Phyre^2

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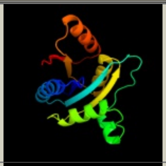
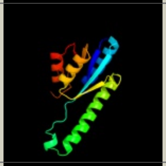
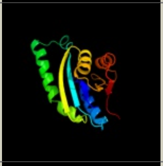
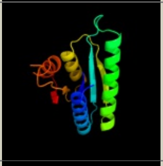
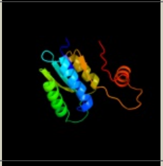
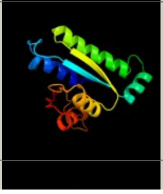
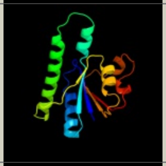
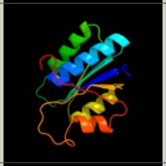
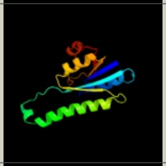
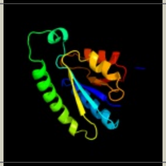
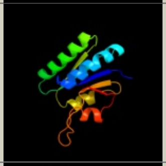
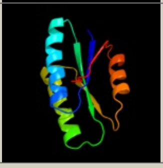
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1jmva_	Alignment		99.9	32	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Adenine nucleotide alpha hydrolases-like **Family:**Universal stress protein-like
2	d2z3va1	Alignment		99.9	20	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Adenine nucleotide alpha hydrolases-like **Family:**Universal stress protein-like
3	c3hgmD_	Alignment		99.9	17	**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
4	d1mjha_	Alignment		99.9	19	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Adenine nucleotide alpha hydrolases-like **Family:**Universal stress protein-like
5	c2dumD_	Alignment		99.9	12	**PDB header:**structural genomics, unknown function **Chain:** D: **PDB Molecule:**hypothetical protein ph0823; **PDBTitle:** crystal structure of hypothetical protein, ph0823
6	c3s3tD_	Alignment		99.9	15	**PDB header:**chaperone **Chain:** D: **PDB Molecule:**nucleotide-binding protein, universal stress protein uspa **PDBTitle:** universal stress protein uspa from lactobacillus plantarum
7	c2pfsA_	Alignment		99.9	26	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**universal stress protein; **PDBTitle:** crystal structure of universal stress protein from nitrosomonas2 europaea
8	c3dloC_	Alignment		99.9	16	**PDB header:**structural genomics, unknown function **Chain:** C: **PDB Molecule:**universal stress protein; **PDBTitle:** structure of universal stress protein from archaeoglobus fulgidus
9	c3fg9B_	Alignment		99.9	13	**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	d1tq8a_	Alignment		99.9	21	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Adenine nucleotide alpha hydrolases-like **Family:**Universal stress protein-like
11	d2gm3a1	Alignment		99.8	11	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Adenine nucleotide alpha hydrolases-like **Family:**Universal stress protein-like

12	c3fh0A_	Alignment		99.8	17	**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	d1q77a_	Alignment		99.8	15	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Adenine nucleotide alpha hydrolases-like **Family:**Universal stress protein-like
14	c3loqA_	Alignment		99.8	13	**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		99.7	16	**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	17	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein pa1789; **PDBTitle:** the crystal structure of a functionally unknown protein pa1789 from2 pseudomonas aeruginosa pao1
17	c3idfA_	Alignment		99.7	16	**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
18	c2jaxA_	Alignment		99.7	11	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**hypothetical protein tb31.7; **PDBTitle:** universal stress protein rv2623 from mycobaterium2 tuberculosis
19	c3ab8B_	Alignment		99.7	12	**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		91.3	18	**PDB header:**ligase/rna **Chain:** B: **PDB Molecule:**trna(ile)-lysidine synthase; **PDBTitle:** crystal structure of tils complexed with trna
21	d1np7a2	Alignment	not modelled	87.9	11	**Fold:**Cryptochrome/photolyase, N-terminal domain **Superfamily:**Cryptochrome/photolyase, N-terminal domain **Family:**Cryptochrome/photolyase, N-terminal domain
22	d1g5qa_	Alignment	not modelled	86.0	15	**Fold:**Homo-oligomeric flavin-containing Cys decarboxylases, HFCD **Superfamily:**Homo-oligomeric flavin-containing Cys decarboxylases, HFCD **Family:**Homo-oligomeric flavin-containing Cys decarboxylases, HFCD
23	c2e21A_	Alignment	not modelled	85.0	20	**PDB header:**ligase **Chain:** A: **PDB Molecule:**trna(ile)-lysidine synthase; **PDBTitle:** crystal structure of tils in a complex with amppnp from aquifex2 aeolicus.
24	c1vl2C_	Alignment	not modelled	80.7	16	**PDB header:**ligase **Chain:** C: **PDB Molecule:**argininosuccinate synthase; **PDBTitle:** crystal structure of argininosuccinate synthase (tm1780) from2 thermotoga maritima at 1.65 a resolution
25	d1vbka1	Alignment	not modelled	77.6	10	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Adenine nucleotide alpha hydrolases-like **Family:**ThiI-like
26	c3tvsA_	Alignment	not modelled	75.0	11	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**cryptochrome-1; **PDBTitle:** structure of full-length drosophila cryptochrome
27	c1kh2D_	Alignment	not modelled	74.7	16	**PDB header:**ligase **Chain:** D: **PDB Molecule:**argininosuccinate synthetase; **PDBTitle:** crystal structure of thermus thermophilus hb82 argininosuccinate synthetase in complex with atp
28	c3qjgD_	Alignment	not modelled	74.4	14	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**epidermin biosynthesis protein epid; **PDBTitle:** epidermin biosynthesis protein epid from staphylococcus aureus

29	d3clsc1	Alignment	not modelled	72.8	18	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Adenine nucleotide alpha hydrolases-like **Family:**ETFP subunits
30	c3lqkA_	Alignment	not modelled	71.1	12	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**dipicolinate synthase subunit b; **PDBTitle:** crystal structure of dipicolinate synthase subunit b from bacillus2 halodurans c
31	d1o94c_	Alignment	not modelled	69.2	17	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Adenine nucleotide alpha hydrolases-like **Family:**ETFP subunits
32	c1np7A_	Alignment	not modelled	68.8	11	**PDB header:**lyase **Chain:** A: **PDB Molecule:**dna photolyase; **PDBTitle:** crystal structure analysis of synechocystis sp. pcc6803 cryptochrome
33	c2xrzA_	Alignment	not modelled	67.0	12	**PDB header:**lyase/dna **Chain:** A: **PDB Molecule:**deoxyribodipyrimidine photolyase; **PDBTitle:** x-ray structure of archaeal class ii cpd photolyase from2 methanosarcina mazei in complex with intact cpd-lesion
34	c2pjuD_	Alignment	not modelled	65.6	8	**PDB header:**transcription **Chain:** D: **PDB Molecule:**propionate catabolism operon regulatory protein; **PDBTitle:** crystal structure of propionate catabolism operon2 regulatory protein prpr
35	d1j20a1	Alignment	not modelled	64.5	17	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Adenine nucleotide alpha hydrolases-like **Family:**N-type ATP pyrophosphatases
36	d1wy5a1	Alignment	not modelled	63.3	18	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Adenine nucleotide alpha hydrolases-like **Family:**PP-loop ATPase
37	c1k97A_	Alignment	not modelled	62.3	14	**PDB header:**ligase **Chain:** A: **PDB Molecule:**argininosuccinate synthase; **PDBTitle:** crystal structure of e. coli argininosuccinate synthetase in complex2 with aspartate and citrulline
38	c1o94D_	Alignment	not modelled	61.5	11	**PDB header:**electron transport **Chain:** D: **PDB Molecule:**electron transfer flavoprotein alpha-subunit; **PDBTitle:** ternary complex between trimethylamine dehydrogenase and2 electron transferring flavoprotein
39	c2nz2A_	Alignment	not modelled	57.8	14	**PDB header:**ligase **Chain:** A: **PDB Molecule:**argininosuccinate synthase; **PDBTitle:** crystal structure of human argininosuccinate synthase in complex with2 aspartate and citrulline
40	c3fy4C_	Alignment	not modelled	57.2	15	**PDB header:**lyase **Chain:** C: **PDB Molecule:**6-4 photolyase; **PDBTitle:** (6-4) photolyase crystal structure
41	d2pjua1	Alignment	not modelled	57.0	8	**Fold:**Chelatase-like **Superfamily:**PrpR receptor domain-like **Family:**PrpR receptor domain-like
42	d1owla2	Alignment	not modelled	54.2	12	**Fold:**Cryptochrome/photolyase, N-terminal domain **Superfamily:**Cryptochrome/photolyase, N-terminal domain **Family:**Cryptochrome/photolyase, N-terminal domain
43	d1efpb_	Alignment	not modelled	53.4	14	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Adenine nucleotide alpha hydrolases-like **Family:**ETFP subunits
44	c1ni5A_	Alignment	not modelled	50.6	25	**PDB header:**cell cycle **Chain:** A: **PDB Molecule:**putative cell cycle protein mesj; **PDBTitle:** structure of the mesj pp-atpase from escherichia coli
45	d1uf3a_	Alignment	not modelled	50.5	15	**Fold:**Metallo-dependent phosphatases **Superfamily:**Metallo-dependent phosphatases **Family:**TT1561-like
46	c3qg5D_	Alignment	not modelled	49.3	16	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**mre11; **PDBTitle:** the mre11:rad50 complex forms an atp dependent molecular clamp in dna2 double-strand break repair
47	c1w2wJ_	Alignment	not modelled	47.5	9	**PDB header:**isomerase **Chain:** J: **PDB Molecule:**5-methylthioribose-1-phosphate isomerase; **PDBTitle:** crystal structure of yeast ypr118w, a methylthioribose-1-2 phosphate isomerase related to regulatory eif2b subunits
48	c2q8uA_	Alignment	not modelled	47.0	14	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**exonuclease, putative; **PDBTitle:** crystal structure of mre11 from thermotoga maritima msb8 (tm1635) at2 2.20 a resolution
49	c3mcuF_	Alignment	not modelled	46.8	22	**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.
50	d1iv0a_	Alignment	not modelled	44.6	18	**Fold:**Ribonuclease H-like motif **Superfamily:**Ribonuclease H-like **Family:**Putative Holliday junction resolvase RuvX
51	d3bzka5	Alignment	not modelled	42.2	18	**Fold:**Ribonuclease H-like motif **Superfamily:**Ribonuclease H-like **Family:**Tex RuvX-like domain-like
52	d1gsoa2	Alignment	not modelled	40.7	39	**Fold:**PreATP-grasp domain **Superfamily:**PreATP-grasp domain **Family:**BC N-terminal domain-like
53	c2ejbA_	Alignment	not modelled	39.8	18	**PDB header:**lyase **Chain:** A: **PDB Molecule:**probable aromatic acid decarboxylase; **PDBTitle:** crystal structure of phenylacrylic acid decarboxylase from2 aquifex aeolicus
54	c1tezB_	Alignment	not modelled	39.8	12	**PDB header:**lyase/dna **Chain:** B: **PDB Molecule:**deoxyribodipyrimidine photolyase; **PDBTitle:** complex between dna and the dna photolyase from

						anacystis nidulans
55	c3zquA_	Alignment	not modelled	39.7	12	**PDB header:**lyase **Chain:** A: **PDB Molecule:**probable aromatic acid decarboxylase; **PDBTitle:** structure of a probable aromatic acid decarboxylase
56	d1p3y1_	Alignment	not modelled	39.2	11	**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	d1nu0a_	Alignment	not modelled	37.9	9	**Fold:**Ribonuclease H-like motif **Superfamily:**Ribonuclease H-like **Family:**Putative Holliday junction resolvase RuvX
58	d3clsd1	Alignment	not modelled	36.9	11	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Adenine nucleotide alpha hydrolases-like **Family:**ETFP subunits
59	c3bl5E_	Alignment	not modelled	36.4	9	**PDB header:**hydrolase **Chain:** E: **PDB Molecule:**queuosine biosynthesis protein quec; **PDBTitle:** crystal structure of quec from bacillus subtilis: an enzyme2 involved in preq1 biosynthesis
60	c3ih5A_	Alignment	not modelled	35.9	19	**PDB header:**electron transport **Chain:** A: **PDB Molecule:**electron transfer flavoprotein alpha-subunit; **PDBTitle:** crystal structure of electron transfer flavoprotein alpha-2 subunit from bacteroides thetaiotaomicron
61	c3t1iC_	Alignment	not modelled	35.4	16	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**double-strand break repair protein mre11a; **PDBTitle:** crystal structure of human mre11: understanding tumorigenic mutations
62	d1vhxa_	Alignment	not modelled	34.8	13	**Fold:**Ribonuclease H-like motif **Superfamily:**Ribonuclease H-like **Family:**Putative Holliday junction resolvase RuvX
63	c2xmoB_	Alignment	not modelled	34.2	17	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**lmo2642 protein; **PDBTitle:** the crystal structure of lmo2642
64	d1sbza_	Alignment	not modelled	34.1	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
65	d2c5sa1	Alignment	not modelled	34.1	14	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Adenine nucleotide alpha hydrolases-like **Family:**ThiI-like
66	c3op1A_	Alignment	not modelled	33.6	12	**PDB header:**transferase **Chain:** A: **PDB Molecule:**macrolide-efflux protein; **PDBTitle:** crystal structure of macrolide-efflux protein sp_1110 from2 streptococcus pneumoniae
67	d1ii7a_	Alignment	not modelled	33.3	16	**Fold:**Metallo-dependent phosphatases **Superfamily:**Metallo-dependent phosphatases **Family:**DNA double-strand break repair nuclease
68	c1mvlA_	Alignment	not modelled	33.3	16	**PDB header:**lyase **Chain:** A: **PDB Molecule:**ppc decarboxylase athal3a; **PDBTitle:** ppc decarboxylase mutant c175s
69	d1mvla_	Alignment	not modelled	33.3	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
70	d1fmfa_	Alignment	not modelled	32.1	11	**Fold:**Flavodoxin-like **Superfamily:**Cobalamin (vitamin B12)-binding domain **Family:**Cobalamin (vitamin B12)-binding domain
71	c3auzA_	Alignment	not modelled	32.1	8	**PDB header:**recombination **Chain:** A: **PDB Molecule:**dna double-strand break repair protein mre11; **PDBTitle:** crystal structure of mre11 with manganese
72	c3umvB_	Alignment	not modelled	31.0	16	**PDB header:**lyase **Chain:** B: **PDB Molecule:**deoxyribodipyrimidine photo-lyase; **PDBTitle:** eukaryotic class ii cpd photolyase structure reveals a basis for2 improved uv-tolerance in plants
73	d1ni5a1	Alignment	not modelled	30.2	24	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Adenine nucleotide alpha hydrolases-like **Family:**PP-loop ATPase
74	d1zuna1	Alignment	not modelled	29.9	12	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Adenine nucleotide alpha hydrolases-like **Family:**PAPS reductase-like
75	d1efvb_	Alignment	not modelled	29.6	11	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Adenine nucleotide alpha hydrolases-like **Family:**ETFP subunits
76	c3uhjE_	Alignment	not modelled	29.5	21	**PDB header:**oxidoreductase **Chain:** E: **PDB Molecule:**probable glycerol dehydrogenase; **PDBTitle:** crystal structure of a probable glycerol dehydrogenase from2 sinorhizobium meliloti 1021
77	c2qf7A_	Alignment	not modelled	29.0	12	**PDB header:**ligase **Chain:** A: **PDB Molecule:**pyruvate carboxylase protein; **PDBTitle:** crystal structure of a complete multifunctional pyruvate carboxylase2 from rhizobium etli
78	d2dbsa1	Alignment	not modelled	28.2	17	**Fold:**TTHC002-like **Superfamily:**TTHC002-like **Family:**TTHC002-like
						PDB header:oxidoreductase **Chain:** C: **PDB Molecule:**3-isopropylmalate dehydrogenase 2,

79	c3r8wC_	Alignment	not modelled	27.6	24	chloroplastic; **PDBTitle:** structure of 3-isopropylmalate dehydrogenase isoform 2 from2 arabidopsis thaliana at 2.2 angstrom resolution
80	c3av0A_	Alignment	not modelled	26.2	12	**PDB header:**recombination **Chain:** A: **PDB Molecule:**dna double-strand break repair protein mre11; **PDBTitle:** crystal structure of mre11-rad50 bound to atp s
81	d3bula2	Alignment	not modelled	25.9	20	**Fold:**Flavodoxin-like **Superfamily:**Cobalamin (vitamin B12)-binding domain **Family:**Cobalamin (vitamin B12)-binding domain
82	c3nhzA_	Alignment	not modelled	25.7	12	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**two component system transcriptional regulator mtra; **PDBTitle:** structure of n-terminal domain of mtra
83	d1e0ta3	Alignment	not modelled	25.6	17	**Fold:**Pyruvate kinase C-terminal domain-like **Superfamily:**PK C-terminal domain-like **Family:**Pyruvate kinase, C-terminal domain
84	c3cvyA_	Alignment	not modelled	25.2	10	**PDB header:**lyase/dna **Chain:** A: **PDB Molecule:**re11660p; **PDBTitle:** drosophila melanogaster (6-4) photolyase bound to repaired2 ds dna
85	c2q5cA_	Alignment	not modelled	24.9	11	**PDB header:**transcription **Chain:** A: **PDB Molecule:**ntrc family transcriptional regulator; **PDBTitle:** crystal structure of ntrc family transcriptional regulator from2 clostridium acetobutylicum
86	d1v53a1	Alignment	not modelled	24.6	28	**Fold:**Isocitrate/Isopropylmalate dehydrogenase-like **Superfamily:**Isocitrate/Isopropylmalate dehydrogenase-like **Family:**Dimeric isocitrate & isopropylmalate dehydrogenases
87	d1s3la_	Alignment	not modelled	24.4	16	**Fold:**Metallo-dependent phosphatases **Superfamily:**Metallo-dependent phosphatases **Family:**YfcE-like
88	c1s3mA_	Alignment	not modelled	24.4	16	**PDB header:**phosphodiesterase **Chain:** A: **PDB Molecule:**hypothetical protein mj0936; **PDBTitle:** structural and functional characterization of a novel2 archaeal phosphodiesterase
89	c2jbvA_	Alignment	not modelled	24.1	12	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**choline oxidase; **PDBTitle:** crystal structure of choline oxidase reveals insights into2 the catalytic mechanism
90	c2j4dA_	Alignment	not modelled	23.9	17	**PDB header:**dna-binding protein **Chain:** A: **PDB Molecule:**cryptochrome dash; **PDBTitle:** cryptochrome 3 from arabidopsis thaliana
91	d1t6t1_	Alignment	not modelled	23.1	9	**Fold:**Toprim domain **Superfamily:**Toprim domain **Family:**Toprim domain
92	c3jzdA_	Alignment	not modelled	22.7	10	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**iron-containing alcohol dehydrogenase; **PDBTitle:** crystal structure of putative alcohol dehedrogenase (yp_298327.1) from2 ralstonia eutropha jmp134 at 2.10 a resolution
93	d1gvfa_	Alignment	not modelled	22.5	10	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class II FBP aldolase
94	d1pkla3	Alignment	not modelled	22.3	7	**Fold:**Pyruvate kinase C-terminal domain-like **Superfamily:**PK C-terminal domain-like **Family:**Pyruvate kinase, C-terminal domain
95	c3psfA_	Alignment	not modelled	21.7	15	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcription elongation factor spt6; **PDBTitle:** crystal structure of the spt6 core domain from saccharomyces2 cerevisiae, form spt6(236-1259)
96	c1zunA_	Alignment	not modelled	21.3	12	**PDB header:**transferase **Chain:** A: **PDB Molecule:**sulfate adenylyltransferase subunit 2; **PDBTitle:** crystal structure of a gtp-regulated atp sulfurylase2 heterodimer from pseudomonas syringae
97	c2yxbA_	Alignment	not modelled	21.2	9	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**coenzyme b12-dependent mutase; **PDBTitle:** crystal structure of the methylmalonyl-coa mutase alpha-subunit from2 aeropyrum pernix
98	d1nuia1	Alignment	not modelled	20.9	11	**Fold:**DNA primase core **Superfamily:**DNA primase core **Family:**Primase fragment of primase-helicase protein
99	c3u9sE_	Alignment	not modelled	20.8	13	**PDB header:**ligase **Chain:** E: **PDB Molecule:**methylcrotonyl-coa carboxylase, alpha-subunit; **PDBTitle:** crystal structure of p. aeruginosa 3-methylcrotonyl-coa carboxylase2 (mcc) 750 kd holoenzyme, coa complex
100	d1cnza_	Alignment	not modelled	20.7	28	**Fold:**Isocitrate/Isopropylmalate dehydrogenase-like **Superfamily:**Isocitrate/Isopropylmalate dehydrogenase-like **Family:**Dimeric isocitrate & isopropylmalate dehydrogenases
101	d1vl2a1	Alignment	not modelled	20.4	13	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Adenine nucleotide alpha hydrolases-like **Family:**N-type ATP pyrophosphatases
102	c3u1hA_	Alignment	not modelled	20.4	32	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**3-isopropylmalate dehydrogenase; **PDBTitle:** crystal structure of ipmdh from the last common ancestor of bacillus
103	d1cm7a_	Alignment	not modelled	20.3	28	**Fold:**Isocitrate/Isopropylmalate dehydrogenase-like **Superfamily:**Isocitrate/Isopropylmalate dehydrogenase-like **Family:**Dimeric isocitrate & isopropylmalate dehydrogenases
104	d1t9ka_	Alignment	not modelled	20.2	9	**Fold:**NagB/RpiA/CoA transferase-like **Superfamily:**NagB/RpiA/CoA transferase-like **Family:**IF2B-like
						Fold: Isocitrate/Isopropylmalate dehydrogenase-like

105	d1xaca_	Alignment	not modelled	20.2	24	**Superfamily:**Isocitrate/Isopropylmalate dehydrogenase-like **Family:**Dimeric isocitrate & isopropylmalate dehydrogenases