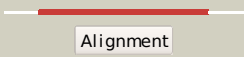

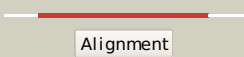

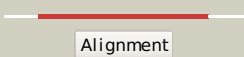

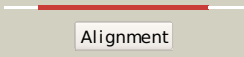
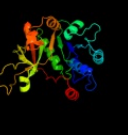
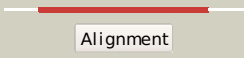

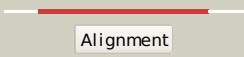

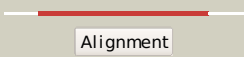

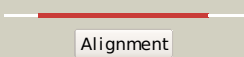

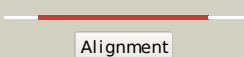

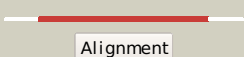

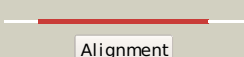











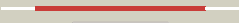
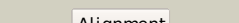
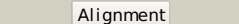
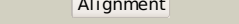
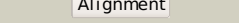
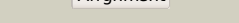


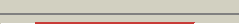



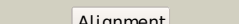
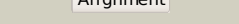
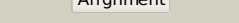
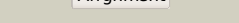
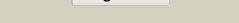
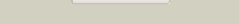






#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3oamD_	 Alignment		100.0	67	PDB header: transferase Chain: D: PDB Molecule: 3-deoxy-manno-octulosonate cytidyltransferase; PDBTitle: crystal structure of cytidyltransferase from vibrio cholerae
2	d1vica_	 Alignment		100.0	64	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: Cytidyltransferase
3	c3polA_	 Alignment		100.0	46	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.
4	d1vh1a_	 Alignment		100.0	97	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: Cytidyltransferase
5	c3tqdA_	 Alignment		100.0	50	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
6	d1h7ea_	 Alignment		100.0	45	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: Cytidyltransferase
7	c2y6pC_	 Alignment		100.0	38	PDB header: transferase Chain: C: PDB Molecule: 3-deoxy-manno-octulosonate cytidyltransferase; PDBTitle: evidence for a two-metal-ion-mechanism in the2 kdsb cytidyltransferase kdsb
8	d1g97a2	 Alignment		100.0	17	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: UDP-glucose pyrophosphorylase
9	d1fxoa_	 Alignment		100.0	20	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: glucose-1-phosphate thymidyltransferase
10	d1h5ra_	 Alignment		100.0	19	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: glucose-1-phosphate thymidyltransferase
11	d2oi6a2	 Alignment		100.0	19	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: UDP-glucose pyrophosphorylase

12	dliina_	Alignment		100.0	18	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: glucose-1-phosphate thymidyltransferase
13	dlvh3a_	Alignment		100.0	59	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: Cytidyltransferase
14	c3hl3A_	Alignment		100.0	20	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.
15	c3pnnA_	Alignment		100.0	12	PDB header: transferase Chain: A: PDB Molecule: conserved domain protein; PDBTitle: the crystal structure of a glycosyltransferase from porphyromonas2 gingivalis w83
16	dlvwva_	Alignment		100.0	18	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: glucose-1-phosphate thymidyltransferase
17	dleyra_	Alignment		100.0	19	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: Cytidyltransferase
18	dlmc3a_	Alignment		100.0	18	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: glucose-1-phosphate thymidyltransferase
19	c2pa4B_	Alignment		100.0	16	PDB header: transferase Chain: B: PDB Molecule: utp-glucose-1-phosphate uridyltransferase; PDBTitle: crystal structure of udp-glucose pyrophosphorylase from corynebacteria2 glutamicum in complex with magnesium and udp-glucose
20	dlqwja_	Alignment		100.0	17	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: Cytidyltransferase
21	c3jukA_	Alignment	not modelled	100.0	15	PDB header: transferase Chain: A: PDB Molecule: udp-glucose pyrophosphorylase (galu); PDBTitle: the crystal structure of udp-glucose pyrophosphorylase complexed with2 udp-glucose
22	c2xwlB_	Alignment	not modelled	100.0	23	PDB header: transferase Chain: B: PDB Molecule: 2-c-methyl-d-erythritol 4-phosphate cytidyltransferase; PDBTitle: crystal structure of ispd from mycobacterium smegmatis in complex2 with ctp and mg
23	dltzfa_	Alignment	not modelled	100.0	16	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: Cytidyltransferase
24	dlvpaa_	Alignment	not modelled	100.0	18	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: Cytidyltransferase
25	dli52a_	Alignment	not modelled	100.0	11	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: Cytidyltransferase
26	c2ux8G_	Alignment	not modelled	100.0	14	PDB header: transferase Chain: G: PDB Molecule: glucose-1-phosphate uridyltransferase; PDBTitle: crystal structure of sphingomonas elodea atcc 31461 glucose-2 1-phosphate uridyltransferase in complex with glucose-3 1-phosphate.
27	c2e3dB_	Alignment	not modelled	100.0	13	PDB header: transferase Chain: B: PDB Molecule: utp--glucose-1-phosphate uridyltransferase; PDBTitle: crystal structure of e. coli glucose-1-phosphate2 uridyltransferase
28	d2cu2a2	Alignment	not modelled	100.0	17	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases

						Family: mannose-1-phosphate guanylyl transferase
29	c3f1cB_	Alignment	not modelled	100.0	16	PDB header: transferase Chain: B: PDB Molecule: putative 2-c-methyl-d-erythritol 4-phosphate PDBTitle: crystal structure of 2-c-methyl-d-erythritol 4-phosphate2 cytidylyltransferase from listeria monocytogenes
30	c1jylC_	Alignment	not modelled	100.0	17	PDB header: transferase Chain: C: PDB Molecule: ctp:phosphocholine cytidylyltransferase; PDBTitle: catalytic mechanism of ctp:phosphocholine2 cytidylyltransferase from streptococcus pneumoniae (liicc)
31	dljyka_	Alignment	not modelled	99.9	16	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: Cytidylyltransferase
32	c1hm8A_	Alignment	not modelled	99.9	17	PDB header: transferase Chain: A: PDB Molecule: udp-n-acetylglucosamine-1-phosphate uridylyltransferase; PDBTitle: crystal structure of s.pneumoniae n-acetylglucosamine-1-phosphate2 uridylyltransferase, glmu, bound to acetyl coenzyme a
33	c1yp3C_	Alignment	not modelled	99.9	15	PDB header: transferase Chain: C: PDB Molecule: glucose-1-phosphate adenlylyltransferase small PDBTitle: crystal structure of potato tuber adp-glucose2 pyrophosphorylase in complex with atp
34	c2cu2A_	Alignment	not modelled	99.9	21	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
35	c3d98A_	Alignment	not modelled	99.9	15	PDB header: transferase Chain: A: PDB Molecule: bifunctional protein glmu; PDBTitle: crystal structure of glmu from mycobacterium tuberculosis, ligand-free2 form
36	dlp2a2	Alignment	not modelled	99.9	12	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: glucose-1-phosphate thymidylyltransferase
37	c2x5sB_	Alignment	not modelled	99.9	16	PDB header: transferase Chain: B: PDB Molecule: mannose-1-phosphate guanylyltransferase; PDBTitle: crystal structure of t. maritima gdp-mannose2 pyrophosphorylase in apo state.
38	c2qkxA_	Alignment	not modelled	99.9	15	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
39	c2px7A_	Alignment	not modelled	99.9	17	PDB header: transferase Chain: A: PDB Molecule: 2-c-methyl-d-erythritol 4-phosphate PDBTitle: crystal structure of 2-c-methyl-d-erythritol 4-phosphate2 cytidylyltransferase from thermus thermophilus hb8
40	dlw55a1	Alignment	not modelled	99.9	13	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: Cytidylyltransferase
41	c2wawA_	Alignment	not modelled	99.9	16	PDB header: unknown function Chain: A: PDB Molecule: moba relate protein; PDBTitle: crystal structure of mycobacterium tuberculosis rv0371c2 homolog from mycobacterium sp. strain jc1
42	c1w57A_	Alignment	not modelled	99.9	13	PDB header: transferase Chain: A: PDB Molecule: ispd/ispf bifunctional enzyme; PDBTitle: structure of the bifunctional ispdf from campylobacter2 jejuni containing zn
43	c2we9A_	Alignment	not modelled	99.9	17	PDB header: unknown function Chain: A: PDB Molecule: moba-related protein; PDBTitle: crystal structure of rv0371c from mycobacterium2 tuberculosis h37rv
44	c3brkX_	Alignment	not modelled	99.9	16	PDB header: transferase Chain: X: PDB Molecule: glucose-1-phosphate adenlylyltransferase; PDBTitle: crystal structure of adp-glucose pyrophosphorylase from2 agrobacterium tumefaciens
45	c3okrA_	Alignment	not modelled	99.9	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)
46	dlvgwa_	Alignment	not modelled	99.9	18	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: Cytidylyltransferase
47	c2v0hA_	Alignment	not modelled	99.9	18	PDB header: transferase Chain: A: PDB Molecule: bifunctional protein glmu; PDBTitle: characterization of substrate binding and catalysis of the2 potential antibacterial target n-acetylglucosamine-1-3 phosphate uridylyltransferase (glmu)
48	c2oi6A_	Alignment	not modelled	99.9	19	PDB header: transferase Chain: A: PDB Molecule: bifunctional protein glmu; PDBTitle: e. coli glmu- complex with udp-glcnac, coa and glcn-1-po4
49	c3ngwA_	Alignment	not modelled	99.9	17	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
50	dlw77a1	Alignment	not modelled	99.9	15	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: Cytidylyltransferase
51	d2dpwa1	Alignment	not modelled	99.9	21	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: TTHA0179-like

52	c1fwyA	 Alignment	not modelled	99.9	20	PDB header: transferase Chain: A: PDB Molecule: udp-n-acetylglucosamine pyrophosphorylase; PDBTitle: crystal structure of n-acetylglucosamine 1-phosphate2 uridylyltransferase bound to udp-glcnac
53	d1e5ka	 Alignment	not modelled	99.9	19	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-di-phospho-sugar transferases Family: Molybdenum cofactor biosynthesis protein MobA
54	c3okrC	 Alignment	not modelled	99.9	17	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 cytidylyltransferase (ispd)
55	c2vshB	 Alignment	not modelled	99.9	14	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
56	c3rsbB	 Alignment	not modelled	99.9	16	PDB header: transferase Chain: B: PDB Molecule: adenosyl cobi nami de-phosphate guanylyltransferase; PDBTitle: structure of the archaeal gtp:adocbi-p guanylyltransferase (coby) from2 methanocaldococcus jannaschii
57	c2ggqA	 Alignment	not modelled	99.9	18	PDB header: transferase Chain: A: PDB Molecule: 401aa long hypothetical glucose-1-phosphate PDBTitle: complex of hypothetical glucose-1-phosphate thymidylyltransferase from2 sulfolobus tokodaii
58	c2qh5B	 Alignment	not modelled	99.9	12	PDB header: isomerase Chain: B: PDB Molecule: mannose-6-phosphate isomerase; PDBTitle: crystal structure of mannose-6-phosphate isomerase from helicobacter2 pylori
59	c2xmhB	 Alignment	not modelled	99.8	14	PDB header: transferase Chain: B: PDB Molecule: ctp-inositol-1-phosphate cytidylyltransferase; PDBTitle: the x-ray structure of ctp:inositol-1-phosphate2 cytidylyltransferase from archaeoglobus fulgidus
60	c2e8bA	 Alignment	not modelled	99.6	21	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
61	c3d5nB	 Alignment	not modelled	99.3	17	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: q97w15_sulso; PDBTitle: crystal structure of the q97w15 sulso protein from2 sulfolobus solfataricus. nesg target ssr125.
62	d1vm8a	 Alignment	not modelled	98.3	17	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-di-phospho-sugar transferases Family: UDP-glucose pyrophosphorylase
63	c3oc9A	 Alignment	not modelled	98.2	15	PDB header: transferase Chain: A: PDB Molecule: udp-n-acetylglucosamine pyrophosphorylase; PDBTitle: crystal structure of putative udp-n-acetylglucosamine2 pyrophosphorylase from entamoeba histolytica
64	c2yqsA	 Alignment	not modelled	98.2	14	PDB header: transferase Chain: A: PDB Molecule: udp-n-acetylglucosamine pyrophosphorylase; PDBTitle: crystal structure of uridine-diphospho-n-acetylglucosamine2 pyrophosphorylase from candida albicans, in the product-binding form
65	d1jv1a	 Alignment	not modelled	98.2	16	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-di-phospho-sugar transferases Family: UDP-glucose pyrophosphorylase
66	d2icya2	 Alignment	not modelled	98.1	12	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-di-phospho-sugar transferases Family: UDP-glucose pyrophosphorylase
67	c2i5kB	 Alignment	not modelled	98.1	10	PDB header: transferase Chain: B: PDB Molecule: utp--glucose-1-phosphate uridylyltransferase; PDBTitle: crystal structure of ugp1p
68	c3cgxA	 Alignment	not modelled	98.0	16	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
69	c3ogzA	 Alignment	not modelled	97.9	17	PDB header: transferase Chain: A: PDB Molecule: udp-sugar pyrophosphorylase; PDBTitle: protein structure of usp from l. major in apo-form
70	c2q4jB	 Alignment	not modelled	97.8	11	PDB header: transferase Chain: B: PDB Molecule: probable utp-glucose-1-phosphate uridylyltransferase 2; PDBTitle: ensemble refinement of the protein crystal structure of gene product2 from arabidopsis thaliana at3g03250, a putative udp-glucose3 pyrophosphorylase
71	d2i5ea1	 Alignment	not modelled	97.7	16	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-di-phospho-sugar transferases Family: MM2497-like
72	c2ffuA	 Alignment	not modelled	97.2	12	PDB header: transferase Chain: A: PDB Molecule: polypeptide n-acetyl galactosaminyltransferase 2; PDBTitle: crystal structure of human ppgalnact-2 complexed with udp2 and ea2
73	c3gueB	 Alignment	not modelled	97.2	9	PDB header: transferase Chain: B: PDB Molecule: utp-glucose-1-phosphate uridylyltransferase 2; PDBTitle: crystal structure of udp-glucose phosphorylase from trypanosoma2 brucei, (tb10.389.0330)
		 Alignment				PDB header: transferase Chain: A: PDB Molecule: polypeptide n-

74	c1xhbA	Alignment	not modelled	96.9	11	acetylgalactosaminyltransferase 1; PDBTitle: the crystal structure of udp-galnac: polypeptide alpha-n-2 acetylgalactosaminyltransferase-t1
75	c2oefA	Alignment	not modelled	96.5	10	PDB header: transferase Chain: A: PDB Molecule: utp-glucose-1-phosphate uridylyltransferase 2, PDBTitle: open and closed structures of the udp-glucose2 pyrophosphorylase from leishmania major
76	c3f1yC	Alignment	not modelled	96.0	12	PDB header: transferase Chain: C: PDB Molecule: mannosyl-3-phosphoglycerate synthase; PDBTitle: mannosyl-3-phosphoglycerate synthase from rubrobacter xylanophilus
77	c3bcvA	Alignment	not modelled	94.7	11	PDB header: transferase Chain: A: PDB Molecule: putative glycosyltransferase protein; PDBTitle: crystal structure of a putative glycosyltransferase from bacteroides2 fragilis
78	c3ckvA	Alignment	not modelled	93.9	16	PDB header: unknown function Chain: A: PDB Molecule: putative uncharacterized protein; PDBTitle: crystal structure of a mycobacterial protein
79	c2qgiA	Alignment	not modelled	93.0	8	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
80	d1xhba2	Alignment	not modelled	89.2	11	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: Polypeptide N-acetylgalactosaminyltransferase 1, N-terminal domain
81	d1omza	Alignment	not modelled	87.4	12	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: Exostosin
82	c2d7iA	Alignment	not modelled	85.2	12	PDB header: transferase Chain: A: PDB Molecule: polypeptide n-acetylgalactosaminyltransferase 10; PDBTitle: crsytal structure of pp-galnac-t10 with udp, galnac and mn2+
83	d2bo4a1	Alignment	not modelled	82.3	11	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: MGS-like
84	c1omxB	Alignment	not modelled	75.7	13	PDB header: transferase Chain: B: PDB Molecule: alpha-1,4-n-acetylhexosaminyltransferase extl2; PDBTitle: crystal structure of mouse alpha-1,4-n-2 acetylhexosaminyltransferase (extl2)
85	c2z86D	Alignment	not modelled	72.0	13	PDB header: transferase Chain: D: PDB Molecule: chondroitin synthase; PDBTitle: crystal structure of chondroitin polymerase from2 escherichia coli strain k4 (k4cp) complexed with udp-glucua3 and udp
86	d1jq5a	Alignment	not modelled	50.0	10	Fold: Dehydroquinase synthase-like Superfamily: Dehydroquinase synthase-like Family: Iron-containing alcohol dehydrogenase
87	c2gpwC	Alignment	not modelled	44.3	14	PDB header: ligase Chain: C: PDB Molecule: biotin carboxylase; PDBTitle: crystal structure of the biotin carboxylase subunit, f363a2 mutant, of acetyl-coa carboxylase from escherichia coli.
88	c2dclB	Alignment	not modelled	41.5	25	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: hypothetical upf0166 protein ph1503; PDBTitle: structure of ph1503 protein from pyrococcus horikoshii ot3
89	d1y9wa1	Alignment	not modelled	36.2	17	Fold: Acyl-CoA N-acyltransferases (Nat) Superfamily: Acyl-CoA N-acyltransferases (Nat) Family: N-acetyl transferase, NAT
90	d1o51a	Alignment	not modelled	35.3	29	Fold: Ferredoxin-like Superfamily: GlnB-like Family: DUF190/COG1993
91	d1j2jb	Alignment	not modelled	34.1	29	Fold: Spectrin repeat-like Superfamily: GAT-like domain Family: GAT domain
92	c2xecD	Alignment	not modelled	32.8	20	PDB header: isomerase Chain: D: PDB Molecule: putative maleate isomerase; PDBTitle: nocardia farcinica maleate cis-trans isomerase bound to2 tris
93	d2g3aa1	Alignment	not modelled	25.0	21	Fold: Acyl-CoA N-acyltransferases (Nat) Superfamily: Acyl-CoA N-acyltransferases (Nat) Family: N-acetyl transferase, NAT
94	d1v7za	Alignment	not modelled	24.4	17	Fold: Creatininase Superfamily: Creatininase Family: Creatininase
95	d1nh9a	Alignment	not modelled	21.7	23	Fold: IF3-like Superfamily: AlbA-like Family: DNA-binding protein AlbA
96	d1qg8a	Alignment	not modelled	20.5	9	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: Spore coat polysaccharide biosynthesis protein SpsA
97	d1ccwa	Alignment	not modelled	19.5	11	Fold: Flavodoxin-like Superfamily: Cobalamin (vitamin B12)-binding domain Family: Cobalamin (vitamin B12)-binding domain
98	c3lubE	Alignment	not modelled	19.5	9	PDB header: hydrolase Chain: E: PDB Molecule: putative creatinine amidohydrolase; PDBTitle: crystal structure of putative creatinine amidohydrolase2 (yp_211512.1) from bacteroides fragilis nctc 9343 at 2.11 a3 resolution
						PDB header: oxidoreductase Chain: A: PDB Molecule: alvcerol dehydrogenase;

99	c3ce9A_	Alignment	not modelled	19.0	9	PDBTitle: crystal structure of glycerol dehydrogenase (np_348253.1) from2 clostridium acetobutylicum at 2.37 a resolution
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