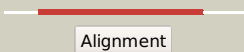

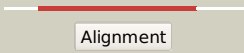



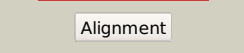



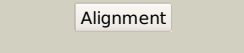

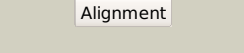



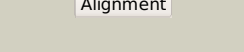

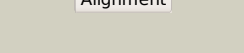

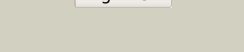



Phyre2

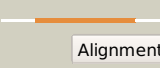
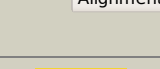
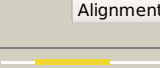
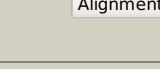
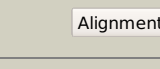
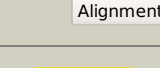
Email	mdejesus@rockefeller.edu
Description	RVBD2957_(-)_3309480_3310307
Date	Thu Aug 8 16:20:11 BST 2019
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Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2z86D_	 Alignment		100.0	20	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
2	d1xhba2	 Alignment		100.0	19	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: Polypeptide N-acetylgalactosaminyltransferase 1, N-terminal domain
3	c2ffuA_	 Alignment		100.0	17	PDB header: transferase Chain: A; PDB Molecule: polypeptide n-acetylgalactosaminyltransferase 2; PDBTitle: crystal structure of human ppgalnact-2 complexed with udp and ea2
4	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+
5	c6h4mA_	 Alignment		100.0	14	PDB header: transferase Chain: A; PDB Molecule: probable ss-1,3-n-acetylglucosaminyltransferase; PDBTitle: tarp-udp-glcnac-3rbop
6	c1xhba_	 Alignment		100.0	21	PDB header: transferase Chain: A; PDB Molecule: polypeptide n-acetylgalactosaminyltransferase 1; PDBTitle: the crystal structure of udp-galnac: polypeptide alpha-n-2 acetylgalactosaminyltransferase-t1
7	c5tz8C_	 Alignment		100.0	23	PDB header: transferase Chain: C; PDB Molecule: glycosyl transferase; PDBTitle: crystal structure of s. aureus tars
8	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
9	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
10	c6iwiqE_	 Alignment		100.0	14	PDB header: transferase Chain: E; PDB Molecule: n-acetylgalactosaminyltransferase 7; PDBTitle: crystal structure of galnac-t7 with mn2+
11	c5heaA_	 Alignment		100.0	21	PDB header: transferase Chain: A; PDB Molecule: putative glycosyltransferase (galt1); PDBTitle: cgt structure in hexamer

12	d1qg8a_	Alignment		99.9	18	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: Spore coat polysaccharide biosynthesis protein SpsA
13	c3f1yC_	Alignment		99.9	16	PDB header: transferase Chain: C: PDB Molecule: mannosyl-3-phosphoglycerate synthase; PDBTitle: mannosyl-3-phosphoglycerate synthase from rubrobacter xylanophilus
14	c3bcvA_	Alignment		99.9	23	PDB header: transferase Chain: A: PDB Molecule: putative glycosyltransferase protein; PDBTitle: crystal structure of a putative glycosyltransferase from bacteroides2 fragilis
15	c5mm1A_	Alignment		99.9	16	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
16	c4hg6A_	Alignment		99.9	17	PDB header: transferase Chain: A: PDB Molecule: cellulose synthase subunit a; PDBTitle: structure of a cellulose synthase - cellulose translocation2 intermediate
17	c3ckvA_	Alignment		99.9	17	PDB header: unknown function Chain: A: PDB Molecule: putative uncharacterized protein; PDBTitle: crystal structure of a mycobacterial protein
18	c4fixA_	Alignment		99.9	19	PDB header: transferase Chain: A: PDB Molecule: udp-galactofuranosyl transferase glft2; PDBTitle: crystal structure of glft2
19	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)
20	c1omxB_	Alignment		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)
21	d1omza_	Alignment	not modelled	99.9	13	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: Exostosin
22	c5ekeB_	Alignment	not modelled	99.9	17	PDB header: transferase Chain: B: PDB Molecule: uncharacterized glycosyltransferase sll0501; PDBTitle: structure of the polyisoprenyl-phosphate glycosyltransferase gtrb2 (f215a mutant)
23	c3zf8A_	Alignment	not modelled	99.9	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.
24	c5z8bB_	Alignment	not modelled	99.8	12	PDB header: transferase Chain: B: PDB Molecule: kfia protein; PDBTitle: truncated n-acetylglucosaminyl transferase kfia from e. coli k5 strain2 apo form
25	c2qgiA_	Alignment	not modelled	99.8	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
26	c5ggfC_	Alignment	not modelled	99.8	13	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	c4irqB_	Alignment	not modelled	99.2	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
						Fold: Nucleotide-diphospho-sugar transferases

28	d1fo8a_	Alignment	not modelled	98.9	10	Superfamily: Nucleotide-diphospho-sugar transferases Family: N-acetylglucosaminyltransferase I
29	d2bo4a1	Alignment	not modelled	98.6	12	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: MGS-like
30	d1pzta_	Alignment	not modelled	98.4	15	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: beta 1,4 galactosyltransferase (b4GalT1)
31	c5vcmA_	Alignment	not modelled	98.2	13	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
32	c6fxyA_	Alignment	not modelled	98.0	14	PDB header: transferase Chain: A: PDB Molecule: procollagen-lysine,2-oxoglutarate 5- dioxxygenase 3; PDBTitle: crystal structure of full-length human lysyl hydroxylase lh3 -2 cocrystal with fe2+, mn2+, udp-gal - structure from long- wavelength3 s-sad
33	c3lw6A_	Alignment	not modelled	98.0	14	PDB header: transferase Chain: A: PDB Molecule: beta-4-galactosyltransferase 7; PDBTitle: crystal structure of drosophila beta1,4- galactosyltransferase-7
34	c4kt7A_	Alignment	not modelled	96.0	13	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
35	c4ys8B_	Alignment	not modelled	95.8	12	PDB header: transferase Chain: B: PDB Molecule: 2-c-methyl-d-erythritol 4-phosphate cytidyltransferase; PDBTitle: crystal structure of 2-c-methyl-d-erythritol 4-phosphate2 cytidyltransferase (ispd) from burkholderia thailandensis
36	c2d0jD_	Alignment	not modelled	95.7	13	PDB header: transferase Chain: D: PDB Molecule: galactosylgalactosylxylosylprotein 3-beta- PDBTitle: crystal structure of human glcat-s apo form
37	d1v82a_	Alignment	not modelled	95.7	14	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: 1,3-glucuronyltransferase
38	d3cu0a1	Alignment	not modelled	95.1	14	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: 1,3-glucuronyltransferase
39	d1fxoa_	Alignment	not modelled	94.7	8	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: glucose-1-phosphate thymidyltransferase
40	c2wawA_	Alignment	not modelled	94.4	12	PDB header: unknown function Chain: A: PDB Molecule: moba relate protein; PDBTitle: crystal structure of mycobacterium tuberculosis rv0371c2 homolog from mycobacterium sp. strain jc1
41	d1h5ra_	Alignment	not modelled	93.2	12	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: glucose-1-phosphate thymidyltransferase
42	c2we9A_	Alignment	not modelled	93.1	18	PDB header: unknown function Chain: A: PDB Molecule: moba-related protein; PDBTitle: crystal structure of rv0371c from mycobacterium2 tuberculosis h37rv
43	c3f1cB_	Alignment	not modelled	91.9	14	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
44	d1lvwa_	Alignment	not modelled	91.1	10	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: glucose-1-phosphate thymidyltransferase
45	d1mc3a_	Alignment	not modelled	91.0	11	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: glucose-1-phosphate thymidyltransferase
46	d1vh3a_	Alignment	not modelled	90.5	10	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: Cytidyltransferase
47	c5vcsB_	Alignment	not modelled	90.4	17	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
48	d1iina_	Alignment	not modelled	90.3	12	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: glucose-1-phosphate thymidyltransferase
49	c2wvmA_	Alignment	not modelled	90.1	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)
50	c2px7A_	Alignment	not modelled	86.1	16	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
51	c4xwiA_	Alignment	not modelled	85.8	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
52	d2oi6a2	Alignment	not modelled	85.2	14	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: UDP-glucose pyrophosphorylase

53	c5ddtA	 Alignment	not modelled	84.9	9	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
54	d1w77a1	 Alignment	not modelled	84.3	10	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: Cytidylyltransferase
55	c3ngwA	 Alignment	not modelled	83.6	9	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
56	c2pa4B	 Alignment	not modelled	80.9	15	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
57	c2qh5B	 Alignment	not modelled	79.8	6	PDB header: isomerase Chain: B: PDB Molecule: mannose-6-phosphate isomerase; PDBTitle: crystal structure of mannose-6-phosphate isomerase from helicobacter2 pylori
58	c5gvvF	 Alignment	not modelled	78.7	10	PDB header: transferase Chain: F: PDB Molecule: glycosyl transferase family 8; PDBTitle: crystal structure of the glycosyltransferase glye in streptococcus2 pneumoniae tigr4
59	c2zu8A	 Alignment	not modelled	78.1	15	PDB header: transferase Chain: A: PDB Molecule: mannosyl-3-phosphoglycerate synthase; PDBTitle: crystal structure of mannosyl-3-phosphoglycerate synthase2 from pyrococcus horikoshii
60	c3polA	 Alignment	not modelled	76.3	13	PDB header: transferase Chain: A: PDB Molecule: 3-deoxy-manno-octulosonate cytidylyltransferase; PDBTitle: 2.3 angstrom crystal structure of 3-deoxy-manno-octulosonate2 cytidylyltransferase (kdsb) from acinetobacter baumannii.
61	c6cglA	 Alignment	not modelled	74.9	19	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
62	c3hl3A	 Alignment	not modelled	74.6	10	PDB header: transferase Chain: A: PDB Molecule: glucose-1-phosphate thymidylyltransferase; PDBTitle: 2.76 angstrom crystal structure of a putative glucose-1-phosphate2 thymidylyltransferase from bacillus anthracis in complex with a3 sucrose.
63	d1eyra	 Alignment	not modelled	74.4	12	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: Cytidylyltransferase
64	c6oewB	 Alignment	not modelled	74.0	9	PDB header: transferase Chain: B: PDB Molecule: cytidylyltransferase; PDBTitle: structure of a cytidylyltransferase from leptospira borgpetersenii2 serovar hardjo-bovis (strain jb197)
65	c6b5kA	 Alignment	not modelled	73.8	8	PDB header: transferase Chain: A: PDB Molecule: glucose-1-phosphate thymidylyltransferase; PDBTitle: mycobacterium tuberculosis rmla in complex with mg/dttp
66	d1vkpa	 Alignment	not modelled	73.0	14	Fold: Pentain, beta/alpha-propeller Superfamily: Pentain Family: Porphyromonas-type peptidylarginine deiminase
67	c5xhwA	 Alignment	not modelled	72.9	13	PDB header: transferase Chain: A: PDB Molecule: putative 6-deoxy-d-mannoheptose pathway protein; PDBTitle: crystal structure of hddc from yersinia pseudotuberculosis
68	c2xwIB	 Alignment	not modelled	72.7	12	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
69	d1vica	 Alignment	not modelled	72.6	9	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: Cytidylyltransferase
70	c3oamD	 Alignment	not modelled	71.5	8	PDB header: transferase Chain: D: PDB Molecule: 3-deoxy-manno-octulosonate cytidylyltransferase; PDBTitle: crystal structure of cytidylyltransferase from vibrio cholerae
71	c2vshB	 Alignment	not modelled	71.2	15	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
72	d1vpaa	 Alignment	not modelled	70.8	10	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: Cytidylyltransferase
73	d1i52a	 Alignment	not modelled	69.5	13	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: Cytidylyltransferase
74	c4ytgA	 Alignment	not modelled	68.8	18	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.
75	c3okrA	 Alignment	not modelled	67.4	16	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 cytidyltransferase (ispd)
76	c4jisB_	Alignment	not modelled	66.6	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
77	c3rsbB_	Alignment	not modelled	66.1	6	PDB header: transferase Chain: B: PDB Molecule: adenosylcobinamide-phosphate guanylyltransferase; PDBTitle: structure of the archaeal gtp:adocbi-p guanylyltransferase (coby) from2 methanocaldococcus jannaschii
78	c6aokA_	Alignment	not modelled	63.7	22	PDB header: hydrolase Chain: A: PDB Molecule: ceg4; PDBTitle: crystal structure of legionella pneumophila effector ceg4 with n-2 terminal tev protease cleavage sequence
79	c3okrC_	Alignment	not modelled	61.1	21	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	c2e8bA_	Alignment	not modelled	60.6	16	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
81	d1qwja_	Alignment	not modelled	59.5	16	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: Cytidylyltransferase
82	c2x5sB_	Alignment	not modelled	55.3	9	PDB header: transferase Chain: B: PDB Molecule: mannose-1-phosphate guanylyltransferase; PDBTitle: crystal structure of t. maritima gdp-mannose2 pyrophosphorylase in apo state.
83	c3d5nB_	Alignment	not modelled	54.7	5	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.
84	d1e5ka_	Alignment	not modelled	54.6	15	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: Molybdenum cofactor biosynthesis protein MobA
85	c2y6pC_	Alignment	not modelled	53.7	10	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
86	c6ifdD_	Alignment	not modelled	50.7	11	PDB header: sugar binding protein Chain: D: PDB Molecule: cmp-n-acetylneuraminate synthetase; PDBTitle: crystal structure of cmp-n-acetylneuraminate synthetase from vibrio2 cholerae in complex with cdp and mg2+.
87	c3d8vA_	Alignment	not modelled	50.7	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
88	d2jera1	Alignment	not modelled	50.5	16	Fold: Pentain, beta/alpha-propeller Superfamily: Pentain Family: Porphyromonas-type peptidylarginine deiminase
89	d1g97a2	Alignment	not modelled	50.0	13	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: UDP-glucose pyrophosphorylase
90	c2jerG_	Alignment	not modelled	48.9	16	PDB header: hydrolase Chain: G: PDB Molecule: agmatine deiminase; PDBTitle: agmatine deiminase of enterococcus faecalis catalyzing its2 reaction.
91	d1h7ea_	Alignment	not modelled	48.5	11	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: Cytidylyltransferase
92	c4y7uA_	Alignment	not modelled	48.3	11	PDB header: transferase Chain: A: PDB Molecule: nucleotidyl transferase; PDBTitle: structural analysis of muru
93	d1w55a1	Alignment	not modelled	47.6	9	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: Cytidylyltransferase
94	d1vgwa_	Alignment	not modelled	45.9	17	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: Cytidylyltransferase
95	c2gamA_	Alignment	not modelled	45.7	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
96	c3tqdA_	Alignment	not modelled	44.6	15	PDB header: transferase Chain: A: PDB Molecule: 3-deoxy-manno-octulosonate cytidyltransferase; PDBTitle: structure of the 3-deoxy-d-manno-octulosonate cytidyltransferase2 (kdsb) from coxiella burnetii
97	c1w57A_	Alignment	not modelled	43.7	9	PDB header: transferase Chain: A: PDB Molecule: ispd/ispf bifunctional enzyme; PDBTitle: structure of the bifunctional ispdf from campylobacter2 jejuni containing zn
98	d1xkna_	Alignment	not modelled	42.8	22	Fold: Pentain, beta/alpha-propeller Superfamily: Pentain Family: Porphyromonas-type peptidylarginine deiminase
99	c4mybA_	Alignment	not modelled	41.6	11	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)

100	d2ewoa1	Alignment	not modelled	40.4	19	Fold: Pentain, beta/alpha-propeller Superfamily: Pentain Family: Porphyromonas-type peptidylarginine deiminase
101	d1zbra1	Alignment	not modelled	37.1	25	Fold: Pentain, beta/alpha-propeller Superfamily: Pentain Family: Porphyromonas-type peptidylarginine deiminase
102	c2xmhB_	Alignment	not modelled	35.0	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
103	c3ssmB_	Alignment	not modelled	32.3	21	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
104	c6b2wB_	Alignment	not modelled	32.0	13	PDB header: hydrolase Chain: B: PDB Molecule: putative peptidyl-arginine deiminase family protein; PDBTitle: c. jejuni c315s agmatine deiminase with substrate bound
105	c5yh1A_	Alignment	not modelled	27.8	21	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
106	c6bwhB_	Alignment	not modelled	27.7	15	PDB header: transferase Chain: B: PDB Molecule: 2-phospho-l-lactate guanylyltransferase; PDBTitle: crystal structure of mycobacterium tuberculosis rv2983 in complex2 with pep
107	c4mndA_	Alignment	not modelled	27.5	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
108	c3tztB_	Alignment	not modelled	27.4	20	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.
109	c2e3dB_	Alignment	not modelled	25.8	18	PDB header: transferase Chain: B: PDB Molecule: utp--glucose-1-phosphate uridylyltransferase; PDBTitle: crystal structure of e. coli glucose-1-phosphate2 uridylyltransferase
110	c1fwyA_	Alignment	not modelled	25.3	16	PDB header: transferase Chain: A: PDB Molecule: udp-n-acetylglucosamine pyrophosphorylase; PDBTitle: crystal structure of n-acetylglucosamine 1-phosphate2 uridylyltransferase bound to udp-glcnac
111	c3jukA_	Alignment	not modelled	24.7	16	PDB header: transferase Chain: A: PDB Molecule: udp-glucose pyrophosphorylase (galu); PDBTitle: the crystal structure of udp-glucose pyrophosphorylase complexed with2 udp-glucose
112	c2cu2A_	Alignment	not modelled	24.2	17	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
113	c2f59B_	Alignment	not modelled	23.1	22	PDB header: transferase Chain: B: PDB Molecule: 6,7-dimethyl-8-ribityllumazine synthase 1; PDBTitle: lumazine synthase ribh1 from brucella abortus (gene bruab1_0785,2 swiss-prot entry q57dy1) complexed with inhibitor 5-nitro-6-(d-3 ribitylamino)-2,4(1h,3h) pyrimidinedione
114	c4jd0A_	Alignment	not modelled	22.0	8	PDB header: transferase Chain: A: PDB Molecule: nucleotidyl transferase; PDBTitle: structure of the inositol-1-phosphate ctp transferase from t.2 maritima.
115	c1jyIC_	Alignment	not modelled	21.4	8	PDB header: transferase Chain: C: PDB Molecule: ctp:phosphocholine cytidyltransferase; PDBTitle: catalytic mechanism of ctp:phosphocholine2 cytidyltransferase from streptococcus pneumoniae (licc)