Phyre2

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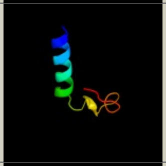
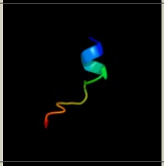
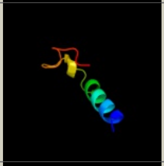
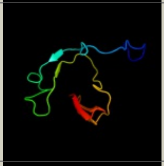
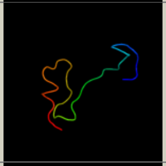
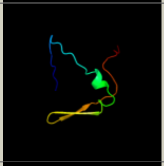
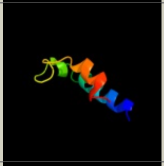
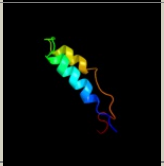
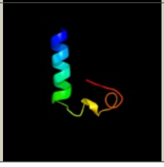
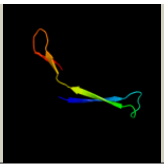
Description	P39293
Date	Thu Jan 5 11:59:00 GMT 2012
Unique Job ID	a6016db73cf1f178

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1wmxa_	 Alignment		19.1	13	**Fold:**Galactose-binding domain-like **Superfamily:**Galactose-binding domain-like **Family:**Family 30 carbohydrate binding module, CBM30 (PKD repeat)
2	c3alxB_	 Alignment		16.9	16	**PDB header:**viral protein/membrane protein **Chain:** B: **PDB Molecule:**hemagglutinin, cdw150; **PDBTitle:** crystal structure of the measles virus hemagglutinin bound to its2 cellular receptor slam (mv-h(l482r)-slam(n102h/r108y) fusion)
3	d1jmxa2	 Alignment		15.5	16	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**Quinohemoprotein amine dehydrogenase A chain, domains 1 and 2
4	c2kxoA_	 Alignment		15.3	33	**PDB header:**cell cycle **Chain:** A: **PDB Molecule:**cell division topological specificity factor; **PDBTitle:** solution nmr structure of the cell division regulator mine protein2 from neisseria gonorrhoeae
5	d1pbya2	 Alignment		12.3	19	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**Quinohemoprotein amine dehydrogenase A chain, domains 1 and 2
6	d1glaf_	 Alignment		9.9	18	**Fold:**Barrel-sandwich hybrid **Superfamily:**Duplicated hybrid motif **Family:**Glucose permease-like
7	c2dhzA_	 Alignment		8.6	20	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**rap guanine nucleotide exchange factor (gef)- **PDBTitle:** solution structure of the ra domain in the human link2 guanine nucleotide exchange factor ii (link-gefii)
8	d3pmga4	 Alignment		7.7	10	**Fold:**TBP-like **Superfamily:**Phosphoglucomutase, C-terminal domain **Family:**Phosphoglucomutase, C-terminal domain
9	c1pbyA_	 Alignment		6.3	20	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**quinohemoprotein amine dehydrogenase 60 kda **PDBTitle:** structure of the phenylhydrazine adduct of the2 quinohemoprotein amine dehydrogenase from paracoccus3 denitrificans at 1.7 a resolution
10	d2bida_	 Alignment		5.8	9	**Fold:**Toxins' membrane translocation domains **Superfamily:**Bcl-2 inhibitors of programmed cell death **Family:**Bcl-2 inhibitors of programmed cell death
11	c1jmxA_	 Alignment		5.5	16	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**amine dehydrogenase; **PDBTitle:** crystal structure of a quinohemoprotein amine dehydrogenase2 from pseudomonas putida

12	d2ewca1	Alignment		5.3	21	**Fold:**Bacillus chorismate mutase-like **Superfamily:**YjgF-like **Family:**YjgF/L-PSP

13	c2jeuA_	Alignment		5.2	8	**PDB header:**transcription **Chain:** A: **PDB Molecule:**regulatory protein e2; **PDBTitle:** transcription activator structure reveals redox control of2 a replication initiation reaction