



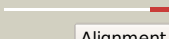























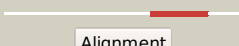











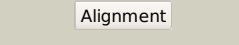
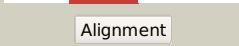
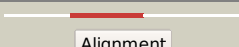

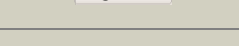




Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2051c_(ppm1)_2308139_2310763
Date	Mon Aug 5 13:25:16 BST 2019
Unique Job ID	4aca70684ab8f2b1

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c5vrhA_	 Alignment		100.0	24	PDB header: transferase Chain: A: PDB Molecule: apolipoprotein n-acyltransferase; PDBTitle: apolipoprotein n-acyltransferase c387s active site mutant
2	c5n6mA_	 Alignment		100.0	24	PDB header: membrane protein Chain: A: PDB Molecule: apolipoprotein n-acyltransferase; PDBTitle: structure of the membrane integral lipoprotein n-acyltransferase lnt2 from p. aeruginosa
3	c5mm1A_	 Alignment		100.0	38	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
4	c5h8lM_	 Alignment		100.0	20	PDB header: hydrolase Chain: M: PDB Molecule: n-carbamoylputrescine amidohydrolase; PDBTitle: crystal structure of medicago truncatula n-carbamoylputrescine2 amidohydrolase (mtcpa) c158s mutant in complex with putrescine
5	d1uf5a_	 Alignment		100.0	18	Fold: Carbon-nitrogen hydrolase Superfamily: Carbon-nitrogen hydrolase Family: Carbamilase
6	c2w1vA_	 Alignment		100.0	21	PDB header: hydrolase Chain: A: PDB Molecule: nitrilase homolog 2; PDBTitle: crystal structure of mouse nitrilase-2 at 1.4a resolution
7	c6i00C_	 Alignment		100.0	21	PDB header: hydrolase Chain: C: PDB Molecule: bifunctional nitrilase/nitrile hydratase nit4; PDBTitle: cryo-em informed directed evolution of nitrilase 4 leads to a change2 in quaternary structure.
8	c1xhbA_	 Alignment		100.0	17	PDB header: transferase Chain: A: PDB Molecule: polypeptide n-acetylgalactosaminyltransferase 1; PDBTitle: the crystal structure of udp-galnac: polypeptide alpha-n-2 acetylgalactosaminyltransferase-t1
9	c6e4rB_	 Alignment		100.0	17	PDB header: transferase Chain: B: PDB Molecule: polypeptide n-acetylgalactosaminyltransferase 9; PDBTitle: crystal structure of the drosophila melanogaster polypeptide n-2 acetylgalactosaminyl transferase pgant9b
10	c6iwiqE_	 Alignment		100.0	16	PDB header: transferase Chain: E: PDB Molecule: n-acetylgalactosaminyltransferase 7; PDBTitle: crystal structure of galnac-t7 with mn2+
11	d1f89a_	 Alignment		100.0	22	Fold: Carbon-nitrogen hydrolase Superfamily: Carbon-nitrogen hydrolase Family: Nitrilase

12	c3wuyA	 Alignment		100.0	20	PDB header: hydrolase Chain: A: PDB Molecule: nitrilase; PDBTitle: crystal structure of nit6803
13	c5nqaA	 Alignment		100.0	15	PDB header: transferase Chain: A: PDB Molecule: polypeptide n-acetylgalactosaminyltransferase 4; PDBTitle: crystal structure of galnac-t4 in complex with the monoglycopeptide 3
14	c5ekeB	 Alignment		100.0	22	PDB header: transferase Chain: B: PDB Molecule: uncharacterized glycosyltransferase slI0501; PDBTitle: structure of the polyisoprenyl-phosphate glycosyltransferase gtrb2 (f215a mutant)
15	c2ffuA	 Alignment		100.0	16	PDB header: transferase Chain: A: PDB Molecule: polypeptide n-acetylgalactosaminyltransferase 2; PDBTitle: crystal structure of human ppgalnact-2 complexed with udp and ea2
16	d1emsa2	 Alignment		100.0	20	Fold: Carbon-nitrogen hydrolase Superfamily: Carbon-nitrogen hydrolase Family: Nitrilase
17	c1emsB	 Alignment		100.0	19	PDB header: antitumor protein Chain: B: PDB Molecule: nit-fragile histidine triad fusion protein; PDBTitle: crystal structure of the c. elegans nitfhit protein
18	c5khaA	 Alignment		100.0	17	PDB header: ligase Chain: A: PDB Molecule: glutamine-dependent nad+ synthetase; PDBTitle: structure of glutamine-dependent nad+ synthetase from acinetobacter2 baumannii in complex with adenosine diphosphate (adp)
19	d1j31a	 Alignment		100.0	20	Fold: Carbon-nitrogen hydrolase Superfamily: Carbon-nitrogen hydrolase Family: Carbamilase
20	c2d7iA	 Alignment		100.0	15	PDB header: transferase Chain: A: PDB Molecule: polypeptide n-acetylgalactosaminyltransferase 10; PDBTitle: crystal structure of pp-galnac-t10 with udp, galnac and mn2+
21	c2plqA	 Alignment	not modelled	100.0	22	PDB header: hydrolase Chain: A: PDB Molecule: aliphatic amidase; PDBTitle: crystal structure of the amidase from geobacillus pallidus rapc8
22	c6mg6D	 Alignment	not modelled	100.0	18	PDB header: hydrolase Chain: D: PDB Molecule: carbon-nitrogen hydrolase; PDBTitle: crystal structure of carbon-nitrogen hydrolase from helicobacter2 pylori g27
23	c3hkaA	 Alignment	not modelled	100.0	21	PDB header: hydrolase Chain: A: PDB Molecule: amidase; PDBTitle: crystal structure analysis of an amidase from nesterenkonia sp.
24	c4hg3C	 Alignment	not modelled	100.0	20	PDB header: hydrolase Chain: C: PDB Molecule: probable hydrolase nit2; PDBTitle: structural insights into yeast nit2: wild-type yeast nit2 in complex2 with alpha-ketoglutarate
25	c2e11B	 Alignment	not modelled	100.0	23	PDB header: hydrolase Chain: B: PDB Molecule: hydrolase; PDBTitle: the crystal structure of xc1258 from xanthomonas campestris: a cn-2 hydrolase superfamily protein with an arsenic adduct in the active3 site
26	d1xhba2	 Alignment	not modelled	100.0	15	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: Polypeptide N-acetylgalactosaminyltransferase 1, N-terminal domain
27	c2e2kC	 Alignment	not modelled	100.0	16	PDB header: hydrolase Chain: C: PDB Molecule: formamidase; PDBTitle: helicobacter pylori formamidase amif contains a fine-tuned cysteine-2 glutamate-lysine catalytic triad
28	c2z86D	 Alignment	not modelled	100.0	16	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
29	c5tz8C	Alignment	not modelled	100.0	18	PDB header: transferase Chain: C: PDB Molecule: glycosyl transferase; PDBTitle: crystal structure of s. aureus tars
30	c3ckvA	Alignment	not modelled	100.0	18	PDB header: unknown function Chain: A: PDB Molecule: putative uncharacterized protein; PDBTitle: crystal structure of a mycobacterial protein
31	c4f4hA	Alignment	not modelled	100.0	21	PDB header: ligase Chain: A: PDB Molecule: glutamine dependent nad+ synthetase; PDBTitle: crystal structure of a glutamine dependent nad+ synthetase from2 burkholderia thailandensis
32	c3f1yC	Alignment	not modelled	100.0	17	PDB header: transferase Chain: C: PDB Molecule: mannosyl-3-phosphoglycerate synthase; PDBTitle: mannosyl-3-phosphoglycerate synthase from rubrobacter xylanophilus
33	c2vhiG	Alignment	not modelled	100.0	21	PDB header: hydrolase Chain: G: PDB Molecule: cg3027-pa; PDBTitle: crystal structure of a pyrimidine degrading enzyme from2 drosophila melanogaster
34	c3n05B	Alignment	not modelled	100.0	19	PDB header: ligase Chain: B: PDB Molecule: nh(3)-dependent nad(+) synthetase; PDBTitle: crystal structure of nh3-dependent nad+ synthetase from streptomyces2 avermitilis
35	c2vhhA	Alignment	not modelled	100.0	20	PDB header: hydrolase Chain: A: PDB Molecule: cg3027-pa; PDBTitle: crystal structure of a pyrimidine degrading enzyme from2 drosophila melanogaster
36	c4hg6A	Alignment	not modelled	100.0	17	PDB header: transferase Chain: A: PDB Molecule: cellulose synthase subunit a; PDBTitle: structure of a cellulose synthase - cellulose translocation2 intermediate
37	c6h4mA	Alignment	not modelled	100.0	13	PDB header: transferase Chain: A: PDB Molecule: probable ss-1,3-n-acetylglucosaminyltransferase; PDBTitle: tarp-udp-glcnaC-3rbop
38	c4fixA	Alignment	not modelled	100.0	14	PDB header: transferase Chain: A: PDB Molecule: udp-galactofuranosyl transferase glft2; PDBTitle: crystal structure of glft2
39	c6ftqA	Alignment	not modelled	100.0	19	PDB header: hydrolase Chain: A: PDB Molecule: beta-ureidopropionase; PDBTitle: crystal structure of human beta-ureidopropionase (beta-alanine2 synthase) - mutant t299c
40	c3bcvA	Alignment	not modelled	100.0	19	PDB header: transferase Chain: A: PDB Molecule: putative glycosyltransferase protein; PDBTitle: crystal structure of a putative glycosyltransferase from bacteroides2 fragilis
41	c5heaA	Alignment	not modelled	99.9	16	PDB header: transferase Chain: A: PDB Molecule: putative glycosyltransferase (galt1); PDBTitle: cgt structure in hexamer
42	c3dlaD	Alignment	not modelled	99.9	18	PDB header: ligase Chain: D: PDB Molecule: glutamine-dependent nad(+) synthetase; PDBTitle: x-ray crystal structure of glutamine-dependent nad+ synthetase from2 mycobacterium tuberculosis bound to naad+ and don
43	c3zf8A	Alignment	not modelled	99.9	8	PDB header: transferase Chain: A: PDB Molecule: mannan polymerase complexes subunit mnn9; PDBTitle: crystal structure of saccharomyces cerevisiae mnn9 in2 complex with gdp and mn.
44	d1qg8a	Alignment	not modelled	99.9	15	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: Spore coat polysaccharide biosynthesis protein SpsA
45	d1omza	Alignment	not modelled	99.9	17	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: Exostosin
46	d2bo4a1	Alignment	not modelled	99.9	20	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: MGS-like
47	c4cyyA	Alignment	not modelled	99.9	16	PDB header: hydrolase Chain: A: PDB Molecule: pantetheinase; PDBTitle: the structure of vanin-1: defining the link between metabolic disease,2 oxidative stress and inflammation
48	c1omxB	Alignment	not modelled	99.9	16	PDB header: transferase Chain: B: PDB Molecule: alpha-1,4-n-acetylhexosaminyltransferase extl2; PDBTitle: crystal structure of mouse alpha-1,4-n-acetylhexosaminyltransferase2 (extl2)
49	c3ilvA	Alignment	not modelled	99.9	19	PDB header: ligase Chain: A: PDB Molecule: glutamine-dependent nad(+) synthetase; PDBTitle: crystal structure of a glutamine-dependent nad(+) synthetase2 from cytophaga hutchinsonii
50	c6p61D	Alignment	not modelled	99.9	18	PDB header: transferase Chain: D: PDB Molecule: glycosyltransferase; PDBTitle: structure of a glycosyltransferase from leptospira borgpetersenii2 serovar hardjo-bovis (strain jb197)
51	c2qgiA	Alignment	not modelled	99.9	10	PDB header: transferase Chain: A: PDB Molecule: atp synthase subunits region orf 6; PDBTitle: the udp complex structure of the sixth gene product of the f1-atpase2 operon of rhodobacter blasticus
52	c5hyyA	Alignment	not modelled	99.9	16	PDB header: hydrolase Chain: A: PDB Molecule: nta1p; PDBTitle: crystal structure of n-terminal amidase
53	c5z8bB	Alignment	not modelled	99.8	9	PDB header: transferase Chain: B: PDB Molecule: kfia protein; PDBTitle: truncated n-acetylglucosaminyl transferase kfia from e. coli k5 strain2 apo form
						PDB header: transferase, sugar binding protein

54	c5ggfC_	Alignment	not modelled	99.7	16	Chain: C; PDB Molecule: protein o-linked-mannose beta-1,2-n- PDBTitle: crystal structure of human protein o-mannose beta-1,2-n-2 acetylglucosaminyltransferase form ii
55	c4irqB_	Alignment	not modelled	99.5	19	PDB header: transferase Chain: B; PDB Molecule: beta-1,4-galactosyltransferase 7; PDBTitle: crystal structure of catalytic domain of human beta1,2 4galactosyltransferase 7 in closed conformation in complex with3 manganese and udp
56	d1pzta_	Alignment	not modelled	99.4	20	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: beta 1,4 galactosyltransferase (b4GalT1)
57	c3lw6A_	Alignment	not modelled	98.9	17	PDB header: transferase Chain: A; PDB Molecule: beta-4-galactosyltransferase 7; PDBTitle: crystal structure of drosophila beta1,4-galactosyltransferase-7
58	c2wvmA_	Alignment	not modelled	98.6	19	PDB header: transferase Chain: A; PDB Molecule: mannosyl-3-phosphoglycerate synthase; PDBTitle: h309a mutant of mannosyl-3-phosphoglycerate synthase from2 thermus thermophilus hb27 in complex with3 gdp-alpha-d-mannose and mg(ii)
59	c2zu8A_	Alignment	not modelled	98.5	17	PDB header: transferase Chain: A; PDB Molecule: mannosyl-3-phosphoglycerate synthase; PDBTitle: crystal structure of mannosyl-3-phosphoglycerate synthase2 from pyrococcus horikoshii
60	c6fxyA_	Alignment	not modelled	98.2	13	PDB header: transferase Chain: A; PDB Molecule: procollagen-lysine,2-oxoglutarate 5-dioxygenase 3; PDBTitle: crystal structure of full-length human lysyl hydroxylase lh3 -2 cocrystal with fe2+, mn2+, udp-gal - structure from long-wavelength3 s-sad
61	d1fo8a_	Alignment	not modelled	98.0	18	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: N-acetylglucosaminyltransferase I
62	d1vh3a_	Alignment	not modelled	97.3	12	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: Cytidylyltransferase
63	d3cu0a1	Alignment	not modelled	97.0	20	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: 1,3-glucuronyltransferase
64	c2d0jD_	Alignment	not modelled	96.8	27	PDB header: transferase Chain: D; PDB Molecule: galactosylgalactosylxylosylprotein 3-beta- PDBTitle: crystal structure of human glcat-s apo form
65	c5vcmA_	Alignment	not modelled	96.8	19	PDB header: transferase Chain: A; PDB Molecule: alpha-1,6-mannosyl-glycoprotein 2-beta-n- PDBTitle: alpha-1,6-mannosyl-glycoprotein 2-beta-n-acetylglucosaminyltransferase2 with bound udp and manganese
66	c4kt7A_	Alignment	not modelled	96.5	10	PDB header: transferase Chain: A; PDB Molecule: 2-c-methyl-d-erythritol 4-phosphate cytidylyltransferase; PDBTitle: the crystal structure of 4-diphosphocytidyl-2c-methyl-d-2 erythritolsynthase from anaerococcus prevotii dsm 20548
67	d1v82a_	Alignment	not modelled	96.4	22	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: 1,3-glucuronyltransferase
68	c3cgxA_	Alignment	not modelled	96.1	17	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
69	c6b5kA_	Alignment	not modelled	95.9	15	PDB header: transferase Chain: A; PDB Molecule: glucose-1-phosphate thymidylyltransferase; PDBTitle: mycobacterium tuberculosis rmla in complex with mg/dttp
70	d1iina_	Alignment	not modelled	95.7	12	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: glucose-1-phosphate thymidylyltransferase
71	c4ys8B_	Alignment	not modelled	95.0	19	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
72	d1h5ra_	Alignment	not modelled	94.9	12	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: glucose-1-phosphate thymidylyltransferase
73	c6bwhB_	Alignment	not modelled	94.9	11	PDB header: transferase Chain: B; PDB Molecule: 2-phospho-l-lactate guanylyltransferase; PDBTitle: crystal structure of mycobacterium tuberculosis rv2983 in complex2 with pep
74	c3foqA_	Alignment	not modelled	94.8	19	PDB header: transferase Chain: A; PDB Molecule: bifunctional protein glmu1; PDBTitle: crystal structure of n-acetylglucosamine-1-phosphate2 uridylyltransferase (glmu) from mycobacterium tuberculosis in3 a cubic space group.
75	c5ddtA_	Alignment	not modelled	94.8	10	PDB header: transferase Chain: A; PDB Molecule: 2-c-methyl-d-erythritol 4-phosphate cytidylyltransferase; PDBTitle: crystal structure of ispd from bacillus subtilis at 1.80 angstroms2 resolution, crystal form i
76	d1i52a_	Alignment	not modelled	94.5	15	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: Cytidylyltransferase
77	d1fxoa_	Alignment	not modelled	94.5	12	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: glucose-1-phosphate thymidylyltransferase

78	d1mc3a_	Alignment	not modelled	94.5	11	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: glucose-1-phosphate thymidyltransferase
79	c3d5nB_	Alignment	not modelled	94.0	9	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: q97w15_sulso; PDBTitle: crystal structure of the q97w15_sulso protein from sulfobolus2 solfataricus. nesg target ssr125.
80	c3d8vA_	Alignment	not modelled	93.9	19	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
81	c3okrA_	Alignment	not modelled	93.7	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	d1w77a1	Alignment	not modelled	93.6	10	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: Cytidyltransferase
83	d1lvwa_	Alignment	not modelled	93.5	13	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: glucose-1-phosphate thymidyltransferase
84	c2xwIB_	Alignment	not modelled	93.3	14	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
85	d1vpaa_	Alignment	not modelled	92.8	5	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: Cytidyltransferase
86	c6oewB_	Alignment	not modelled	92.8	15	PDB header: transferase Chain: B: PDB Molecule: cytidyltransferase; PDBTitle: structure of a cytidyltransferase from leptospira borgpeterseni2 serovar hardjo-bovis (strain jb197)
87	c4jisB_	Alignment	not modelled	92.7	10	PDB header: transferase Chain: B: PDB Molecule: ribitol-5-phosphate cytidyltransferase; PDBTitle: crystal structure of ribitol 5-phosphate cytidyltransferase (tari)2 from bacillus subtilis
88	c2px7A_	Alignment	not modelled	92.4	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
89	c3d98A_	Alignment	not modelled	92.2	18	PDB header: transferase Chain: A: PDB Molecule: bifunctional protein glmu; PDBTitle: crystal structure of glmu from mycobacterium tuberculosis, ligand-free2 form
90	d2oi6a2	Alignment	not modelled	91.9	15	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: UDP-glucose pyrophosphorylase
91	d1w55a1	Alignment	not modelled	91.6	10	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: Cytidyltransferase
92	c2wawA_	Alignment	not modelled	91.4	6	PDB header: unknown function Chain: A: PDB Molecule: moba relate protein; PDBTitle: crystal structure of mycobacterium tuberculosis rv0371c2 homolog from mycobacterium sp. strain jc1
93	d1yp2a2	Alignment	not modelled	91.2	8	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: glucose-1-phosphate thymidyltransferase
94	c1w57A_	Alignment	not modelled	91.0	7	PDB header: transferase Chain: A: PDB Molecule: ispd/ispf bifunctional enzyme; PDBTitle: structure of the bifunctional ispdf from campylobacter2 jejuni containing zn
95	c3oamD_	Alignment	not modelled	90.9	18	PDB header: transferase Chain: D: PDB Molecule: 3-deoxy-manno-octulosonate cytidyltransferase; PDBTitle: crystal structure of cytidyltransferase from vibrio cholerae
96	c2cu2A_	Alignment	not modelled	90.0	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
97	d1vgwa_	Alignment	not modelled	89.2	16	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: Cytidyltransferase
98	c4xwiA_	Alignment	not modelled	88.9	14	PDB header: transferase Chain: A: PDB Molecule: 3-deoxy-manno-octulosonate cytidyltransferase; PDBTitle: x-ray crystal structure of cmp-kdo synthase from pseudomonas2 aeruginosa
99	c2pa4B_	Alignment	not modelled	88.4	13	PDB header: transferase Chain: B: PDB Molecule: utp-glucose-1-phosphate uridyltransferase; PDBTitle: crystal structure of udp-glucose pyrophosphorylase from corynebacteria2 glutamicum in complex with magnesium and udp-glucose
100	c5xhwA_	Alignment	not modelled	88.3	10	PDB header: transferase Chain: A: PDB Molecule: putative 6-deoxy-d-mannoheptose pathway protein; PDBTitle: crystal structure of hddc from yersinia pseudotuberculosis
101	d1vkpa_	Alignment	not modelled	87.0	19	Fold: Pentain, beta/alpha-propeller Superfamily: Pentain Family: Porphyromonas-type peptidylarginine deiminase PDB header: transferase

102	c5vcsB_	Alignment	not modelled	86.9	19	Chain: B: PDB Molecule: alpha-1,6-mannosyl-glycoprotein 2-beta-n- PDBTitle: alpha-1,6-mannosyl-glycoprotein 2-beta-n-acetylglucosaminyltransferase2 with bound acceptor
103	d2cu2a2	Alignment	not modelled	86.8	23	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: mannose-1-phosphate guanylyl transferase
104	c3okrC_	Alignment	not modelled	86.7	17	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)
105	c5i1fA_	Alignment	not modelled	86.6	13	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
106	c4mndA_	Alignment	not modelled	86.5	9	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
107	c3brkX_	Alignment	not modelled	85.5	11	PDB header: transferase Chain: X: PDB Molecule: glucose-1-phosphate adenyltransferase; PDBTitle: crystal structure of adp-glucose pyrophosphorylase from agrobacterium2 tumefaciens
108	c2qkxA_	Alignment	not modelled	84.9	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
109	d1e5ka_	Alignment	not modelled	84.4	16	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: Molybdenum cofactor biosynthesis protein MobA
110	c2vshB_	Alignment	not modelled	84.3	13	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
111	c2c0nA_	Alignment	not modelled	84.3	16	PDB header: viral protein/transferase Chain: A: PDB Molecule: a197; PDBTitle: crystal structure of a197 from stiv
112	c4ytqA_	Alignment	not modelled	84.0	17	PDB header: hydrolase Chain: A: PDB Molecule: peptidylarginine deiminase; PDBTitle: crystal structure of porphyromonas gingivalis peptidylarginine2 deiminase (ppad) mutant c351a in complex with dipeptide met-arg.
113	c5gvvF_	Alignment	not modelled	83.2	9	PDB header: transferase Chain: F: PDB Molecule: glycosyl transferase family 8; PDBTitle: crystal structure of the glycosyltransferase glye in streptococcus2 pneumoniae tigr4
114	c2j0bA_	Alignment	not modelled	81.8	19	PDB header: transferase Chain: A: PDB Molecule: beta-1,3-n-acetylglucosaminyltransferase manic fringe; PDBTitle: structure of the catalytic domain of mouse manic fringe in2 complex with udp and manganese
115	c2qh5B_	Alignment	not modelled	81.2	9	PDB header: isomerase Chain: B: PDB Molecule: mannose-6-phosphate isomerase; PDBTitle: crystal structure of mannose-6-phosphate isomerase from helicobacter2 pylori
116	c2x5sB_	Alignment	not modelled	80.1	14	PDB header: transferase Chain: B: PDB Molecule: mannose-1-phosphate guanylyltransferase; PDBTitle: crystal structure of t. maritima gdp-mannose2 pyrophosphorylase in apo state.
117	c3polA_	Alignment	not modelled	80.1	10	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.
118	c3tqdA_	Alignment	not modelled	79.5	11	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
119	d1sgva1	Alignment	not modelled	77.1	23	Fold: PUA domain-like Superfamily: PUA domain-like Family: PUA domain
120	c2gamA_	Alignment	not modelled	77.0	13	PDB header: transferase Chain: A: PDB Molecule: beta-1,6-n-acetylglucosaminyltransferase; PDBTitle: x-ray crystal structure of murine leukocyte-type core 2 b1,6-n-2 acetylglucosaminyltransferase (c2gnt-l) in complex with galb1,3galnac