Phyre^{2}

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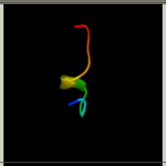
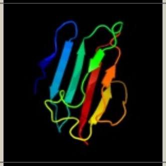
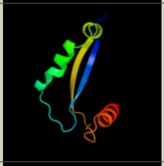
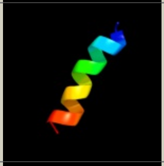
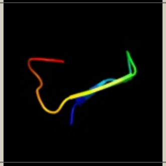
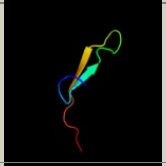
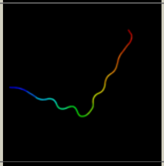
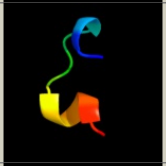
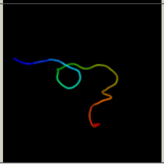
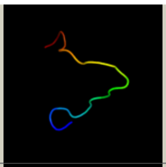
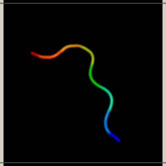
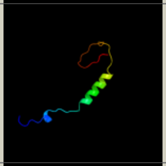
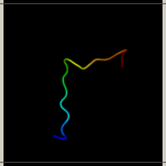
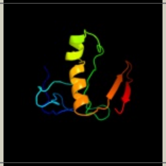
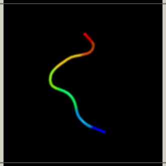
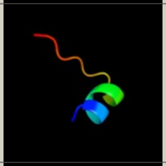
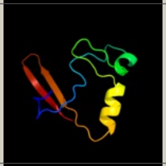
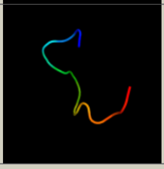
Description	P19381
Date	Thu Jan 5 11:37:20 GMT 2012
Unique Job ID	0899464f9c269c60

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d3d85d1	Alignment		45.0	50	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**Immunoglobulin **Family:**I set domains
2	c2voyG_	Alignment		34.7	42	**PDB header:**hydrolase **Chain:** G: **PDB Molecule:**sarcoplasmic/endoplasmic reticulum calcium **PDBTitle:** cryoem model of copa, the copper transporting atpase from2 archaeoglobus fulgidus
3	d1r46a1	Alignment		32.3	18	**Fold:**Glycosyl hydrolase domain **Superfamily:**Glycosyl hydrolase domain **Family:**alpha-Amylases, C-terminal beta-sheet domain
4	c3p24C_	Alignment		25.6	19	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**bft-3; **PDBTitle:** structure of profragilysin-3 from bacteroides fragilis
5	c2kncB_	Alignment		22.8	35	**PDB header:**cell adhesion **Chain:** B: **PDB Molecule:**integrin beta-3; **PDBTitle:** platelet integrin alfaiib-beta3 transmembrane-cytoplasmic2 heterocomplex
6	c2kvgA_	Alignment		20.5	35	**PDB header:**transcription **Chain:** A: **PDB Molecule:**zinc finger and btb domain-containing protein 32; **PDBTitle:** structure of the three-cys2his2 domain of mouse testis zinc2 finger protein
7	c2jgsA_	Alignment		20.3	43	**PDB header:**biotin-binding protein **Chain:** A: **PDB Molecule:**circular permutant of avidin; **PDBTitle:** circular permutant of avidin
8	c3fkhB_	Alignment		18.8	35	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**putative pyridoxamine 5'-phosphate oxidase; **PDBTitle:** crystal structure of putative pyridoxamine 5'-phosphate oxidase2 (np_601736.1) from corynebacterium glutamicum atcc 13032 kitasato at3 2.51 a resolution
9	d1htwa_	Alignment		17.4	30	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**YjeE-like
10	c3idwA_	Alignment		15.3	46	**PDB header:**endocytosis **Chain:** A: **PDB Molecule:**actin cytoskeleton-regulatory complex protein sla1; **PDBTitle:** crystal structure of sla1 homology domain 2
11	c2g9tT_	Alignment		13.8	30	**PDB header:**viral protein **Chain:** T: **PDB Molecule:** **PDBTitle:** crystal structure of the sars coronavirus nsp10 at 2.1a

12	c2a45L_	Alignment		13.3	30	**PDB header:**hydrolase/hydrolase inhibitor **Chain:** L: **PDB Molecule:**fibrinogen gamma chain; **PDBTitle:** crystal structure of the complex between thrombin and the central "e"2 region of fibrin
13	d2okqa1	Alignment		11.6	25	**Fold:**Ferredoxin-like **Superfamily:**Dimeric alpha+beta barrel **Family:**YbaA-like
14	c3nicA_	Alignment		11.5	28	**PDB header:**hydrolase/dna **Chain:** A: **PDB Molecule:**eco29kir; **PDBTitle:** dna binding and cleavage by the giy-yig endonuclease r.eco29ki2 inactive variant y49f
15	d2ea9a1	Alignment		11.1	47	**Fold:**Profilin-like **Superfamily:**YeeU-like **Family:**YagB/YeeU/YfjZ-like
16	d1lwub1	Alignment		10.3	17	**Fold:**Fibrinogen C-terminal domain-like **Superfamily:**Fibrinogen C-terminal domain-like **Family:**Fibrinogen C-terminal domain-like
17	c2okqB_	Alignment		10.0	29	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**hypothetical protein ybaa; **PDBTitle:** crystal structure of unknown conserved ybaa protein from2 shigella flexneri
18	c2ph7B_	Alignment		9.6	36	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**uncharacterized protein af_2093; **PDBTitle:** crystal structure of af2093 from archaeoglobus fulgidus
19	c1ei3E_	Alignment		9.2	12	**PDB header:** **PDB COMPND:**
20	c2gbxF_	Alignment		9.2	40	**PDB header:**oxidoreductase **Chain:** F: **PDB Molecule:**biphenyl 2,3-dioxygenase beta subunit; **PDBTitle:** crystal structure of biphenyl 2,3-dioxygenase from sphingomonas2 yanoikuyae b1 bound to biphenyl
21	c3izxE_	Alignment	not modelled	9.2	11	**PDB header:**virus **Chain:** E: **PDB Molecule:**viral structural protein 5; **PDBTitle:** 3.1 angstrom cryoem structure of cytoplasmic polyhedrosis virus
22	d1u5tb1	Alignment	not modelled	8.7	38	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Vacuolar sorting protein domain
23	d2h28a1	Alignment	not modelled	8.1	35	**Fold:**Profilin-like **Superfamily:**YeeU-like **Family:**YagB/YeeU/YfjZ-like
24	c1tolA_	Alignment	not modelled	8.1	18	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**protein (fusion protein consisting of minor coat **PDBTitle:** fusion of n-terminal domain of the minor coat protein from2 gene iii in phage m13, and c-terminal domain of e. coli3 protein-tola
25	c3qa8A_	Alignment	not modelled	8.0	25	**PDB header:**immune system, signaling protein **Chain:** A: **PDB Molecule:**mgc80376 protein; **PDBTitle:** crystal structure of inhibitor of kappa b kinase beta
26	c1jdmA_	Alignment	not modelled	8.0	44	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**sarcolipin; **PDBTitle:** nmr structure of sarcolipin
27	c2vbeA_	Alignment	not modelled	7.8	71	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**tailspike-protein; **PDBTitle:** tailspike protein of bacteriophage sf6
28	c1deqO_	Alignment	not modelled	7.6	20	**PDB header:** **PDB COMPND:**

29	d1f60a2	Alignment	not modelled	7.6	22	**Fold:**Elongation factor/aminomethyltransferase common domain **Superfamily:**EF-Tu/eEF-1alpha/eIF2-gamma C-terminal domain **Family:**EF-Tu/eEF-1alpha/eIF2-gamma C-terminal domain
30	d2inwa1	Alignment	not modelled	7.5	35	**Fold:**Profilin-like **Superfamily:**YeeU-like **Family:**YagB/YeeU/YfjZ-like
31	c2kbcA_	Alignment	not modelled	7.4	63	**PDB header:**hormone **Chain:** A: **PDB Molecule:**insl5_a-chain; **PDBTitle:** solution structure of human insulin-like peptide 5 (insl5)
32	c2k1vA_	Alignment	not modelled	7.4	63	**PDB header:**hormone **Chain:** A: **PDB Molecule:**insulin-like peptide insl5; **PDBTitle:** r3/i5 relaxin chimera
33	c2jmbA_	Alignment	not modelled	7.3	50	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein atu4866; **PDBTitle:** solution structure of the protein atu4866 from agrobacterium2 tumefaciens
34	c2kzvA_	Alignment	not modelled	7.1	28	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** solution nmr structure of cv_0373(175-257) protein from2 chromobacterium violaceum, northeast structural genomics consortium3 target cvr118a
35	c3rykB_	Alignment	not modelled	6.8	30	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**dtdp-4-dehydrorhamnose 3,5-epimerase; **PDBTitle:** 1.63 angstrom resolution crystal structure of dtdp-4-dehydrorhamnose2 3,5-epimerase (rfbc) from bacillus anthracis str. ames with tdp and3 ppi bound
36	c2wryA_	Alignment	not modelled	6.6	14	**PDB header:**immune system **Chain:** A: **PDB Molecule:**interleukin-1beta; **PDBTitle:** crystal structure of chicken cytokine interleukin 1 beta
37	d1zunb2	Alignment	not modelled	6.4	28	**Fold:**Elongation factor/aminomethyltransferase common domain **Superfamily:**EF-Tu/eEF-1alpha/eIF2-gamma C-terminal domain **Family:**EF-Tu/eEF-1alpha/eIF2-gamma C-terminal domain
38	d2bo9b2	Alignment	not modelled	6.0	20	**Fold:**Cystatin-like **Superfamily:**Cystatin/monellin **Family:**Latexin-like
39	d1l8na1	Alignment	not modelled	5.8	18	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**alpha-D-glucuronidase/Hyaluronidase catalytic domain
40	d2f0ca2	Alignment	not modelled	5.7	53	**Fold:**Triple-stranded beta-helix **Superfamily:**Phage fibre proteins **Family:**Lactophage receptor-binding protein domain
41	c1s8kA_	Alignment	not modelled	5.6	45	**PDB header:**toxin **Chain:** A: **PDB Molecule:**toxin bmkk4; **PDBTitle:** solution structure of bmkk4, a novel potassium channel2 blocker from scorpion buthus martensii karsch, 253 structures
42	d1jnya2	Alignment	not modelled	5.4	33	**Fold:**Elongation factor/aminomethyltransferase common domain **Superfamily:**EF-Tu/eEF-1alpha/eIF2-gamma C-terminal domain **Family:**EF-Tu/eEF-1alpha/eIF2-gamma C-terminal domain
43	c2zx3B_	Alignment	not modelled	5.3	30	**PDB header:**immune system, sugar binding protein **Chain:** B: **PDB Molecule:**csl3; **PDBTitle:** rhamnose-binding lectin csl3
44	d1cmwa1	Alignment	not modelled	5.3	40	**Fold:**SAM domain-like **Superfamily:**5' to 3' exonuclease, C-terminal subdomain **Family:**5' to 3' exonuclease, C-terminal subdomain
45	c1fqjC_	Alignment	not modelled	5.2	30	**PDB header:**signaling protein **Chain:** C: **PDB Molecule:**retinal rod rhodopsin-sensitive cgmp 3',5'- **PDBTitle:** crystal structure of the heterotrimeric complex of the rgs2 domain of rgs9, the gamma subunit of phosphodiesterase and3 the gt/i1 chimera alpha subunit [(rgs9)-(pdegamma)-4 (gt/i1alpha)-(gdp)-(alf4-)-(mg2+)]