Phyre2

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Description	P0A7A9
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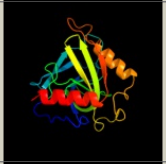
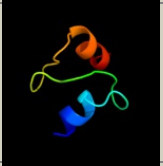
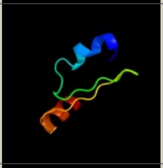
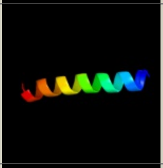
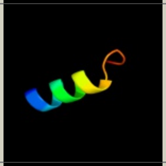
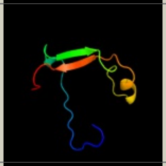
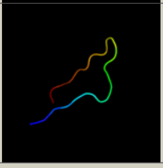
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1i40a_	Alignment		100.0	99	**Fold:**OB-fold **Superfamily:**Inorganic pyrophosphatase **Family:**Inorganic pyrophosphatase
2	c3fq3H_	Alignment		100.0	54	**PDB header:**hydrolase **Chain:** H: **PDB Molecule:**inorganic pyrophosphatase:bacterial/archaeal inorganic **PDBTitle:** crystal structure of inorganic phosphatase from brucella melitensis
3	d2prda_	Alignment		100.0	48	**Fold:**OB-fold **Superfamily:**Inorganic pyrophosphatase **Family:**Inorganic pyrophosphatase
4	c3d63B_	Alignment		100.0	61	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**inorganic pyrophosphatase; **PDBTitle:** crystal structure of inorganic pyrophosphatase from burkholderia2 pseudomallei
5	c1ygzC_	Alignment		100.0	46	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**inorganic pyrophosphatase; **PDBTitle:** crystal structure of inorganic pyrophosphatase from helicobacter2 pylori
6	d1qeza_	Alignment		100.0	53	**Fold:**OB-fold **Superfamily:**Inorganic pyrophosphatase **Family:**Inorganic pyrophosphatase
7	d1udea_	Alignment		100.0	44	**Fold:**OB-fold **Superfamily:**Inorganic pyrophosphatase **Family:**Inorganic pyrophosphatase
8	d1twla_	Alignment		100.0	43	**Fold:**OB-fold **Superfamily:**Inorganic pyrophosphatase **Family:**Inorganic pyrophosphatase
9	c3emjL_	Alignment		100.0	64	**PDB header:**hydrolase **Chain:** L: **PDB Molecule:**inorganic pyrophosphatase; **PDBTitle:** 2.2 a crystal structure of inorganic pyrophosphatase from2 rickettsia prowazekii (p21 form)
10	c2uxsA_	Alignment		100.0	46	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**inorganic pyrophosphatase; **PDBTitle:** 2.7a crystal structure of inorganic pyrophosphatase (rv3628)2 from mycobacterium tuberculosis at ph 7.5
11	d1e9ga_	Alignment		100.0	25	**Fold:**OB-fold **Superfamily:**Inorganic pyrophosphatase **Family:**Inorganic pyrophosphatase

12	c3lo0A_	Alignment		100.0	51	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**inorganic pyrophosphatase; **PDBTitle:** crystal structure of inorganic pyrophosphatase from2 ehrlichia chaffeensis
13	c2dhxA_	Alignment		25.9	14	**PDB header:**rna binding protein **Chain:** A: **PDB Molecule:**poly (adp-ribose) polymerase family, member 10 **PDBTitle:** solution structure of the rrm domain in the human poly (adp-2 ribose) polymerase family, member 10 variant
14	c1wwhB_	Alignment		21.4	12	**PDB header:**protein transport **Chain:** B: **PDB Molecule:**nucleoporin 35; **PDBTitle:** crystal structure of the mppn domain of mouse nup35
15	c2yueA_	Alignment		19.9	10	**PDB header:**rna binding protein **Chain:** A: **PDB Molecule:**protein neuralized; **PDBTitle:** solution structure of the neuz (nhr) domain in neuralized2 from drosophila melanogaster
16	d2ghpa1	Alignment		14.0	8	**Fold:**Ferredoxin-like **Superfamily:**RNA-binding domain, RBD **Family:**Canonical RBD
17	c3kztB_	Alignment		13.7	21	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of protein of unknown function (np_812423.1) from2 bacteroides thetaiotaomicron vpi-5482 at 2.10 a resolution
18	d1d02a_	Alignment		12.6	24	**Fold:**Restriction endonuclease-like **Superfamily:**Restriction endonuclease-like **Family:**Restriction endonuclease MunI
19	d2o0qa1	Alignment		12.4	15	**Fold:**ADP-ribosylation **Superfamily:**ADP-ribosylation **Family:**CC0527-like
20	c2e63A_	Alignment		11.8	33	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**kiaa1787 protein; **PDBTitle:** solution structure of the neuz domain in kiaa1787 protein
21	d1go3e1	Alignment	not modelled	11.3	25	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
22	d1wwha1	Alignment	not modelled	11.0	12	**Fold:**Ferredoxin-like **Superfamily:**RNA-binding domain, RBD **Family:**Canonical RBD
23	c1p0yA_	Alignment	not modelled	10.6	19	**PDB header:**transferase **Chain:** A: **PDB Molecule:**ribulose-1,5 bisphosphate carboxylase/oxygenase **PDBTitle:** crystal structure of the set domain of lsmt bound to2 melysine and adohcy
24	c2opdA_	Alignment	not modelled	10.4	29	**PDB header:**cell adhesion **Chain:** A: **PDB Molecule:**pilx; **PDBTitle:** structure of the neisseria meningitidis minor type iv pilin,2 pilx
25	d1x9na2	Alignment	not modelled	10.3	14	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**DNA ligase/mRNA capping enzyme postcatalytic domain
26	c3ideD_	Alignment	not modelled	8.6	26	**PDB header:**virus like particle **Chain:** D: **PDB Molecule:**capsid protein vp2; **PDBTitle:** structure of ipnv subviral particle
27	c3e9mC_	Alignment	not modelled	8.2	13	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**oxidoreductase, gfo/idh/moca family; **PDBTitle:** crystal structure of an oxidoreductase from enterococcus2 faecalis
28	d1efva2	Alignment	not modelled	7.5	13	**Fold:**DHS-like NAD/FAD-binding domain **Superfamily:**DHS-like NAD/FAD-binding domain **Family:**C-terminal domain of the electron transfer flavoprotein alpha subunit

29	d1q1oa_	Alignment	not modelled	7.4	23	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**CAD & PB1 domains **Family:**PB1 domain
30	d1wexa_	Alignment	not modelled	7.2	18	**Fold:**Ferredoxin-like **Superfamily:**RNA-binding domain, RBD **Family:**Canonical RBD
31	c3nzlA_	Alignment	not modelled	7.0	18	**PDB header:**transcription **Chain:** A: **PDB Molecule:**dna-binding protein satb1; **PDBTitle:** crystal structure of the n-terminal domain of dna-binding protein2 satb1 from homo sapiens, northeast structural genomics consortium3 target hr4435b
32	d1p9qc3	Alignment	not modelled	6.9	21	**Fold:**Ferredoxin-like **Superfamily:**EF-G C-terminal domain-like **Family:**Hypothetical protein AF0491, C-terminal domain
33	c2jnsA_	Alignment	not modelled	6.8	7	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**bromodomain-containing protein 4; **PDBTitle:** solution structure of the bromodomain-containing protein 42 et domain
34	c2vtvA_	Alignment	not modelled	6.5	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**phb depolymerase phaz7; **PDBTitle:** phaz7 depolymerase from paucimonas lemoignei
35	d1t95a3	Alignment	not modelled	6.5	21	**Fold:**Ferredoxin-like **Superfamily:**EF-G C-terminal domain-like **Family:**Hypothetical protein AF0491, C-terminal domain
36	d3bida1	Alignment	not modelled	6.3	23	**Fold:**YegP-like **Superfamily:**YegP-like **Family:**YegP-like
37	d2ghpa2	Alignment	not modelled	6.1	20	**Fold:**Ferredoxin-like **Superfamily:**RNA-binding domain, RBD **Family:**Canonical RBD
38	d1efpa2	Alignment	not modelled	6.0	11	**Fold:**DHS-like NAD/FAD-binding domain **Superfamily:**DHS-like NAD/FAD-binding domain **Family:**C-terminal domain of the electron transfer flavoprotein alpha subunit
39	d1ej7s_	Alignment	not modelled	5.9	19	**Fold:**RuBisCO, small subunit **Superfamily:**RuBisCO, small subunit **Family:**RuBisCO, small subunit
40	d2fgea4	Alignment	not modelled	5.8	14	**Fold:**LuxS/MPP-like metallohydrolase **Superfamily:**LuxS/MPP-like metallohydrolase **Family:**MPP-like
41	d8ruci_	Alignment	not modelled	5.8	10	**Fold:**RuBisCO, small subunit **Superfamily:**RuBisCO, small subunit **Family:**RuBisCO, small subunit
42	c2l76A_	Alignment	not modelled	5.7	18	**PDB header:**transcription **Chain:** A: **PDB Molecule:**nfatc2-interacting protein; **PDBTitle:** solution nmr structure of human nfatc2ip ubiquitin-like domain,2 nfatc2ip_244_338, nesg target ht65a/ocsp target hs00387_244_338/sgc-3 toronto
43	c2df7H_	Alignment	not modelled	5.5	31	**PDB header:**virus like particle **Chain:** H: **PDB Molecule:**structural polyprotein vp2; **PDBTitle:** crystal structure of infectious bursal disease virus vp2 subviral2 particle
44	d1gk8i_	Alignment	not modelled	5.5	24	**Fold:**RuBisCO, small subunit **Superfamily:**RuBisCO, small subunit **Family:**RuBisCO, small subunit
45	d2r9ga1	Alignment	not modelled	5.3	25	**Fold:**post-AAA+ oligomerization domain-like **Superfamily:**post-AAA+ oligomerization domain-like **Family:**MgsA/YrvN C-terminal domain-like
46	d1wdds_	Alignment	not modelled	5.3	14	**Fold:**RuBisCO, small subunit **Superfamily:**RuBisCO, small subunit **Family:**RuBisCO, small subunit
47	c2ytcA_	Alignment	not modelled	5.2	13	**PDB header:**transcription **Chain:** A: **PDB Molecule:**pre-mrna-splicing factor rbm22; **PDBTitle:** solution structure of rna binding domain in pre-mrna-2 splicing factor rbm22
48	d2df7a1	Alignment	not modelled	5.2	31	**Fold:**Nucleoplasmin-like/VP (viral coat and capsid proteins) **Superfamily:**Positive stranded ssRNA viruses **Family:**Birnaviridae-like VP
49	d1hr6a1	Alignment	not modelled	5.1	13	**Fold:**LuxS/MPP-like metallohydrolase **Superfamily:**LuxS/MPP-like metallohydrolase **Family:**MPP-like
50	d2pyta1	Alignment	not modelled	5.1	21	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**EutQ-like