Phyre2

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Description	P75910
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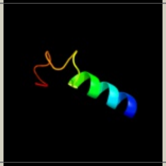
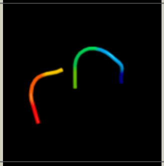
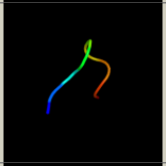
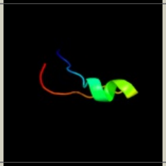
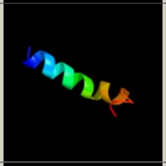
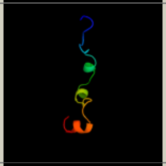
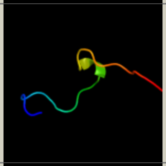
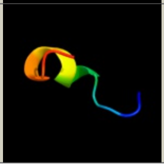
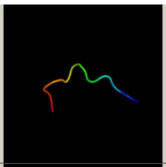
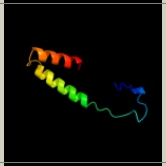
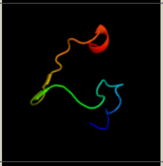
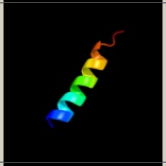
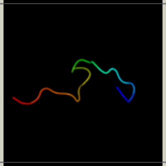
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1vzmB_	Alignment		19.7	100	**PDB header:**calcium-binding protein **Chain:** B: **PDB Molecule:**osteocalcin; **PDBTitle:** osteocalcin from fish argyrosomus regius
2	d2cqka1	Alignment		17.9	29	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**La domain
3	d1zh5a1	Alignment		15.4	24	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**La domain
4	c3pf6C_	Alignment		13.0	45	**PDB header:**structural genomics, unknown function **Chain:** C: **PDB Molecule:**hypothetical protein pp-luz7_gp033; **PDBTitle:** the structure of uncharacterized protein pp-luz7_gp033 from2 pseudomonas phage luz7.
5	d2k0bx1	Alignment		12.7	67	**Fold:**RuvA C-terminal domain-like **Superfamily:**UBA-like **Family:**UBA domain
6	d2nrqa1	Alignment		12.7	48	**Fold:**RL5-like **Superfamily:**RL5-like **Family:**SSO1042-like
7	d1s29a_	Alignment		12.0	20	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**La domain
8	c2qnlA_	Alignment		11.7	32	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of a putative dna damage-inducible protein2 (chu_0679) from cytophaga hutchinsonii atcc 33406 at 1.50 a3 resolution
9	d1rzhh1	Alignment		10.5	14	**Fold:**PRC-barrel domain **Superfamily:**PRC-barrel domain **Family:**Photosynthetic reaction centre, H-chain, cytoplasmic domain
10	c2i6hA_	Alignment		10.3	46	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein atu0120; **PDBTitle:** structure of protein of unknown function atu0120 from agrobacterium2 tumefaciens
11	d2i6ha1	Alignment		10.3	46	**Fold:**alpha-alpha superhelix **Superfamily:**TPR-like **Family:**Atu0120-like

12	d2r48a1	Alignment		10.0	17	**Fold:**Phosphotyrosine protein phosphatases I-like **Superfamily:**PTS system IIB component-like **Family:**PTS system, Fructose specific IIB subunit-like
13	d2r4qa1	Alignment		9.7	33	**Fold:**Phosphotyrosine protein phosphatases I-like **Superfamily:**PTS system IIB component-like **Family:**PTS system, Fructose specific IIB subunit-like
14	c2k1aA_	Alignment		8.7	46	**PDB header:**cell adhesion **Chain:** A: **PDB Molecule:**integrin alpha-iib; **PDBTitle:** bicelle-embedded integrin alpha(iib) transmembrane segment
15	d1hf8a1	Alignment		8.7	20	**Fold:**Spectrin repeat-like **Superfamily:**GAT-like domain **Family:**Phosphoinositide-binding clathrin adaptor, domain 2
16	d1dfma_	Alignment		8.4	32	**Fold:**Restriction endonuclease-like **Superfamily:**Restriction endonuclease-like **Family:**Restriction endonuclease BglII
17	c2kncA_	Alignment		7.8	46	**PDB header:**cell adhesion **Chain:** A: **PDB Molecule:**integrin alpha-iib; **PDBTitle:** platelet integrin alfaiib-beta3 transmembrane-cytoplasmic2 heterocomplex
18	d2jdid1	Alignment		7.6	30	**Fold:**Left-handed superhelix **Superfamily:**C-terminal domain of alpha and beta subunits of F1 ATP synthase **Family:**C-terminal domain of alpha and beta subunits of F1 ATP synthase
19	c2i5nH_	Alignment		7.5	32	**PDB header:**photosynthesis **Chain:** H: **PDB Molecule:**reaction center protein h chain; **PDBTitle:** 1.96 a x-ray structure of photosynthetic reaction center from2 rhodopseudomonas viridis:crystals grown by microfluidic technique
20	d2gica1	Alignment		7.4	38	**Fold:**Rhabdovirus nucleoprotein-like **Superfamily:**Rhabdovirus nucleoprotein-like **Family:**Rhabdovirus nucleocapsid protein
21	c3izxE_	Alignment	not modelled	7.2	23	**PDB header:**virus **Chain:** E: **PDB Molecule:**viral structural protein 5; **PDBTitle:** 3.1 angstrom cryoem structure of cytoplasmic polyhedrosis virus
22	c1eysH_	Alignment	not modelled	7.2	25	**PDB header:**electron transport **Chain:** H: **PDB Molecule:**photosynthetic reaction center; **PDBTitle:** crystal structure of photosynthetic reaction center from a2 thermophilic bacterium, thermochromatium tepidum
23	d2ogka1	Alignment	not modelled	7.2	29	**Fold:**RL5-like **Superfamily:**RL5-like **Family:**SSO1042-like
24	d1hx8a1	Alignment	not modelled	7.0	15	**Fold:**Spectrin repeat-like **Superfamily:**GAT-like domain **Family:**Phosphoinositide-binding clathrin adaptor, domain 2
25	c3e5aB_	Alignment	not modelled	6.8	69	**PDB header:**transferase **Chain:** B: **PDB Molecule:**targeting protein for xklp2; **PDBTitle:** crystal structure of aurora a in complex with vx-680 and tpx2
26	c2ks1B_	Alignment	not modelled	6.8	56	**PDB header:**transferase **Chain:** B: **PDB Molecule:**epidermal growth factor receptor; **PDBTitle:** heterodimeric association of transmembrane domains of erbb1 and erbb22 receptors enabling kinase activation
27	d1lghb_	Alignment	not modelled	6.7	60	**Fold:**Light-harvesting complex subunits **Superfamily:**Light-harvesting complex subunits **Family:**Light-harvesting complex subunits
28	c3lpzA_	Alignment	not modelled	6.4	16	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**get4 (yor164c homolog); **PDBTitle:** crystal structure of c. therm. get4
						PDB header:structural genomics

29	c2xvoB_	Alignment	not modelled	5.7	47	**Chain:** B: **PDB Molecule:**sso1725; **PDBTitle:** sso1725, a protein involved in the crispr/cas pathway
30	d1e6yb2	Alignment	not modelled	5.7	31	**Fold:**Ferredoxin-like **Superfamily:**Methyl-coenzyme M reductase subunits **Family:**Methyl-coenzyme M reductase alpha and beta chain N-terminal domain
31	c1ponB_	Alignment	not modelled	5.7	50	**PDB header:**calcium-binding protein **Chain:** B: **PDB Molecule:**troponin c; **PDBTitle:** site iii-site iv troponin c heterodimer, nmr
32	c3pryA_	Alignment	not modelled	5.7	70	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**heat shock protein hsp 90-beta; **PDBTitle:** crystal structure of the middle domain of human hsp90-beta refined at2 2.3 a resolution
33	c2pqlA_	Alignment	not modelled	5.7	40	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**d7r4 protein; **PDBTitle:** crystal structure of anopheles gambiae d7r4-tryptamine complex
34	d1qkya_	Alignment	not modelled	5.6	80	**Fold:**Knottins (small inhibitors, toxins, lectins) **Superfamily:**Scorpion toxin-like **Family:**Short-chain scorpion toxins
35	c2wnyB_	Alignment	not modelled	5.6	43	**PDB header:**unknown function **Chain:** B: **PDB Molecule:**conserved protein mth689; **PDBTitle:** structure of mth689, a duf54 protein from methanothermobacter2 thermautotrophicus
36	d1h5wa_	Alignment	not modelled	5.6	18	**Fold:**Upper collar protein gp10 (connector protein) **Superfamily:**Upper collar protein gp10 (connector protein) **Family:**Upper collar protein gp10 (connector protein)
37	c2nr1A_	Alignment	not modelled	5.4	57	**PDB header:**receptor **Chain:** A: **PDB Molecule:**nr1 m2; **PDBTitle:** transmembrane segment 2 of nmda receptor nr1, nmr, 102 structures
38	c1y6zA_	Alignment	not modelled	5.4	60	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**heat shock protein, putative; **PDBTitle:** middle domain of plasmodium falciparum putative heat shock protein2 pf14_0417
39	d2v7qi1	Alignment	not modelled	5.4	44	**Fold:**Non-globular all-alpha subunits of globular proteins **Superfamily:**Epsilon subunit of mitochondrial F1F0-ATP synthase **Family:**Epsilon subunit of mitochondrial F1F0-ATP synthase
40	d1q90g_	Alignment	not modelled	5.3	56	**Fold:**Single transmembrane helix **Superfamily:**PetG subunit of the cytochrome b6f complex **Family:**PetG subunit of the cytochrome b6f complex
41	c1q90G_	Alignment	not modelled	5.3	56	**PDB header:**photosynthesis **Chain:** G: **PDB Molecule:**cytochrome b6f complex subunit petg; **PDBTitle:** structure of the cytochrome b6f (plastohydroquinone : plastocyanin2 oxidoreductase) from chlamydomonas reinhardtii
42	d3d85d2	Alignment	not modelled	5.1	38	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**Fibronectin type III **Family:**Fibronectin type III