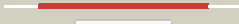



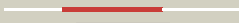














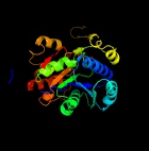




Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3808c_glfT_4270544_4272457
Date	Fri Aug 9 18:20:51 BST 2019
Unique Job ID	cf51559be86058da

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c4fixA_	 Alignment		100.0	100	PDB header: transferase Chain: A: PDB Molecule: udp-galactofuranosyl transferase glft2; PDBTitle: crystal structure of glft2
2	c1xhbA_	 Alignment		100.0	12	PDB header: transferase Chain: A: PDB Molecule: polypeptide n-acetylgalactosaminyltransferase 1; PDBTitle: the crystal structure of udp-galnac: polypeptide alpha-n-2 acetylgalactosaminyltransferase-t1
3	c2ffuA_	 Alignment		100.0	12	PDB header: transferase Chain: A: PDB Molecule: polypeptide n-acetylgalactosaminyltransferase 2; PDBTitle: crystal structure of human ppgalnact-2 complexed with udp and ea2
4	c6e4rB_	 Alignment		100.0	10	PDB header: transferase Chain: B: PDB Molecule: polypeptide n-acetylgalactosaminyltransferase 9; PDBTitle: crystal structure of the drosophila melanogaster polypeptide n-2 acetylgalactosaminyl transferase pgant9b
5	c2d7iA_	 Alignment		100.0	12	PDB header: transferase Chain: A: PDB Molecule: polypeptide n-acetylgalactosaminyltransferase 10; PDBTitle: crystal structure of pp-galnac-t10 with udp, galnac and mn2+
6	c5nqaA_	 Alignment		100.0	10	PDB header: transferase Chain: A: PDB Molecule: polypeptide n-acetylgalactosaminyltransferase 4; PDBTitle: crystal structure of galnac-t4 in complex with the monoglycopeptide 3
7	c6iwqE_	 Alignment		100.0	12	PDB header: transferase Chain: E: PDB Molecule: n-acetylgalactosaminyltransferase 7; PDBTitle: crystal structure of galnac-t7 with mn2+
8	d1xhbA2	 Alignment		100.0	10	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: Polypeptide N-acetylgalactosaminyltransferase 1, N-terminal domain
9	c3zf8A_	 Alignment		100.0	11	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.
10	c2z86D_	 Alignment		100.0	12	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
11	c6h4mA_	 Alignment		100.0	10	PDB header: transferase Chain: A: PDB Molecule: probable ss-1,3-n-acetylglucosaminyltransferase; PDBTitle: tarp-udp-glcnac-3rbop

12	c5tz8C_	Alignment		99.9	13	PDB header: transferase Chain: C: PDB Molecule: glycosyl transferase; PDBTitle: crystal structure of s. aureus tars
13	c4hg6A_	Alignment		99.9	14	PDB header: transferase Chain: A: PDB Molecule: cellulose synthase subunit a; PDBTitle: structure of a cellulose synthase - cellulose translocation2 intermediate
14	c3bcvA_	Alignment		99.9	14	PDB header: transferase Chain: A: PDB Molecule: putative glycosyltransferase protein; PDBTitle: crystal structure of a putative glycosyltransferase from bacteroides2 fragilis
15	c5heaA_	Alignment		99.9	13	PDB header: transferase Chain: A: PDB Molecule: putative glycosyltransferase (galt1); PDBTitle: cgt structure in hexamer
16	c6p61D_	Alignment		99.9	14	PDB header: transferase Chain: D: PDB Molecule: glycosyltransferase; PDBTitle: structure of a glycosyltransferase from leptospira borgpetersenii2 serovar hardjo-bovis (strain jb197)
17	d1qq8a_	Alignment		99.9	14	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: Spore coat polysaccharide biosynthesis protein SpsA
18	c5z8bB_	Alignment		99.9	16	PDB header: transferase Chain: B: PDB Molecule: kfia protein; PDBTitle: truncated n-acetylglucosaminyl transferase kfia from e. coli k5 strain2 apo form
19	c3f1yC_	Alignment		99.9	13	PDB header: transferase Chain: C: PDB Molecule: mannosyl-3-phosphoglycerate synthase; PDBTitle: mannosyl-3-phosphoglycerate synthase from rubrobacter xylanophilus
20	c5mm1A_	Alignment		99.9	12	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
21	c2qgiA_	Alignment	not modelled	99.9	13	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
22	c3ckvA_	Alignment	not modelled	99.9	13	PDB header: unknown function Chain: A: PDB Molecule: putative uncharacterized protein; PDBTitle: crystal structure of a mycobacterial protein
23	c1omxB_	Alignment	not modelled	99.9	12	PDB header: transferase Chain: B: PDB Molecule: alpha-1,4-n-acetylhexosaminyltransferase extl2; PDBTitle: crystal structure of mouse alpha-1,4-n-acetylhexosaminyltransferase2 (extl2)
24	c5ekeB_	Alignment	not modelled	99.8	14	PDB header: transferase Chain: B: PDB Molecule: uncharacterized glycosyltransferase sli0501; PDBTitle: structure of the polyisoprenyl-phosphate glycosyltransferase gtrb2 (f215a mutant)
25	d1omza_	Alignment	not modelled	99.8	12	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: Exostosin
26	c5ggfC_	Alignment	not modelled	99.7	20	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
27	d1pzta_	Alignment	not modelled	99.4	22	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: beta 1,4 galactosyltransferase (b4GalT1)
28	c4irqB_	Alignment	not modelled	99.3	17	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	c6fxyA	Alignment	not modelled	99.0	9	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
30	d2bo4a1	Alignment	not modelled	98.9	14	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: MGS-like
31	d1fo8a	Alignment	not modelled	98.9	18	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: N-acetylglucosaminyltransferase I
32	c3lw6A	Alignment	not modelled	98.3	18	PDB header: transferase Chain: A; PDB Molecule: beta-4-galactosyltransferase 7; PDBTitle: crystal structure of drosophila beta1,4-galactosyltransferase-7
33	c5vcmA	Alignment	not modelled	98.3	15	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
34	d1vh3a	Alignment	not modelled	96.8	10	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: Cytidyltransferase
35	d1v82a	Alignment	not modelled	96.6	21	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: 1,3-glucuronyltransferase
36	c2d0jD	Alignment	not modelled	96.5	17	PDB header: transferase Chain: D; PDB Molecule: galactosylgalactosylxylosylprotein 3-beta- PDBTitle: crystal structure of human gcat-s apo form
37	c5vcsB	Alignment	not modelled	96.5	18	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
38	c2zu8A	Alignment	not modelled	96.2	16	PDB header: transferase Chain: A; PDB Molecule: mannosyl-3-phosphoglycerate synthase; PDBTitle: crystal structure of mannosyl-3-phosphoglycerate synthase2 from pyrococcus horikoshii
39	c2wvmA	Alignment	not modelled	95.8	15	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)
40	d3cu0a1	Alignment	not modelled	95.7	15	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: 1,3-glucuronyltransferase
41	c3polA	Alignment	not modelled	94.9	12	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.
42	c3tqdA	Alignment	not modelled	94.2	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
43	c4ys8B	Alignment	not modelled	93.6	17	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
44	c6gym1	Alignment	not modelled	93.3	13	PDB header: transcription Chain: 1; PDB Molecule: general transcription and dna repair factor iih subunit PDBTitle: structure of a yeast closed complex with distorted dna (ccdist)
45	c5oqm1	Alignment	not modelled	93.0	14	PDB header: transcription Chain: 1; PDB Molecule: general transcription and dna repair factor iih subunit PDBTitle: structure of yeast transcription pre-initiation complex with tfiih and2 core mediator
46	c5oqj1	Alignment	not modelled	92.7	14	PDB header: transcription Chain: 1; PDB Molecule: rna polymerase ii transcription factor b subunit 1; PDBTitle: structure of yeast transcription pre-initiation complex with tfiih
47	c6o9l1	Alignment	not modelled	92.6	11	PDB header: transcription/dna Chain: 1; PDB Molecule: general transcription factor iih subunit 1; PDBTitle: human holo-pic in the closed state
48	c6nmiC	Alignment	not modelled	92.4	11	PDB header: transcription Chain: C; PDB Molecule: general transcription factor iih subunit 1, p62; PDBTitle: cryo-em structure of the human tfiih core complex
49	c6ejeA	Alignment	not modelled	91.8	12	PDB header: transferase Chain: A; PDB Molecule: xylosyltransferase 1; PDBTitle: human xylosyltransferase 1 in complex with peptide paaegsgeqdf
50	c4xwiA	Alignment	not modelled	91.1	13	PDB header: transferase Chain: A; PDB Molecule: 3-deoxy-manno-octulosonate cytidyltransferase; PDBTitle: x-ray crystal structure of cmp-kdo synthase from pseudomonas2 aeruginosa
51	c4mybA	Alignment	not modelled	89.9	8	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)
52	c2j0bA_	Alignment	not modelled	89.9	24	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
53	c4kt7A_	Alignment	not modelled	89.7	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
54	c3oamD_	Alignment	not modelled	89.3	12	PDB header: transferase Chain: D: PDB Molecule: 3-deoxy-manno-octulosonate cytidyltransferase; PDBTitle: crystal structure of cytidyltransferase from vibrio cholerae
55	d1vgwa_	Alignment	not modelled	88.9	11	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: Cytidyltransferase
56	c2xwB_	Alignment	not modelled	87.4	18	PDB header: transferase Chain: B: PDB Molecule: 2-c-methyl-d-erythritol 4-phosphate cytidyltransferase; PDBTitle: crystal structure of ispd from mycobacterium smegmatis in complex with2 ctp and mg
57	c2gamA_	Alignment	not modelled	86.4	12	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
58	c2px7A_	Alignment	not modelled	85.7	20	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
59	c3okrA_	Alignment	not modelled	85.2	21	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)
60	c6bwhB_	Alignment	not modelled	84.7	14	PDB header: transferase Chain: B: PDB Molecule: 2-phospho-l-lactate guanylyltransferase; PDBTitle: crystal structure of mycobacterium tuberculosis rv2983 in complex2 with pep
61	c5gvvF_	Alignment	not modelled	84.5	13	PDB header: transferase Chain: F: PDB Molecule: glycosyl transferase family 8; PDBTitle: crystal structure of the glycosyltransferase glye in streptococcus2 pneumoniae tigr4
62	d1vica_	Alignment	not modelled	84.5	13	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: Cytidyltransferase
63	d1w77a1	Alignment	not modelled	80.9	9	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: Cytidyltransferase
64	c1w57A_	Alignment	not modelled	80.6	11	PDB header: transferase Chain: A: PDB Molecule: ispd/ispf bifunctional enzyme; PDBTitle: structure of the bifunctional ispdf from campylobacter2 jejuni containing zn
65	d1vpaa_	Alignment	not modelled	79.5	18	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: Cytidyltransferase
66	c2xmhB_	Alignment	not modelled	78.8	12	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	c3d5nB_	Alignment	not modelled	77.9	10	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: q97w15_sulso; PDBTitle: crystal structure of the q97w15_sulso protein from sulfolobus2 solfataricus. nesc target ssr125.
68	d1i52a_	Alignment	not modelled	76.7	14	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: Cytidyltransferase
69	c2wawA_	Alignment	not modelled	75.0	14	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	c6b5kA_	Alignment	not modelled	73.6	8	PDB header: transferase Chain: A: PDB Molecule: glucose-1-phosphate thymidyltransferase; PDBTitle: mycobacterium tuberculosis rmla in complex with mg/dttp
71	c6cglA_	Alignment	not modelled	70.8	13	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
72	c3f1cB_	Alignment	not modelled	64.9	10	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
73	c4jd0A_	Alignment	not modelled	63.2	13	PDB header: transferase Chain: A: PDB Molecule: nucleotidyl transferase; PDBTitle: structure of the inositol-1-phosphate ctp transferase from t.2 maritima.
74	d1e5ka_	Alignment	not modelled	61.8	15	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: Molybdenum cofactor biosynthesis protein MobA
						PDB header: transferase Chain: A: PDB Molecule: ctp l-myo-inositol-1-phosphate

75	c4mndA_	Alignment	not modelled	61.4	14	cytidyltransferase/cdp-l PDBTitle: crystal structure of archaeoglobus fulgidus ipct-dipps bifunctional2 membrane protein
76	c6aokA_	Alignment	not modelled	61.3	24	PDB header: hydrolase Chain: A: PDB Molecule: ceg4; PDBTitle: crystal structure of legionella pneumophila effector ceg4 with n-2 terminal tev protease cleavage sequence
77	d1eyra_	Alignment	not modelled	56.3	10	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: Cytidyltransferase
78	c6oewB_	Alignment	not modelled	56.3	9	PDB header: transferase Chain: B: PDB Molecule: cytidyltransferase; PDBTitle: structure of a cytidyltransferase from leptospira borgpetersenii2 serovar hardjo-bovis (strain jb197)
79	c3okrC_	Alignment	not modelled	51.9	23	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)
80	c3brkX_	Alignment	not modelled	49.1	6	PDB header: transferase Chain: X: PDB Molecule: glucose-1-phosphate adenyltransferase; PDBTitle: crystal structure of adp-glucose pyrophosphorylase from agrobacterium2 tumefaciens
81	c1zctB_	Alignment	not modelled	49.0	15	PDB header: transferase Chain: B: PDB Molecule: glycogenin-1; PDBTitle: structure of glycogenin truncated at residue 270 in a complex with udp
82	c2vshB_	Alignment	not modelled	48.4	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
83	c3cqxA_	Alignment	not modelled	48.3	9	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
84	c2we9A_	Alignment	not modelled	47.0	12	PDB header: unknown function Chain: A: PDB Molecule: moba-related protein; PDBTitle: crystal structure of rv0371c from mycobacterium2 tuberculosis h37rv
85	d2diiA1	Alignment	not modelled	46.3	17	Fold: BSD domain-like Superfamily: BSD domain-like Family: BSD domain
86	c6bsvB_	Alignment	not modelled	46.0	12	PDB header: transferase Chain: B: PDB Molecule: xyloglucan 6-xylosyltransferase 1; PDBTitle: crystal structure of xyloglucan xylosyltransferase binary form
87	d1h5ra_	Alignment	not modelled	44.1	8	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: glucose-1-phosphate thymidyltransferase
88	c2diiA_	Alignment	not modelled	42.9	15	PDB header: transcription Chain: A: PDB Molecule: tfiih basal transcription factor complex p62 PDBTitle: solution structure of the bsd domain of human tfiih basal2 transcription factor complex p62 subunit
89	c5ddtA_	Alignment	not modelled	42.4	12	PDB header: transferase Chain: A: PDB Molecule: 2-c-methyl-d-erythritol 4-phosphate cytidyltransferase; PDBTitle: crystal structure of ispd from bacillus subtilis at 1.80 angstroms2 resolution, crystal form i
90	d3bswa1	Alignment	not modelled	42.0	26	Fold: Single-stranded left-handed beta-helix Superfamily: Trimeric LpxA-like enzymes Family: PgID-like
91	d1fxoa_	Alignment	not modelled	41.2	9	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: glucose-1-phosphate thymidyltransferase
92	c2cu2A_	Alignment	not modelled	41.1	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
93	d1w55a1	Alignment	not modelled	40.8	10	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: Cytidyltransferase
94	c6ifdD_	Alignment	not modelled	40.0	10	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+
95	c2e8bA_	Alignment	not modelled	39.7	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
96	d1mc3a_	Alignment	not modelled	39.1	13	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: glucose-1-phosphate thymidyltransferase
97	d1x3aa1	Alignment	not modelled	38.1	13	Fold: BSD domain-like Superfamily: BSD domain-like Family: BSD domain
98	c3ngwA_	Alignment	not modelled	36.3	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
						PDB header: transferase

99	c3pnnA	Alignment	not modelled	36.2	7	Chain: A; PDB Molecule: conserved domain protein; PDBTitle: the crystal structure of a glycosyltransferase from porphyromonas2 gingivalis w83
100	d1iina	Alignment	not modelled	35.9	8	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: glucose-1-phosphate thymidyltransferase
101	c3hl3A	Alignment	not modelled	35.8	12	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.
102	c4wfgA	Alignment	not modelled	35.3	10	PDB header: transcription Chain: A; PDB Molecule: suppressor of stem-loop protein 1; PDBTitle: crystal structure of tfiih subunit
103	c3d98A	Alignment	not modelled	33.2	18	PDB header: transferase Chain: A; PDB Molecule: bifunctional protein glmu; PDBTitle: crystal structure of glmu from mycobacterium tuberculosis, ligand-free2 form
104	c3me5A	Alignment	not modelled	29.0	22	PDB header: transferase Chain: A; PDB Molecule: cytosine-specific methyltransferase; PDBTitle: crystal structure of putative dna cytosine methylase from shigella2 flexneri 2a str. 2457t
105	d2ihta3	Alignment	not modelled	28.0	15	Fold: Thiamin diphosphate-binding fold (THDP-binding) Superfamily: Thiamin diphosphate-binding fold (THDP-binding) Family: Pyruvate oxidase and decarboxylase PP module
106	d1h7ea	Alignment	not modelled	26.4	13	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: Cytidyltransferase
107	d1lwva	Alignment	not modelled	26.2	12	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: glucose-1-phosphate thymidyltransferase
108	c1zcyA	Alignment	not modelled	25.8	10	PDB header: transferase Chain: A; PDB Molecule: glycogenin-1; PDBTitle: apo form of a mutant of glycogenin in which asp159 is replaced by ser
109	c4ea8A	Alignment	not modelled	25.8	30	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
110	d1yp2a2	Alignment	not modelled	25.3	10	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: glucose-1-phosphate thymidyltransferase
111	c3tztB	Alignment	not modelled	24.8	11	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.
112	c4xijA	Alignment	not modelled	24.3	18	PDB header: oxidoreductase Chain: A; PDB Molecule: shikimate 5-dehydrogenase; PDBTitle: crystal structure of a shikimate 5-dehydrogenase from mycobacterium2 fortuitum determined by iodide sad phasing
113	c2w6hG	Alignment	not modelled	23.3	18	PDB header: hydrolase Chain: G; PDB Molecule: atp synthase subunit gamma, mitochondrial; PDBTitle: low resolution structures of bovine mitochondrial f1-atpase during2 controlled dehydration: hydration state 4a.
114	d1qwja	Alignment	not modelled	22.3	16	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: Cytidyltransferase
115	c4uegB	Alignment	not modelled	21.8	10	PDB header: transferase Chain: B; PDB Molecule: glycogenin-2; PDBTitle: crystal structure of human glycogenin-2 catalytic domain
116	c4y7uA	Alignment	not modelled	20.8	15	PDB header: transferase Chain: A; PDB Molecule: nucleotidyl transferase; PDBTitle: structural analysis of muru
117	c2xokG	Alignment	not modelled	20.7	17	PDB header: hydrolase Chain: G; PDB Molecule: atp synthase subunit gamma, mitochondrial; PDBTitle: refined structure of yeast f1c10 atpase complex to 3 a resolution
118	c5xhwA	Alignment	not modelled	20.6	11	PDB header: transferase Chain: A; PDB Molecule: putative 6-deoxy-d-mannoheptose pathway protein; PDBTitle: crystal structure of hddc from yersinia pseudotuberculosis