Phyre2

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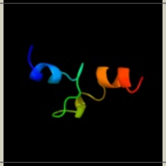
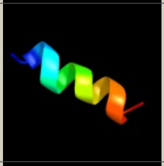
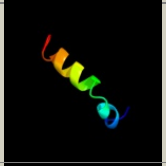
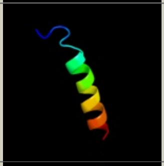
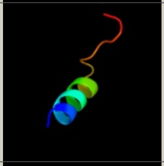
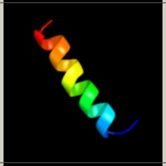
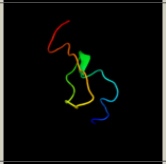
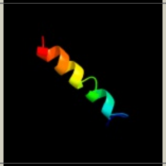
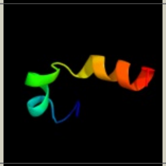
Description	P0A9R2
Date	Thu Jan 5 11:11:03 GMT 2012
Unique Job ID	2515e4372549def7

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2l2tA_	Alignment		32.0	26	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**receptor tyrosine-protein kinase erbb-4; **PDBTitle:** solution nmr structure of the erbb4 dimeric membrane domain
2	c2qjxA_	Alignment		24.2	32	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**protein bim1; **PDBTitle:** structural basis of microtubule plus end tracking by2 xmap215, clip-170 and eb1
3	c3kdpG_	Alignment		23.1	36	**PDB header:**hydrolase **Chain:** G: **PDB Molecule:**na+/k+ atpase gamma subunit transcript variant a; **PDBTitle:** crystal structure of the sodium-potassium pump
4	c3kdpH_	Alignment		23.1	36	**PDB header:**hydrolase **Chain:** H: **PDB Molecule:**na+/k+ atpase gamma subunit transcript variant a; **PDBTitle:** crystal structure of the sodium-potassium pump
5	c1wyoA_	Alignment		16.9	32	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**microtubule-associated protein rp/eb family **PDBTitle:** solution structure of the ch domain of human microtubule-2 associated protein rp/eb family member 3
6	d2gbsa1	Alignment		11.3	33	**Fold:**PUA domain-like **Superfamily:**PUA domain-like **Family:**Atu2648/PH1033-like
7	d2qjza1	Alignment		10.2	30	**Fold:**CH domain-like **Superfamily:**Calponin-homology domain, CH-domain **Family:**Calponin-homology domain, CH-domain
8	c3ixzB_	Alignment		10.1	18	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**potassium-transporting atpase subunit beta; **PDBTitle:** pig gastric h+/k+-atpase complexed with aluminium fluoride
9	c3bq9A_	Alignment		9.7	32	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**predicted rossmann fold nucleotide-binding domain- **PDBTitle:** crystal structure of predicted nucleotide-binding protein from2 idiomarina baltica os145
10	c3o0rC_	Alignment		9.6	35	**PDB header:**immune system/oxidoreductase **Chain:** C: **PDB Molecule:**nitric oxide reductase subunit c; **PDBTitle:** crystal structure of nitric oxide reductase from pseudomonas2 aeruginosa in complex with antibody fragment
11	d1m56d_	Alignment		9.5	40	**Fold:**Single transmembrane helix **Superfamily:**Bacterial aa3 type cytochrome c oxidase subunit IV **Family:**Bacterial aa3 type cytochrome c oxidase subunit IV

12	c2kdnA_	Alignment		9.2	17	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**putative uncharacterized protein pfe0790c; **PDBTitle:** solution structure of pfe0790c, a putative bola-like2 protein from the protozoan parasite plasmodium falciparum.
13	d1v5ka_	Alignment		8.9	32	**Fold:**CH domain-like **Superfamily:**Calponin-homology domain, CH-domain **Family:**Calponin-homology domain, CH-domain
14	c3b8eB_	Alignment		8.8	23	**PDB header:**hydrolase/transport protein **Chain:** B: **PDB Molecule:**sodium/potassium-transporting atpase subunit **PDBTitle:** crystal structure of the sodium-potassium pump
15	d1eysh2	Alignment		8.7	40	**Fold:**Single transmembrane helix **Superfamily:**Photosystem II reaction centre subunit H, transmembrane region **Family:**Photosystem II reaction centre subunit H, transmembrane region
16	c3dl8D_	Alignment		8.7	28	**PDB header:**protein transport **Chain:** D: **PDB Molecule:**sece; **PDBTitle:** structure of the complex of aquifex aeolicus secyeg and2 bacillus subtilis seca
17	c3o2eA_	Alignment		7.7	50	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**bola-like protein; **PDBTitle:** crystal structure of a bol-like protein from babesia bovis
18	c2veqA_	Alignment		7.5	31	**PDB header:**cell cycle **Chain:** A: **PDB Molecule:**centromere dna-binding protein complex cbf3 **PDBTitle:** insights into kinetochore-dna interactions from the2 structure of cep3p
19	d1ny8a_	Alignment		7.3	44	**Fold:**Alpha-lytic protease prodomain-like **Superfamily:**BolA-like **Family:**BolA-like
20	d1v9ja_	Alignment		6.8	50	**Fold:**Alpha-lytic protease prodomain-like **Superfamily:**BolA-like **Family:**BolA-like
21	c3eopB_	Alignment	not modelled	6.5	20	**PDB header:**unknown function **Chain:** B: **PDB Molecule:**thymocyte nuclear protein 1; **PDBTitle:** crystal structure of the duf55 domain of human thymocyte nuclear2 protein 1
22	c3htuE_	Alignment	not modelled	5.7	25	**PDB header:**protein transport **Chain:** E: **PDB Molecule:**vacuolar protein-sorting-associated protein 25; **PDBTitle:** crystal structure of the human vps25-vps20 subcomplex
23	d1vk5a_	Alignment	not modelled	5.5	36	**Fold:**Hypothetical protein At3g22680 **Superfamily:**Hypothetical protein At3g22680 **Family:**Hypothetical protein At3g22680