Phyre2

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Description	P76061
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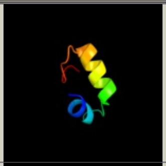
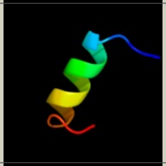
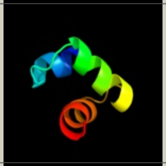
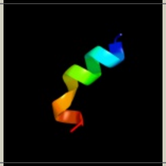
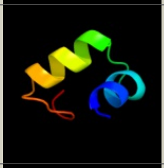
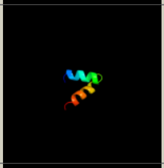
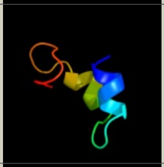
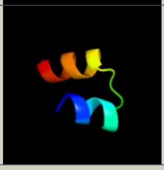
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1ifya_	Alignment		76.4	23	**Fold:**RuvA C-terminal domain-like **Superfamily:**UBA-like **Family:**UBA domain
2	d1v92a_	Alignment		60.7	24	**Fold:**RuvA C-terminal domain-like **Superfamily:**UBA-like **Family:**TAP-C domain-like
3	d1oqya1	Alignment		53.1	23	**Fold:**RuvA C-terminal domain-like **Superfamily:**UBA-like **Family:**UBA domain
4	d2g3qa1	Alignment		43.0	44	**Fold:**RuvA C-terminal domain-like **Superfamily:**UBA-like **Family:**UBA domain
5	d1i9sa_	Alignment		25.1	14	**Fold:**(Phosphotyrosine protein) phosphatases II **Superfamily:**(Phosphotyrosine protein) phosphatases II **Family:**Dual specificity phosphatase-like
6	c2gwoC_	Alignment		22.7	32	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**dual specificity protein phosphatase 13; **PDBTitle:** crystal structure of tmdp
7	c2fw9A_	Alignment		22.3	17	**PDB header:**lyase **Chain:** A: **PDB Molecule:**n5-carboxyaminoimidazole ribonucleotide mutase; **PDBTitle:** structure of pure (n5-carboxyaminoimidazole ribonucleotide mutase)2 h59f from the acidophilic bacterium acetobacter aceti, at ph 8
8	d1u11a_	Alignment		21.9	17	**Fold:**Flavodoxin-like **Superfamily:**N5-CAIR mutase (phosphoribosylaminoimidazole carboxylase, PurE) **Family:**N5-CAIR mutase (phosphoribosylaminoimidazole carboxylase, PurE)
9	d1wiva_	Alignment		20.8	24	**Fold:**RuvA C-terminal domain-like **Superfamily:**UBA-like **Family:**UBA domain
10	c3echC_	Alignment		20.4	47	**PDB header:**transcription, transcription regulation **Chain:** C: **PDB Molecule:**25-mer fragment of protein armr; **PDBTitle:** the marr-family repressor mexr in complex with its antirepressor armr
11	c3trhI_	Alignment		18.5	30	**PDB header:**lyase **Chain:** I: **PDB Molecule:**phosphoribosylaminoimidazole carboxylase **PDBTitle:** structure of a phosphoribosylaminoimidazole carboxylase catalytic2 subunit (pure) from coxiella burnetii

12	c3bq3A_	Alignment		17.6	16	**PDB header:**cell cycle, ligase **Chain:** A: **PDB Molecule:**defective in cullin neddylation protein 1; **PDBTitle:** crystal structure of s. cerevisiae dcn1
13	c1yn9B_	Alignment		16.9	32	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**polynucleotide 5'-phosphatase; **PDBTitle:** crystal structure of baculovirus rna 5'-phosphatase2 complexed with phosphate
14	c2ekkA_	Alignment		16.8	38	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**uba domain from e3 ubiquitin-protein ligase **PDBTitle:** solution structure of ruh-074, a human uba domain
15	c3nmeA_	Alignment		15.6	23	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**sex4 glucan phosphatase; **PDBTitle:** structure of a plant phosphatase
16	c2jp7A_	Alignment		15.2	14	**PDB header:**translation **Chain:** A: **PDB Molecule:**mrna export factor mex67; **PDBTitle:** nmr structure of the mex67 uba domain
17	c2dakA_	Alignment		14.9	30	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**ubiquitin carboxyl-terminal hydrolase 5; **PDBTitle:** solution structure of the second uba domain in the human2 ubiquitin specific protease 5 (isopeptidase 5)
18	d2dkla1	Alignment		14.7	37	**Fold:**RuvA C-terminal domain-like **Superfamily:**UBA-like **Family:**UBA domain
19	d1oqya2	Alignment		13.9	20	**Fold:**RuvA C-terminal domain-like **Superfamily:**UBA-like **Family:**UBA domain
20	c2esbA_	Alignment		12.9	23	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**dual specificity protein phosphatase 18; **PDBTitle:** crystal structure of human dusp18
21	c3lp6D_	Alignment	not modelled	12.5	27	**PDB header:**lyase **Chain:** D: **PDB Molecule:**phosphoribosylaminoimidazole carboxylase catalytic subunit; **PDBTitle:** crystal structure of rv3275c-e60a from mycobacterium tuberculosis at2 1.7a resolution
22	c2y96A_	Alignment	not modelled	12.3	35	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**dual specificity phosphatase dupd1; **PDBTitle:** structure of human dual-specificity phosphatase 27
23	c2ywxA_	Alignment	not modelled	11.9	18	**PDB header:**lyase **Chain:** A: **PDB Molecule:**phosphoribosylaminoimidazole carboxylase catalytic subunit; **PDBTitle:** crystal structure of phosphoribosylaminoimidazole carboxylase2 catalytic subunit from methanocaldococcus jannaschii
24	c2imgA_	Alignment	not modelled	11.4	23	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**dual specificity protein phosphatase 23; **PDBTitle:** crystal structure of dual specificity protein phosphatase2 23 from homo sapiens in complex with ligand malate ion
25	c2c46B_	Alignment	not modelled	11.4	13	**PDB header:**transferase **Chain:** B: **PDB Molecule:**mrna capping enzyme; **PDBTitle:** crystal structure of the human rna guanylyltransferase and2 5'-phosphatase
26	d1qcza_	Alignment	not modelled	11.0	30	**Fold:**Flavodoxin-like **Superfamily:**N5-CAIR mutase (phosphoribosylaminoimidazole carboxylase, PurE) **Family:**N5-CAIR mutase (phosphoribosylaminoimidazole carboxylase, PurE)
27	d1o4va_	Alignment	not modelled	10.8	9	**Fold:**Flavodoxin-like **Superfamily:**N5-CAIR mutase (phosphoribosylaminoimidazole carboxylase, PurE) **Family:**N5-CAIR mutase (phosphoribosylaminoimidazole carboxylase, PurE)

28	c2r0bA_	Alignment	not modelled	10.4	27	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**serine/threonine/tyrosine-interacting protein; **PDBTitle:** crystal structure of human tyrosine phosphatase-like2 serine/threonine/tyrosine-interacting protein
29	c3orsD_	Alignment	not modelled	10.4	18	**PDB header:**isomerase,biosynthetic protein **Chain:** D: **PDB Molecule:**n5-carboxyaminoimidazole ribonucleotide mutase; **PDBTitle:** crystal structure of n5-carboxyaminoimidazole ribonucleotide mutase2 from staphylococcus aureus
30	d1xmpa_	Alignment	not modelled	10.1	30	**Fold:**Flavodoxin-like **Superfamily:**N5-CAIR mutase (phosphoribosylaminoimidazole carboxylase, PurE) **Family:**N5-CAIR mutase (phosphoribosylaminoimidazole carboxylase, PurE)
31	d1oaia_	Alignment	not modelled	9.5	23	**Fold:**RuvA C-terminal domain-like **Superfamily:**UBA-like **Family:**TAP-C domain-like
32	c2h31A_	Alignment	not modelled	9.5	22	**PDB header:**ligase, lyase **Chain:** A: **PDB Molecule:**multifunctional protein ade2; **PDBTitle:** crystal structure of human paics, a bifunctional carboxylase and2 synthetase in purine biosynthesis
33	c3emuA_	Alignment	not modelled	9.5	18	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**leucine rich repeat and phosphatase domain **PDBTitle:** crystal structure of a leucine rich repeat and phosphatase2 domain containing protein from entamoeba histolytica
34	c3rggD_	Alignment	not modelled	9.2	9	**PDB header:**lyase **Chain:** D: **PDB Molecule:**phosphoribosylaminoimidazole carboxylase, pure protein; **PDBTitle:** crystal structure of treponema denticola pure bound to air
35	c2hcmA_	Alignment	not modelled	9.0	32	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**dual specificity protein phosphatase; **PDBTitle:** crystal structure of mouse putative dual specificity phosphatase2 complexed with zinc tungstate, new york structural genomics3 consortium
36	c3pcsB_	Alignment	not modelled	8.5	36	**PDB header:**protein transport/transferase **Chain:** B: **PDB Molecule:**espg; **PDBTitle:** structure of espg-pak2 autoinhibitory ialpha3 helix complex
37	d1vega_	Alignment	not modelled	7.9	27	**Fold:**RuvA C-terminal domain-like **Superfamily:**UBA-like **Family:**UBA domain
38	c2crnA_	Alignment	not modelled	7.8	24	**PDB header:**immune system **Chain:** A: **PDB Molecule:**ubash3a protein; **PDBTitle:** solution structure of the uba domain of human ubash3a2 protein
39	d1go5a_	Alignment	not modelled	7.7	22	**Fold:**RuvA C-terminal domain-like **Superfamily:**UBA-like **Family:**TAP-C domain-like
40	d1gyza_	Alignment	not modelled	7.3	21	**Fold:**PABP domain-like **Superfamily:**Ribosomal protein L20 **Family:**Ribosomal protein L20
41	c1tr8A_	Alignment	not modelled	7.2	23	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**conserved protein (mth177); **PDBTitle:** crystal structure of archaeal nascent polypeptide-associated complex2 (aenac)
42	d1mkpa_	Alignment	not modelled	6.9	27	**Fold:**(Phosphotyrosine protein) phosphatases II **Superfamily:**(Phosphotyrosine protein) phosphatases II **Family:**Dual specificity phosphatase-like
43	c2daiA_	Alignment	not modelled	6.5	24	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**ubiquitin associated domain containing 1; **PDBTitle:** solution structure of the first uba domain in the human2 ubiquitin associated domain containing 1 (ubadc1)
44	c1wrmA_	Alignment	not modelled	6.5	23	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**dual specificity phosphatase 22; **PDBTitle:** crystal structure of jsp-1
45	d1wj7a1	Alignment	not modelled	6.4	32	**Fold:**RuvA C-terminal domain-like **Superfamily:**UBA-like **Family:**UBA domain
46	c2e0tA_	Alignment	not modelled	6.3	27	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**dual specificity phosphatase 26; **PDBTitle:** crystal structure of catalytic domain of dual specificity phosphatase2 26, ms0830 from homo sapiens
47	d1veka_	Alignment	not modelled	6.0	24	**Fold:**RuvA C-terminal domain-like **Superfamily:**UBA-like **Family:**UBA domain
48	c3s4oB_	Alignment	not modelled	6.0	18	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**protein tyrosine phosphatase-like protein; **PDBTitle:** protein tyrosine phosphatase (putative) from leishmania major
49	d1pk1c1	Alignment	not modelled	5.8	16	**Fold:**SAM domain-like **Superfamily:**SAM/Pointed domain **Family:**SAM (sterile alpha motif) domain
50	d1xb2b1	Alignment	not modelled	5.7	26	**Fold:**RuvA C-terminal domain-like **Superfamily:**UBA-like **Family:**TS-N domain
51	d1h2vc1	Alignment	not modelled	5.7	27	**Fold:**alpha-alpha superhelix **Superfamily:**ARM repeat **Family:**MIF4G domain-like
						Fold:SAM domain-like

52	d1uqva_	Alignment	not modelled	5.5	22	**Superfamily:**SAM/Pointed domain **Family:**SAM (sterile alpha motif) domain
53	d1wuua2	Alignment	not modelled	5.3	46	**Fold:**Ferredoxin-like **Superfamily:**GHMP Kinase, C-terminal domain **Family:**Galactokinase