Phyre2

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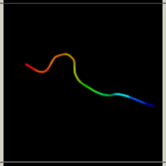
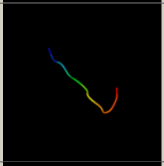
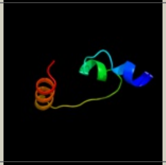
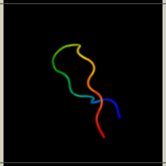
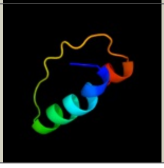
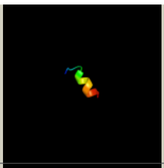
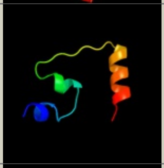
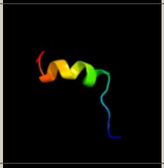
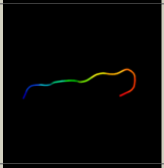
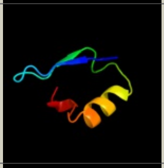
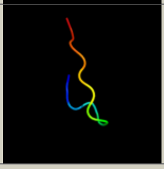
Description	P0A8W5
Date	Thu Jan 5 11:08:51 GMT 2012
Unique Job ID	9ebb4b598eec2dd3

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d2gzoa1	Alignment		100.0	45	**Fold:**VC0467-like **Superfamily:**VC0467-like **Family:**VC0467-like
2	d2do8a1	Alignment		100.0	41	**Fold:**VC0467-like **Superfamily:**VC0467-like **Family:**VC0467-like
3	c2aj2A_	Alignment		100.0	45	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**hypothetical upf0301 protein vc0467; **PDBTitle:** x-ray crystal structure of protein vc0467 from vibrio2 cholerae. northeast structural genomics consortium target3 vcr8.
4	d2hafa1	Alignment		100.0	47	**Fold:**VC0467-like **Superfamily:**VC0467-like **Family:**VC0467-like
5	d2ew0a1	Alignment		100.0	40	**Fold:**VC0467-like **Superfamily:**VC0467-like **Family:**VC0467-like
6	d2gs5a1	Alignment		100.0	19	**Fold:**VC0467-like **Superfamily:**VC0467-like **Family:**VC0467-like
7	d1vpqa_	Alignment		15.5	20	**Fold:**TIM beta/alpha-barrel **Superfamily:**TM1631-like **Family:**TM1631-like
8	d1jl3a_	Alignment		11.4	18	**Fold:**Phosphotyrosine protein phosphatases I-like **Superfamily:**Phosphotyrosine protein phosphatases I **Family:**Low-molecular-weight phosphotyrosine protein phosphatases
9	d2ovra1	Alignment		9.3	13	**Fold:**Skp1 dimerisation domain-like **Superfamily:**Skp1 dimerisation domain-like **Family:**Skp1 dimerisation domain-like
10	d1sy6a1	Alignment		8.2	27	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**Immunoglobulin **Family:**I set domains
11	d1vm6a3	Alignment		8.1	15	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain

12	c2eapA_	Alignment		7.7	15	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**lymphocyte cytosolic protein 2; **PDBTitle:** solution structure of the n-terminal sam-domain of human2 lymphocyte cytosolic protein 2
13	c2dgdD_	Alignment		7.2	16	**PDB header:**lyase **Chain:** D: **PDB Molecule:**223aa long hypothetical arylmalonate decarboxylase; **PDBTitle:** crystal structure of st0656, a function unknown protein from2 sulfolobus tokodaii
14	c2ovqA_	Alignment		6.7	14	**PDB header:**transcription/cell cycle **Chain:** A: **PDB Molecule:**s-phase kinase-associated protein 1a; **PDBTitle:** structure of the skp1-fbw7-cyclinedegc complex
15	c1byyA_	Alignment		6.1	25	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**protein (sodium channel alpha-subunit); **PDBTitle:** sodium channel iia inactivation gate
16	d1j6oa_	Alignment		6.0	10	**Fold:**TIM beta/alpha-barrel **Superfamily:**Metallo-dependent hydrolases **Family:**TatD Mg-dependent DNase-like
17	d1jf8a_	Alignment		5.9	18	**Fold:**Phosphotyrosine protein phosphatases I-like **Superfamily:**Phosphotyrosine protein phosphatases I **Family:**Low-molecular-weight phosphotyrosine protein phosphatases
18	d1p9ea_	Alignment		5.8	19	**Fold:**Metallo-hydrolase/oxidoreductase **Superfamily:**Metallo-hydrolase/oxidoreductase **Family:**Methyl parathion hydrolase
19	c1p9eA_	Alignment		5.8	19	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**methyl parathion hydrolase; **PDBTitle:** crystal structure analysis of methyl parathion hydrolase from2 pseudomonas sp wbc-3
20	d1jbja1	Alignment		5.6	23	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**Immunoglobulin **Family:**I set domains
21	c2y75F_	Alignment	not modelled	5.6	14	**PDB header:**transcription **Chain:** F: **PDB Molecule:**hth-type transcriptional regulator cymr; **PDBTitle:** the structure of cymr (yrzc) the global cysteine regulator2 of b. subtilis
22	d1yl7a1	Alignment	not modelled	5.4	15	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
23	c3lwfD_	Alignment	not modelled	5.3	24	**PDB header:**transcription regulator **Chain:** D: **PDB Molecule:**putative transcriptional regulator; **PDBTitle:** crystal structure of putative transcriptional regulator (np_470886.1)2 from listeria innocua at 2.06 a resolution
24	d1miua1	Alignment	not modelled	5.3	24	**Fold:**BRCA2 helical domain **Superfamily:**BRCA2 helical domain **Family:**BRCA2 helical domain
25	c2p1nD_	Alignment	not modelled	5.3	14	**PDB header:**signaling protein **Chain:** D: **PDB Molecule:**skp1-like protein 1a; **PDBTitle:** mechanism of auxin perception by the tir1 ubiqutin ligase