Phyre^2

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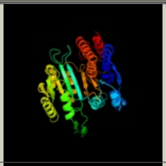
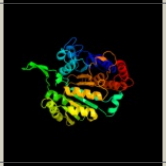
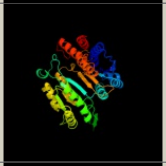
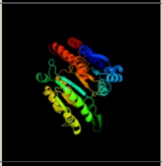
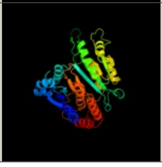
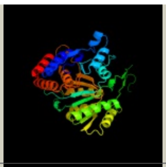
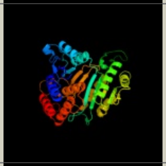
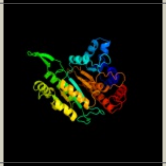
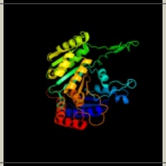
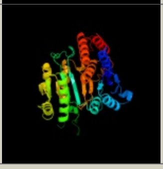
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3fmxX_	Alignment		100.0	78	**PDB header:**oxidoreductase **Chain:** X: **PDB Molecule:**tartrate dehydrogenase/decarboxylase; **PDBTitle:** crystal structure of tartrate dehydrogenase from pseudomonas2 putida complexed with nadh
2	c2d1cB_	Alignment		100.0	35	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**isocitrate dehydrogenase; **PDBTitle:** crystal structure of tt0538 protein from thermus thermophilus hb8
3	d1cm7a_	Alignment		100.0	38	**Fold:**Isocitrate/Isopropylmalate dehydrogenase-like **Superfamily:**Isocitrate/Isopropylmalate dehydrogenase-like **Family:**Dimeric isocitrate & isopropylmalate dehydrogenases
4	d1pb1a_	Alignment		100.0	29	**Fold:**Isocitrate/Isopropylmalate dehydrogenase-like **Superfamily:**Isocitrate/Isopropylmalate dehydrogenase-like **Family:**Dimeric isocitrate & isopropylmalate dehydrogenases
5	d1v53a1	Alignment		100.0	36	**Fold:**Isocitrate/Isopropylmalate dehydrogenase-like **Superfamily:**Isocitrate/Isopropylmalate dehydrogenase-like **Family:**Dimeric isocitrate & isopropylmalate dehydrogenases
6	d1cnza_	Alignment		100.0	37	**Fold:**Isocitrate/Isopropylmalate dehydrogenase-like **Superfamily:**Isocitrate/Isopropylmalate dehydrogenase-like **Family:**Dimeric isocitrate & isopropylmalate dehydrogenases
7	d1a05a_	Alignment		100.0	34	**Fold:**Isocitrate/Isopropylmalate dehydrogenase-like **Superfamily:**Isocitrate/Isopropylmalate dehydrogenase-like **Family:**Dimeric isocitrate & isopropylmalate dehydrogenases
8	c3r8wC_	Alignment		100.0	36	**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
9	c2d4vD_	Alignment		100.0	29	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**isocitrate dehydrogenase; **PDBTitle:** crystal structure of nad dependent isocitrate dehydrogenase2 from acidithiobacillus thiooxidans
10	d1g2ua_	Alignment		100.0	36	**Fold:**Isocitrate/Isopropylmalate dehydrogenase-like **Superfamily:**Isocitrate/Isopropylmalate dehydrogenase-like **Family:**Dimeric isocitrate & isopropylmalate dehydrogenases
11	d1xaca_	Alignment		100.0	36	**Fold:**Isocitrate/Isopropylmalate dehydrogenase-like **Superfamily:**Isocitrate/Isopropylmalate dehydrogenase-like **Family:**Dimeric isocitrate & isopropylmalate dehydrogenases

12	d1hqsa_	Alignment		100.0	31	**Fold:**Isocitrate/Isopropylmalate dehydrogenase-like **Superfamily:**Isocitrate/Isopropylmalate dehydrogenase-like **Family:**Dimeric isocitrate & isopropylmalate dehydrogenases
13	d1vlca_	Alignment		100.0	36	**Fold:**Isocitrate/Isopropylmalate dehydrogenase-like **Superfamily:**Isocitrate/Isopropylmalate dehydrogenase-like **Family:**Dimeric isocitrate & isopropylmalate dehydrogenases
14	c2e0cA_	Alignment		100.0	30	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**409aa long hypothetical nadp-dependent isocitrate **PDBTitle:** crystal structure of isocitrate dehydrogenase from sulfolobus tokodaii2 strain7 at 2.0 a resolution
15	c3u1hA_	Alignment		100.0	40	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**3-isopropylmalate dehydrogenase; **PDBTitle:** crystal structure of ipmdh from the last common ancestor of bacillus
16	d1wpwa_	Alignment		100.0	34	**Fold:**Isocitrate/Isopropylmalate dehydrogenase-like **Superfamily:**Isocitrate/Isopropylmalate dehydrogenase-like **Family:**Dimeric isocitrate & isopropylmalate dehydrogenases
17	c1x0lB_	Alignment		100.0	42	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**homoisocitrate dehydrogenase; **PDBTitle:** crystal structure of tetrameric homoisocitrate dehydrogenase from an2 extreme thermophile, thermus thermophilus
18	d1w0da_	Alignment		100.0	41	**Fold:**Isocitrate/Isopropylmalate dehydrogenase-like **Superfamily:**Isocitrate/Isopropylmalate dehydrogenase-like **Family:**Dimeric isocitrate & isopropylmalate dehydrogenases
19	c3blxL_	Alignment		100.0	33	**PDB header:**oxidoreductase **Chain:** L: **PDB Molecule:**isocitrate dehydrogenase [nad] subunit 2; **PDBTitle:** yeast isocitrate dehydrogenase (apo form)
20	c1tyoA_	Alignment		100.0	26	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**isocitrate dehydrogenase; **PDBTitle:** isocitrate dehydrogenase from the hyperthermophile aeropyrum pernix in2 complex with etheno-nadp
21	c3blxM_	Alignment	not modelled	100.0	31	**PDB header:**oxidoreductase **Chain:** M: **PDB Molecule:**isocitrate dehydrogenase [nad] subunit 1; **PDBTitle:** yeast isocitrate dehydrogenase (apo form)
22	c1zorB_	Alignment	not modelled	100.0	18	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**isocitrate dehydrogenase; **PDBTitle:** isocitrate dehydrogenase from the hyperthermophile thermotoga maritima
23	c2uxqB_	Alignment	not modelled	100.0	20	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**isocitrate dehydrogenase native; **PDBTitle:** isocitrate dehydrogenase from the psychrophilic bacterium2 desulfotalea psychrophila: biochemical properties and3 crystal structure analysis
24	d1lwda_	Alignment	not modelled	100.0	18	**Fold:**Isocitrate/Isopropylmalate dehydrogenase-like **Superfamily:**Isocitrate/Isopropylmalate dehydrogenase-like **Family:**Dimeric isocitrate & isopropylmalate dehydrogenases
25	c3us8A_	Alignment	not modelled	100.0	16	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**isocitrate dehydrogenase [nadp]; **PDBTitle:** crystal structure of an isocitrate dehydrogenase from sinorhizobium2 meliloti 1021
26	d1t0la_	Alignment	not modelled	100.0	17	**Fold:**Isocitrate/Isopropylmalate dehydrogenase-like **Superfamily:**Isocitrate/Isopropylmalate dehydrogenase-like **Family:**Dimeric isocitrate & isopropylmalate dehydrogenases
27	c2qfyE_	Alignment	not modelled	100.0	19	**PDB header:**oxidoreductase **Chain:** E: **PDB Molecule:**isocitrate dehydrogenase [nadp]; **PDBTitle:** crystal structure of saccharomyces cerevesiae mitochondrial nadp(+)-2 dependent isocitrate dehydrogenase in complex with a-ketoglutarate
28	c2iv0A_	Alignment	not modelled	100.0	32	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**isocitrate dehydrogenase; **PDBTitle:** thermal stability of isocitrate dehydrogenase from2

						archaeoglobus fulgidus studied by crystal structure3 analysis and engineering of chimers
29	c2hi1A_	Alignment	not modelled	99.0	16	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**4-hydroxythreonine-4-phosphate dehydrogenase 2; **PDBTitle:** the structure of a putative 4-hydroxythreonine-4-phosphate2 dehydrogenase from salmonella typhimurium.
30	d1ptma_	Alignment	not modelled	99.0	16	**Fold:**Isocitrate/Isopropylmalate dehydrogenase-like **Superfamily:**Isocitrate/Isopropylmalate dehydrogenase-like **Family:**PdxA-like
31	d1r8ka_	Alignment	not modelled	98.8	17	**Fold:**Isocitrate/Isopropylmalate dehydrogenase-like **Superfamily:**Isocitrate/Isopropylmalate dehydrogenase-like **Family:**PdxA-like
32	c1yxoB_	Alignment	not modelled	98.5	16	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**4-hydroxythreonine-4-phosphate dehydrogenase 1; **PDBTitle:** crystal structure of pyridoxal phosphate biosynthetic protein pdxa2 pa0593
33	d1itwa_	Alignment	not modelled	98.1	18	**Fold:**Isocitrate/Isopropylmalate dehydrogenase-like **Superfamily:**Isocitrate/Isopropylmalate dehydrogenase-like **Family:**Monomeric isocitrate dehydrogenase
34	c2b0tA_	Alignment	not modelled	98.0	14	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**nadp isocitrate dehydrogenase; **PDBTitle:** structure of monomeric nadp isocitrate dehydrogenase
35	c2q62A_	Alignment	not modelled	77.0	10	**PDB header:**flavoprotein **Chain:** A: **PDB Molecule:**arsh; **PDBTitle:** crystal structure of arsh from sinorhizobium meliloti
36	d2fpoa1	Alignment	not modelled	66.7	10	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**YhhF-like
37	c1p84E_	Alignment	not modelled	57.1	32	**PDB header:**oxidoreductase **Chain:** E: **PDB Molecule:**ubiquinol-cytochrome c reductase iron-sulfur **PDBTitle:** hdbt inhibited yeast cytochrome bc1 complex
38	d2onsa1	Alignment	not modelled	53.1	13	**Fold:**Periplasmic binding protein-like II **Superfamily:**Periplasmic binding protein-like II **Family:**Phosphate binding protein-like
39	c3cfxA_	Alignment	not modelled	53.0	12	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**upf0100 protein ma_0280; **PDBTitle:** crystal structure of m. acetivorans periplasmic binding protein2 moda/wtpa with bound tungstate
40	c2fyuE_	Alignment	not modelled	51.8	32	**PDB header:**oxidoreductase **Chain:** E: **PDB Molecule:**ubiquinol-cytochrome c reductase iron-sulfur subunit, **PDBTitle:** crystal structure of bovine heart mitochondrial bc1 with jg1442 inhibitor
41	c3s40C_	Alignment	not modelled	49.1	11	**PDB header:**transferase **Chain:** C: **PDB Molecule:**diacylglycerol kinase; **PDBTitle:** the crystal structure of a diacylglycerol kinases from bacillus2 anthracis str. sterne
42	c3cfzA_	Alignment	not modelled	48.2	9	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**upf0100 protein mj1186; **PDBTitle:** crystal structure of m. jannaschii periplasmic binding2 protein moda/wtpa with bound tungstate
43	d3thia_	Alignment	not modelled	44.0	18	**Fold:**Periplasmic binding protein-like II **Superfamily:**Periplasmic binding protein-like II **Family:**Phosphate binding protein-like
44	d1riea_	Alignment	not modelled	41.0	32	**Fold:**ISP domain **Superfamily:**ISP domain **Family:**Rieske iron-sulfur protein (ISP)
45	c3k6wA_	Alignment	not modelled	40.4	12	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**solute-binding protein ma_0280; **PDBTitle:** apo and ligand bound structures of moda from the archaeon2 methanosarcina acetivorans
46	c2fynO_	Alignment	not modelled	39.6	29	**PDB header:**oxidoreductase **Chain:** O: **PDB Molecule:**ubiquinol-cytochrome c reductase iron-sulfur **PDBTitle:** crystal structure analysis of the double mutant rhodobacter2 sphaeroides bc1 complex
47	c1orhA_	Alignment	not modelled	37.3	10	**PDB header:**transferase **Chain:** A: **PDB Molecule:**protein arginine n-methyltransferase 1; **PDBTitle:** structure of the predominant protein arginine methyltransferase prmt1
48	d1oria_	Alignment	not modelled	36.4	10	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**Arginine methyltransferase
49	d3cx5e1	Alignment	not modelled	32.1	32	**Fold:**ISP domain **Superfamily:**ISP domain **Family:**Rieske iron-sulfur protein (ISP)
50	c2e76D_	Alignment	not modelled	28.5	38	**PDB header:**photosynthesis **Chain:** D: **PDB Molecule:**cytochrome b6-f complex iron-sulfur subunit; **PDBTitle:** crystal structure of the cytochrome b6f complex with tridecyl-2 stigmatellin (tds) from m.laminosus
51	c1twyG_	Alignment	not modelled	26.8	16	**PDB header:**structural genomics, unknown function **Chain:** G: **PDB Molecule:**abc transporter, periplasmic substrate-binding protein; **PDBTitle:** crystal structure of an abc-type phosphate transport receptor from2 vibrio cholerae
52	d1twya_	Alignment	not modelled	26.8	16	**Fold:**Periplasmic binding protein-like II **Superfamily:**Periplasmic binding protein-like II **Family:**Phosphate binding protein-like
53	c3fzgA_	Alignment	not modelled	25.7	6	**PDB header:**transferase **Chain:** A: **PDB Molecule:**16s rrna methylase;

						PDBTitle: structure of the 16s rrna methylase arma
54	c3grzA_	Alignment	not modelled	24.6	23	**PDB header:**transferase **Chain:** A: **PDB Molecule:**ribosomal protein l11 methyltransferase; **PDBTitle:** crystal structure of ribosomal protein l11 methylase from2 lactobacillus delbrueckii subsp. bulgaricus
55	c2nvgA_	Alignment	not modelled	24.1	26	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**ubiquinol-cytochrome c reductase iron-sulfur subunit; **PDBTitle:** soluble domain of rieske iron sulfur protein.
56	c3qd7X_	Alignment	not modelled	23.5	5	**PDB header:**hydrolase **Chain:** X: **PDB Molecule:**uncharacterized protein ydal; **PDBTitle:** crystal structure of ydal, a stand-alone small muts-related protein2 from escherichia coli
57	d1ydga_	Alignment	not modelled	23.1	15	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**WrbA-like
58	d2fyta1	Alignment	not modelled	22.9	12	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**Arginine methyltransferase
59	c2huzB_	Alignment	not modelled	17.2	13	**PDB header:**structural genomics, transferase **Chain:** B: **PDB Molecule:**glucosamine 6-phosphate n-acetyltransferase; **PDBTitle:** crystal structure of gnpnat1
60	d2fcaa1	Alignment	not modelled	16.2	10	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**TrmB-like
61	c3lwzC_	Alignment	not modelled	16.1	24	**PDB header:**lyase **Chain:** C: **PDB Molecule:**3-dehydroquinate dehydratase; **PDBTitle:** 1.65 angstrom resolution crystal structure of type ii 3-2 dehydroquinate dehydratase (aroq) from yersinia pestis
62	d2z3va1	Alignment	not modelled	16.0	12	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Adenine nucleotide alpha hydrolases-like **Family:**Universal stress protein-like
63	d1t0ia_	Alignment	not modelled	15.8	19	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**NADPH-dependent FMN reductase
64	d1yzha1	Alignment	not modelled	15.5	6	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**TrmB-like
65	d1g6q1_	Alignment	not modelled	15.3	10	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**Arginine methyltransferase
66	c3ksmA_	Alignment	not modelled	15.2	13	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**abc-type sugar transport system, periplasmic component; **PDBTitle:** crystal structure of abc-type sugar transport system, periplasmic2 component from hahella chejuensis
67	c2pebB_	Alignment	not modelled	15.1	22	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**putative dioxygenase; **PDBTitle:** crystal structure of a putative dioxygenase (npun_f1925) from nostoc2 punctiforme pcc 73102 at 1.46 a resolution
68	c2qhxB_	Alignment	not modelled	15.0	18	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**pteridine reductase 1; **PDBTitle:** structure of pteridine reductase from leishmania major2 complexed with a ligand
69	d1n1jb_	Alignment	not modelled	14.9	11	**Fold:**Histone-fold **Superfamily:**Histone-fold **Family:**TBP-associated factors, TAFs
70	d1tzyb_	Alignment	not modelled	14.8	38	**Fold:**Histone-fold **Superfamily:**Histone-fold **Family:**Nucleosome core histones
71	c3fg9B_	Alignment	not modelled	14.6	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
72	d1ofda1	Alignment	not modelled	14.6	19	**Fold:**Single-stranded right-handed beta-helix **Superfamily:**Alpha subunit of glutamate synthase, C-terminal domain **Family:**Alpha subunit of glutamate synthase, C-terminal domain
73	d1hioa_	Alignment	not modelled	13.4	11	**Fold:**Histone-fold **Superfamily:**Histone-fold **Family:**Nucleosome core histones
74	d1cyxa_	Alignment	not modelled	13.3	21	**Fold:**Cupredoxin-like **Superfamily:**Cupredoxins **Family:**Periplasmic domain of cytochrome c oxidase subunit II
75	c1cyxA_	Alignment	not modelled	13.3	21	**PDB header:**electron transport **Chain:** A: **PDB Molecule:**cyoa; **PDBTitle:** quinol oxidase (periplasmic fragment of subunit ii with2 engineered cu-a binding site)(cyoa)
76	d1r5ja_	Alignment	not modelled	13.2	17	**Fold:**Isocitrate/Isopropylmalate dehydrogenase-like **Superfamily:**Isocitrate/Isopropylmalate dehydrogenase-like **Family:**Phosphotransacetylase
77	c2uvgA_	Alignment	not modelled	13.2	14	**PDB header:**sugar-binding protein **Chain:** A: **PDB Molecule:**abc type periplasmic sugar-binding protein; **PDBTitle:** structure of a periplasmic oligogalacturonide binding2 protein from yersinia enterocolitica
78	c1f66C_	Alignment	not modelled	12.6	11	**PDB header:**structural protein/dna **Chain:** C: **PDB Molecule:**histone h2a.z; **PDBTitle:** 2.6 a crystal structure of a nucleosome core particle2 containing the variant histone h2a.z
						Fold: Histone-fold

79	d1f66c_	Alignment	not modelled	12.6	11	**Superfamily:**Histone-fold **Family:**Nucleosome core histones
80	c2hxrA_	Alignment	not modelled	11.9	15	**PDB header:**transcription **Chain:** A: **PDB Molecule:**hth-type transcriptional regulator cynr; **PDBTitle:** structure of the ligand binding domain of e. coli cynr, a2 transcriptional regulator controlling cyanate metabolism
81	c3er6D_	Alignment	not modelled	11.8	17	**PDB header:**structural genomics, unknown function **Chain:** D: **PDB Molecule:**putative transcriptional regulator protein; **PDBTitle:** crystal structure of a putative transcriptional regulator2 protein from vibrio parahaemolyticus
82	d1id3d_	Alignment	not modelled	11.8	29	**Fold:**Histone-fold **Superfamily:**Histone-fold **Family:**Nucleosome core histones
83	d1n1ja_	Alignment	not modelled	11.6	16	**Fold:**Histone-fold **Superfamily:**Histone-fold **Family:**TBP-associated factors, TAFs
84	c3b3jA_	Alignment	not modelled	11.6	14	**PDB header:**transferase **Chain:** A: **PDB Molecule:**histone-arginine methyltransferase carm1; **PDBTitle:** the 2.55 a crystal structure of the apo catalytic domain of2 coactivator-associated arginine methyl transferase i(carm1:28-507,3 residues 28-146 and 479-507 not ordered)
85	d1i27a_	Alignment	not modelled	11.5	22	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**C-terminal domain of the rap74 subunit of TFIIF
86	d2jssa1	Alignment	not modelled	11.5	14	**Fold:**Histone-fold **Superfamily:**Histone-fold **Family:**Nucleosome core histones
87	c2f8nK_	Alignment	not modelled	11.4	11	**PDB header:**structural protein/dna **Chain:** K: **PDB Molecule:**histone h2a type 1; **PDBTitle:** 2.9 angstrom x-ray structure of hybrid macroh2a nucleosomes
88	c3c6kC_	Alignment	not modelled	11.2	10	**PDB header:**transferase **Chain:** C: **PDB Molecule:**spermine synthase; **PDBTitle:** crystal structure of human spermine synthase in complex2 with spermidine and 5-methylthioadenosine
89	c2qv7A_	Alignment	not modelled	11.0	13	**PDB header:**transferase **Chain:** A: **PDB Molecule:**diacylglycerol kinase dgkb; **PDBTitle:** crystal structure of diacylglycerol kinase dgkb in complex with adp2 and mg
90	d1fftb1	Alignment	not modelled	10.8	21	**Fold:**Cupredoxin-like **Superfamily:**Cupredoxins **Family:**Periplasmic domain of cytochrome c oxidase subunit II
91	d1e7wa_	Alignment	not modelled	10.7	18	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
92	d1i7na1	Alignment	not modelled	10.6	25	**Fold:**PreATP-grasp domain **Superfamily:**PreATP-grasp domain **Family:**Synapsin domain
93	d1jq4a_	Alignment	not modelled	10.4	23	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**2Fe-2S ferredoxin-like **Family:**2Fe-2S ferredoxin domains from multidomain proteins
94	d1p3mh_	Alignment	not modelled	10.4	38	**Fold:**Histone-fold **Superfamily:**Histone-fold **Family:**Nucleosome core histones
95	c2zqeA_	Alignment	not modelled	10.3	11	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**muts2 protein; **PDBTitle:** crystal structure of the smr domain of thermus thermophilus muts2
96	d1q77a_	Alignment	not modelled	10.3	13	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Adenine nucleotide alpha hydrolases-like **Family:**Universal stress protein-like
97	d1ku5a_	Alignment	not modelled	10.1	33	**Fold:**Histone-fold **Superfamily:**Histone-fold **Family:**Archaeal histone
98	d1hiob_	Alignment	not modelled	10.0	38	**Fold:**Histone-fold **Superfamily:**Histone-fold **Family:**Nucleosome core histones
99	d1tzya_	Alignment	not modelled	10.0	11	**Fold:**Histone-fold **Superfamily:**Histone-fold **Family:**Nucleosome core histones