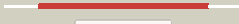



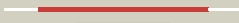



















Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1208 (-)_1352150_1353124
Date	Wed Jul 31 22:05:29 BST 2019
Unique Job ID	097db47090e6a379

Detailed template
information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3ckvA_	 Alignment		100.0	83	PDB header: unknown function Chain: A; PDB Molecule: putative uncharacterized protein; PDBTitle: crystal structure of a mycobacterial protein
2	c3f1yC_	 Alignment		100.0	38	PDB header: transferase Chain: C; PDB Molecule: mannosyl-3-phosphoglycerate synthase; PDBTitle: mannosyl-3-phosphoglycerate synthase from rubrobacter xylanophilus
3	c5mm1A_	 Alignment		100.0	19	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	d1xhba2	 Alignment		100.0	14	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: Polypeptide N-acetylgalactosaminyltransferase 1, N-terminal domain
5	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
6	c2ffuA_	 Alignment		100.0	15	PDB header: transferase Chain: A; PDB Molecule: polypeptide n-acetylgalactosaminyltransferase 2; PDBTitle: crystal structure of human ppgalnact-2 complexed with udp and ea2
7	c1xhbA_	 Alignment		100.0	15	PDB header: transferase Chain: A; PDB Molecule: polypeptide n-acetylgalactosaminyltransferase 1; PDBTitle: the crystal structure of udp-galnac: polypeptide alpha-n-2 acetylgalactosaminyltransferase-t1
8	c6iwqE_	 Alignment		100.0	16	PDB header: transferase Chain: E; PDB Molecule: n-acetylgalactosaminyltransferase 7; PDBTitle: crystal structure of galnac-t7 with mn2+
9	c6e4rB_	 Alignment		100.0	15	PDB header: transferase Chain: B; PDB Molecule: polypeptide n-acetylgalactosaminyltransferase 9; PDBTitle: crystal structure of the drosophila melanogaster polypeptide n-2 acetylgalactosaminyl transferase pgant9b
10	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+
11	c2z86D_	 Alignment		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

12	c5tz8C_	Alignment		100.0	16	PDB header: transferase Chain: C: PDB Molecule: glycosyl transferase; PDBTitle: crystal structure of s. aureus tars
13	c6h4mA_	Alignment		100.0	13	PDB header: transferase Chain: A: PDB Molecule: probable ss-1,3-n-acetylglucosaminyltransferase; PDBTitle: tarp-udp-glcnac-3rbop
14	c4hg6A_	Alignment		100.0	14	PDB header: transferase Chain: A: PDB Molecule: cellulose synthase subunit a; PDBTitle: structure of a cellulose synthase - cellulose translocation2 intermediate
15	c5ekeB_	Alignment		100.0	23	PDB header: transferase Chain: B: PDB Molecule: uncharacterized glycosyltransferase slI0501; PDBTitle: structure of the polyisoprenyl-phosphate glycosyltransferase gtrb2 (f215a mutant)
16	d1omza_	Alignment		100.0	10	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: Exostosin
17	d2bo4a1	Alignment		100.0	23	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: MGS-like
18	d1qq8a_	Alignment		100.0	14	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: Spore coat polysaccharide biosynthesis protein SpsA
19	c1omxB_	Alignment		100.0	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)
20	c5heaA_	Alignment		100.0	15	PDB header: transferase Chain: A: PDB Molecule: putative glycosyltransferase (galt1); PDBTitle: cgt structure in hexamer
21	c4fixA_	Alignment	not modelled	100.0	15	PDB header: transferase Chain: A: PDB Molecule: udp-galactofuranosyl transferase glft2; PDBTitle: crystal structure of glft2
22	c3bcvA_	Alignment	not modelled	100.0	15	PDB header: transferase Chain: A: PDB Molecule: putative glycosyltransferase protein; PDBTitle: crystal structure of a putative glycosyltransferase from bacteroides2 fragilis
23	c3zf8A_	Alignment	not modelled	99.9	14	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.
24	c6p61D_	Alignment	not modelled	99.9	22	PDB header: transferase Chain: D: PDB Molecule: glycosyltransferase; PDBTitle: structure of a glycosyltransferase from leptospira borgpetersenii2 serovar hardjo-bovis (strain jb197)
25	c2qgiA_	Alignment	not modelled	99.9	14	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
26	c5z8bB_	Alignment	not modelled	99.9	13	PDB header: transferase Chain: B: PDB Molecule: kfia protein; PDBTitle: truncated n-acetylglucosaminyl transferase kfia from e. coli k5 strain2 apo form
27	c5ggfC_	Alignment	not modelled	99.8	14	PDB header: transferase, sugar binding protein 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
28	c2wvmA_	Alignment	not modelled	99.5	22	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)
29	c2zu8A_	Alignment	not modelled	99.4	18	PDB header: transferase Chain: A: PDB Molecule: mannosyl-3-phosphoglycerate synthase; PDBTitle: crystal structure of mannosyl-3-phosphoglycerate synthase2 from pyrococcus horikoshii
30	c4irqB_	Alignment	not modelled	99.3	11	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
31	d1pzta_	Alignment	not modelled	98.7	18	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: beta 1,4 galactosyltransferase (b4GalT1)
32	d1fo8a_	Alignment	not modelled	98.7	14	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: N-acetylglucosaminyltransferase I
33	c6fxyA_	Alignment	not modelled	98.4	10	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
34	c3lw6A_	Alignment	not modelled	98.1	13	PDB header: transferase Chain: A: PDB Molecule: beta-4-galactosyltransferase 7; PDBTitle: crystal structure of drosophila beta1,4-galactosyltransferase-7
35	c5vcmA_	Alignment	not modelled	97.0	14	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
36	d1vh3a_	Alignment	not modelled	96.9	15	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: Cytidylyltransferase
37	c4kt7A_	Alignment	not modelled	96.5	17	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
38	c4xwiA_	Alignment	not modelled	96.4	16	PDB header: transferase Chain: A: PDB Molecule: 3-deoxy-manno-octulosonate cytidylyltransferase; PDBTitle: x-ray crystal structure of cmp-kdo synthase from pseudomonas2 aeruginosa
39	d1w77a1	Alignment	not modelled	96.3	15	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: Cytidylyltransferase
40	c2cu2A_	Alignment	not modelled	95.8	19	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
41	c2qh5B_	Alignment	not modelled	95.5	11	PDB header: isomerase Chain: B: PDB Molecule: mannose-6-phosphate isomerase; PDBTitle: crystal structure of mannose-6-phosphate isomerase from helicobacter2 pylori
42	c2wawA_	Alignment	not modelled	95.4	13	PDB header: unknown function Chain: A: PDB Molecule: moba relate protein; PDBTitle: crystal structure of mycobacterium tuberculosis rv0371c2 homolog from mycobacterium sp. strain jc1
43	c3okrA_	Alignment	not modelled	95.1	19	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 cytidylyltransferase (ispd)
44	c4ys8B_	Alignment	not modelled	95.1	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
45	c1w57A_	Alignment	not modelled	95.0	12	PDB header: transferase Chain: A: PDB Molecule: ispdf/ispf bifunctional enzyme; PDBTitle: structure of the bifunctional ispdf from campylobacter2 jejuni containing zn
46	c3d5nB_	Alignment	not modelled	94.5	12	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: q97w15_sulso; PDBTitle: crystal structure of the q97w15_sulso protein from sulfobolus2 solfataricus. nseg target ssr125.
47	c4mybA_	Alignment	not modelled	93.9	9	PDB header: transferase Chain: A: PDB Molecule: 2-c-methyl-d-erythritol 4-phosphate cytidylyltransferase; PDBTitle: crystal structure of francisella tularensis 2-c-methyl-d-erythritol 4-2 phosphate cytidylyltransferase (ispd)
48	c2xwIB_	Alignment	not modelled	93.7	15	PDB header: transferase Chain: B: PDB Molecule: 2-c-methyl-d-erythritol 4-phosphate cytidylyltransferase; PDBTitle: crystal structure of ispdf from mycobacterium smegmatis in complex with2 ctp and mg
49	d1vica_	Alignment	not modelled	93.2	15	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: Cytidylyltransferase
50	c2px7A_	Alignment	not modelled	93.2	16	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
51	c3okrC_	Alignment	not modelled	93.0	20	PDB header: transferase Chain: C: PDB Molecule: 2-c-methyl-d-erythritol 4-phosphate cytidylyltransferase; PDBTitle: structure of mtb apo 2-c-methyl-d-erythritol 4-

						phosphate2 cytidyltransferase (ispd)
52	d1v82a_	Alignment	not modelled	92.2	18	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: 1,3-glucuronyltransferase
53	d3cu0a1	Alignment	not modelled	92.0	18	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: 1,3-glucuronyltransferase
54	c4cvhA_	Alignment	not modelled	91.2	13	PDB header: transferase Chain: A: PDB Molecule: isoprenoid synthase domain-containing protein; PDBTitle: crystal structure of human isoprenoid synthase domain-containing2 protein
55	c2we9A_	Alignment	not modelled	91.2	11	PDB header: unknown function Chain: A: PDB Molecule: moba-related protein; PDBTitle: crystal structure of rv0371c from mycobacterium2 tuberculosis h37rv
56	d1i52a_	Alignment	not modelled	91.0	12	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: Cytidyltransferase
57	d1w55a1	Alignment	not modelled	90.9	11	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: Cytidyltransferase
58	c5ddtA_	Alignment	not modelled	90.4	8	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
59	c2d0jD_	Alignment	not modelled	89.9	12	PDB header: transferase Chain: D: PDB Molecule: galactosylgalactosylxylosylprotein 3-beta- PDBTitle: crystal structure of human glcat-s apo form
60	c3oamD_	Alignment	not modelled	89.7	19	PDB header: transferase Chain: D: PDB Molecule: 3-deoxy-manno-octulosonate cytidyltransferase; PDBTitle: crystal structure of cytidyltransferase from vibrio cholerae
61	c6ifdD_	Alignment	not modelled	89.4	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+.
62	c2e8bA_	Alignment	not modelled	89.1	13	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
63	c6bwhB_	Alignment	not modelled	89.1	13	PDB header: transferase Chain: B: PDB Molecule: 2-phospho-l-lactate guanylyltransferase; PDBTitle: crystal structure of mycobacterium tuberculosis rv2983 in complex2 with pep
64	d1vgwa_	Alignment	not modelled	89.0	15	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: Cytidyltransferase
65	d1h7ea_	Alignment	not modelled	88.5	18	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: Cytidyltransferase
66	c3polA_	Alignment	not modelled	87.3	16	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.
67	c6b5kA_	Alignment	not modelled	87.3	12	PDB header: transferase Chain: A: PDB Molecule: glucose-1-phosphate thymidyltransferase; PDBTitle: mycobacterium tuberculosis rmla in complex with mg/dttp
68	d1fxoa_	Alignment	not modelled	84.5	14	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: glucose-1-phosphate thymidyltransferase
69	c6oewB_	Alignment	not modelled	84.0	12	PDB header: transferase Chain: B: PDB Molecule: cytidyltransferase; PDBTitle: structure of a cytidyltransferase from leptospira borgpetersenii2 serovar hardjo-bovis (strain jb197)
70	c4jisB_	Alignment	not modelled	83.8	12	PDB header: transferase Chain: B: PDB Molecule: ribitol-5-phosphate cytidyltransferase; PDBTitle: crystal structure of ribitol 5-phosphate cytidyltransferase (tari)2 from bacillus subtilis
71	d1e5ka_	Alignment	not modelled	83.1	17	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: Molybdenum cofactor biosynthesis protein MobA
72	d1vpaa_	Alignment	not modelled	81.8	11	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: Cytidyltransferase
73	d1mc3a_	Alignment	not modelled	81.8	12	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: glucose-1-phosphate thymidyltransferase
74	c2vshB_	Alignment	not modelled	80.3	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
75	d1lwaa_	Alignment	not modelled	79.1	7	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: glucose-1-phosphate thymidyltransferase
76	d1vh1a_	Alignment	not modelled	78.7	16	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases

					Family:Cytidylyltransferase
77	d1eyra_	Alignment	not modelled	78.3	14 Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: Cytidylyltransferase
78	c3rsbB_	Alignment	not modelled	77.9	17 PDB header: transferase Chain: B: PDB Molecule: adenosylcobinamide-phosphate guanylyltransferase; PDBTitle: structure of the archaeal gtp:adocbi-p guanylyltransferase (coby) from2 methanocaldococcus jannaschii
79	c2x5sB_	Alignment	not modelled	77.2	19 PDB header: transferase Chain: B: PDB Molecule: mannose-1-phosphate guanylyltransferase; PDBTitle: crystal structure of t. maritima gdp-mannose2 pyrophosphorylase in apo state.
80	c5xhwA_	Alignment	not modelled	77.1	14 PDB header: transferase Chain: A: PDB Molecule: putative 6-deoxy-d-mannoheptose pathway protein; PDBTitle: crystal structure of hddc from yersinia pseudotuberculosis
81	d1h5ra_	Alignment	not modelled	73.4	17 Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: glucose-1-phosphate thymidyltransferase
82	c3cgxA_	Alignment	not modelled	73.2	14 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
83	c4jd0A_	Alignment	not modelled	71.7	9 PDB header: transferase Chain: A: PDB Molecule: nucleotidyl transferase; PDBTitle: structure of the inositol-1-phosphate ctp transferase from t.2 maritima.
84	c5gvvF_	Alignment	not modelled	70.3	14 PDB header: transferase Chain: F: PDB Molecule: glycosyl transferase family 8; PDBTitle: crystal structure of the glycosyltransferase glye in streptococcus2 pneumoniae tigr4
85	c4rg1A_	Alignment	not modelled	69.5	29 PDB header: transferase Chain: A: PDB Molecule: c9orf114; PDBTitle: methyltransferase domain of c9orf114
86	c3d8vA_	Alignment	not modelled	68.1	16 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
87	c3f1cB_	Alignment	not modelled	64.5	12 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
88	c3foqA_	Alignment	not modelled	64.3	18 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.
89	c2y6pC_	Alignment	not modelled	63.0	11 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
90	c2pa4B_	Alignment	not modelled	62.8	12 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
91	c2xmhB_	Alignment	not modelled	61.5	18 PDB header: transferase Chain: B: PDB Molecule: ctp-inositol-1-phosphate cytidyltransferase; PDBTitle: the x-ray structure of ctp:inositol-1-phosphate cytidyltransferase2 from archaeoglobus fulgidus
92	c3tqdA_	Alignment	not modelled	60.1	14 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
93	d2cu2a2	Alignment	not modelled	58.5	19 Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: mannose-1-phosphate guanylyl transferase
94	d1qwja_	Alignment	not modelled	53.3	18 Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: Cytidylyltransferase
95	d1k3ra2	Alignment	not modelled	52.8	8 Fold: alpha/beta knot Superfamily: alpha/beta knot Family: Hypothetical protein MTH1 (MT0001), dimerisation domain
96	c4mndA_	Alignment	not modelled	52.6	14 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
97	c1k3ra_	Alignment	not modelled	52.5	8 PDB header: structural genomics, unknown function Chain: A: PDB Molecule: conserved protein mt0001; PDBTitle: crystal structure of the methyltransferase with a knot from2 methanobacterium thermoautotrophicum
98	c3hl3A_	Alignment	not modelled	52.1	15 PDB header: transferase Chain: A: PDB Molecule: glucose-1-phosphate thymidyltransferase; PDBTitle: 2.76 angstrom crystal structure of a putative glucose-1-phosphate2 thymidyltransferase from bacillus anthracis in complex with a3 sucrose.

99	c6cglA	Alignment	not modelled	47.3	16	PDB header: hydrolase Chain: A: PDB Molecule: effector protein lem4 (lpg1101); PDBTitle: structure of the had domain of effector protein lem4 (lpg1101) from2 legionella pneumophila
100	c2r6r1	Alignment	not modelled	45.7	25	PDB header: cell cycle Chain: 1: PDB Molecule: cell division protein ftsz; PDBTitle: aquifex aeolicus ftsz
101	c2rhoB	Alignment	not modelled	43.4	27	PDB header: cell cycle Chain: B: PDB Molecule: cell division protein ftsz; PDBTitle: synthetic gene encoded bacillus subtilis ftsz ncs dimer with bound gdp2 and gtp-gamma-s
102	c1w5fA	Alignment	not modelled	43.4	23	PDB header: cell division Chain: A: PDB Molecule: cell division protein ftsz; PDBTitle: ftsz, t7 mutated, domain swapped (t. maritima)
103	d1rq2a1	Alignment	not modelled	43.1	23	Fold: Tubulin nucleotide-binding domain-like Superfamily: Tubulin nucleotide-binding domain-like Family: Tubulin, GTPase domain
104	d1iina	Alignment	not modelled	42.4	17	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: glucose-1-phosphate thymidyltransferase
105	d2oi6a2	Alignment	not modelled	42.4	10	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: UDP-glucose pyrophosphorylase
106	c5vcsB	Alignment	not modelled	40.8	16	PDB header: transferase 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
107	d2dpwa1	Alignment	not modelled	40.0	13	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: TTHA0179-like
108	c1jylC	Alignment	not modelled	39.5	14	PDB header: transferase Chain: C: PDB Molecule: ctp:phosphocholine cytidyltransferase; PDBTitle: catalytic mechanism of ctp:phosphocholine2 cytidyltransferase from streptococcus pneumoniae (licc)
109	c3ngwA	Alignment	not modelled	39.3	13	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
110	c1w59B	Alignment	not modelled	39.3	23	PDB header: cell division Chain: B: PDB Molecule: cell division protein ftsz homolog 1; PDBTitle: ftsz dimer, empty (m. jannaschii)
111	c3ssmB	Alignment	not modelled	37.5	17	PDB header: transferase Chain: B: PDB Molecule: methyltransferase; PDBTitle: myce methyltransferase from the mycinamycin biosynthetic pathway in2 complex with mg and sah, crystal form 1
112	c3tztB	Alignment	not modelled	36.2	12	PDB header: transferase Chain: B: PDB Molecule: glycosyl transferase family 8; PDBTitle: the structure of a protein in glycosyl transferase family 8 from2 anaerococcus prevotii.
113	c5yh1A	Alignment	not modelled	34.5	23	PDB header: ribosomal protein Chain: A: PDB Molecule: member of s1p family of ribosomal proteins; PDBTitle: member of s1p family of ribosomal proteins pf0399 dhh domain
114	d1ga8a	Alignment	not modelled	32.6	19	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: Galactosyltransferase LgtC
115	c1ga8A	Alignment	not modelled	32.6	19	PDB header: transferase Chain: A: PDB Molecule: galactosyl transferase lgtc; PDBTitle: crystal structure of galactosyltransferase lgtc in complex2 with donor and acceptor sugar analogs.
116	c4evwB	Alignment	not modelled	31.5	12	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.
117	c3ssoE	Alignment	not modelled	30.1	17	PDB header: transferase Chain: E: PDB Molecule: methyltransferase; PDBTitle: myce methyltransferase from the mycinamycin biosynthetic pathway in2 complex with mg and sah, crystal form 2
118	c3d98A	Alignment	not modelled	29.9	16	PDB header: transferase Chain: A: PDB Molecule: bifunctional protein glmu; PDBTitle: crystal structure of glmu from mycobacterium tuberculosis, ligand-free2 form
119	c4y7uA	Alignment	not modelled	29.2	10	PDB header: transferase Chain: A: PDB Molecule: nucleotidyl transferase; PDBTitle: structural analysis of muru
120	c4dxdA	Alignment	not modelled	29.2	20	PDB header: cell cycle/inhibitor Chain: A: PDB Molecule: cell division protein ftsz; PDBTitle: staphylococcal aureus ftsz in complex with 723