Phyre^2

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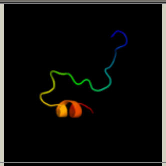
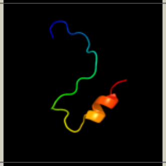
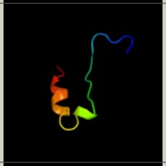
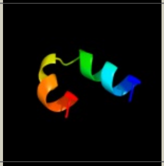
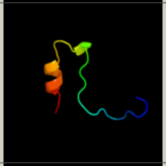
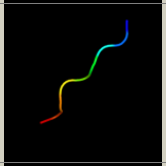
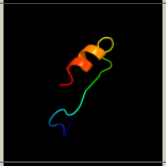
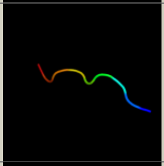
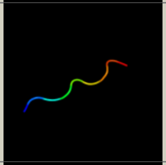
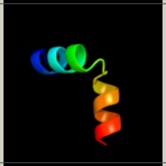
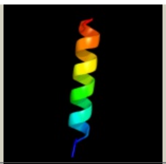
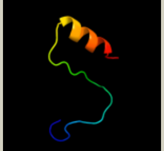
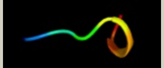
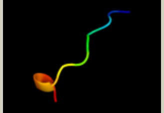
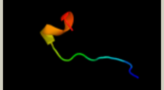
Description	P0ADJ3
Date	Thu Jan 5 11:21:09 GMT 2012
Unique Job ID	e27ec5437bc475b9

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1gq2a2	Alignment		27.2	32	**Fold:**Aminoacid dehydrogenase-like, N-terminal domain **Superfamily:**Aminoacid dehydrogenase-like, N-terminal domain **Family:**Malic enzyme N-domain
2	d1pj3a2	Alignment		21.8	25	**Fold:**Aminoacid dehydrogenase-like, N-terminal domain **Superfamily:**Aminoacid dehydrogenase-like, N-terminal domain **Family:**Malic enzyme N-domain
3	c2aw5A_	Alignment		14.4	29	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**nadp-dependent malic enzyme; **PDBTitle:** crystal structure of a human malic enzyme
4	c3ps9A_	Alignment		13.1	50	**PDB header:**transferase **Chain:** A: **PDB Molecule:**trna 5-methylaminomethyl-2-thiouridine biosynthesis **PDBTitle:** crystal structure of mnmc from e. coli
5	c1gz3B_	Alignment		11.9	25	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**nad-dependent malic enzyme; **PDBTitle:** molecular mechanism for the regulation of human mitochondrial2 nad(p)+-dependent malic enzyme by atp and fumarate
6	d1dt0a1	Alignment		11.3	56	**Fold:**Long alpha-hairpin **Superfamily:**Fe,Mn superoxide dismutase (SOD), N-terminal domain **Family:**Fe,Mn superoxide dismutase (SOD), N-terminal domain
7	c1qr6A_	Alignment		10.6	25	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**malic enzyme 2; **PDBTitle:** human mitochondrial nad(p)-dependent malic enzyme
8	d1y67a1	Alignment		10.1	44	**Fold:**Long alpha-hairpin **Superfamily:**Fe,Mn superoxide dismutase (SOD), N-terminal domain **Family:**Fe,Mn superoxide dismutase (SOD), N-terminal domain
9	d1my6a1	Alignment		9.0	22	**Fold:**Long alpha-hairpin **Superfamily:**Fe,Mn superoxide dismutase (SOD), N-terminal domain **Family:**Fe,Mn superoxide dismutase (SOD), N-terminal domain
10	d1zkea1	Alignment		8.8	30	**Fold:**ROP-like **Superfamily:**HP1531-like **Family:**HP1531-like
11	d1ix9a1	Alignment		8.1	33	**Fold:**Long alpha-hairpin **Superfamily:**Fe,Mn superoxide dismutase (SOD), N-terminal domain **Family:**Fe,Mn superoxide dismutase (SOD), N-terminal domain

12	d1regx_	Alignment		8.0	27	**Fold:**Ferredoxin-like **Superfamily:**Translational regulator protein regA **Family:**Translational regulator protein regA
13	d1o0sa2	Alignment		7.8	16	**Fold:**Aminoacid dehydrogenase-like, N-terminal domain **Superfamily:**Aminoacid dehydrogenase-like, N-terminal domain **Family:**Malic enzyme N-domain
14	d2j8ba1	Alignment		7.5	6	**Fold:**Snake toxin-like **Superfamily:**Snake toxin-like **Family:**Extracellular domain of cell surface receptors
15	c3rnvA_	Alignment		7.5	24	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**helper component proteinase; **PDBTitle:** structure of the autocatalytic cysteine protease domain of potyvirus2 helper-component proteinase
16	c2hdlA_	Alignment		7.1	50	**PDB header:**cytokine **Chain:** A: **PDB Molecule:**small inducible cytokine b14; **PDBTitle:** solution structure of brak/cxcl14
17	d2nyba1	Alignment		7.1	44	**Fold:**Long alpha-hairpin **Superfamily:**Fe,Mn superoxide dismutase (SOD), N-terminal domain **Family:**Fe,Mn superoxide dismutase (SOD), N-terminal domain
18	c3lrrB_	Alignment		7.1	27	**PDB header:**hydrolase/rna **Chain:** B: **PDB Molecule:**probable atp-dependent rna helicase ddx58; **PDBTitle:** crystal structure of human rig-i ctd bound to a 12 bp au rich 5' ppp2 dsrna
19	d2g6ta1	Alignment		6.8	25	**Fold:**CAC2185-like **Superfamily:**CAC2185-like **Family:**CAC2185-like
20	c3ga3A_	Alignment		6.5	27	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**interferon-induced helicase c domain-containing **PDBTitle:** crystal structure of the c-terminal domain of human mda5
21	c3ol4B_	Alignment	not modelled	5.7	25	**PDB header:**unknown function **Chain:** B: **PDB Molecule:**putative uncharacterized protein; **PDBTitle:** crystal structure of a putative uncharacterized protein from2 mycobacterium smegmatis, an ortholog of rv0543c
22	c1o0sB_	Alignment	not modelled	5.2	16	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**nad-dependent malic enzyme; **PDBTitle:** crystal structure of ascaris suum malic enzyme complexed with nadh
23	d2hi3a1	Alignment	not modelled	5.1	17	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Homeodomain
24	c1zmrA_	Alignment	not modelled	5.0	18	**PDB header:**transferase **Chain:** A: **PDB Molecule:**phosphoglycerate kinase; **PDBTitle:** crystal structure of the e. coli phosphoglycerate kinase