Phyre2

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Description	P31991
Date	Thu Jan 5 11:48:56 GMT 2012
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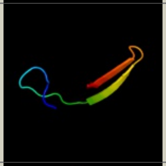
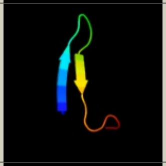
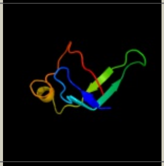
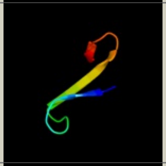
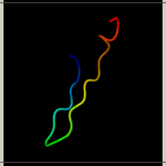
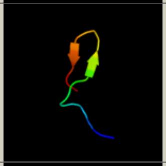
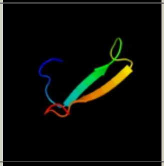
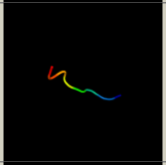
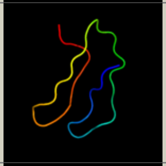
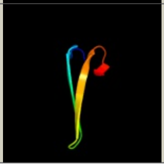
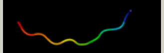
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3gt2A_	Alignment		25.0	35	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**putative uncharacterized protein; **PDBTitle:** crystal structure of the p60 domain from m. avium2 paratuberculosis antigen map1272c
2	c2yxyA_	Alignment		16.8	48	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical conserved protein, gk0453; **PDBTitle:** crystarl structure of hypothetical conserved protein, gk0453
3	c3ipjB_	Alignment		16.4	30	**PDB header:**transferase **Chain:** B: **PDB Molecule:**pts system, iiabc component; **PDBTitle:** the crystal structure of one domain of the pts system, iiabc component2 from clostridium difficile
4	c2eqnA_	Alignment		14.8	16	**PDB header:**transcription **Chain:** A: **PDB Molecule:**hypothetical protein loc92345; **PDBTitle:** solution structure of the naf1 domain of hypothetical2 protein bc008207 [homo sapiens]
5	c3pbiA_	Alignment		14.7	30	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**invasion protein; **PDBTitle:** structure of the peptidoglycan hydrolase ripb (rv1478) from2 mycobacterium tuberculosis at 1.6 resolution
6	c1ibaA_	Alignment		8.7	35	**PDB header:**phoshphotransferase **Chain:** A: **PDB Molecule:**glucose permease; **PDBTitle:** glucose permease (domain iib), nmr, 11 structures
7	c3e8vA_	Alignment		8.6	28	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**possible transglutaminase-family protein; **PDBTitle:** crystal structure of a possible transglutaminase-family2 protein proteolytic fragment from bacteroides fragilis
8	c2xivA_	Alignment		8.4	27	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**hypothetical invasion protein; **PDBTitle:** structure of rv1477, hypothetical invasion protein of2 mycobacterium tuberculosis
9	c2yujA_	Alignment		7.7	63	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**ubiquitin fusion degradation 1-like; **PDBTitle:** solution structure of human ubiquitin fusion degradation2 protein 1 homolog ufd1
10	d1drsa_	Alignment		7.7	32	**Fold:**Snake toxin-like **Superfamily:**Snake toxin-like **Family:**Dendroaspin
11	c3npfB_	Alignment		7.0	47	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**putative dipeptidyl-peptidase vi; **PDBTitle:** crystal structure of a putative dipeptidyl-peptidase vi (bacova_00612)2 from bacteroides ovatus at 1.72 a resolution

12	d1d0na6	Alignment		7.0	24	**Fold:**Gelsolin-like **Superfamily:**Actin depolymerizing proteins **Family:**Gelsolin-like
13	c1zc1A_	Alignment		6.5	36	**PDB header:**protein turnover **Chain:** A: **PDB Molecule:**ubiquitin fusion degradation protein 1; **PDBTitle:** ufd1 exhibits the aaa-atpase fold with two distinct2 ubiquitin interaction sites
14	d1sf9a_	Alignment		6.4	43	**Fold:**SH3-like barrel **Superfamily:**Hypothetical protein YfhH **Family:**Hypothetical protein YfhH
15	c1ik9C_	Alignment		5.8	57	**PDB header:**gene regulation/ligase **Chain:** C: **PDB Molecule:**dna ligase iv; **PDBTitle:** crystal structure of a xrcc4-dna ligase iv complex
16	d1gjwa1	Alignment		5.7	83	**Fold:**Glycosyl hydrolase domain **Superfamily:**Glycosyl hydrolase domain **Family:**alpha-Amylases, C-terminal beta-sheet domain
17	d1ig8a1	Alignment		5.5	10	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**Hexokinase
18	d2esla1	Alignment		5.1	25	**Fold:**Cyclophilin-like **Superfamily:**Cyclophilin-like **Family:**Cyclophilin (peptidylprolyl isomerase)
19	d1tifa_	Alignment		5.1	25	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**Translation initiation factor IF3, N-terminal domain **Family:**Translation initiation factor IF3, N-terminal domain

20	c2kmfA_	Alignment		5.0	17	**PDB header:**photosynthesis **Chain:** A: **PDB Molecule:**photosystem ii 11 kda protein; **PDBTitle:** solution structure of psb27 from cyanobacterial photosystem2 ii