Phyre2

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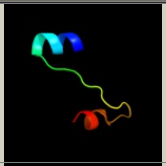
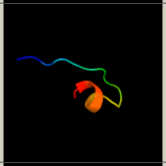
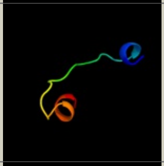
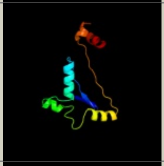
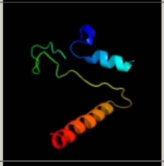
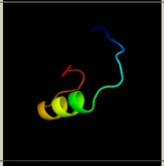
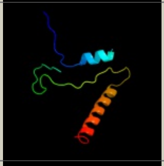
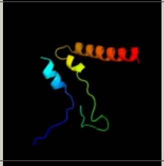
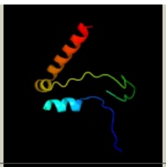
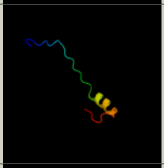
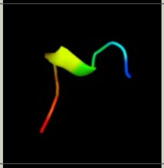
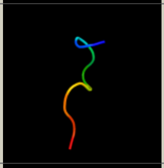
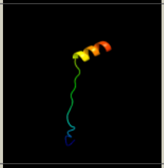
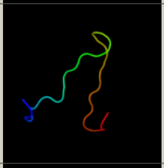
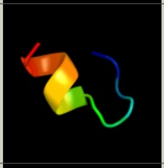
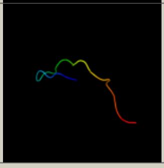
Description	P36661
Date	Thu Jan 5 11:53:33 GMT 2012
Unique Job ID	20c5f8f862434c9d

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3pfyA_	Alignment		93.3	26	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**otu domain-containing protein 5; **PDBTitle:** the catalytic domain of human otud5
2	c2zfyA_	Alignment		80.8	31	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**ubiquitin thioesterase otub1; **PDBTitle:** crystal structure of human otubain 1
3	c3c0rC_	Alignment		80.5	47	**PDB header:**cell cycle, hydrolase **Chain:** C: **PDB Molecule:**ubiquitin thioesterase otu1; **PDBTitle:** structure of ovarian tumor (otu) domain in complex with ubiquitin
4	c3pt2A_	Alignment		72.8	27	**PDB header:**hydrolase/protein binding **Chain:** A: **PDB Molecule:**rna polymerase; **PDBTitle:** structure of a viral otu domain protease bound to ubiquitin
5	d1tffa_	Alignment		69.4	31	**Fold:**Cysteine proteinases **Superfamily:**Cysteine proteinases **Family:**Ubiquitin thiolesterase protein OTUB2 (Otubain-2)
6	d2d32a1	Alignment		51.7	31	**Fold:**Glutamine synthetase/guanido kinase **Superfamily:**Glutamine synthetase/guanido kinase **Family:**Glutamate-cysteine ligase
7	c3i7fA_	Alignment		41.2	19	**PDB header:**ligase **Chain:** A: **PDB Molecule:**aspartyl-trna synthetase; **PDBTitle:** aspartyl trna synthetase from entamoeba histolytica
8	c1u9pA_	Alignment		39.3	25	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**parc; **PDBTitle:** permuted single-chain arc
9	c1asyA_	Alignment		36.1	19	**PDB header:**complex (aminoacyl-trna synthase/trna) **Chain:** A: **PDB Molecule:**aspartyl-trna synthetase; **PDBTitle:** class ii aminoacyl transfer rna synthetases: crystal2 structure of yeast aspartyl-trna synthetase complexed with3 trna asp
10	c3m4qA_	Alignment		35.9	19	**PDB header:**ligase **Chain:** A: **PDB Molecule:**asparaginyl-trna synthetase, putative; **PDBTitle:** entamoeba histolytica asparaginyl-trna synthetase (asnrs)
11	d1mnta_	Alignment		27.8	27	**Fold:**Ribbon-helix-helix **Superfamily:**Ribbon-helix-helix **Family:**Arc/Mnt-like phage repressors

12	c1b8aB_	Alignment		23.7	15	**PDB header:**ligase **Chain:** B: **PDB Molecule:**protein (aspartyl-trna synthetase); **PDBTitle:** aspartyl-trna synthetase
13	c3ln7A_	Alignment		23.4	32	**PDB header:**ligase **Chain:** A: **PDB Molecule:**glutathione biosynthesis bifunctional protein gshab; **PDBTitle:** crystal structure of a bifunctional glutathione synthetase from2 pasteurella multocida
14	d1ppjw_	Alignment		20.5	60	**Fold:**Single transmembrane helix **Superfamily:**Subunit X (non-heme 7 kDa protein) of cytochrome bc1 complex (Ubiquinol-cytochrome c reductase) **Family:**Subunit X (non-heme 7 kDa protein) of cytochrome bc1 complex (Ubiquinol-cytochrome c reductase)
15	d1ppjj_	Alignment		19.0	60	**Fold:**Single transmembrane helix **Superfamily:**Subunit X (non-heme 7 kDa protein) of cytochrome bc1 complex (Ubiquinol-cytochrome c reductase) **Family:**Subunit X (non-heme 7 kDa protein) of cytochrome bc1 complex (Ubiquinol-cytochrome c reductase)
16	d2outa1	Alignment		17.3	43	**Fold:**LEM/SAP HeH motif **Superfamily:**Rho N-terminal domain-like **Family:**YqbF C-terminal domain-like
17	c3ln6A_	Alignment		16.6	33	**PDB header:**ligase **Chain:** A: **PDB Molecule:**glutathione biosynthesis bifunctional protein gshab; **PDBTitle:** crystal structure of a bifunctional glutathione synthetase from2 streptococcus agalactiae
18	d2gp4a1	Alignment		16.1	38	**Fold:**The "swivelling" beta/beta/alpha domain **Superfamily:**LeuD/IlvD-like **Family:**IlvD/EDD C-terminal domain-like
19	c2vfjA_	Alignment		16.1	46	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**tumor necrosis factor; **PDBTitle:** structure of the a20 ovarian tumour (otu) domain
20	d1y1oa_	Alignment		16.0	46	**Fold:**Restriction endonuclease-like **Superfamily:**Restriction endonuclease-like **Family:**RecU-like
21	c1y1oC_	Alignment	not modelled	16.0	46	**PDB header:**recombination **Chain:** C: **PDB Molecule:**penicillin-binding protein-related factor a; **PDBTitle:** x-ray crystal structure of penicillin-binding protein-2 related factor a from bacillus stearothermophilus
22	c3dkbA_	Alignment	not modelled	15.9	46	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**tumor necrosis factor, alpha-induced protein 3; **PDBTitle:** crystal structure of a20, 2.5 angstrom
23	c3c0mB_	Alignment	not modelled	13.6	28	**PDB header:**toxin **Chain:** B: **PDB Molecule:**aerolysin; **PDBTitle:** crystal structure of the proaerolysin mutant y221g
24	d1thqa_	Alignment	not modelled	11.8	45	**Fold:**Transmembrane beta-barrels **Superfamily:**OMPA-like **Family:**Outer membrane enzyme PagP
25	d1sg7a1	Alignment	not modelled	11.6	47	**Fold:**ChaB-like **Superfamily:**ChaB-like **Family:**ChaB-like
26	c1sg7A_	Alignment	not modelled	11.6	47	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**putative cation transport regulator chab; **PDBTitle:** nmr solution structure of the putative cation transport2 regulator chab
27	d1r4xa2	Alignment	not modelled	11.6	24	**Fold:**Subdomain of clathrin and coatomer appendage domain **Superfamily:**Subdomain of clathrin and coatomer appendage domain **Family:**Coatomer appendage domain
28	c2xgtB_	Alignment	not modelled	10.9	29	**PDB header:**ligase **Chain:** B: **PDB Molecule:**asparaginyl-trna synthetase, cytoplasmic; **PDBTitle:** asparaginyl-trna synthetase from brugia malayi

						complexed2 with the sulphamoyl analogue of asparaginyl-adenylate
29	c3oakC_	Alignment	not modelled	10.8	86	**PDB header:**transcription **Chain:** C: **PDB Molecule:**transcription elongation factor spt6; **PDBTitle:** crystal structure of a spn1 (iws1)-spt6 complex
30	d2ftxb1	Alignment	not modelled	10.3	28	**Fold:**Kinetochore globular domain-like **Superfamily:**Kinetochore globular domain **Family:**Spc24-like
31	c2fv4B_	Alignment	not modelled	10.2	28	**PDB header:**structural protein, protein binding **Chain:** B: **PDB Molecule:**hypothetical 24.6 kda protein in ilv2-ade17 **PDBTitle:** nmr solution structure of the yeast kinetochore spc24/spc252 globular domain
32	c2vxdA_	Alignment	not modelled	9.8	11	**PDB header:**nuclear protein **Chain:** A: **PDB Molecule:**nucleophosmin; **PDBTitle:** the structure of the c-terminal domain of nucleophosmin
33	c1ykuB_	Alignment	not modelled	9.8	19	**PDB header:**unknown function **Chain:** B: **PDB Molecule:**hypothetical protein pxo2-61; **PDBTitle:** crystal structure of a sensor domain homolog
34	c2rodB_	Alignment	not modelled	9.6	53	**PDB header:**apoptosis **Chain:** B: **PDB Molecule:**noxa; **PDBTitle:** solution structure of mcl-1 complexed with noxaa
35	c1e22A_	Alignment	not modelled	9.5	21	**PDB header:**ligase **Chain:** A: **PDB Molecule:**lysyl-trna synthetase; **PDBTitle:** lysyl-trna synthetase (lysu) hexagonal form complexed with2 lysine and the non-hydrolysable atp analogue amp-pcp
36	d2cura2	Alignment	not modelled	9.5	100	**Fold:**Glucocorticoid receptor-like (DNA-binding domain) **Superfamily:**Glucocorticoid receptor-like (DNA-binding domain) **Family:**LIM domain
37	c2yfvC_	Alignment	not modelled	9.3	33	**PDB header:**cell cycle **Chain:** C: **PDB Molecule:**scm3; **PDBTitle:** the heterotrimeric complex of kluyveromyces lactis scm3, cse4 and h4
38	c1p5kA_	Alignment	not modelled	9.3	64	**PDB header:**ribosome **Chain:** A: **PDB Molecule:**19-mer peptide from 50s ribosomal protein l1; **PDBTitle:** hp (2-20) substitution ser to leu11 modification in sds-d252 micelles
39	c2jwnB_	Alignment	not modelled	8.4	34	**PDB header:**rna binding protein **Chain:** B: **PDB Molecule:**embryonic polyadenylate-binding protein 2-b; **PDBTitle:** solution nmr structure of the protease-resistent domain of2 xenopus laevis epabp2
40	c2npiB_	Alignment	not modelled	8.2	26	**PDB header:**transcription **Chain:** B: **PDB Molecule:**protein clp1; **PDBTitle:** clp1-atp-pcf11 complex
41	c3nztA_	Alignment	not modelled	8.1	27	**PDB header:**ligase **Chain:** A: **PDB Molecule:**glutamate--cysteine ligase; **PDBTitle:** 2.0 angstrom crystal structure of glutamate--cysteine ligase (gsha)2 ftom francisella tularensis in complex with amp
42	d2d8za1	Alignment	not modelled	7.7	67	**Fold:**Glucocorticoid receptor-like (DNA-binding domain) **Superfamily:**Glucocorticoid receptor-like (DNA-binding domain) **Family:**LIM domain
43	c2lc0A_	Alignment	not modelled	7.6	18	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**putative uncharacterized protein tb39.8; **PDBTitle:** rv0020c_nter structure
44	c3bjuB_	Alignment	not modelled	7.6	24	**PDB header:**ligase **Chain:** B: **PDB Molecule:**lysyl-trna synthetase; **PDBTitle:** crystal structure of tetrameric form of human lysyl-trna2 synthetase
45	d1o57a1	Alignment	not modelled	7.6	27	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**N-terminal domain of Bacillus PurR
46	c1sfcD_	Alignment	not modelled	7.5	20	**PDB header:**transport protein **Chain:** D: **PDB Molecule:**protein (snap-25b); **PDBTitle:** neuronal synaptic fusion complex
47	c2v4oB_	Alignment	not modelled	6.9	46	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**multifunctional protein sur e; **PDBTitle:** crystal structure of salmonella typhimurium sure at 2.752 angstrom resolution in monoclinic form
48	d2i9fa1	Alignment	not modelled	6.9	44	**Fold:**Nucleocapsid protein dimerization domain **Superfamily:**Nucleocapsid protein dimerization domain **Family:**Arterivirus nucleocapsid protein
49	c2gloA_	Alignment	not modelled	6.9	32	**PDB header:**transcription/dna **Chain:** A: **PDB Molecule:**brinker cg9653-pa; **PDBTitle:** solution structure of the brinker dna binding domain in2 complex with the omb enhancer
50	c2yv5A_	Alignment	not modelled	6.9	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**yjeq protein; **PDBTitle:** crystal structure of yjeq from aquifex aeolicus
51	c3c2vA_	Alignment	not modelled	6.7	20	**PDB header:**transferase **Chain:** A: **PDB Molecule:**nicotinate-nucleotide pyrophosphorylase; **PDBTitle:** crystal structure of the quinolinate phosphoribosyl2 transferase (bna6) from saccharomyces cerevisiae complexed3 with prpp and the inhibitor phthalate
52	c2f0cC_	Alignment	not modelled	6.7	28	**PDB header:**virus/viral protein **Chain:** C: **PDB Molecule:**phage tp901-1 orf49 (bpp); **PDBTitle:** structure of the receptor binding protein (orf49, bbp) from lactophage2 tp901-1
53	c1wydB_	Alignment	not modelled	6.6	23	**PDB header:**ligase **Chain:** B: **PDB Molecule:**hypothetical aspartyl-trna synthetase; **PDBTitle:** crystal structure of aspartyl-trna synthetase from sulfolobus tokodaii

54	c1aq5C_	Alignment	not modelled	6.4	58	**PDB header:**coiled-coil **Chain:** C: **PDB Molecule:**cartilage matrix protein; **PDBTitle:** high-resolution solution nmr structure of the trimeric coiled-coil2 domain of chicken cartilage matrix protein, 20 structures
55	c1x55A_	Alignment	not modelled	6.4	21	**PDB header:**ligase **Chain:** A: **PDB Molecule:**asparaginyl-trna synthetase; **PDBTitle:** crystal structure of asparaginyl-trna synthetase from pyrococcus2 horikoshii complexed with asparaginyl-adenylate analogue
56	c3e9hB_	Alignment	not modelled	6.3	18	**PDB header:**ligase **Chain:** B: **PDB Molecule:**lysyl-trna synthetase; **PDBTitle:** lysyl-trna synthetase from bacillus stearothermophilus2 complexed with l-lysylsulfamoyl adenosine
57	d2enga_	Alignment	not modelled	6.2	38	**Fold:**Double psi beta-barrel **Superfamily:**Barwin-like endoglucanases **Family:**Eng V-like
58	d1eova2	Alignment	not modelled	6.1	18	**Fold:**Class II aaRS and biotin synthetases **Superfamily:**Class II aaRS and biotin synthetases **Family:**Class II aminoacyl-tRNA synthetase (aaRS)-like, catalytic domain
59	d1f0la3	Alignment	not modelled	6.0	25	**Fold:**Toxins' membrane translocation domains **Superfamily:**Diphtheria toxin, middle domain **Family:**Diphtheria toxin, middle domain
60	d2duca1	Alignment	not modelled	5.8	26	**Fold:**Trypsin-like serine proteases **Superfamily:**Trypsin-like serine proteases **Family:**Viral cysteine protease of trypsin fold
61	c2i8bB_	Alignment	not modelled	5.8	30	**PDB header:**viral protein **Chain:** B: **PDB Molecule:**minor nucleoprotein vp30; **PDBTitle:** crystal structure of the c-terminal domain of ebola virus vp30
62	d2al6a2	Alignment	not modelled	5.7	83	**Fold:**PH domain-like barrel **Superfamily:**PH domain-like **Family:**Third domain of FERM
63	d2cs7a1	Alignment	not modelled	5.6	24	**Fold:**IL8-like **Superfamily:**PhtA domain-like **Family:**PhtA domain-like
64	c1p5lA_	Alignment	not modelled	5.6	64	**PDB header:**ribosome **Chain:** A: **PDB Molecule:**19-mer peptide from 50s ribosomal protein l1; **PDBTitle:** hp (2-20) substitution phe5 to ser modification in sds-d252 micelles
65	c1p0gA_	Alignment	not modelled	5.4	64	**PDB header:**ribosome **Chain:** A: **PDB Molecule:**19-mer peptide from 50s ribosomal protein l1; **PDBTitle:** structure of antimicrobial peptide, hp (2-20) and its2 analogues derived from helicobacter pylori, as determined3 by 1h nmr spectroscopy
66	c2e6gI_	Alignment	not modelled	5.4	31	**PDB header:**hydrolase **Chain:** I: **PDB Molecule:**5'-nucleotidase sure; **PDBTitle:** crystal structure of the stationary phase survival protein sure from2 thermus thermophilus hb8 in complex with phosphate
67	c3pmdA_	Alignment	not modelled	5.2	24	**PDB header:**lipid binding protein **Chain:** A: **PDB Molecule:**conserved domain protein; **PDBTitle:** crystal structure of the sporulation inhibitor pxo1-118 from bacillus2 anthracis
68	d2saka_	Alignment	not modelled	5.1	21	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**Staphylokinase/streptokinase **Family:**Staphylokinase/streptokinase