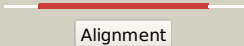

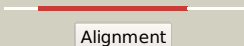

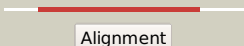







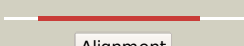




















Phyre2

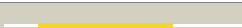






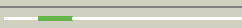
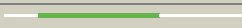




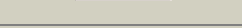

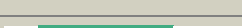




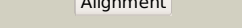


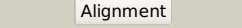
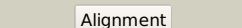
Email	mdejesus@rockefeller.edu
Description	RVBD3782_(-)_4228525_4229439
Date	Fri Aug 9 18:20:49 BST 2019
Unique Job ID	1f721abc397b27cd

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c4fixA_	 Alignment		100.0	17	PDB header: transferase Chain: A: PDB Molecule: udp-galactofuranosyl transferase glft2; PDBTitle: crystal structure of glft2
2	d1xhba2	 Alignment		100.0	14	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: Polypeptide N-acetylgalactosaminyltransferase 1, N-terminal domain
3	c2ffuA_	 Alignment		100.0	14	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	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
5	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+
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	c1xhba_	 Alignment		100.0	13	PDB header: transferase Chain: A: PDB Molecule: polypeptide n-acetylgalactosaminyltransferase 1; PDBTitle: the crystal structure of udp-galnac: polypeptide alpha-n-2 acetylgalactosaminyltransferase-t1
8	c6iwqE_	 Alignment		100.0	15	PDB header: transferase Chain: E: PDB Molecule: n-acetylgalactosaminyltransferase 7; PDBTitle: crystal structure of galnac-t7 with mn2+
9	c2z86D_	 Alignment		100.0	14	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	11	PDB header: transferase Chain: A: PDB Molecule: probable ss-1,3-n-acetylglucosaminyltransferase; PDBTitle: tarp-udp-glcnac-3rbop
11	c5tz8C_	 Alignment		100.0	15	PDB header: transferase Chain: C: PDB Molecule: glycosyl transferase; PDBTitle: crystal structure of s. aureus tars

12	c5heaA	Alignment		100.0	15	PDB header: transferase Chain: A: PDB Molecule: putative glycosyltransferase (galt1); PDBTitle: cgt structure in hexamer
13	c3bcvA	Alignment		100.0	11	PDB header: transferase Chain: A: PDB Molecule: putative glycosyltransferase protein; PDBTitle: crystal structure of a putative glycosyltransferase from bacteroides2 fragilis
14	c5mm1A	Alignment		100.0	10	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
15	d1qq8a	Alignment		100.0	14	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: Spore coat polysaccharide biosynthesis protein SpsA
16	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
17	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)
18	c3zf8A	Alignment		99.9	10	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.
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	c3ckvA	Alignment		99.9	14	PDB header: unknown function Chain: A: PDB Molecule: putative uncharacterized protein; PDBTitle: crystal structure of a mycobacterial protein
21	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)
22	d1omza	Alignment	not modelled	99.9	14	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: Exostosin
23	c5ekeB	Alignment	not modelled	99.9	13	PDB header: transferase Chain: B: PDB Molecule: uncharacterized glycosyltransferase sll0501; PDBTitle: structure of the polyisoprenyl-phosphate glycosyltransferase gtrb2 (f215a mutant)
24	c5z8bB	Alignment	not modelled	99.9	14	PDB header: transferase Chain: B: PDB Molecule: kfia protein; PDBTitle: truncated n-acetylglucosaminyl transferase kfia from e. coli k5 strain2 apo form
25	c2qqiA	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	99.7	16	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	99.3	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
						Fold: Nucleotide-diphospho-sugar transferases

28	d1pzta_	Alignment	not modelled	99.0	17	Superfamily: Nucleotide-diphospho-sugar transferases Family: beta 1,4 galactosyltransferase (b4GalT1)
29	d2bo4a1	Alignment	not modelled	98.7	12	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: MGS-like
30	d1fo8a_	Alignment	not modelled	98.6	15	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: N-acetylglucosaminyltransferase I
31	c5vcmA_	Alignment	not modelled	98.6	11	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	98.4	11	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
33	c3lw6A_	Alignment	not modelled	98.4	15	PDB header: transferase Chain: A: PDB Molecule: beta-4-galactosyltransferase 7; PDBTitle: crystal structure of drosophila beta1,4- galactosyltransferase-7
34	d1vh3a_	Alignment	not modelled	96.7	11	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: Cytidyltransferase
35	c5vcsB_	Alignment	not modelled	95.1	12	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
36	d3cu0a1	Alignment	not modelled	95.0	18	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: 1,3-glucuronyltransferase
37	c2d0jD_	Alignment	not modelled	93.1	19	PDB header: transferase Chain: D: PDB Molecule: galactosylgalactosylxylosylprotein 3-beta- PDBTitle: crystal structure of human gcat-s apo form
38	c4xwiA_	Alignment	not modelled	92.9	14	PDB header: transferase Chain: A: PDB Molecule: 3-deoxy-manno-octulosonate cytidyltransferase; PDBTitle: x-ray crystal structure of cmp-kdo synthase from pseudomonas2 aeruginosa
39	d1w77a1	Alignment	not modelled	92.6	9	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: Cytidyltransferase
40	d1v82a_	Alignment	not modelled	91.8	21	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: 1,3-glucuronyltransferase
41	c3oamD_	Alignment	not modelled	88.4	11	PDB header: transferase Chain: D: PDB Molecule: 3-deoxy-manno-octulosonate cytidyltransferase; PDBTitle: crystal structure of cytidyltransferase from vibrio cholerae
42	c2wawA_	Alignment	not modelled	86.4	13	PDB header: unknown function Chain: A: PDB Molecule: moba relate protein; PDBTitle: crystal structure of mycobacterium tuberculosis rv0371c2 homolog from mycobacterium sp. strain jc1
43	d1vica_	Alignment	not modelled	85.8	13	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: Cytidyltransferase
44	c4kt7A_	Alignment	not modelled	85.6	8	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
45	c2wvmA_	Alignment	not modelled	85.1	22	PDB header: transferase Chain: A: PDB Molecule: mannosyl-3-phosphoglycerate synthase; PDBTitle: h309a mutant of mannosyl-3-phosphoglycerate synthase from2 thermus thermophilus hb27 in complex with3 gdp-alpha-d- mannose and mg(ii)
46	c3polA_	Alignment	not modelled	84.5	10	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.
47	c4ys8B_	Alignment	not modelled	82.1	19	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
48	c6cglA_	Alignment	not modelled	80.0	11	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
49	c2pa4B_	Alignment	not modelled	79.7	11	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
50	c5gvvF_	Alignment	not modelled	78.0	11	PDB header: transferase Chain: F: PDB Molecule: glycosyl transferase family 8; PDBTitle: crystal structure of the glycosyltransferase glye in streptococcus2 pneumoniae tigr4
51	d1h7ea_	Alignment	not modelled	75.2	11	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: Cytidyltransferase

52	c3tqdA_	 Alignment	not modelled	75.1	9	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
53	c6aokA_	 Alignment	not modelled	70.9	16	PDB header: hydrolase Chain: A: PDB Molecule: ceg4; PDBTitle: crystal structure of legionella pneumophila effector ceg4 with n-2 terminal tev protease cleavage sequence
54	c2zu8A_	 Alignment	not modelled	67.4	16	PDB header: transferase Chain: A: PDB Molecule: mannosyl-3-phosphoglycerate synthase; PDBTitle: crystal structure of mannosyl-3-phosphoglycerate synthase2 from pyrococcus horikoshii
55	c2gamA_	 Alignment	not modelled	64.2	8	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
56	d1vh1a_	 Alignment	not modelled	63.7	9	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: Cytidylyltransferase
57	d1lwva_	 Alignment	not modelled	61.5	11	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: glucose-1-phosphate thymidylyltransferase
58	d1eyra_	 Alignment	not modelled	61.0	8	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: Cytidylyltransferase
59	d1vkpa_	 Alignment	not modelled	58.5	14	Fold: Pentain, beta/alpha-propeller Superfamily: Pentain Family: Porphyromonas-type peptidylarginine deiminase
60	d1qwja_	 Alignment	not modelled	58.2	7	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: Cytidylyltransferase
61	c2px7A_	 Alignment	not modelled	57.4	17	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
62	d1ll2a_	 Alignment	not modelled	55.7	9	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: Glycogenin
63	c4jd0A_	 Alignment	not modelled	55.6	7	PDB header: transferase Chain: A: PDB Molecule: nucleotidyl transferase; PDBTitle: structure of the inositol-1-phosphate ctp transferase from t.2 maritima.
64	c1zcyA_	 Alignment	not modelled	54.7	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
65	d1h5ra_	 Alignment	not modelled	49.5	11	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: glucose-1-phosphate thymidylyltransferase
66	d1mc3a_	 Alignment	not modelled	49.0	8	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: glucose-1-phosphate thymidylyltransferase
67	d1iina_	 Alignment	not modelled	48.5	13	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: glucose-1-phosphate thymidylyltransferase
68	d1fxoa_	 Alignment	not modelled	47.6	9	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: glucose-1-phosphate thymidylyltransferase
69	d1xkna_	 Alignment	not modelled	40.0	19	Fold: Pentain, beta/alpha-propeller Superfamily: Pentain Family: Porphyromonas-type peptidylarginine deiminase
70	c4ytgA_	 Alignment	not modelled	39.1	14	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.
71	c3d8vA_	 Alignment	not modelled	36.9	16	PDB header: transferase Chain: A: PDB Molecule: bifunctional protein glmu; PDBTitle: crystal structure of glmu from mycobacterium tuberculosis2 in complex with uridine-diphosphate-n-acetylglucosamine
72	c1zctB_	 Alignment	not modelled	36.1	9	PDB header: transferase Chain: B: PDB Molecule: glycogenin-1; PDBTitle: structure of glycogenin truncated at residue 270 in a complex with udp
73	d1vpaa_	 Alignment	not modelled	34.0	7	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: Cytidylyltransferase
74	d1zbra1	 Alignment	not modelled	33.3	16	Fold: Pentain, beta/alpha-propeller Superfamily: Pentain Family: Porphyromonas-type peptidylarginine deiminase
75	c6b5kA_	 Alignment	not modelled	32.0	11	PDB header: transferase Chain: A: PDB Molecule: glucose-1-phosphate thymidylyltransferase; PDBTitle: mycobacterium tuberculosis rmla in complex with mg/dttp
76	c6b2wB_	 Alignment	not modelled	27.9	13	PDB header: hydrolase Chain: B: PDB Molecule: putative peptidyl-arginine deiminase family protein; PDBTitle: c. jejuni c315s agmatine deiminase with substrate bound PDB header: transcription

77	c2qu7B_	Alignment	not modelled	26.1	8	Chain: B: PDB Molecule: putative transcriptional regulator; PDBTitle: crystal structure of a putative transcription regulator from 2 staphylococcus saprophyticus subsp. saprophyticus
78	c4rndB_	Alignment	not modelled	25.4	4	PDB header: hydrolase Chain: B: PDB Molecule: v-type proton atpase subunit f; PDBTitle: crystal structure of the subunit df-assembly of the eukaryotic v-2 atpase.
79	c6ifdD_	Alignment	not modelled	24.7	9	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+.
80	c3d98A_	Alignment	not modelled	24.2	15	PDB header: transferase Chain: A: PDB Molecule: bifunctional protein glmu; PDBTitle: crystal structure of glmu from mycobacterium tuberculosis, ligand-free2 form
81	c3foqA_	Alignment	not modelled	23.8	14	PDB header: transferase Chain: A: PDB Molecule: bifunctional protein glmu; PDBTitle: crystal structure of n-acetylglucosamine-1-phosphate2 uridylyltransferase (glmu) from mycobacterium tuberculosis in3 a cubic space group.
82	c4rg1A_	Alignment	not modelled	23.5	12	PDB header: transferase Chain: A: PDB Molecule: c9orf114; PDBTitle: methyltransferase domain of c9orf114
83	c2qkxA_	Alignment	not modelled	20.0	14	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
84	c3tztB_	Alignment	not modelled	18.7	6	PDB header: transferase Chain: B: PDB Molecule: glycosyl transferase family 8; PDBTitle: the structure of a protein in glycosyl transferase family 8 from 2 anaerococcus prevotii.
85	c5ddtA_	Alignment	not modelled	17.2	10	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
86	c2y6pC_	Alignment	not modelled	16.1	11	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	c3gybB_	Alignment	not modelled	15.8	11	PDB header: transcription regulator Chain: B: PDB Molecule: transcriptional regulators (laci-family) PDBTitle: crystal structure of a laci-family transcriptional2 regulatory protein from corynebacterium glutamicum
88	c3brcA_	Alignment	not modelled	15.2	4	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 from 2 methanobacterium thermoautotrophicum
89	c3hl3A_	Alignment	not modelled	15.2	8	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.
90	c3d54D_	Alignment	not modelled	15.1	16	PDB header: ligase Chain: D: PDB Molecule: phosphoribosylformylglycinamide synthase 1; PDBTitle: structure of purlqs from thermotoga maritima
91	c4evwB_	Alignment	not modelled	15.0	9	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	c1k3rA_	Alignment	not modelled	15.0	15	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: conserved protein mt0001; PDBTitle: crystal structure of the methyltransferase with a knot from 2 methanobacterium thermoautotrophicum
93	d1d4aa_	Alignment	not modelled	14.6	10	Fold: Flavodoxin-like Superfamily: Flavoproteins Family: Quinone reductase
94	c5d5pC_	Alignment	not modelled	14.5	11	PDB header: transferase Chain: C: PDB Molecule: hcgb; PDBTitle: hcgb from methanococcus maripaludis
95	d2oi6a2	Alignment	not modelled	14.5	8	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: UDP-glucose pyrophosphorylase
96	d1vgwa_	Alignment	not modelled	14.4	16	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: Cytidylyltransferase
97	c6fmgC_	Alignment	not modelled	13.9	15	PDB header: transferase Chain: C: PDB Molecule: pts system mannose-specific transporter subunit iiab; PDBTitle: structure of the mannose transporter iia domain from streptococcus2 pneumoniae
98	c5l6sF_	Alignment	not modelled	13.7	10	PDB header: transferase Chain: F: PDB Molecule: glucose-1-phosphate adenilyltransferase; PDBTitle: crystal structure of e. coli adp-glucose pyrophosphorylase (aggase) in2 complex with a positive allosteric regulator beta-fructose-1,6-3 diphosphate (fbp) - aggase*fbp
99	c4ix9A_	Alignment	not modelled	13.6	4	PDB header: hydrolase Chain: A: PDB Molecule: v-type proton atpase subunit f; PDBTitle: crystal structure of subunit f of v-atpase from s. cerevisiae