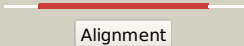

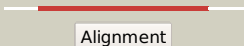

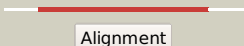







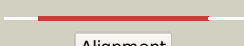











Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1213_(glgC)_1355842_1357056
Date	Wed Jul 31 22:05:30 BST 2019
Unique Job ID	5227273b05f03e1b

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c5l6sF_	 Alignment		100.0	40	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
2	c3brkX_	 Alignment		100.0	40	PDB header: transferase Chain: X; PDB Molecule: glucose-1-phosphate adenylyltransferase; PDBTitle: crystal structure of adp-glucose pyrophosphorylase from agrobacterium2 tumefaciens
3	c1yp3C_	 Alignment		100.0	35	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
4	c6jlwJ_	 Alignment		100.0	15	PDB header: translation Chain: J; PDB Molecule: translation initiation factor eif-2b subunit epsilon; PDBTitle: eif2 - eif2b complex
5	c3d98A_	 Alignment		100.0	18	PDB header: transferase Chain: A; PDB Molecule: bifunctional protein glmu; PDBTitle: crystal structure of glmu from mycobacterium tuberculosis, ligand-free2 form
6	c6j3mG_	 Alignment		100.0	15	PDB header: translation Chain: G; PDB Molecule: translation initiation factor eif-2b subunit epsilon; PDBTitle: eif2b:eif2 complex, phosphorylated on eif2 alpha serine 52.
7	c2qkxA_	 Alignment		100.0	17	PDB header: transferase Chain: A; PDB Molecule: bifunctional protein glmu; PDBTitle: n-acetyl glucosamine 1-phosphate uridyltransferase from mycobacterium2 tuberculosis complex with n-acetyl glucosamine 1-phosphate
8	c5b04I_	 Alignment		100.0	14	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
9	c3d8vA_	 Alignment		100.0	17	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
10	c5b04F_	 Alignment		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
11	c6qq2F_	 Alignment		100.0	15	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)

12	c1hm8A_	Alignment		100.0	17	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
13	c2v0hA_	Alignment		100.0	18	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)
14	c1fwyA_	Alignment		100.0	16	PDB header: transferase Chain: A: PDB Molecule: udp-n-acetylglucosamine pyrophosphorylase; PDBTitle: crystal structure of n-acetylglucosamine 1-phosphate2 uridylyltransferase bound to udp-glcnaC
15	c6ezoF_	Alignment		100.0	17	PDB header: membrane protein Chain: F: PDB Molecule: translation initiation factor eif-2b subunit gamma; PDBTitle: eukaryotic initiation factor eif2b in complex with isrib
16	c6ezoJ_	Alignment		100.0	13	PDB header: membrane protein Chain: J: PDB Molecule: human eukaryotic initiation factor eif2b epsilon subunits; PDBTitle: eukaryotic initiation factor eif2b in complex with isrib
17	c2oi6A_	Alignment		100.0	15	PDB header: transferase Chain: A: PDB Molecule: bifunctional protein glmu; PDBTitle: e. coli glmu- complex with udp-glcnaC, coa and glcN-1-po4
18	c3foqA_	Alignment		100.0	19	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.
19	c5vmkB_	Alignment		100.0	19	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
20	c2ggqA_	Alignment		100.0	22	PDB header: transferase Chain: A: PDB Molecule: 401aa long hypothetical glucose-1-phosphate PDBTitle: complex of hypothetical glucose-1-phosphate thymidyltransferase from2 sulfobolus tokodaii
21	d1lvwa_	Alignment	not modelled	100.0	26	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: glucose-1-phosphate thymidyltransferase
22	d1yp2a2	Alignment	not modelled	100.0	34	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: glucose-1-phosphate thymidyltransferase
23	d1fxoa_	Alignment	not modelled	100.0	24	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: glucose-1-phosphate thymidyltransferase
24	d1liina_	Alignment	not modelled	100.0	25	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: glucose-1-phosphate thymidyltransferase
25	d1h5ra_	Alignment	not modelled	100.0	27	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: glucose-1-phosphate thymidyltransferase
26	d1mc3a_	Alignment	not modelled	100.0	27	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: glucose-1-phosphate thymidyltransferase
27	c5i1fA_	Alignment	not modelled	100.0	20	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 PDB header: transferase
28	c2ux8G_	Alignment	not modelled	100.0	18	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. PDB header: transferase

29	c2pa4B	Alignment	not modelled	100.0	17	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
30	c2e3dB	Alignment	not modelled	100.0	20	PDB header: transferase Chain: B; PDB Molecule: utp--glucose-1-phosphate uridylyltransferase; PDBTitle: crystal structure of e. coli glucose-1-phosphate2 uridylyltransferase
31	c2cu2A	Alignment	not modelled	100.0	23	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
32	c6b5kA	Alignment	not modelled	100.0	24	PDB header: transferase Chain: A; PDB Molecule: glucose-1-phosphate thymidylyltransferase; PDBTitle: mycobacterium tuberculosis rmla in complex with mg/dttp
33	c3jukA	Alignment	not modelled	100.0	19	PDB header: transferase Chain: A; PDB Molecule: udp-glucose pyrophosphorylase (galu); PDBTitle: the crystal structure of udp-glucose pyrophosphorylase complexed with2 udp-glucose
34	c2x5sB	Alignment	not modelled	100.0	18	PDB header: transferase Chain: B; PDB Molecule: mannose-1-phosphate guanylyltransferase; PDBTitle: crystal structure of t. maritima gdp-mannose2 pyrophosphorylase in apo state.
35	c3hl3A	Alignment	not modelled	100.0	25	PDB header: transferase Chain: A; PDB Molecule: glucose-1-phosphate thymidylyltransferase; PDBTitle: 2.76 angstrom crystal structure of a putative glucose-1-phosphate2 thymidylyltransferase from bacillus anthracis in complex with a3 sucrose.
36	d2cu2a2	Alignment	not modelled	100.0	21	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: mannose-1-phosphate guanylyl transferase
37	d1tzfa	Alignment	not modelled	100.0	19	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: Cytidylyltransferase
38	c5xhwA	Alignment	not modelled	100.0	24	PDB header: transferase Chain: A; PDB Molecule: putative 6-deoxy-d-mannoheptose pathway protein; PDBTitle: crystal structure of hddc from yersinia pseudotuberculosis
39	c3pnnA	Alignment	not modelled	100.0	17	PDB header: transferase Chain: A; PDB Molecule: conserved domain protein; PDBTitle: the crystal structure of a glycosyltransferase from porphyromonas2 gingivalis w83
40	d1g97a2	Alignment	not modelled	100.0	18	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: UDP-glucose pyrophosphorylase
41	c4evwB	Alignment	not modelled	100.0	13	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 (nsg) target vcr193.
42	d2oi6a2	Alignment	not modelled	100.0	14	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: UDP-glucose pyrophosphorylase
43	c4y7uA	Alignment	not modelled	100.0	21	PDB header: transferase Chain: A; PDB Molecule: nucleotidyl transferase; PDBTitle: structural analysis of muru
44	c4jd0A	Alignment	not modelled	100.0	18	PDB header: transferase Chain: A; PDB Molecule: nucleotidyl transferase; PDBTitle: structure of the inositol-1-phosphate ctp transferase from t.2 maritima.
45	c6i7tl	Alignment	not modelled	100.0	12	PDB header: translation Chain: I; PDB Molecule: translation initiation factor eif-2b subunit gamma; PDBTitle: eif2b:eif2 complex
46	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
47	c1jvC	Alignment	not modelled	99.9	16	PDB header: transferase Chain: C; PDB Molecule: ctp:phosphocholine cytidylyltransferase; PDBTitle: catalytic mechanism of ctp:phosphocholine2 cytidylyltransferase from streptococcus pneumoniae (licc)
48	d1jyka	Alignment	not modelled	99.9	16	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: Cytidylyltransferase
49	c2qh5B	Alignment	not modelled	99.9	19	PDB header: isomerase Chain: B; PDB Molecule: mannose-6-phosphate isomerase; PDBTitle: crystal structure of mannose-6-phosphate isomerase from helicobacter2 pylori
50	d1vica	Alignment	not modelled	99.9	15	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: Cytidylyltransferase
51	c2xmhB	Alignment	not modelled	99.9	17	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
						PDB header: transferase Chain: D; PDB Molecule: 3-deoxy-manno-octulosonate

52	c3oamD_	Alignment	not modelled	99.9	13	cytidyltransferase; PDBTitle: crystal structure of cytidyltransferase from vibrio cholerae
53	c4xwiA_	Alignment	not modelled	99.9	16	PDB header: transferase Chain: A: PDB Molecule: 3-deoxy-manno-octulosonate cytidyltransferase; PDBTitle: x-ray crystal structure of cmp-kdo synthase from pseudomonas2 aeruginosa
54	c2xwlB_	Alignment	not modelled	99.9	18	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	d1h7ea_	Alignment	not modelled	99.8	12	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: Cytidyltransferase
56	c3polA_	Alignment	not modelled	99.8	14	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	c5ddtA_	Alignment	not modelled	99.8	12	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
58	d1vh1a_	Alignment	not modelled	99.8	16	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: Cytidyltransferase
59	c3tqdA_	Alignment	not modelled	99.8	12	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
60	c2y6pC_	Alignment	not modelled	99.8	20	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
61	d1vpaa_	Alignment	not modelled	99.8	13	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: Cytidyltransferase
62	d1i52a_	Alignment	not modelled	99.8	16	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: Cytidyltransferase
63	d1eyra_	Alignment	not modelled	99.8	14	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: Cytidyltransferase
64	d1qwja_	Alignment	not modelled	99.8	16	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: Cytidyltransferase
65	c4kt7A_	Alignment	not modelled	99.8	13	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	d1vh3a_	Alignment	not modelled	99.8	13	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: Cytidyltransferase
67	c4mybA_	Alignment	not modelled	99.7	15	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)
68	d1w55a1	Alignment	not modelled	99.7	16	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: Cytidyltransferase
69	c3f1cB_	Alignment	not modelled	99.7	15	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
70	d2dpwa1	Alignment	not modelled	99.7	22	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: TTHA0179-like
71	c2wawA_	Alignment	not modelled	99.7	19	PDB header: unknown function Chain: A: PDB Molecule: moba relate protein; PDBTitle: crystal structure of mycobacterium tuberculosis rv0371c2 homolog from mycobacterium sp. strain jc1
72	c2we9A_	Alignment	not modelled	99.7	14	PDB header: unknown function Chain: A: PDB Molecule: moba-related protein; PDBTitle: crystal structure of rv0371c from mycobacterium2 tuberculosis h37rv
73	c6ifdD_	Alignment	not modelled	99.7	12	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+.
74	c2i5kB_	Alignment	not modelled	99.7	12	PDB header: transferase Chain: B: PDB Molecule: utp--glucose-1-phosphate uridyltransferase; PDBTitle: crystal structure of ugp1p
75	d1w77a1	Alignment	not modelled	99.6	14	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: Cytidyltransferase
						Fold: Nucleotide-diphospho-sugar transferases

76	d1e5ka_	Alignment	not modelled	99.6	14	Superfamily: Nucleotide-diphospho-sugar transferases Family: Molybdenum cofactor biosynthesis protein MobA
77	c3ngwA_	Alignment	not modelled	99.6	18	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
78	c3rsbB_	Alignment	not modelled	99.6	18	PDB header: transferase Chain: B: PDB Molecule: adenosylcobinamide-phosphate guanylyltransferase; PDBTitle: structure of the archaeal gtp:adocbi-p guanylyltransferase (coby) from2 methanocaldococcus jannaschii
79	c3okrA_	Alignment	not modelled	99.6	17	PDB header: transferase Chain: A: PDB Molecule: 2-c-methyl-d-erythritol 4-phosphate cytidylyltransferase; PDBTitle: structure of mtb apo 2-c-methyl-d-erythritol 4-phosphate2 cytidyltransferase (ispd)
80	c2vshB_	Alignment	not modelled	99.6	16	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
81	c4jisB_	Alignment	not modelled	99.6	13	PDB header: transferase Chain: B: PDB Molecule: ribitol-5-phosphate cytidylyltransferase; PDBTitle: crystal structure of ribitol 5-phosphate cytidylyltransferase (tari)2 from bacillus subtilis
82	c6oewB_	Alignment	not modelled	99.6	16	PDB header: transferase Chain: B: PDB Molecule: cytidylyltransferase; PDBTitle: structure of a cytidylyltransferase from leptospira borgpetersenii2 serovar hardjo-bovis (strain jb197)
83	d1vgwa_	Alignment	not modelled	99.6	15	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: Cytidylyltransferase
84	d1yp2a1	Alignment	not modelled	99.6	29	Fold: Single-stranded left-handed beta-helix Superfamily: Trimeric LpxA-like enzymes Family: GlmU C-terminal domain-like
85	c4ys8B_	Alignment	not modelled	99.6	15	PDB header: transferase Chain: B: PDB Molecule: 2-c-methyl-d-erythritol 4-phosphate cytidylyltransferase; PDBTitle: crystal structure of 2-c-methyl-d-erythritol 4-phosphate2 cytidylyltransferase (ispd) from burkholderia thailandensis
86	c3r2wB_	Alignment	not modelled	99.5	13	PDB header: transferase Chain: B: PDB Molecule: utp--glucose-1-phosphate uridylyltransferase; PDBTitle: crystal structure of udp-glucose pyrophosphorylase of homo sapiens
87	c2px7A_	Alignment	not modelled	99.5	17	PDB header: transferase Chain: A: PDB Molecule: 2-c-methyl-d-erythritol 4-phosphate cytidylyltransferase; PDBTitle: crystal structure of 2-c-methyl-d-erythritol 4-phosphate2 cytidylyltransferase from thermus thermophilus hb8
88	c3c8vA_	Alignment	not modelled	99.5	12	PDB header: transferase Chain: A: PDB Molecule: putative acetyltransferase; PDBTitle: crystal structure of putative acetyltransferase (yp_390128.1) from2 desulfovibrio desulfuricans g20 at 2.28 a resolution
89	c2q4jB_	Alignment	not modelled	99.5	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
90	c2e8bA_	Alignment	not modelled	99.5	21	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
91	c3gueB_	Alignment	not modelled	99.4	13	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)
92	c1w57A_	Alignment	not modelled	99.4	18	PDB header: transferase Chain: A: PDB Molecule: ispd/ispf bifunctional enzyme; PDBTitle: structure of the bifunctional ispdf from campylobacter2 jejuni containing zn
93	c3pmoA_	Alignment	not modelled	99.4	18	PDB header: transferase Chain: A: PDB Molecule: udp-3-o-[3-hydroxymyristoyl] glucosamine n-acyltransferase; PDBTitle: the structure of lpxd from pseudomonas aeruginosa at 1.3 a resolution
94	c3r5dA_	Alignment	not modelled	99.4	12	PDB header: transferase Chain: A: PDB Molecule: tetrahydrodipicolinate n-succinyletransferase; PDBTitle: pseudomonas aeruginosa dapd (pa3666) apoprotein
95	c4e75A_	Alignment	not modelled	99.4	15	PDB header: transferase Chain: A: PDB Molecule: udp-3-o-acylglucosamine n-acyltransferase; PDBTitle: structure of lpxd from acinetobacter baumannii at 2.85a resolution2 (p21 form)
96	c6ckta_	Alignment	not modelled	99.4	17	PDB header: transferase Chain: A: PDB Molecule: 2,3,4,5-tetrahydropyridine-2,6-dicarboxylate n-dicarbonyltransferase PDBTitle: crystal structure of 2,3,4,5-tetrahydropyridine-2,6-dicarboxylate n-2 succinyltransferase from legionella pneumophila philadelphia 1
97	c2oefa_	Alignment	not modelled	99.3	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

98	d3tdta_	Alignment	not modelled	99.3	15	Fold: Single-stranded left-handed beta-helix Superfamily: Trimeric LpxA-like enzymes Family: Tetrahydrodipicolinate-N-succinyltransferase, THDP-succinyltransferase, DapD
99	c3kwcD_	Alignment	not modelled	99.3	19	PDB header: lyase, protein binding, photosynthesis Chain: D: PDB Molecule: carbon dioxide concentrating mechanism protein; PDBTitle: oxidized, active structure of the beta-carboxysomal gamma-carbonic2 anhydrase, cccmm
100	c3eg4A_	Alignment	not modelled	99.3	15	PDB header: transferase Chain: A: PDB Molecule: 2,3,4,5-tetrahydropyridine-2,6-dicarboxylate n- PDBTitle: crystal structure of 2,3,4,5-tetrahydropyridine-2-2 carboxylate n-succinyltransferase from brucella melitensis3 biovar abortus 2308
101	c3eh0C_	Alignment	not modelled	99.3	14	PDB header: transferase Chain: C: PDB Molecule: udp-3-o-[3-hydroxymyristoyl] glucosamine n- PDBTitle: crystal structure of lpxd from escherichia coli
102	c2iu9C_	Alignment	not modelled	99.3	13	PDB header: transferase Chain: C: PDB Molecule: udp-3-o-[3-hydroxymyristoyl] glucosamine PDBTitle: chlamydia trachomatis lpxd with 100mm udpglcnac (complex ii)
103	d1fxja1	Alignment	not modelled	99.2	24	Fold: Single-stranded left-handed beta-helix Superfamily: Trimeric LpxA-like enzymes Family: GlmU C-terminal domain-like
104	d2icya2	Alignment	not modelled	99.2	11	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: UDP-glucose pyrophosphorylase
105	c5afuU_	Alignment	not modelled	99.2	13	PDB header: motor protein Chain: U: PDB Molecule: dynactin; PDBTitle: cryo-em structure of dynein tail-dynactin-bicd2n complex
106	d1jv1a_	Alignment	not modelled	99.2	15	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: UDP-glucose pyrophosphorylase
107	d1vm8a_	Alignment	not modelled	99.1	16	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: UDP-glucose pyrophosphorylase
108	c3oc9A_	Alignment	not modelled	99.1	12	PDB header: transferase Chain: A: PDB Molecule: udp-n-acetylglucosamine pyrophosphorylase; PDBTitle: crystal structure of putative udp-n-acetylglucosamine2 pyrophosphorylase from entamoeba histolytica
109	c3fsyC_	Alignment	not modelled	99.1	17	PDB header: transferase Chain: C: PDB Molecule: tetrahydrodipicolinate n-succinyltransferase; PDBTitle: structure of tetrahydrodipicolinate n-succinyltransferase2 (rv1201c;dapd) in complex with succinyl-coa from mycobacterium3 tuberculosis
110	c3i3aC_	Alignment	not modelled	99.1	14	PDB header: transferase Chain: C: PDB Molecule: acyl-[acyl-carrier-protein]-udp-n- PDBTitle: structural basis for the sugar nucleotide and acyl chain2 selectivity of leptospira interrogans lpxa
111	c3t57A_	Alignment	not modelled	99.1	18	PDB header: transferase Chain: A: PDB Molecule: udp-n-acetylglucosamine o-acyltransferase domain-containing PDBTitle: activity and crystal structure of arabidopsis udp-n-acetylglucosamine2 acyltransferase
112	c4cvhA_	Alignment	not modelled	99.1	17	PDB header: transferase Chain: A: PDB Molecule: isoprenoid synthase domain-containing protein; PDBTitle: crystal structure of human isoprenoid synthase domain-containing2 protein
113	c5f42B_	Alignment	not modelled	99.1	17	PDB header: transferase Chain: B: PDB Molecule: acyl-[acyl-carrier-protein]-udp-n-acetylglucosamine o- PDBTitle: activity and crystal structure of francisella novicida udp-n-2 acetylglucosamine acyltransferase
114	c4bmaB_	Alignment	not modelled	99.1	13	PDB header: transferase Chain: B: PDB Molecule: udp-n-acetylglucosamine pyrophosphorylase; PDBTitle: structural of aspergillus fumigatus udp-n-acetylglucosamine2 pyrophosphorylase
115	c4mzuG_	Alignment	not modelled	99.1	15	PDB header: isomerase, transferase Chain: G: PDB Molecule: wxcm-like protein; PDBTitle: crystal structure of fdtd, a bifunctional ketoisomerase/n-2 acetyltransferase from shewanella denitrificans
116	c3r3rA_	Alignment	not modelled	99.1	17	PDB header: transferase Chain: A: PDB Molecule: ferripyochelin binding protein; PDBTitle: structure of the yrdA ferripyochelin binding protein from salmonella2 enterica
117	d1qrea_	Alignment	not modelled	99.1	21	Fold: Single-stranded left-handed beta-helix Superfamily: Trimeric LpxA-like enzymes Family: gamma-carbonic anhydrase-like
118	c1qreA_	Alignment	not modelled	99.1	21	PDB header: lyase Chain: A: PDB Molecule: carbonic anhydrase; PDBTitle: a closer look at the active site of gamma-carbonic anhydrases: high2 resolution crystallographic studies of the carbonic anhydrase from3 methanosarcina thermophila
119	c4bqhA_	Alignment	not modelled	99.1	14	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
120	c4ea8A_	Alignment	not modelled	99.1	14	PDB header: transferase Chain: A: PDB Molecule: perosamine n-acetyltransferase; PDBTitle: x-ray crystal structure of perb from caulobacter crescentus in complex2 with coenzyme a and gdp-n-

