Phyre2

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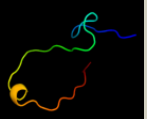
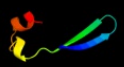
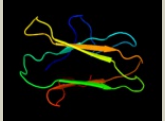
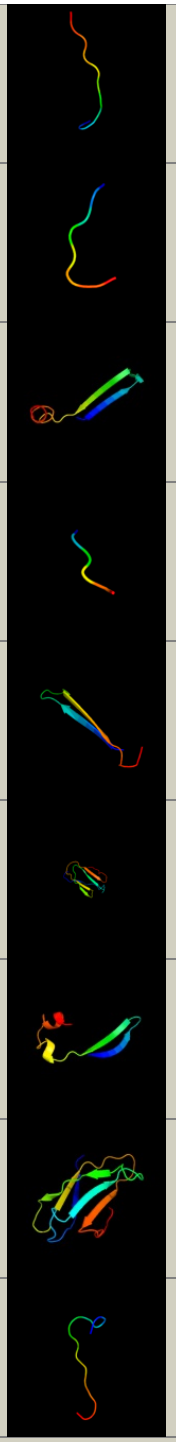
Description	P0AE91
Date	Thu Jan 5 11:22:48 GMT 2012
Unique Job ID	29157def408eab84

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3qsqA_	Alignment		41.1	31	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**capsid polyprotein; **PDBTitle:** crystal structure of the projection domain of the human astrovirus2 capsid protein
2	c3bdkB_	Alignment		41.0	17	**PDB header:**lyase **Chain:** B: **PDB Molecule:**d-mannonate dehydratase; **PDBTitle:** crystal structure of streptococcus suis mannonate2 dehydratase complexed with substrate analogue
3	d1tz9a_	Alignment		27.6	22	**Fold:**TIM beta/alpha-barrel **Superfamily:**Xylose isomerase-like **Family:**UxuA-like
4	c3ba3A_	Alignment		22.0	22	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**pyridoxamine 5'-phosphate oxidase-like protein; **PDBTitle:** crystal structure of pyridoxamine 5'-phosphate oxidase-like protein2 (np_783940.1) from lactobacillus plantarum at 1.55 a resolution
5	c3cnkB_	Alignment		19.0	14	**PDB header:**structural protein **Chain:** B: **PDB Molecule:**filamin-a; **PDBTitle:** crystal structure of the dimerization domain of human2 filamin a
6	d2d7ma1	Alignment		12.9	18	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**E set domains **Family:**Filamin repeat (rod domain)
7	d2q79a1	Alignment		12.2	19	**Fold:**Ferredoxin-like **Superfamily:**Viral DNA-binding domain **Family:**Viral DNA-binding domain
8	d2bp3a1	Alignment		11.3	18	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**E set domains **Family:**Filamin repeat (rod domain)
9	d1gk8a2	Alignment		10.7	26	**Fold:**Ferredoxin-like **Superfamily:**RuBisCO, large subunit, small (N-terminal) domain **Family:**Ribulose 1,5-bisphosphate carboxylase-oxygenase
10	d1rbla2	Alignment		10.7	21	**Fold:**Ferredoxin-like **Superfamily:**RuBisCO, large subunit, small (N-terminal) domain **Family:**Ribulose 1,5-bisphosphate carboxylase-oxygenase
11	c3iswA_	Alignment		9.6	14	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**filamin-a; **PDBTitle:** crystal structure of filamin-a immunoglobulin-like repeat 21 bound to2 an n-terminal peptide of cftr

12	d1wf9a1	Alignment		9.6	36	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**Ubiquitin-like **Family:**Ubiquitin-related
13	c2nytB_	Alignment		9.0	63	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**probable c->u-editing enzyme apobec-2; **PDBTitle:** the apobec2 crystal structure and functional implications2 for aid
14	c1vknC_	Alignment		9.0	19	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**n-acetyl-gamma-glutamyl-phosphate reductase; **PDBTitle:** crystal structure of n-acetyl-gamma-glutamyl-phosphate reductase2 (tm1782) from thermotoga maritima at 1.80 a resolution
15	c2kboA_	Alignment		8.8	67	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**dna dc->du-editing enzyme apobec-3g; **PDBTitle:** structure, interaction, and real-time monitoring of the2 enzymatic reaction of wild type apobec3g
16	d2o62a2	Alignment		8.7	24	**Fold:**Lipocalins **Superfamily:**Lipocalins **Family:**All1756-like
17	c2eecA_	Alignment		8.4	23	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**filamin-b; **PDBTitle:** solution structure of the 23th filamin domain from human2 filamin-b
18	d8ruca2	Alignment		7.8	21	**Fold:**Ferredoxin-like **Superfamily:**RuBisCO, large subunit, small (N-terminal) domain **Family:**Ribulose 1,5-bisphosphate carboxylase-oxygenase
19	d2e9ia1	Alignment		7.5	16	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**E set domains **Family:**Filamin repeat (rod domain)
20	c2zw3B_	Alignment		7.5	40	**PDB header:**cell adhesion **Chain:** B: **PDB Molecule:**gap junction beta-2 protein; **PDBTitle:** structure of the connexin-26 gap junction channel at 3.52 angstrom resolution
21	c3khpB_	Alignment	not modelled	7.3	14	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**maoc family protein; **PDBTitle:** crystal structure of a possible dehydrogenase from2 mycobacterium tuberculosis at 2.3a resolution
22	c1moxB_	Alignment	not modelled	7.2	14	**PDB header:**transferase/growth factor **Chain:** B: **PDB Molecule:**epidermal growth factor receptor; **PDBTitle:** crystal structure of human epidermal growth factor receptor (residues2 1-501) in complex with tgf-alpha
23	d1zl0a2	Alignment	not modelled	6.9	54	**Fold:**Flavodoxin-like **Superfamily:**Class I glutamine amidotransferase-like **Family:**LD-carboxypeptidase A N-terminal domain-like
24	c3hsbB_	Alignment	not modelled	6.7	42	**PDB header:**rna binding protein/rna **Chain:** B: **PDB Molecule:**protein hfq; **PDBTitle:** crystal structure of ymah (hfq) from bacillus subtilis in complex with2 an rna aptamer
25	d1k8wa3	Alignment	not modelled	6.6	17	**Fold:**PUA domain-like **Superfamily:**PUA domain-like **Family:**PUA domain
26	c2e9jA_	Alignment	not modelled	6.3	18	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**filamin-b; **PDBTitle:** solution structure of the 14th filamin domain from human2 filamin-b
27	d2o62a1	Alignment	not modelled	6.3	25	**Fold:**Lipocalins **Superfamily:**Lipocalins **Family:**All1756-like
28	c2jf1A_	Alignment	not modelled	6.2	18	**PDB header:**cell adhesion **Chain:** A: **PDB Molecule:**filamin-a; **PDBTitle:** crystal structure of the filamin a repeat 21 complexed with2 the integrin beta2 cytoplasmic tail peptide
						Fold: Ferredoxin-like

29	d1ej7l2	Alignment	not modelled	6.0	29	**Superfamily:**RuBisCO, large subunit, small (N-terminal) domain **Family:**Ribulose 1,5-bisphosphate carboxylase-oxygenase
30	c2e2zA_	Alignment	not modelled	5.9	35	**PDB header:**protein transport, chaperone regulator **Chain:** A: **PDB Molecule:**tim15; **PDBTitle:** solution nmr structure of yeast tim15, co-chaperone of2 mitochondrial hsp70
31	d1bwva2	Alignment	not modelled	5.9	26	**Fold:**Ferredoxin-like **Superfamily:**RuBisCO, large subunit, small (N-terminal) domain **Family:**Ribulose 1,5-bisphosphate carboxylase-oxygenase
32	d1dbda_	Alignment	not modelled	5.8	13	**Fold:**Ferredoxin-like **Superfamily:**Viral DNA-binding domain **Family:**Viral DNA-binding domain
33	d1hk9a_	Alignment	not modelled	5.8	39	**Fold:**Sm-like fold **Superfamily:**Sm-like ribonucleoproteins **Family:**Pleiotropic translational regulator Hfq
34	d1f9fa_	Alignment	not modelled	5.7	5	**Fold:**Ferredoxin-like **Superfamily:**Viral DNA-binding domain **Family:**Viral DNA-binding domain
35	d1bxna2	Alignment	not modelled	5.7	24	**Fold:**Ferredoxin-like **Superfamily:**RuBisCO, large subunit, small (N-terminal) domain **Family:**Ribulose 1,5-bisphosphate carboxylase-oxygenase
36	d2b59b2	Alignment	not modelled	5.6	28	**Fold:**Prealbumin-like **Superfamily:**Carboxypeptidase regulatory domain-like **Family:**Pre-dockerin domain
37	c3g23A_	Alignment	not modelled	5.6	23	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**ld-carboxypeptidase a; **PDBTitle:** crystal structure of a ld-carboxypeptidase a (saro_1426) from2 novosphingobium aromaticivorans dsm at 1.89 a resolution
38	c1rcxH_	Alignment	not modelled	5.6	24	**PDB header:**lyase (carbon-carbon) **Chain:** H: **PDB Molecule:**ribulose bisphosphate carboxylase/oxygenase; **PDBTitle:** non-activated spinach rubisco in complex with its substrate2 ribulose-1,5-bisphosphate
39	c2q49B_	Alignment	not modelled	5.4	19	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**probable n-acetyl-gamma-glutamyl-phosphate reductase; **PDBTitle:** ensemble refinement of the protein crystal structure of gene product2 from arabidopsis thaliana at2g19940
40	d1svda2	Alignment	not modelled	5.4	24	**Fold:**Ferredoxin-like **Superfamily:**RuBisCO, large subunit, small (N-terminal) domain **Family:**Ribulose 1,5-bisphosphate carboxylase-oxygenase
41	d2dtge4	Alignment	not modelled	5.4	21	**Fold:**Leucine-rich repeat, LRR (right-handed beta-alpha superhelix) **Superfamily:**L domain-like **Family:**L domain
42	d2auna2	Alignment	not modelled	5.3	54	**Fold:**Flavodoxin-like **Superfamily:**Class I glutamine amidotransferase-like **Family:**LD-carboxypeptidase A N-terminal domain-like
43	c3b2ul_	Alignment	not modelled	5.2	14	**PDB header:**immune system/transferase **Chain:** I: **PDB Molecule:**epidermal growth factor receptor; **PDBTitle:** crystal structure of isolated domain iii of the extracellular region2 of the epidermal growth factor receptor in complex with the fab3 fragment of imc-11f8