Phyre2

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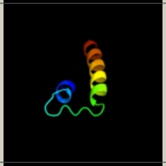
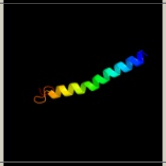
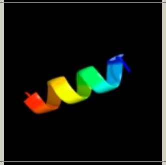
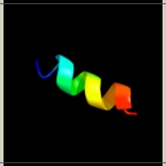
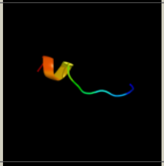
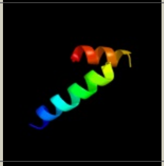
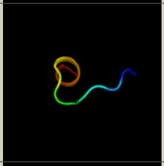
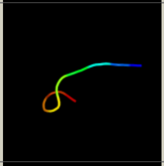
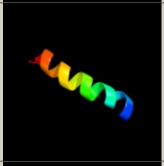
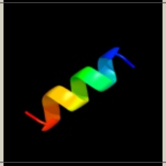
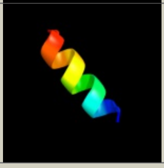
Description	Q9JMT1
Date	Thu Jan 5 12:38:06 GMT 2012
Unique Job ID	2ffc0a056acf1cb6

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1gm5a1	Alignment		39.1	13	**Fold:**Four-helical up-and-down bundle **Superfamily:**RecG, N-terminal domain **Family:**RecG, N-terminal domain
2	c3bhpA_	Alignment		30.7	19	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**upf0291 protein ynzc; **PDBTitle:** crystal structure of upf0291 protein ynzc from bacillus2 subtilis at resolution 2.0 a. northeast structural3 genomics consortium target sr384
3	c2rf4B_	Alignment		17.9	23	**PDB header:**transferase **Chain:** B: **PDB Molecule:**dna-directed rna polymerase i subunit rpa4; **PDBTitle:** crystal structure of the rna polymerase i subcomplex a14/43
4	d2f23a2	Alignment		17.9	25	**Fold:**FKBP-like **Superfamily:**FKBP-like **Family:**GreA transcript cleavage factor, C-terminal domain
5	c2etnA_	Alignment		17.5	25	**PDB header:**transcription **Chain:** A: **PDB Molecule:**anti-cleavage anti-grea transcription factor **PDBTitle:** crystal structure of thermus aquaticus gfh1
6	d2etna2	Alignment		16.1	25	**Fold:**FKBP-like **Superfamily:**FKBP-like **Family:**GreA transcript cleavage factor, C-terminal domain
7	d1w0ba_	Alignment		14.2	12	**Fold:**Spectrin repeat-like **Superfamily:**Alpha-hemoglobin stabilizing protein AHSP **Family:**Alpha-hemoglobin stabilizing protein AHSP
8	c1grjA_	Alignment		12.4	17	**PDB header:**transcription regulation **Chain:** A: **PDB Molecule:**grea protein; **PDBTitle:** grea transcript cleavage factor from escherichia coli
9	c1unyA_	Alignment		11.9	38	**PDB header:**four helix bundle **Chain:** A: **PDB Molecule:**general control protein gcn4; **PDBTitle:** structure based engineering of internal molecular surfaces2 of four helix bundles
10	c1u9gA_	Alignment		11.4	38	**PDB header:**transcription **Chain:** A: **PDB Molecule:**general control protein gcn4; **PDBTitle:** heterocyclic peptide backbone modification in gcn4-pli based coiled2 coils: replacement of k(8)l(9)
11	c1u9gB_	Alignment		11.4	38	**PDB header:**transcription **Chain:** B: **PDB Molecule:**general control protein gcn4; **PDBTitle:** heterocyclic peptide backbone modification in gcn4-pli based coiled2 coils: replacement of k(8)l(9)

12	c1unvA_	Alignment		11.4	38	**PDB header:**four helix bundle **Chain:** A: **PDB Molecule:**general control protein gcn4; **PDBTitle:** structure based engineering of internal molecular surfaces2 of four helix bundles
13	c2p4vA_	Alignment		11.2	25	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcription elongation factor greb; **PDBTitle:** crystal structure of the transcript cleavage factor, greb2 at 2.6a resolution
14	c1unvB_	Alignment		11.2	38	**PDB header:**four helix bundle **Chain:** B: **PDB Molecule:**general control protein gcn4; **PDBTitle:** structure based engineering of internal molecular surfaces2 of four helix bundles
15	d1n1ba1	Alignment		10.7	3	**Fold:**alpha/alpha toroid **Superfamily:**Terpenoid cyclases/Protein prenyltransferases **Family:**Terpenoid cyclase N-terminal domain
16	d1grja2	Alignment		10.5	14	**Fold:**FKBP-like **Superfamily:**FKBP-like **Family:**GreA transcript cleavage factor, C-terminal domain
17	d1u7na_	Alignment		10.3	22	**Fold:**Isocitrate/Isopropylmalate dehydrogenase-like **Superfamily:**Isocitrate/Isopropylmalate dehydrogenase-like **Family:**PlsX-like
18	c1x4qA_	Alignment		10.3	19	**PDB header:**rna binding protein **Chain:** A: **PDB Molecule:**u4/u6 small nuclear ribonucleoprotein prp3; **PDBTitle:** solution structure of pwi domain in u4/u6 small nuclear2 ribonucleoprotein prp3(hprp3)
19	c1unzA_	Alignment		10.1	38	**PDB header:**four helix bundle **Chain:** A: **PDB Molecule:**general control protein gcn4; **PDBTitle:** structure based engineering of internal molecular surfaces2 of four helix bundles
20	c1unzB_	Alignment		10.1	38	**PDB header:**four helix bundle **Chain:** B: **PDB Molecule:**general control protein gcn4; **PDBTitle:** structure based engineering of internal molecular surfaces2 of four helix bundles
21	d1am9a_	Alignment	not modelled	9.9	16	**Fold:**HLH-like **Superfamily:**HLH, helix-loop-helix DNA-binding domain **Family:**HLH, helix-loop-helix DNA-binding domain
22	d2ovra1	Alignment	not modelled	9.9	19	**Fold:**Skp1 dimerisation domain-like **Superfamily:**Skp1 dimerisation domain-like **Family:**Skp1 dimerisation domain-like
23	c1n20A_	Alignment	not modelled	9.4	3	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**(+)-bornyl diphosphate synthase; **PDBTitle:** (+)-bornyl diphosphate synthase: complex with mg and 3-aza-2 2,3-dihydrogeranyl diphosphate
24	c2jvdA_	Alignment	not modelled	7.9	24	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**upf0291 protein ynzc; **PDBTitle:** solution nmr structure of the folded n-terminal fragment of2 upf0291 protein ynzc from bacillus subtilis. northeast3 structural genomics target sr384-1-46
25	d1ee8a1	Alignment	not modelled	7.3	15	**Fold:**S13-like H2TH domain **Superfamily:**S13-like H2TH domain **Family:**Middle domain of MutM-like DNA repair proteins
26	c2g9pA_	Alignment	not modelled	7.3	38	**PDB header:**antimicrobial protein **Chain:** A: **PDB Molecule:**antimicrobial peptide latarcin 2a; **PDBTitle:** nmr structure of a novel antimicrobial peptide, latarcin 2a,2 from spider (lachesana tarabaevi) venom
27	c1u2uB_	Alignment	not modelled	7.1	50	**PDB header:**transcription **Chain:** B: **PDB Molecule:**general control protein gcn4; **PDBTitle:** nmr solution structure of a designed heterodimeric leucine2 zipper
28	c3if8A_	Alignment	not modelled	6.7	7	**PDB header:**cell cycle **Chain:** A: **PDB Molecule:**protein zwilch homolog; **PDBTitle:** crystal structure of zwilch, a member of the rzz kinetochore complex

29	d2cg4a1	Alignment	not modelled	6.2	10	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Lrp/AsnC-like transcriptional regulator N-terminal domain
30	d1iega_	Alignment	not modelled	5.7	19	**Fold:**Herpes virus serine proteinase, assemblin **Superfamily:**Herpes virus serine proteinase, assemblin **Family:**Herpes virus serine proteinase, assemblin
31	c1u7mB_	Alignment	not modelled	5.6	24	**PDB header:**de novo protein **Chain:** B: **PDB Molecule:**four-helix bundle model; **PDBTitle:** solution structure of a diiron protein model: due ferri(ii)2 turn mutant
32	d2v0ea1	Alignment	not modelled	5.4	25	**Fold:**GYF/BRK domain-like **Superfamily:**BRK domain-like **Family:**BRK domain-like
33	c1r7gA_	Alignment	not modelled	5.4	8	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**genome polyprotein; **PDBTitle:** nmr structure of the membrane anchor domain (1-31) of the2 nonstructural protein 5a (ns5a) of hepatitis c virus3 (minimized average structure, sample in 100mm dpc)