Phyre^2

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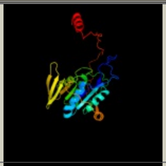
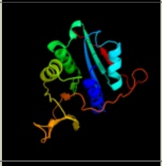
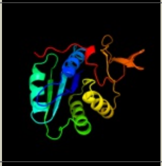
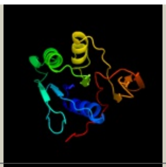
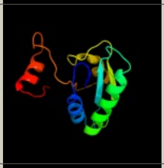
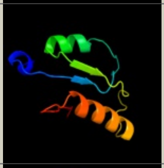
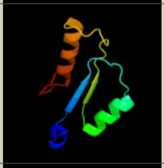
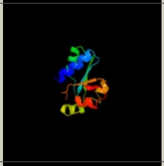
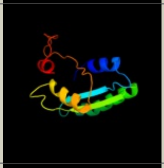
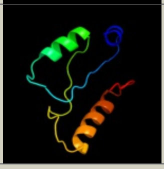
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1efvb_	Alignment		100.0	24	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Adenine nucleotide alpha hydrolases-like **Family:**ETFP subunits
2	d1efpb_	Alignment		100.0	27	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Adenine nucleotide alpha hydrolases-like **Family:**ETFP subunits
3	d3clsc1	Alignment		100.0	23	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Adenine nucleotide alpha hydrolases-like **Family:**ETFP subunits
4	d1o94c_	Alignment		100.0	25	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Adenine nucleotide alpha hydrolases-like **Family:**ETFP subunits
5	c1o94D_	Alignment		100.0	15	**PDB header:**electron transport **Chain:** D: **PDB Molecule:**electron transfer flavoprotein alpha-subunit; **PDBTitle:** ternary complex between trimethylamine dehydrogenase and2 electron transferring flavoprotein
6	d3clsd1	Alignment		100.0	16	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Adenine nucleotide alpha hydrolases-like **Family:**ETFP subunits
7	c3ih5A_	Alignment		99.9	16	**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
8	d1efva1	Alignment		99.9	17	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Adenine nucleotide alpha hydrolases-like **Family:**ETFP subunits
9	c1t9gR_	Alignment		99.9	17	**PDB header:**oxidoreductase, electron transport **Chain:** R: **PDB Molecule:**electron transfer flavoprotein alpha-subunit, **PDBTitle:** structure of the human mcad:etf complex
10	c1efpC_	Alignment		99.9	15	**PDB header:**electron transport **Chain:** C: **PDB Molecule:**protein (electron transfer flavoprotein); **PDBTitle:** electron transfer flavoprotein (etf) from paracoccus2 denitrificans
11	d1efpa1	Alignment		99.8	17	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Adenine nucleotide alpha hydrolases-like **Family:**ETFP subunits

12	c3fetA_	Alignment		99.7	11	**PDB header:**electron transport **Chain:** A: **PDB Molecule:**electron transfer flavoprotein subunit alpha related **PDBTitle:** crystal structure of the electron transfer flavoprotein subunit alpha2 related protein ta0212 from thermoplasma acidophilum
13	d1tq8a_	Alignment		95.9	17	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Adenine nucleotide alpha hydrolases-like **Family:**Universal stress protein-like
14	c2ixdB_	Alignment		95.2	10	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**lmbe-related protein; **PDBTitle:** crystal structure of the putative deacetylase bc1534 from2 bacilus cereus
15	d1uana_	Alignment		95.0	11	**Fold:**LmbE-like **Superfamily:**LmbE-like **Family:**LmbE-like
16	c3fg9B_	Alignment		94.2	19	**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
17	c2pfsA_	Alignment		94.0	20	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**universal stress protein; **PDBTitle:** crystal structure of universal stress protein from nitrosomonas2 europaea
18	c3mt0A_	Alignment		93.6	14	**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
19	c3fh0A_	Alignment		93.6	20	**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
20	d1q74a_	Alignment		92.4	15	**Fold:**LmbE-like **Superfamily:**LmbE-like **Family:**LmbE-like
21	d2z3va1	Alignment	not modelled	92.0	14	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Adenine nucleotide alpha hydrolases-like **Family:**Universal stress protein-like
22	d1q77a_	Alignment	not modelled	90.8	13	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Adenine nucleotide alpha hydrolases-like **Family:**Universal stress protein-like
23	c1q7tA_	Alignment	not modelled	89.9	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**hypothetical protein rv1170; **PDBTitle:** rv1170 (mshb) from mycobacterium tuberculosis
24	c3lpnB_	Alignment	not modelled	89.6	14	**PDB header:**transferase **Chain:** B: **PDB Molecule:**ribose-phosphate pyrophosphokinase; **PDBTitle:** crystal structure of the phosphoribosylpyrophosphate (prpp) synthetase2 from thermoplasma volcanium in complex with an atp analog (ampcpp).
25	c3hgmD_	Alignment	not modelled	89.5	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
26	c3loqA_	Alignment	not modelled	88.6	14	**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
27	d1miob_	Alignment	not modelled	88.2	15	**Fold:**Chelatase-like **Superfamily:**"Helical backbone" metal receptor **Family:**Nitrogenase iron-molybdenum protein
28	d1m1na_	Alignment	not modelled	84.8	13	**Fold:**Chelatase-like **Superfamily:**"Helical backbone" metal receptor **Family:**Nitrogenase iron-molybdenum protein

29	d1m1nb_	Alignment	not modelled	83.6	17	**Fold:**Chelatase-like **Superfamily:**"Helical backbone" metal receptor **Family:**Nitrogenase iron-molybdenum protein
30	c3dloC_	Alignment	not modelled	83.5	9	**PDB header:**structural genomics, unknown function **Chain:** C: **PDB Molecule:**universal stress protein; **PDBTitle:** structure of universal stress protein from archaeoglobus fulgidus
31	c1u9yD_	Alignment	not modelled	83.2	12	**PDB header:**transferase **Chain:** D: **PDB Molecule:**ribose-phosphate pyrophosphokinase; **PDBTitle:** crystal structure of phosphoribosyl diphosphate synthase2 from methanocaldococcus jannaschii
32	d1qh8b_	Alignment	not modelled	82.1	14	**Fold:**Chelatase-like **Superfamily:**"Helical backbone" metal receptor **Family:**Nitrogenase iron-molybdenum protein
33	d1ozha1	Alignment	not modelled	81.9	11	**Fold:**DHS-like NAD/FAD-binding domain **Superfamily:**DHS-like NAD/FAD-binding domain **Family:**Pyruvate oxidase and decarboxylase, middle domain
34	c3dfiA_	Alignment	not modelled	80.8	12	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**pseudoaglycone deacetylase dbv21; **PDBTitle:** the crystal structure of antimicrobial reagent a40926 pseudoaglycone2 deacetylase dbv21
35	c1dkrB_	Alignment	not modelled	80.3	12	**PDB header:**transferase **Chain:** B: **PDB Molecule:**phosphoribosyl pyrophosphate synthetase; **PDBTitle:** crystal structures of bacillus subtilis phosphoribosylpyrophosphate2 synthetase: molecular basis of allosteric inhibition and activation.
36	c3pdiG_	Alignment	not modelled	77.6	12	**PDB header:**protein binding **Chain:** G: **PDB Molecule:**nitrogenase mofe cofactor biosynthesis protein nife; **PDBTitle:** precursor bound nifen
37	d2gm3a1	Alignment	not modelled	77.4	11	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Adenine nucleotide alpha hydrolases-like **Family:**Universal stress protein-like
38	d1f6da_	Alignment	not modelled	77.2	15	**Fold:**UDP-Glycosyltransferase/glycogen phosphorylase **Superfamily:**UDP-Glycosyltransferase/glycogen phosphorylase **Family:**UDP-N-acetylglucosamine 2-epimerase
39	d2ji7a1	Alignment	not modelled	76.9	12	**Fold:**DHS-like NAD/FAD-binding domain **Superfamily:**DHS-like NAD/FAD-binding domain **Family:**Pyruvate oxidase and decarboxylase, middle domain
40	d2iyva1	Alignment	not modelled	76.5	10	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Shikimate kinase (AroK)
41	c2dy0A_	Alignment	not modelled	75.0	13	**PDB header:**transferase **Chain:** A: **PDB Molecule:**adenine phosphoribosyltransferase; **PDBTitle:** crystal structure of project jw0458 from escherichia coli
42	d1qh8a_	Alignment	not modelled	74.7	16	**Fold:**Chelatase-like **Superfamily:**"Helical backbone" metal receptor **Family:**Nitrogenase iron-molybdenum protein
43	d1a9xa3	Alignment	not modelled	73.5	16	**Fold:**PreATP-grasp domain **Superfamily:**PreATP-grasp domain **Family:**BC N-terminal domain-like
44	d1a9xa4	Alignment	not modelled	73.1	19	**Fold:**PreATP-grasp domain **Superfamily:**PreATP-grasp domain **Family:**BC N-terminal domain-like
45	d1jmva_	Alignment	not modelled	72.8	17	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Adenine nucleotide alpha hydrolases-like **Family:**Universal stress protein-like
46	c2ebdB_	Alignment	not modelled	71.9	16	**PDB header:**transferase **Chain:** B: **PDB Molecule:**3-oxoacyl-[acyl-carrier-protein] synthase 3; **PDBTitle:** crystal structure of 3-oxoacyl-[acyl-carrier-protein] synthase iii2 from aquifex aeolicus vf5
47	d1o57a2	Alignment	not modelled	71.8	17	**Fold:**PRTase-like **Superfamily:**PRTase-like **Family:**Phosphoribosyltransferases (PRTases)
48	c3s3tD_	Alignment	not modelled	71.4	17	**PDB header:**chaperone **Chain:** D: **PDB Molecule:**nucleotide-binding protein, universal stress protein uspa **PDBTitle:** universal stress protein uspa from lactobacillus plantarum
49	d1rkba_	Alignment	not modelled	70.4	20	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Nucleotide and nucleoside kinases
50	d1l1qa_	Alignment	not modelled	69.6	12	**Fold:**PRTase-like **Superfamily:**PRTase-like **Family:**Phosphoribosyltransferases (PRTases)
51	d1y0ba1	Alignment	not modelled	69.3	17	**Fold:**PRTase-like **Superfamily:**PRTase-like **Family:**Phosphoribosyltransferases (PRTases)
52	d1v4va_	Alignment	not modelled	69.2	21	**Fold:**UDP-Glycosyltransferase/glycogen phosphorylase **Superfamily:**UDP-Glycosyltransferase/glycogen phosphorylase **Family:**UDP-N-acetylglucosamine 2-epimerase
53	d1kaga_	Alignment	not modelled	69.2	9	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Shikimate kinase (AroK)
54	c3il5D_	Alignment	not modelled	68.9	11	**PDB header:**transferase **Chain:** D: **PDB Molecule:**3-oxoacyl-[acyl-carrier-protein] synthase 3; **PDBTitle:** structure of e. faecalis fabh in complex with 2-({4-

						bromo-3-2 [(diethylamino)sulfonyl]benzoyl}amino)benzoic acid
55	d1iowa1	Alignment	not modelled	68.0	20	**Fold:**PreATP-grasp domain **Superfamily:**PreATP-grasp domain **Family:**D-Alanine ligase N-terminal domain
56	c2c4kD_	Alignment	not modelled	67.1	11	**PDB header:**regulatory protein **Chain:** D: **PDB Molecule:**phosphoribosyl pyrophosphate synthetase- **PDBTitle:** crystal structure of human phosphoribosylpyrophosphate2 synthetase-associated protein 39 (pap39)
57	d1g2qa_	Alignment	not modelled	67.0	15	**Fold:**PRTase-like **Superfamily:**PRTase-like **Family:**Phosphoribosyltransferases (PRTases)
58	d1o6ca_	Alignment	not modelled	66.8	13	**Fold:**UDP-Glycosyltransferase/glycogen phosphorylase **Superfamily:**UDP-Glycosyltransferase/glycogen phosphorylase **Family:**UDP-N-acetylglucosamine 2-epimerase
59	c2qv5A_	Alignment	not modelled	66.6	12	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein atu2773; **PDBTitle:** crystal structure of uncharacterized protein atu2773 from2 agrobacterium tumefaciens c58
60	c3efhB_	Alignment	not modelled	65.5	11	**PDB header:**transferase **Chain:** B: **PDB Molecule:**ribose-phosphate pyrophosphokinase 1; **PDBTitle:** crystal structure of human phosphoribosyl pyrophosphate2 synthetase 1
61	c3olqA_	Alignment	not modelled	64.4	19	**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
62	c2ip4A_	Alignment	not modelled	63.5	20	**PDB header:**ligase **Chain:** A: **PDB Molecule:**phosphoribosylamine--glycine ligase; **PDBTitle:** crystal structure of glycinamide ribonucleotide synthetase from2 thermus thermophilus hb8
63	c1zuiA_	Alignment	not modelled	61.6	21	**PDB header:**transferase **Chain:** A: **PDB Molecule:**shikimate kinase; **PDBTitle:** structural basis for shikimate-binding specificity of helicobacter2 pylori shikimate kinase
64	c3ab8B_	Alignment	not modelled	61.6	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.
65	c2dumD_	Alignment	not modelled	61.5	18	**PDB header:**structural genomics, unknown function **Chain:** D: **PDB Molecule:**hypothetical protein ph0823; **PDBTitle:** crystal structure of hypothetical protein, ph0823
66	d2djia1	Alignment	not modelled	61.0	15	**Fold:**DHS-like NAD/FAD-binding domain **Superfamily:**DHS-like NAD/FAD-binding domain **Family:**Pyruvate oxidase and decarboxylase, middle domain
67	d2ez9a1	Alignment	not modelled	60.0	13	**Fold:**DHS-like NAD/FAD-binding domain **Superfamily:**DHS-like NAD/FAD-binding domain **Family:**Pyruvate oxidase and decarboxylase, middle domain
68	c3ot5D_	Alignment	not modelled	59.9	10	**PDB header:**isomerase **Chain:** D: **PDB Molecule:**udp-n-acetylglucosamine 2-epimerase; **PDBTitle:** 2.2 angstrom resolution crystal structure of putative udp-n-2 acetylglucosamine 2-epimerase from listeria monocytogenes
69	d1ybha1	Alignment	not modelled	59.5	17	**Fold:**DHS-like NAD/FAD-binding domain **Superfamily:**DHS-like NAD/FAD-binding domain **Family:**Pyruvate oxidase and decarboxylase, middle domain
70	c1kbiB_	Alignment	not modelled	58.9	16	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**cytochrome b2; **PDBTitle:** crystallographic study of the recombinant flavin-binding domain of2 baker's yeast flavocytochrome b2: comparison with the intact wild-3 type enzyme
71	c1o57A_	Alignment	not modelled	58.8	14	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**pur operon repressor; **PDBTitle:** crystal structure of the purine operon repressor of2 bacillus subtilis
72	c2nz2A_	Alignment	not modelled	58.5	15	**PDB header:**ligase **Chain:** A: **PDB Molecule:**argininosuccinate synthase; **PDBTitle:** crystal structure of human argininosuccinate synthase in complex with2 aspartate and citrulline
73	d2ptza1	Alignment	not modelled	58.1	9	**Fold:**TIM beta/alpha-barrel **Superfamily:**Enolase C-terminal domain-like **Family:**Enolase
74	d1viaa_	Alignment	not modelled	57.6	11	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Shikimate kinase (AroK)
75	d1e6ca_	Alignment	not modelled	57.6	14	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Shikimate kinase (AroK)
76	c3dfmA_	Alignment	not modelled	57.5	18	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**teicoplanin pseudoaglycone deacetylase orf2; **PDBTitle:** the crystal structure of the zinc inhibited form of2 teicoplanin deacetylase orf2
77	c1w96B_	Alignment	not modelled	57.0	10	**PDB header:**ligase **Chain:** B: **PDB Molecule:**acetyl-coenzyme a carboxylase; **PDBTitle:** crystal structure of biotin carboxylase domain of acetyl-2 coenzyme a carboxylase from saccharomyces cerevisiae in3 complex with soraphen a
78	c3s29C_	Alignment	not modelled	56.8	19	**PDB header:**transferase **Chain:** C: **PDB Molecule:**sucrose synthase 1; **PDBTitle:** the crystal structure of sucrose synthase-1 from arabidopsis thaliana2 and its functional implications.
79	c3op1A_	Alignment	not modelled	56.6	20	**PDB header:**transferase **Chain:** A: **PDB Molecule:**macrolide-efflux protein;

79	c3op1A_	Alignment	not modelled	56.6	20	**PDBTitle:** crystal structure of macrolide-efflux protein sp_1110 from2 streptococcus pneumoniae
80	d1vcfa1	Alignment	not modelled	56.5	13	**Fold:**TIM beta/alpha-barrel **Superfamily:**FMN-linked oxidoreductases **Family:**FMN-linked oxidoreductases
81	d1w0ma_	Alignment	not modelled	56.4	14	**Fold:**TIM beta/alpha-barrel **Superfamily:**Triosephosphate isomerase (TIM) **Family:**Triosephosphate isomerase (TIM)
82	c2pt5D_	Alignment	not modelled	56.3	22	**PDB header:**transferase **Chain:** D: **PDB Molecule:**shikimate kinase; **PDBTitle:** crystal structure of shikimate kinase (aq_2177) from aquifex aeolicus2 vf5
83	d1jlja_	Alignment	not modelled	55.3	13	**Fold:**Molybdenum cofactor biosynthesis proteins **Superfamily:**Molybdenum cofactor biosynthesis proteins **Family:**MogA-like
84	c3t61A_	Alignment	not modelled	54.8	18	**PDB header:**transferase **Chain:** A: **PDB Molecule:**gluconokinase; **PDBTitle:** crystal structure of a gluconokinase from sinorhizobium meliloti 1021
85	d1s3ga1	Alignment	not modelled	54.7	14	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Nucleotide and nucleoside kinases
86	c3fdiA_	Alignment	not modelled	54.3	19	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of uncharacterized protein from eubacterium2 ventriosum atcc 27560.
87	d2cdna1	Alignment	not modelled	53.7	21	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Nucleotide and nucleoside kinases
88	d1qb7a_	Alignment	not modelled	53.2	14	**Fold:**PRTase-like **Superfamily:**PRTase-like **Family:**Phosphoribosyltransferases (PRTases)
89	c1kh2D_	Alignment	not modelled	52.4	19	**PDB header:**ligase **Chain:** D: **PDB Molecule:**argininosuccinate synthetase; **PDBTitle:** crystal structure of thermus thermophilus hb82 argininosuccinate synthetase in complex with atp
90	d1ovma1	Alignment	not modelled	52.4	12	**Fold:**DHS-like NAD/FAD-binding domain **Superfamily:**DHS-like NAD/FAD-binding domain **Family:**Pyruvate oxidase and decarboxylase, middle domain
91	d1zpda1	Alignment	not modelled	52.3	13	**Fold:**DHS-like NAD/FAD-binding domain **Superfamily:**DHS-like NAD/FAD-binding domain **Family:**Pyruvate oxidase and decarboxylase, middle domain
92	c2v4wB_	Alignment	not modelled	52.0	11	**PDB header:**transferase **Chain:** B: **PDB Molecule:**hydroxymethylglutaryl-coa synthase, **PDBTitle:** crystal structure of human mitochondrial 3-hydroxy-3-2 methylglutaryl-coenzyme a synthase 2 (hmgcs2)
93	c3jyfB_	Alignment	not modelled	51.7	18	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**2',3'-cyclic nucleotide 2'-phosphodiesterase/3'- **PDBTitle:** the crystal structure of a 2,3-cyclic nucleotide 2-2 phosphodiesterase/3-nucleotidase bifunctional periplasmic precursor3 protein from klebsiella pneumoniae subsp. pneumoniae mgh 78578
94	c2h92C_	Alignment	not modelled	51.2	11	**PDB header:**transferase **Chain:** C: **PDB Molecule:**cytidylate kinase; **PDBTitle:** crystal structure of staphylococcus aureus cytidine2 monophosphate kinase in complex with cytidine-5'-3 monophosphate
95	c2vu2D_	Alignment	not modelled	50.8	11	**PDB header:**transferase **Chain:** D: **PDB Molecule:**acetyl-coa acetyltransferase; **PDBTitle:** biosynthetic thiolase from z. ramigera. complex with s-2 pantetheine-11-pivalate.
96	c3gwaA_	Alignment	not modelled	50.8	13	**PDB header:**transferase **Chain:** A: **PDB Molecule:**3-oxoacyl-(acyl-carrier-protein) synthase iii; **PDBTitle:** 1.6 angstrom crystal structure of 3-oxoacyl-(acyl-carrier-protein)2 synthase iii
97	c3gmtB_	Alignment	not modelled	50.8	18	**PDB header:**transferase **Chain:** B: **PDB Molecule:**adenylate kinase; **PDBTitle:** crystal structure of adenylate kinase from burkholderia pseudomallei
98	d1zina1	Alignment	not modelled	50.5	14	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Nucleotide and nucleoside kinases
99	c2eu8B_	Alignment	not modelled	50.3	21	**PDB header:**transferase **Chain:** B: **PDB Molecule:**adenylate kinase; **PDBTitle:** crystal structure of a thermostable mutant of bacillus2 subtilis adenylate kinase (q199r)
100	c3hdtB_	Alignment	not modelled	50.1	21	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**putative kinase; **PDBTitle:** crystal structure of putative kinase from clostridium symbiosum atcc2 14940
101	c1m6vE_	Alignment	not modelled	50.0	16	**PDB header:**ligase **Chain:** E: **PDB Molecule:**carbamoyl phosphate synthetase large chain; **PDBTitle:** crystal structure of the g359f (small subunit) point mutant of2 carbamoyl phosphate synthetase
102	c2bwjC_	Alignment	not modelled	49.7	11	**PDB header:**transferase **Chain:** C: **PDB Molecule:**adenylate kinase 5; **PDBTitle:** structure of adenylate kinase 5
103	c2grjH_	Alignment	not modelled	49.6	14	**PDB header:**transferase **Chain:** H: **PDB Molecule:**dephospho-coa kinase; **PDBTitle:** crystal structure of dephospho-coa kinase (ec 2.7.1.24)2 (dephosphocoenzyme a kinase) (tm1387) from thermotoga maritima at3 2.60 a resolution

104	d1di6a_	Alignment	not modelled	49.5	10	**Fold:**Molybdenum cofactor biosynthesis proteins **Superfamily:**Molybdenum cofactor biosynthesis proteins **Family:**MogA-like
105	c2ar7A_	Alignment	not modelled	49.5	14	**PDB header:**transferase **Chain:** A: **PDB Molecule:**adenylate kinase 4; **PDBTitle:** crystal structure of human adenylate kinase 4, ak4
106	d1e4va1	Alignment	not modelled	49.3	14	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Nucleotide and nucleoside kinases
107	d1vcha1	Alignment	not modelled	48.7	22	**Fold:**PRTase-like **Superfamily:**PRTase-like **Family:**Phosphoribosyltransferases (PRTases)
108	c1ankA_	Alignment	not modelled	48.4	14	**PDB header:**transferase(phosphotransferase) **Chain:** A: **PDB Molecule:**adenylate kinase; **PDBTitle:** the closed conformation of a highly flexible protein: the2 structure of e. coli adenylate kinase with bound amp and3 amppnp
109	c3be4A_	Alignment	not modelled	48.1	9	**PDB header:**transferase **Chain:** A: **PDB Molecule:**adenylate kinase; **PDBTitle:** crystal structure of cryptosporidium parvum adenylate kinase cgd5_3360
110	d1mzva_	Alignment	not modelled	48.0	14	**Fold:**PRTase-like **Superfamily:**PRTase-like **Family:**Phosphoribosyltransferases (PRTases)
111	d1zaka1	Alignment	not modelled	48.0	21	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Nucleotide and nucleoside kinases
112	d1rqba2	Alignment	not modelled	47.9	14	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**HMGL-like
113	c2rhmD_	Alignment	not modelled	47.9	14	**PDB header:**unknown function **Chain:** D: **PDB Molecule:**putative kinase; **PDBTitle:** crystal structure of a putative kinase (caur_3907) from chloroflexus2 aurantiacus j-10-fl at 1.70 a resolution
114	d1knqa_	Alignment	not modelled	47.9	18	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Gluconate kinase
115	d1zn7a1	Alignment	not modelled	47.6	20	**Fold:**PRTase-like **Superfamily:**PRTase-like **Family:**Phosphoribosyltransferases (PRTases)
116	d2ihta1	Alignment	not modelled	47.5	23	**Fold:**DHS-like NAD/FAD-binding domain **Superfamily:**DHS-like NAD/FAD-binding domain **Family:**Pyruvate oxidase and decarboxylase, middle domain
117	c3r8cB_	Alignment	not modelled	47.0	11	**PDB header:**transferase **Chain:** B: **PDB Molecule:**cytidylate kinase; **PDBTitle:** crystal structure of cytidylate kinase (cmk) from mycobacterium2 abscessus
118	c2vliB_	Alignment	not modelled	46.8	14	**PDB header:**transferase **Chain:** B: **PDB Molecule:**antibiotic resistance protein; **PDBTitle:** structure of deinococcus radiodurans tunicamycin resistance2 protein
119	c1s3gA_	Alignment	not modelled	46.2	14	**PDB header:**transferase **Chain:** A: **PDB Molecule:**adenylate kinase; **PDBTitle:** crystal structure of adenylate kinase from bacillus2 globisporus
120	c3trfB_	Alignment	not modelled	45.8	11	**PDB header:**transferase **Chain:** B: **PDB Molecule:**shikimate kinase; **PDBTitle:** structure of a shikimate kinase (arok) from coxiella burnetii