Phyre^2

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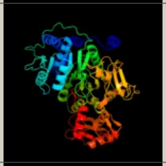
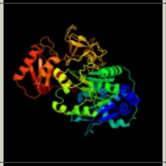
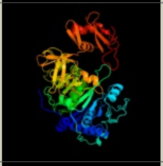
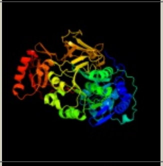
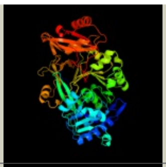
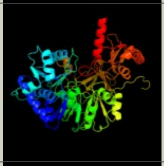
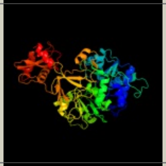
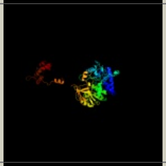
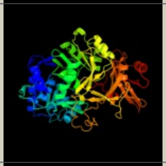
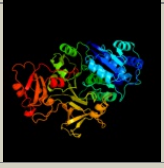
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1pg4a_	Alignment		100.0	23	**Fold:**Acetyl-CoA synthetase-like **Superfamily:**Acetyl-CoA synthetase-like **Family:**Acetyl-CoA synthetase-like
2	d1mdba_	Alignment		100.0	29	**Fold:**Acetyl-CoA synthetase-like **Superfamily:**Acetyl-CoA synthetase-like **Family:**Acetyl-CoA synthetase-like
3	d1ry2a_	Alignment		100.0	22	**Fold:**Acetyl-CoA synthetase-like **Superfamily:**Acetyl-CoA synthetase-like **Family:**Acetyl-CoA synthetase-like
4	c3e7wA_	Alignment		100.0	19	**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
5	c2vsqA_	Alignment		100.0	24	**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
6	d3cw9a1	Alignment		100.0	21	**Fold:**Acetyl-CoA synthetase-like **Superfamily:**Acetyl-CoA synthetase-like **Family:**Acetyl-CoA synthetase-like
7	c3ni2A_	Alignment		100.0	26	**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	c3etcB_	Alignment		100.0	24	**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
9	c3eynB_	Alignment		100.0	25	**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	d1amua_	Alignment		100.0	21	**Fold:**Acetyl-CoA synthetase-like **Superfamily:**Acetyl-CoA synthetase-like **Family:**Acetyl-CoA synthetase-like
11	c2d1tA_	Alignment		100.0	25	**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

12	c1amuB_	Alignment		100.0	22	**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
13	c3gqwB_	Alignment		100.0	22	**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
14	c3dhvA_	Alignment		100.0	22	**PDB header:**ligase **Chain:** A: **PDB Molecule:**d-alanine-poly(phosphoribitol) ligase; **PDBTitle:** crystal structure of dlta protein in complex with d-alanine2 adenylate
15	c3kxwA_	Alignment		100.0	19	**PDB header:**ligase **Chain:** A: **PDB Molecule:**saframycin mx1 synthetase b; **PDBTitle:** the crystal structure of fatty acid amp ligase from legionella2 pneumophila
16	c3iteB_	Alignment		100.0	20	**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	d1lcia_	Alignment		100.0	23	**Fold:**Acetyl-CoA synthetase-like **Superfamily:**Acetyl-CoA synthetase-like **Family:**Acetyl-CoA synthetase-like
18	c3tsyA_	Alignment		100.0	22	**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
19	c2v7bB_	Alignment		100.0	24	**PDB header:**ligase **Chain:** B: **PDB Molecule:**benzoate-coenzyme a ligase; **PDBTitle:** crystal structures of a benzoate coa ligase from2 burkholderia xenovorans lb400
20	c3l8cA_	Alignment		100.0	18	**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	d1v25a_	Alignment	not modelled	100.0	24	**Fold:**Acetyl-CoA synthetase-like **Superfamily:**Acetyl-CoA synthetase-like **Family:**Acetyl-CoA synthetase-like
22	c3ipIB_	Alignment	not modelled	100.0	25	**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	c3nyrA_	Alignment	not modelled	100.0	28	**PDB header:**ligase **Chain:** A: **PDB Molecule:**malonyl-coa ligase; **PDBTitle:** malonyl-coa ligase ternary product complex with malonyl-coa and amp2 bound
24	c3g7sA_	Alignment	not modelled	100.0	21	**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	26	**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	25	**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	26	**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
		Alignment				**PDB header:**ligase

28	c3e53A_	Alignment	not modelled	100.0	22	**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	18	**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	16	**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	c3laxA_	Alignment	not modelled	99.6	15	**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
33	c3hguB_	Alignment	not modelled	99.5	17	**PDB header:**biosynthetic protein **Chain:** B: **PDB Molecule:**ehpf; **PDBTitle:** structure of phenazine antibiotic biosynthesis protein
34	d2ayia1	Alignment	not modelled	85.0	20	**Fold:**Thermophilic metalloprotease-like **Superfamily:**Thermophilic metalloprotease-like **Family:**Thermophilic metalloprotease (M29)
35	c3l6cA_	Alignment	not modelled	78.8	8	**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
36	d1piwa2	Alignment	not modelled	66.2	9	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Alcohol dehydrogenase-like, C-terminal domain
37	c3smaD_	Alignment	not modelled	58.2	20	**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
38	d2nyga1	Alignment	not modelled	53.8	18	**Fold:**TTHA0583/YokD-like **Superfamily:**TTHA0583/YokD-like **Family:**Aminoglycoside 3-N-acetyltransferase-like
39	d1pl8a2	Alignment	not modelled	53.8	14	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Alcohol dehydrogenase-like, C-terminal domain
40	d1llua2	Alignment	not modelled	52.8	9	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Alcohol dehydrogenase-like, C-terminal domain
41	c3ippA_	Alignment	not modelled	52.1	10	**PDB header:**transferase **Chain:** A: **PDB Molecule:**putative thiosulfate sulfurtransferase ynje; **PDBTitle:** crystal structure of sulfur-free ynje
42	d1kola2	Alignment	not modelled	51.5	12	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Alcohol dehydrogenase-like, C-terminal domain
43	d1f06a2	Alignment	not modelled	46.8	20	**Fold:**FwdE/GAPDH domain-like **Superfamily:**Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain **Family:**Dihydrodipicolinate reductase-like
44	d1e3ja2	Alignment	not modelled	46.7	13	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Alcohol dehydrogenase-like, C-terminal domain
45	c1uarA_	Alignment	not modelled	46.3	13	**PDB header:**transferase **Chain:** A: **PDB Molecule:**rhodanese; **PDBTitle:** crystal structure of rhodanese from thermus thermophilus hb8
46	c3e4fB_	Alignment	not modelled	45.6	20	**PDB header:**transferase **Chain:** B: **PDB Molecule:**aminoglycoside n3-acetyltransferase; **PDBTitle:** crystal structure of ba2930- a putative aminoglycoside n3-2 acetyltransferase from bacillus anthracis
47	d1d1ta2	Alignment	not modelled	43.8	8	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Alcohol dehydrogenase-like, C-terminal domain
48	d1z7wa1	Alignment	not modelled	42.7	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
49	d1v71a1	Alignment	not modelled	41.0	8	**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
50	c3olhA_	Alignment	not modelled	39.3	8	**PDB header:**transferase **Chain:** A: **PDB Molecule:**3-mercaptopyruvate sulfurtransferase; **PDBTitle:** human 3-mercaptopyruvate sulfurtransferase
51	d1iz0a2	Alignment	not modelled	39.0	11	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Alcohol dehydrogenase-like, C-terminal domain
52	d1jvba2	Alignment	not modelled	38.4	8	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Alcohol dehydrogenase-like, C-terminal domain
53	c3bcxA_	Alignment	not modelled	37.9	9	**PDB header:**transferase **Chain:** A: **PDB Molecule:**cdp-6-deoxy-l-threo-d-glycero-4-hexulose-3-

						PDBTitle: e1 dehydrase
54	d1vjka_	Alignment	not modelled	37.4	15	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**MoaD/ThiS **Family:**MoaD
55	d1e3ia2	Alignment	not modelled	37.2	10	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Alcohol dehydrogenase-like, C-terminal domain
56	c2jwlB_	Alignment	not modelled	35.4	14	**PDB header:**membrane protein **Chain:** B: **PDB Molecule:**protein tolr; **PDBTitle:** solution structure of periplasmic domain of tolr from h.2 influenzae with saxs data
57	d1p0fa2	Alignment	not modelled	33.8	11	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Alcohol dehydrogenase-like, C-terminal domain
58	d1uufa2	Alignment	not modelled	33.4	11	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Alcohol dehydrogenase-like, C-terminal domain
59	d1ykfa2	Alignment	not modelled	32.5	13	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Alcohol dehydrogenase-like, C-terminal domain
60	c2ywiA_	Alignment	not modelled	31.6	13	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical conserved protein; **PDBTitle:** crystal structure of uncharacterized conserved protein from2 geobacillus kaustophilus
61	c3pc3A_	Alignment	not modelled	30.4	20	**PDB header:**lyase **Chain:** A: **PDB Molecule:**cg1753, isoform a; **PDBTitle:** full length structure of cystathionine beta-synthase from drosophila2 in complex with aminoacrylate
62	c2zy3A_	Alignment	not modelled	29.8	24	**PDB header:**lyase **Chain:** A: **PDB Molecule:**l-aspartate beta-decarboxylase; **PDBTitle:** dodecameric l-aspartate beta-decarboxylase
63	d1uara2	Alignment	not modelled	29.5	13	**Fold:**Rhodanese/Cell cycle control phosphatase **Superfamily:**Rhodanese/Cell cycle control phosphatase **Family:**Multidomain sulfurtransferase (rhodanese)
64	d1jqba2	Alignment	not modelled	29.2	15	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Alcohol dehydrogenase-like, C-terminal domain
65	d1rjwa2	Alignment	not modelled	28.4	12	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Alcohol dehydrogenase-like, C-terminal domain
66	d2fzwa2	Alignment	not modelled	26.2	10	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Alcohol dehydrogenase-like, C-terminal domain
67	d1udxa3	Alignment	not modelled	25.6	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
68	d1zjca1	Alignment	not modelled	25.5	10	**Fold:**Thermophilic metalloprotease-like **Superfamily:**Thermophilic metalloprotease-like **Family:**Thermophilic metalloprotease (M29)
69	d1ja1a1	Alignment	not modelled	25.4	23	**Fold:**Reductase/isomerase/elongation factor common domain **Superfamily:**Riboflavin synthase domain-like **Family:**NADPH-cytochrome p450 reductase FAD-binding domain-like
70	d1liua3	Alignment	not modelled	25.4	11	**Fold:**Pyruvate kinase C-terminal domain-like **Superfamily:**PK C-terminal domain-like **Family:**Pyruvate kinase, C-terminal domain
71	d1okga1	Alignment	not modelled	25.2	10	**Fold:**Rhodanese/Cell cycle control phosphatase **Superfamily:**Rhodanese/Cell cycle control phosphatase **Family:**Multidomain sulfurtransferase (rhodanese)
72	c3aaxB_	Alignment	not modelled	24.9	10	**PDB header:**transferase **Chain:** B: **PDB Molecule:**putative thiosulfate sulfurtransferase; **PDBTitle:** crystal structure of probable thiosulfate sulfurtransferase2 cysa3 (rv3117) from mycobacterium tuberculosis: monoclinic3 form
73	d2jhfa2	Alignment	not modelled	24.4	11	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Alcohol dehydrogenase-like, C-terminal domain
74	d1uaaa2	Alignment	not modelled	23.4	9	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Tandem AAA-ATPase domain
75	d1f20a1	Alignment	not modelled	22.2	11	**Fold:**Reductase/isomerase/elongation factor common domain **Superfamily:**Riboflavin synthase domain-like **Family:**NADPH-cytochrome p450 reductase FAD-binding domain-like
76	d1qora2	Alignment	not modelled	22.1	10	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Alcohol dehydrogenase-like, C-terminal domain
77	d1wkva1	Alignment	not modelled	21.8	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
78	d1cdoa2	Alignment	not modelled	21.7	10	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Alcohol dehydrogenase-like, C-terminal domain
79	d1y7la1	Alignment	not modelled	21.1	9	**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
80	d1u3wa2	Alignment	not modelled	21.1	9	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Alcohol dehydrogenase-like, C-terminal domain
81	d2g50a3	Alignment	not modelled	21.0	14	**Fold:**Pyruvate kinase C-terminal domain-like **Superfamily:**PK C-terminal domain-like **Family:**Pyruvate kinase, C-terminal domain
82	c1okgA_	Alignment	not modelled	20.5	12	**PDB header:**transferase **Chain:** A: **PDB Molecule:**possible 3-mercaptopyruvate sulfurtransferase; **PDBTitle:** 3-mercaptopyruvate sulfurtransferase from leishmania major
83	c1l9xA_	Alignment	not modelled	20.4	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**gamma-glutamyl hydrolase; **PDBTitle:** structure of gamma-glutamyl hydrolase
84	d1l9xa_	Alignment	not modelled	20.4	17	**Fold:**Flavodoxin-like **Superfamily:**Class I glutamine amidotransferase-like **Family:**Class I glutamine amidotransferases (GAT)
85	c3hjtB_	Alignment	not modelled	20.2	9	**PDB header:**cell adhesion, transport protein **Chain:** B: **PDB Molecule:**lmb; **PDBTitle:** structure of laminin binding protein (lmb) of streptococcus2 agalactiae a bifunctional protein with adhesin and metal3 transporting activity
86	d2gy9p1	Alignment	not modelled	19.6	17	**Fold:**Ribosomal protein S16 **Superfamily:**Ribosomal protein S16 **Family:**Ribosomal protein S16
87	d1aisa1	Alignment	not modelled	19.4	16	**Fold:**TBP-like **Superfamily:**TATA-box binding protein-like **Family:**TATA-box binding protein (TBP), C-terminal domain
88	c2qjlA_	Alignment	not modelled	18.9	19	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**ubiquitin-related modifier 1; **PDBTitle:** crystal structure of urm1
89	d1f8fa2	Alignment	not modelled	18.8	10	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Alcohol dehydrogenase-like, C-terminal domain
90	d1m5wa_	Alignment	not modelled	18.6	8	**Fold:**TIM beta/alpha-barrel **Superfamily:**Pyridoxine 5'-phosphate synthase **Family:**Pyridoxine 5'-phosphate synthase
91	c3iauA_	Alignment	not modelled	18.4	12	**PDB header:**lyase **Chain:** A: **PDB Molecule:**threonine deaminase; **PDBTitle:** the structure of the processed form of threonine deaminase isoform 22 from solanum lycopersicum
92	d1pwha_	Alignment	not modelled	18.3	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
93	c1aqfB_	Alignment	not modelled	18.3	15	**PDB header:**transferase **Chain:** B: **PDB Molecule:**pyruvate kinase; **PDBTitle:** pyruvate kinase from rabbit muscle with mg, k, and l-2 phospholactate
94	d1k92a1	Alignment	not modelled	18.2	25	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Adenine nucleotide alpha hydrolases-like **Family:**N-type ATP pyrophosphatases
95	d1nula_	Alignment	not modelled	18.1	20	**Fold:**PRTase-like **Superfamily:**PRTase-like **Family:**Phosphoribosyltransferases (PRTases)
96	c3a2kB_	Alignment	not modelled	17.8	14	**PDB header:**ligase/rna **Chain:** B: **PDB Molecule:**trna(ile)-lysidine synthase; **PDBTitle:** crystal structure of tils complexed with trna
97	d1yb5a2	Alignment	not modelled	17.7	8	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Alcohol dehydrogenase-like, C-terminal domain
98	d1o69a_	Alignment	not modelled	17.2	14	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**GABA-aminotransferase-like
99	d1ddga1	Alignment	not modelled	17.1	12	**Fold:**Reductase/isomerase/elongation factor common domain **Superfamily:**Riboflavin synthase domain-like **Family:**NADPH-cytochrome p450 reductase FAD-binding domain-like