Phyre2

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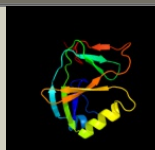
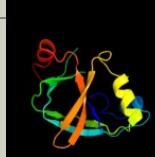
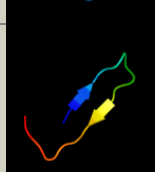
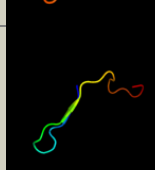
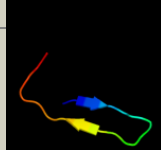
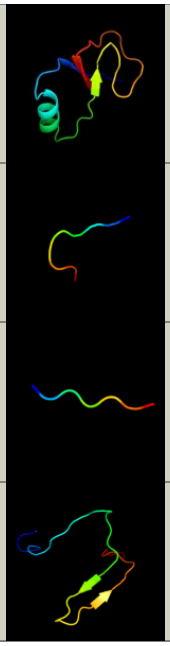
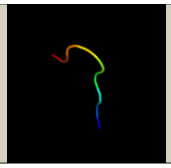
Description	P0AE48
Date	Thu Jan 5 11:22:31 GMT 2012
Unique Job ID	fe17f078b16ff208

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1xhsa_	Alignment		100.0	100	**Fold:**Gamma-glutamyl cyclotransferase-like **Superfamily:**Gamma-glutamyl cyclotransferase-like **Family:**Gamma-glutamyl cyclotransferase-like
2	d1v30a_	Alignment		100.0	32	**Fold:**Gamma-glutamyl cyclotransferase-like **Superfamily:**Gamma-glutamyl cyclotransferase-like **Family:**Gamma-glutamyl cyclotransferase-like
3	c2qikA_	Alignment		100.0	29	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**upf0131 protein ykqa; **PDBTitle:** crystal structure of ykqa from bacillus subtilis. northeast2 structural genomics target sr631
4	d1vkba_	Alignment		99.9	31	**Fold:**Gamma-glutamyl cyclotransferase-like **Superfamily:**Gamma-glutamyl cyclotransferase-like **Family:**Gamma-glutamyl cyclotransferase-like
5	c3jubA_	Alignment		99.9	27	**PDB header:**transferase **Chain:** A: **PDB Molecule:**aig2-like domain-containing protein 1; **PDBTitle:** human gamma-glutamylamine cyclotransferase
6	c2jqvA_	Alignment		99.9	25	**PDB header:**structural genomics **Chain:** A: **PDB Molecule:**aig2 protein-like; **PDBTitle:** solution structure at3g28950.1 from arabidopsis thaliana
7	c2g0qA_	Alignment		99.9	26	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**at5g39720.1 protein; **PDBTitle:** solution structure of at5g39720.1 from arabidopsis thaliana
8	c2rbhA_	Alignment		99.8	20	**PDB header:**transferase **Chain:** A: **PDB Molecule:**gamma-glutamyl cyclotransferase; **PDBTitle:** gamma-glutamyl cyclotransferase
9	d2o8ra4	Alignment		49.4	22	**Fold:**Phospholipase D/nuclease **Superfamily:**Phospholipase D/nuclease **Family:**Polyphosphate kinase C-terminal domain
10	d1xdpa4	Alignment		45.9	26	**Fold:**Phospholipase D/nuclease **Superfamily:**Phospholipase D/nuclease **Family:**Polyphosphate kinase C-terminal domain
11	c2o8rA_	Alignment		25.8	22	**PDB header:**transferase **Chain:** A: **PDB Molecule:**polyphosphate kinase; **PDBTitle:** crystal structure of polyphosphate kinase from2 porphyromonas gingivalis

12	c3eoiB_	Alignment		11.8	14	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**pilm; **PDBTitle:** crystal structure of putative protein pilm from escherichia coli b7a
13	d1hf2a1	Alignment		8.2	22	**Fold:**Single-stranded right-handed beta-helix **Superfamily:**Cell-division inhibitor MinC, C-terminal domain **Family:**Cell-division inhibitor MinC, C-terminal domain
14	d1ynha1	Alignment		7.9	71	**Fold:**Pentein, beta/alpha-propeller **Superfamily:**Pentein **Family:**Succinylarginine dihydrolase-like
15	c1xdoB_	Alignment		6.7	17	**PDB header:**transferase **Chain:** B: **PDB Molecule:**polyphosphate kinase; **PDBTitle:** crystal structure of escherichia coli polyphosphate kinase

16	c1hf2A_	Alignment		5.4	22	**PDB header:**cell division protein **Chain:** A: **PDB Molecule:**septum site-determining protein minc; **PDBTitle:** crystal structure of the bacterial cell-division inhibitor2 minc from t. maritima