Phyre2

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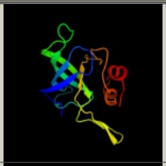
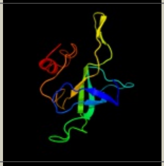
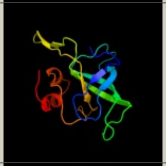
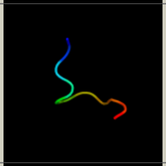
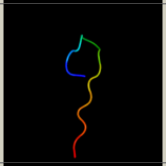
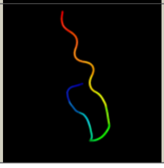
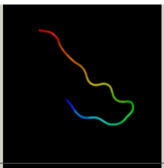
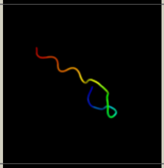
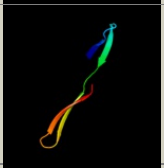
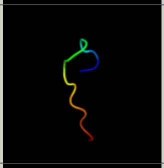
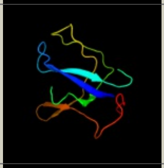
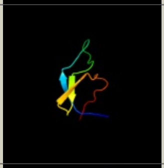
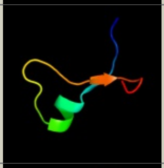
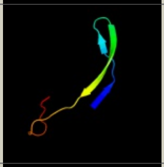
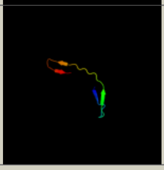
Description	P0ADY3
Date	Wed Jan 25 15:20:29 GMT 2012
Unique Job ID	ff02aebd34072e44

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1whia_	Alignment		100.0	69	**Fold:**Ribosomal protein L14 **Superfamily:**Ribosomal protein L14 **Family:**Ribosomal protein L14
2	d2j01o1	Alignment		100.0	69	**Fold:**Ribosomal protein L14 **Superfamily:**Ribosomal protein L14 **Family:**Ribosomal protein L14
3	d2zjrh1	Alignment		100.0	66	**Fold:**Ribosomal protein L14 **Superfamily:**Ribosomal protein L14 **Family:**Ribosomal protein L14
4	d2gyci1	Alignment		100.0	100	**Fold:**Ribosomal protein L14 **Superfamily:**Ribosomal protein L14 **Family:**Ribosomal protein L14
5	c3bboM_	Alignment		100.0	59	**PDB header:**ribosome **Chain:** M: **PDB Molecule:**ribosomal protein l14; **PDBTitle:** homology model for the spinach chloroplast 50s subunit2 fitted to 9.4a cryo-em map of the 70s chlororibosome
6	c2zkrk_	Alignment		100.0	38	**PDB header:**ribosomal protein/rna **Chain:** K: **PDB Molecule:**rna expansion segment es19; **PDBTitle:** structure of a mammalian ribosomal 60s subunit within an2 80s complex obtained by docking homology models of the rna3 and proteins into an 8.7 a cryo-em map
7	d1vqok1	Alignment		100.0	39	**Fold:**Ribosomal protein L14 **Superfamily:**Ribosomal protein L14 **Family:**Ribosomal protein L14
8	d1zv9a1	Alignment		21.2	33	**Fold:**Common fold of diphtheria toxin/transcription factors/cytochrome f **Superfamily:**Carbohydrate-binding domain **Family:**Cellulose-binding domain family III
9	d1wyha1	Alignment		20.3	64	**Fold:**Glucocorticoid receptor-like (DNA-binding domain) **Superfamily:**Glucocorticoid receptor-like (DNA-binding domain) **Family:**LIM domain
10	d1tyja1	Alignment		19.0	33	**Fold:**Common fold of diphtheria toxin/transcription factors/cytochrome f **Superfamily:**Carbohydrate-binding domain **Family:**Cellulose-binding domain family III
11	c3ghpA_	Alignment		17.9	53	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**cellulosomal scaffoldin adaptor protein b; **PDBTitle:** structure of the second type ii cohesin module from the2 adaptor scaa scaffoldin of acetivibrio cellulolyticus3 (including long c-terminal linker)

12	d2bm3a1	Alignment		17.2	40	**Fold:**Common fold of diphtheria toxin/transcription factors/cytochrome f **Superfamily:**Carbohydrate-binding domain **Family:**Cellulose-binding domain family III
13	c2b59A_	Alignment		17.1	40	**PDB header:**hydrolase/structural protein **Chain:** A: **PDB Molecule:**cog1196: chromosome segregation atpases; **PDBTitle:** the type ii cohesin dockerin complex
14	d1oj5a_	Alignment		16.5	10	**Fold:**Profilin-like **Superfamily:**PYP-like sensor domain (PAS domain) **Family:**PAS domain of steroid receptor coactivator 1A, NCo-A1
15	c3fnkA_	Alignment		16.3	53	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**cellulosomal scaffoldin adaptor protein b; **PDBTitle:** crystal structure of the second type ii cohesin module from2 the cellulosomal adaptor scaa scaffoldin of acetivibrio3 cellulolyticus
16	d1gd7a_	Alignment		13.5	23	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Myf domain
17	c2e5qA_	Alignment		9.6	15	**PDB header:**transcription **Chain:** A: **PDB Molecule:**phd finger protein 19; **PDBTitle:** solution structure of the tudor domain of phd finger2 protein 19, isoform b [homo sapiens]
18	c2xk0A_	Alignment		9.2	25	**PDB header:**transcription **Chain:** A: **PDB Molecule:**polycomb protein pcl; **PDBTitle:** solution structure of the tudor domain from drosophila2 polycomblike (pcl)
19	c3icyB_	Alignment		9.2	9	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**sensor protein; **PDBTitle:** the crystal structure of sensory box histidine2 kinase/response regulator domain from chlorobium tepidum3 tls
20	c3ewkA_	Alignment		9.1	11	**PDB header:**flavoprotein **Chain:** A: **PDB Molecule:**sensor protein; **PDBTitle:** structure of the redox sensor domain of methylococcus capsulatus2 (bath) mmos
21	d1b12a_	Alignment	not modelled	9.0	13	**Fold:**LexA/Signal peptidase **Superfamily:**LexA/Signal peptidase **Family:**Type 1 signal peptidase
22	c2q2iA_	Alignment	not modelled	7.6	18	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**secretion chaperone; **PDBTitle:** crystal structure of the protein secretion chaperone csaa from2 agrobacterium tumefaciens.
23	d1ijdb_	Alignment	not modelled	7.3	44	**Fold:**Light-harvesting complex subunits **Superfamily:**Light-harvesting complex subunits **Family:**Light-harvesting complex subunits
24	c3s6xA_	Alignment	not modelled	6.3	21	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**outer capsid protein sigma-1; **PDBTitle:** structure of reovirus attachment protein sigma1 in complex with alpha-2 2,3-sialyllactose
25	d2do3a1	Alignment	not modelled	6.3	24	**Fold:**SH3-like barrel **Superfamily:**Translation proteins SH3-like domain **Family:**SPT5 KOW domain-like
26	d1k8ke_	Alignment	not modelled	6.1	25	**Fold:**Arp2/3 complex 21 kDa subunit ARPC3 **Superfamily:**Arp2/3 complex 21 kDa subunit ARPC3 **Family:**Arp2/3 complex 21 kDa subunit ARPC3
27	d2zjrm1	Alignment	not modelled	5.7	19	**Fold:**SH3-like barrel **Superfamily:**Translation proteins SH3-like domain **Family:**Ribosomal protein L19
28	c2eqjA_	Alignment	not modelled	5.7	13	**PDB header:**transcription **Chain:** A: **PDB Molecule:**metal-response element-binding transcription **PDBTitle:** solution structure of the tudor domain of metal-response2 element-binding transcription factor 2
						PDB header:protein turnover/protein turnover

29	c2dyoB_	Alignment	not modelled	5.1	100	**Chain:** B: **PDB Molecule:**autophagy protein 16; **PDBTitle:** the crystal structure of saccharomyces cerevisiae atg5-2 atg16(1-57) complex
30	d1mb4a1	Alignment	not modelled	5.1	13	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
31	d1x4ka1	Alignment	not modelled	5.1	50	**Fold:**Glucocorticoid receptor-like (DNA-binding domain) **Superfamily:**Glucocorticoid receptor-like (DNA-binding domain) **Family:**LIM domain
32	d1t3ta4	Alignment	not modelled	5.1	33	**Fold:**Bacillus chorismate mutase-like **Superfamily:**PurM N-terminal domain-like **Family:**PurM N-terminal domain-like