


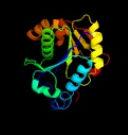



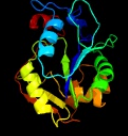
















# Phyre2

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 Description RVBD2453c\_(mobA)\_2753028\_2753633  
 Date Wed Aug 7 12:50:08 BST 2019  
 Unique Job ID 4f8e1c26b4a86f48

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">d1e5ka_</a>	 Alignment		100.0	27	<b>Fold:</b> Nucleotide-diphospho-sugar transferases <b>Superfamily:</b> Nucleotide-diphospho-sugar transferases <b>Family:</b> Molybdenum cofactor biosynthesis protein MobA
2	<a href="#">c2e8bA_</a>	 Alignment		100.0	23	<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
3	<a href="#">c3ngwA_</a>	 Alignment		100.0	21	<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
4	<a href="#">c2wawA_</a>	 Alignment		100.0	18	<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="#">c2we9A_</a>	 Alignment		100.0	17	<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
6	<a href="#">d1w55a1</a>	 Alignment		99.9	11	<b>Fold:</b> Nucleotide-diphospho-sugar transferases <b>Superfamily:</b> Nucleotide-diphospho-sugar transferases <b>Family:</b> Cytidylyltransferase
7	<a href="#">d1i52a_</a>	 Alignment		99.9	19	<b>Fold:</b> Nucleotide-diphospho-sugar transferases <b>Superfamily:</b> Nucleotide-diphospho-sugar transferases <b>Family:</b> Cytidylyltransferase
8	<a href="#">d1vpaa_</a>	 Alignment		99.9	17	<b>Fold:</b> Nucleotide-diphospho-sugar transferases <b>Superfamily:</b> Nucleotide-diphospho-sugar transferases <b>Family:</b> Cytidylyltransferase
9	<a href="#">c2xwIB_</a>	 Alignment		99.9	20	<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 ispd from mycobacterium smegmatis in complex with2 ctp and mg
10	<a href="#">c5ddtA_</a>	 Alignment		99.9	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> crystal structure of ispd from bacillus subtilis at 1.80 angstroms2 resolution, crystal form i
11	<a href="#">d2oi6a2</a>	 Alignment		99.9	16	<b>Fold:</b> Nucleotide-diphospho-sugar transferases <b>Superfamily:</b> Nucleotide-diphospho-sugar transferases <b>Family:</b> UDP-glucose pyrophosphorylase

12	<a href="#">c1w57A_</a>	Alignment		99.9	13	<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="#">c3d5nB_</a>	Alignment		99.9	16	<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.
14	<a href="#">c4mybA_</a>	Alignment		99.9	13	<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)
15	<a href="#">c6oewB_</a>	Alignment		99.9	10	<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)
16	<a href="#">c4kt7A_</a>	Alignment		99.9	13	<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
17	<a href="#">c4mndA_</a>	Alignment		99.9	17	<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
18	<a href="#">c3oamD_</a>	Alignment		99.9	14	<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
19	<a href="#">c3rsbB_</a>	Alignment		99.9	16	<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
20	<a href="#">d2dpwa1</a>	Alignment		99.9	23	<b>Fold:</b> Nucleotide-diphospho-sugar transferases <b>Superfamily:</b> Nucleotide-diphospho-sugar transferases <b>Family:</b> TTHA0179-like
21	<a href="#">c4xwiA_</a>	Alignment	not modelled	99.9	17	<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
22	<a href="#">d1w77a1</a>	Alignment	not modelled	99.9	18	<b>Fold:</b> Nucleotide-diphospho-sugar transferases <b>Superfamily:</b> Nucleotide-diphospho-sugar transferases <b>Family:</b> Cytidylyltransferase
23	<a href="#">c3polA_</a>	Alignment	not modelled	99.9	18	<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.
24	<a href="#">d1vica_</a>	Alignment	not modelled	99.9	16	<b>Fold:</b> Nucleotide-diphospho-sugar transferases <b>Superfamily:</b> Nucleotide-diphospho-sugar transferases <b>Family:</b> Cytidylyltransferase
25	<a href="#">c3pnnA_</a>	Alignment	not modelled	99.9	19	<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
26	<a href="#">c2px7A_</a>	Alignment	not modelled	99.9	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
27	<a href="#">d1eyra_</a>	Alignment	not modelled	99.9	15	<b>Fold:</b> Nucleotide-diphospho-sugar transferases <b>Superfamily:</b> Nucleotide-diphospho-sugar transferases <b>Family:</b> Cytidylyltransferase
						<b>Fold:</b> Nucleotide-diphospho-sugar transferases

28	<a href="#">d1g97a2</a>	Alignment	not modelled	99.9	16	<b>Superfamily:</b> Nucleotide-diphospho-sugar transferases <b>Family:</b> UDP-glucose pyrophosphorylase
29	<a href="#">c3foqA_</a>	Alignment	not modelled	99.9	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.
30	<a href="#">d1qwja_</a>	Alignment	not modelled	99.9	13	<b>Fold:</b> Nucleotide-diphospho-sugar transferases <b>Superfamily:</b> Nucleotide-diphospho-sugar transferases <b>Family:</b> Cytidylyltransferase
31	<a href="#">c3d8vA_</a>	Alignment	not modelled	99.9	17	<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
32	<a href="#">c4jd0A_</a>	Alignment	not modelled	99.8	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.
33	<a href="#">c3f1cB_</a>	Alignment	not modelled	99.8	15	<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
34	<a href="#">c2y6pC_</a>	Alignment	not modelled	99.8	18	<b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> 3-deoxy-manno-octulosonate cytidylyltransferase; <b>PDBTitle:</b> evidence for a two-metal-ion-mechanism in the kdo-2 cytidylyltransferase kdsb
35	<a href="#">c4y7uA_</a>	Alignment	not modelled	99.8	16	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> nucleotidyl transferase; <b>PDBTitle:</b> structural analysis of muru
36	<a href="#">d1h7ea_</a>	Alignment	not modelled	99.8	16	<b>Fold:</b> Nucleotide-diphospho-sugar transferases <b>Superfamily:</b> Nucleotide-diphospho-sugar transferases <b>Family:</b> Cytidylyltransferase
37	<a href="#">d1jyka_</a>	Alignment	not modelled	99.8	12	<b>Fold:</b> Nucleotide-diphospho-sugar transferases <b>Superfamily:</b> Nucleotide-diphospho-sugar transferases <b>Family:</b> Cytidylyltransferase
38	<a href="#">c1jyC_</a>	Alignment	not modelled	99.8	13	<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)
39	<a href="#">c3tqdA_</a>	Alignment	not modelled	99.8	15	<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
40	<a href="#">d1iina_</a>	Alignment	not modelled	99.8	14	<b>Fold:</b> Nucleotide-diphospho-sugar transferases <b>Superfamily:</b> Nucleotide-diphospho-sugar transferases <b>Family:</b> glucose-1-phosphate thymidylyltransferase
41	<a href="#">d1h5ra_</a>	Alignment	not modelled	99.8	17	<b>Fold:</b> Nucleotide-diphospho-sugar transferases <b>Superfamily:</b> Nucleotide-diphospho-sugar transferases <b>Family:</b> glucose-1-phosphate thymidylyltransferase
42	<a href="#">c3hl3A_</a>	Alignment	not modelled	99.8	16	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> glucose-1-phosphate thymidylyltransferase; <b>PDBTitle:</b> 2.76 angstrom crystal structure of a putative glucose-1-phosphate2 thymidylyltransferase from bacillus anthracis in complex with a3 sucrose.
43	<a href="#">d1fxoa_</a>	Alignment	not modelled	99.8	17	<b>Fold:</b> Nucleotide-diphospho-sugar transferases <b>Superfamily:</b> Nucleotide-diphospho-sugar transferases <b>Family:</b> glucose-1-phosphate thymidylyltransferase
44	<a href="#">c5xhwA_</a>	Alignment	not modelled	99.8	12	<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
45	<a href="#">c2pa4B_</a>	Alignment	not modelled	99.8	15	<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
46	<a href="#">c5i1fA_</a>	Alignment	not modelled	99.8	14	<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
47	<a href="#">c3jukA_</a>	Alignment	not modelled	99.8	12	<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
48	<a href="#">d1mc3a_</a>	Alignment	not modelled	99.8	13	<b>Fold:</b> Nucleotide-diphospho-sugar transferases <b>Superfamily:</b> Nucleotide-diphospho-sugar transferases <b>Family:</b> glucose-1-phosphate thymidylyltransferase
49	<a href="#">c2e3dB_</a>	Alignment	not modelled	99.8	15	<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
50	<a href="#">d1lwva_</a>	Alignment	not modelled	99.8	14	<b>Fold:</b> Nucleotide-diphospho-sugar transferases <b>Superfamily:</b> Nucleotide-diphospho-sugar transferases <b>Family:</b> glucose-1-phosphate thymidylyltransferase
51	<a href="#">c6b5kA_</a>	Alignment	not modelled	99.8	15	<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
52	<a href="#">c3okrA_</a>	Alignment	not modelled	99.8	19	<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)
53	<a href="#">c4ys8B_</a>	Alignment	not modelled	99.8	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 2-c-methyl-d-erythritol 4-phosphate2 cytidyltransferase (ispd) from burkholderia thailandensis
54	<a href="#">d1vgwa_</a>	Alignment	not modelled	99.8	16	<b>Fold:</b> Nucleotide-diphospho-sugar transferases <b>Superfamily:</b> Nucleotide-diphospho-sugar transferases <b>Family:</b> Cytidylyltransferase
55	<a href="#">c6bwhB_</a>	Alignment	not modelled	99.8	16	<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
56	<a href="#">c2ux8G_</a>	Alignment	not modelled	99.8	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.
57	<a href="#">c1hm8A_</a>	Alignment	not modelled	99.7	16	<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
58	<a href="#">c2oi6A_</a>	Alignment	not modelled	99.7	13	<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
59	<a href="#">c4evwB_</a>	Alignment	not modelled	99.7	16	<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.
60	<a href="#">c2vshB_</a>	Alignment	not modelled	99.7	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
61	<a href="#">c2qkxA_</a>	Alignment	not modelled	99.7	24	<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
62	<a href="#">c3d98A_</a>	Alignment	not modelled	99.7	21	<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="#">d1tzfa_</a>	Alignment	not modelled	99.7	14	<b>Fold:</b> Nucleotide-diphospho-sugar transferases <b>Superfamily:</b> Nucleotide-diphospho-sugar transferases <b>Family:</b> Cytidylyltransferase
64	<a href="#">d2cu2a2</a>	Alignment	not modelled	99.7	24	<b>Fold:</b> Nucleotide-diphospho-sugar transferases <b>Superfamily:</b> Nucleotide-diphospho-sugar transferases <b>Family:</b> mannose-1-phosphate guanylyl transferase
65	<a href="#">c2v0hA_</a>	Alignment	not modelled	99.7	20	<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)
66	<a href="#">c1fwyA_</a>	Alignment	not modelled	99.7	18	<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
67	<a href="#">c2cu2A_</a>	Alignment	not modelled	99.7	21	<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
68	<a href="#">c4jisB_</a>	Alignment	not modelled	99.7	13	<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
69	<a href="#">d1vh1a_</a>	Alignment	not modelled	99.7	14	<b>Fold:</b> Nucleotide-diphospho-sugar transferases <b>Superfamily:</b> Nucleotide-diphospho-sugar transferases <b>Family:</b> Cytidylyltransferase
70	<a href="#">c5l6sF_</a>	Alignment	not modelled	99.6	16	<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
71	<a href="#">c1yp3C_</a>	Alignment	not modelled	99.6	16	<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
72	<a href="#">c3okrC_</a>	Alignment	not modelled	99.6	18	<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 cytidyltransferase (ispd)
73	<a href="#">c4cvhA_</a>	Alignment	not modelled	99.6	16	<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
						<b>PDB header:</b> transferase

74	<a href="#">c5vmkB_</a>	Alignment	not modelled	99.6	16	<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 from <i>Acinetobacter baumannii</i>
75	<a href="#">c3brkX_</a>	Alignment	not modelled	99.6	15	<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 <i>Agrobacterium tumefaciens</i>
76	<a href="#">d1yp2a2</a>	Alignment	not modelled	99.6	15	<b>Fold:</b> Nucleotide-diphospho-sugar transferases <b>Superfamily:</b> Nucleotide-diphospho-sugar transferases <b>Family:</b> glucose-1-phosphate thymidyltransferase
77	<a href="#">c6ifdD_</a>	Alignment	not modelled	99.6	16	<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 <i>Vibrio cholerae</i> in complex with cdp and mg2+
78	<a href="#">c2x5sB_</a>	Alignment	not modelled	99.5	18	<b>PDB header:</b> transferase <b>Chain:</b> B; <b>PDB Molecule:</b> mannose-1-phosphate guanylyltransferase; <b>PDBTitle:</b> crystal structure of <i>T. maritima</i> gdp-mannose2 pyrophosphorylase in apo state.
79	<a href="#">c2ggqA_</a>	Alignment	not modelled	99.5	17	<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 from <i>Sulfolobus tokodaii</i>
80	<a href="#">c5b04I_</a>	Alignment	not modelled	99.5	14	<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 <i>Schizosaccharomyces pombe</i>
81	<a href="#">c6i3mG_</a>	Alignment	not modelled	99.4	12	<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.
82	<a href="#">c2xmhB_</a>	Alignment	not modelled	99.4	15	<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 <i>Archaeoglobus fulgidus</i>
83	<a href="#">c6ezoF_</a>	Alignment	not modelled	99.4	16	<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
84	<a href="#">c6jlwJ_</a>	Alignment	not modelled	99.3	13	<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
85	<a href="#">c5b04F_</a>	Alignment	not modelled	99.3	12	<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 <i>Schizosaccharomyces pombe</i>
86	<a href="#">c2qh5B_</a>	Alignment	not modelled	99.3	14	<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 <i>Helicobacter pylori</i>
87	<a href="#">c6qq2F_</a>	Alignment	not modelled	99.2	12	<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)
88	<a href="#">d1vh3a_</a>	Alignment	not modelled	99.1	10	<b>Fold:</b> Nucleotide-diphospho-sugar transferases <b>Superfamily:</b> Nucleotide-diphospho-sugar transferases <b>Family:</b> Cytidyltransferase
89	<a href="#">c3cgxA_</a>	Alignment	not modelled	99.1	17	<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 <i>Desulfovibrio desulfuricans</i> g20 at 1.90 a3 resolution
90	<a href="#">d2i5ea1</a>	Alignment	not modelled	98.8	11	<b>Fold:</b> Nucleotide-diphospho-sugar transferases <b>Superfamily:</b> Nucleotide-diphospho-sugar transferases <b>Family:</b> MM2497-like
91	<a href="#">d2icya2</a>	Alignment	not modelled	98.0	15	<b>Fold:</b> Nucleotide-diphospho-sugar transferases <b>Superfamily:</b> Nucleotide-diphospho-sugar transferases <b>Family:</b> UDP-glucose pyrophosphorylase
92	<a href="#">c3r2wB_</a>	Alignment	not modelled	97.9	22	<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 of <i>Homo sapiens</i>
93	<a href="#">c3oc9A_</a>	Alignment	not modelled	97.9	17	<b>PDB header:</b> transferase <b>Chain:</b> A; <b>PDB Molecule:</b> udp-n-acetylglucosamine pyrophosphorylase; <b>PDBTitle:</b> crystal structure of putative udp-n-acetylglucosamine2 pyrophosphorylase from <i>Entamoeba histolytica</i>
94	<a href="#">c4bqhA_</a>	Alignment	not modelled	97.8	18	<b>PDB header:</b> transferase <b>Chain:</b> A; <b>PDB Molecule:</b> udp-n-acetylglucosamine pyrophosphorylase; <b>PDBTitle:</b> crystal structure of the uridine diphosphate n-2 acetylglucosamine pyrophosphorylase from <i>Trypanosoma brucei</i> in complex with inhibitor
95	<a href="#">d1vm8a_</a>	Alignment	not modelled	97.7	24	<b>Fold:</b> Nucleotide-diphospho-sugar transferases <b>Superfamily:</b> Nucleotide-diphospho-sugar transferases <b>Family:</b> UDP-glucose pyrophosphorylase
96	<a href="#">c2x4iB_</a>	Alignment	not modelled	97.7	22	<b>PDB header:</b> transferase <b>Chain:</b> B; <b>PDB Molecule:</b> probable utp-glucose-1-phosphate uridylyltransferase 2;

96	<a href="#">c2q4pB</a>	Alignment	not modelled	97.7	22	<b>PDBTitle:</b> ensemble refinement of the protein crystal structure of gene product2 from arabidopsis thaliana at3g03250, a putative udp-glucose3 pyrophosphorylase
97	<a href="#">c4bmaB</a>	Alignment	not modelled	97.7	21	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> udp-n-acetylglucosamine pyrophosphorylase; <b>PDBTitle:</b> structural of aspergillus fumigatus udp-n-acetylglucosamine2 pyrophosphorylase
98	<a href="#">d1jv1a</a>	Alignment	not modelled	97.7	24	<b>Fold:</b> Nucleotide-diphospho-sugar transferases <b>Superfamily:</b> Nucleotide-diphospho-sugar transferases <b>Family:</b> UDP-glucose pyrophosphorylase
99	<a href="#">c2yqsA</a>	Alignment	not modelled	97.7	17	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> udp-n-acetylglucosamine pyrophosphorylase; <b>PDBTitle:</b> crystal structure of uridine-diphospho-n-acetylglucosamine2 pyrophosphorylase from candida albicans, in the product-binding form
100	<a href="#">c2i5kB</a>	Alignment	not modelled	97.6	24	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> utp--glucose-1-phosphate uridylyltransferase; <b>PDBTitle:</b> crystal structure of ugp1p
101	<a href="#">c2oefA</a>	Alignment	not modelled	97.6	17	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> utp-glucose-1-phosphate uridylyltransferase 2, <b>PDBTitle:</b> open and closed structures of the udp-glucose2 pyrophosphorylase from leishmania major
102	<a href="#">c3gueB</a>	Alignment	not modelled	97.5	22	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> utp-glucose-1-phosphate uridylyltransferase 2; <b>PDBTitle:</b> crystal structure of udp-glucose phosphorylase from trypanosoma2 brucei, (tb10.389.0330)
103	<a href="#">c6ezoJ</a>	Alignment	not modelled	97.3	13	<b>PDB header:</b> membrane protein <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
104	<a href="#">c3ogzA</a>	Alignment	not modelled	97.2	24	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> udp-sugar pyrophosphorylase; <b>PDBTitle:</b> protein structure of usp from l. major in apo-form
105	<a href="#">c6i7tI</a>	Alignment	not modelled	97.2	13	<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
106	<a href="#">d1omza</a>	Alignment	not modelled	90.4	6	<b>Fold:</b> Nucleotide-diphospho-sugar transferases <b>Superfamily:</b> Nucleotide-diphospho-sugar transferases <b>Family:</b> Exostosin
107	<a href="#">c5mm1A</a>	Alignment	not modelled	90.2	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
108	<a href="#">c4fixA</a>	Alignment	not modelled	86.3	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
109	<a href="#">c5ekeB</a>	Alignment	not modelled	84.9	17	<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)
110	<a href="#">c3ckvA</a>	Alignment	not modelled	83.3	12	<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
111	<a href="#">c1omxB</a>	Alignment	not modelled	82.2	6	<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)
112	<a href="#">c5tz8C</a>	Alignment	not modelled	75.9	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
113	<a href="#">c2z86D</a>	Alignment	not modelled	68.8	15	<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-glucua and udp
114	<a href="#">c5z8bB</a>	Alignment	not modelled	67.2	7	<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
115	<a href="#">d1xhba2</a>	Alignment	not modelled	58.2	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
116	<a href="#">c6h4mA</a>	Alignment	not modelled	57.9	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
117	<a href="#">c2ffuA</a>	Alignment	not modelled	53.3	15	<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
118	<a href="#">c1xhBA</a>	Alignment	not modelled	52.0	17	<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
119	<a href="#">c3f1yC</a>	Alignment	not modelled	45.2	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

120	<a href="#">c4hg6A</a>	Alignment	not modelled	39.4	14	<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
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