Phyre2

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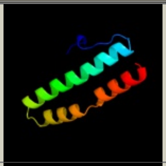
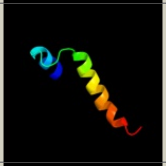
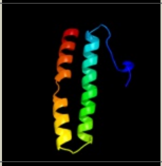
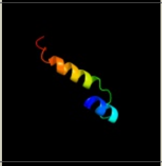
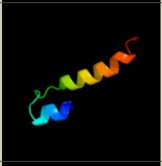
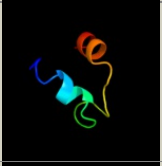
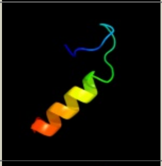
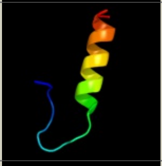
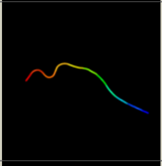
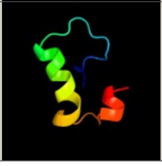
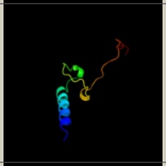
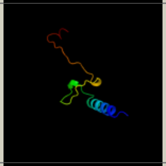
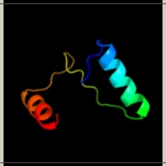
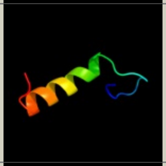
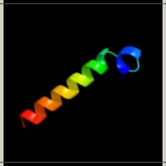
Description	P77427
Date	Thu Jan 5 12:29:11 GMT 2012
Unique Job ID	ff499a8ef9317652

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d2cwla1	Alignment		34.0	8	**Fold:**Ferritin-like **Superfamily:**Ferritin-like **Family:**Manganese catalase (T-catalase)
2	c2jobA_	Alignment		25.6	14	**PDB header:**lipid binding protein **Chain:** A: **PDB Molecule:**antilipopolysaccharide factor; **PDBTitle:** solution structure of an antilipopolysaccharide factor from2 shrimp and its possible lipid a binding site
3	d1joga_	Alignment		24.7	9	**Fold:**Four-helical up-and-down bundle **Superfamily:**Nucleotidyltransferase substrate binding subunit/domain **Family:**Family 1 bi-partite nucleotidyltransferase subunit
4	d1jkva_	Alignment		23.8	4	**Fold:**Ferritin-like **Superfamily:**Ferritin-like **Family:**Manganese catalase (T-catalase)
5	c1wwpA_	Alignment		20.3	18	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein ttha0636; **PDBTitle:** crystal structure of ttk003001694 from thermus thermophilus2 hb8
6	d1wtya_	Alignment		20.1	15	**Fold:**Four-helical up-and-down bundle **Superfamily:**Nucleotidyltransferase substrate binding subunit/domain **Family:**Family 1 bi-partite nucleotidyltransferase subunit
7	c2lhuA_	Alignment		19.0	17	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**mybpc3 protein; **PDBTitle:** structural insight into the unique cardiac myosin binding protein-c2 motif: a partially folded domain
8	d1tz7a1	Alignment		17.0	19	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
9	d1eswa_	Alignment		14.9	11	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
10	c2advB_	Alignment		14.6	18	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**glutaryl 7- aminocephalosporanic acid acylase; **PDBTitle:** crystal structures of glutaryl 7-aminocephalosporanic acid acylase:2 mutational study of activation mechanism
11	d2oa4a1	Alignment		12.5	19	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**TrpR-like **Family:**SPO1678-like

12	d2gykb1	Alignment		12.2	14	**Fold:**His-Me finger endonucleases **Superfamily:**His-Me finger endonucleases **Family:**HNH-motif
13	c2jrtA_	Alignment		11.1	19	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** nmr solution structure of the protein coded by gene2 rhos4_12090 of rhodobacter sphaeroides. northeast3 structural genomics target rhr5
14	d1e8oa_	Alignment		9.9	30	**Fold:**Signal recognition particle alu RNA binding heterodimer, SRP9/14 **Superfamily:**Signal recognition particle alu RNA binding heterodimer, SRP9/14 **Family:**Signal recognition particle alu RNA binding heterodimer, SRP9/14
15	c2fxhB_	Alignment		7.0	17	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**catalase-peroxidase protein; **PDBTitle:** crystal structure of katg at ph 6.5
16	c2b2qB_	Alignment		7.0	17	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**catalase-peroxidase; **PDBTitle:** crystal structure of native catalase-peroxidase katg at2 ph7.5
17	c3rdwB_	Alignment		6.9	11	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**putative arsenate reductase; **PDBTitle:** putative arsenate reductase from yersinia pestis
18	d1x1na1	Alignment		6.8	11	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
19	d2p12a1	Alignment		6.8	3	**Fold:**FomD barrel-like **Superfamily:**FomD-like **Family:**FomD-like
20	c2jg6A_	Alignment		6.2	14	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**dna-3-methyladenine glycosidase; **PDBTitle:** crystal structure of a 3-methyladenine dna glycosylase i2 from staphylococcus aureus
21	c1dpuA_	Alignment	not modelled	6.0	18	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**replication protein a (rpa32) c-terminal domain; **PDBTitle:** solution structure of the c-terminal domain of human rpa322 complexed with ung2(73-88)
22	d1dpua_	Alignment	not modelled	6.0	18	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**C-terminal domain of RPA32
23	c2k5eA_	Alignment	not modelled	6.0	21	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** solution structure of putative uncharacterized protein2 gsu1278 from methanocaldococcus jannaschii, northeast3 structural genomics consortium (nesg) target gsr195
24	c3dmlA_	Alignment	not modelled	5.9	15	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**putative uncharacterized protein; **PDBTitle:** crystal structure of the periplasmic thioredoxin soxs from2 paracoccus pantotrophus (reduced form)
25	d1jvaa2	Alignment	not modelled	5.7	32	**Fold:**Homing endonuclease-like **Superfamily:**Homing endonucleases **Family:**Intein endonuclease
26	c3gkxB_	Alignment	not modelled	5.5	12	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**putative arsc family related protein; **PDBTitle:** crystal structure of putative arsc family related protein from2 bacteroides fragilis
27	d2gsca1	Alignment	not modelled	5.5	6	**Fold:**Bromodomain-like **Superfamily:**IVS-encoded protein-like **Family:**IVS-encoded protein-like
28	d1nkua_	Alignment	not modelled	5.4	6	**Fold:**DNA-glycosylase **Superfamily:**DNA-glycosylase **Family:**3-Methyladenine DNA glycosylase I (Tag)

29	d1fsha_	Alignment	not modelled	5.2	21	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**DEP domain