Phyre2

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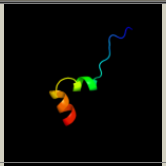
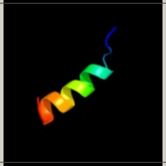
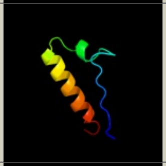
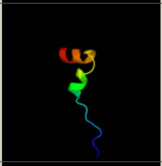
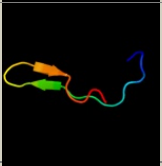
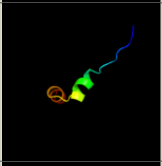
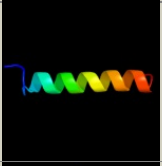
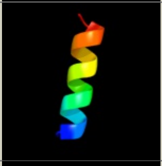
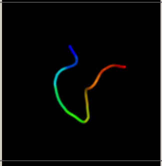
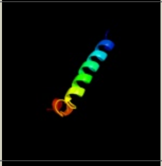
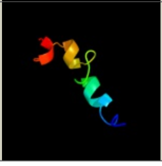
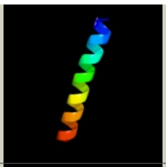
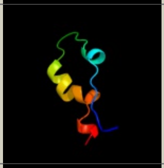
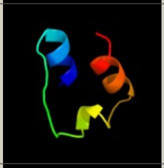
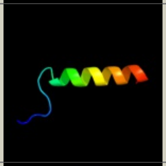
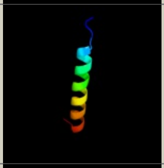
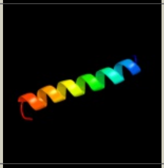
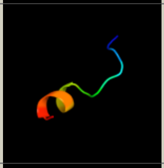
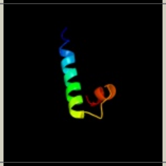
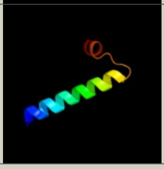
Description	P0AEV7
Date	Thu Jan 5 11:24:22 GMT 2012
Unique Job ID	4f3311e04e73af5a

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1a6ca1	Alignment		70.4	30	**Fold:**Nucleoplasmin-like/VP (viral coat and capsid proteins) **Superfamily:**Positive stranded ssRNA viruses **Family:**Comoviridae-like VP
2	d1wiia_	Alignment		26.8	44	**Fold:**Rubredoxin-like **Superfamily:**Zinc beta-ribbon **Family:**Putative zinc binding domain
3	d3e11a1	Alignment		19.3	24	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**TTHA0227-like
4	c1a6cA_	Alignment		16.2	30	**PDB header:**virus **Chain:** A: **PDB Molecule:**tobacco ringspot virus capsid protein; **PDBTitle:** structure of tobacco ringspot virus
5	c2gk9D_	Alignment		16.1	41	**PDB header:**transferase **Chain:** D: **PDB Molecule:**phosphatidylinositol-4-phosphate 5-kinase, type **PDBTitle:** human phosphatidylinositol-4-phosphate 5-kinase, type ii,2 gamma
6	c2y7uM_	Alignment		13.8	19	**PDB header:**virus **Chain:** M: **PDB Molecule:**coat protein; **PDBTitle:** x-ray structure of the grapevine fanleaf virus
7	c2q9lA_	Alignment		13.8	27	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**hypothetical protein; **PDBTitle:** crystal structure of imazg from vibrio dat 722: ctag-imazg (p43212)
8	c3dl8D_	Alignment		12.6	50	**PDB header:**protein transport **Chain:** D: **PDB Molecule:**sece; **PDBTitle:** structure of the complex of aquifex aeolicus secyeg and2 bacillus subtilis seca
9	d1dxqa_	Alignment		10.6	60	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Quinone reductase
10	c3obcB_	Alignment		9.7	21	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**pyrophosphatase; **PDBTitle:** crystal structure of a pyrophosphatase (af1178) from archaeoglobus2 fulgidus at 1.80 a resolution
11	c2khsB_	Alignment		9.6	27	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**nuclease; **PDBTitle:** solution structure of snase121:snase(111-143) complex

12	d2oiea1	Alignment		8.6	27	**Fold:**all-alpha NTP pyrophosphatases **Superfamily:**all-alpha NTP pyrophosphatases **Family:**MazG-like
13	d2ejqa1	Alignment		8.4	19	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**TTHA0227-like
14	d1ebfa1	Alignment		8.4	9	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
15	d2gtad1	Alignment		8.3	12	**Fold:**all-alpha NTP pyrophosphatases **Superfamily:**all-alpha NTP pyrophosphatases **Family:**MazG-like
16	d2gtaa1	Alignment		8.1	12	**Fold:**all-alpha NTP pyrophosphatases **Superfamily:**all-alpha NTP pyrophosphatases **Family:**MazG-like
17	d1vmga_	Alignment		7.5	19	**Fold:**all-alpha NTP pyrophosphatases **Superfamily:**all-alpha NTP pyrophosphatases **Family:**MazG-like
18	d1cmca_	Alignment		7.3	21	**Fold:**Ribbon-helix-helix **Superfamily:**Ribbon-helix-helix **Family:**Met repressor, MetJ (MetR)
19	d1qgpa_	Alignment		7.1	11	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Z-DNA binding domain
20	c2q4pA_	Alignment		7.1	24	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**protein rs21-c6; **PDBTitle:** ensemble refinement of the crystal structure of protein from mus2 musculus mm.29898
21	d2a3qa1	Alignment	not modelled	7.1	24	**Fold:**all-alpha NTP pyrophosphatases **Superfamily:**all-alpha NTP pyrophosphatases **Family:**MazG-like
22	c2p7vA_	Alignment	not modelled	6.9	24	**PDB header:**transcription **Chain:** A: **PDB Molecule:**regulator of sigma d; **PDBTitle:** crystal structure of the escherichia coli regulator of sigma 70, rsd,2 in complex with sigma 70 domain 4
23	c3lj4i_	Alignment	not modelled	6.9	20	**PDB header:**viral protein **Chain:** I: **PDB Molecule:**portal protein; **PDBTitle:** bacteriophage p22 portal protein bound to middle tail factor gp4. this2 file contain the first biological assembly
24	d1xq5a_	Alignment	not modelled	6.8	7	**Fold:**Globin-like **Superfamily:**Globin-like **Family:**Globins
25	c2dzjA_	Alignment	not modelled	6.0	33	**PDB header:**sugar binding protein **Chain:** A: **PDB Molecule:**synaptic glycoprotein sc2; **PDBTitle:** 2dzj/solution structure of the n-terminal ubiquitin-like2 domain in human synaptic glycoprotein sc2
26	d2yzca2	Alignment	not modelled	6.0	15	**Fold:**T-fold **Superfamily:**Tetrahydrobiopterin biosynthesis enzymes-like **Family:**Urate oxidase (uricase)
27	c3efyB_	Alignment	not modelled	6.0	15	**PDB header:**cell cycle **Chain:** B: **PDB Molecule:**cif (cell cycle inhibiting factor); **PDBTitle:** structure of the cyclomodulin cif from pathogenic2 escherichia coli
28	d1pcfa_	Alignment	not modelled	5.9	13	**Fold:**ssDNA-binding transcriptional regulator domain **Superfamily:**ssDNA-binding transcriptional regulator domain **Family:**Transcriptional coactivator PC4 C-terminal domain
						Fold: Globin-like

29	d1jl6a_	Alignment	not modelled	5.6	13	**Superfamily:**Globin-like **Family:**Globins
30	c1otpA_	 Alignment	not modelled	5.2	24	**PDB header:**phosphorylase **Chain:** A: **PDB Molecule:**thymidine phosphorylase; **PDBTitle:** structural and theoretical studies suggest domain movement produces an2 active conformation of thymidine phosphorylase