Phyre^2

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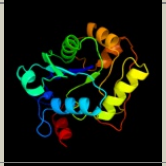
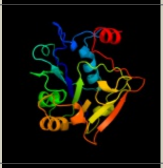
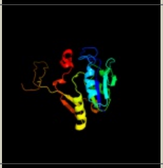
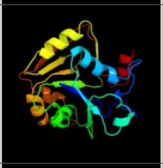
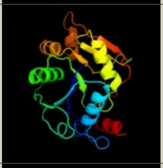
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1e5ka_	Alignment		100.0	100	**Fold:**Nucleotide-diphospho-sugar transferases **Superfamily:**Nucleotide-diphospho-sugar transferases **Family:**Molybdenum cofactor biosynthesis protein MobA
2	c2wawA_	Alignment		100.0	22	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**moba relate protein; **PDBTitle:** crystal structure of mycobacterium tuberculosis rv0371c2 homolog from mycobacterium sp. strain jc1
3	c2we9A_	Alignment		100.0	17	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**moba-related protein; **PDBTitle:** crystal structure of rv0371c from mycobacterium2 tuberculosis h37rv
4	c2e8bA_	Alignment		100.0	22	**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
5	c3ngwA_	Alignment		100.0	21	**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
6	d1w55a1	Alignment		100.0	15	**Fold:**Nucleotide-diphospho-sugar transferases **Superfamily:**Nucleotide-diphospho-sugar transferases **Family:**Cytidylytransferase
7	c2xwlB_	Alignment		100.0	16	**PDB header:**transferase **Chain:** B: **PDB Molecule:**2-c-methyl-d-erythritol 4-phosphate cytidylyltransferase; **PDBTitle:** crystal structure of ispd from mycobacterium smegmatis in complex2 with ctp and mg
8	d1i52a_	Alignment		100.0	18	**Fold:**Nucleotide-diphospho-sugar transferases **Superfamily:**Nucleotide-diphospho-sugar transferases **Family:**Cytidylytransferase
9	d2oi6a2	Alignment		100.0	26	**Fold:**Nucleotide-diphospho-sugar transferases **Superfamily:**Nucleotide-diphospho-sugar transferases **Family:**UDP-glucose pyrophosphorylase
10	c3rsbB_	Alignment		100.0	15	**PDB header:**transferase **Chain:** B: **PDB Molecule:**adenosylcobinamide-phosphate guanylyltransferase; **PDBTitle:** structure of the archaeal gtp:adocbi-p guanylyltransferase (coby) from2 methanocaldococcus jannaschii
11	d1vpaa_	Alignment		100.0	15	**Fold:**Nucleotide-diphospho-sugar transferases **Superfamily:**Nucleotide-diphospho-sugar transferases **Family:**Cytidylytransferase

12	c1w57A_	Alignment		99.9	16	**PDB header:**transferase **Chain:** A: **PDB Molecule:**ispd/ispf bifunctional enzyme; **PDBTitle:** structure of the bifunctional ispdf from campylobacter2 jejuni containing zn
13	d1eyra_	Alignment		99.9	15	**Fold:**Nucleotide-diphospho-sugar transferases **Superfamily:**Nucleotide-diphospho-sugar transferases **Family:**Cytidylytransferase
14	c3hl3A_	Alignment		99.9	15	**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.
15	d1iina_	Alignment		99.9	18	**Fold:**Nucleotide-diphospho-sugar transferases **Superfamily:**Nucleotide-diphospho-sugar transferases **Family:**glucose-1-phosphate thymidylyltransferase
16	c3oamD_	Alignment		99.9	23	**PDB header:**transferase **Chain:** D: **PDB Molecule:**3-deoxy-manno-octulosonate cytidylyltransferase; **PDBTitle:** crystal structure of cytidylyltransferase from vibrio cholerae
17	d1qwja_	Alignment		99.9	16	**Fold:**Nucleotide-diphospho-sugar transferases **Superfamily:**Nucleotide-diphospho-sugar transferases **Family:**Cytidylytransferase
18	d1mc3a_	Alignment		99.9	18	**Fold:**Nucleotide-diphospho-sugar transferases **Superfamily:**Nucleotide-diphospho-sugar transferases **Family:**glucose-1-phosphate thymidylyltransferase
19	d1vica_	Alignment		99.9	23	**Fold:**Nucleotide-diphospho-sugar transferases **Superfamily:**Nucleotide-diphospho-sugar transferases **Family:**Cytidylytransferase
20	c2px7A_	Alignment		99.9	14	**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
21	d1w77a1	Alignment	not modelled	99.9	13	**Fold:**Nucleotide-diphospho-sugar transferases **Superfamily:**Nucleotide-diphospho-sugar transferases **Family:**Cytidylytransferase
22	d1h5ra_	Alignment	not modelled	99.9	19	**Fold:**Nucleotide-diphospho-sugar transferases **Superfamily:**Nucleotide-diphospho-sugar transferases **Family:**glucose-1-phosphate thymidylyltransferase
23	c3f1cB_	Alignment	not modelled	99.9	13	**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
24	c2y6pC_	Alignment	not modelled	99.9	18	**PDB header:**transferase **Chain:** C: **PDB Molecule:**3-deoxy-manno-octulosonate cytidylyltransferase; **PDBTitle:** evidence for a two-metal-ion-mechanism in the2 kdo-cytidylyltransferase kdsb
25	d1fxoa_	Alignment	not modelled	99.9	19	**Fold:**Nucleotide-diphospho-sugar transferases **Superfamily:**Nucleotide-diphospho-sugar transferases **Family:**glucose-1-phosphate thymidylyltransferase
26	d2dpwa1	Alignment	not modelled	99.9	20	**Fold:**Nucleotide-diphospho-sugar transferases **Superfamily:**Nucleotide-diphospho-sugar transferases **Family:**TTHA0179-like
27	c1jylC_	Alignment	not modelled	99.9	12	**PDB header:**transferase **Chain:** C: **PDB Molecule:**ctp:phosphocholine cytidylyltransferase; **PDBTitle:** catalytic mechanism of ctp:phosphocholine2 cytidylyltransferase from streptococcus pneumoniae (licc)
28	d1jyka_	Alignment	not modelled	99.9	11	**Fold:**Nucleotide-diphospho-sugar transferases **Superfamily:**Nucleotide-diphospho-sugar transferases **Family:**Cytidylytransferase

29	c2pa4B_	Alignment	not modelled	99.9	18	**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
30	c3polA_	Alignment	not modelled	99.9	18	**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.
31	c3d5nB_	Alignment	not modelled	99.9	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.
32	d1h7ea_	Alignment	not modelled	99.9	18	**Fold:**Nucleotide-diphospho-sugar transferases **Superfamily:**Nucleotide-diphospho-sugar transferases **Family:**Cytidylyltransferase
33	c3pnnA_	Alignment	not modelled	99.9	16	**PDB header:**transferase **Chain:** A: **PDB Molecule:**conserved domain protein; **PDBTitle:** the crystal structure of a glycosyltransferase from porphyromonas2 gingivalis w83
34	c2ux8G_	Alignment	not modelled	99.9	11	**PDB header:**transferase **Chain:** G: **PDB Molecule:**glucose-1-phosphate uridylyltransferase; **PDBTitle:** crystal structure of sphingomonas elodea atcc 31461 glucose-2 1-phosphate uridylyltransferase in complex with glucose-3 1-phosphate.
35	d1lvwa_	Alignment	not modelled	99.9	17	**Fold:**Nucleotide-diphospho-sugar transferases **Superfamily:**Nucleotide-diphospho-sugar transferases **Family:**glucose-1-phosphate thymidylyltransferase
36	c3jukA_	Alignment	not modelled	99.9	16	**PDB header:**transferase **Chain:** A: **PDB Molecule:**udp-glucose pyrophosphorylase (galu); **PDBTitle:** the crystal structure of udp-glucose pyrophosphorylase complexed with2 udp-glucose
37	d1g97a2	Alignment	not modelled	99.9	18	**Fold:**Nucleotide-diphospho-sugar transferases **Superfamily:**Nucleotide-diphospho-sugar transferases **Family:**UDP-glucose pyrophosphorylase
38	c2e3dB_	Alignment	not modelled	99.9	16	**PDB header:**transferase **Chain:** B: **PDB Molecule:**utp--glucose-1-phosphate uridylyltransferase; **PDBTitle:** crystal structure of e. coli glucose-1-phosphate2 uridylyltransferase
39	c3tqdA_	Alignment	not modelled	99.9	23	**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
40	d1vh1a_	Alignment	not modelled	99.9	19	**Fold:**Nucleotide-diphospho-sugar transferases **Superfamily:**Nucleotide-diphospho-sugar transferases **Family:**Cytidylyltransferase
41	d1tzfa_	Alignment	not modelled	99.9	14	**Fold:**Nucleotide-diphospho-sugar transferases **Superfamily:**Nucleotide-diphospho-sugar transferases **Family:**Cytidylyltransferase
42	d1vgwa_	Alignment	not modelled	99.9	13	**Fold:**Nucleotide-diphospho-sugar transferases **Superfamily:**Nucleotide-diphospho-sugar transferases **Family:**Cytidylyltransferase
43	c3okrA_	Alignment	not modelled	99.8	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)
44	d2cu2a2	Alignment	not modelled	99.8	18	**Fold:**Nucleotide-diphospho-sugar transferases **Superfamily:**Nucleotide-diphospho-sugar transferases **Family:**mannose-1-phosphate guanylyl transferase
45	c2vshB_	Alignment	not modelled	99.8	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
46	c2oi6A_	Alignment	not modelled	99.8	25	**PDB header:**transferase **Chain:** A: **PDB Molecule:**bifunctional protein glmu; **PDBTitle:** e. coli glmu- complex with udp-glcnac, coa and glcn-1-po4
47	c1fwyA_	Alignment	not modelled	99.8	26	**PDB header:**transferase **Chain:** A: **PDB Molecule:**udp-n-acetylglucosamine pyrophosphorylase; **PDBTitle:** crystal structure of n-acetylglucosamine 1-phosphate2 uridyltransferase bound to udp-glcnac
48	c2v0hA_	Alignment	not modelled	99.8	19	**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 uridyltransferase (glmu)
49	c3brkX_	Alignment	not modelled	99.8	16	**PDB header:**transferase **Chain:** X: **PDB Molecule:**glucose-1-phosphate adenylyltransferase; **PDBTitle:** crystal structure of adp-glucose pyrophosphorylase from2 agrobacterium tumefaciens
50	c2qkxA_	Alignment	not modelled	99.8	20	**PDB header:**transferase **Chain:** A: **PDB Molecule:**bifunctional protein glmu; **PDBTitle:** n-acetyl glucosamine 1-phosphate uridyltransferase from mycobacterium2 tuberculosis complex with n-acetyl glucosamine 1-phosphate
51	c3d98A_	Alignment	not modelled	99.8	20	**PDB header:**transferase **Chain:** A: **PDB Molecule:**bifunctional protein glmu; **PDBTitle:** crystal structure of glmu from mycobacterium tuberculosis, ligand-free2 form
						PDB header:transferase

52	c2cu2A_	Alignment	not modelled	99.8	18	**Chain:** A: **PDB Molecule:**putative mannose-1-phosphate guanylyl transferase; **PDBTitle:** crystal structure of mannose-1-phosphate geranyltransferase from2 thermus thermophilus hb8
53	c3okrC_	Alignment	not modelled	99.8	16	**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)
54	c1hm8A_	Alignment	not modelled	99.8	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**udp-n-acetylglucosamine-1-phosphate uridyltransferase; **PDBTitle:** crystal structure of s.pneumoniae n-acetylglucosamine-1-phosphate2 uridyltransferase, glmu, bound to acetyl coenzyme a
55	c2ggqA_	Alignment	not modelled	99.8	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**401aa long hypothetical glucose-1-phosphate **PDBTitle:** complex of hypothetical glucose-1-phosphate thymidylyltransferase from2 sulfolobus tokodaii
56	d1yp2a2	Alignment	not modelled	99.7	13	**Fold:**Nucleotide-diphospho-sugar transferases **Superfamily:**Nucleotide-diphospho-sugar transferases **Family:**glucose-1-phosphate thymidylyltransferase
57	c2x5sB_	Alignment	not modelled	99.7	12	**PDB header:**transferase **Chain:** B: **PDB Molecule:**mannose-1-phosphate guanylyltransferase; **PDBTitle:** crystal structure of t. maritima gdp-mannose2 pyrophosphorylase in apo state.
58	c2xmhB_	Alignment	not modelled	99.7	15	**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
59	c1yp3C_	Alignment	not modelled	99.7	16	**PDB header:**transferase **Chain:** C: **PDB Molecule:**glucose-1-phosphate adenylyltransferase small **PDBTitle:** crystal structure of potato tuber adp-glucose2 pyrophosphorylase in complex with atp
60	c2qh5B_	Alignment	not modelled	99.4	11	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**mannose-6-phosphate isomerase; **PDBTitle:** crystal structure of mannose-6-phosphate isomerase from helicobacter2 pylori
61	d1vh3a_	Alignment	not modelled	99.1	19	**Fold:**Nucleotide-diphospho-sugar transferases **Superfamily:**Nucleotide-diphospho-sugar transferases **Family:**Cytidylytransferase
62	c3cgxA_	Alignment	not modelled	98.9	9	**PDB header:**transferase **Chain:** A: **PDB Molecule:**putative nucleotide-diphospho-sugar transferase; **PDBTitle:** crystal structure of putative nucleotide-diphospho-sugar transferase2 (yp_389115.1) from desulfovibrio desulfuricans g20 at 1.90 a3 resolution
63	d2i5ea1	Alignment	not modelled	98.6	14	**Fold:**Nucleotide-diphospho-sugar transferases **Superfamily:**Nucleotide-diphospho-sugar transferases **Family:**MM2497-like
64	c2q4jB_	Alignment	not modelled	98.4	15	**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
65	c3oc9A_	Alignment	not modelled	98.4	27	**PDB header:**transferase **Chain:** A: **PDB Molecule:**udp-n-acetylglucosamine pyrophosphorylase; **PDBTitle:** crystal structure of putative udp-n-acetylglucosamine2 pyrophosphorylase from entamoeba histolytica
66	d2icya2	Alignment	not modelled	98.4	19	**Fold:**Nucleotide-diphospho-sugar transferases **Superfamily:**Nucleotide-diphospho-sugar transferases **Family:**UDP-glucose pyrophosphorylase
67	d1jv1a_	Alignment	not modelled	98.4	18	**Fold:**Nucleotide-diphospho-sugar transferases **Superfamily:**Nucleotide-diphospho-sugar transferases **Family:**UDP-glucose pyrophosphorylase
68	c3gueB_	Alignment	not modelled	98.2	29	**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)
69	c2i5kB_	Alignment	not modelled	98.2	17	**PDB header:**transferase **Chain:** B: **PDB Molecule:**utp--glucose-1-phosphate uridylyltransferase; **PDBTitle:** crystal structure of ugp1p
70	c2oefA_	Alignment	not modelled	98.1	27	**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
71	d1vm8a_	Alignment	not modelled	98.1	29	**Fold:**Nucleotide-diphospho-sugar transferases **Superfamily:**Nucleotide-diphospho-sugar transferases **Family:**UDP-glucose pyrophosphorylase
72	c2yqsA_	Alignment	not modelled	98.1	26	**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
73	c3ogzA_	Alignment	not modelled	97.8	20	**PDB header:**transferase **Chain:** A: **PDB Molecule:**udp-sugar pyrophosphorylase; **PDBTitle:** protein structure of usp from l. major in apo-form
74	c3ckvA_	Alignment	not modelled	88.0	16	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**putative uncharacterized protein;

						PDBTitle: crystal structure of a mycobacterial protein
75	c3f1yC_	Alignment	not modelled	84.9	19	**PDB header:**transferase **Chain:** C: **PDB Molecule:**mannosyl-3-phosphoglycerate synthase; **PDBTitle:** mannosyl-3-phosphoglycerate synthase from rubrobacter xylanophilus
76	d1omza_	Alignment	not modelled	82.1	16	**Fold:**Nucleotide-diphospho-sugar transferases **Superfamily:**Nucleotide-diphospho-sugar transferases **Family:**Exostosin
77	c2ffuA_	Alignment	not modelled	80.3	7	**PDB header:**transferase **Chain:** A: **PDB Molecule:**polypeptide n-acetylgalactosaminyltransferase 2; **PDBTitle:** crystal structure of human ppgalnact-2 complexed with udp2 and ea2
78	d1xhba2	Alignment	not modelled	76.3	8	**Fold:**Nucleotide-diphospho-sugar transferases **Superfamily:**Nucleotide-diphospho-sugar transferases **Family:**Polypeptide N-acetylgalactosaminyltransferase 1, N-terminal domain
79	c1xhbA_	Alignment	not modelled	76.1	10	**PDB header:**transferase **Chain:** A: **PDB Molecule:**polypeptide n-acetylgalactosaminyltransferase 1; **PDBTitle:** the crystal structure of udp-galnac: polypeptide alpha-n-2 acetylgalactosaminyltransferase-t1
80	c1omxB_	Alignment	not modelled	72.1	15	**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)
81	c2z86D_	Alignment	not modelled	63.7	9	**PDB header:**transferase **Chain:** D: **PDB Molecule:**chondroitin synthase; **PDBTitle:** crystal structure of chondroitin polymerase from2 escherichia coli strain k4 (k4cp) complexed with udp-glcua3 and udp
82	c2d7iA_	Alignment	not modelled	39.3	10	**PDB header:**transferase **Chain:** A: **PDB Molecule:**polypeptide n-acetylgalactosaminyltransferase 10; **PDBTitle:** crsytal structure of pp-galnac-t10 with udp, galnac and mn2+
83	c2dclB_	Alignment	not modelled	37.6	11	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**hypothetical upf0166 protein ph1503; **PDBTitle:** structure of ph1503 protein from pyrococcus horikoshii ot3
84	d1o51a_	Alignment	not modelled	25.6	18	**Fold:**Ferredoxin-like **Superfamily:**GlnB-like **Family:**DUF190/COG1993
85	c2gpwC_	Alignment	not modelled	22.5	10	**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.
86	d1kyqa1	Alignment	not modelled	20.3	14	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Siroheme synthase N-terminal domain-like
87	c3bcvA_	Alignment	not modelled	18.2	16	**PDB header:**transferase **Chain:** A: **PDB Molecule:**putative glycosyltransferase protein; **PDBTitle:** crystal structure of a putative glycosyltransferase from bacteroides2 fragilis
88	d1mlda1	Alignment	not modelled	17.7	15	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**LDH N-terminal domain-like
89	d1zs9a1	Alignment	not modelled	17.2	17	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**Enolase-phosphatase E1
90	d1wj6a_	Alignment	not modelled	13.2	17	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**CAD & PB1 domains **Family:**PB1 domain
91	d1ajza_	Alignment	not modelled	12.0	13	**Fold:**TIM beta/alpha-barrel **Superfamily:**Dihydropteroate synthetase-like **Family:**Dihydropteroate synthetase
92	d1nh9a_	Alignment	not modelled	11.8	24	**Fold:**IF3-like **Superfamily:**AlbA-like **Family:**DNA-binding protein AlbA
93	c2ki0A_	Alignment	not modelled	9.5	50	**PDB header:**de novo protein **Chain:** A: **PDB Molecule:**ds119; **PDBTitle:** nmr structure of a de novo designed beta alpha beta
94	c3dfzB_	Alignment	not modelled	8.4	9	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**precorrin-2 dehydrogenase; **PDBTitle:** sirc, precorrin-2 dehydrogenase
95	d1ip9a_	Alignment	not modelled	7.8	3	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**CAD & PB1 domains **Family:**PB1 domain
96	c1kyqC_	Alignment	not modelled	7.5	14	**PDB header:**oxidoreductase, lyase **Chain:** C: **PDB Molecule:**siroheme biosynthesis protein met8; **PDBTitle:** met8p: a bifunctional nad-dependent dehydrogenase and2 ferrochelatase involved in siroheme synthesis.
97	c2qgiA_	Alignment	not modelled	6.7	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
98	d1o6za1	Alignment	not modelled	5.7	19	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**LDH N-terminal domain-like
99	d2od0a1	Alignment	not modelled	5.4	11	**Fold:**Secretion chaperone-like **Superfamily:**YgaC/TfoX-N like **Family:**TfoX N-terminal domain-like