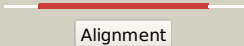

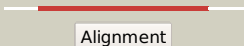

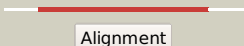







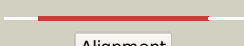











Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3264c_(manB)_3644895_3645974
Date	Thu Aug 8 16:20:47 BST 2019
Unique Job ID	14819a470a33fa42

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c6i3mG_	 Alignment		100.0	20	PDB header: translation Chain: G: PDB Molecule: translation initiation factor eif-2b subunit epsilon; PDBTitle: eif2b:eif2 complex, phosphorylated on eif2 alpha serine 52.
2	c6j1wJ_	 Alignment		100.0	17	PDB header: translation Chain: J: PDB Molecule: translation initiation factor eif-2b subunit epsilon; PDBTitle: eif2 - eif2b complex
3	c5b04I_	 Alignment		100.0	19	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
4	c3brkX_	 Alignment		100.0	23	PDB header: transferase Chain: X: PDB Molecule: glucose-1-phosphate adenylyltransferase; PDBTitle: crystal structure of adp-glucose pyrophosphorylase from agrobacterium2 tumefaciens
5	c2qkxA_	 Alignment		100.0	25	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
6	c3d98A_	 Alignment		100.0	25	PDB header: transferase Chain: A: PDB Molecule: bifunctional protein glmu; PDBTitle: crystal structure of glmu from mycobacterium tuberculosis, ligand-free2 form
7	c5l6sF_	 Alignment		100.0	23	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
8	c5b04F_	 Alignment		100.0	19	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
9	c1yp3C_	 Alignment		100.0	23	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
10	c3d8vA_	 Alignment		100.0	27	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
11	c6qg2F_	 Alignment		100.0	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)

12	c1hm8A_	Alignment		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
13	c2v0hA_	Alignment		100.0	21	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	c2oi6A_	Alignment		100.0	21	PDB header: transferase Chain: A: PDB Molecule: bifunctional protein glmu; PDBTitle: e. coli glmu- complex with udp-glcnac, coa and glcn-1-p04
15	c6ezoJ_	Alignment		100.0	17	PDB header: membrane protein Chain: J: PDB Molecule: human eukaryotic initiation factor eif2b epsilon subunits; PDBTitle: eukaryotic initiation factor eif2b in complex with isrib
16	c6ezoF_	Alignment		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
17	c1fwyA_	Alignment		100.0	20	PDB header: transferase Chain: A: PDB Molecule: udp-n-acetylglucosamine pyrophosphorylase; PDBTitle: crystal structure of n-acetylglucosamine 1-phosphate2 uridylyltransferase bound to udp-glcnac
18	c3foqA_	Alignment		100.0	26	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	c2ggqA_	Alignment		100.0	21	PDB header: transferase Chain: A: PDB Molecule: 401aa long hypothetical glucose-1-phosphate PDBTitle: complex of hypothetical glucose-1-phosphate thymidyllyltransferase from2 sulfobolus tokodaii
20	c5vmkB_	Alignment		100.0	21	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
21	d1lwva_	Alignment	not modelled	100.0	23	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: glucose-1-phosphate thymidyllyltransferase
22	d1fxoa_	Alignment	not modelled	100.0	25	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: glucose-1-phosphate thymidyllyltransferase
23	d1h5ra_	Alignment	not modelled	100.0	24	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: glucose-1-phosphate thymidyllyltransferase
24	d1mc3a_	Alignment	not modelled	100.0	25	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: glucose-1-phosphate thymidyllyltransferase
25	d1iina_	Alignment	not modelled	100.0	24	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: glucose-1-phosphate thymidyllyltransferase
26	c5i1fA_	Alignment	not modelled	100.0	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
27	c6b5kA_	Alignment	not modelled	100.0	22	PDB header: transferase Chain: A: PDB Molecule: glucose-1-phosphate thymidyllyltransferase; PDBTitle: mycobacterium tuberculosis rmla in complex with mg/dttp
28	c2pa4B_	Alignment	not modelled	100.0	23	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
29	c2ux8G_	Alignment	not modelled	100.0	23	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.
30	c2e3dB_	Alignment	not modelled	100.0	24	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	22	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	d1yp2a2	Alignment	not modelled	100.0	22	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: glucose-1-phosphate thymidylyltransferase
33	c3hl3A_	Alignment	not modelled	100.0	19	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.
34	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
35	c5xhwA_	Alignment	not modelled	100.0	28	PDB header: transferase Chain: A: PDB Molecule: putative 6-deoxy-d-mannoheptose pathway protein; PDBTitle: crystal structure of hddc from yersinia pseudotuberculosis
36	c2x5sB_	Alignment	not modelled	100.0	20	PDB header: transferase Chain: B: PDB Molecule: mannose-1-phosphate guanylyltransferase; PDBTitle: crystal structure of t. maritima gdp-mannose2 pyrophosphorylase in apo state.
37	c3pnnA_	Alignment	not modelled	100.0	20	PDB header: transferase Chain: A: PDB Molecule: conserved domain protein; PDBTitle: the crystal structure of a glycosyltransferase from porphyromonas2 gingivalis w83
38	d2cu2a2	Alignment	not modelled	100.0	22	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: mannose-1-phosphate guanylyl transferase
39	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 (nesg) target vcr193.
40	d1tzfa_	Alignment	not modelled	100.0	27	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: Cytidylyltransferase
41	c4y7uA_	Alignment	not modelled	100.0	31	PDB header: transferase Chain: A: PDB Molecule: nucleotidyl transferase; PDBTitle: structural analysis of muru
42	c4jd0A_	Alignment	not modelled	100.0	17	PDB header: transferase Chain: A: PDB Molecule: nucleotidyl transferase; PDBTitle: structure of the inositol-1-phosphate ctp transferase from t.2 maritima.
43	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
44	d1g97a2	Alignment	not modelled	100.0	21	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: UDP-glucose pyrophosphorylase
45	d2oi6a2	Alignment	not modelled	100.0	19	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: UDP-glucose pyrophosphorylase
46	d1jyka_	Alignment	not modelled	100.0	17	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: Cytidylyltransferase
47	c1jylC_	Alignment	not modelled	100.0	15	PDB header: transferase Chain: C: PDB Molecule: ctp:phosphocholine cytidylyltransferase; PDBTitle: catalytic mechanism of ctp:phosphocholine2 cytidylyltransferase from streptococcus pneumoniae (licc)
48	c6i7tl_	Alignment	not modelled	100.0	10	PDB header: translation Chain: I: PDB Molecule: translation initiation factor eif-2b subunit gamma; PDBTitle: eif2b:eif2 complex
49	c2xmhB_	Alignment	not modelled	100.0	16	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
50	c2qh5B_	Alignment	not modelled	100.0	21	PDB header: isomerase Chain: B: PDB Molecule: mannose-6-phosphate isomerase; PDBTitle: crystal structure of mannose-6-phosphate isomerase from helicobacter2 pylori
51	d1vica_	Alignment	not modelled	99.9	18	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: Cytidylyltransferase
						PDB header: transferase

52	c3oamD_	Alignment	not modelled	99.9	20	Chain: D: PDB Molecule: 3-deoxy-manno-octulosonate cytidyltransferase; PDBTitle: crystal structure of cytidyltransferase from vibrio cholerae
53	c4xwiA_	Alignment	not modelled	99.9	17	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	c2xwIB_	Alignment	not modelled	99.9	19	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	c3polA_	Alignment	not modelled	99.9	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.
56	d1eyra_	Alignment	not modelled	99.9	12	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: Cytidyltransferase
57	d1h7ea_	Alignment	not modelled	99.9	19	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: Cytidyltransferase
58	d1vh1a_	Alignment	not modelled	99.9	17	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: Cytidyltransferase
59	c3tqdA_	Alignment	not modelled	99.9	15	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	d1i52a_	Alignment	not modelled	99.9	14	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: Cytidyltransferase
61	d1vpaa_	Alignment	not modelled	99.9	13	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: Cytidyltransferase
62	c5ddtA_	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 ispd from bacillus subtilis at 1.80 angstroms2 resolution, crystal form i
63	c2y6pC_	Alignment	not modelled	99.9	18	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
64	d1vh3a_	Alignment	not modelled	99.8	19	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: Cytidyltransferase
65	d1w55a1	Alignment	not modelled	99.8	12	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: Cytidyltransferase
66	c4mybA_	Alignment	not modelled	99.8	14	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)
67	d1qwja_	Alignment	not modelled	99.8	15	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: Cytidyltransferase
68	c4kt7A_	Alignment	not modelled	99.8	15	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
69	c2wawA_	Alignment	not modelled	99.8	22	PDB header: unknown function Chain: A: PDB Molecule: moba relate protein; PDBTitle: crystal structure of mycobacterium tuberculosis rv0371c2 homolog from mycobacterium sp. strain jc1
70	c2we9A_	Alignment	not modelled	99.8	24	PDB header: unknown function Chain: A: PDB Molecule: moba-related protein; PDBTitle: crystal structure of rv0371c from mycobacterium2 tuberculosis h37rv
71	d2dpwa1	Alignment	not modelled	99.8	22	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: TTHA0179-like
72	c3c8vA_	Alignment	not modelled	99.8	23	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
73	c3eg4A_	Alignment	not modelled	99.7	19	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
74	d1e5ka_	Alignment	not modelled	99.7	18	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: Molybdenum cofactor biosynthesis protein MobA
						PDB header: transferase Chain: A: PDB Molecule: 2,3,4,5-tetrahydropyridine-2,6-

75	c6cktA	Alignment	not modelled	99.7	24	dicarboxylate n- PDBTitle: crystal structure of 2,3,4,5-tetrahydropyridine-2,6-dicarboxylate n-2 succinyltransferase from legionella pneumophila philadelphia 1
76	d3tdta	Alignment	not modelled	99.7	21	Fold: Single-stranded left-handed beta-helix Superfamily: Trimeric LpxA-like enzymes Family: Tetrahydrodipicolinate-N-succinyltransferase, THDP-succinyltransferase, DapD
77	c6oewB	Alignment	not modelled	99.7	15	PDB header: transferase Chain: B: PDB Molecule: cytidyltransferase; PDBTitle: structure of a cytidyltransferase from leptospira borgpetersenii2 serovar hardjo-bovis (strain jb197)
78	d1w77a1	Alignment	not modelled	99.7	13	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: Cytidyltransferase
79	c1w57A	Alignment	not modelled	99.7	15	PDB header: transferase Chain: A: PDB Molecule: ispd/ispf bifunctional enzyme; PDBTitle: structure of the bifunctional ispdf from campylobacter2 jejuni containing zn
80	c6ifdD	Alignment	not modelled	99.7	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+.
81	c3okrA	Alignment	not modelled	99.7	14	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)
82	c3rsbB	Alignment	not modelled	99.7	17	PDB header: transferase Chain: B: PDB Molecule: adenosylcobinamide-phosphate guanylyltransferase; PDBTitle: structure of the archaeal gtp:adocbi-p guanylyltransferase (coby) from2 methanocaldococcus jannaschii
83	c3f1cB	Alignment	not modelled	99.7	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
84	c4ys8B	Alignment	not modelled	99.7	12	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
85	c3kwcD	Alignment	not modelled	99.7	28	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, ccmm
86	c3ngwA	Alignment	not modelled	99.6	16	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
87	d1vgwa	Alignment	not modelled	99.6	13	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: Cytidyltransferase
88	c3eh0C	Alignment	not modelled	99.6	19	PDB header: transferase Chain: C: PDB Molecule: udp-3-o-[3-hydroxymyristoyl] glucosamine n- PDBTitle: crystal structure of lpxd from escherichia coli
89	c2px7A	Alignment	not modelled	99.6	17	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
90	c4e75A	Alignment	not modelled	99.6	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)
91	c5f42B	Alignment	not modelled	99.6	27	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
92	c3i3aC	Alignment	not modelled	99.6	18	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
93	c4eqyC	Alignment	not modelled	99.6	29	PDB header: transferase Chain: C: PDB Molecule: acyl-[acyl-carrier-protein]-udp-n-acetylglucosamine o- PDBTitle: crystal structure of acyl-[acyl-carrier-protein]-udp-n-2 acetylglucosamine o-acyltransferase from burkholderia thailandensis
94	d2jf2a1	Alignment	not modelled	99.6	28	Fold: Single-stranded left-handed beta-helix Superfamily: Trimeric LpxA-like enzymes Family: UDP N-acetylglucosamine acyltransferase
95	c2e8bA	Alignment	not modelled	99.6	15	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
96	c2iu9C	Alignment	not modelled	99.6	21	PDB header: transferase Chain: C: PDB Molecule: udp-3-o-[3-hydroxymyristoyl] glucosamine PDBTitle: chlamydia trachomatis lpxd with 100mm udpglcnaC (complex ii)
97	c5jxxC	Alignment	not modelled	99.6	26	PDB header: transferase Chain: C: PDB Molecule: acyl-[acyl-carrier-protein]-udp-n-acetylglucosamine o- PDBTitle: crystal structure of udp-n-acetylglucosamine o-

						acyltransferase (lpxa)2 from moraxella catarrhalis rh4.
98	c5afuU	Alignment	not modelled	99.6	22	PDB header: motor protein Chain: U: PDB Molecule: dyndactin; PDBTitle: cryo-em structure of dynein tail-dyndactin-bicd2n complex
99	d1j2za	Alignment	not modelled	99.6	24	Fold: Single-stranded left-handed beta-helix Superfamily: Trimeric LpxA-like enzymes Family: UDP N-acetylglucosamine acyltransferase
100	c4mzuG	Alignment	not modelled	99.6	24	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
101	c3r0sA	Alignment	not modelled	99.6	30	PDB header: transferase Chain: A: PDB Molecule: acyl-[acyl-carrier-protein]-udp-n-acetylglucosamine o- PDBTitle: udp-n-acetylglucosamine acyltransferase from campylobacter jejuni
102	c4ea8A	Alignment	not modelled	99.6	17	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-acetylperosamine at 1 angstrom resolution
103	c3pmoA	Alignment	not modelled	99.6	21	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
104	c2vshB	Alignment	not modelled	99.6	11	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
105	c3cj8B	Alignment	not modelled	99.6	29	PDB header: transferase Chain: B: PDB Molecule: 2,3,4,5-tetrahydropyridine-2,6-dicarboxylate n- PDBTitle: crystal structure of 2,3,4,5-tetrahydropyridine-2-carboxylate n-2 succinyltransferase from enterococcus faecalis v583
106	c4r36A	Alignment	not modelled	99.6	31	PDB header: transferase Chain: A: PDB Molecule: putative acyl-[acyl-carrier-protein]-udp-n-acetylglucosamine2 acyltransferase analysis of lpxa, a udp-n-acetylglucosamine2 acyltransferase from bacteroides fragilis 9343
107	c4jisB	Alignment	not modelled	99.5	11	PDB header: transferase Chain: B: PDB Molecule: ribitol-5-phosphate cytidyltransferase; PDBTitle: crystal structure of ribitol 5-phosphate cytidyltransferase (tari)2 from bacillus subtilis
108	d1qrea	Alignment	not modelled	99.5	23	Fold: Single-stranded left-handed beta-helix Superfamily: Trimeric LpxA-like enzymes Family: gamma-carbonic anhydrase-like
109	c1qreA	Alignment	not modelled	99.5	23	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
110	c4e6tA	Alignment	not modelled	99.5	12	PDB header: transferase Chain: A: PDB Molecule: acyl-[acyl-carrier-protein]-udp-n-acetylglucosamine o- PDBTitle: structure of lpxa from acinetobacter baumannii at 1.8a resolution2 (p212121 form)
111	c4m98A	Alignment	not modelled	99.5	22	PDB header: transferase Chain: A: PDB Molecule: pilin glycosylation protein; PDBTitle: acetyltransferase domain of pglb from neisseria gonorrhoeae fa1090
112	c5dg3D	Alignment	not modelled	99.5	27	PDB header: transferase Chain: D: PDB Molecule: acyl-[acyl-carrier-protein]-udp-n-acetylglucosamine o- PDBTitle: structure of pseudomonas aeruginosa lpxa in complex with udp-3-o-(r-3-2 hydroxydecanoyl)-glcnae
113	c3t57A	Alignment	not modelled	99.5	19	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
114	c2i5kB	Alignment	not modelled	99.5	18	PDB header: transferase Chain: B: PDB Molecule: utp--glucose-1-phosphate uridylyltransferase; PDBTitle: crystal structure of ugp1p
115	d1yp2a1	Alignment	not modelled	99.5	24	Fold: Single-stranded left-handed beta-helix Superfamily: Trimeric LpxA-like enzymes Family: GlmU C-terminal domain-like
116	c3r3rA	Alignment	not modelled	99.5	18	PDB header: transferase Chain: A: PDB Molecule: ferripyochelin binding protein; PDBTitle: structure of the yrdA ferripyochelin binding protein from salmonella2 enterica
117	c3r8yD	Alignment	not modelled	99.5	22	PDB header: transferase Chain: D: PDB Molecule: 2,3,4,5-tetrahydropyridine-2,6-dicarboxylate n- PDBTitle: structure of the bacillus anthracis tetrahydropicolinate2 succinyltransferase
118	c3tv0A	Alignment	not modelled	99.5	21	PDB header: structural protein Chain: A: PDB Molecule: dyndactin subunit 6; PDBTitle: structure of dyndactin p27 subunit
119	c3ixcA	Alignment	not modelled	99.5	22	PDB header: transferase Chain: A: PDB Molecule: hexapeptide transferase family protein; PDBTitle: crystal structure of hexapeptide transferase family protein from2 anaplasma phagocytophilum
120	c4n27D	Alignment	not modelled	99.5	29	PDB header: transferase Chain: D: PDB Molecule: bacterial transferase hexapeptide repeat; PDBTitle: x-ray structure of brucella abortus rica