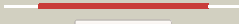



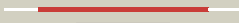



















# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2983 (-) _3339128_3339772
Date	Thu Aug 8 16:20:14 BST 2019
Unique Job ID	0da16308d5ad7239

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c6bwhB_</a>	 Alignment		100.0	100	<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
2	<a href="#">d2i5ea1</a>	 Alignment		100.0	24	<b>Fold:</b> Nucleotide-diphospho-sugar transferases <b>Superfamily:</b> Nucleotide-diphospho-sugar transferases <b>Family:</b> MM2497-like
3	<a href="#">c3cqxA_</a>	 Alignment		100.0	16	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> putative nucleotide-diphospho-sugar transferase; <b>PDBTitle:</b> crystal structure of putative nucleotide-diphospho-sugar transferase2 (yp_389115.1) from desulfovibrio desulfuricans g20 at 1.90 a3 resolution
4	<a href="#">c2wawA_</a>	 Alignment		99.9	19	<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
5	<a href="#">c2xwlB_</a>	 Alignment		99.8	16	<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
6	<a href="#">c2we9A_</a>	 Alignment		99.8	22	<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
7	<a href="#">d1vpaa_</a>	 Alignment		99.8	15	<b>Fold:</b> Nucleotide-diphospho-sugar transferases <b>Superfamily:</b> Nucleotide-diphospho-sugar transferases <b>Family:</b> Cytidyltransferase
8	<a href="#">d1w55a1</a>	 Alignment		99.8	11	<b>Fold:</b> Nucleotide-diphospho-sugar transferases <b>Superfamily:</b> Nucleotide-diphospho-sugar transferases <b>Family:</b> Cytidyltransferase
9	<a href="#">d1w77a1</a>	 Alignment		99.8	9	<b>Fold:</b> Nucleotide-diphospho-sugar transferases <b>Superfamily:</b> Nucleotide-diphospho-sugar transferases <b>Family:</b> Cytidyltransferase
10	<a href="#">c4kt7A_</a>	 Alignment		99.7	12	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> 2-c-methyl-d-erythritol 4-phosphate cytidyltransferase; <b>PDBTitle:</b> the crystal structure of 4-diphosphocytidyl-2c-methyl-d-2 erythritolsynthase from anaerococcus prevotii dsm 20548
11	<a href="#">c3okrA_</a>	 Alignment		99.7	17	<b>PDB header:</b> transferase <b>Chain:</b> A: <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)

12	<a href="#">c1w57A_</a>	Alignment		99.7	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
13	<a href="#">c5ddtA_</a>	Alignment		99.7	15	<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
14	<a href="#">c3okrC_</a>	Alignment		99.7	14	<b>PDB header:</b> transferase <b>Chain:</b> C: <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 cytidylyltransferase (ispd)
15	<a href="#">c3polA_</a>	Alignment		99.7	22	<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.
16	<a href="#">c6oewB_</a>	Alignment		99.7	14	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> cytidylyltransferase; <b>PDBTitle:</b> structure of a cytidylyltransferase from leptospira borgpetersenii2 serovar hardjo-bovis (strain jb197)
17	<a href="#">d1i52a_</a>	Alignment		99.7	17	<b>Fold:</b> Nucleotide-diphospho-sugar transferases <b>Superfamily:</b> Nucleotide-diphospho-sugar transferases <b>Family:</b> Cytidylyltransferase
18	<a href="#">c4ys8B_</a>	Alignment		99.7	18	<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
19	<a href="#">c4mybA_</a>	Alignment		99.7	11	<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)
20	<a href="#">dleyra_</a>	Alignment		99.7	19	<b>Fold:</b> Nucleotide-diphospho-sugar transferases <b>Superfamily:</b> Nucleotide-diphospho-sugar transferases <b>Family:</b> Cytidylyltransferase
21	<a href="#">c3f1cB_</a>	Alignment	not modelled	99.7	17	<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
22	<a href="#">d1qwja_</a>	Alignment	not modelled	99.7	15	<b>Fold:</b> Nucleotide-diphospho-sugar transferases <b>Superfamily:</b> Nucleotide-diphospho-sugar transferases <b>Family:</b> Cytidylyltransferase
23	<a href="#">d1e5ka_</a>	Alignment	not modelled	99.6	10	<b>Fold:</b> Nucleotide-diphospho-sugar transferases <b>Superfamily:</b> Nucleotide-diphospho-sugar transferases <b>Family:</b> Molybdenum cofactor biosynthesis protein MobA
24	<a href="#">d1vgwa_</a>	Alignment	not modelled	99.6	16	<b>Fold:</b> Nucleotide-diphospho-sugar transferases <b>Superfamily:</b> Nucleotide-diphospho-sugar transferases <b>Family:</b> Cytidylyltransferase
25	<a href="#">c3tqdA_</a>	Alignment	not modelled	99.6	21	<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
26	<a href="#">c4jisB_</a>	Alignment	not modelled	99.6	14	<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
27	<a href="#">c3rsbB_</a>	Alignment	not modelled	99.6	11	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> adenosylcobinamide-phosphate guanylyltransferase; <b>PDBTitle:</b> structure of the archaeal gtp:adocbi-p guanylyltransferase (coby) from2 methanocaldococcus jannaschii
						<b>PDB header:</b> transferase <b>Chain:</b> D: <b>PDB Molecule:</b> 3-deoxy-manno-octulosonate

28	<a href="#">c3oamD_</a>	Alignment	not modelled	99.6	17	cytidyltransferase; <b>PDBTitle:</b> crystal structure of cytidyltransferase from vibrio cholerae
29	<a href="#">c2px7A_</a>	Alignment	not modelled	99.6	13	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> 2-c-methyl-d-erythritol 4-phosphate cytidyltransferase; <b>PDBTitle:</b> crystal structure of 2-c-methyl-d-erythritol 4-phosphate2 cytidyltransferase from thermus thermophilus hb8
30	<a href="#">d1vica_</a>	Alignment	not modelled	99.6	20	<b>Fold:</b> Nucleotide-diphospho-sugar transferases <b>Superfamily:</b> Nucleotide-diphospho-sugar transferases <b>Family:</b> Cytidyltransferase
31	<a href="#">c2vshB_</a>	Alignment	not modelled	99.6	15	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> 2-c-methyl-d-erythritol 4-phosphate <b>PDBTitle:</b> synthesis of cdp-activated ribitol for teichoic acid2 precursors in streptococcus pneumoniae
32	<a href="#">c4cvhA_</a>	Alignment	not modelled	99.6	14	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> isoprenoid synthase domain-containing protein; <b>PDBTitle:</b> crystal structure of human isoprenoid synthase domain-containing2 protein
33	<a href="#">c4xwiA_</a>	Alignment	not modelled	99.6	24	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> 3-deoxy-manno-octulosonate cytidyltransferase; <b>PDBTitle:</b> x-ray crystal structure of cmp-kdo synthase from pseudomonas2 aeruginosa
34	<a href="#">d2oi6a2</a>	Alignment	not modelled	99.6	18	<b>Fold:</b> Nucleotide-diphospho-sugar transferases <b>Superfamily:</b> Nucleotide-diphospho-sugar transferases <b>Family:</b> UDP-glucose pyrophosphorylase
35	<a href="#">c3ngwA_</a>	Alignment	not modelled	99.6	14	<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
36	<a href="#">c3d5nB_</a>	Alignment	not modelled	99.6	15	<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.
37	<a href="#">d1h7ea_</a>	Alignment	not modelled	99.6	23	<b>Fold:</b> Nucleotide-diphospho-sugar transferases <b>Superfamily:</b> Nucleotide-diphospho-sugar transferases <b>Family:</b> Cytidyltransferase
38	<a href="#">d2dpwa1</a>	Alignment	not modelled	99.5	22	<b>Fold:</b> Nucleotide-diphospho-sugar transferases <b>Superfamily:</b> Nucleotide-diphospho-sugar transferases <b>Family:</b> TTHA0179-like
39	<a href="#">c6ifdD_</a>	Alignment	not modelled	99.5	20	<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+.
40	<a href="#">c2y6pC_</a>	Alignment	not modelled	99.5	18	<b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> 3-deoxy-manno-octulosonate cytidyltransferase; <b>PDBTitle:</b> evidence for a two-metal-ion-mechanism in the kdo-2 cytidyltransferase kdsb
41	<a href="#">c2e8bA_</a>	Alignment	not modelled	99.4	13	<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
42	<a href="#">d1g97a2</a>	Alignment	not modelled	99.4	16	<b>Fold:</b> Nucleotide-diphospho-sugar transferases <b>Superfamily:</b> Nucleotide-diphospho-sugar transferases <b>Family:</b> UDP-glucose pyrophosphorylase
43	<a href="#">d1vh1a_</a>	Alignment	not modelled	99.3	26	<b>Fold:</b> Nucleotide-diphospho-sugar transferases <b>Superfamily:</b> Nucleotide-diphospho-sugar transferases <b>Family:</b> Cytidyltransferase
44	<a href="#">c4mndA_</a>	Alignment	not modelled	99.3	14	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> ctp l-myo-inositol-1-phosphate cytidyltransferase/cdp-l- <b>PDBTitle:</b> crystal structure of archaeoglobus fulgidus ipct-dipps bifunctional2 membrane protein
45	<a href="#">c4jd0A_</a>	Alignment	not modelled	99.2	14	<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.
46	<a href="#">c5xhwA_</a>	Alignment	not modelled	99.2	17	<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
47	<a href="#">c4y7uA_</a>	Alignment	not modelled	99.2	17	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> nucleotidyl transferase; <b>PDBTitle:</b> structural analysis of muru
48	<a href="#">c3hl3A_</a>	Alignment	not modelled	99.2	14	<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.
49	<a href="#">d1vh3a_</a>	Alignment	not modelled	99.1	17	<b>Fold:</b> Nucleotide-diphospho-sugar transferases <b>Superfamily:</b> Nucleotide-diphospho-sugar transferases <b>Family:</b> Cytidyltransferase
50	<a href="#">d1jyka_</a>	Alignment	not modelled	99.0	10	<b>Fold:</b> Nucleotide-diphospho-sugar transferases <b>Superfamily:</b> Nucleotide-diphospho-sugar transferases <b>Family:</b> Cytidyltransferase
51	<a href="#">c3d8vA_</a>	Alignment	not modelled	98.9	24	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> bifunctional protein glmu; <b>PDBTitle:</b> crystal structure of uridine from mycobacterium tuberculosis2 in complex with uridine-diphosphate-n-acetylglucosamine

52	<a href="#">c3pnnA</a>	Alignment	not modelled	98.8	16	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> conserved domain protein; <b>PDBTitle:</b> the crystal structure of a glycosyltransferase from porphyromonas2 gingivalis w83
53	<a href="#">c1hm8A</a>	Alignment	not modelled	98.8	14	<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
54	<a href="#">c1jylC</a>	Alignment	not modelled	98.8	11	<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)
55	<a href="#">c3foqA</a>	Alignment	not modelled	98.8	25	<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.
56	<a href="#">c2v0hA</a>	Alignment	not modelled	98.8	18	<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)
57	<a href="#">c2oi6A</a>	Alignment	not modelled	98.8	16	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> bifunctional protein glmu; <b>PDBTitle:</b> e. coli glmu- complex with udp-glcnac, coa and glcn-1-po4
58	<a href="#">d1tzfa</a>	Alignment	not modelled	98.7	13	<b>Fold:</b> Nucleotide-diphospho-sugar transferases <b>Superfamily:</b> Nucleotide-diphospho-sugar transferases <b>Family:</b> Cytidylyltransferase
59	<a href="#">c2pa4B</a>	Alignment	not modelled	98.7	20	<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
60	<a href="#">d1h5ra</a>	Alignment	not modelled	98.6	21	<b>Fold:</b> Nucleotide-diphospho-sugar transferases <b>Superfamily:</b> Nucleotide-diphospho-sugar transferases <b>Family:</b> glucose-1-phosphate thymidylyltransferase
61	<a href="#">c5i1fA</a>	Alignment	not modelled	98.6	19	<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
62	<a href="#">c3d98A</a>	Alignment	not modelled	98.6	26	<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
63	<a href="#">d1fxoa</a>	Alignment	not modelled	98.6	20	<b>Fold:</b> Nucleotide-diphospho-sugar transferases <b>Superfamily:</b> Nucleotide-diphospho-sugar transferases <b>Family:</b> glucose-1-phosphate thymidylyltransferase
64	<a href="#">c3jukA</a>	Alignment	not modelled	98.6	16	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> udp-glucose pyrophosphorylase (galu); <b>PDBTitle:</b> the crystal structure of udp-glucose pyrophosphorylase complexed with2 udp-glucose
65	<a href="#">c5vmkB</a>	Alignment	not modelled	98.5	14	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> bifunctional protein glmu; <b>PDBTitle:</b> crystal structure of a bifunctional glmu udp-n-acetylglucosamine2 diphosphorylase/glucosamine-1- phosphate n-acetyltransferase from3 acinetobacter baumannii
66	<a href="#">c4evwB</a>	Alignment	not modelled	98.5	11	<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 (nesh) target vcr193.
67	<a href="#">c1fwyA</a>	Alignment	not modelled	98.5	17	<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-glcnac
68	<a href="#">c2qkxA</a>	Alignment	not modelled	98.5	25	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> bifunctional protein glmu; <b>PDBTitle:</b> n-acetyl glucosamine 1-phosphate uridylyltransferase from mycobacterium2 tuberculosis complex with n-acetyl glucosamine 1-phosphate
69	<a href="#">d1iina</a>	Alignment	not modelled	98.4	20	<b>Fold:</b> Nucleotide-diphospho-sugar transferases <b>Superfamily:</b> Nucleotide-diphospho-sugar transferases <b>Family:</b> glucose-1-phosphate thymidylyltransferase
70	<a href="#">c2e3dB</a>	Alignment	not modelled	98.4	14	<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
71	<a href="#">d1mc3a</a>	Alignment	not modelled	98.4	16	<b>Fold:</b> Nucleotide-diphospho-sugar transferases <b>Superfamily:</b> Nucleotide-diphospho-sugar transferases <b>Family:</b> glucose-1-phosphate thymidylyltransferase
72	<a href="#">c2cu2A</a>	Alignment	not modelled	98.4	16	<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
73	<a href="#">c2x5sB</a>	Alignment	not modelled	98.3	15	<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.
						<b>Fold:</b> Nucleotide-diphospho-sugar transferases

74	<a href="#">d2cu2a2</a>	Alignment	not modelled	98.2	21	<b>Superfamily:</b> Nucleotide-diphospho-sugar transferases <b>Family:</b> mannose-1-phosphate guanylyl transferase
75	<a href="#">c6b5kA</a>	Alignment	not modelled	98.2	16	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> glucose-1-phosphate thymidyltransferase; <b>PDBTitle:</b> mycobacterium tuberculosis rmla in complex with mg/dttp
76	<a href="#">c2ux8G</a>	Alignment	not modelled	98.1	15	<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.
77	<a href="#">c1yp3C</a>	Alignment	not modelled	98.0	19	<b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> glucose-1-phosphate adenyllyltransferase small <b>PDBTitle:</b> crystal structure of potato tuber adp-glucose2 pyrophosphorylase in complex with atp
78	<a href="#">d1lvwa</a>	Alignment	not modelled	98.0	14	<b>Fold:</b> Nucleotide-diphospho-sugar transferases <b>Superfamily:</b> Nucleotide-diphospho-sugar transferases <b>Family:</b> glucose-1-phosphate thymidyltransferase
79	<a href="#">d1yp2a2</a>	Alignment	not modelled	97.9	15	<b>Fold:</b> Nucleotide-diphospho-sugar transferases <b>Superfamily:</b> Nucleotide-diphospho-sugar transferases <b>Family:</b> glucose-1-phosphate thymidyltransferase
80	<a href="#">c2qh5B</a>	Alignment	not modelled	97.9	12	<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="#">c5l6sF</a>	Alignment	not modelled	97.8	15	<b>PDB header:</b> transferase <b>Chain:</b> F: <b>PDB Molecule:</b> glucose-1-phosphate adenyllyltransferase; <b>PDBTitle:</b> crystal structure of e. coli adp-glucose pyrophosphorylase (agpase) in2 complex with a positive allosteric regulator beta-fructose-1,6-3 diphosphate (fbp) - agpase*fbp
82	<a href="#">c6jlwJ</a>	Alignment	not modelled	97.7	10	<b>PDB header:</b> translation <b>Chain:</b> J: <b>PDB Molecule:</b> translation initiation factor eif-2b subunit epsilon; <b>PDBTitle:</b> eif2 - eif2b complex
83	<a href="#">c5b04I</a>	Alignment	not modelled	97.6	8	<b>PDB header:</b> translation <b>Chain:</b> I: <b>PDB Molecule:</b> probable translation initiation factor eif-2b subunit <b>PDBTitle:</b> crystal structure of the eukaryotic translation initiation factor 2b2 from schizosaccharomyces pombe
84	<a href="#">c3brkX</a>	Alignment	not modelled	97.6	15	<b>PDB header:</b> transferase <b>Chain:</b> X: <b>PDB Molecule:</b> glucose-1-phosphate adenyllyltransferase; <b>PDBTitle:</b> crystal structure of adp-glucose pyrophosphorylase from agrobacterium2 tumefaciens
85	<a href="#">c6i3mG</a>	Alignment	not modelled	97.3	8	<b>PDB header:</b> translation <b>Chain:</b> G: <b>PDB Molecule:</b> translation initiation factor eif-2b subunit epsilon; <b>PDBTitle:</b> eif2b:eif2 complex, phosphorylated on eif2 alpha serine 52.
86	<a href="#">c5b04F</a>	Alignment	not modelled	97.2	18	<b>PDB header:</b> translation <b>Chain:</b> F: <b>PDB Molecule:</b> probable translation initiation factor eif-2b subunit <b>PDBTitle:</b> crystal structure of the eukaryotic translation initiation factor 2b2 from schizosaccharomyces pombe
87	<a href="#">c2ggqA</a>	Alignment	not modelled	97.2	11	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> 401aa long hypothetical glucose-1-phosphate <b>PDBTitle:</b> complex of hypothetical glucose-1-phosphate thymidyltransferase from2 sulfolobus tokodaii
88	<a href="#">c2xmhB</a>	Alignment	not modelled	96.7	11	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> ctp-inositol-1-phosphate cytidyltransferase; <b>PDBTitle:</b> the x-ray structure of ctp:inositol-1-phosphate cytidyltransferase2 from archaeoglobus fulgidus
89	<a href="#">c6qq2F</a>	Alignment	not modelled	96.4	9	<b>PDB header:</b> translation <b>Chain:</b> F: <b>PDB Molecule:</b> translation initiation factor eif-2b subunit gamma; <b>PDBTitle:</b> structure of eif2b-eif2 (phosphorylated at ser51) complex (model a)
90	<a href="#">c6ezoF</a>	Alignment	not modelled	95.4	17	<b>PDB header:</b> membrane protein <b>Chain:</b> F: <b>PDB Molecule:</b> translation initiation factor eif-2b subunit gamma; <b>PDBTitle:</b> eukaryotic initiation factor eif2b in complex with isrib
91	<a href="#">c3ckvA</a>	Alignment	not modelled	94.1	13	<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
92	<a href="#">c5mm1A</a>	Alignment	not modelled	92.6	17	<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
93	<a href="#">c4fixA</a>	Alignment	not modelled	90.5	14	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> udp-galactofuranosyl transferase glft2; <b>PDBTitle:</b> crystal structure of glft2
94	<a href="#">d1omza</a>	Alignment	not modelled	88.7	13	<b>Fold:</b> Nucleotide-diphospho-sugar transferases <b>Superfamily:</b> Nucleotide-diphospho-sugar transferases <b>Family:</b> Exostosin
95	<a href="#">c1omxB</a>	Alignment	not modelled	86.9	18	<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)
96	<a href="#">c2ffuA</a>	Alignment	not modelled	85.6	14	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> polypeptide n-acetylgalactosaminyltransferase 2; <b>PDBTitle:</b> crystal structure of human ppgalnact-2 complexed with udp and ea2 <b>PDB header:</b> membrane protein



97	<a href="#">c6ezoJ_</a>	Alignment	not modelled	79.6	12	<b>Chain:</b> J: <b>PDB Molecule:</b> human eukaryotic initiation factor eif2b epsilon subunits; <b>PDBTitle:</b> eukaryotic initiation factor eif2b in complex with isrib
98	<a href="#">c3f1yC_</a>	Alignment	not modelled	79.3	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
99	<a href="#">c2z86D_</a>	Alignment	not modelled	74.5	11	<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
100	<a href="#">c1xhbA_</a>	Alignment	not modelled	70.9	14	<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
101	<a href="#">c5nqaA_</a>	Alignment	not modelled	65.0	9	<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
102	<a href="#">c6i7tI_</a>	Alignment	not modelled	63.5	12	<b>PDB header:</b> translation <b>Chain:</b> I: <b>PDB Molecule:</b> translation initiation factor eif-2b subunit gamma; <b>PDBTitle:</b> eif2b:eif2 complex
103	<a href="#">c6e4rB_</a>	Alignment	not modelled	60.8	10	<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
104	<a href="#">d2bo4a1</a>	Alignment	not modelled	59.6	14	<b>Fold:</b> Nucleotide-diphospho-sugar transferases <b>Superfamily:</b> Nucleotide-diphospho-sugar transferases <b>Family:</b> MGS-like
105	<a href="#">c5ekeB_</a>	Alignment	not modelled	54.3	12	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> uncharacterized glycosyltransferase sll0501; <b>PDBTitle:</b> structure of the polyisoprenyl-phosphate glycosyltransferase gtrb2 (f215a mutant)
106	<a href="#">c2d7iA_</a>	Alignment	not modelled	50.9	10	<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+
107	<a href="#">c5tz8C_</a>	Alignment	not modelled	44.1	12	<b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> glycosyl transferase; <b>PDBTitle:</b> crystal structure of s. aureus tars
108	<a href="#">c4hg6A_</a>	Alignment	not modelled	43.2	20	<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
109	<a href="#">c6h4mA_</a>	Alignment	not modelled	42.9	11	<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
110	<a href="#">c6iwiqE_</a>	Alignment	not modelled	34.6	10	<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+
111	<a href="#">d1xhba2</a>	Alignment	not modelled	24.9	15	<b>Fold:</b> Nucleotide-diphospho-sugar transferases <b>Superfamily:</b> Nucleotide-diphospho-sugar transferases <b>Family:</b> Polypeptide N-acetylgalactosaminyltransferase 1, N-terminal domain