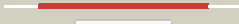



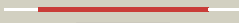



















Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0334_(rmlA)_398658_399524
Date	Tue Jul 23 14:50:40 BST 2019
Unique Job ID	11d7960106c22057

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1mc3a_	 Alignment		100.0	58	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: glucose-1-phosphate thymidyltransferase
2	d1lvwa_	 Alignment		100.0	57	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: glucose-1-phosphate thymidyltransferase
3	d1fxoa_	 Alignment		100.0	61	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: glucose-1-phosphate thymidyltransferase
4	d1h5ra_	 Alignment		100.0	62	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: glucose-1-phosphate thymidyltransferase
5	c6b5kA_	 Alignment		100.0	99	PDB header: transferase Chain: A: PDB Molecule: glucose-1-phosphate thymidyltransferase; PDBTitle: mycobacterium tuberculosis rmla in complex with mg/dttp
6	d1iina_	 Alignment		100.0	60	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: glucose-1-phosphate thymidyltransferase
7	c2pa4B_	 Alignment		100.0	26	PDB header: transferase Chain: B: PDB Molecule: utp-glucose-1-phosphate uridylyltransferase; PDBTitle: crystal structure of udp-glucose pyrophosphorylase from corynebacteria2 glutamicum in complex with magnesium and udp-glucose
8	c5i1fA_	 Alignment		100.0	27	PDB header: transferase Chain: A: PDB Molecule: utp--glucose-1-phosphate uridylyltransferase; PDBTitle: crystal structure of utp-glucose-1-phosphate uridylyltransferase from2 burkholderia vietnamiensis in complex with uridine-5'-diphosphate-3 glucose
9	c2ux8G_	 Alignment		100.0	28	PDB header: transferase Chain: G: PDB Molecule: glucose-1-phosphate uridylyltransferase; PDBTitle: crystal structure of sphingomonas elodea atcc 31461 glucose-2 1-phosphate uridylyltransferase in complex with glucose-3 1-phosphate.
10	c2e3dB_	 Alignment		100.0	26	PDB header: transferase Chain: B: PDB Molecule: utp--glucose-1-phosphate uridylyltransferase; PDBTitle: crystal structure of e. coli glucose-1-phosphate2 uridylyltransferase
11	c3d8vA_	 Alignment		100.0	18	PDB header: transferase Chain: A: PDB Molecule: bifunctional protein glmu; PDBTitle: crystal structure of glmu from mycobacterium tuberculosis2 in complex with uridine-diphosphate-n-acetylglucosamine

12	c5l6sF_	Alignment		100.0	21	PDB header: transferase Chain: F; PDB Molecule: glucose-1-phosphate adenylyltransferase; PDBTitle: 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
13	c3hl3A_	Alignment		100.0	36	PDB header: transferase Chain: A; PDB Molecule: glucose-1-phosphate thymidyltransferase; PDBTitle: 2.76 angstrom crystal structure of a putative glucose-1-phosphate2 thymidyltransferase from bacillus anthracis in complex with a3 sucrose.
14	c3jukA_	Alignment		100.0	27	PDB header: transferase Chain: A; PDB Molecule: udp-glucose pyrophosphorylase (galu); PDBTitle: the crystal structure of udp-glucose pyrophosphorylase complexed with2 udp-glucose
15	c1yp3C_	Alignment		100.0	21	PDB header: transferase Chain: C; PDB Molecule: glucose-1-phosphate adenylyltransferase small PDBTitle: crystal structure of potato tuber adp-glucose2 pyrophosphorylase in complex with atp
16	c3pnnA_	Alignment		100.0	19	PDB header: transferase Chain: A; PDB Molecule: conserved domain protein; PDBTitle: the crystal structure of a glycosyltransferase from porphyromonas2 gingivalis w83
17	c3brkX_	Alignment		100.0	20	PDB header: transferase Chain: X; PDB Molecule: glucose-1-phosphate adenylyltransferase; PDBTitle: crystal structure of adp-glucose pyrophosphorylase from agrobacterium2 tumefaciens
18	c6i3mG_	Alignment		100.0	12	PDB header: translation Chain: G; PDB Molecule: translation initiation factor eif-2b subunit epsilon; PDBTitle: eif2b:eif2 complex, phosphorylated on eif2 alpha serine 52.
19	c2x5sB_	Alignment		100.0	21	PDB header: transferase Chain: B; PDB Molecule: mannose-1-phosphate guanylyltransferase; PDBTitle: crystal structure of t. maritima gdp-mannose2 pyrophosphorylase in apo state.
20	c3d98A_	Alignment		100.0	19	PDB header: transferase Chain: A; PDB Molecule: bifunctional protein glmu; PDBTitle: crystal structure of glmu from mycobacterium tuberculosis, ligand-free2 form
21	c2cu2A_	Alignment	not modelled	100.0	18	PDB header: transferase Chain: A; PDB Molecule: putative mannose-1-phosphate guanylyl transferase; PDBTitle: crystal structure of mannose-1-phosphate geranyltransferase from2 thermus thermophilus hb8
22	d1yp2a2	Alignment	not modelled	100.0	22	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: glucose-1-phosphate thymidyltransferase
23	c5b04l_	Alignment	not modelled	100.0	13	PDB header: translation Chain: l; PDB Molecule: probable translation initiation factor eif-2b subunit PDBTitle: crystal structure of the eukaryotic translation initiation factor 2b2 from schizosaccharomyces pombe
24	c2qkxA_	Alignment	not modelled	100.0	18	PDB header: transferase Chain: A; PDB Molecule: bifunctional protein glmu; PDBTitle: n-acetyl glucosamine 1-phosphate uridylyltransferase from mycobacterium2 tuberculosis complex with n-acetyl glucosamine 1-phosphate
25	c1hm8A_	Alignment	not modelled	100.0	21	PDB header: transferase Chain: A; PDB Molecule: udp-n-acetylglucosamine-1-phosphate uridylyltransferase; PDBTitle: crystal structure of s.pneumoniae n-acetylglucosamine-1-phosphate2 uridylyltransferase, glmu, bound to acetyl coenzyme a
26	c1fwyA_	Alignment	not modelled	100.0	19	PDB header: transferase Chain: A; PDB Molecule: udp-n-acetylglucosamine pyrophosphorylase; PDBTitle: crystal structure of n-acetylglucosamine 1-phosphate2 uridylyltransferase bound to udp-glcnac
27	c2oi6A_	Alignment	not modelled	100.0	17	PDB header: transferase Chain: A; PDB Molecule: bifunctional protein glmu; PDBTitle: e. coli glmu- complex with udp-glcnac, coa and glcn-1-p04
						PDB header: translation

28	c6jlwJ_	Alignment	not modelled	100.0	12	Chain: J; PDB Molecule: translation initiation factor eif-2b subunit epsilon; PDBTitle: eif2 - eif2b complex
29	c5b04F_	Alignment	not modelled	100.0	18	PDB header: translation Chain: F; PDB Molecule: probable translation initiation factor eif-2b subunit PDBTitle: crystal structure of the eukaryotic translation initiation factor 2b2 from schizosaccharomyces pombe
30	c2ggqA_	Alignment	not modelled	100.0	26	PDB header: transferase Chain: A; PDB Molecule: 401aa long hypothetical glucose-1-phosphate PDBTitle: complex of hypothetical glucose-1-phosphate thymidyltransferase from2 sulfolobus tokodaii
31	c2v0hA_	Alignment	not modelled	100.0	19	PDB header: transferase Chain: A; PDB Molecule: bifunctional protein glmu; PDBTitle: characterization of substrate binding and catalysis of the2 potential antibacterial target n-acetylglucosamine-1-3 phosphate uridytransferase (glmu)
32	c4jd0A_	Alignment	not modelled	100.0	16	PDB header: transferase Chain: A; PDB Molecule: nucleotidyl transferase; PDBTitle: structure of the inositol-1-phosphate ctp transferase from t.2 maritima.
33	c6gg2F_	Alignment	not modelled	100.0	13	PDB header: translation Chain: F; PDB Molecule: translation initiation factor eif-2b subunit gamma; PDBTitle: structure of eif2b-eif2 (phosphorylated at ser51) complex (model a)
34	c5xhwA_	Alignment	not modelled	100.0	20	PDB header: transferase Chain: A; PDB Molecule: putative 6-deoxy-d-mannoheptose pathway protein; PDBTitle: crystal structure of hddc from yersinia pseudotuberculosis
35	c4evwB_	Alignment	not modelled	100.0	14	PDB header: transferase Chain: B; PDB Molecule: nucleoside-diphosphate-sugar pyrophosphorylase; PDBTitle: crystal structure of the nucleoside-diphosphate-sugar2 pyrophosphorylase from vibrio cholerae rc9. northeast structural3 genomics consortium (nesh) target vcr193.
36	d2cu2a2	Alignment	not modelled	100.0	22	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: mannose-1-phosphate guanylyl transferase
37	c4y7uA_	Alignment	not modelled	100.0	19	PDB header: transferase Chain: A; PDB Molecule: nucleotidyl transferase; PDBTitle: structural analysis of muru
38	d1tzfa_	Alignment	not modelled	100.0	14	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: Cytidylyltransferase
39	d2oi6a2	Alignment	not modelled	100.0	18	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: UDP-glucose pyrophosphorylase
40	d1g97a2	Alignment	not modelled	100.0	21	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: UDP-glucose pyrophosphorylase
41	c3foqA_	Alignment	not modelled	100.0	16	PDB header: transferase Chain: A; PDB Molecule: bifunctional protein glmu; PDBTitle: crystal structure of n-acetylglucosamine-1-phosphate2 uridytransferase (glmu) from mycobacterium tuberculosis in3 a cubic space group.
42	c4mndA_	Alignment	not modelled	100.0	18	PDB header: transferase Chain: A; PDB Molecule: ctp l-myo-inositol-1-phosphate cytidylyltransferase/cdp-l- PDBTitle: crystal structure of archaeoglobus fulgidus ipct-dipps bifunctional2 membrane protein
43	c6ezoF_	Alignment	not modelled	100.0	18	PDB header: membrane protein Chain: F; PDB Molecule: translation initiation factor eif-2b subunit gamma; PDBTitle: eukaryotic initiation factor eif2b in complex with isrib
44	c5vmkB_	Alignment	not modelled	100.0	17	PDB header: transferase Chain: B; PDB Molecule: bifunctional protein glmu; PDBTitle: crystal structure of a bifunctional glmu udp-n-acetylglucosamine2 diphosphorylase/glucosamine-1- phosphate n-acetyltransferase from3 acinetobacter baumannii
45	d1jyka_	Alignment	not modelled	100.0	17	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: Cytidylyltransferase
46	c1jyC_	Alignment	not modelled	100.0	16	PDB header: transferase Chain: C; PDB Molecule: ctp:phosphocholine cytidylyltransferase; PDBTitle: catalytic mechanism of ctp:phosphocholine2 cytidylyltransferase from streptococcus pneumoniae (licc)
47	c6ezol_	Alignment	not modelled	100.0	12	PDB header: membrane protein Chain: J; PDB Molecule: human eukaryotic initiation factor eif2b epsilon subunits; PDBTitle: eukaryotic initiation factor eif2b in complex with isrib
48	d1vica_	Alignment	not modelled	100.0	16	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: Cytidylyltransferase
49	c3oamD_	Alignment	not modelled	100.0	19	PDB header: transferase Chain: D; PDB Molecule: 3-deoxy-manno-octulosonate cytidylyltransferase; PDBTitle: crystal structure of cytidylyltransferase from vibrio cholerae
50	c2qh5B_	Alignment	not modelled	100.0	15	PDB header: isomerase Chain: B; PDB Molecule: mannose-6-phosphate isomerase; PDBTitle: crystal structure of mannose-6-phosphate isomerase from helicobacter2 pylori
51	c4xwiA_	Alignment	not modelled	100.0	19	PDB header: transferase Chain: A; PDB Molecule: 3-deoxy-manno-octulosonate cytidylyltransferase; PDBTitle: x-ray crystal structure of cmp-kdo synthase from

						pseudomonas2 aeruginosa
52	c2xmhB_	Alignment	not modelled	100.0	16	PDB header: transferase Chain: B: PDB Molecule: ctp-inositol-1-phosphate cytidyltransferase; PDBTitle: the x-ray structure of ctp:inositol-1-phosphate cytidyltransferase2 from archaeoglobus fulgidus
53	c5ddtA_	Alignment	not modelled	100.0	15	PDB header: transferase Chain: A: PDB Molecule: 2-c-methyl-d-erythritol 4-phosphate cytidyltransferase; PDBTitle: crystal structure of ispd from bacillus subtilis at 1.80 angstroms2 resolution, crystal form i
54	c2xwIB_	Alignment	not modelled	100.0	17	PDB header: transferase Chain: B: PDB Molecule: 2-c-methyl-d-erythritol 4-phosphate cytidyltransferase; PDBTitle: crystal structure of ispd from mycobacterium smegmatis in complex with2 ctp and mg
55	d1i52a_	Alignment	not modelled	100.0	15	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: Cytidylytransferase
56	c3polA_	Alignment	not modelled	99.9	17	PDB header: transferase Chain: A: PDB Molecule: 3-deoxy-manno-octulosonate cytidyltransferase; PDBTitle: 2.3 angstrom crystal structure of 3-deoxy-manno-octulosonate2 cytidyltransferase (kdsb) from acinetobacter baumannii.
57	d1h7ea_	Alignment	not modelled	99.9	16	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: Cytidylytransferase
58	d1vpaa_	Alignment	not modelled	99.9	16	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: Cytidylytransferase
59	c2y6pC_	Alignment	not modelled	99.9	17	PDB header: transferase Chain: C: PDB Molecule: 3-deoxy-manno-octulosonate cytidyltransferase; PDBTitle: evidence for a two-metal-ion-mechanism in the kdo-2 cytidyltransferase kdsb
60	c3tqdA_	Alignment	not modelled	99.9	18	PDB header: transferase Chain: A: PDB Molecule: 3-deoxy-manno-octulosonate cytidyltransferase; PDBTitle: structure of the 3-deoxy-d-manno-octulosonate cytidyltransferase2 (kdsb) from coxiella burnetii
61	d1vh1a_	Alignment	not modelled	99.9	20	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: Cytidylytransferase
62	c6i7tl_	Alignment	not modelled	99.9	15	PDB header: translation Chain: I: PDB Molecule: translation initiation factor eif-2b subunit gamma; PDBTitle: eif2b:eif2 complex
63	d1eyra_	Alignment	not modelled	99.9	13	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: Cytidylytransferase
64	c4mybA_	Alignment	not modelled	99.9	13	PDB header: transferase Chain: A: PDB Molecule: 2-c-methyl-d-erythritol 4-phosphate cytidyltransferase; PDBTitle: crystal structure of francisella tularensis 2-c-methyl-d-erythritol 4-2 phosphate cytidyltransferase (ispd)
65	c4kt7A_	Alignment	not modelled	99.9	12	PDB header: transferase Chain: A: PDB Molecule: 2-c-methyl-d-erythritol 4-phosphate cytidyltransferase; PDBTitle: the crystal structure of 4-diphosphocytidyl-2c-methyl-d-2 erythritolsynthase from anaerococcus prevotii dsm 20548
66	c3f1cB_	Alignment	not modelled	99.9	13	PDB header: transferase Chain: B: PDB Molecule: putative 2-c-methyl-d-erythritol 4-phosphate PDBTitle: crystal structure of 2-c-methyl-d-erythritol 4-phosphate2 cytidyltransferase from listeria monocytogenes
67	d1w55a1	Alignment	not modelled	99.9	18	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: Cytidylytransferase
68	d1qwja_	Alignment	not modelled	99.9	18	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: Cytidylytransferase
69	c3okrA_	Alignment	not modelled	99.9	15	PDB header: transferase Chain: A: PDB Molecule: 2-c-methyl-d-erythritol 4-phosphate cytidyltransferase; PDBTitle: structure of mtb apo 2-c-methyl-d-erythritol 4-phosphate2 cytidyltransferase (ispd)
70	d1e5ka_	Alignment	not modelled	99.9	18	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: Molybdenum cofactor biosynthesis protein MobA
71	d2dpwa1	Alignment	not modelled	99.9	17	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: TTHA0179-like
72	c2wawA_	Alignment	not modelled	99.9	17	PDB header: unknown function Chain: A: PDB Molecule: moba relate protein; PDBTitle: crystal structure of mycobacterium tuberculosis rv0371c2 homolog from mycobacterium sp. strain jc1
73	d1vh3a_	Alignment	not modelled	99.9	13	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: Cytidylytransferase
74	c2vshB_	Alignment	not modelled	99.9	15	PDB header: transferase Chain: B: PDB Molecule: 2-c-methyl-d-erythritol 4-phosphate PDBTitle: synthesis of cdp-activated ribitol for teichoic acid2 precursors in streptococcus pneumoniae
75	c2we9A_	Alignment	not modelled	99.9	20	PDB header: unknown function Chain: A: PDB Molecule: moba-related protein;

75	c2we9A	Alignment	not modelled	99.9	20	PDBTitle: crystal structure of rv0371c from mycobacterium2 tuberculosis h37rv PDB header: biosynthetic protein Chain: A: PDB Molecule: molybdopterin-guanine dinucleotide biosynthesis protein a
76	c3ngwA	Alignment	not modelled	99.8	15	PDBTitle: crystal structure of molybdopterin-guanine dinucleotide biosynthesis2 protein a from archaeoglobus fulgidus, northeast structural genomics3 consortium target gr189 PDB header: transferase Chain: B: PDB Molecule: 2-c-methyl-d-erythritol 4-phosphate cytidyltransferase;
77	c4ys8B	Alignment	not modelled	99.8	12	PDBTitle: crystal structure of 2-c-methyl-d-erythritol 4-phosphate2 cytidyltransferase (ispd) from burkholderia thailandensis PDB header: transferase Chain: A: PDB Molecule: 2-c-methyl-d-erythritol 4-phosphate cytidyltransferase;
78	c2px7A	Alignment	not modelled	99.8	13	PDBTitle: crystal structure of 2-c-methyl-d-erythritol 4-phosphate2 cytidyltransferase from thermus thermophilus hb8
79	d1w77a1	Alignment	not modelled	99.8	18	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: Cytidylyltransferase
80	c4jisB	Alignment	not modelled	99.8	9	PDB header: transferase Chain: B: PDB Molecule: ribitol-5-phosphate cytidyltransferase; PDBTitle: crystal structure of ribitol 5-phosphate cytidyltransferase (tari)2 from bacillus subtilis
81	c6ifdD	Alignment	not modelled	99.8	11	PDB header: sugar binding protein Chain: D: PDB Molecule: cmp-n-acetylneuraminate synthetase; PDBTitle: crystal structure of cmp-n-acetylneuraminate synthetase from vibrio2 cholerae in complex with cdp and mg2+.
82	c3rsbB	Alignment	not modelled	99.8	14	PDB header: transferase Chain: B: PDB Molecule: adenosylcobinamide-phosphate guanylyltransferase; PDBTitle: structure of the archaeal gtp:adocbi-p guanylyltransferase (coby) from2 methanocaldococcus jannaschii
83	d1vgwa	Alignment	not modelled	99.8	12	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: Cytidylyltransferase
84	c1w57A	Alignment	not modelled	99.8	18	PDB header: transferase Chain: A: PDB Molecule: ispd/ispf bifunctional enzyme; PDBTitle: structure of the bifunctional ispdf from campylobacter2 jejuni containing zn
85	c6oewB	Alignment	not modelled	99.8	13	PDB header: transferase Chain: B: PDB Molecule: cytidyltransferase; PDBTitle: structure of a cytidyltransferase from leptospira borgpetersenii2 serovar hardjo-bovis (strain jb197)
86	c4cvhA	Alignment	not modelled	99.7	17	PDB header: transferase Chain: A: PDB Molecule: isoprenoid synthase domain-containing protein; PDBTitle: crystal structure of human isoprenoid synthase domain-containing2 protein
87	c3okrC	Alignment	not modelled	99.7	16	PDB header: transferase Chain: C: PDB Molecule: 2-c-methyl-d-erythritol 4-phosphate cytidyltransferase; PDBTitle: structure of mtb apo 2-c-methyl-d-erythritol 4-phosphate2 cytidyltransferase (ispd)
88	c2e8bA	Alignment	not modelled	99.6	14	PDB header: biosynthetic protein Chain: A: PDB Molecule: probable molybdopterin-guanine dinucleotide biosynthesis PDBTitle: crystal structure of the putative protein (aq1419) from aquifex2 aeolicus vf5
89	c3d5nB	Alignment	not modelled	99.2	20	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: q97w15_sulso; PDBTitle: crystal structure of the q97w15_sulso protein from sulfolobus2 solfataricus. nesg target ssr125.
90	d2icya2	Alignment	not modelled	98.9	18	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: UDP-glucose pyrophosphorylase
91	c3oc9A	Alignment	not modelled	98.9	19	PDB header: transferase Chain: A: PDB Molecule: udp-n-acetylglucosamine pyrophosphorylase; PDBTitle: crystal structure of putative udp-n-acetylglucosamine2 pyrophosphorylase from entamoeba histolytica
92	d1vm8a	Alignment	not modelled	98.9	18	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: UDP-glucose pyrophosphorylase
93	d1jv1a	Alignment	not modelled	98.8	18	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: UDP-glucose pyrophosphorylase
94	c4bmaB	Alignment	not modelled	98.8	15	PDB header: transferase Chain: B: PDB Molecule: udp-n-acetylglucosamine pyrophosphorylase; PDBTitle: structural of aspergillus fumigatus udp-n-acetylglucosamine2 pyrophosphorylase
95	c2q4jB	Alignment	not modelled	98.8	17	PDB header: transferase Chain: B: PDB Molecule: probable utp-glucose-1-phosphate uridylyltransferase 2; PDBTitle: ensemble refinement of the protein crystal structure of gene product2 from arabidopsis thaliana at3g03250, a putative udp-glucose3 pyrophosphorylase
96	c3r2wB	Alignment	not modelled	98.7	15	PDB header: transferase Chain: B: PDB Molecule: utp--glucose-1-phosphate uridylyltransferase; PDBTitle: crystal structure of udp-glucose pyrophosphorylase of homo sapiens
97	c4bqhA	Alignment	not modelled	98.7	20	PDB header: transferase Chain: A: PDB Molecule: udp-n-acetylglucosamine pyrophosphorylase; PDBTitle: crystal structure of the uridine diphosphate n-2 acetylglucosamine pyrophosphorylase from trypanosoma3 Brucei in complex with inhibitor

98	c2yqsA	Alignment	not modelled	98.7	16	PDB header: transferase Chain: A: PDB Molecule: udp-n-acetylglucosamine pyrophosphorylase; PDBTitle: crystal structure of uridine-diphospho-n-acetylglucosamine2 pyrophosphorylase from candida albicans, in the product-binding form
99	c2i5kB	Alignment	not modelled	98.6	16	PDB header: transferase Chain: B: PDB Molecule: utp--glucose-1-phosphate uridylyltransferase; PDBTitle: crystal structure of ugp1p
100	c3gueB	Alignment	not modelled	98.5	16	PDB header: transferase Chain: B: PDB Molecule: utp-glucose-1-phosphate uridylyltransferase 2; PDBTitle: crystal structure of udp-glucose phosphorylase from trypanosoma2 brucei, (tb10.389.0330)
101	c3ogzA	Alignment	not modelled	98.3	20	PDB header: transferase Chain: A: PDB Molecule: udp-sugar pyrophosphorylase; PDBTitle: protein structure of usp from I. major in apo-form
102	c2oefA	Alignment	not modelled	98.2	15	PDB header: transferase Chain: A: PDB Molecule: utp-glucose-1-phosphate uridylyltransferase 2, PDBTitle: open and closed structures of the udp-glucose2 pyrophosphorylase from leishmania major
103	c6bwhB	Alignment	not modelled	97.2	22	PDB header: transferase Chain: B: PDB Molecule: 2-phospho-l-lactate guanylyltransferase; PDBTitle: crystal structure of mycobacterium tuberculosis rv2983 in complex2 with pep
104	c5tz8C	Alignment	not modelled	96.2	9	PDB header: transferase Chain: C: PDB Molecule: glycosyl transferase; PDBTitle: crystal structure of s. aureus tars
105	c2z86D	Alignment	not modelled	94.4	13	PDB header: transferase Chain: D: PDB Molecule: chondroitin synthase; PDBTitle: crystal structure of chondroitin polymerase from escherichia coli2 strain k4 (k4cp) complexed with udp-glcua and udp
106	d1xhba2	Alignment	not modelled	94.1	13	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: Polypeptide N-acetylgalactosaminyltransferase 1, N-terminal domain
107	c6h4mA	Alignment	not modelled	94.0	11	PDB header: transferase Chain: A: PDB Molecule: probable ss-1,3-n-acetylglucosaminyltransferase; PDBTitle: tarp-udp-glcnaC-3rbop
108	d1omza	Alignment	not modelled	93.9	10	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: Exostosin
109	c6e4rB	Alignment	not modelled	93.6	15	PDB header: transferase Chain: B: PDB Molecule: polypeptide n-acetylgalactosaminyltransferase 9; PDBTitle: crystal structure of the drosophila melanogaster polypeptide n-2 acetylgalactosaminyl transferase pgant9b
110	c1omxB	Alignment	not modelled	93.4	10	PDB header: transferase Chain: B: PDB Molecule: alpha-1,4-n-acetylhexosaminyltransferase extl2; PDBTitle: crystal structure of mouse alpha-1,4-n-acetylhexosaminyltransferase2 (extl2)
111	c5nqaA	Alignment	not modelled	93.1	11	PDB header: transferase Chain: A: PDB Molecule: polypeptide n-acetylgalactosaminyltransferase 4; PDBTitle: crystal structure of galnac-t4 in complex with the monoglycopeptide 3
112	c5mm1A	Alignment	not modelled	92.9	12	PDB header: membrane protein Chain: A: PDB Molecule: dolichol monophosphate mannose synthase; PDBTitle: dolichyl phosphate mannose synthase in complex with gdp and dolichyl2 phosphate mannose
113	c2d7iA	Alignment	not modelled	90.0	14	PDB header: transferase Chain: A: PDB Molecule: polypeptide n-acetylgalactosaminyltransferase 10; PDBTitle: crystal structure of pp-galnac-t10 with udp, galnac and mn2+
114	c1xhba	Alignment	not modelled	89.9	14	PDB header: transferase Chain: A: PDB Molecule: polypeptide n-acetylgalactosaminyltransferase 1; PDBTitle: the crystal structure of udp-galnac: polypeptide alpha-n-2 acetylgalactosaminyltransferase-t1
115	c2ffuA	Alignment	not modelled	88.2	15	PDB header: transferase Chain: A: PDB Molecule: polypeptide n-acetylgalactosaminyltransferase 2; PDBTitle: crystal structure of human ppgalnact-2 complexed with udp and ea2
116	c3f1yC	Alignment	not modelled	85.8	15	PDB header: transferase Chain: C: PDB Molecule: mannosyl-3-phosphoglycerate synthase; PDBTitle: mannosyl-3-phosphoglycerate synthase from rubrobacter xylanophilus
117	c3bcvA	Alignment	not modelled	85.4	19	PDB header: transferase Chain: A: PDB Molecule: putative glycosyltransferase protein; PDBTitle: crystal structure of a putative glycosyltransferase from bacteroides2 fragilis
118	c5ekeB	Alignment	not modelled	83.8	13	PDB header: transferase Chain: B: PDB Molecule: uncharacterized glycosyltransferase sll0501; PDBTitle: structure of the polyisoprenyl-phosphate glycosyltransferase gtrb2 (f215a mutant)
119	c3r5dA	Alignment	not modelled	78.3	14	PDB header: transferase Chain: A: PDB Molecule: tetrahydrodipicolinate n-succinyletransferase; PDBTitle: pseudomonas aeruginosa dapd (pa3666) apoprotein
120	c5heaA	Alignment	not modelled	75.9	13	PDB header: transferase Chain: A: PDB Molecule: putative glycosyltransferase (galt1); PDBTitle: cgt structure in hexamer