Phyre2

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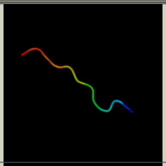
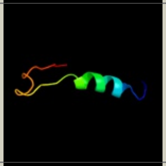
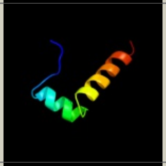
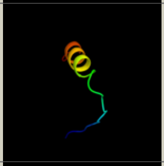
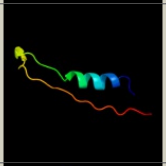
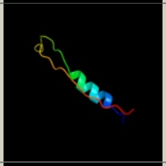
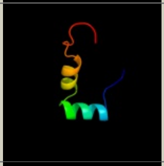
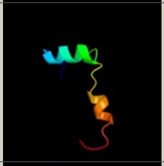
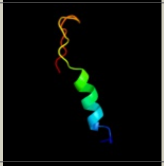
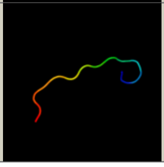
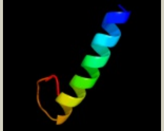
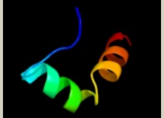
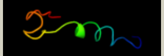
Description	P76023
Date	Thu Jan 5 12:17:31 GMT 2012
Unique Job ID	f31614f42c3531f5

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1f3ua_	Alignment		16.7	42	**Fold:**triple barrel **Superfamily:**Rap30/74 interaction domains **Family:**Rap30/74 interaction domains
2	d2jdia3	Alignment		12.9	27	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**RecA protein-like (ATPase-domain)
3	d1mala2	Alignment		12.3	22	**Fold:**Fe,Mn superoxide dismutase (SOD), C-terminal domain **Superfamily:**Fe,Mn superoxide dismutase (SOD), C-terminal domain **Family:**Fe,Mn superoxide dismutase (SOD), C-terminal domain
4	c2rjbD_	Alignment		12.2	44	**PDB header:**structural genomics, unknown function **Chain:** D: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of uncharacterized protein ydcj (sf1787)2 from shigella flexneri which includes domain duf1338.3 northeast structural genomics consortium target sfr276
5	c2w6fA_	Alignment		11.8	21	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**atp synthase subunit alpha heart isoform, **PDBTitle:** low resolution structures of bovine mitochondrial f1-atpase2 during controlled dehydration: hydration state 2.
6	c1w0jB_	Alignment		10.7	21	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**atp synthase alpha chain heart isoform, **PDBTitle:** beryllium fluoride inhibited bovine f1-atpase
7	c2r9vA_	Alignment		10.3	21	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**atp synthase subunit alpha; **PDBTitle:** crystal structure of atp synthase subunit alpha (tm1612) from2 thermotoga maritima at 2.10 a resolution
8	d1ix9a2	Alignment		10.1	31	**Fold:**Fe,Mn superoxide dismutase (SOD), C-terminal domain **Superfamily:**Fe,Mn superoxide dismutase (SOD), C-terminal domain **Family:**Fe,Mn superoxide dismutase (SOD), C-terminal domain
9	d1b06a2	Alignment		8.8	26	**Fold:**Fe,Mn superoxide dismutase (SOD), C-terminal domain **Superfamily:**Fe,Mn superoxide dismutase (SOD), C-terminal domain **Family:**Fe,Mn superoxide dismutase (SOD), C-terminal domain
10	d1skyb3	Alignment		8.7	27	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**RecA protein-like (ATPase-domain)
11	c3hh7A_	Alignment		8.6	43	**PDB header:**toxin **Chain:** A: **PDB Molecule:**muscarinic toxin-like protein 3 homolog; **PDBTitle:** structural and functional characterization of a novel2 homodimeric three-finger neurotoxin from the venom of3 ophiophagus hannah (king cobra)

12	c3h0dB_	Alignment		8.2	29	**PDB header:**transcription/dna **Chain:** B: **PDB Molecule:**ctsr; **PDBTitle:** crystal structure of ctsr in complex with a 26bp dna duplex
13	d1q9ca_	Alignment		7.8	28	**Fold:**Histone-fold **Superfamily:**Histone-fold **Family:**TBP-associated factors, TAFs
14	d1uera2	Alignment		6.4	25	**Fold:**Fe,Mn superoxide dismutase (SOD), C-terminal domain **Superfamily:**Fe,Mn superoxide dismutase (SOD), C-terminal domain **Family:**Fe,Mn superoxide dismutase (SOD), C-terminal domain
15	d1wb8a2	Alignment		6.4	23	**Fold:**Fe,Mn superoxide dismutase (SOD), C-terminal domain **Superfamily:**Fe,Mn superoxide dismutase (SOD), C-terminal domain **Family:**Fe,Mn superoxide dismutase (SOD), C-terminal domain
16	d2nyba2	Alignment		6.3	23	**Fold:**Fe,Mn superoxide dismutase (SOD), C-terminal domain **Superfamily:**Fe,Mn superoxide dismutase (SOD), C-terminal domain **Family:**Fe,Mn superoxide dismutase (SOD), C-terminal domain
17	d1fx0a3	Alignment		5.8	27	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**RecA protein-like (ATPase-domain)

18	d1dt0a2	Alignment		5.8	25	**Fold:**Fe,Mn superoxide dismutase (SOD), C-terminal domain **Superfamily:**Fe,Mn superoxide dismutase (SOD), C-terminal domain **Family:**Fe,Mn superoxide dismutase (SOD), C-terminal domain