Phyre2

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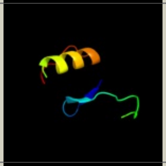
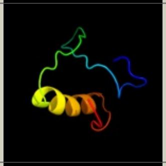
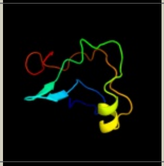
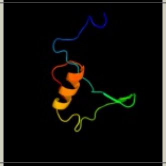
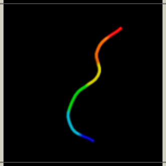
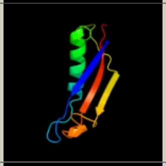
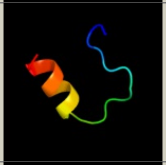
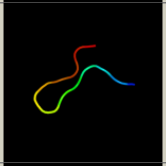
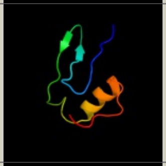
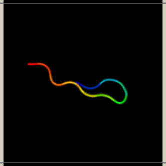
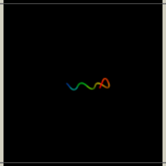
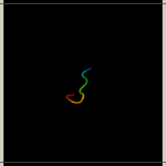
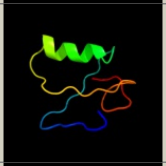
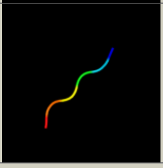
Description	P76308
Date	Wed Jan 25 15:21:07 GMT 2012
Unique Job ID	854eaae1dd96e142

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1z8ga2	Alignment		47.5	13	**Fold:**SRCR-like **Superfamily:**SRCR-like **Family:**Hepsin, N-terminal domain
2	c1z8gA_	Alignment		45.7	18	**PDB header:**hydrolase/hydrolase inhibitor **Chain:** A: **PDB Molecule:**serine protease hepsin; **PDBTitle:** crystal structure of the extracellular region of the transmembrane2 serine protease hepsin with covalently bound preferred substrate.
3	c2ottY_	Alignment		41.6	14	**PDB header:**immune system **Chain:** Y: **PDB Molecule:**t-cell surface glycoprotein cd5; **PDBTitle:** crystal structure of cd5_diii
4	c2jopA_	Alignment		26.6	9	**PDB header:**immune system **Chain:** A: **PDB Molecule:**t-cell surface glycoprotein cd5; **PDBTitle:** solution structure of the n-terminal extracellular domain2 of the lymphocyte receptor cd5 (cd5 domain 1)
5	c2oyaA_	Alignment		24.4	13	**PDB header:**ligand binding protein **Chain:** A: **PDB Molecule:**macrophage receptor marco; **PDBTitle:** crystal structure analysis of the dimeric form of the srcr domain of2 mouse marco
6	d1dx5i1	Alignment		14.4	50	**Fold:**Knottins (small inhibitors, toxins, lectins) **Superfamily:**EGF/Laminin **Family:**EGF-type module
7	c2y1bA_	Alignment		14.1	19	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**putative outer membrane protein, signal; **PDBTitle:** crystal structure of the e. coli outer membrane lipoprotein2 rcsf
8	d1ji8a_	Alignment		13.5	24	**Fold:**DsrC, the gamma subunit of dissimilatory sulfite reductase **Superfamily:**DsrC, the gamma subunit of dissimilatory sulfite reductase **Family:**DsrC, the gamma subunit of dissimilatory sulfite reductase
9	c1yx3A_	Alignment		11.9	14	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein dsrc; **PDBTitle:** nmr structure of allochromatium vinosum dsrc: northeast2 structural genomics consortium target op4
10	d1a0ea_	Alignment		9.4	29	**Fold:**TIM beta/alpha-barrel **Superfamily:**Xylose isomerase-like **Family:**Xylose isomerase
11	d1fvia1	Alignment		9.3	31	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**DNA ligase/mRNA capping enzyme postcatalytic domain

12	d2v4jc1	Alignment		8.8	9	**Fold:**DsrC, the gamma subunit of dissimilatory sulfite reductase **Superfamily:**DsrC, the gamma subunit of dissimilatory sulfite reductase **Family:**DsrC, the gamma subunit of dissimilatory sulfite reductase
13	d1a0ca_	Alignment		8.5	14	**Fold:**TIM beta/alpha-barrel **Superfamily:**Xylose isomerase-like **Family:**Xylose isomerase
14	c2a5wC_	Alignment		8.4	32	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**sulfite reductase, desulfoviridin-type subunit gamma **PDBTitle:** crystal structure of the oxidized gamma-subunit of the dissimilatory2 sulfite reductase (dsrc) from archaeoglobus fulgidus
15	d1by2a_	Alignment		7.5	15	**Fold:**SRCR-like **Superfamily:**SRCR-like **Family:**Scavenger receptor cysteine-rich (SRCR) domain
16	d1xiwb_	Alignment		7.4	36	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**Immunoglobulin **Family:**I set domains
17	d1xzpa3	Alignment		6.6	22	**Fold:**Folate-binding domain **Superfamily:**Folate-binding domain **Family:**TrmE formyl-THF-binding domain
18	c1xzqB_	Alignment		6.6	22	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**probable trna modification gtpase trme; **PDBTitle:** structure of the gtp-binding protein trme from thermotoga2 maritima complexed with 5-formyl-thf
19	c2j8jA_	Alignment		6.5	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**coagulation factor xi; **PDBTitle:** solution structure of the a4 domain of blood coagulation2 factor xi
20	d1sy6a1	Alignment		6.4	67	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**Immunoglobulin **Family:**I set domains
21	d1a0da_	Alignment	not modelled	6.3	21	**Fold:**TIM beta/alpha-barrel **Superfamily:**Xylose isomerase-like **Family:**Xylose isomerase
22	c2j8jB_	Alignment	not modelled	6.3	16	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**coagulation factor xi; **PDBTitle:** solution structure of the a4 domain of blood coagulation2 factor xi
23	c2j8lA_	Alignment	not modelled	6.2	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**coagulation factor xi; **PDBTitle:** fxi apple 4 domain loop-out conformation