Phyre2

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Description	P0AED0
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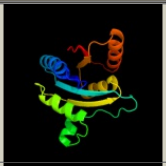
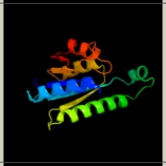
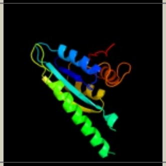
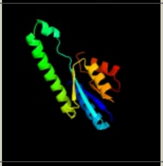
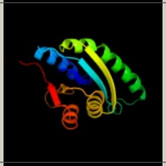
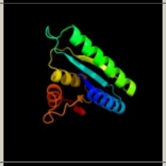
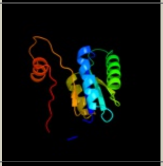
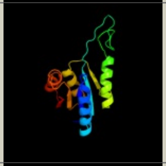
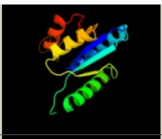
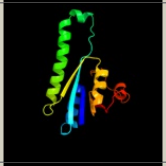
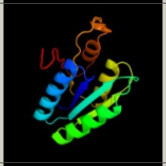
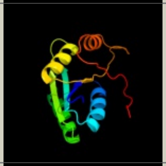
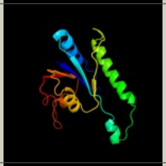
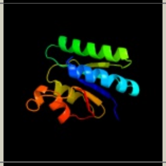
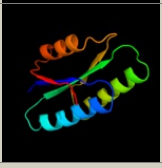
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1jmva_	Alignment		99.9	68	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Adenine nucleotide alpha hydrolases-like **Family:**Universal stress protein-like
2	c3hgmD_	Alignment		99.9	23	**PDB header:**signaling protein **Chain:** D: **PDB Molecule:**universal stress protein tead; **PDBTitle:** universal stress protein tead from the trap transporter2 teaabc of halomonas elongata
3	d1mjha_	Alignment		99.9	16	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Adenine nucleotide alpha hydrolases-like **Family:**Universal stress protein-like
4	d2z3va1	Alignment		99.9	24	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Adenine nucleotide alpha hydrolases-like **Family:**Universal stress protein-like
5	c3s3tD_	Alignment		99.9	18	**PDB header:**chaperone **Chain:** D: **PDB Molecule:**nucleotide-binding protein, universal stress protein uspa **PDBTitle:** universal stress protein uspa from lactobacillus plantarum
6	c2dumD_	Alignment		99.9	15	**PDB header:**structural genomics, unknown function **Chain:** D: **PDB Molecule:**hypothetical protein ph0823; **PDBTitle:** crystal structure of hypothetical protein, ph0823
7	c3dloC_	Alignment		99.9	18	**PDB header:**structural genomics, unknown function **Chain:** C: **PDB Molecule:**universal stress protein; **PDBTitle:** structure of universal stress protein from archaeoglobus fulgidus
8	d1tq8a_	Alignment		99.9	25	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Adenine nucleotide alpha hydrolases-like **Family:**Universal stress protein-like
9	c3fg9B_	Alignment		99.9	18	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**protein of universal stress protein uspa family; **PDBTitle:** the crystal structure of an universal stress protein uspa2 family protein from lactobacillus plantarum wcfs1
10	c2pfsA_	Alignment		99.9	27	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**universal stress protein; **PDBTitle:** crystal structure of universal stress protein from nitrosomonas2 europaea
11	d2gm3a1	Alignment		99.8	16	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Adenine nucleotide alpha hydrolases-like **Family:**Universal stress protein-like

12	c3fh0A_	Alignment		99.8	23	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**putative universal stress protein kpn_01444; **PDBTitle:** crystal structure of putative universal stress protein kpn_01444 -2 atpase
13	c3idfA_	Alignment		99.8	13	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**usp-like protein; **PDBTitle:** the crystal structure of a usp-like protein from wolinella2 succinogenes to 2.0a
14	c3loqA_	Alignment		99.8	17	**PDB header:**structure genomics, unknown function **Chain:** A: **PDB Molecule:**universal stress protein; **PDBTitle:** the crystal structure of a universal stress protein from2 archaeoglobus fulgidus dsm 4304
15	c3olqA_	Alignment		99.8	13	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**universal stress protein e; **PDBTitle:** the crystal structure of a universal stress protein e from proteus2 mirabilis hi4320
16	c3mt0A_	Alignment		99.7	14	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein pa1789; **PDBTitle:** crystal structure of a functionally unknown protein pa1789 from2 pseudomonas aeruginosa pao1
17	d1q77a_	Alignment		99.7	16	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Adenine nucleotide alpha hydrolases-like **Family:**Universal stress protein-like
18	c2jaxA_	Alignment		99.6	14	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**hypothetical protein tb31.7; **PDBTitle:** universal stress protein rv2623 from mycobaterium2 tuberculosis
19	c3ab8B_	Alignment		99.6	20	**PDB header:**unknown function **Chain:** B: **PDB Molecule:**putative uncharacterized protein ttha0350; **PDBTitle:** crystal structure of the hypothetical tandem-type universal stress2 protein ttha0350 complexed with atps.
20	c3a2kB_	Alignment		75.0	23	**PDB header:**ligase/rna **Chain:** B: **PDB Molecule:**trna(ile)-lysidine synthase; **PDBTitle:** crystal structure of tils complexed with trna
21	c1ni5A_	Alignment	not modelled	65.6	14	**PDB header:**cell cycle **Chain:** A: **PDB Molecule:**putative cell cycle protein mesj; **PDBTitle:** structure of the mesj pp-atpase from escherichia coli
22	c3mcuF_	Alignment	not modelled	65.6	16	**PDB header:**oxidoreductase **Chain:** F: **PDB Molecule:**dipicolinate synthase, b chain; **PDBTitle:** crystal structure of the dipicolinate synthase chain b from2 bacillus cereus. northeast structural genomics consortium3 target bcr215.
23	d3clsc1	Alignment	not modelled	51.5	16	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Adenine nucleotide alpha hydrolases-like **Family:**ETFP subunits
24	c3lqkA_	Alignment	not modelled	50.6	22	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**dipicolinate synthase subunit b; **PDBTitle:** crystal structure of dipicolinate synthase subunit b from bacillus2 halodurans c
25	d1ni5a1	Alignment	not modelled	49.9	14	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Adenine nucleotide alpha hydrolases-like **Family:**PP-loop ATPase
26	d1zuna1	Alignment	not modelled	49.2	18	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Adenine nucleotide alpha hydrolases-like **Family:**PAPS reductase-like
27	d1g5qa_	Alignment	not modelled	48.1	18	**Fold:**Homo-oligomeric flavin-containing Cys decarboxylases, HFCD **Superfamily:**Homo-oligomeric flavin-containing Cys decarboxylases, HFCD **Family:**Homo-oligomeric flavin-containing Cys decarboxylases, HFCD
28	d1efpb_	Alignment	not modelled	47.9	12	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Adenine nucleotide alpha hydrolases-like **Family:**ETFP subunits

29	c2e21A_	Alignment	not modelled	46.2	19	**PDB header:**ligase **Chain:** A: **PDB Molecule:**trna(ile)-lysidine synthase; **PDBTitle:** crystal structure of tils in a complex with amppnp from aquifex2 aeolicus.
30	d1o94c_	Alignment	not modelled	44.2	16	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Adenine nucleotide alpha hydrolases-like **Family:**ETFP subunits
31	d1p3y1_	Alignment	not modelled	42.3	14	**Fold:**Homo-oligomeric flavin-containing Cys decarboxylases, HFCD **Superfamily:**Homo-oligomeric flavin-containing Cys decarboxylases, HFCD **Family:**Homo-oligomeric flavin-containing Cys decarboxylases, HFCD
32	c1zunA_	Alignment	not modelled	41.8	18	**PDB header:**transferase **Chain:** A: **PDB Molecule:**sulfate adenylyltransferase subunit 2; **PDBTitle:** crystal structure of a gtp-regulated atp sulfurylase2 heterodimer from pseudomonas syringae
33	c2ejbA_	Alignment	not modelled	40.6	9	**PDB header:**lyase **Chain:** A: **PDB Molecule:**probable aromatic acid decarboxylase; **PDBTitle:** crystal structure of phenylacrylic acid decarboxylase from2 aquifex aeolicus
34	c3zquA_	Alignment	not modelled	39.5	9	**PDB header:**lyase **Chain:** A: **PDB Molecule:**probable aromatic acid decarboxylase; **PDBTitle:** structure of a probable aromatic acid decarboxylase
35	c1o94D_	Alignment	not modelled	39.0	27	**PDB header:**electron transport **Chain:** D: **PDB Molecule:**electron transfer flavoprotein alpha-subunit; **PDBTitle:** ternary complex between trimethylamine dehydrogenase and2 electron transferring flavoprotein
36	c3qjgD_	Alignment	not modelled	39.0	18	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**epidermin biosynthesis protein epid; **PDBTitle:** epidermin biosynthesis protein epid from staphylococcus aureus
37	d1sbza_	Alignment	not modelled	38.6	9	**Fold:**Homo-oligomeric flavin-containing Cys decarboxylases, HFCD **Superfamily:**Homo-oligomeric flavin-containing Cys decarboxylases, HFCD **Family:**Homo-oligomeric flavin-containing Cys decarboxylases, HFCD
38	d1gph11	Alignment	not modelled	37.8	17	**Fold:**PRTase-like **Superfamily:**PRTase-like **Family:**Phosphoribosyltransferases (PRTases)
39	d1efvb_	Alignment	not modelled	35.6	15	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Adenine nucleotide alpha hydrolases-like **Family:**ETFP subunits
40	d1mvla_	Alignment	not modelled	34.8	16	**Fold:**Homo-oligomeric flavin-containing Cys decarboxylases, HFCD **Superfamily:**Homo-oligomeric flavin-containing Cys decarboxylases, HFCD **Family:**Homo-oligomeric flavin-containing Cys decarboxylases, HFCD
41	c1mvlA_	Alignment	not modelled	34.8	16	**PDB header:**lyase **Chain:** A: **PDB Molecule:**ppc decarboxylase athal3a; **PDBTitle:** ppc decarboxylase mutant c175s
42	c1vl2C_	Alignment	not modelled	34.2	9	**PDB header:**ligase **Chain:** C: **PDB Molecule:**argininosuccinate synthase; **PDBTitle:** crystal structure of argininosuccinate synthase (tm1780) from2 thermotoga maritima at 1.65 a resolution
43	d2dbsa1	Alignment	not modelled	32.2	17	**Fold:**TTHC002-like **Superfamily:**TTHC002-like **Family:**TTHC002-like
44	d1wy5a1	Alignment	not modelled	31.6	15	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Adenine nucleotide alpha hydrolases-like **Family:**PP-loop ATPase
45	d1p5dx1	Alignment	not modelled	31.6	14	**Fold:**Phosphoglucomutase, first 3 domains **Superfamily:**Phosphoglucomutase, first 3 domains **Family:**Phosphoglucomutase, first 3 domains
46	c2pjuD_	Alignment	not modelled	29.9	9	**PDB header:**transcription **Chain:** D: **PDB Molecule:**propionate catabolism operon regulatory protein; **PDBTitle:** crystal structure of propionate catabolism operon2 regulatory protein prpr
47	d1vl2a1	Alignment	not modelled	28.8	9	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Adenine nucleotide alpha hydrolases-like **Family:**N-type ATP pyrophosphatases
48	d1np7a2	Alignment	not modelled	26.3	13	**Fold:**Cryptochrome/photolyase, N-terminal domain **Superfamily:**Cryptochrome/photolyase, N-terminal domain **Family:**Cryptochrome/photolyase, N-terminal domain
49	d2iela1	Alignment	not modelled	26.0	15	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Adenine nucleotide alpha hydrolases-like **Family:**Universal stress protein-like
50	d1vbka1	Alignment	not modelled	25.5	9	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Adenine nucleotide alpha hydrolases-like **Family:**ThiI-like
51	c2xrzA_	Alignment	not modelled	25.1	16	**PDB header:**lyase/dna **Chain:** C: **PDB Molecule:**deoxyribodipyrimidine photolyase; **PDBTitle:** x-ray structure of archaeal class ii cpd photolyase from2 methanosarcina mazei in complex with intact cpd-lesion
52	c2ywxA_	Alignment	not modelled	24.9	7	**PDB header:**lyase **Chain:** A: **PDB Molecule:**phosphoribosylaminoimidazole carboxylase catalytic subunit; **PDBTitle:** crystal structure of phosphoribosylaminoimidazole carboxylase2 catalytic subunit from methanocaldococcus jannaschii
						PDB header:isomerase

53	c3c04A_	Alignment	not modelled	24.5	14	**Chain:** A: **PDB Molecule:**phosphomannomutase/phosphoglucomutase; **PDBTitle:** structure of the p368g mutant of pmm/pgm from p. aeruginosa
54	c1kh2D_	Alignment	not modelled	24.1	16	**PDB header:**ligase **Chain:** D: **PDB Molecule:**argininosuccinate synthetase; **PDBTitle:** crystal structure of thermus thermophilus hb82 argininosuccinate synthetase in complex with atp
55	d1t6t1_	Alignment	not modelled	23.6	12	**Fold:**Toprim domain **Superfamily:**Toprim domain **Family:**Toprim domain
56	d1qzua_	Alignment	not modelled	22.2	19	**Fold:**Homo-oligomeric flavin-containing Cys decarboxylases, HFCD **Superfamily:**Homo-oligomeric flavin-containing Cys decarboxylases, HFCD **Family:**Homo-oligomeric flavin-containing Cys decarboxylases, HFCD
57	c3r8wC_	Alignment	not modelled	20.4	20	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**3-isopropylmalate dehydrogenase 2, chloroplastic; **PDBTitle:** structure of 3-isopropylmalate dehydrogenase isoform 2 from2 arabidopsis thaliana at 2.2 angstrom resolution
58	d1j20a1	Alignment	not modelled	18.8	16	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Adenine nucleotide alpha hydrolases-like **Family:**N-type ATP pyrophosphatases
59	d1ylqa1	Alignment	not modelled	18.4	19	**Fold:**Nucleotidyltransferase **Superfamily:**Nucleotidyltransferase **Family:**Catalytic subunit of bi-partite nucleotidyltransferase
60	d1v53a1	Alignment	not modelled	18.4	24	**Fold:**Isocitrate/Isopropylmalate dehydrogenase-like **Superfamily:**Isocitrate/Isopropylmalate dehydrogenase-like **Family:**Dimeric isocitrate & isopropylmalate dehydrogenases
61	d2pjua1	Alignment	not modelled	18.0	9	**Fold:**Chelatase-like **Superfamily:**PrpR receptor domain-like **Family:**PrpR receptor domain-like
62	c2qf7A_	Alignment	not modelled	17.4	16	**PDB header:**ligase **Chain:** A: **PDB Molecule:**pyruvate carboxylase protein; **PDBTitle:** crystal structure of a complete multifunctional pyruvate carboxylase2 from rhizobium etli
63	d1m7ja3	Alignment	not modelled	17.1	17	**Fold:**TIM beta/alpha-barrel **Superfamily:**Metallo-dependent hydrolases **Family:**D-aminoacylase, catalytic domain
64	c3tvsA_	Alignment	not modelled	16.9	10	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**cryptochrome-1; **PDBTitle:** structure of full-length drosophila cryptochrome
65	c2nz2A_	Alignment	not modelled	16.7	6	**PDB header:**ligase **Chain:** A: **PDB Molecule:**argininosuccinate synthase; **PDBTitle:** crystal structure of human argininosuccinate synthase in complex with2 aspartate and citrulline
66	c1gph1_	Alignment	not modelled	16.2	17	**PDB header:**transferase(glutamine amidotransferase) **Chain:** 1: **PDB Molecule:**glutamine phosphoribosyl-pyrophosphate amidotransferase; **PDBTitle:** structure of the allosteric regulatory enzyme of purine biosynthesis
67	d2e1za2	Alignment	not modelled	16.1	21	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**Acetokinase-like
68	c1k97A_	Alignment	not modelled	15.4	18	**PDB header:**ligase **Chain:** A: **PDB Molecule:**argininosuccinate synthase; **PDBTitle:** crystal structure of e. coli argininosuccinate synthetase in complex2 with aspartate and citrulline
69	d1cnza_	Alignment	not modelled	15.3	28	**Fold:**Isocitrate/Isopropylmalate dehydrogenase-like **Superfamily:**Isocitrate/Isopropylmalate dehydrogenase-like **Family:**Dimeric isocitrate & isopropylmalate dehydrogenases
70	d2c5sa1	Alignment	not modelled	15.0	13	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Adenine nucleotide alpha hydrolases-like **Family:**ThiI-like
71	d1tifa_	Alignment	not modelled	14.9	16	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**Translation initiation factor IF3, N-terminal domain **Family:**Translation initiation factor IF3, N-terminal domain
72	c3trhI_	Alignment	not modelled	14.7	9	**PDB header:**lyase **Chain:** I: **PDB Molecule:**phosphoribosylaminoimidazole carboxylase **PDBTitle:** structure of a phosphoribosylaminoimidazole carboxylase catalytic2 subunit (pure) from coxiella burnetii
73	c3i3wB_	Alignment	not modelled	14.4	16	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**phosphoglucosamine mutase; **PDBTitle:** structure of a phosphoglucosamine mutase from francisella tularensis
74	d2j07a2	Alignment	not modelled	14.1	13	**Fold:**Cryptochrome/photolyase, N-terminal domain **Superfamily:**Cryptochrome/photolyase, N-terminal domain **Family:**Cryptochrome/photolyase, N-terminal domain
75	c1nuiA_	Alignment	not modelled	14.0	18	**PDB header:**replication **Chain:** A: **PDB Molecule:**dna primase/helicase; **PDBTitle:** crystal structure of the primase fragment of bacteriophage t7 primase-2 helicase protein
76	d1xaca_	Alignment	not modelled	14.0	24	**Fold:**Isocitrate/Isopropylmalate dehydrogenase-like **Superfamily:**Isocitrate/Isopropylmalate dehydrogenase-like **Family:**Dimeric isocitrate & isopropylmalate dehydrogenases
77	d1g99a2	Alignment	not modelled	13.9	21	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**Acetokinase-like
						PDB header:oxidoreductase **Chain:** B: **PDB Molecule:**phosphoadenosine phosphosulfate

78	c2oq2B_	Alignment	not modelled	13.8	13	reductase; **PDBTitle:** crystal structure of yeast paps reductase with pap, a product complex
79	d1pkla3	Alignment	not modelled	13.8	22	**Fold:**Pyruvate kinase C-terminal domain-like **Superfamily:**PK C-terminal domain-like **Family:**Pyruvate kinase, C-terminal domain
80	c2f7lA_	Alignment	not modelled	13.7	15	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**455aa long hypothetical phospho-sugar mutase; **PDBTitle:** crystal structure of sulfolobus tokodaii2 phosphomannomutase/phosphoglucomutase
81	d1nuia1	Alignment	not modelled	13.6	18	**Fold:**DNA primase core **Superfamily:**DNA primase core **Family:**Primase fragment of primase-helicase protein
82	d1cm7a_	Alignment	not modelled	13.1	28	**Fold:**Isocitrate/Isopropylmalate dehydrogenase-like **Superfamily:**Isocitrate/Isopropylmalate dehydrogenase-like **Family:**Dimeric isocitrate & isopropylmalate dehydrogenases
83	c3u1hA_	Alignment	not modelled	13.1	24	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**3-isopropylmalate dehydrogenase; **PDBTitle:** crystal structure of ipmdh from the last common ancestor of bacillus
84	d1t0la_	Alignment	not modelled	13.0	9	**Fold:**Isocitrate/Isopropylmalate dehydrogenase-like **Superfamily:**Isocitrate/Isopropylmalate dehydrogenase-like **Family:**Dimeric isocitrate & isopropylmalate dehydrogenases
85	c3us8A_	Alignment	not modelled	12.8	12	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**isocitrate dehydrogenase [nadp]; **PDBTitle:** crystal structure of an isocitrate dehydrogenase from sinorhizobium2 meliloti 1021
86	d1uf3a_	Alignment	not modelled	12.4	19	**Fold:**Metallo-dependent phosphatases **Superfamily:**Metallo-dependent phosphatases **Family:**TT1561-like
87	d1nmpa_	Alignment	not modelled	12.3	21	**Fold:**NIF3 (NGG1p interacting factor 3)-like **Superfamily:**NIF3 (NGG1p interacting factor 3)-like **Family:**NIF3 (NGG1p interacting factor 3)-like
88	d1g2ua_	Alignment	not modelled	12.1	24	**Fold:**Isocitrate/Isopropylmalate dehydrogenase-like **Superfamily:**Isocitrate/Isopropylmalate dehydrogenase-like **Family:**Dimeric isocitrate & isopropylmalate dehydrogenases
89	d1lwda_	Alignment	not modelled	11.8	3	**Fold:**Isocitrate/Isopropylmalate dehydrogenase-like **Superfamily:**Isocitrate/Isopropylmalate dehydrogenase-like **Family:**Dimeric isocitrate & isopropylmalate dehydrogenases
90	d3pmga1	Alignment	not modelled	11.7	14	**Fold:**Phosphoglucomutase, first 3 domains **Superfamily:**Phosphoglucomutase, first 3 domains **Family:**Phosphoglucomutase, first 3 domains
91	c2iirJ_	Alignment	not modelled	11.6	36	**PDB header:**transferase **Chain:** J: **PDB Molecule:**acetate kinase; **PDBTitle:** acetate kinase from a hypothermophile thermotoga maritima
92	c3pdkB_	Alignment	not modelled	11.4	18	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**phosphoglucosamine mutase; **PDBTitle:** crystal structure of phosphoglucosamine mutase from b. anthracis
93	d3clsd1	Alignment	not modelled	11.3	26	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Adenine nucleotide alpha hydrolases-like **Family:**ETFP subunits
94	d1k92a1	Alignment	not modelled	11.2	13	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Adenine nucleotide alpha hydrolases-like **Family:**N-type ATP pyrophosphatases
95	c2au3A_	Alignment	not modelled	10.6	14	**PDB header:**transferase **Chain:** A: **PDB Molecule:**dna primase; **PDBTitle:** crystal structure of the aquifex aeolicus primase (zinc binding and2 rna polymerase domains)
96	c1ecjB_	Alignment	not modelled	10.6	22	**PDB header:**transferase **Chain:** B: **PDB Molecule:**glutamine phosphoribosylpyrophosphate **PDBTitle:** escherichia coli glutamine phosphoribosylpyrophosphate2 (prpp) amidotransferase complexed with 2 amp per tetramer
97	c1dd9A_	Alignment	not modelled	10.5	11	**PDB header:**transferase **Chain:** A: **PDB Molecule:**dna primase; **PDBTitle:** structure of the dnag catalytic core
98	d1dd9a_	Alignment	not modelled	10.5	11	**Fold:**DNA primase core **Superfamily:**DNA primase core **Family:**DNA primase DnaG catalytic core
99	c3p4iA_	Alignment	not modelled	10.5	29	**PDB header:**transferase **Chain:** A: **PDB Molecule:**acetate kinase; **PDBTitle:** crystal structure of acetate kinase from mycobacterium avium