Phyre2

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Description	P10378
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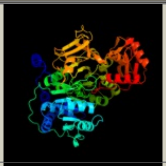
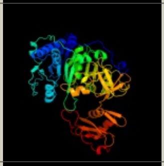
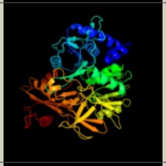
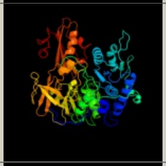
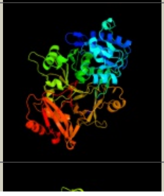
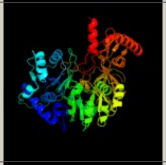
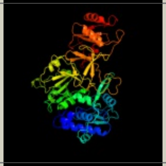
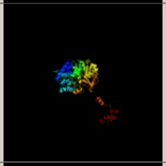
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1mdba_	Alignment		100.0	47	**Fold:**Acetyl-CoA synthetase-like **Superfamily:**Acetyl-CoA synthetase-like **Family:**Acetyl-CoA synthetase-like
2	d1pg4a_	Alignment		100.0	21	**Fold:**Acetyl-CoA synthetase-like **Superfamily:**Acetyl-CoA synthetase-like **Family:**Acetyl-CoA synthetase-like
3	d1ry2a_	Alignment		100.0	20	**Fold:**Acetyl-CoA synthetase-like **Superfamily:**Acetyl-CoA synthetase-like **Family:**Acetyl-CoA synthetase-like
4	c2vsqA_	Alignment		100.0	23	**PDB header:**ligase **Chain:** A: **PDB Molecule:**surfactin synthetase subunit 3; **PDBTitle:** structure of surfactin a synthetase c (srfa-c), a2 nonribosomal peptide synthetase termination module
5	d3cw9a1	Alignment		100.0	20	**Fold:**Acetyl-CoA synthetase-like **Superfamily:**Acetyl-CoA synthetase-like **Family:**Acetyl-CoA synthetase-like
6	c3e7wA_	Alignment		100.0	18	**PDB header:**ligase **Chain:** A: **PDB Molecule:**d-alanine--poly(phosphoribitol) ligase subunit 1; **PDBTitle:** crystal structure of dlta: implications for the reaction2 mechanism of non-ribosomal peptide synthetase (nrps)3 adenylation domains
7	c3ni2A_	Alignment		100.0	20	**PDB header:**ligase **Chain:** A: **PDB Molecule:**4-coumarate:coa ligase; **PDBTitle:** crystal structures and enzymatic mechanisms of a populus tomentosa 4-2 coumarate:coa ligase
8	d1amua_	Alignment		100.0	20	**Fold:**Acetyl-CoA synthetase-like **Superfamily:**Acetyl-CoA synthetase-like **Family:**Acetyl-CoA synthetase-like
9	c3eynB_	Alignment		100.0	20	**PDB header:**ligase **Chain:** B: **PDB Molecule:**acyl-coenzyme a synthetase acsm2a; **PDBTitle:** crystal structure of human acyl-coa synthetase medium-chain2 family member 2a (l64p mutation) in a complex with coa
10	c3etcB_	Alignment		100.0	18	**PDB header:**ligase **Chain:** B: **PDB Molecule:**amp-binding protein; **PDBTitle:** 2.1 a structure of acyl-adenylate synthetase from methanosarcina2 acetivorans containing a link between lys256 and cys298
11	c1amuB_	Alignment		100.0	19	**PDB header:**peptide synthetase **Chain:** B: **PDB Molecule:**gramicidin synthetase 1; **PDBTitle:** phenylalanine activating domain of gramicidin synthetase 12 in a complex with amp and phenylalanine

12	c2d1tA_	Alignment		100.0	18	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**luciferin 4-monooxygenase; **PDBTitle:** crystal structure of the thermostable japanese firefly2 luciferase red-color emission s286n mutant complexed with3 high-energy intermediate analogue
13	c3dhvA_	Alignment		100.0	18	**PDB header:**ligase **Chain:** A: **PDB Molecule:**d-alanine-poly(phosphoribitol) ligase; **PDBTitle:** crystal structure of dlta protein in complex with d-alanine2 adenylate
14	c3gqwB_	Alignment		100.0	18	**PDB header:**ligase **Chain:** B: **PDB Molecule:**fatty acid amp ligase; **PDBTitle:** crystal structure of a fatty acid amp ligase from e. coli with an acyl2 adenylate product bound
15	c2v7bB_	Alignment		100.0	23	**PDB header:**ligase **Chain:** B: **PDB Molecule:**benzoate-coenzyme a ligase; **PDBTitle:** crystal structures of a benzoate coa ligase from2 burkholderia xenovorans lb400
16	c3iteB_	Alignment		100.0	15	**PDB header:**ligase **Chain:** B: **PDB Molecule:**sidn siderophore synthetase; **PDBTitle:** the third adenylation domain of the fungal sidn non-2 ribosomal peptide synthetase
17	c3kxwA_	Alignment		100.0	16	**PDB header:**ligase **Chain:** A: **PDB Molecule:**saframycin mx1 synthetase b; **PDBTitle:** the crystal structure of fatty acid amp ligase from legionella2 pneumophila
18	d1lcia_	Alignment		100.0	19	**Fold:**Acetyl-CoA synthetase-like **Superfamily:**Acetyl-CoA synthetase-like **Family:**Acetyl-CoA synthetase-like
19	c3tsyA_	Alignment		100.0	19	**PDB header:**ligase, transferase **Chain:** A: **PDB Molecule:**fusion protein 4-coumarate--coa ligase 1, resveratrol **PDBTitle:** 4-coumaroyl-coa ligase::stilbene synthase fusion protein
20	c3l8cA_	Alignment		100.0	19	**PDB header:**ligase **Chain:** A: **PDB Molecule:**d-alanine--poly(phosphoribitol) ligase subunit 1; **PDBTitle:** structure of probable d-alanine--poly(phosphoribitol) ligase2 subunit-1 from streptococcus pyogenes
21	c3nyrA_	Alignment	not modelled	100.0	27	**PDB header:**ligase **Chain:** A: **PDB Molecule:**malonyl-coa ligase; **PDBTitle:** malonyl-coa ligase ternary product complex with malonyl-coa and amp2 bound
22	c3iplB_	Alignment	not modelled	100.0	24	**PDB header:**ligase **Chain:** B: **PDB Molecule:**2-succinylbenzoate--coa ligase; **PDBTitle:** crystal structure of o-succinylbenzoic acid-coa ligase from2 staphylococcus aureus subsp. aureus mu50
23	d1v25a_	Alignment	not modelled	100.0	21	**Fold:**Acetyl-CoA synthetase-like **Superfamily:**Acetyl-CoA synthetase-like **Family:**Acetyl-CoA synthetase-like
24	c3g7sA_	Alignment	not modelled	100.0	23	**PDB header:**ligase **Chain:** A: **PDB Molecule:**long-chain-fatty-acid--coa ligase (fadd-1); **PDBTitle:** crystal structure of a long-chain-fatty-acid-coa ligase2 (fadd1) from archaeoglobus fulgidus
25	c3o82B_	Alignment	not modelled	100.0	53	**PDB header:**ligase **Chain:** B: **PDB Molecule:**peptide arylation enzyme; **PDBTitle:** structure of base n-terminal domain from acinetobacter baumannii bound2 to 5'-o-[n-(2,3-dihydroxybenzoyl)sulfamoyl] adenosine
26	c3o82A_	Alignment	not modelled	100.0	53	**PDB header:**ligase **Chain:** A: **PDB Molecule:**peptide arylation enzyme; **PDBTitle:** structure of base n-terminal domain from acinetobacter baumannii bound2 to 5'-o-[n-(2,3-dihydroxybenzoyl)sulfamoyl] adenosine
27	c3ivrA_	Alignment	not modelled	100.0	22	**PDB header:**ligase **Chain:** A: **PDB Molecule:**putative long-chain-fatty-acid coa ligase; **PDBTitle:** crystal structure of putative long-chain-fatty-acid coa ligase from2 rhodopseudomonas palustris cga009
28	c3e53A_	Alignment	not modelled	100.0	17	**PDB header:**ligase **Chain:** A: **PDB Molecule:**fatty-acid-coa ligase fadd28; **PDBTitle:** crystal structure of n-terminal domain of a fatty acyl

						amp2 ligase faal28 from mycobacterium tuberculosis
29	c2y4oA_	Alignment	not modelled	100.0	16	**PDB header:**ligase **Chain:** A: **PDB Molecule:**phenylacetate-coenzyme a ligase; **PDBTitle:** crystal structure of paak2 in complex with phenylacetyl adenylate
30	c2y27B_	Alignment	not modelled	100.0	14	**PDB header:**ligase **Chain:** B: **PDB Molecule:**phenylacetate-coenzyme a ligase; **PDBTitle:** crystal structure of paak1 in complex with atp from2 burkholderia cenocepacia
31	c3qovD_	Alignment	not modelled	100.0	15	**PDB header:**ligase **Chain:** D: **PDB Molecule:**phenylacetate-coenzyme a ligase; **PDBTitle:** crystal structure of a hypothetical acyl-coa ligase (bt_0428) from2 bacteroides thetaiotaomicron vpi-5482 at 2.20 a resolution
32	c3hguB_	Alignment	not modelled	99.7	13	**PDB header:**biosynthetic protein **Chain:** B: **PDB Molecule:**ehpf; **PDBTitle:** structure of phenazine antibiotic biosynthesis protein
33	c3laxA_	Alignment	not modelled	99.6	23	**PDB header:**ligase **Chain:** A: **PDB Molecule:**phenylacetate-coenzyme a ligase; **PDBTitle:** the crystal structure of a domain of phenylacetate-coenzyme2 a ligase from bacteroides vulgatus atcc 8482
34	d1f06a2	Alignment	not modelled	82.4	21	**Fold:**FwdE/GAPDH domain-like **Superfamily:**Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain **Family:**Dihydrodipicolinate reductase-like
35	d2ayia1	Alignment	not modelled	76.3	13	**Fold:**Thermophilic metalloprotease-like **Superfamily:**Thermophilic metalloprotease-like **Family:**Thermophilic metalloprotease (M29)
36	d1pl8a2	Alignment	not modelled	72.4	15	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Alcohol dehydrogenase-like, C-terminal domain
37	d1piwa2	Alignment	not modelled	68.8	17	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Alcohol dehydrogenase-like, C-terminal domain
38	d1e3ja2	Alignment	not modelled	65.7	19	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Alcohol dehydrogenase-like, C-terminal domain
39	c3smaD_	Alignment	not modelled	65.2	30	**PDB header:**transferase **Chain:** D: **PDB Molecule:**frbf; **PDBTitle:** a new n-acetyltransferase fold in the structure and mechanism of the2 phosphonate biosynthetic enzyme frbf
40	c3e4fB_	Alignment	not modelled	61.1	30	**PDB header:**transferase **Chain:** B: **PDB Molecule:**aminoglycoside n3-acetyltransferase; **PDBTitle:** crystal structure of ba2930- a putative aminoglycoside n3-2 acetyltransferase from bacillus anthracis
41	d1kola2	Alignment	not modelled	60.1	16	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Alcohol dehydrogenase-like, C-terminal domain
42	d1z7wa1	Alignment	not modelled	55.0	11	**Fold:**Tryptophan synthase beta subunit-like PLP-dependent enzymes **Superfamily:**Tryptophan synthase beta subunit-like PLP-dependent enzymes **Family:**Tryptophan synthase beta subunit-like PLP-dependent enzymes
43	d1rjwa2	Alignment	not modelled	54.2	15	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Alcohol dehydrogenase-like, C-terminal domain
44	d2nyga1	Alignment	not modelled	53.6	25	**Fold:**TTHA0583/YokD-like **Superfamily:**TTHA0583/YokD-like **Family:**Aminoglycoside 3-N-acetyltransferase-like
45	d1d1ta2	Alignment	not modelled	46.9	12	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Alcohol dehydrogenase-like, C-terminal domain
46	d1iz0a2	Alignment	not modelled	45.1	22	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Alcohol dehydrogenase-like, C-terminal domain
47	d1fcja_	Alignment	not modelled	42.3	12	**Fold:**Tryptophan synthase beta subunit-like PLP-dependent enzymes **Superfamily:**Tryptophan synthase beta subunit-like PLP-dependent enzymes **Family:**Tryptophan synthase beta subunit-like PLP-dependent enzymes
48	d1llua2	Alignment	not modelled	41.8	14	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Alcohol dehydrogenase-like, C-terminal domain
49	d1ykfa2	Alignment	not modelled	41.8	15	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Alcohol dehydrogenase-like, C-terminal domain
50	d1uufa2	Alignment	not modelled	40.7	15	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Alcohol dehydrogenase-like, C-terminal domain
51	d1e3ia2	Alignment	not modelled	40.6	8	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Alcohol dehydrogenase-like, C-terminal domain
52	d1udxa3	Alignment	not modelled	39.3	17	**Fold:**Obg GTP-binding protein C-terminal domain **Superfamily:**Obg GTP-binding protein C-terminal domain **Family:**Obg GTP-binding protein C-terminal domain
53	c3ippA_	Alignment	not modelled	37.1	20	**PDB header:**transferase **Chain:** A: **PDB Molecule:**putative thiosulfate sulfurtransferase ynje; **PDBTitle:** crystal structure of sulfur-free ynje
						Fold:NAD(P)-binding Rossmann-fold domains

54	d1jqba2	Alignment	not modelled	35.9	13	**Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Alcohol dehydrogenase-like, C-terminal domain
55	d1p0fa2	Alignment	not modelled	35.8	8	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Alcohol dehydrogenase-like, C-terminal domain
56	c1uarA_	Alignment	not modelled	32.5	18	**PDB header:**transferase **Chain:** A: **PDB Molecule:**rhodanese; **PDBTitle:** crystal structure of rhodanese from thermus thermophilus hb8
57	d1jvba2	Alignment	not modelled	32.0	15	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Alcohol dehydrogenase-like, C-terminal domain
58	c2ywiA_	Alignment	not modelled	29.8	20	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical conserved protein; **PDBTitle:** crystal structure of uncharacterized conserved protein from2 geobacillus kaustophilus
59	c2jx2A_	Alignment	not modelled	29.5	17	**PDB header:**transcription **Chain:** A: **PDB Molecule:**negative elongation factor e; **PDBTitle:** solution conformation of rna-bound nelf-e rrm
60	c2q3bA_	Alignment	not modelled	28.9	8	**PDB header:**transferase **Chain:** A: **PDB Molecule:**cysteine synthase a; **PDBTitle:** 1.8 a resolution crystal structure of o-acetylserine sulfhydrylase2 (oass) holoenzyme from mycobacterium tuberculosis
61	d2fzwa2	Alignment	not modelled	28.9	7	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Alcohol dehydrogenase-like, C-terminal domain
62	c3olhA_	Alignment	not modelled	27.5	5	**PDB header:**transferase **Chain:** A: **PDB Molecule:**3-mercaptopyruvate sulfurtransferase; **PDBTitle:** human 3-mercaptopyruvate sulfurtransferase
63	d2jhfa2	Alignment	not modelled	26.5	7	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Alcohol dehydrogenase-like, C-terminal domain
64	c3bcxA_	Alignment	not modelled	26.4	23	**PDB header:**transferase **Chain:** A: **PDB Molecule:**cdp-6-deoxy-l-threo-d-glycero-4-hexulose-3- **PDBTitle:** e1 dehydrase
65	d1y7la1	Alignment	not modelled	26.2	12	**Fold:**Tryptophan synthase beta subunit-like PLP-dependent enzymes **Superfamily:**Tryptophan synthase beta subunit-like PLP-dependent enzymes **Family:**Tryptophan synthase beta subunit-like PLP-dependent enzymes
66	d1u3wa2	Alignment	not modelled	25.4	8	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Alcohol dehydrogenase-like, C-terminal domain
67	d1cdoa2	Alignment	not modelled	23.6	10	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Alcohol dehydrogenase-like, C-terminal domain
68	c3nnkC_	Alignment	not modelled	23.2	11	**PDB header:**transferase **Chain:** C: **PDB Molecule:**ureidoglycine-glyoxylate aminotransferase; **PDBTitle:** biochemical and structural characterization of a ureidoglycine2 aminotransferase in the klebsiella pneumoniae uric acid catabolic3 pathway
69	d1zjca1	Alignment	not modelled	23.1	10	**Fold:**Thermophilic metalloprotease-like **Superfamily:**Thermophilic metalloprotease-like **Family:**Thermophilic metalloprotease (M29)
70	c3l6cA_	Alignment	not modelled	22.2	9	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**serine racemase; **PDBTitle:** x-ray crystal structure of rat serine racemase in complex with2 malonate a potent inhibitor
71	d1yb5a2	Alignment	not modelled	21.1	14	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Alcohol dehydrogenase-like, C-terminal domain
72	d1f8fa2	Alignment	not modelled	21.1	10	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Alcohol dehydrogenase-like, C-terminal domain
73	d1pqwa_	Alignment	not modelled	20.4	17	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Alcohol dehydrogenase-like, C-terminal domain
74	d1nula_	Alignment	not modelled	19.3	14	**Fold:**PRTase-like **Superfamily:**PRTase-like **Family:**Phosphoribosyltransferases (PRTases)
75	d2bhsa1	Alignment	not modelled	19.2	10	**Fold:**Tryptophan synthase beta subunit-like PLP-dependent enzymes **Superfamily:**Tryptophan synthase beta subunit-like PLP-dependent enzymes **Family:**Tryptophan synthase beta subunit-like PLP-dependent enzymes
76	c2jkzB_	Alignment	not modelled	19.1	21	**PDB header:**transferase **Chain:** B: **PDB Molecule:**hypoxanthine-guanine phosphoribosyltransferase; **PDBTitle:** saccharomyces cerevisiae hypoxanthine-guanine2 phosphoribosyltransferase in complex with gmp (guanosine 5'3 -monophosphate) (orthorhombic crystal form)
77	d1qora2	Alignment	not modelled	19.1	15	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Alcohol dehydrogenase-like, C-terminal domain
78	d1v3va2	Alignment	not modelled	19.0	25	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Alcohol dehydrogenase-like, C-terminal domain

79	c1okgA_	Alignment	not modelled	19.0	12	**PDB header:**transferase **Chain:** A: **PDB Molecule:**possible 3-mercaptopyruvate sulfurtransferase; **PDBTitle:** 3-mercaptopyruvate sulfurtransferase from leishmania major
80	d1okga1	Alignment	not modelled	17.4	12	**Fold:**Rhodanese/Cell cycle control phosphatase **Superfamily:**Rhodanese/Cell cycle control phosphatase **Family:**Multidomain sulfurtransferase (rhodanese)
81	d1ja1a1	Alignment	not modelled	17.3	19	**Fold:**Reductase/isomerase/elongation factor common domain **Superfamily:**Riboflavin synthase domain-like **Family:**NADPH-cytochrome p450 reductase FAD-binding domain-like
82	d1l9xa_	Alignment	not modelled	16.1	15	**Fold:**Flavodoxin-like **Superfamily:**Class I glutamine amidotransferase-like **Family:**Class I glutamine amidotransferases (GAT)
83	c1l9xA_	Alignment	not modelled	16.1	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**gamma-glutamyl hydrolase; **PDBTitle:** structure of gamma-glutamyl hydrolase
84	c2zy3A_	Alignment	not modelled	16.0	19	**PDB header:**lyase **Chain:** A: **PDB Molecule:**l-aspartate beta-decarboxylase; **PDBTitle:** dodecameric l-aspartate beta-decarboxylase
85	c3dwgA_	Alignment	not modelled	15.8	7	**PDB header:**transferase **Chain:** A: **PDB Molecule:**cysteine synthase b; **PDBTitle:** crystal structure of a sulfur carrier protein complex found in the2 cysteine biosynthetic pathway of mycobacterium tuberculosis
86	c2uv0G_	Alignment	not modelled	15.3	14	**PDB header:**transcription **Chain:** G: **PDB Molecule:**transcriptional activator protein lasr; **PDBTitle:** structure of the p. aeruginosa lasr ligand-binding domain2 bound to its autoinducer
87	c3aaxB_	Alignment	not modelled	15.3	20	**PDB header:**transferase **Chain:** B: **PDB Molecule:**putative thiosulfate sulfurtransferase; **PDBTitle:** crystal structure of probable thiosulfate sulfurtransferase2 cysa3 (rv3117) from mycobacterium tuberculosis: monoclinic3 form
88	c2eguA_	Alignment	not modelled	15.2	9	**PDB header:**transferase **Chain:** A: **PDB Molecule:**cysteine synthase; **PDBTitle:** crystal structure of o-acetylserine sulfhydrase from geobacillus2 kaustophilus hta426
89	d1uara2	Alignment	not modelled	15.0	18	**Fold:**Rhodanese/Cell cycle control phosphatase **Superfamily:**Rhodanese/Cell cycle control phosphatase **Family:**Multidomain sulfurtransferase (rhodanese)
90	d1i1ga2	Alignment	not modelled	14.7	16	**Fold:**Ferredoxin-like **Superfamily:**Dimeric alpha+beta barrel **Family:**Lrp/AsnC-like transcriptional regulator C-terminal domain
91	d1a3xa3	Alignment	not modelled	14.7	20	**Fold:**Pyruvate kinase C-terminal domain-like **Superfamily:**PK C-terminal domain-like **Family:**Pyruvate kinase, C-terminal domain
92	d1v71a1	Alignment	not modelled	14.6	11	**Fold:**Tryptophan synthase beta subunit-like PLP-dependent enzymes **Superfamily:**Tryptophan synthase beta subunit-like PLP-dependent enzymes **Family:**Tryptophan synthase beta subunit-like PLP-dependent enzymes
93	d1qz9a_	Alignment	not modelled	13.2	11	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**Cystathionine synthase-like
94	d1liua3	Alignment	not modelled	13.1	13	**Fold:**Pyruvate kinase C-terminal domain-like **Superfamily:**PK C-terminal domain-like **Family:**Pyruvate kinase, C-terminal domain
95	d1ve1a1	Alignment	not modelled	13.0	12	**Fold:**Tryptophan synthase beta subunit-like PLP-dependent enzymes **Superfamily:**Tryptophan synthase beta subunit-like PLP-dependent enzymes **Family:**Tryptophan synthase beta subunit-like PLP-dependent enzymes
96	d1f20a1	Alignment	not modelled	12.9	26	**Fold:**Reductase/isomerase/elongation factor common domain **Superfamily:**Riboflavin synthase domain-like **Family:**NADPH-cytochrome p450 reductase FAD-binding domain-like
97	d1l3la2	Alignment	not modelled	12.1	13	**Fold:**Profilin-like **Superfamily:**Pheromone-binding domain of LuxR-like quorum-sensing transcription factors **Family:**Pheromone-binding domain of LuxR-like quorum-sensing transcription factors
98	c3g8qA_	Alignment	not modelled	11.9	17	**PDB header:**rna binding protein **Chain:** A: **PDB Molecule:**predicted rna-binding protein, contains thump **PDBTitle:** a cytidine deaminase edits c-to-u in transfer rnas in2 archaea
99	d1jjcb4	Alignment	not modelled	11.6	24	**Fold:**Ferredoxin-like **Superfamily:**Anticodon-binding domain of PheRS **Family:**Anticodon-binding domain of PheRS