



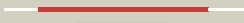

















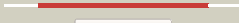

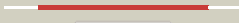













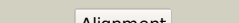









Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3631 (-) _4070693_4071418
Date	Fri Aug 9 18:20:31 BST 2019
Unique Job ID	fccbe34a07119ffb

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1xhba2	 Alignment		100.0	15	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: Polypeptide N-acetylgalactosaminyltransferase 1, N-terminal domain
2	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
3	c5nqaA_	 Alignment		100.0	14	PDB header: transferase Chain: A; PDB Molecule: polypeptide n-acetylgalactosaminyltransferase 4; PDBTitle: crystal structure of galnac-t4 in complex with the monoglycopeptide 3
4	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
5	c6e4rB_	 Alignment		100.0	14	PDB header: transferase Chain: B; PDB Molecule: polypeptide n-acetylgalactosaminyltransferase 9; PDBTitle: crystal structure of the drosophila melanogaster polypeptide n-2 acetylgalactosaminyl transferase pgant9b
6	c2d7iA_	 Alignment		100.0	13	PDB header: transferase Chain: A; PDB Molecule: polypeptide n-acetylgalactosaminyltransferase 10; PDBTitle: crystal structure of pp-galnac-t10 with udp, galnac and mn2+
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	c5mm1A_	 Alignment		100.0	18	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
9	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
10	c6h4mA_	 Alignment		100.0	15	PDB header: transferase Chain: A; PDB Molecule: probable ss-1,3-n-acetylglucosaminyltransferase; PDBTitle: tarp-udp-glcnac-3rbop
11	c5tz8C_	 Alignment		100.0	16	PDB header: transferase Chain: C; PDB Molecule: glycosyl transferase; PDBTitle: crystal structure of s. aureus tars

12	c5heaA	 Alignment		100.0	12	PDB header: transferase Chain: A: PDB Molecule: putative glycosyltransferase (galt1); PDBTitle: cgt structure in hexamer
13	c3flyC	 Alignment		100.0	14	PDB header: transferase Chain: C: PDB Molecule: mannosyl-3-phosphoglycerate synthase; PDBTitle: mannosyl-3-phosphoglycerate synthase from rubrobacter xylanophilus
14	c4hg6A	 Alignment		100.0	12	PDB header: transferase Chain: A: PDB Molecule: cellulose synthase subunit a; PDBTitle: structure of a cellulose synthase - cellulose translocation2 intermediate
15	c4fixA	 Alignment		100.0	15	PDB header: transferase Chain: A: PDB Molecule: udp-galactofuranosyl transferase glft2; PDBTitle: crystal structure of glft2
16	c3ckvA	 Alignment		100.0	18	PDB header: unknown function Chain: A: PDB Molecule: putative uncharacterized protein; PDBTitle: crystal structure of a mycobacterial protein
17	c3bcvA	 Alignment		100.0	13	PDB header: transferase Chain: A: PDB Molecule: putative glycosyltransferase protein; PDBTitle: crystal structure of a putative glycosyltransferase from bacteroides2 fragilis
18	c5ekeB	 Alignment		100.0	18	PDB header: transferase Chain: B: PDB Molecule: uncharacterized glycosyltransferase sll0501; PDBTitle: structure of the polyisoprenyl-phosphate glycosyltransferase gtrb2 (f215a mutant)
19	d1qg8a	 Alignment		100.0	12	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: Spore coat polysaccharide biosynthesis protein SpsA
20	d1omza	 Alignment		100.0	7	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: Exostosin
21	c1omxB	 Alignment	not modelled	100.0	10	PDB header: transferase Chain: B: PDB Molecule: alpha-1,4-n-acetylhexosaminyltransferase extl2; PDBTitle: crystal structure of mouse alpha-1,4-n-acetylhexosaminyltransferase2 (extl2)
22	c6p61D	 Alignment	not modelled	99.9	9	PDB header: transferase Chain: D: PDB Molecule: glycosyltransferase; PDBTitle: structure of a glycosyltransferase from leptospira borgpetersenii2 serovar hardjo-bovis (strain jb197)
23	c3zf8A	 Alignment	not modelled	99.9	8	PDB header: transferase Chain: A: PDB Molecule: mannan polymerase complexes subunit mnn9; PDBTitle: crystal structure of saccharomyces cerevisiae mnn9 in2 complex with gdp and mn.
24	c5z8bB	 Alignment	not modelled	99.9	11	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	99.9	10	PDB header: transferase Chain: A: PDB Molecule: atp synthase subunits region orf 6; PDBTitle: the udp complex structure of the sixth gene product of the f1-atpase2 operon of rhodobacter blasticus
26	c5ggfC	 Alignment	not modelled	99.8	12	PDB header: transferase, sugar binding protein Chain: C: PDB Molecule: protein o-linked-mannose beta-1,2-n-2 acetylglucosaminyltransferase form ii PDBTitle: crystal structure of human protein o-mannose beta-1,2-n-2 acetylglucosaminyltransferase form ii
27	d2bo4a1	 Alignment	not modelled	99.7	15	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: MGS-like
		 Alignment				PDB header: transferase Chain: B: PDB Molecule: beta-1,4-galactosyltransferase 7;

28	c4irqB_	Alignment	not modelled	99.4	9	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	99.1	14	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: beta 1,4 galactosyltransferase (b4GalT1)
30	d1fo8a_	Alignment	not modelled	98.9	5	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: N-acetylglucosaminyltransferase I
31	c5vcmA_	Alignment	not modelled	98.4	9	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	c3lw6A_	Alignment	not modelled	98.3	8	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	98.2	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	d1vh3a_	Alignment	not modelled	97.5	14	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: Cytidylyltransferase
35	c4xwiA_	Alignment	not modelled	96.4	13	PDB header: transferase Chain: A: PDB Molecule: 3-deoxy-manno-octulosonate cytidylyltransferase; PDBTitle: x-ray crystal structure of cmp-kdo synthase from pseudomonas2 aeruginosa
36	d1v82a_	Alignment	not modelled	96.1	18	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: 1,3-glucuronyltransferase
37	c2d0jD_	Alignment	not modelled	95.9	13	PDB header: transferase Chain: D: PDB Molecule: galactosylgalactosylxylosylprotein 3-beta- PDBTitle: crystal structure of human glcat-s apo form
38	d3cu0a1	Alignment	not modelled	95.7	23	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: 1,3-glucuronyltransferase
39	c2wvma_	Alignment	not modelled	95.7	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	c3oamD_	Alignment	not modelled	95.2	13	PDB header: transferase Chain: D: PDB Molecule: 3-deoxy-manno-octulosonate cytidylyltransferase; PDBTitle: crystal structure of cytidylyltransferase from vibrio cholerae
41	c3polA_	Alignment	not modelled	94.1	14	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.
42	c3tqdA_	Alignment	not modelled	94.0	13	PDB header: transferase Chain: A: PDB Molecule: 3-deoxy-manno-octulosonate cytidylyltransferase; PDBTitle: structure of the 3-deoxy-d-manno-octulosonate cytidylyltransferase2 (kdsb) from coxiella burnetii
43	c2zu8A_	Alignment	not modelled	93.8	18	PDB header: transferase Chain: A: PDB Molecule: mannosyl-3-phosphoglycerate synthase; PDBTitle: crystal structure of mannosyl-3-phosphoglycerate synthase2 from pyrococcus horikoshii
44	d1vica_	Alignment	not modelled	93.4	13	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: Cytidylyltransferase
45	c2px7A_	Alignment	not modelled	92.0	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
46	c4ys8B_	Alignment	not modelled	91.8	15	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
47	c4kt7A_	Alignment	not modelled	90.7	13	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
48	c2wawA_	Alignment	not modelled	89.5	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
49	d1h5ra_	Alignment	not modelled	89.0	8	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: glucose-1-phosphate thymidylyltransferase
50	d1fxoa_	Alignment	not modelled	88.2	9	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: glucose-1-phosphate thymidylyltransferase
51	c5ddtA_	Alignment	not modelled	86.9	8	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
52	d1vh1a_	Alignment	not modelled	86.2	10	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: Cytidylyltransferase
53	c4jd0A_	Alignment	not modelled	82.5	10	PDB header: transferase Chain: A: PDB Molecule: nucleotidyl transferase; PDBTitle: structure of the inositol-1-phosphate ctp transferase from t.2 maritima.
54	d1lvwa_	Alignment	not modelled	82.5	10	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: glucose-1-phosphate thymidylyltransferase
55	c4mybA_	Alignment	not modelled	82.3	5	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)
56	c1w57A_	Alignment	not modelled	81.3	9	PDB header: transferase Chain: A: PDB Molecule: ispd/ispf bifunctional enzyme; PDBTitle: structure of the bifunctional ispdf from campylobacter2 jejuni containing zn
57	c6b5kA_	Alignment	not modelled	80.2	11	PDB header: transferase Chain: A: PDB Molecule: glucose-1-phosphate thymidylyltransferase; PDBTitle: mycobacterium tuberculosis rmla in complex with mg/dttp
58	c2we9A_	Alignment	not modelled	79.9	13	PDB header: unknown function Chain: A: PDB Molecule: moba-related protein; PDBTitle: crystal structure of rv0371c from mycobacterium2 tuberculosis h37rv
59	d1liia_	Alignment	not modelled	74.5	8	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: glucose-1-phosphate thymidylyltransferase
60	d1w77a1	Alignment	not modelled	73.9	12	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: Cytidylyltransferase
61	c6cgjA_	Alignment	not modelled	72.0	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	d1mc3a_	Alignment	not modelled	70.4	8	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: glucose-1-phosphate thymidylyltransferase
63	c2e3dB_	Alignment	not modelled	70.0	14	PDB header: transferase Chain: B: PDB Molecule: utp--glucose-1-phosphate uridylyltransferase; PDBTitle: crystal structure of e. coli glucose-1-phosphate2 uridylyltransferase
64	d1vgwa_	Alignment	not modelled	69.0	11	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: Cytidylyltransferase
65	c3okrA_	Alignment	not modelled	68.9	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)
66	d1i52a_	Alignment	not modelled	66.7	13	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: Cytidylyltransferase
67	d1h7ea_	Alignment	not modelled	64.2	12	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: Cytidylyltransferase
68	c5gvvF_	Alignment	not modelled	63.4	8	PDB header: transferase Chain: F: PDB Molecule: glycosyl transferase family 8; PDBTitle: crystal structure of the glycosyltransferase glye in streptococcus2 pneumoniae tigr4
69	c2j0bA_	Alignment	not modelled	59.9	13	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
70	c3okrC_	Alignment	not modelled	59.5	19	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)
71	c5vcsB_	Alignment	not modelled	57.0	13	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
72	c5xhwA_	Alignment	not modelled	55.9	10	PDB header: transferase Chain: A: PDB Molecule: putative 6-deoxy-d-mannoheptose pathway protein; PDBTitle: crystal structure of hddc from yersinia pseudotuberculosis
73	c2qh5B_	Alignment	not modelled	54.7	5	PDB header: isomerase Chain: B: PDB Molecule: mannose-6-phosphate isomerase; PDBTitle: crystal structure of mannose-6-phosphate isomerase from helicobacter2 pylori
74	c2gamA_	Alignment	not modelled	49.8	6	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
75	d1g97a2	Alignment	not modelled	47.8	9	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: UDP-glucose pyrophosphorylase
						Fold: Nucleotide-diphospho-sugar transferases

76	d1vpaa_	Alignment	not modelled	46.4	9	Superfamily: Nucleotide-diphospho-sugar transferases Family: Cytidylyltransferase
77	d2oi6a2	Alignment	not modelled	45.9	10	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: UDP-glucose pyrophosphorylase
78	c6aokA_	Alignment	not modelled	42.9	38	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	c2c0nA_	Alignment	not modelled	42.8	13	PDB header: viral protein/transferase Chain: A: PDB Molecule: a197; PDBTitle: crystal structure of a197 from stiv
80	c2pa4B_	Alignment	not modelled	41.0	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
81	c2xwB_	Alignment	not modelled	40.5	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
82	d1w55a1	Alignment	not modelled	39.3	8	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: Cytidylyltransferase
83	c3tztB_	Alignment	not modelled	35.7	7	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.
84	c5i1fA_	Alignment	not modelled	35.6	14	PDB header: transferase Chain: A: PDB Molecule: utp--glucose-1-phosphate uridylyltransferase; PDBTitle: crystal structure of utp-glucose-1-phosphate uridylyltransferase from2 burkholderia vietnamiensis in complex with uridine-5'-diphosphate-3 glucose
85	c6ifdD_	Alignment	not modelled	33.6	13	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+.
86	c2y6pC_	Alignment	not modelled	32.0	10	PDB header: transferase Chain: C: PDB Molecule: 3-deoxy-manno-octulosonate cytidylyltransferase; PDBTitle: evidence for a two-metal-ion-mechanism in the kdo-2 cytidylyltransferase kdsb
87	c2vshB_	Alignment	not modelled	30.9	12	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
88	c3ngwA_	Alignment	not modelled	28.9	12	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
89	c3d5nB_	Alignment	not modelled	27.0	8	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.
90	c2xmhB_	Alignment	not modelled	26.2	10	PDB header: transferase Chain: B: PDB Molecule: ctp-inositol-1-phosphate cytidylyltransferase; PDBTitle: the x-ray structure of ctp:inositol-1-phosphate cytidylyltransferase2 from archaeoglobus fulgidus
91	c4evwB_	Alignment	not modelled	24.2	8	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.
92	c2e8bA_	Alignment	not modelled	24.0	18	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
93	c4jisB_	Alignment	not modelled	23.5	11	PDB header: transferase Chain: B: PDB Molecule: ribitol-5-phosphate cytidylyltransferase; PDBTitle: crystal structure of ribitol 5-phosphate cytidylyltransferase (tari)2 from bacillus subtilis
94	c3hl3A_	Alignment	not modelled	23.4	6	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.
95	d1qwja_	Alignment	not modelled	22.9	10	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: Cytidylyltransferase
96	c6bwhB_	Alignment	not modelled	21.6	16	PDB header: transferase Chain: B: PDB Molecule: 2-phospho-l-lactate guanylyltransferase; PDBTitle: crystal structure of mycobacterium tuberculosis rv2983 in complex2 with pep
97	c6oewB_	Alignment	not modelled	21.4	11	PDB header: transferase Chain: B: PDB Molecule: cytidylyltransferase; PDBTitle: structure of a cytidylyltransferase from leptospira borgpeterseni2 serovar hardjo-bovis (strain jb197)
98	d1yp2a2	Alignment	not modelled	21.2	13	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: glucose-1-phosphate thymidylyltransferase

99	c2l82a	Alignment	not modelled	20.9	19	PDB header: de novo protein Chain: A: PDB Molecule: designed protein or32; PDBTitle: solution nmr structure of de novo designed protein, p-loop ntpase2 fold, northeast structural genomics consortium target or32
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