Phyre^2

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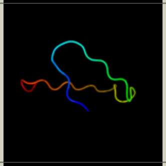
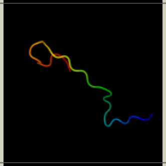
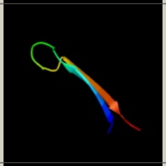
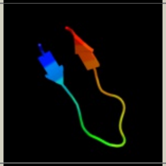
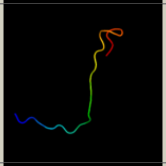
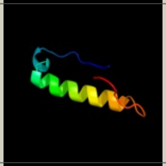
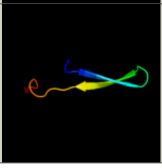
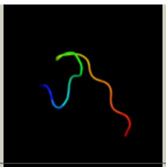
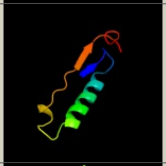
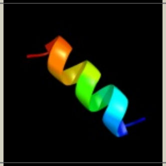
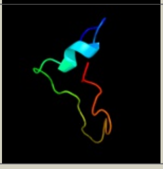
Description	P75677
Date	Thu Jan 5 12:12:54 GMT 2012
Unique Job ID	1181e3a095c44de3

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d2hjja1	Alignment		100.0	100	**Fold:**dsRBD-like **Superfamily:**YcfA/nrd intein domain **Family:**YkfF-like
2	c2hjjA_	Alignment		100.0	100	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein ykff; **PDBTitle:** solution nmr structure of protein ykff from escherichia coli.2 northeast structural genomics target er397.
3	c3fcgB_	Alignment		26.9	26	**PDB header:**membrane protein, protein transport **Chain:** B: **PDB Molecule:**f1 capsule-anchoring protein; **PDBTitle:** crystal structure analysis of the middle domain of the2 caf1a usher
4	c3isyA_	Alignment		22.9	36	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**intracellular proteinase inhibitor; **PDBTitle:** crystal structure of an intracellular proteinase inhibitor (ipi,2 bsu11130) from bacillus subtilis at 2.61 a resolution
5	c3hx8A_	Alignment		19.2	29	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**putative ketosteroid isomerase; **PDBTitle:** crystal structure of putative ketosteroid isomerase2 (np_103587.1) from mesorhizobium loti at 1.45 a resolution
6	c3ffeB_	Alignment		17.2	31	**PDB header:**biosynthetic protein **Chain:** B: **PDB Molecule:**acsd; **PDBTitle:** structure of achromobactin synthetase protein d, (acsd)
7	c1xs3A_	Alignment		16.3	27	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein xc975; **PDBTitle:** solution structure analysis of the xc975 protein
8	c2dhmA_	Alignment		16.1	19	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**protein bola; **PDBTitle:** solution structure of the bola protein from escherichia coli
9	d1xdna_	Alignment		14.7	17	**Fold:**ATP-grasp **Superfamily:**DNA ligase/mRNA capping enzyme, catalytic domain **Family:**RNA ligase
10	d1k1sa1	Alignment		13.8	16	**Fold:**Lesion bypass DNA polymerase (Y-family), little finger domain **Superfamily:**Lesion bypass DNA polymerase (Y-family), little finger domain **Family:**Lesion bypass DNA polymerase (Y-family), little finger domain
11	c2w02A_	Alignment		13.0	31	**PDB header:**metal transport **Chain:** A: **PDB Molecule:**acsd; **PDBTitle:** co-complex structure of achromobactin synthetase protein d (2 acsd) with atp from pectobacterium chrysanthemi

12	c3tr3A_	Alignment		11.7	33	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**bola; **PDBTitle:** structure of a bola protein homologue from coxiella burnetii
13	c1yewF_	Alignment		11.1	50	**PDB header:**oxidoreductase, membrane protein **Chain:** F: **PDB Molecule:**particulate methane monooxygenase, a subunit; **PDBTitle:** crystal structure of particulate methane monooxygenase
14	c2flzC_	Alignment		10.6	13	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**cis-3-chloroacrylic acid dehalogenase; **PDBTitle:** the x-ray structure of cis-3-chloroacrylic acid dehalogenase (cis-2 caad) with a sulfate ion bound in the active site
15	c3o2eA_	Alignment		10.3	20	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**bola-like protein; **PDBTitle:** crystal structure of a bol-like protein from babesia bovis
16	c2zt9F_	Alignment		9.5	36	**PDB header:**photosynthesis **Chain:** F: **PDB Molecule:**cytochrome b6-f complex subunit 7; **PDBTitle:** crystal structure of the cytochrome b6f complex from nostoc sp. pcc2 7120
17	c2kdnA_	Alignment		9.4	33	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**putative uncharacterized protein pfe0790c; **PDBTitle:** solution structure of pfe0790c, a putative bola-like2 protein from the protozoan parasite plasmodium falciparum.
18	c3lrmB_	Alignment		9.2	23	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**alpha-galactosidase 1; **PDBTitle:** structure of alfa-galactosidase from saccharomyces cerevisiae with2 raffinose
19	c3chxF_	Alignment		8.5	50	**PDB header:**membrane protein **Chain:** F: **PDB Molecule:**pmoa; **PDBTitle:** crystal structure of methylosinus trichosporium ob3b2 particulate methane monooxygenase (pmmo)
20	d1f1sa4	Alignment		8.0	21	**Fold:**Supersandwich **Superfamily:**Galactose mutarotase-like **Family:**Hyaluronate lyase-like, central domain
21	c2f4qA_	Alignment	not modelled	7.9	26	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**type i topoisomerase, putative; **PDBTitle:** crystal structure of deinococcus radiodurans topoisomerase ib
22	d1ny8a_	Alignment	not modelled	7.8	36	**Fold:**Alpha-lytic protease prodomain-like **Superfamily:**BolA-like **Family:**BolA-like
23	c2h7fX_	Alignment	not modelled	6.5	14	**PDB header:**isomerase/dna **Chain:** X: **PDB Molecule:**dna topoisomerase 1; **PDBTitle:** structure of variola topoisomerase covalently bound to dna
24	c2knrA_	Alignment	not modelled	6.5	18	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein atc0905; **PDBTitle:** solution structure of protein atu0922 from a. tumefaciens. northeast2 structural genomics consortium target att13. ontario center for3 structural proteomics target atc0905
25	d2oa4a1	Alignment	not modelled	6.3	58	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**TrpR-like **Family:**SPO1678-like
26	d1v9ja_	Alignment	not modelled	6.2	33	**Fold:**Alpha-lytic protease prodomain-like **Superfamily:**BolA-like **Family:**BolA-like
27	c3iydB_	Alignment	not modelled	6.2	19	**PDB header:**transcription/dna **Chain:** B: **PDB Molecule:**dna-directed rna polymerase subunit alpha; **PDBTitle:** three-dimensional em structure of an intact activator-dependent2 transcription initiation complex
28	d1x7fa2	Alignment	not modelled	5.8	28	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Outer surface protein, N-terminal domain

29	d1szwa_	Alignment	not modelled	5.6	30	**Fold:**Pseudouridine synthase **Superfamily:**Pseudouridine synthase **Family:**tRNA pseudouridine synthase TruD
30	c1v60A_	Alignment	not modelled	5.6	22	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**riken cdna 1810037g04; **PDBTitle:** solution structure of bola1 protein from mus musculus
31	d1ik0a_	Alignment	not modelled	5.3	57	**Fold:**4-helical cytokines **Superfamily:**4-helical cytokines **Family:**Short-chain cytokines
32	c2kz3A_	Alignment	not modelled	5.3	28	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**putative uncharacterized protein rad51l3; **PDBTitle:** backbone 1h, 13c, and 15n chemical shift assignments for human rad51d2 from 1 to 83
33	c2k17A_	Alignment	not modelled	5.3	26	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcription initiation factor tfiid subunit 3; **PDBTitle:** solution structure of the taf3 phd domain in complex with a2 h3k4me3 peptide