b>PDB Molecule:</b> probable molybdopterin-guanine dinucleotide biosynthesis <b>PDBTitle:</b> crystal structure of the putative protein (aq1419) from aquifex2 aeolicus vf5
73	<a href="#">c5i1fA_</a>	Alignment	not modelled	80.2	11	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> utp--glucose-1-phosphate uridylyltransferase; <b>PDBTitle:</b> crystal structure of utp-glucose-1-phosphate uridylyltransferase from2 burkholderia vietnamiensis in complex with uridine-5'-diphosphate-3 glucose
74	<a href="#">d1w77a1</a>	Alignment	not modelled	79.3	13	<b>Fold:</b> Nucleotide-diphospho-sugar transferases <b>Superfamily:</b> Nucleotide-diphospho-sugar transferases <b>Family:</b> Cytidylyltransferase <b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> 3-deoxv-manno-octulosonate

75	<a href="#">c2y6pC_</a>	Alignment	not modelled	78.6	12	cytidyltransferase; <b>PDBTitle:</b> evidence for a two-metal-ion-mechanism in the kdo-2 cytidyltransferase kdsb
76	<a href="#">d1w55a1</a>	Alignment	not modelled	78.0	11	<b>Fold:</b> Nucleotide-diphospho-sugar transferases <b>Superfamily:</b> Nucleotide-diphospho-sugar transferases <b>Family:</b> Cytidyltransferase
77	<a href="#">c2ux8G_</a>	Alignment	not modelled	77.0	12	<b>PDB header:</b> transferase <b>Chain:</b> G: <b>PDB Molecule:</b> glucose-1-phosphate uridylyltransferase; <b>PDBTitle:</b> crystal structure of sphingomonas elodea atcc 31461 glucose-2 1-phosphate uridylyltransferase in complex with glucose-3 1-phosphate.
78	<a href="#">c2xwIB_</a>	Alignment	not modelled	76.9	13	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> 2-c-methyl-d-erythritol 4-phosphate cytidyltransferase; <b>PDBTitle:</b> crystal structure of ispd from mycobacterium smegmatis in complex with2 ctp and mg
79	<a href="#">c2cu2A_</a>	Alignment	not modelled	75.5	17	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> putative mannose-1-phosphate guanylyl transferase; <b>PDBTitle:</b> crystal structure of mannose-1-phosphate geranyltransferase from2 thermus thermophilus hb8
80	<a href="#">c2qh5B_</a>	Alignment	not modelled	73.6	11	<b>PDB header:</b> isomerase <b>Chain:</b> B: <b>PDB Molecule:</b> mannose-6-phosphate isomerase; <b>PDBTitle:</b> crystal structure of mannose-6-phosphate isomerase from helicobacter2 pylori
81	<a href="#">c1hm8A_</a>	Alignment	not modelled	72.6	9	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> udp-n-acetylglucosamine-1-phosphate uridylyltransferase; <b>PDBTitle:</b> crystal structure of s.pneumoniae n-acetylglucosamine-1-phosphate2 uridylyltransferase, glmu, bound to acetyl coenzyme a
82	<a href="#">c2e3dB_</a>	Alignment	not modelled	72.2	13	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> utp--glucose-1-phosphate uridylyltransferase; <b>PDBTitle:</b> crystal structure of e. coli glucose-1-phosphate2 uridylyltransferase
83	<a href="#">c5gvvF_</a>	Alignment	not modelled	70.3	17	<b>PDB header:</b> transferase <b>Chain:</b> F: <b>PDB Molecule:</b> glycosyl transferase family 8; <b>PDBTitle:</b> crystal structure of the glycosyltransferase glye in streptococcus2 pneumoniae tigr4
84	<a href="#">c1w57A_</a>	Alignment	not modelled	68.8	12	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> ispd/ispf bifunctional enzyme; <b>PDBTitle:</b> structure of the bifunctional ispdf from campylobacter2 jejuni containing zn
85	<a href="#">c3foqA_</a>	Alignment	not modelled	68.2	19	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> bifunctional protein glmu; <b>PDBTitle:</b> crystal structure of n-acetylglucosamine-1-phosphate2 uridylyltransferase (glmu) from mycobacterium tuberculosis in3 a cubic space group.
86	<a href="#">d1e5ka_</a>	Alignment	not modelled	67.3	14	<b>Fold:</b> Nucleotide-diphospho-sugar transferases <b>Superfamily:</b> Nucleotide-diphospho-sugar transferases <b>Family:</b> Molybdenum cofactor biosynthesis protein MobA
87	<a href="#">c3ngwA_</a>	Alignment	not modelled	66.4	10	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> A: <b>PDB Molecule:</b> molybdopterin-guanine dinucleotide biosynthesis protein a <b>PDBTitle:</b> crystal structure of molybdopterin-guanine dinucleotide biosynthesis2 protein a from archaeoglobus fulgidus, northeast structural genomics3 consortium target gr189
88	<a href="#">c3hl3A_</a>	Alignment	not modelled	65.9	12	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> glucose-1-phosphate thymidyltransferase; <b>PDBTitle:</b> 2.76 angstrom crystal structure of a putative glucose-1-phosphate2 thymidyltransferase from bacillus anthracis in complex with a3 sucrose.
89	<a href="#">c2c0nA_</a>	Alignment	not modelled	65.7	21	<b>PDB header:</b> viral protein/transferase <b>Chain:</b> A: <b>PDB Molecule:</b> a197; <b>PDBTitle:</b> crystal structure of a197 from stiv
90	<a href="#">c2x5sB_</a>	Alignment	not modelled	65.5	14	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> mannose-1-phosphate guanylyltransferase; <b>PDBTitle:</b> crystal structure of t. maritima gdp-mannose2 pyrophosphorylase in apo state.
91	<a href="#">d1yp2a2</a>	Alignment	not modelled	64.0	10	<b>Fold:</b> Nucleotide-diphospho-sugar transferases <b>Superfamily:</b> Nucleotide-diphospho-sugar transferases <b>Family:</b> glucose-1-phosphate thymidyltransferase
92	<a href="#">c3brkX_</a>	Alignment	not modelled	62.8	13	<b>PDB header:</b> transferase <b>Chain:</b> X: <b>PDB Molecule:</b> glucose-1-phosphate adenyltransferase; <b>PDBTitle:</b> crystal structure of adp-glucose pyrophosphorylase from agrobacterium2 tumefaciens
93	<a href="#">c3okrC_</a>	Alignment	not modelled	62.3	17	<b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> 2-c-methyl-d-erythritol 4-phosphate cytidyltransferase; <b>PDBTitle:</b> structure of mtb apo 2-c-methyl-d-erythritol 4-phosphate2 cytidyltransferase (ispd)
94	<a href="#">c1fwyA_</a>	Alignment	not modelled	59.2	9	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> udp-n-acetylglucosamine pyrophosphorylase; <b>PDBTitle:</b> crystal structure of n-acetylglucosamine 1-phosphate2 uridylyltransferase bound to udp-glcna
95	<a href="#">c2v0hA_</a>	Alignment	not modelled	59.0	11	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> bifunctional protein glmu; <b>PDBTitle:</b> characterization of substrate binding and catalysis of the2 potential antibacterial target n-acetylglucosamine-1-3 phosphate uridylyltransferase (glmu)
96	<a href="#">c6oewB_</a>	Alignment	not modelled	56.7	8	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> cytidyltransferase; <b>PDBTitle:</b> structure of a cytidyltransferase from leptospira borgpetersenii2 serovar hardjo-bovis (strain jb197)
97	<a href="#">d1g97a2</a>	Alignment	not modelled	55.6	9	<b>Fold:</b> Nucleotide-diphospho-sugar transferases <b>Superfamily:</b> Nucleotide-diphospho-sugar transferases <b>Family:</b> UDP-glucose pyrophosphorylase

98	<a href="#">c3f1cB</a>	 Alignment	not modelled	53.5	8	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> putative 2-c-methyl-d-erythritol 4-phosphate <b>PDBTitle:</b> crystal structure of 2-c-methyl-d-erythritol 4-phosphate2 cytidylyltransferase from listeria monocytogenes
99	<a href="#">c2we9A</a>	 Alignment	not modelled	52.9	7	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> moba-related protein; <b>PDBTitle:</b> crystal structure of rv0371c from mycobacterium2 tuberculosis h37rv
100	<a href="#">d1vgwa</a>	 Alignment	not modelled	51.5	9	<b>Fold:</b> Nucleotide-diphospho-sugar transferases <b>Superfamily:</b> Nucleotide-diphospho-sugar transferases <b>Family:</b> Cytidylyltransferase
101	<a href="#">c4y7uA</a>	 Alignment	not modelled	49.5	10	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> nucleotidyl transferase; <b>PDBTitle:</b> structural analysis of muru
102	<a href="#">c6ifdD</a>	 Alignment	not modelled	47.5	6	<b>PDB header:</b> sugar binding protein <b>Chain:</b> D: <b>PDB Molecule:</b> cmp-n-acetylneuraminate synthetase; <b>PDBTitle:</b> crystal structure of cmp-n-acetylneuraminate synthetase from vibrio2 cholerae in complex with cdp and mg2+
103	<a href="#">c4jisB</a>	 Alignment	not modelled	47.1	9	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> ribitol-5-phosphate cytidylyltransferase; <b>PDBTitle:</b> crystal structure of ribitol 5-phosphate cytidylyltransferase (tari)2 from bacillus subtilis
104	<a href="#">d1qwja</a>	 Alignment	not modelled	45.7	8	<b>Fold:</b> Nucleotide-diphospho-sugar transferases <b>Superfamily:</b> Nucleotide-diphospho-sugar transferases <b>Family:</b> Cytidylyltransferase
105	<a href="#">c2we7A</a>	 Alignment	not modelled	42.9	14	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> xanthine dehydrogenase; <b>PDBTitle:</b> crystal structure of mycobacterium tuberculosis tuberculosis rv0376c2 homologue from mycobacterium smegmatis
106	<a href="#">d1vpaA</a>	 Alignment	not modelled	42.6	9	<b>Fold:</b> Nucleotide-diphospho-sugar transferases <b>Superfamily:</b> Nucleotide-diphospho-sugar transferases <b>Family:</b> Cytidylyltransferase
107	<a href="#">c5yh1A</a>	 Alignment	not modelled	39.6	14	<b>PDB header:</b> ribosomal protein <b>Chain:</b> A: <b>PDB Molecule:</b> member of s1p family of ribosomal proteins; <b>PDBTitle:</b> member of s1p family of ribosomal proteins pf0399 dhh domain
108	<a href="#">c4evwB</a>	 Alignment	not modelled	39.5	12	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> nucleoside-diphosphate-sugar pyrophosphorylase; <b>PDBTitle:</b> crystal structure of the nucleoside-diphosphate-sugar2 pyrophosphorylase from vibrio cholerae rc9. northeast structural3 genomics consortium (nesg) target vcr193.
109	<a href="#">c3gqnA</a>	 Alignment	not modelled	38.3	14	<b>PDB header:</b> viral protein <b>Chain:</b> A: <b>PDB Molecule:</b> preneck appendage protein; <b>PDBTitle:</b> crystal structure of the pre-mature bacteriophage phi29 gene product2 12
110	<a href="#">c3ssoE</a>	 Alignment	not modelled	35.9	29	<b>PDB header:</b> transferase <b>Chain:</b> E: <b>PDB Molecule:</b> methyltransferase; <b>PDBTitle:</b> myce methyltransferase from the mycinamycin biosynthetic pathway in2 complex with mg and sah, crystal form 2
111	<a href="#">c6cglA</a>	 Alignment	not modelled	35.3	29	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> effector protein lem4 (lpg1101); <b>PDBTitle:</b> structure of the had domain of effector protein lem4 (lpg1101) from2 legionella pneumophila
112	<a href="#">c6aokA</a>	 Alignment	not modelled	34.0	33	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> ceg4; <b>PDBTitle:</b> crystal structure of legionella pneumophila effector ceg4 with n-2 terminal tev protease cleavage sequence
113	<a href="#">d1eyra</a>	 Alignment	not modelled	33.6	11	<b>Fold:</b> Nucleotide-diphospho-sugar transferases <b>Superfamily:</b> Nucleotide-diphospho-sugar transferases <b>Family:</b> Cytidylyltransferase
114	<a href="#">d2cu2a2</a>	 Alignment	not modelled	33.2	17	<b>Fold:</b> Nucleotide-diphospho-sugar transferases <b>Superfamily:</b> Nucleotide-diphospho-sugar transferases <b>Family:</b> mannose-1-phosphate guanylyl transferase
115	<a href="#">c3d98A</a>	 Alignment	not modelled	31.9	15	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> bifunctional protein glmu; <b>PDBTitle:</b> crystal structure of glmu from mycobacterium tuberculosis, ligand-free2 form
116	<a href="#">c3tztB</a>	 Alignment	not modelled	29.9	12	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> glycosyl transferase family 8; <b>PDBTitle:</b> the structure of a protein in glycosyl transferase family 8 from2 anaerococcus prevotii.
117	<a href="#">c5l6sF</a>	 Alignment	not modelled	29.6	14	<b>PDB header:</b> transferase <b>Chain:</b> F: <b>PDB Molecule:</b> glucose-1-phosphate adenyltransferase; <b>PDBTitle:</b> crystal structure of e. coli adp-glucose pyrophosphorylase (aggpase) in2 complex with a positive allosteric regulator beta-fructose-1,6-3 diphosphate (fbp) - agpase*fbp
118	<a href="#">c1jylC</a>	 Alignment	not modelled	27.1	10	<b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> ctp:phosphocholine cytidylyltransferase; <b>PDBTitle:</b> catalytic mechanism of ctp:phosphocholine2 cytidylyltransferase from streptococcus pneumoniae (licc)
119	<a href="#">c3ssmB</a>	 Alignment	not modelled	27.1	29	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> methyltransferase; <b>PDBTitle:</b> myce methyltransferase from the mycinamycin biosynthetic pathway in2 complex with mg and sah, crystal form 1
120	<a href="#">c4ehxA</a>	 Alignment	not modelled	26.5	24	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> tetraacyldisaccharide 4'-kinase; <b>PDBTitle:</b> crystal structure of lpxk from aquifex aeolicus at 1.9 angstrom2 resolution