Phyre²

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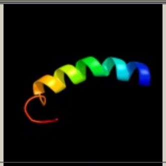
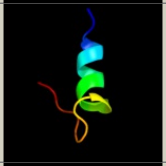
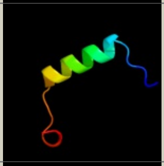
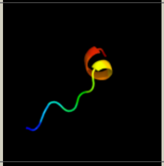
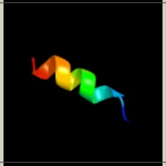
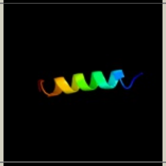
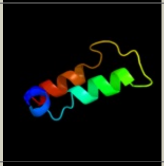
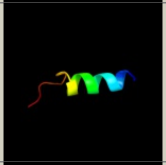
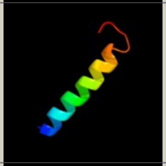
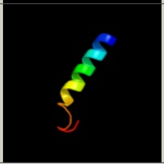
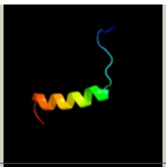
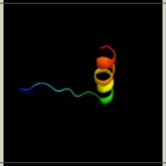
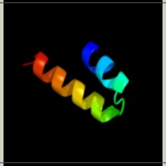
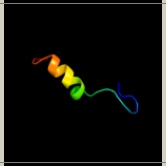
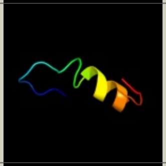
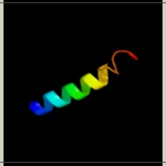
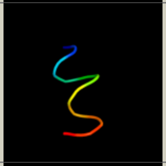
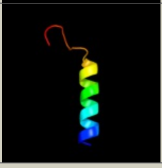
Description	P0AAS9
Date	Thu Jan 5 11:13:44 GMT 2012
Unique Job ID	178075ed28fff211

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1i1rb_	Alignment		40.1	12	**Fold:**4-helical cytokines **Superfamily:**4-helical cytokines **Family:**Long-chain cytokines
2	d1alua_	Alignment		27.0	17	**Fold:**4-helical cytokines **Superfamily:**4-helical cytokines **Family:**Long-chain cytokines
3	c2ghfA_	Alignment		20.5	29	**PDB header:**transcription, metal binding protein **Chain:** A: **PDB Molecule:**zinc fingers and homeoboxes protein 1; **PDBTitle:** solution structure of the complete zinc-finger region of2 human zinc-fingers and homeoboxes 1 (zhx1)
4	c4a19Q_	Alignment		18.4	19	**PDB header:**ribosome **Chain:** Q: **PDB Molecule:**60s ribosomal protein l36; **PDBTitle:** t.thermophila 60s ribosomal subunit in complex with2 initiation factor 6. this file contains 26s rrna and3 proteins of molecule 2.
5	d2ffsa1	Alignment		18.0	0	**Fold:**TBP-like **Superfamily:**Bet v1-like **Family:**PA1206-like
6	c1bh0A_	Alignment		17.8	23	**PDB header:**synthetic hormone **Chain:** A: **PDB Molecule:**glucagon; **PDBTitle:** structure of a glucagon analog
7	c2l3yA_	Alignment		15.2	36	**PDB header:**transcription **Chain:** A: **PDB Molecule:**interleukin-6; **PDBTitle:** solution structure of mouse il-6
8	c1tjlD_	Alignment		13.2	23	**PDB header:**transcription **Chain:** D: **PDB Molecule:**dnak suppressor protein; **PDBTitle:** crystal structure of transcription factor dksa from e. coli
9	c2ct1A_	Alignment		11.6	19	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcriptional repressor ctcf; **PDBTitle:** solution structure of the zinc finger domain of2 transcriptional repressor ctcf protein
10	c3izck_	Alignment		11.4	12	**PDB header:**ribosome **Chain:** K: **PDB Molecule:**60s ribosomal protein rpl16 (l13p); **PDBTitle:** localization of the large subunit ribosomal proteins into a 6.1 a2 cryo-em map of saccharomyces cerevisiae translating 80s ribosome
11	d1rhga_	Alignment		11.1	17	**Fold:**4-helical cytokines **Superfamily:**4-helical cytokines **Family:**Long-chain cytokines

12	d1odma_	Alignment		10.3	14	**Fold:**Double-stranded beta-helix **Superfamily:**Clavaminate synthase-like **Family:**Penicillin synthase-like
13	c3hs2H_	Alignment		10.1	12	**PDB header:**antitoxin **Chain:** H: **PDB Molecule:**prevent host death protein; **PDBTitle:** crystal structure of phd truncated to residue 57 in an orthorhombic2 space group
14	c1puoA_	Alignment		9.8	20	**PDB header:**allergen **Chain:** A: **PDB Molecule:**major allergen i polypeptide, fused chain 2, **PDBTitle:** crystal structure of fel d 1- the major cat allergen
15	c3izbU_	Alignment		8.8	24	**PDB header:**ribosome **Chain:** U: **PDB Molecule:**40s ribosomal protein s24; **PDBTitle:** localization of the small subunit ribosomal proteins into a 6.1 a2 cryo-em map of saccharomyces cerevisiae translating 80s ribosome
16	d2g1da1	Alignment		8.7	16	**Fold:**Ribosomal proteins S24e, L23 and L15e **Superfamily:**Ribosomal proteins S24e, L23 and L15e **Family:**Ribosomal protein S24e
17	c2kncB_	Alignment		8.5	25	**PDB header:**cell adhesion **Chain:** B: **PDB Molecule:**integrin beta-3; **PDBTitle:** platelet integrin alfaiib-beta3 transmembrane-cytoplasmic2 heterocomplex
18	d1bgea_	Alignment		8.0	18	**Fold:**4-helical cytokines **Superfamily:**4-helical cytokines **Family:**Long-chain cytokines
19	c1kuzB_	Alignment		7.7	36	**PDB header:**cell adhesion **Chain:** B: **PDB Molecule:**integrin beta-3; **PDBTitle:** solution structure of the membrane proximal regions of2 alpha-iib and beta-3 integrins
20	d1bgca_	Alignment		7.5	17	**Fold:**4-helical cytokines **Superfamily:**4-helical cytokines **Family:**Long-chain cytokines
21	c2hu9B_	Alignment	not modelled	7.3	43	**PDB header:**metal transport **Chain:** B: **PDB Molecule:**mercuric transport protein periplasmic component; **PDBTitle:** x-ray structure of the archaeoglobus fulgidus copz n-2 terminal domain
22	c1nauA_	Alignment	not modelled	6.8	25	**PDB header:**hormone/growth factor **Chain:** A: **PDB Molecule:**glucagon; **PDBTitle:** nmr solution structure of the glucagon antagonist [deshis1,2 desphe6, glu9]glucagon amide in the presence of3 perdeuterated dodecylphosphocholine micelles
23	d2diia1	Alignment	not modelled	6.8	36	**Fold:**BSD domain-like **Superfamily:**BSD domain-like **Family:**BSD domain
24	c3g9wC_	Alignment	not modelled	6.5	15	**PDB header:**cell adhesion **Chain:** C: **PDB Molecule:**integrin beta-1d; **PDBTitle:** crystal structure of talin2 f2-f3 in complex with the integrin beta1d2 cytoplasmic tail
25	d2ejna1	Alignment	not modelled	6.5	20	**Fold:**Uteroglobin-like **Superfamily:**Uteroglobin-like **Family:**Uteroglobin-like
26	d1mtyd_	Alignment	not modelled	6.2	11	**Fold:**Ferritin-like **Superfamily:**Ferritin-like **Family:**Ribonucleotide reductase-like
27	c3iz5k_	Alignment	not modelled	6.1	13	**PDB header:**ribosome **Chain:** K: **PDB Molecule:**60s ribosomal protein l13a (l13p); **PDBTitle:** localization of the large subunit ribosomal proteins into a 5.5 a2 cryo-em map of triticum aestivum translating 80s ribosome
28	c1d0rA_	Alignment	not modelled	5.9	23	**PDB header:**hormone/growth factor **Chain:** A: **PDB Molecule:**glucagon-like peptide-1-(7-36)-amide; **PDBTitle:** solution structure of glucagon-like peptide-1-(7-36)-

						amide2 in trifluoroethanol/water
29	c2diiA_	Alignment	not modelled	5.7	36	**PDB header:**transcription **Chain:** A: **PDB Molecule:**tfiih basal transcription factor complex p62 **PDBTitle:** solution structure of the bsd domain of human tfiih basal2 transcription factor complex p62 subunit
30	d2v94a1	Alignment	not modelled	5.6	12	**Fold:**Ribosomal proteins S24e, L23 and L15e **Superfamily:**Ribosomal proteins S24e, L23 and L15e **Family:**Ribosomal protein S24e
31	c3e53A_	Alignment	not modelled	5.4	14	**PDB header:**ligase **Chain:** A: **PDB Molecule:**fatty-acid-coa ligase fadd28; **PDBTitle:** crystal structure of n-terminal domain of a fatty acyl amp2 ligase faal28 from mycobacterium tuberculosis
32	d1fmta1	Alignment	not modelled	5.3	8	**Fold:**FMT C-terminal domain-like **Superfamily:**FMT C-terminal domain-like **Family:**Post formyltransferase domain
33	c2l9vA_	Alignment	not modelled	5.3	50	**PDB header:**rna binding protein **Chain:** A: **PDB Molecule:**pre-mrna-processing factor 40 homolog a; **PDBTitle:** nmr structure of the ff domain l24a mutant's folding transition state