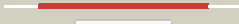



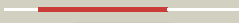



















Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1500_(-)_1690856_1691884
Date	Fri Aug 2 13:30:08 BST 2019
Unique Job ID	5d8c565e163c56fa

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c5ekeB_	 Alignment		100.0	32	PDB header: transferase Chain: B: PDB Molecule: uncharacterized glycosyltransferase slI0501; PDBTitle: structure of the polyisoprenyl-phosphate glycosyltransferase gtrb2 (f215a mutant)
2	c5mm1A_	 Alignment		100.0	17	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
3	c3f1yC_	 Alignment		100.0	17	PDB header: transferase Chain: C: PDB Molecule: mannosyl-3-phosphoglycerate synthase; PDBTitle: mannosyl-3-phosphoglycerate synthase from rubrobacter xylanophilus
4	c3ckvA_	 Alignment		100.0	18	PDB header: unknown function Chain: A: PDB Molecule: putative uncharacterized protein; PDBTitle: crystal structure of a mycobacterial protein
5	c5tz8C_	 Alignment		100.0	17	PDB header: transferase Chain: C: PDB Molecule: glycosyl transferase; PDBTitle: crystal structure of s. aureus tars
6	c5nqaA_	 Alignment		100.0	19	PDB header: transferase Chain: A: PDB Molecule: polypeptide n-acetylgalactosaminyltransferase 4; PDBTitle: crystal structure of galnac-t4 in complex with the monoglycopeptide 3
7	c6e4rB_	 Alignment		100.0	18	PDB header: transferase Chain: B: PDB Molecule: polypeptide n-acetylgalactosaminyltransferase 9; PDBTitle: crystal structure of the drosophila melanogaster polypeptide n-2 acetylgalactosaminyl transferase pgant9b
8	c1xhbA_	 Alignment		100.0	19	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	c2ffuA_	 Alignment		100.0	18	PDB header: transferase Chain: A: PDB Molecule: polypeptide n-acetylgalactosaminyltransferase 2; PDBTitle: crystal structure of human ppgalnact-2 complexed with udp and ea2
10	d1xhb2	 Alignment		100.0	17	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: Polypeptide N-acetylgalactosaminyltransferase 1, N-terminal domain
11	c4hg6A_	 Alignment		100.0	11	PDB header: transferase Chain: A: PDB Molecule: cellulose synthase subunit a; PDBTitle: structure of a cellulose synthase - cellulose translocation2 intermediate

12	c2d7iA_	Alignment		100.0	19	PDB header: transferase Chain: A: PDB Molecule: polypeptide n-acetylgalactosaminyltransferase 10; PDBTitle: crystal structure of pp-galnac-t10 with udp, galnac and mn2+
13	c6iwqE_	Alignment		100.0	14	PDB header: transferase Chain: E: PDB Molecule: n-acetylgalactosaminyltransferase 7; PDBTitle: crystal structure of galnac-t7 with mn2+
14	c2z86D_	Alignment		100.0	18	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
15	c6h4mA_	Alignment		100.0	13	PDB header: transferase Chain: A: PDB Molecule: probable ss-1,3-n-acetylglucosaminyltransferase; PDBTitle: tarp-udp-glcna-3rbop
16	d1omza_	Alignment		99.9	11	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: Exostosin
17	c1omxB_	Alignment		99.9	9	PDB header: transferase Chain: B: PDB Molecule: alpha-1,4-n-acetylhexosaminyltransferase extl2; PDBTitle: crystal structure of mouse alpha-1,4-n-acetylhexosaminyltransferase2 (extl2)
18	c3bcvA_	Alignment		99.9	20	PDB header: transferase Chain: A: PDB Molecule: putative glycosyltransferase protein; PDBTitle: crystal structure of a putative glycosyltransferase from bacteroides2 fragilis
19	c5heaA_	Alignment		99.9	15	PDB header: transferase Chain: A: PDB Molecule: putative glycosyltransferase (galt1); PDBTitle: cgt structure in hexamer
20	c4fixA_	Alignment		99.9	10	PDB header: transferase Chain: A: PDB Molecule: udp-galactofuranosyl transferase glft2; PDBTitle: crystal structure of glft2
21	d1qg8a_	Alignment	not modelled	99.9	19	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: Spore coat polysaccharide biosynthesis protein SpsA
22	d2bo4a1	Alignment	not modelled	99.9	13	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: MGS-like
23	c5z8bB_	Alignment	not modelled	99.7	15	PDB header: transferase Chain: B: PDB Molecule: kfia protein; PDBTitle: truncated n-acetylglucosaminyl transferase kfia from e. coli k5 strain2 apo form
24	c3zf8A_	Alignment	not modelled	99.7	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.
25	c6p61D_	Alignment	not modelled	99.7	11	PDB header: transferase Chain: D: PDB Molecule: glycosyltransferase; PDBTitle: structure of a glycosyltransferase from leptospira borgpetersenii2 serovar hardjo-bovis (strain jb197)
26	c2qgiA_	Alignment	not modelled	99.7	11	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
27	c5ggfC_	Alignment	not modelled	99.4	9	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	c4irqB_	Alignment	not modelled	99.1	14	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

29	d1pzta_	Alignment	not modelled	98.6	12	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: beta 1,4 galactosyltransferase (b4GalT1)
30	c2zu8A_	Alignment	not modelled	98.6	11	PDB header: transferase Chain: A: PDB Molecule: mannosyl-3-phosphoglycerate synthase; PDBTitle: crystal structure of mannosyl-3-phosphoglycerate synthase2 from pyrococcus horikoshii
31	c2wvmA_	Alignment	not modelled	98.5	17	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)
32	c3lw6A_	Alignment	not modelled	98.0	13	PDB header: transferase Chain: A: PDB Molecule: beta-4-galactosyltransferase 7; PDBTitle: crystal structure of drosophila beta1,4-galactosyltransferase-7
33	c6fxyA_	Alignment	not modelled	98.0	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
34	d1fo8a_	Alignment	not modelled	97.6	18	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: N-acetylglucosaminyltransferase I
35	c5ddtA_	Alignment	not modelled	96.9	14	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
36	c2px7A_	Alignment	not modelled	96.5	15	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
37	c3oamD_	Alignment	not modelled	96.5	15	PDB header: transferase Chain: D: PDB Molecule: 3-deoxy-manno-octulosonate cytidylyltransferase; PDBTitle: crystal structure of cytidylyltransferase from vibrio cholerae
38	c5vcmA_	Alignment	not modelled	96.3	20	PDB header: transferase Chain: A: PDB Molecule: alpha-1,6-mannosyl-glycoprotein 2-beta-n-acetylglucosaminyltransferase2 with bound udp and manganese
39	c6oewB_	Alignment	not modelled	96.2	11	PDB header: transferase Chain: B: PDB Molecule: cytidylyltransferase; PDBTitle: structure of a cytidylyltransferase from leptospira borgpetersenii2 serovar hardjo-bovis (strain jb197)
40	d1i52a_	Alignment	not modelled	96.1	11	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: Cytidylyltransferase
41	d1w55a1	Alignment	not modelled	96.0	9	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: Cytidylyltransferase
42	c2xwIB_	Alignment	not modelled	94.9	16	PDB header: transferase Chain: B: PDB Molecule: 2-c-methyl-d-erythritol 4-phosphate cytidylyltransferase; PDBTitle: crystal structure of ispd from mycobacterium smegmatis in complex with2 ctp and mg
43	d1vpaa_	Alignment	not modelled	94.4	12	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: Cytidylyltransferase
44	d1fxoa_	Alignment	not modelled	94.3	8	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: glucose-1-phosphate thymidylyltransferase
45	c5xhwA_	Alignment	not modelled	94.1	10	PDB header: transferase Chain: A: PDB Molecule: putative 6-deoxy-d-mannoheptose pathway protein; PDBTitle: crystal structure of hddc from yersinia pseudotuberculosis
46	d1vica_	Alignment	not modelled	93.9	12	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: Cytidylyltransferase
47	c6b5kA_	Alignment	not modelled	93.9	14	PDB header: transferase Chain: A: PDB Molecule: glucose-1-phosphate thymidylyltransferase; PDBTitle: mycobacterium tuberculosis rmla in complex with mg/dttp
48	d1lwva_	Alignment	not modelled	93.8	10	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: glucose-1-phosphate thymidylyltransferase
49	d1h5ra_	Alignment	not modelled	93.7	10	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: glucose-1-phosphate thymidylyltransferase
50	c1w57A_	Alignment	not modelled	93.1	10	PDB header: transferase Chain: A: PDB Molecule: ispd/ispf bifunctional enzyme; PDBTitle: structure of the bifunctional ispdf from campylobacter2 jejuni containing zn
51	d1v82a_	Alignment	not modelled	93.0	16	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: 1,3-glucuronyltransferase
52	c2x5sB_	Alignment	not modelled	92.2	16	PDB header: transferase Chain: B: PDB Molecule: mannose-1-phosphate guanylyltransferase; PDBTitle: crystal structure of t. maritima gdp-mannose2 pyrophosphorylase in apo state.
						Fold: Nucleotide-diphospho-sugar transferases

53	d3cu0a1	Alignment	not modelled	92.1	20	Superfamily: Nucleotide-diphospho-sugar transferases Family: 1,3-glucuronyltransferase
54	c4xwiA	Alignment	not modelled	91.5	12	PDB header: transferase Chain: A: PDB Molecule: 3-deoxy-manno-octulosonate cytidyltransferase; PDBTitle: x-ray crystal structure of cmp-kdo synthase from pseudomonas2 aeruginosa
55	d1iina	Alignment	not modelled	91.2	9	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: glucose-1-phosphate thymidyltransferase
56	d1mc3a	Alignment	not modelled	91.1	7	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: glucose-1-phosphate thymidyltransferase
57	c2wawA	Alignment	not modelled	90.6	12	PDB header: unknown function Chain: A: PDB Molecule: smoba relate protein; PDBTitle: crystal structure of mycobacterium tuberculosis rv0371c2 homolog from mycobacterium sp. strain jc1
58	c4mybA	Alignment	not modelled	90.2	10	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)
59	c4kt7A	Alignment	not modelled	89.8	14	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
60	c3hl3A	Alignment	not modelled	89.8	9	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.
61	d1w77a1	Alignment	not modelled	89.4	13	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: Cytidyltransferase
62	c3okrA	Alignment	not modelled	89.3	17	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)
63	c3d5nB	Alignment	not modelled	87.9	13	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: q97w15_sulso; PDBTitle: crystal structure of the q97w15_sulso protein from sulfolobus2 solfataricus. nesg target ssr125.
64	c2qh5B	Alignment	not modelled	86.4	19	PDB header: isomerase Chain: B: PDB Molecule: mannose-6-phosphate isomerase; PDBTitle: crystal structure of mannose-6-phosphate isomerase from helicobacter2 pylori
65	c4y7uA	Alignment	not modelled	86.0	14	PDB header: transferase Chain: A: PDB Molecule: nucleotidyl transferase; PDBTitle: structural analysis of muru
66	c2xmhB	Alignment	not modelled	85.3	15	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
67	d1vh3a	Alignment	not modelled	84.7	13	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: Cytidyltransferase
68	c3foqA	Alignment	not modelled	84.1	16	PDB header: transferase Chain: A: PDB Molecule: bifunctional protein glmu; PDBTitle: crystal structure of n-acetylglucosamine-1-phosphate2 uridyltransferase (glmu) from mycobacterium tuberculosis in3 a cubic space group.
69	c2gamA	Alignment	not modelled	81.1	9	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
70	c4mndA	Alignment	not modelled	80.9	13	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
71	c4evwB	Alignment	not modelled	79.0	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.
72	c1jylC	Alignment	not modelled	77.4	8	PDB header: transferase Chain: C: PDB Molecule: ctp:phosphocholine cytidyltransferase; PDBTitle: catalytic mechanism of ctp:phosphocholine2 cytidyltransferase from streptococcus pneumoniae (licc)
73	c4ys8B	Alignment	not modelled	76.5	9	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
74	c3okrC	Alignment	not modelled	74.9	14	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)
75	c2d0jD	Alignment	not modelled	71.8	16	PDB header: transferase Chain: D: PDB Molecule: galactosylgalactosylxylosylprotein 3-beta- PDBTitle: crystal structure of human gcat-s apo form

76	d1o6da_	Alignment	not modelled	70.8	16	Fold: alpha/beta knot Superfamily: alpha/beta knot Family: YbeA-like
77	d1h7ea_	Alignment	not modelled	70.4	12	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: Cytidylyltransferase
78	d1vh0a_	Alignment	not modelled	70.2	15	Fold: alpha/beta knot Superfamily: alpha/beta knot Family: YbeA-like
79	c3d8vA_	Alignment	not modelled	70.1	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
80	d1vgwa_	Alignment	not modelled	68.7	12	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: Cytidylyltransferase
81	c5gvvF_	Alignment	not modelled	67.6	16	PDB header: transferase Chain: F: PDB Molecule: glycosyl transferase family 8; PDBTitle: crystal structure of the glycosyltransferase glye in streptococcus2 pneumoniae tigr4
82	c2cu2A_	Alignment	not modelled	66.9	14	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
83	c3ngwA_	Alignment	not modelled	63.1	22	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
84	c4jisB_	Alignment	not modelled	62.8	9	PDB header: transferase Chain: B: PDB Molecule: ribitol-5-phosphate cytidylyltransferase; PDBTitle: crystal structure of ribitol 5-phosphate cytidylyltransferase (tari)2 from bacillus subtilis
85	c6bwhB_	Alignment	not modelled	61.9	14	PDB header: transferase Chain: B: PDB Molecule: 2-phospho-l-lactate guanylyltransferase; PDBTitle: crystal structure of mycobacterium tuberculosis rv2983 in complex2 with pep
86	c4jd0A_	Alignment	not modelled	60.5	14	PDB header: transferase Chain: A: PDB Molecule: nucleotidyl transferase; PDBTitle: structure of the inositol-1-phosphate ctp transferase from t.2 maritima.
87	d1jyka_	Alignment	not modelled	59.5	8	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: Cytidylyltransferase
88	d1e5ka_	Alignment	not modelled	57.8	11	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: Molybdenum cofactor biosynthesis protein MobA
89	c1zcyA_	Alignment	not modelled	56.5	8	PDB header: transferase Chain: A: PDB Molecule: glycogenin-1; PDBTitle: apo form of a mutant of glycogenin in which asp159 is replaced by ser
90	c4c76A_	Alignment	not modelled	55.7	12	PDB header: oxidoreductase Chain: A: PDB Molecule: fmn reductase (nadph); PDBTitle: crystal structure of the fmn-reductase msue from pseudomonas putida2 kt2440.
91	d1eyra_	Alignment	not modelled	55.0	12	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: Cytidylyltransferase
92	c3f1cB_	Alignment	not modelled	54.4	11	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 cytidylyltransferase from listeria monocytogenes
93	c3d98A_	Alignment	not modelled	54.1	19	PDB header: transferase Chain: A: PDB Molecule: bifunctional protein glmu; PDBTitle: crystal structure of glmu from mycobacterium tuberculosis, ligand-free2 form
94	c3tztB_	Alignment	not modelled	53.0	9	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.
95	c5vcsB_	Alignment	not modelled	52.5	26	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
96	c1yp3C_	Alignment	not modelled	52.1	17	PDB header: transferase Chain: C: PDB Molecule: glucose-1-phosphate adenyltransferase small PDBTitle: crystal structure of potato tuber adp-glucose2 pyrophosphorylase in complex with atp
97	c2vshB_	Alignment	not modelled	52.0	10	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
98	d1k3ra2	Alignment	not modelled	49.7	15	Fold: alpha/beta knot Superfamily: alpha/beta knot Family: Hypothetical protein MTH1 (MT0001), dimerisation domain
99	c2pa4B_	Alignment	not modelled	45.7	13	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
100	c1k3rA	Alignment	not modelled	45.0	15	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: conserved protein mt0001;

100	c1k31A	Alignment	not modelled	43.0	15	PDBTitle: crystal structure of the methyltransferase with a knot from2 methanobacterium thermoautotrophicum PDB header: unknown function
101	c2we9A	Alignment	not modelled	43.7	16	Chain: A; PDB Molecule: moba-related protein; PDBTitle: crystal structure of rv0371c from mycobacterium2 tuberculosis h37rv
102	c2yswB	Alignment	not modelled	43.4	12	PDB header: lyase Chain: B; PDB Molecule: 3-dehydroquinatase; PDBTitle: crystal structure of the 3-dehydroquinatase dehydratase from aquifex2 aeolicus vf5
103	c3s99A	Alignment	not modelled	41.9	7	PDB header: lipid binding protein Chain: A; PDB Molecule: basic membrane lipoprotein; PDBTitle: crystal structure of a basic membrane lipoprotein from brucella2 melitensis, iodide soak
104	c1zctB	Alignment	not modelled	41.7	11	PDB header: transferase Chain: B; PDB Molecule: glycogenin-1; PDBTitle: structure of glycogenin truncated at residue 270 in a complex with udp
105	d2oi6a2	Alignment	not modelled	40.3	13	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: UDP-glucose pyrophosphorylase
106	d1g97a2	Alignment	not modelled	40.0	10	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: UDP-glucose pyrophosphorylase
107	c4rxuA	Alignment	not modelled	35.8	23	PDB header: transport protein Chain: A; PDB Molecule: periplasmic sugar-binding protein; PDBTitle: crystal structure of carbohydrate transporter solute binding protein2 caur_1924 from chloroflexus aurantiacus, target efi-511158, in3 complex with d-glucose
108	c3tqdA	Alignment	not modelled	35.5	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
109	c4z0nA	Alignment	not modelled	35.2	16	PDB header: transcription Chain: A; PDB Molecule: periplasmic binding protein/laci transcriptional regulator; PDBTitle: crystal structure of a periplasmic solute binding protein (ipr025997)2 from streptobacillus moniliformis dsm-12112 (smon_0317, target efi-3_511281) with bound d-galactose
110	d1wp0a1	Alignment	not modelled	34.9	11	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: Glutathione peroxidase-like
111	c2qkxA	Alignment	not modelled	34.4	16	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
112	d1ll2a	Alignment	not modelled	34.3	11	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: Glycogenin
113	c6dspB	Alignment	not modelled	34.0	10	PDB header: signaling protein Chain: B; PDB Molecule: autoinducer 2-binding protein lsrB; PDBTitle: lsrB from clostridium saccharobutylicum in complex with ai-2
114	c3kyiB	Alignment	not modelled	33.1	23	PDB header: transferase Chain: B; PDB Molecule: chey6 protein; PDBTitle: crystal structure of the phosphorylated p1 domain of chea3 in complex2 with chey6 from r. sphaeroides
115	c2c0nA	Alignment	not modelled	32.5	23	PDB header: viral protein/transferase Chain: A; PDB Molecule: a197; PDBTitle: crystal structure of a197 from stiv
116	c3lpnB	Alignment	not modelled	32.0	13	PDB header: transferase Chain: B; PDB Molecule: ribose-phosphate pyrophosphokinase; PDBTitle: crystal structure of the phosphoribosylpyrophosphate (prpp) synthetase2 from thermoplasma volcanium in complex with an atp analog (ampcpp).
117	c3brcA	Alignment	not modelled	31.8	11	PDB header: structural genomics, unknown function Chain: A; PDB Molecule: conserved protein of unknown function; PDBTitle: crystal structure of a conserved protein of unknown function from2 methanobacterium thermoautotrophicum
118	c3pnnA	Alignment	not modelled	31.5	11	PDB header: transferase Chain: A; PDB Molecule: conserved domain protein; PDBTitle: the crystal structure of a glycosyltransferase from porphyromonas2 gingivalis w83
119	c5n80A	Alignment	not modelled	30.3	7	PDB header: transferase Chain: A; PDB Molecule: lipopolysaccharide 1,6-galactosyltransferase; PDBTitle: glycosyltransferase lps biosynthesis in complex with udp
120	c2ywrA	Alignment	not modelled	29.8	8	PDB header: transferase Chain: A; PDB Molecule: phosphoribosylglycinamide formyltransferase; PDBTitle: crystal structure of gar transformylase from aquifex aeolicus