Phyre2

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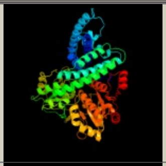
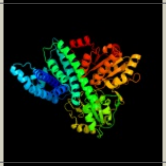
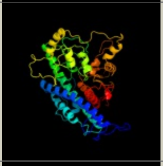
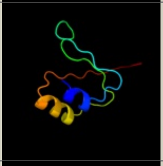
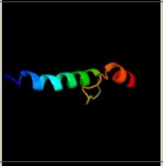
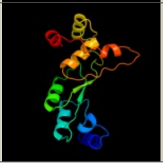
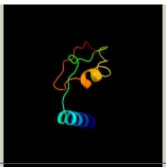
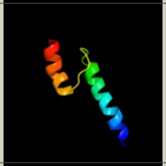
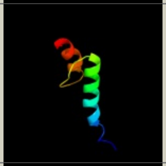
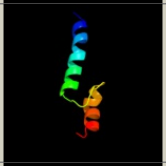
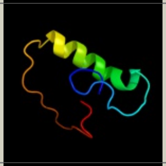
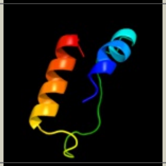
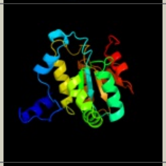
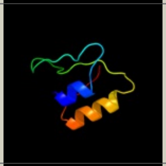
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1gnta_	Alignment		100.0	41	**Fold:**Prismane protein-like **Superfamily:**Prismane protein-like **Family:**Hybrid cluster protein (prismane protein)
2	d1gnla_	Alignment		100.0	42	**Fold:**Prismane protein-like **Superfamily:**Prismane protein-like **Family:**Hybrid cluster protein (prismane protein)
3	d1oaoa_	Alignment		100.0	20	**Fold:**Prismane protein-like **Superfamily:**Prismane protein-like **Family:**Carbon monoxide dehydrogenase
4	d1su7a_	Alignment		100.0	20	**Fold:**Prismane protein-like **Superfamily:**Prismane protein-like **Family:**Carbon monoxide dehydrogenase
5	d1jqka_	Alignment		100.0	21	**Fold:**Prismane protein-like **Superfamily:**Prismane protein-like **Family:**Carbon monoxide dehydrogenase
6	c1jqkE_	Alignment		100.0	21	**PDB header:**oxidoreductase **Chain:** E: **PDB Molecule:**carbon monoxide dehydrogenase; **PDBTitle:** crystal structure of carbon monoxide dehydrogenase from2 rhodospirillum rubrum
7	c3cf4A_	Alignment		100.0	18	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**acetyl-coa decarboxylase/synthase alpha subunit; **PDBTitle:** structure of the codh component of the m. barkeri acds complex
8	d1ru3a_	Alignment		97.6	15	**Fold:**Prismane protein-like **Superfamily:**Prismane protein-like **Family:**Acetyl-CoA synthase
9	d1h3da2	Alignment		56.9	17	**Fold:**Ferredoxin-like **Superfamily:**GlnB-like **Family:**ATP phosphoribosyltransferase (ATP-PRTase, HisG), regulatory C-terminal domain
10	c3hrdF_	Alignment		52.9	10	**PDB header:**oxidoreductase **Chain:** F: **PDB Molecule:**nicotinate dehydrogenase medium molybdopterin **PDBTitle:** crystal structure of nicotinate dehydrogenase
11	c3h7uA_	Alignment		51.3	14	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**aldo-keto reductase; **PDBTitle:** crystal structure of the plant stress-response enzyme akr4c9

12	d2gp4a2	Alignment		50.1	18	**Fold:**IlvD/EDD N-terminal domain-like **Superfamily:**IlvD/EDD N-terminal domain-like **Family:**IvD/EDD N-terminal domain-like
13	d1n62b2	Alignment		47.9	14	**Fold:**Molybdenum cofactor-binding domain **Superfamily:**Molybdenum cofactor-binding domain **Family:**Molybdenum cofactor-binding domain
14	d1rm6a2	Alignment		43.8	23	**Fold:**Molybdenum cofactor-binding domain **Superfamily:**Molybdenum cofactor-binding domain **Family:**Molybdenum cofactor-binding domain
15	c1n62E_	Alignment		41.5	14	**PDB header:**oxidoreductase **Chain:** E: **PDB Molecule:**carbon monoxide dehydrogenase large chain; **PDBTitle:** crystal structure of the mo,cu-co dehydrogenase (codh), n-2 butylisocyanide-bound state
16	d1ws6a1	Alignment		41.1	19	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**YhhF-like
17	d1pama4	Alignment		39.8	23	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
18	d1oaoc_	Alignment		37.5	11	**Fold:**Prismane protein-like **Superfamily:**Prismane protein-like **Family:**Acetyl-CoA synthase
19	d1nh8a2	Alignment		36.9	13	**Fold:**Ferredoxin-like **Superfamily:**GlnB-like **Family:**ATP phosphoribosyltransferase (ATP-PRTase, HisG), regulatory C-terminal domain
20	c3ijdB_	Alignment		35.4	14	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**uncharacterized protein; **PDBTitle:** uncharacterized protein cthe_2304 from clostridium2 thermocellum binds two copies of 5-methyl-5,6,7,8-3 tetrahydrofolic acid
21	c3enoB_	Alignment	not modelled	35.2	12	**PDB header:**hydrolase/unknown function **Chain:** B: **PDB Molecule:**putative o-sialoglycoprotein endopeptidase; **PDBTitle:** crystal structure of pyrococcus furiosus pcc1 in complex2 with thermoplasma acidophilum kae1
22	c3rxyA_	Alignment	not modelled	34.1	25	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**nif3 protein; **PDBTitle:** crystal structure of nif3 superfamily protein from sphaerobacter2 thermophilus
23	d2h5fa1	Alignment	not modelled	32.9	41	**Fold:**Snake toxin-like **Superfamily:**Snake toxin-like **Family:**Snake venom toxins
24	c2dy0A_	Alignment	not modelled	32.9	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**adenine phosphoribosyltransferase; **PDBTitle:** crystal structure of project jw0458 from escherichia coli
25	d2ex2a1	Alignment	not modelled	31.8	19	**Fold:**beta-lactamase/transpeptidase-like **Superfamily:**beta-lactamase/transpeptidase-like **Family:**Dac-like
26	d1dx5i2	Alignment	not modelled	31.3	47	**Fold:**Knottins (small inhibitors, toxins, lectins) **Superfamily:**EGF/Laminin **Family:**EGF-type module
27	d2c4ka2	Alignment	not modelled	30.0	21	**Fold:**PRTase-like **Superfamily:**PRTase-like **Family:**Phosphoribosylpyrophosphate synthetase-like
28	c3lpnB_	Alignment	not modelled	29.1	24	**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).

29	c2ivoC_	Alignment	not modelled	27.8	14	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**up1; **PDBTitle:** structure of up1 protein
30	d1hw6a_	Alignment	not modelled	27.6	14	**Fold:**TIM beta/alpha-barrel **Superfamily:**NAD(P)-linked oxidoreductase **Family:**Aldo-keto reductases (NADP)
31	c1sb3D_	Alignment	not modelled	26.6	23	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**4-hydroxybenzoyl-coa reductase alpha subunit; **PDBTitle:** structure of 4-hydroxybenzoyl-coa reductase from thauera2 aromatica
32	c2vd3B_	Alignment	not modelled	24.8	20	**PDB header:**transferase **Chain:** B: **PDB Molecule:**atp phosphoribosyltransferase; **PDBTitle:** the structure of histidine inhibited hisg from2 methanobacterium thermoautotrophicum
33	d1mmca_	Alignment	not modelled	24.6	32	**Fold:**Knottins (small inhibitors, toxins, lectins) **Superfamily:**Plant lectins/antimicrobial peptides **Family:**Antimicrobial peptide 2, AC-AMP2
34	c3cixA_	Alignment	not modelled	24.3	14	**PDB header:**adomet binding protein **Chain:** A: **PDB Molecule:**fefe-hydrogenase maturase; **PDBTitle:** x-ray structure of the [fefe]-hydrogenase maturase hyde from2 thermotoga maritima in complex with thiocyanate
35	c3it4C_	Alignment	not modelled	23.9	18	**PDB header:**transferase **Chain:** C: **PDB Molecule:**arginine biosynthesis bifunctional protein argj **PDBTitle:** the crystal structure of ornithine acetyltransferase from2 mycobacterium tuberculosis (rv1653) at 1.7 a
36	d1p94a_	Alignment	not modelled	23.8	25	**Fold:**Ribbon-helix-helix **Superfamily:**Ribbon-helix-helix **Family:**CopG-like
37	d1vlba4	Alignment	not modelled	23.7	13	**Fold:**Molybdenum cofactor-binding domain **Superfamily:**Molybdenum cofactor-binding domain **Family:**Molybdenum cofactor-binding domain
38	d1ffvb2	Alignment	not modelled	23.6	13	**Fold:**Molybdenum cofactor-binding domain **Superfamily:**Molybdenum cofactor-binding domain **Family:**Molybdenum cofactor-binding domain
39	d1s0ya_	Alignment	not modelled	23.3	53	**Fold:**Tautomerase/MIF **Superfamily:**Tautomerase/MIF **Family:**4-oxalocrotonate tautomerase-like
40	d2h7za1	Alignment	not modelled	23.2	35	**Fold:**Snake toxin-like **Superfamily:**Snake toxin-like **Family:**Snake venom toxins
41	d1dkua2	Alignment	not modelled	22.0	21	**Fold:**PRTase-like **Superfamily:**PRTase-like **Family:**Phosphoribosylpyrophosphate synthetase-like
42	c3e5aB_	Alignment	not modelled	21.5	86	**PDB header:**transferase **Chain:** B: **PDB Molecule:**targeting protein for xklp2; **PDBTitle:** crystal structure of aurora a in complex with vx-680 and tpx2
43	d1pyfa_	Alignment	not modelled	20.5	18	**Fold:**TIM beta/alpha-barrel **Superfamily:**NAD(P)-linked oxidoreductase **Family:**Aldo-keto reductases (NADP)
44	c2wtoB_	Alignment	not modelled	20.5	26	**PDB header:**metal binding protein **Chain:** B: **PDB Molecule:**orf131 protein; **PDBTitle:** crystal structure of apo-form czce from c. metallidurans ch34
45	d1t3qb2	Alignment	not modelled	20.3	8	**Fold:**Molybdenum cofactor-binding domain **Superfamily:**Molybdenum cofactor-binding domain **Family:**Molybdenum cofactor-binding domain
46	c3ktbD_	Alignment	not modelled	19.9	20	**PDB header:**transcription regulator **Chain:** D: **PDB Molecule:**arsenical resistance operon trans-acting repressor; **PDBTitle:** crystal structure of arsenical resistance operon trans-acting2 repressor from bacteroides vulgatus atcc 8482
47	d2h7zb1	Alignment	not modelled	19.9	24	**Fold:**Snake toxin-like **Superfamily:**Snake toxin-like **Family:**Snake venom toxins
48	c1q1kA_	Alignment	not modelled	19.7	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**atp phosphoribosyltransferase; **PDBTitle:** structure of atp-phosphoribosyltransferase from e. coli complexed with2 pr-atp
49	d1cjba_	Alignment	not modelled	19.3	27	**Fold:**PRTase-like **Superfamily:**PRTase-like **Family:**Phosphoribosyltransferases (PRTases)
50	d3bmva4	Alignment	not modelled	19.0	26	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
51	d1cxla4	Alignment	not modelled	18.4	25	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
52	d1pj3a2	Alignment	not modelled	18.2	30	**Fold:**Aminoacid dehydrogenase-like, N-terminal domain **Superfamily:**Aminoacid dehydrogenase-like, N-terminal domain **Family:**Malic enzyme N-domain
53	d1o98a1	Alignment	not modelled	18.1	20	**Fold:**2,3-Bisphosphoglycerate-independent phosphoglycerate mutase, substrate-binding domain **Superfamily:**2,3-Bisphosphoglycerate-independent phosphoglycerate mutase, substrate-binding domain **Family:**2,3-Bisphosphoglycerate-independent phosphoglycerate mutase, substrate-binding domain
54	c1zwuA_	Alignment	not modelled	17.3	32	**PDB header:**antimicrobial protein **Chain:** A: **PDB Molecule:**amaranthus caudatus antimicrobial peptide 2 (acmp2);

						PDBTitle: 30 nmr structures of acamp2-like peptide with non natural beta-(2-2 naphthyl)-alanine residue.
55	c3dahB_	Alignment	not modelled	16.7	17	**PDB header:**transferase **Chain:** B: **PDB Molecule:**ribose-phosphate pyrophosphokinase; **PDBTitle:** 2.3 a crystal structure of ribose-phosphate pyrophosphokinase from2 burkholderia pseudomallei
56	d1whqa_	Alignment	not modelled	16.2	18	**Fold:**dsRBD-like **Superfamily:**dsRNA-binding domain-like **Family:**Double-stranded RNA-binding domain (dsRBD)
57	c1ldbA_	Alignment	not modelled	16.0	15	**PDB header:**oxidoreductase(choh(d)-nad(a)) **Chain:** A: **PDB Molecule:**apo-l-lactate dehydrogenase; **PDBTitle:** structure determination and refinement of bacillus2 stearothermophilus lactate dehydrogenase
58	c1dkrB_	Alignment	not modelled	15.9	21	**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.
59	d1z7ga1	Alignment	not modelled	15.9	26	**Fold:**PRTase-like **Superfamily:**PRTase-like **Family:**Phosphoribosyltransferases (PRTases)
60	d2fpoa1	Alignment	not modelled	15.3	17	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**YhhF-like
61	c3outC_	Alignment	not modelled	14.9	18	**PDB header:**isomerase **Chain:** C: **PDB Molecule:**glutamate racemase; **PDBTitle:** crystal structure of glutamate racemase from francisella tularensis2 subsp. tularensis schu s4 in complex with d-glutamate.
62	d1dgja4	Alignment	not modelled	14.9	16	**Fold:**Molybdenum cofactor-binding domain **Superfamily:**Molybdenum cofactor-binding domain **Family:**Molybdenum cofactor-binding domain
63	c1hygA_	Alignment	not modelled	14.8	13	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**l-lactate/malate dehydrogenase; **PDBTitle:** crystal structure of mj0490 gene product, the family of2 lactate/malate dehydrogenase
64	c2v4iA_	Alignment	not modelled	14.6	14	**PDB header:**transferase **Chain:** A: **PDB Molecule:**glutamate n-acetyltransferase 2 alpha chain; **PDBTitle:** structure of a novel n-acyl-enzyme intermediate of an n-2 terminal nucleophile (ntn) hydrolase, oat2
65	c2jq4A_	Alignment	not modelled	14.6	21	**PDB header:**structural genomics **Chain:** A: **PDB Molecule:**hypothetical protein atu2571; **PDBTitle:** complete resonance assignments and solution structure2 calculation of atc2521 (nesg id: att6) from agrobacterium3 tumefaciens
66	d2jq4a1	Alignment	not modelled	14.6	21	**Fold:**Acyl carrier protein-like **Superfamily:**ACP-like **Family:**Acyl-carrier protein (ACP)
67	d1u9ya2	Alignment	not modelled	14.5	17	**Fold:**PRTase-like **Superfamily:**PRTase-like **Family:**Phosphoribosylpyrophosphate synthetase-like
68	d2f2ab2	Alignment	not modelled	14.4	16	**Fold:**Glutamine synthetase/guanido kinase **Superfamily:**Glutamine synthetase/guanido kinase **Family:**GatB/GatE catalytic domain-like
69	c3dm5A_	Alignment	not modelled	14.3	13	**PDB header:**rna binding protein, transport protein **Chain:** A: **PDB Molecule:**signal recognition 54 kda protein; **PDBTitle:** structures of srp54 and srp19, the two proteins assembling2 the ribonucleic core of the signal recognition particle3 from the archaeon pyrococcus furiosus.
70	c1o98A_	Alignment	not modelled	14.2	17	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**2,3-bisphosphoglycerate-independent **PDBTitle:** 1.4a crystal structure of phosphoglycerate mutase from2 bacillus stearothermophilus complexed with3 2-phosphoglycerate
71	d1ugpa_	Alignment	not modelled	14.1	23	**Fold:**Nitrile hydratase alpha chain **Superfamily:**Nitrile hydratase alpha chain **Family:**Nitrile hydratase alpha chain
72	d1o6za2	Alignment	not modelled	13.8	21	**Fold:**LDH C-terminal domain-like **Superfamily:**LDH C-terminal domain-like **Family:**Lactate & malate dehydrogenases, C-terminal domain
73	c2eoyA_	Alignment	not modelled	13.6	57	**PDB header:**transcription **Chain:** A: **PDB Molecule:**zinc finger protein 473; **PDBTitle:** solution structure of the c2h2 type zinc finger (region 557-2 589) of human zinc finger protein 473
74	c3omtA_	Alignment	not modelled	13.6	28	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** putative antitoxin component, chu_2935 protein, from xre family from2 prevotella buccae.
75	d1utxa_	Alignment	not modelled	13.2	28	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**SinR domain-like
76	c1u9yD_	Alignment	not modelled	13.0	17	**PDB header:**transferase **Chain:** D: **PDB Molecule:**ribose-phosphate pyrophosphokinase; **PDBTitle:** crystal structure of phosphoribosyl diphosphate synthase2 from methanocaldococcus jannaschii
77	c2j37W_	Alignment	not modelled	12.9	10	**PDB header:**ribosome **Chain:** W: **PDB Molecule:**signal recognition particle 54 kda protein **PDBTitle:** model of mammalian srp bound to 80s rncs
78	c2l9fA_	Alignment	not modelled	12.8	14	**PDB header:**transferase **Chain:** A: **PDB Molecule:**cale8; **PDBTitle:** nmr solution structure of meacp
79	c3p9xB_	Alignment	not modelled	12.6	15	**PDB header:**transferase **Chain:** B: **PDB Molecule:**phosphoribosylglycinamide formyltransferase;

						PDBTitle: crystal structure of phosphoribosylglycinamide formyltransferase from2 bacillus halodurans
80	c1ex1A_	Alignment	not modelled	12.5	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**protein (beta-d-glucan exohydrolase isoenzyme exo1); **PDBTitle:** beta-d-glucan exohydrolase from barley
81	d1cyga4	Alignment	not modelled	12.5	23	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
82	d1lgya_	Alignment	not modelled	12.4	29	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Fungal lipases
83	d2d6fc3	Alignment	not modelled	12.3	30	**Fold:**Glutamine synthetase/guanido kinase **Superfamily:**Glutamine synthetase/guanido kinase **Family:**GatB/GatE catalytic domain-like
84	d1lmb3_	Alignment	not modelled	12.1	28	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**Phage repressors
85	d2nlya1	Alignment	not modelled	12.0	12	**Fold:**7-stranded beta/alpha barrel **Superfamily:**Glycoside hydrolase/deacetylase **Family:**Divergent polysaccharide deacetylase
86	c3jruB_	Alignment	not modelled	12.0	15	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**probable cytosol aminopeptidase; **PDBTitle:** crystal structure of leucyl aminopeptidase (pepa) from xoo0834,2 xanthomonas oryzae pv. oryzae kacc10331
87	c1qr6A_	Alignment	not modelled	12.0	30	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**malic enzyme 2; **PDBTitle:** human mitochondrial nad(p)-dependent malic enzyme
88	c3bs3A_	Alignment	not modelled	11.9	28	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**putative dna-binding protein; **PDBTitle:** crystal structure of a putative dna-binding protein from bacteroides2 fragilis
89	c3t76A_	Alignment	not modelled	11.8	22	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**transcriptional regulator vanug; **PDBTitle:** crystal structure of transcriptional regulator vanug, form ii
90	c3igzB_	Alignment	not modelled	11.7	10	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**cofactor-independent phosphoglycerate mutase; **PDBTitle:** crystal structures of leishmania mexicana phosphoglycerate2 mutase at low cobalt concentration
91	d1fsga_	Alignment	not modelled	11.5	23	**Fold:**PRTase-like **Superfamily:**PRTase-like **Family:**Phosphoribosyltransferases (PRTases)
92	c3fybA_	Alignment	not modelled	11.3	60	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**protein of unknown function (duf1244); **PDBTitle:** crystal structure of a protein of unknown function (duf1244) from2 alcanivorax borkumensis
93	d1jsda_	Alignment	not modelled	11.1	5	**Fold:**Viral protein domain **Superfamily:**Viral protein domain **Family:**Influenza hemagglutinin headpiece
94	d1iuka_	Alignment	not modelled	11.1	13	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**CoA-binding domain
95	c3al0B_	Alignment	not modelled	11.1	26	**PDB header:**ligase/rna **Chain:** B: **PDB Molecule:**aspartyl/glutamyl-trna(asn/gln) amidotransferase subunit b; **PDBTitle:** crystal structure of the glutamine transamidosome from thermotoga2 maritima in the glutamylation state.
96	c1vraA_	Alignment	not modelled	10.9	16	**PDB header:**transferase **Chain:** A: **PDB Molecule:**arginine biosynthesis bifunctional protein argj; **PDBTitle:** crystal structure of arginine biosynthesis bifunctional protein argj2 (10175521) from bacillus halodurans at 2.00 a resolution
97	d1p17b_	Alignment	not modelled	10.9	18	**Fold:**PRTase-like **Superfamily:**PRTase-like **Family:**Phosphoribosyltransferases (PRTases)
98	d1f7ua3	Alignment	not modelled	10.8	14	**Fold:**RRF/tRNA synthetase additional domain-like **Superfamily:**Arginyl-tRNA synthetase (ArgRS), N-terminal 'additional' domain **Family:**Arginyl-tRNA synthetase (ArgRS), N-terminal 'additional' domain
99	c2c4kD_	Alignment	not modelled	10.8	21	**PDB header:**regulatory protein **Chain:** D: **PDB Molecule:**phosphoribosyl pyrophosphate synthetase- **PDBTitle:** crystal structure of human phosphoribosylpyrophosphate2 synthetase-associated protein 39 (pap39)