Phyre^2

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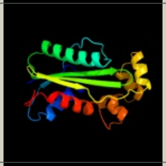
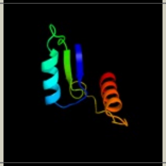
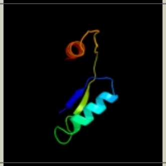
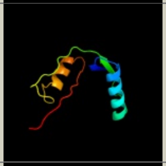
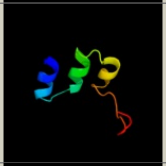
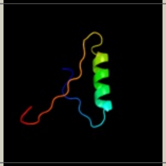
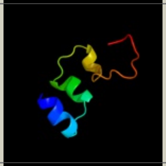
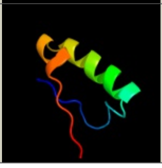
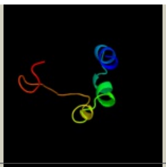
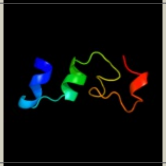
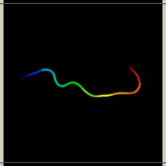
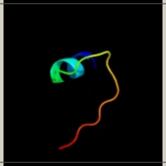
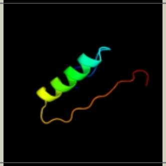
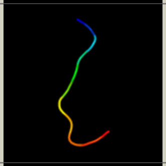
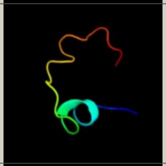
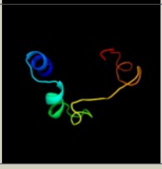
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1u14a_	Alignment		100.0	88	**Fold:**Anticodon-binding domain-like **Superfamily:**ITPase-like **Family:**YjjX-like
2	d1u5wa1	Alignment		100.0	99	**Fold:**Anticodon-binding domain-like **Superfamily:**ITPase-like **Family:**YjjX-like
3	d1zwya1	Alignment		100.0	46	**Fold:**Anticodon-binding domain-like **Superfamily:**ITPase-like **Family:**YjjX-like
4	d1k7ka_	Alignment		83.4	20	**Fold:**Anticodon-binding domain-like **Superfamily:**ITPase-like **Family:**ITPase (Ham1)
5	d1v7ra_	Alignment		62.3	15	**Fold:**Anticodon-binding domain-like **Superfamily:**ITPase-like **Family:**ITPase (Ham1)
6	c3brcA_	Alignment		58.3	18	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**conserved protein of unknown function; **PDBTitle:** crystal structure of a conserved protein of unknown function from2 methanobacterium thermoautotrophicum
7	d2cara1	Alignment		51.4	20	**Fold:**Anticodon-binding domain-like **Superfamily:**ITPase-like **Family:**ITPase (Ham1)
8	c2kgjA_	Alignment		41.2	12	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**peptidyl-prolyl cis-trans isomerase d; **PDBTitle:** solution structure of parvulin domain of ppid from e.coli
9	d1bwvs_	Alignment		37.1	12	**Fold:**RuBisCO, small subunit **Superfamily:**RuBisCO, small subunit **Family:**RuBisCO, small subunit
10	c2rqsA_	Alignment		35.2	22	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**parvulin-like peptidyl-prolyl isomerase; **PDBTitle:** 3d structure of pin from the psychrophilic archeon cenarcheaum2 symbiosum (cspin)
11	d1o66a_	Alignment		22.9	29	**Fold:**TIM beta/alpha-barrel **Superfamily:**Phosphoenolpyruvate/pyruvate domain **Family:**Ketopantoate hydroxymethyltransferase PanB

12	c2jzvA_	Alignment		22.3	16	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**foldase protein prsa; **PDBTitle:** solution structure of s. aureus prsa-ppiase
13	d1m5ya3	Alignment		18.9	12	**Fold:**FKBP-like **Superfamily:**FKBP-like **Family:**FKBP immunophilin/proline isomerase
14	d1rdua_	Alignment		17.5	18	**Fold:**Ribonuclease H-like motif **Superfamily:**Nitrogenase accessory factor-like **Family:**MTH1175-like
15	c3cgiD_	Alignment		17.5	19	**PDB header:**unknown function **Chain:** D: **PDB Molecule:**propanediol utilization protein pduu; **PDBTitle:** crystal structure of the pduu shell protein from the pdu2 microcompartment
16	d1svdm1	Alignment		14.8	10	**Fold:**RuBisCO, small subunit **Superfamily:**RuBisCO, small subunit **Family:**RuBisCO, small subunit
17	c2wfbA_	Alignment		14.0	18	**PDB header:**biosynthetic protein **Chain:** A: **PDB Molecule:**putative uncharacterized protein orp; **PDBTitle:** high resolution structure of the apo form of the orange2 protein (orp) from desulfovibrio gigas
18	c2h29A_	Alignment		12.9	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**probable nicotinate-nucleotide **PDBTitle:** crystal structure of nicotinic acid mononucleotide2 adenylyltransferase from staphylococcus aureus: product3 bound form 1
19	d1s6la1	Alignment		12.4	30	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**MerB N-terminal domain-like
20	c1yw5A_	Alignment		12.2	21	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**peptidyl prolyl cis/trans isomerase; **PDBTitle:** peptidyl-prolyl isomerase ess1 from candida albicans
21	c3tquD_	Alignment	not modelled	12.0	18	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**non-canonical purine ntp pyrophosphatase; **PDBTitle:** structure of a ham1 protein from coxiella burnetii
22	c2l33A_	Alignment	not modelled	11.8	30	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**interleukin enhancer-binding factor 3; **PDBTitle:** solution nmr structure of drbm 2 domain of interleukin enhancer-2 binding factor 3 from homo sapiens, northeast structural genomics3 consortium target hr4527e
23	c3d3kD_	Alignment	not modelled	11.5	9	**PDB header:**protein binding **Chain:** D: **PDB Molecule:**enhancer of mrna-decapping protein 3; **PDBTitle:** crystal structure of human edc3p
24	d1oy0a_	Alignment	not modelled	11.2	28	**Fold:**TIM beta/alpha-barrel **Superfamily:**Phosphoenolpyruvate/pyruvate domain **Family:**Ketopantoate hydroxymethyltransferase PanB
25	c2gezF_	Alignment	not modelled	10.7	18	**PDB header:**hydrolase **Chain:** F: **PDB Molecule:**l-asparaginase beta subunit; **PDBTitle:** crystal structure of potassium-independent plant asparaginase
26	d1eq3a_	Alignment	not modelled	10.7	26	**Fold:**FKBP-like **Superfamily:**FKBP-like **Family:**FKBP immunophilin/proline isomerase
27	c3gpkA_	Alignment	not modelled	10.5	17	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**ppic-type peptidyl-prolyl cis-trans isomerase; **PDBTitle:** crystal structure of ppic-type peptidyl-prolyl cis-trans isomerase2 domain at 1.55a resolution.
28	d1jnsa_	Alignment	not modelled	10.5	23	**Fold:**FKBP-like **Superfamily:**FKBP-like **Family:**FKBP immunophilin/proline isomerase

29	d1vp2a_	Alignment	not modelled	9.3	25	**Fold:**Anticodon-binding domain-like **Superfamily:**ITPase-like **Family:**ITPase (Ham1)
30	d2pv2a1	Alignment	not modelled	8.9	20	**Fold:**FKBP-like **Superfamily:**FKBP-like **Family:**FKBP immunophilin/proline isomerase
31	c2kwvA_	Alignment	not modelled	8.6	43	**PDB header:**protein binding/signaling protein **Chain:** A: **PDB Molecule:**dna polymerase iota; **PDBTitle:** solution structure of ubm1 of murine polymerase iota in complex with2 ubiquitin
32	c1apzB_	Alignment	not modelled	7.9	23	**PDB header:**complex (hydrolase/peptide) **Chain:** B: **PDB Molecule:**aspartylglucosaminidase; **PDBTitle:** human aspartylglucosaminidase complex with reaction product
33	c3pe0B_	Alignment	not modelled	7.8	14	**PDB header:**structural protein **Chain:** B: **PDB Molecule:**plectin; **PDBTitle:** structure of the central region of the plakin domain of plectin
34	d1bxni_	Alignment	not modelled	7.6	11	**Fold:**RuBisCO, small subunit **Superfamily:**RuBisCO, small subunit **Family:**RuBisCO, small subunit
35	d1c1da2	Alignment	not modelled	7.3	9	**Fold:**Aminoacid dehydrogenase-like, N-terminal domain **Superfamily:**Aminoacid dehydrogenase-like, N-terminal domain **Family:**Aminoacid dehydrogenases
36	c3e27B_	Alignment	not modelled	7.3	11	**PDB header:**transferase **Chain:** B: **PDB Molecule:**nicotinate (nicotinamide) nucleotide **PDBTitle:** nicotinic acid mononucleotide (namn) adenylyltransferase2 from bacillus anthracis: product complex
37	c3bd1B_	Alignment	not modelled	7.1	18	**PDB header:**transcription **Chain:** B: **PDB Molecule:**cro protein; **PDBTitle:** structure of the cro protein from putative prophage element xfaso 1 in2 xylella fastidiosa strain ann-1
38	d1b78a_	Alignment	not modelled	7.0	24	**Fold:**Anticodon-binding domain-like **Superfamily:**ITPase-like **Family:**ITPase (Ham1)
39	d1jzta_	Alignment	not modelled	6.3	38	**Fold:**YjeF N-terminal domain-like **Superfamily:**YjeF N-terminal domain-like **Family:**YjeF N-terminal domain-like
40	d2ozza1	Alignment	not modelled	6.2	32	**Fold:**Periplasmic binding protein-like II **Superfamily:**Periplasmic binding protein-like II **Family:**Phosphate binding protein-like
41	c3idfA_	Alignment	not modelled	6.1	11	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**usp-like protein; **PDBTitle:** the crystal structure of a usp-like protein from wolinella2 succinogenes to 2.0a
42	c1zk6A_	Alignment	not modelled	5.9	12	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**foldase protein prsa; **PDBTitle:** nmr solution structure of b. subtilis prsa ppiase
43	d1hcua_	Alignment	not modelled	5.8	26	**Fold:**alpha/alpha toroid **Superfamily:**Seven-hairpin glycosidases **Family:**Class I alpha-1;2-mannosidase, catalytic domain
44	d1j6ya_	Alignment	not modelled	5.8	22	**Fold:**FKBP-like **Superfamily:**FKBP-like **Family:**FKBP immunophilin/proline isomerase
45	d1e8ca2	Alignment	not modelled	5.7	11	**Fold:**MurD-like peptide ligases, peptide-binding domain **Superfamily:**MurD-like peptide ligases, peptide-binding domain **Family:**MurCDEF C-terminal domain
46	d2b7va1	Alignment	not modelled	5.4	28	**Fold:**dsRBD-like **Superfamily:**dsRNA-binding domain-like **Family:**Double-stranded RNA-binding domain (dsRBD)
47	c3mvnA_	Alignment	not modelled	5.4	21	**PDB header:**ligase **Chain:** A: **PDB Molecule:**udp-n-acetylmuramate:l-alanyl-gamma-d-glutamayl-medo- **PDBTitle:** crystal structure of a domain from a putative udp-n-acetylmuramate:l-2 alanyl-gamma-d-glutamayl-medo-diaminopimelate ligase from haemophilus3 ducreyi 35000hp
48	c3d3jA_	Alignment	not modelled	5.2	8	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**enhancer of mrna-decapping protein 3; **PDBTitle:** crystal structure of human edc3p
49	d2a9sa1	Alignment	not modelled	5.1	29	**Fold:**Anticodon-binding domain-like **Superfamily:**CinA-like **Family:**CinA-like
50	d1zbsa2	Alignment	not modelled	5.1	21	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**BadF/BadG/BcrA/BcrD-like