Phyre^2

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Description	P67338
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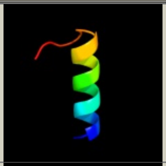
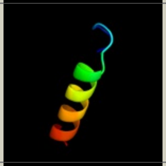
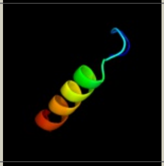
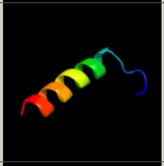
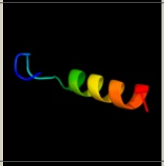
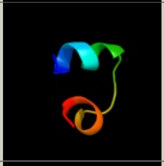
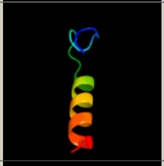
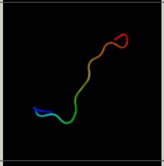
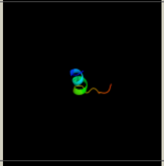
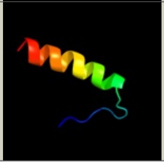
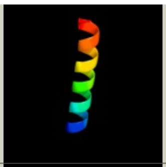
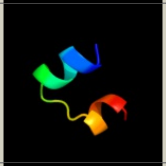
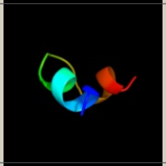
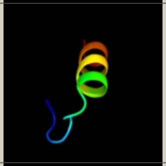
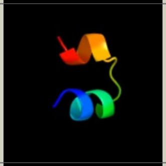
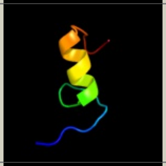
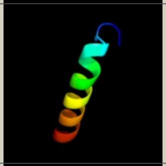
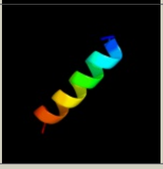
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1wi9a_	Alignment		68.9	42	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**PCI domain (PINT motif)
2	d1svdm1	Alignment		32.2	30	**Fold:**RuBisCO, small subunit **Superfamily:**RuBisCO, small subunit **Family:**RuBisCO, small subunit
3	d1iwga4	Alignment		28.9	40	**Fold:**Ferredoxin-like **Superfamily:**Multidrug efflux transporter AcrB pore domain; PN1, PN2, PC1 and PC2 subdomains **Family:**Multidrug efflux transporter AcrB pore domain; PN1, PN2, PC1 and PC2 subdomains
4	d1rbli_	Alignment		28.8	30	**Fold:**RuBisCO, small subunit **Superfamily:**RuBisCO, small subunit **Family:**RuBisCO, small subunit
5	c3m20A_	Alignment		26.0	27	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**4-oxalocrotonate tautomerase, putative; **PDBTitle:** crystal structure of dmpi from archaeoglobus fulgidus determined to2 2.37 angstroms resolution
6	d1uzhc1	Alignment		22.5	30	**Fold:**RuBisCO, small subunit **Superfamily:**RuBisCO, small subunit **Family:**RuBisCO, small subunit
7	c2jnhA_	Alignment		22.4	24	**PDB header:**ligase **Chain:** A: **PDB Molecule:**e3 ubiquitin-protein ligase cbl-b; **PDBTitle:** solution structure of the uba domain from cbl-b
8	d1ir1s_	Alignment		21.3	22	**Fold:**RuBisCO, small subunit **Superfamily:**RuBisCO, small subunit **Family:**RuBisCO, small subunit
9	d1bcoa1	Alignment		20.5	25	**Fold:**mu transposase, C-terminal domain **Superfamily:**mu transposase, C-terminal domain **Family:**mu transposase, C-terminal domain
10	c3itfA_	Alignment		19.9	38	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**periplasmic adaptor protein cpxp; **PDBTitle:** structural basis for the inhibitory function of the cpxp adaptor2 protein
11	c2kjwA_	Alignment		18.0	22	**PDB header:**ribosomal protein **Chain:** A: **PDB Molecule:**30s ribosomal protein s6; **PDBTitle:** solution structure and backbone dynamics of the permutant2 p54-55

12	c2r9iA_	Alignment		16.9	33	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**putative phage capsid protein; **PDBTitle:** crystal structure of putative phage capsid protein domain from2 corynebacterium diphtheriae
13	c2d9sA_	Alignment		16.1	35	**PDB header:**ligase **Chain:** A: **PDB Molecule:**cbl e3 ubiquitin protein ligase; **PDBTitle:** solution structure of rsgi ruh-049, a uba domain from mouse2 cdna
14	d2g3qa1	Alignment		15.8	22	**Fold:**RuvA C-terminal domain-like **Superfamily:**UBA-like **Family:**UBA domain
15	c2rd0A_	Alignment		15.3	21	**PDB header:**transferase/oncoprotein **Chain:** A: **PDB Molecule:**phosphatidylinositol-4,5-bisphosphate 3-kinase catalytic **PDBTitle:** structure of a human p110alpha/p85alpha complex
16	c3gyuA_	Alignment		14.7	21	**PDB header:**transcription **Chain:** A: **PDB Molecule:**nuclear hormone receptor of the steroid/thyroid **PDBTitle:** nuclear receptor daf-12 from parasitic nematode2 strongyloides stercoralis in complex with its physiological3 ligand dafachronic acid delta 7
17	c2do6A_	Alignment		14.3	24	**PDB header:**ligase **Chain:** A: **PDB Molecule:**e3 ubiquitin-protein ligase cbl-b; **PDBTitle:** solution structure of rsgi ruh-065, a uba domain from human2 cdna
18	d1fsea_	Alignment		13.9	27	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**C-terminal effector domain of the bipartite response regulators **Family:**GerE-like (LuxR/UhpA family of transcriptional regulators)
19	c3g0tA_	Alignment		11.7	30	**PDB header:**transferase **Chain:** A: **PDB Molecule:**putative aminotransferase; **PDBTitle:** crystal structure of putative aspartate aminotransferase (np_905498.1)2 from porphyromonas gingivalis w83 at 1.75 a resolution
20	d1gyxa_	Alignment		11.4	16	**Fold:**Tautomerase/MIF **Superfamily:**Tautomerase/MIF **Family:**4-oxalocrotonate tautomerase-like
21	d1g4us1	Alignment	not modelled	11.2	17	**Fold:**Four-helical up-and-down bundle **Superfamily:**Bacterial GAP domain **Family:**Bacterial GAP domain
22	d1lq1a_	Alignment	not modelled	11.2	41	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**C-terminal effector domain of the bipartite response regulators **Family:**Spo0A
23	d1cuka1	Alignment	not modelled	11.1	27	**Fold:**RuvA C-terminal domain-like **Superfamily:**DNA helicase RuvA subunit, C-terminal domain **Family:**DNA helicase RuvA subunit, C-terminal domain
24	d1fc3a_	Alignment	not modelled	10.4	39	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**C-terminal effector domain of the bipartite response regulators **Family:**Spo0A
25	d1pgya_	Alignment	not modelled	10.4	40	**Fold:**RuvA C-terminal domain-like **Superfamily:**UBA-like **Family:**UBA domain
26	d1he1a_	Alignment	not modelled	10.1	11	**Fold:**Four-helical up-and-down bundle **Superfamily:**Bacterial GAP domain **Family:**Bacterial GAP domain
27	d1oqya2	Alignment	not modelled	9.3	33	**Fold:**RuvA C-terminal domain-like **Superfamily:**UBA-like **Family:**UBA domain
28	d1ifya_	Alignment	not modelled	8.9	22	**Fold:**RuvA C-terminal domain-like **Superfamily:**UBA-like **Family:**UBA domain
29	d1hy5a_	Alignment	not modelled	8.4	22	**Fold:**Four-helical up-and-down bundle **Superfamily:**Bacterial GAP domain

						Family: Bacterial GAP domain
30	d1nzja_	Alignment	not modelled	8.1	32	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Nucleotidylyl transferase **Family:**Class I aminoacyl-tRNA synthetases (RS), catalytic domain
31	d1g1xb_	Alignment	not modelled	8.0	19	**Fold:**S15/NS1 RNA-binding domain **Superfamily:**S15/NS1 RNA-binding domain **Family:**Ribosomal protein S15
32	c1yueA_	Alignment	not modelled	7.5	32	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**head vertex protein gp24; **PDBTitle:** bacteriophage t4 capsid vertex protein gp24
33	d1bwvs_	Alignment	not modelled	7.3	42	**Fold:**RuBisCO, small subunit **Superfamily:**RuBisCO, small subunit **Family:**RuBisCO, small subunit
34	d3c2wa1	Alignment	not modelled	7.0	20	**Fold:**Profilin-like **Superfamily:**GAF domain-like **Family:**GAF domain
35	d1oqya1	Alignment	not modelled	6.5	22	**Fold:**RuvA C-terminal domain-like **Superfamily:**UBA-like **Family:**UBA domain
36	d1a04a1	Alignment	not modelled	5.8	29	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**C-terminal effector domain of the bipartite response regulators **Family:**GerE-like (LuxR/UhpA family of transcriptional regulators)
37	d1bxni_	Alignment	not modelled	5.7	47	**Fold:**RuBisCO, small subunit **Superfamily:**RuBisCO, small subunit **Family:**RuBisCO, small subunit
38	d2ctma1	Alignment	not modelled	5.5	19	**Fold:**Eukaryotic type KH-domain (KH-domain type I) **Superfamily:**Eukaryotic type KH-domain (KH-domain type I) **Family:**Eukaryotic type KH-domain (KH-domain type I)
39	c1zljE_	Alignment	not modelled	5.5	24	**PDB header:**transcription **Chain:** E: **PDB Molecule:**dormancy survival regulator; **PDBTitle:** crystal structure of the mycobacterium tuberculosis hypoxic2 response regulator dosr c-terminal domain
40	c2c4mA_	Alignment	not modelled	5.2	26	**PDB header:**transferase **Chain:** A: **PDB Molecule:**glycogen phosphorylase; **PDBTitle:** starch phosphorylase: structural studies explain oxyanion-2 dependent kinetic stability and regulatory control.
41	c3cnfB_	Alignment	not modelled	5.1	31	**PDB header:**virus **Chain:** B: **PDB Molecule:**vp1; **PDBTitle:** 3.88 angstrom structure of cytoplasmic polyhedrosis virus2 by cryo-electron microscopy
42	c1n93X_	Alignment	not modelled	5.1	39	**PDB header:**viral protein **Chain:** X: **PDB Molecule:**p40 nucleoprotein; **PDBTitle:** crystal structure of the borna disease virus nucleoprotein