Phyre^2

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Description	P0A7G2
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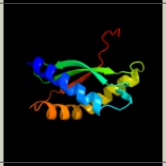
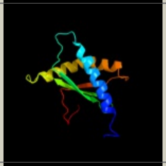
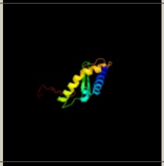
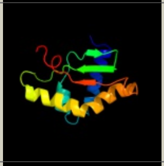
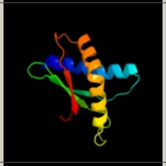
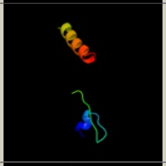
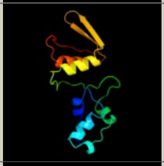
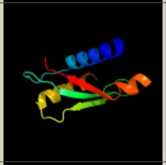
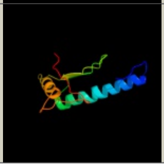
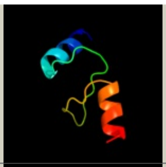
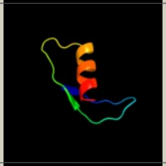
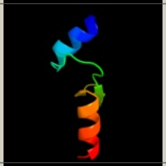
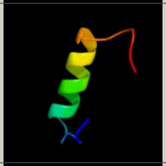
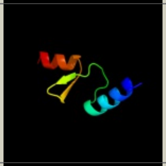
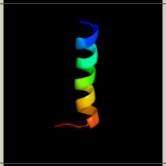
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1kkga_	Alignment		100.0	100	**Fold:**Alpha-lytic protease prodomain-like **Superfamily:**Ribosome-binding factor A, RbfA **Family:**Ribosome-binding factor A, RbfA
2	d1josa_	Alignment		100.0	71	**Fold:**Alpha-lytic protease prodomain-like **Superfamily:**Ribosome-binding factor A, RbfA **Family:**Ribosome-binding factor A, RbfA
3	c2kzfA_	Alignment		100.0	36	**PDB header:**ribosomal protein **Chain:** A: **PDB Molecule:**ribosome-binding factor a; **PDBTitle:** solution nmr structure of the thermotoga maritima protein tm0855 a2 putative ribosome binding factor a
4	d2e7ga1	Alignment		100.0	18	**Fold:**Alpha-lytic protease prodomain-like **Superfamily:**Ribosome-binding factor A, RbfA **Family:**Ribosome-binding factor A, RbfA
5	d1pa4a_	Alignment		100.0	20	**Fold:**Alpha-lytic protease prodomain-like **Superfamily:**Ribosome-binding factor A, RbfA **Family:**Ribosome-binding factor A, RbfA
6	d2dyja1	Alignment		100.0	27	**Fold:**Alpha-lytic protease prodomain-like **Superfamily:**Ribosome-binding factor A, RbfA **Family:**Ribosome-binding factor A, RbfA
7	c2qsiB_	Alignment		12.4	10	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**putative hydrogenase expression/formation protein hupg; **PDBTitle:** crystal structure of putative hydrogenase expression/formation protein2 hupg from rhodopseudomonas palustris cga009
8	c3ereD_	Alignment		9.6	17	**PDB header:**dna binding protein/dna **Chain:** D: **PDB Molecule:**arginine repressor; **PDBTitle:** crystal structure of the arginine repressor protein from mycobacterium2 tuberculosis in complex with the dna operator
9	d1lr0a_	Alignment		9.2	14	**Fold:**TolA/TonB C-terminal domain **Superfamily:**TolA/TonB C-terminal domain **Family:**TolA
10	c3kh0A_	Alignment		9.2	20	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**ral guanine nucleotide dissociation stimulator; **PDBTitle:** crystal structure of the ras-association (ra) domain of2 ralgds
11	d1jmta_	Alignment		7.6	19	**Fold:**Ferredoxin-like **Superfamily:**RNA-binding domain, RBD **Family:**Splicing factor U2AF subunits

12	c3c1sA_	Alignment		7.4	15	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**glutaredoxin-1; **PDBTitle:** crystal structure of grx1 in glutathionylated form
13	d2rgfa_	Alignment		7.1	20	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**Ubiquitin-like **Family:**Ras-binding domain, RBD
14	c2jacA_	Alignment		7.0	16	**PDB header:**electron transport **Chain:** A: **PDB Molecule:**glutaredoxin-1; **PDBTitle:** glutaredoxin grx1p c30s mutant from yeast
15	d2b3aa1	Alignment		6.9	20	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**Ubiquitin-like **Family:**Ras-binding domain, RBD
16	d1ug8a_	Alignment		6.7	20	**Fold:**IF3-like **Superfamily:**R3H domain **Family:**R3H domain
17	c3fzaA_	Alignment		6.6	15	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**glutaredoxin; **PDBTitle:** crystal structure of poplar glutaredoxin s12 in complex with2 glutathione and beta-mercaptoethanol
18	d1lfda_	Alignment		6.4	20	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**Ubiquitin-like **Family:**Ras-binding domain, RBD
19	d1l0wa2	Alignment		6.4	24	**Fold:**DCoH-like **Superfamily:**GAD domain-like **Family:**GAD domain
20	c3ipzA_	Alignment		6.3	11	**PDB header:**electron transport, oxidoreductase **Chain:** A: **PDB Molecule:**monothiol glutaredoxin-s14, chloroplastic; **PDBTitle:** crystal structure of arabidopsis monothiol glutaredoxin atgrxcp
21	d1xmka1	Alignment	not modelled	6.3	15	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Z-DNA binding domain
22	c2gboB_	Alignment	not modelled	6.2	17	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**upf0358 protein ef2458; **PDBTitle:** protein of unknown function ef2458 from enterococcus faecalis
23	d2gboa1	Alignment	not modelled	6.2	17	**Fold:**Open three-helical up-and-down bundle **Superfamily:**EF2458-like **Family:**EF2458-like
24	d1whxa_	Alignment	not modelled	6.2	16	**Fold:**Ferredoxin-like **Superfamily:**RNA-binding domain, RBD **Family:**Canonical RBD
25	c3d5jB_	Alignment	not modelled	5.8	13	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**glutaredoxin-2, mitochondrial; **PDBTitle:** structure of yeast grx2-c30s mutant with glutathionyl mixed2 disulfide
26	c3nm7D_	Alignment	not modelled	5.7	19	**PDB header:**nucleic acid binding protein **Chain:** D: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of borrelia burgdorferi pur-alpha
27	d1hska2	Alignment	not modelled	5.2	17	**Fold:**Uridine diphospho-N-Acetylenolpyruvylglucosamine reductase, MurB, C-terminal domain **Superfamily:**Uridine diphospho-N-Acetylenolpyruvylglucosamine reductase, MurB, C-terminal domain **Family:**Uridine diphospho-N-Acetylenolpyruvylglucosamine reductase, MurB, C-terminal domain
28	d1ep7a_	Alignment	not modelled	5.1	15	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Thioltransferase