Phyre^2

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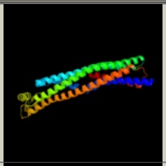
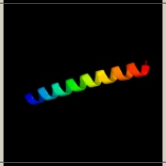
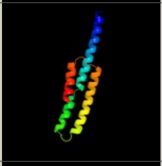
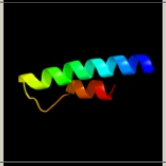
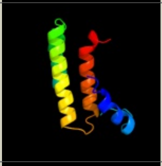
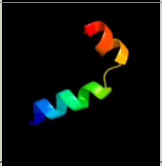
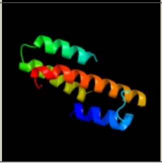
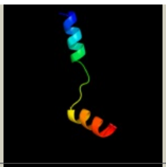
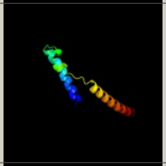
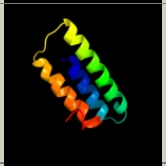
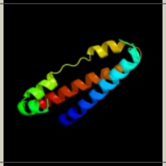
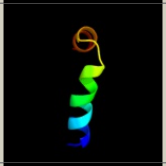
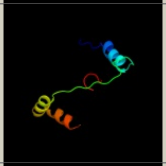
Description	P77335
Date	Thu Jan 5 12:27:57 GMT 2012
Unique Job ID	0c5a8cd2ce0f7b9a

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1qoyA_	Alignment		100.0	99	**PDB header:**toxin **Chain:** A: **PDB Molecule:**hemolysin e; **PDBTitle:** e.coli hemolysin e (hlye, clya, shea)
2	c3brvB_	Alignment		20.7	6	**PDB header:**transferase/transcription **Chain:** B: **PDB Molecule:**nf-kappa-b essential modulator; **PDBTitle:** nemo/ikkb association domain structure
3	d1pcaa1	Alignment		17.1	14	**Fold:**Ferredoxin-like **Superfamily:**Protease propeptides/inhibitors **Family:**Pancreatic carboxypeptidase, activation domain
4	d2coba1	Alignment		15.3	26	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Psq domain
5	d1r11a3	Alignment		14.0	29	**Fold:**MutS N-terminal domain-like **Superfamily:**tRNA-intron endonuclease N-terminal domain-like **Family:**tRNA-intron endonuclease N-terminal domain-like
6	c3pjaK_	Alignment		13.8	15	**PDB header:**hydrolase **Chain:** K: **PDB Molecule:**translin-associated protein x; **PDBTitle:** crystal structure of human c3po complex
7	c2q1kA_	Alignment		12.6	14	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**asce; **PDBTitle:** cyrstal structure of asce from aeromonas hydrophilla
8	d1f6fa_	Alignment		12.4	10	**Fold:**4-helical cytokines **Superfamily:**4-helical cytokines **Family:**Long-chain cytokines
9	d1pfva1	Alignment		12.0	16	**Fold:**Anticodon-binding domain of a subclass of class I aminoacyl-tRNA synthetases **Superfamily:**Anticodon-binding domain of a subclass of class I aminoacyl-tRNA synthetases **Family:**Anticodon-binding domain of a subclass of class I aminoacyl-tRNA synthetases
10	c4a9zD_	Alignment		11.2	13	**PDB header:**transcription **Chain:** D: **PDB Molecule:**tumor protein 63; **PDBTitle:** crystal structure of human p63 tetramerization domain
11	d1rqga1	Alignment		10.5	16	**Fold:**Anticodon-binding domain of a subclass of class I aminoacyl-tRNA synthetases **Superfamily:**Anticodon-binding domain of a subclass of class I aminoacyl-tRNA synthetases **Family:**Anticodon-binding domain of a subclass of class I aminoacyl-tRNA synthetases

12	d1gg2g_	Alignment		10.3	23	**Fold:**Non-globular all-alpha subunits of globular proteins **Superfamily:**Transducin (heterotrimeric G protein), gamma chain **Family:**Transducin (heterotrimeric G protein), gamma chain
13	c3f1iH_	Alignment		10.1	13	**PDB header:**protein binding **Chain:** H: **PDB Molecule:**hepatocyte growth factor-regulated tyrosine kinase **PDBTitle:** human escrt-0 core complex
14	d1h3na1	Alignment		10.1	14	**Fold:**Anticodon-binding domain of a subclass of class I aminoacyl-tRNA synthetases **Superfamily:**Anticodon-binding domain of a subclass of class I aminoacyl-tRNA synthetases **Family:**Anticodon-binding domain of a subclass of class I aminoacyl-tRNA synthetases
15	d1rw5a1	Alignment		9.9	7	**Fold:**4-helical cytokines **Superfamily:**4-helical cytokines **Family:**Long-chain cytokines
16	c3zy1A_	Alignment		9.9	13	**PDB header:**transcription **Chain:** A: **PDB Molecule:**tumor protein 63; **PDBTitle:** crystal structure of the human p63 tetramerization domain
17	c3kwlA_	Alignment		9.4	18	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of a hypothetical protein from helicobacter pylori
18	c1ciiA_	Alignment		9.4	13	**PDB header:**transmembrane protein **Chain:** A: **PDB Molecule:**colicin ia; **PDBTitle:** colicin ia
19	c2ql2A_	Alignment		8.9	23	**PDB header:**transcription/dna **Chain:** A: **PDB Molecule:**transcription factor e2-alpha; **PDBTitle:** crystal structure of the basic-helix-loop-helix domains of2 the heterodimer e47/neurod1 bound to dna
20	d2ezwa1	Alignment		8.9	27	**Fold:**Dimerization-anchoring domain of cAMP-dependent PK regulatory subunit **Superfamily:**Dimerization-anchoring domain of cAMP-dependent PK regulatory subunit **Family:**Dimerization-anchoring domain of cAMP-dependent PK regulatory subunit
21	d1b0na1	Alignment	not modelled	8.5	12	**Fold:**Dimerisation interlock **Superfamily:**SinR repressor dimerisation domain-like **Family:**SinR repressor dimerisation domain-like
22	d1omwg_	Alignment	not modelled	8.4	17	**Fold:**Non-globular all-alpha subunits of globular proteins **Superfamily:**Transducin (heterotrimeric G protein), gamma chain **Family:**Transducin (heterotrimeric G protein), gamma chain
23	c2k29A_	Alignment	not modelled	8.1	24	**PDB header:**transcription **Chain:** A: **PDB Molecule:**antitoxin relb; **PDBTitle:** structure of the dbd domain of e. coli antitoxin relb
24	d1ggpa_	Alignment	not modelled	7.7	16	**Fold:**Ribosome inactivating proteins (RIP) **Superfamily:**Ribosome inactivating proteins (RIP) **Family:**Plant cytotoxins
25	d1gotg_	Alignment	not modelled	7.2	9	**Fold:**Non-globular all-alpha subunits of globular proteins **Superfamily:**Transducin (heterotrimeric G protein), gamma chain **Family:**Transducin (heterotrimeric G protein), gamma chain
26	d1xppa_	Alignment	not modelled	7.2	8	**Fold:**DCoH-like **Superfamily:**RBP11-like subunits of RNA polymerase **Family:**RBP11/RpoL
27	d1tbge_	Alignment	not modelled	6.3	9	**Fold:**Non-globular all-alpha subunits of globular proteins **Superfamily:**Transducin (heterotrimeric G protein), gamma chain **Family:**Transducin (heterotrimeric G protein), gamma chain
28	c1gaxB_	Alignment	not modelled	6.2	15	**PDB header:**ligase/rna **Chain:** B: **PDB Molecule:**valyl-trna synthetase; **PDBTitle:** crystal structure of thermus thermophilus valyl-trna2 synthetase complexed with trna(val) and valyl-adenylate3 analogue
29	c2zwmA_	Alignment	not modelled	6.1	14	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcriptional regulatory protein yycf;

29	c2zwmA_	Alignment	not modelled	6.1	14	**PDBTitle:** crystal structure of yycf receiver domain from bacillus2 subtilis
30	c2rlwA_	Alignment	not modelled	5.9	16	**PDB header:**toxin **Chain:** A: **PDB Molecule:**plnf; **PDBTitle:** three-dimensional structure of the two peptides that2 constitute the two-peptide bacteriocin plantaracin ef
31	c3qqwC_	Alignment	not modelled	5.9	19	**PDB header:**lyase **Chain:** C: **PDB Molecule:**putative citrate lyase; **PDBTitle:** crystal structure of a hypothetical lyase (reut_b4148) from ralstonia2 eutropha jmp134 at 2.44 a resolution
32	c3hisA_	Alignment	not modelled	5.9	11	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**vacuolar saporin; **PDBTitle:** crystal structure of saporin-l1 from saponaria officinalis
33	c3df8A_	Alignment	not modelled	5.8	12	**PDB header:**transcription **Chain:** A: **PDB Molecule:**possible hxlr family transcriptional factor; **PDBTitle:** the crystal structure of a possible hxlr family transcriptional factor2 from thermoplasma volcanium gss1
34	c2xzmV_	Alignment	not modelled	5.7	20	**PDB header:**ribosome **Chain:** V: **PDB Molecule:**rps17e; **PDBTitle:** crystal structure of the eukaryotic 40s ribosomal2 subunit in complex with initiation factor 1. this file3 contains the 40s subunit and initiation factor for4 molecule 1
35	d1vcsa1	Alignment	not modelled	5.6	14	**Fold:**STAT-like **Superfamily:**t-snare proteins **Family:**t-snare proteins
36	c1jsdB_	Alignment	not modelled	5.5	23	**PDB header:**viral protein **Chain:** B: **PDB Molecule:**haemagglutinin (ha2 chain); **PDBTitle:** crystal structure of swine h9 haemagglutinin
37	c1lt1G_	Alignment	not modelled	5.4	11	**PDB header:**de novo protein **Chain:** G: **PDB Molecule:**l13g-df1; **PDBTitle:** sliding helix induced change of coordination geometry in a2 model di-mn(ii) protein
38	c3i5pA_	Alignment	not modelled	5.4	18	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**nucleoporin nup170; **PDBTitle:** nup170(aa979-1502), s.cerevisiae
39	c2uwjE_	Alignment	not modelled	5.3	11	**PDB header:**chaperone **Chain:** E: **PDB Molecule:**type iii export protein psce; **PDBTitle:** structure of the heterotrimeric complex which regulates2 type iii secretion needle formation
40	d1d9ca_	Alignment	not modelled	5.3	16	**Fold:**4-helical cytokines **Superfamily:**4-helical cytokines **Family:**Interferons/interleukin-10 (IL-10)
41	d1twfk_	Alignment	not modelled	5.1	16	**Fold:**DCoH-like **Superfamily:**RBP11-like subunits of RNA polymerase **Family:**RBP11/RpoL