Phyre2

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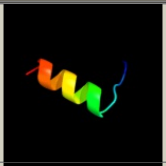
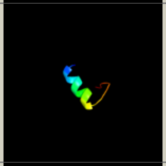
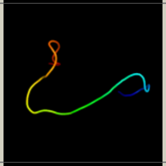
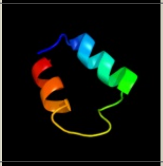
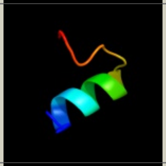
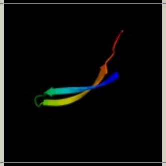
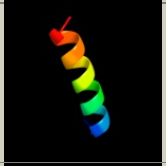
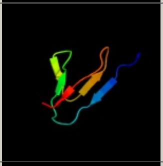
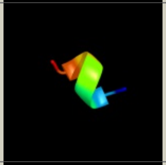
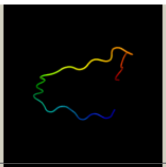
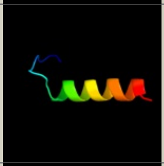
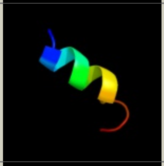
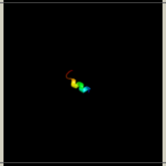
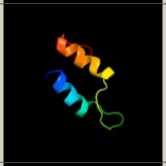
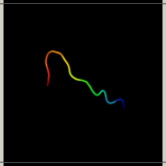
Description	P0ADU7
Date	Thu Jan 5 11:21:53 GMT 2012
Unique Job ID	43e82381ebce0c66

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1m47a_	Alignment		42.7	41	**Fold:**4-helical cytokines **Superfamily:**4-helical cytokines **Family:**Short-chain cytokines
2	c2kebA_	Alignment		27.5	5	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**dna polymerase subunit alpha b; **PDBTitle:** nmr solution structure of the n-terminal domain of the dna polymerase2 alpha p68 subunit
3	c3igeA_	Alignment		23.5	41	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**soc small outer capsid protein; **PDBTitle:** small outer capsid protein (soc) from bacteriophage rb69
4	d3b7sa1	Alignment		20.3	23	**Fold:**alpha-alpha superhelix **Superfamily:**ARM repeat **Family:**Leukotriene A4 hydrolase C-terminal domain
5	d1f44a1	Alignment		19.3	17	**Fold:**SAM domain-like **Superfamily:**lambda integrase-like, N-terminal domain **Family:**lambda integrase-like, N-terminal domain
6	c3iabB_	Alignment		15.5	15	**PDB header:**hydrolase/rna **Chain:** B: **PDB Molecule:**ribonucleases p/mrp protein subunit pop7; **PDBTitle:** crystal structure of rnase p /rnase mrp proteins pop6, pop72 in a complex with the p3 domain of rnase mrp rna
7	c3h6pD_	Alignment		15.4	32	**PDB header:**structural genomics, unknown function **Chain:** D: **PDB Molecule:**esat-6-like protein esxr; **PDBTitle:** crystal structure of rv3019c-rv3020c from mycobacterium tuberculosis
8	d1iv8a1	Alignment		14.6	28	**Fold:**Glycosyl hydrolase domain **Superfamily:**Glycosyl hydrolase domain **Family:**alpha-Amylases, C-terminal beta-sheet domain
9	c3g36D_	Alignment		14.6	57	**PDB header:**nuclear protein **Chain:** D: **PDB Molecule:**protein dpy-30 homolog; **PDBTitle:** crystal structure of the human dpy-30-like c-terminal domain
10	d2dsya1	Alignment		13.6	26	**Fold:**TTHA1013/TTHA0281-like **Superfamily:**TTHA1013/TTHA0281-like **Family:**TTHA0281-like
11	c3iu0A_	Alignment		12.4	26	**PDB header:**transferase **Chain:** A: **PDB Molecule:**protein-glutamine gamma-glutamyltransferase; **PDBTitle:** structural basis for zymogen activation and substrate binding of2 transglutaminase from streptomyces mobaraense

12	d1xsqa_	Alignment		10.4	23	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Ureidoglycolate hydrolase AllA
13	d1ufoa_	Alignment		10.1	17	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Hypothetical protein TT1662
14	d1mkya3	Alignment		9.1	40	**Fold:**Alpha-lytic protease prodomain-like **Superfamily:**Probable GTPase Der, C-terminal domain **Family:**Probable GTPase Der, C-terminal domain
15	d1t15a1	Alignment		8.6	9	**Fold:**BRCT domain **Superfamily:**BRCT domain **Family:**BRCT domain
16	d1xhmb1	Alignment		8.4	43	**Fold:**Non-globular all-alpha subunits of globular proteins **Superfamily:**Transducin (heterotrimeric G protein), gamma chain **Family:**Transducin (heterotrimeric G protein), gamma chain
17	c1xhmB_	Alignment		8.2	43	**PDB header:**signaling protein **Chain:** B: **PDB Molecule:**guanine nucleotide-binding protein g(i)/g(s) **PDBTitle:** the crystal structure of a biologically active peptide2 (sigk) bound to a g protein beta:gamma heterodimer
18	d1iu4a_	Alignment		7.7	26	**Fold:**Cysteine proteinases **Superfamily:**Cysteine proteinases **Family:**Microbial transglutaminase
19	c2jyaA_	Alignment		6.5	33	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein atu1810; **PDBTitle:** nmr solution structure of protein atu1810 from agrobacterium2 tumefaciens. northeast structural genomics consortium target atr23,3 ontario centre for structural proteomics target atc1776
20	d1l0ba1	Alignment		6.4	9	**Fold:**BRCT domain **Superfamily:**BRCT domain **Family:**BRCT domain
21	c3ktfB_	Alignment	not modelled	6.3	36	**PDB header:**cell cycle **Chain:** B: **PDB Molecule:**microcephalin; **PDBTitle:** structure of the n-terminal brct domain of human2 microcephalin (mcph1).
22	c3ebrA_	Alignment	not modelled	6.2	43	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**uncharacterized rmlc-like cupin; **PDBTitle:** crystal structure of an rmlc-like cupin protein (reut_a0381) from2 ralstonia eutropha jmp134 at 2.60 a resolution
23	c2cokA_	Alignment	not modelled	5.3	19	**PDB header:**transferase **Chain:** A: **PDB Molecule:**poly [adp-ribose] polymerase-1; **PDBTitle:** solution structure of brct domain of poly(adp-ribose)2 polymerase-1