Phyre^2

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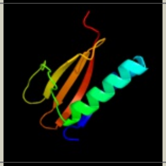
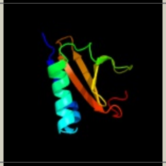
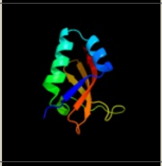
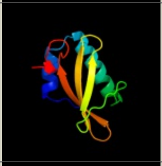
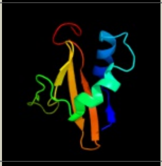
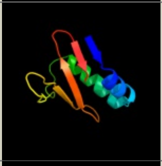
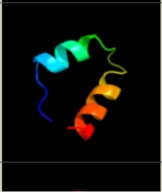
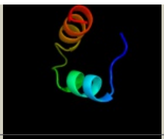
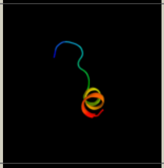
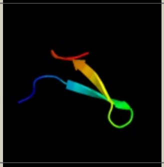
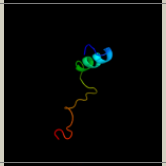
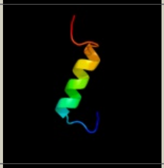
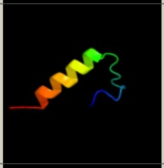
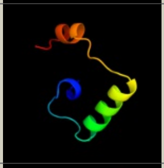
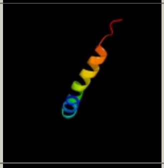
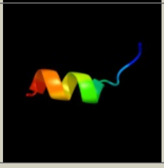
Description	P0C077
Date	Thu Jan 5 11:29:47 GMT 2012
Unique Job ID	f1c5a71d773acdb6

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3kixy_	Alignment		100.0	100	**PDB header:**ribosome **Chain:** Y: **PDB Molecule:** **PDBTitle:** structure of rele nuclease bound to the 70s ribosome2 (postcleavage state; part 3 of 4)
2	d1wmia1	Alignment		99.9	20	**Fold:**RelE-like **Superfamily:**RelE-like **Family:**RelE-like
3	c2kheA_	Alignment		99.9	34	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**toxin-like protein; **PDBTitle:** solution structure of the bacterial toxin rele from thermus2 thermophilus hb8
4	c3g5oC_	Alignment		99.9	22	**PDB header:**toxin/antitoxin **Chain:** C: **PDB Molecule:**uncharacterized protein rv2866; **PDBTitle:** the crystal structure of the toxin-antitoxin complex relbe2 (rv2865-2 2866) from mycobacterium tuberculosis
5	c3bpqD_	Alignment		99.8	21	**PDB header:**toxin **Chain:** D: **PDB Molecule:**toxin rele3; **PDBTitle:** crystal structure of relb-rele antitoxin-toxin complex from2 methanococcus jannaschii
6	c2otrA_	Alignment		99.3	18	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein hp0892; **PDBTitle:** solution structure of conserved hypothetical protein hp0892 from2 helicobacter pylori
7	c3oeiH_	Alignment		99.1	21	**PDB header:**toxin, protein binding **Chain:** H: **PDB Molecule:**relk (toxin rv3358); **PDBTitle:** crystal structure of mycobacterium tuberculosis reljk (rv3357-rv3358-2 relbe3)
8	d2a6sa1	Alignment		99.0	16	**Fold:**RelE-like **Superfamily:**RelE-like **Family:**YoeB/Txe-like
9	d1z8ma1	Alignment		98.4	21	**Fold:**RelE-like **Superfamily:**RelE-like **Family:**RelE-like
10	c3kxeB_	Alignment		97.6	15	**PDB header:**protein binding **Chain:** B: **PDB Molecule:**toxin protein pare-1; **PDBTitle:** a conserved mode of protein recognition and binding in a2 pard-pare toxin-antitoxin complex
11	c2kruA_	Alignment		81.2	23	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**light-independent protochlorophyllide reductase **PDBTitle:** solution nmr structure of the pcp_red domain of light-2 independent protochlorophyllide reductase subunit b from3 chlorobium tepidum. northeast structural genomics4 consortium target ctr69a (casp target)

12	c2l09A_	Alignment		73.1	17	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**asr4154 protein; **PDBTitle:** solution nmr structure of protein asr4154 from nostoc sp. pcc71202 northeast structural genomics consortium target id nsr143
13	c2apnA_	Alignment		16.1	33	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**protein hi1723; **PDBTitle:** hi1723 solution structure
14	d1ugja_	Alignment		10.1	17	**Fold:**PRC-barrel domain **Superfamily:**PRC-barrel domain **Family:**RIKEN cDNA 2310057j16 protein (KIAA1543)
15	c1v9xA_	Alignment		10.1	8	**PDB header:**transferase **Chain:** A: **PDB Molecule:**poly (adp-ribose) polymerase; **PDBTitle:** solution structure of the first zn-finger domain of2 poly(adp-ribose) polymerase-1
16	c2dmjA_	Alignment		8.8	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**poly (adp-ribose) polymerase family, member 1; **PDBTitle:** solution structure of the first zf-parp domain of human2 poly(adp-ribose)polymerase-1
17	c1v85A_	Alignment		8.2	19	**PDB header:**apoptosis **Chain:** A: **PDB Molecule:**similar to ring finger protein 36; **PDBTitle:** sterile alpha motif (sam) domain of mouse bifunctional2 apoptosis regulator
18	d1efaa1	Alignment		7.7	20	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**GalR/LacI-like bacterial regulator
19	d1wixa_	Alignment		7.3	12	**Fold:**CH domain-like **Superfamily:**Hook domain **Family:**Hook domain
20	d1nwba_	Alignment		7.0	21	**Fold:**HesB-like domain **Superfamily:**HesB-like domain **Family:**HesB-like domain
21	d1zdna1	Alignment	not modelled	6.9	10	**Fold:**UBC-like **Superfamily:**UBC-like **Family:**UBC-related
22	c2eamA_	Alignment	not modelled	6.6	19	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**putative 47 kda protein; **PDBTitle:** solution structure of the n-terminal sam-domain of a human2 putative 47 kda protein
23	d1v38a_	Alignment	not modelled	6.5	23	**Fold:**SAM domain-like **Superfamily:**SAM/Pointed domain **Family:**SAM (sterile alpha motif) domain
24	c1hk7A_	Alignment	not modelled	6.5	16	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**heat shock protein hsp82; **PDBTitle:** middle domain of hsp90
25	c2dl0A_	Alignment	not modelled	6.4	17	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**sam and sh3 domain-containing protein 1; **PDBTitle:** solution structure of the sam-domain of the sam and sh32 domain containing protein 1
26	c2lc0A_	Alignment	not modelled	6.3	8	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**putative uncharacterized protein tb39.8; **PDBTitle:** rv0020c_nter structure
27	c1x0gA_	Alignment	not modelled	6.2	21	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**isca; **PDBTitle:** crystal structure of isca with the [2fe-2s] cluster
28	c3djmA_	Alignment	not modelled	5.9	19	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein duf427; **PDBTitle:** crystal structure of a protein of unknown function from duf427 family2 (rsph17029_0682) from rhodobacter sphaeroides 2.4.1 at 2.51 a3 resolution
						Fold: Mediator hinge subcomplex-like

29	d1ykha1	Alignment	not modelled	5.8	18	**Superfamily:**Mediator hinge subcomplex-like **Family:**MED7 hinge region
30	c2d2aA_	Alignment	not modelled	5.6	29	**PDB header:**metal transport **Chain:** A: **PDB Molecule:**sufa protein; **PDBTitle:** crystal structure of escherichia coli sufa involved in2 biosynthesis of iron-sulfur clusters
31	d2hsga1	Alignment	not modelled	5.6	13	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**GalR/LacI-like bacterial regulator
32	d1nexa2	Alignment	not modelled	5.2	12	**Fold:**POZ domain **Superfamily:**POZ domain **Family:**BTB/POZ domain
33	d1qpza1	Alignment	not modelled	5.1	19	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**GalR/LacI-like bacterial regulator