



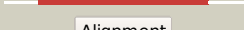

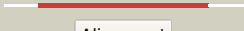









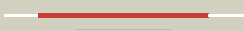













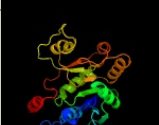


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3582c_(ispD)_4024523_4025218
Date	Fri Aug 9 18:20:26 BST 2019
Unique Job ID	6b27334ad66d6298

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2xw1B_	 Alignment		100.0	61	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
2	d1i52a_	 Alignment		100.0	29	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: Cytidylytransferase
3	c5ddtA_	 Alignment		100.0	25	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
4	d1vpaa_	 Alignment		100.0	30	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: Cytidylytransferase
5	c4mybA_	 Alignment		100.0	26	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)
6	c4kt7A_	 Alignment		100.0	26	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
7	c3okrA_	 Alignment		100.0	89	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)
8	c1w57A_	 Alignment		100.0	29	PDB header: transferase Chain: A: PDB Molecule: ispd/ispf bifunctional enzyme; PDBTitle: structure of the bifunctional ispdf from campylobacter2 jejuni containing zn
9	d1w55a1	 Alignment		100.0	28	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: Cytidylytransferase
10	d2oi6a2	 Alignment		100.0	18	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: UDP-glucose pyrophosphorylase
11	c3f1cB_	 Alignment		100.0	25	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

12	c4cvhA	Alignment		100.0	28	PDB header: transferase Chain: A: PDB Molecule: isoprenoid synthase domain-containing protein; PDBTitle: crystal structure of human isoprenoid synthase domain-containing2 protein
13	c3okrC	Alignment		100.0	97	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)
14	d1vgwa	Alignment		100.0	33	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: Cytidylytransferase
15	c2px7A	Alignment		100.0	37	PDB header: transferase Chain: A: PDB Molecule: 2-c-methyl-d-erythritol 4-phosphate cytidyltransferase; PDBTitle: crystal structure of 2-c-methyl-d-erythritol 4-phosphate2 cytidyltransferase from thermus thermophilus hb8
16	c4ys8B	Alignment		100.0	29	PDB header: transferase Chain: B: PDB Molecule: 2-c-methyl-d-erythritol 4-phosphate cytidyltransferase; PDBTitle: crystal structure of 2-c-methyl-d-erythritol 4-phosphate2 cytidyltransferase (ispd) from burkholderia thailandensis
17	c4xwiA	Alignment		100.0	24	PDB header: transferase Chain: A: PDB Molecule: 3-deoxy-manno-octulosonate cytidyltransferase; PDBTitle: x-ray crystal structure of cmp-kdo synthase from pseudomonas2 aeruginosa
18	d1g97a2	Alignment		100.0	16	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: UDP-glucose pyrophosphorylase
19	d1w77a1	Alignment		100.0	25	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: Cytidylytransferase
20	c3polA	Alignment		100.0	18	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.
21	c3oamD	Alignment	not modelled	100.0	18	PDB header: transferase Chain: D: PDB Molecule: 3-deoxy-manno-octulosonate cytidyltransferase; PDBTitle: crystal structure of cytidyltransferase from vibrio cholerae
22	d1vica	Alignment	not modelled	100.0	18	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: Cytidylytransferase
23	c2vshB	Alignment	not modelled	100.0	25	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
24	d1h7ea	Alignment	not modelled	100.0	19	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: Cytidylytransferase
25	c3d8vA	Alignment	not modelled	100.0	20	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
26	c4jisB	Alignment	not modelled	100.0	26	PDB header: transferase Chain: B: PDB Molecule: ribitol-5-phosphate cytidyltransferase; PDBTitle: crystal structure of ribitol 5-phosphate cytidyltransferase (tari)2 from bacillus subtilis
27	c3pnnA	Alignment	not modelled	100.0	21	PDB header: transferase Chain: A: PDB Molecule: conserved domain protein; PDBTitle: the crystal structure of a glycosyltransferase from porphyromonas2 gingivalis w83
28	d1qwja	Alignment	not modelled	100.0	15	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: Cytidylytransferase
						PDB header: transferase

29	c3hl3A_	Alignment	not modelled	100.0	15	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.
30	d1eyra_	Alignment	not modelled	100.0	15	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: Cytidyltransferase
31	d1h5ra_	Alignment	not modelled	100.0	15	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: glucose-1-phosphate thymidyltransferase
32	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
33	d1fxoa_	Alignment	not modelled	99.9	13	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: glucose-1-phosphate thymidyltransferase
34	d1iina_	Alignment	not modelled	99.9	14	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: glucose-1-phosphate thymidyltransferase
35	c2y6pC_	Alignment	not modelled	99.9	15	PDB header: transferase Chain: C: PDB Molecule: 3-deoxy-manno-octulosonate cytidyltransferase; PDBTitle: evidence for a two-metal-ion-mechanism in the kdsb cytidyltransferase kdsb
36	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
37	c6oewB_	Alignment	not modelled	99.9	11	PDB header: transferase Chain: B: PDB Molecule: cytidyltransferase; PDBTitle: structure of a cytidyltransferase from leptospira borgpetersenii2 serovar hardjo-bovis (strain jb197)
38	c4jd0A_	Alignment	not modelled	99.9	21	PDB header: transferase Chain: A: PDB Molecule: nucleotidyl transferase; PDBTitle: structure of the inositol-1-phosphate ctp transferase from t.2 maritima.
39	c2we9A_	Alignment	not modelled	99.9	14	PDB header: unknown function Chain: A: PDB Molecule: moba-related protein; PDBTitle: crystal structure of rv0371c from mycobacterium2 tuberculosis h37rv
40	d1mc3a_	Alignment	not modelled	99.9	14	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: glucose-1-phosphate thymidyltransferase
41	c5i1fA_	Alignment	not modelled	99.9	22	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
42	c5xhwA_	Alignment	not modelled	99.9	14	PDB header: transferase Chain: A: PDB Molecule: putative 6-deoxy-d-mannoheptose pathway protein; PDBTitle: crystal structure of hddc from yersinia pseudotuberculosis
43	c2pa4B_	Alignment	not modelled	99.9	16	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
44	d1lwva_	Alignment	not modelled	99.9	16	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: glucose-1-phosphate thymidyltransferase
45	d1vh1a_	Alignment	not modelled	99.9	17	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: Cytidyltransferase
46	c3foqA_	Alignment	not modelled	99.9	20	PDB header: transferase Chain: A: PDB Molecule: bifunctional protein glmu; PDBTitle: crystal structure of n-acetylglucosamine-1-phosphate2 uridylyltransferase (glmu) from mycobacterium tuberculosis in3 a cubic space group.
47	d1e5ka_	Alignment	not modelled	99.9	18	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: Molybdenum cofactor biosynthesis protein MobA
48	c3jukA_	Alignment	not modelled	99.9	13	PDB header: transferase Chain: A: PDB Molecule: udp-glucose pyrophosphorylase (galu); PDBTitle: the crystal structure of udp-glucose pyrophosphorylase complexed with2 udp-glucose
49	c4y7uA_	Alignment	not modelled	99.9	17	PDB header: transferase Chain: A: PDB Molecule: nucleotidyl transferase; PDBTitle: structural analysis of muru
50	c2oi6A_	Alignment	not modelled	99.9	19	PDB header: transferase Chain: A: PDB Molecule: bifunctional protein glmu; PDBTitle: e. coli glmu- complex with udp-glcnac, coa and glcn-1-po4
51	c2v0hA_	Alignment	not modelled	99.9	17	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 uridylyltransferase (glmu)
52	c1hm8A_	Alignment	not modelled	99.9	16	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

53	c4mndA	Alignment	not modelled	99.9	16	PDB header: transferase Chain: A: PDB Molecule: ctp l-myo-inositol-1-phosphate cytidyltransferase/cdp-l PDBTitle: crystal structure of archaeoglobus fulgidus ipct-dipps bifunctional2 membrane protein
54	c3d98A	Alignment	not modelled	99.9	21	PDB header: transferase Chain: A: PDB Molecule: bifunctional protein glmu; PDBTitle: crystal structure of glmu from mycobacterium tuberculosis, ligand-free2 form
55	c2ux8G	Alignment	not modelled	99.9	17	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.
56	c1jyC	Alignment	not modelled	99.9	18	PDB header: transferase Chain: C: PDB Molecule: ctp:phosphocholine cytidyltransferase; PDBTitle: catalytic mechanism of ctp:phosphocholine2 cytidyltransferase from streptococcus pneumoniae (licc)
57	d1jyka	Alignment	not modelled	99.9	18	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: Cytidylyltransferase
58	c4evwB	Alignment	not modelled	99.9	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.
59	d2dpwa1	Alignment	not modelled	99.9	16	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: TTHA0179-like
60	c6b5kA	Alignment	not modelled	99.9	16	PDB header: transferase Chain: A: PDB Molecule: glucose-1-phosphate thymidyltransferase; PDBTitle: mycobacterium tuberculosis rmla in complex with mg/dttp
61	c1fwyA	Alignment	not modelled	99.9	19	PDB header: transferase Chain: A: PDB Molecule: udp-n-acetylglucosamine pyrophosphorylase; PDBTitle: crystal structure of n-acetylglucosamine 1-phosphate2 uridylyltransferase bound to udp-glcna
62	d2cu2a2	Alignment	not modelled	99.9	21	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: mannose-1-phosphate guanylyl transferase
63	d1tzfa	Alignment	not modelled	99.9	10	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: Cytidylyltransferase
64	c2qkxA	Alignment	not modelled	99.9	20	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
65	c3ngwA	Alignment	not modelled	99.9	15	PDB header: biosynthetic protein Chain: A: PDB Molecule: molybdopterin-guanine dinucleotide biosynthesis protein a PDBTitle: crystal structure of molybdopterin-guanine dinucleotide biosynthesis2 protein a from archaeoglobus fulgidus, northeast structural genomics3 consortium target gr189
66	c2e3dB	Alignment	not modelled	99.9	18	PDB header: transferase Chain: B: PDB Molecule: utp--glucose-1-phosphate uridylyltransferase; PDBTitle: crystal structure of e. coli glucose-1-phosphate2 uridylyltransferase
67	c1yp3C	Alignment	not modelled	99.9	17	PDB header: transferase Chain: C: PDB Molecule: glucose-1-phosphate adenyltransferase small PDBTitle: crystal structure of potato tuber adp-glucose2 pyrophosphorylase in complex with atp
68	c6ifdD	Alignment	not modelled	99.9	17	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+
69	c3rsbB	Alignment	not modelled	99.9	22	PDB header: transferase Chain: B: PDB Molecule: adenosylcobinamide-phosphate guanylyltransferase; PDBTitle: structure of the archaeal gtp:adocbi-p guanylyltransferase (coby) from2 methanocaldococcus jannaschii
70	c2x5sB	Alignment	not modelled	99.9	18	PDB header: transferase Chain: B: PDB Molecule: mannose-1-phosphate guanylyltransferase; PDBTitle: crystal structure of t. maritima gdp-mannose2 pyrophosphorylase in apo state.
71	d1yp2a2	Alignment	not modelled	99.9	17	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: glucose-1-phosphate thymidyltransferase
72	c2cu2A	Alignment	not modelled	99.9	21	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
73	c5vmkB	Alignment	not modelled	99.9	14	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
74	c5l6sF	Alignment	not modelled	99.9	14	PDB header: transferase Chain: F: PDB Molecule: glucose-1-phosphate adenyltransferase; 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 PDB header: transferase

75	c3brkX	Alignment	not modelled	99.8	15	Chain: X: PDB Molecule: glucose-1-phosphate adenyltransferase; PDBTitle: crystal structure of adp-glucose pyrophosphorylase from agrobacterium2 tumefaciens
76	c6i3mG	Alignment	not modelled	99.8	10	PDB header: translation Chain: G: PDB Molecule: translation initiation factor eif-2b subunit epsilon; PDBTitle: eif2b:eif2 complex, phosphorylated on eif2 alpha serine 52.
77	c2ggqA	Alignment	not modelled	99.8	16	PDB header: transferase Chain: A: PDB Molecule: 401aa long hypothetical glucose-1-phosphate PDBTitle: complex of hypothetical glucose-1-phosphate thymidyltransferase from2 sulfolobus tokodaii
78	c5b04I	Alignment	not modelled	99.8	11	PDB header: translation Chain: I: PDB Molecule: probable translation initiation factor eif-2b subunit PDBTitle: crystal structure of the eukaryotic translation initiation factor 2b2 from schizosaccharomyces pombe
79	c2e8bA	Alignment	not modelled	99.7	19	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
80	c2qh5B	Alignment	not modelled	99.7	12	PDB header: isomerase Chain: B: PDB Molecule: mannose-6-phosphate isomerase; PDBTitle: crystal structure of mannose-6-phosphate isomerase from helicobacter2 pylori
81	c6jlwJ	Alignment	not modelled	99.7	14	PDB header: translation Chain: J: PDB Molecule: translation initiation factor eif-2b subunit epsilon; PDBTitle: eif2 - eif2b complex
82	c5b04F	Alignment	not modelled	99.6	11	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
83	d1vh3a	Alignment	not modelled	99.6	14	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: Cytidylyltransferase
84	c6bwhB	Alignment	not modelled	99.6	17	PDB header: transferase Chain: B: PDB Molecule: 2-phospho-l-lactate guanylyltransferase; PDBTitle: crystal structure of mycoibacterium tuberculosis rv2983 in complex2 with pep
85	c6ezoF	Alignment	not modelled	99.6	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
86	c2xmhB	Alignment	not modelled	99.6	12	PDB header: transferase Chain: B: PDB Molecule: ctp-inositol-1-phosphate cytidylyltransferase; PDBTitle: the x-ray structure of ctp:inositol-1-phosphate cytidylyltransferase2 from archaeoglobus fulgidus
87	c3d5nB	Alignment	not modelled	99.6	16	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.
88	c6qq2F	Alignment	not modelled	99.5	14	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)
89	c6ezoJ	Alignment	not modelled	99.0	14	PDB header: membrane protein Chain: J: PDB Molecule: human eukaryotic initiation factor eif2b epsilon subunits; PDBTitle: eukaryotic initiation factor eif2b in complex with isrib
90	d2icya2	Alignment	not modelled	98.6	14	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: UDP-glucose pyrophosphorylase
91	c2q4jB	Alignment	not modelled	98.6	14	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
92	c3oc9A	Alignment	not modelled	98.5	31	PDB header: transferase Chain: A: PDB Molecule: udp-n-acetylglucosamine pyrophosphorylase; PDBTitle: crystal structure of putative udp-n-acetylglucosamine2 pyrophosphorylase from entamoeba histolytica
93	c3r2wB	Alignment	not modelled	98.5	12	PDB header: transferase Chain: B: PDB Molecule: utp--glucose-1-phosphate uridylyltransferase; PDBTitle: crystal structure of udp-glucose pyrophosphorylase of homo sapiens
94	c3cqxA	Alignment	not modelled	98.5	15	PDB header: transferase Chain: A: PDB Molecule: putative nucleotide-diphospho-sugar transferase; PDBTitle: crystal structure of putative nucleotide-diphospho-sugar transferase2 (yp_389115.1) from desulfovibrio desulfuricans g20 at 1.90 a3 resolution
95	c6i7tI	Alignment	not modelled	98.5	9	PDB header: translation Chain: I: PDB Molecule: translation initiation factor eif-2b subunit gamma; PDBTitle: eif2b:eif2 complex
96	c2i5kB	Alignment	not modelled	98.4	12	PDB header: transferase Chain: B: PDB Molecule: utp--glucose-1-phosphate uridylyltransferase; PDBTitle: crystal structure of ugp1p
97	c4bmaB	Alignment	not modelled	98.4	21	PDB header: transferase Chain: B: PDB Molecule: udp-n-acetylglucosamine pyrophosphorylase; PDBTitle: structural of aspergillus fumigatus udp-n-

						acetylglucosamine2 pyrophosphorylase
98	c3ogzA_	Alignment	not modelled	98.3	20	PDB header: transferase Chain: A: PDB Molecule: udp-sugar pyrophosphorylase; PDBTitle: protein structure of usp from l. major in apo-form
99	c2yqsA_	Alignment	not modelled	98.3	20	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
100	d1jv1a_	Alignment	not modelled	98.3	31	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: UDP-glucose pyrophosphorylase
101	d1vm8a_	Alignment	not modelled	98.3	30	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: UDP-glucose pyrophosphorylase
102	c2oefA_	Alignment	not modelled	98.2	17	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	c3gueB_	Alignment	not modelled	98.2	24	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)
104	d2i5ea1	Alignment	not modelled	98.1	16	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: MM2497-like
105	c4bqhA_	Alignment	not modelled	98.1	29	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
106	c5tz8C_	Alignment	not modelled	96.3	12	PDB header: transferase Chain: C: PDB Molecule: glycosyl transferase; PDBTitle: crystal structure of s. aureus tars
107	c5mm1A_	Alignment	not modelled	95.6	14	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
108	c5ekeB_	Alignment	not modelled	95.1	19	PDB header: transferase Chain: B: PDB Molecule: uncharacterized glycosyltransferase slI0501; PDBTitle: structure of the polyisoprenyl-phosphate glycosyltransferase gtrb2 (f215a mutant)
109	d1omza_	Alignment	not modelled	94.6	12	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: Exostosin
110	c2ffuA_	Alignment	not modelled	94.3	11	PDB header: transferase Chain: A: PDB Molecule: polypeptide n-acetylgalactosaminyltransferase 2; PDBTitle: crystal structure of human ppgalnact-2 complexed with udp and ea2
111	c6h4mA_	Alignment	not modelled	94.3	7	PDB header: transferase Chain: A: PDB Molecule: probable ss-1,3-n-acetylglucosaminyltransferase; PDBTitle: tarp-udp-glcnac-3rbop
112	c2z86D_	Alignment	not modelled	94.2	12	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
113	d1xhba2	Alignment	not modelled	94.0	9	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: Polypeptide N-acetylgalactosaminyltransferase 1, N-terminal domain
114	d2bo4a1	Alignment	not modelled	93.3	16	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: MGS-like
115	c2d7iA_	Alignment	not modelled	92.7	8	PDB header: transferase Chain: A: PDB Molecule: polypeptide n-acetylgalactosaminyltransferase 10; PDBTitle: crystal structure of pp-galnac-t10 with udp, galnac and mn2+
116	c4hg6A_	Alignment	not modelled	92.5	15	PDB header: transferase Chain: A: PDB Molecule: cellulose synthase subunit a; PDBTitle: structure of a cellulose synthase - cellulose translocation2 intermediate
117	c1omxB_	Alignment	not modelled	92.3	10	PDB header: transferase Chain: B: PDB Molecule: alpha-1,4-n-acetylhexosaminyltransferase extI2; PDBTitle: crystal structure of mouse alpha-1,4-n-acetylhexosaminyltransferase2 (extI2)
118	c3ckvA_	Alignment	not modelled	90.9	17	PDB header: unknown function Chain: A: PDB Molecule: putative uncharacterized protein; PDBTitle: crystal structure of a mycobacterial protein
119	c6e4rB_	Alignment	not modelled	90.8	9	PDB header: transferase Chain: B: PDB Molecule: polypeptide n-acetylgalactosaminyltransferase 9; PDBTitle: crystal structure of the drosophila melanogaster polypeptide n-2 acetylgalactosaminyl transferase pgant9b
120	c3f1yC_	Alignment	not modelled	90.7	17	PDB header: transferase Chain: C: PDB Molecule: mannosyl-3-phosphoglycerate synthase; PDBTitle: mannosyl-3-phosphoglycerate synthase from rubrobacter xylanophilus