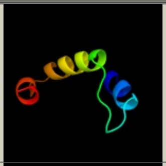
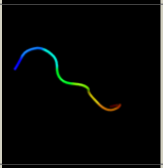
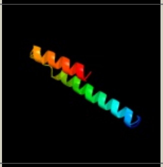
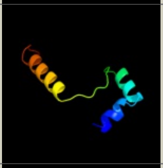
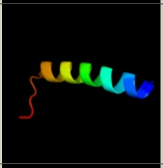
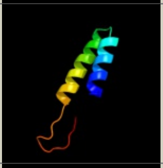
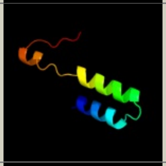
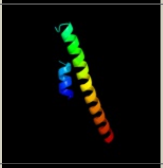
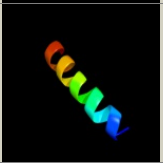
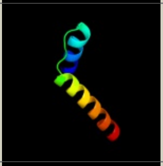
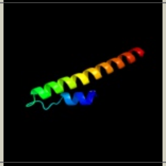
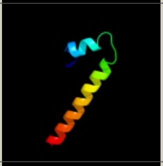
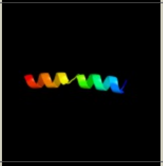
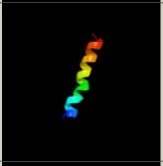
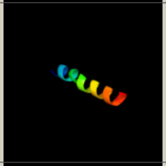
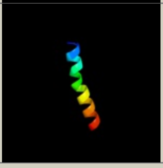
Phyre2

Email	l.a.kelley@imperial.ac.uk
Description	P0A8H6
Date	Thu Jan 5 11:07:51 GMT 2012
Unique Job ID	ae2a70226869e8df

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2k0mA_	Alignment		62.9	21	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** solution nmr structure of the uncharacterized protein from2 rhodospirillum rubrum gene locus rru_a0810. northeast3 structural genomics target rrr43
2	c8tfvA_	Alignment		61.2	56	**PDB header:**antimicrobial **Chain:** A: **PDB Molecule:**protein (thanatin); **PDBTitle:** insect defense peptide
3	c2wl8D_	Alignment		54.1	14	**PDB header:**protein transport **Chain:** D: **PDB Molecule:**peroxisomal biogenesis factor 19; **PDBTitle:** x-ray crystal structure of pex19p
4	c2dvzA_	Alignment		52.2	15	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**putative exported protein; **PDBTitle:** structure of a periplasmic transporter
5	c2qpqC_	Alignment		50.8	31	**PDB header:**transport protein **Chain:** C: **PDB Molecule:**protein bug27; **PDBTitle:** structure of bug27 from bordetella pertussis
6	c2xi7B_	Alignment		38.0	24	**PDB header:**transferase **Chain:** B: **PDB Molecule:**rna polymerase l; **PDBTitle:** n-terminal endonuclease domain of la crosse virus l-protein
7	c2xi5D_	Alignment		37.9	24	**PDB header:**transferase **Chain:** D: **PDB Molecule:**rna polymerase l; **PDBTitle:** n-terminal endonuclease domain of la crosse virus l-protein
8	d1vp7a_	Alignment		32.7	20	**Fold:**Spectrin repeat-like **Superfamily:**XseB-like **Family:**XseB-like
9	d1vp7b_	Alignment		30.8	18	**Fold:**Spectrin repeat-like **Superfamily:**XseB-like **Family:**XseB-like
10	c2hbpA_	Alignment		28.5	31	**PDB header:**endocytosis, protein binding **Chain:** A: **PDB Molecule:**cytoskeleton assembly control protein sla1; **PDBTitle:** solution structure of sla1 homology domain 1
11	d1ug8a_	Alignment		20.3	20	**Fold:**IF3-like **Superfamily:**R3H domain **Family:**R3H domain

12	d1tf5a4	Alignment		19.7	28	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Tandem AAA-ATPase domain
13	d2choa1	Alignment		18.2	13	**Fold:**Hyaluronidase domain-like **Superfamily:**Hyaluronidase post-catalytic domain-like **Family:**Hyaluronidase post-catalytic domain-like
14	c2is9A_	Alignment		17.8	19	**PDB header:**transcription **Chain:** A: **PDB Molecule:**defective in cullin neddylation protein 1; **PDBTitle:** structure of yeast dcn-1
15	c1vp7D_	Alignment		17.8	20	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**exodeoxyribonuclease vii small subunit; **PDBTitle:** crystal structure of exodeoxyribonuclease vii small subunit2 (np_881400.1) from bordetella pertussis at 2.40 a resolution
16	d2c42a2	Alignment		17.4	19	**Fold:**Thiamin diphosphate-binding fold (THDP-binding) **Superfamily:**Thiamin diphosphate-binding fold (THDP-binding) **Family:**PFOR PP module
17	c3h5fC_	Alignment		17.1	39	**PDB header:**de novo protein **Chain:** C: **PDB Molecule:**coil ser l16l-pen; **PDBTitle:** switching the chirality of the metal environment alters the2 coordination mode in designed peptides.
18	c3h5gA_	Alignment		17.1	39	**PDB header:**de novo protein **Chain:** A: **PDB Molecule:**coil ser l16d-pen; **PDBTitle:** switching the chirality of the metal environment alters the2 coordination mode in designed peptides.
19	c3h5gB_	Alignment		17.1	39	**PDB header:**de novo protein **Chain:** B: **PDB Molecule:**coil ser l16d-pen; **PDBTitle:** switching the chirality of the metal environment alters the2 coordination mode in designed peptides.
20	c3h5gC_	Alignment		17.1	39	**PDB header:**de novo protein **Chain:** C: **PDB Molecule:**coil ser l16d-pen; **PDBTitle:** switching the chirality of the metal environment alters the2 coordination mode in designed peptides.
21	c3h5fB_	Alignment	not modelled	17.1	39	**PDB header:**de novo protein **Chain:** B: **PDB Molecule:**coil ser l16l-pen; **PDBTitle:** switching the chirality of the metal environment alters the2 coordination mode in designed peptides.
22	c3h5fA_	Alignment	not modelled	17.1	39	**PDB header:**de novo protein **Chain:** A: **PDB Molecule:**coil ser l16l-pen; **PDBTitle:** switching the chirality of the metal environment alters the2 coordination mode in designed peptides.
23	d1uoua1	Alignment	not modelled	17.0	22	**Fold:**Methionine synthase domain-like **Superfamily:**Nucleoside phosphorylase/phosphoribosyltransferase N-terminal domain **Family:**Nucleoside phosphorylase/phosphoribosyltransferase N-terminal domain
24	d1khda1	Alignment	not modelled	16.4	24	**Fold:**Methionine synthase domain-like **Superfamily:**Nucleoside phosphorylase/phosphoribosyltransferase N-terminal domain **Family:**Nucleoside phosphorylase/phosphoribosyltransferase N-terminal domain
25	c2c3yA_	Alignment	not modelled	16.0	20	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**pyruvate-ferredoxin oxidoreductase; **PDBTitle:** crystal structure of the radical form of2 pyruvate:ferredoxin oxidoreductase from desulfovibrio3 africanus
26	c2xlfA_	Alignment	not modelled	14.9	28	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**sll1785 protein; **PDBTitle:** structure and metal-loading of a soluble periplasm cupro-protein:2 apo-cuca-closed (semet)
27	c3nr7A_	Alignment	not modelled	14.6	20	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**dna-binding protein h-ns; **PDBTitle:** crystal structure of s. typhimurium h-ns 1-83
						Fold: Methionine synthase domain-like **Superfamily:**Nucleoside

28	d2elca1	Alignment	not modelled	14.5	32	phosphorylase/phosphoribosyltransferase N-terminal domain **Family:**Nucleoside phosphorylase/phosphoribosyltransferase N-terminal domain
29	d2ofya1	Alignment	not modelled	14.3	30	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**SinR domain-like
30	d1o17a1	Alignment	not modelled	12.8	18	**Fold:**Methionine synthase domain-like **Superfamily:**Nucleoside phosphorylase/phosphoribosyltransferase N-terminal domain **Family:**Nucleoside phosphorylase/phosphoribosyltransferase N-terminal domain
31	d2acaa1	Alignment	not modelled	12.2	29	**Fold:**CYTH-like phosphatases **Superfamily:**CYTH-like phosphatases **Family:**CYTH domain
32	d1xp3a1	Alignment	not modelled	11.9	20	**Fold:**TIM beta/alpha-barrel **Superfamily:**Xylose isomerase-like **Family:**Endonuclease IV
33	c3ovkD_	Alignment	not modelled	11.7	16	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**aminopeptidase p, xaa-pro dipeptidase; **PDBTitle:** crystal structure of an xxa-pro aminopeptidase from streptococcus2 pyogenes
34	c3sp1B_	Alignment	not modelled	11.0	14	**PDB header:**ligase **Chain:** B: **PDB Molecule:**cysteinyl-trna synthetase; **PDBTitle:** crystal structure of cysteinyl-trna synthetase (cyss) from borrelia2 burgdorferi
35	d1yg2a_	Alignment	not modelled	10.8	16	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**PadR-like
36	d1h3na3	Alignment	not modelled	10.6	26	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Nucleotidylyl transferase **Family:**Class I aminoacyl-tRNA synthetases (RS), catalytic domain
37	c1u0bB_	Alignment	not modelled	10.3	19	**PDB header:**ligase/rna **Chain:** B: **PDB Molecule:**cysteinyl trna; **PDBTitle:** crystal structure of cysteinyl-trna synthetase binary2 complex with trnacys
38	d1tc3c_	Alignment	not modelled	10.3	45	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Recombinase DNA-binding domain
39	c3lutA_	Alignment	not modelled	9.5	18	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**voltage-gated potassium channel subunit beta-2; **PDBTitle:** a structural model for the full-length shaker potassium channel kv1.2
40	d1knza_	Alignment	not modelled	9.3	38	**Fold:**NSP3 homodimer **Superfamily:**NSP3 homodimer **Family:**NSP3 homodimer
41	d3eaua1	Alignment	not modelled	9.0	18	**Fold:**TIM beta/alpha-barrel **Superfamily:**NAD(P)-linked oxidoreductase **Family:**Aldo-keto reductases (NADP)
42	d1v8ga1	Alignment	not modelled	8.7	32	**Fold:**Methionine synthase domain-like **Superfamily:**Nucleoside phosphorylase/phosphoribosyltransferase N-terminal domain **Family:**Nucleoside phosphorylase/phosphoribosyltransferase N-terminal domain
43	c3bq3A_	Alignment	not modelled	8.5	19	**PDB header:**cell cycle, ligase **Chain:** A: **PDB Molecule:**defective in cullin neddylation protein 1; **PDBTitle:** crystal structure of s. cerevisiae dcn1
44	c3bm3A_	Alignment	not modelled	7.8	22	**PDB header:**hydrolase/dna **Chain:** A: **PDB Molecule:**pspgi restriction endonuclease; **PDBTitle:** restriction endonuclease pspgi-substrate dna complex
45	d1biaa1	Alignment	not modelled	7.8	38	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Biotin repressor-like
46	c2zi0B_	Alignment	not modelled	7.4	26	**PDB header:**gene regulation/rna **Chain:** B: **PDB Molecule:**protein 2b; **PDBTitle:** crystal structure of tav2b/sirna complex
47	c3t76A_	Alignment	not modelled	7.4	25	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**transcriptional regulator vanug; **PDBTitle:** crystal structure of transcriptional regulator vanug, form ii
48	c2fjtA_	Alignment	not modelled	7.4	19	**PDB header:**lyase **Chain:** A: **PDB Molecule:**adenylyl cyclase class iv; **PDBTitle:** adenylyl cyclase class iv from yersinia pestis
49	d1oj7a_	Alignment	not modelled	7.1	12	**Fold:**Dehydroquinate synthase-like **Superfamily:**Dehydroquinate synthase-like **Family:**Iron-containing alcohol dehydrogenase
50	c3p2fA_	Alignment	not modelled	7.0	15	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**ahl synthase; **PDBTitle:** crystal structure of tofi in an apo form
51	c3au4B_	Alignment	not modelled	6.9	26	**PDB header:**motor protein/apoptosis **Chain:** B: **PDB Molecule:**netrin receptor dcc; **PDBTitle:** structure of the human myosin-x myth4-ferm cassette bound to its2 specific cargo, dcc
52	c2l9vA_	Alignment	not modelled	6.8	24	**PDB header:**rna binding protein **Chain:** A: **PDB Molecule:**pre-mrna-processing factor 40 homolog a; **PDBTitle:** nmr structure of the ff domain l24a mutant's folding transition state
53	d1dgna_	Alignment	not modelled	6.8	28	**Fold:**DEATH domain **Superfamily:**DEATH domain **Family:**Caspase recruitment domain, CARD

54	d2outa2	Alignment	not modelled	6.6	50	**Fold:**GINS/PriA/YqbF domain **Superfamily:**PriA/YqbF domain **Family:**YqbF N-terminal domain-like
55	c3pzdB_	Alignment	not modelled	6.6	26	**PDB header:**motor protein/apoptosis **Chain:** B: **PDB Molecule:**netrin receptor dcc; **PDBTitle:** structure of the myosin x myth4-ferm/dcc complex
56	d2jmua1	Alignment	not modelled	6.6	30	**Fold:**CYTH-like phosphatases **Superfamily:**CYTH-like phosphatases **Family:**CYTH domain
57	d1j99a_	Alignment	not modelled	6.3	15	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**PAPS sulfotransferase
58	c2outA_	Alignment	not modelled	6.3	50	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**mu-like prophage flumu protein gp35, protein **PDBTitle:** solution structure of hi1506, a novel two domain protein2 from haemophilus influenzae
59	d1a32a_	Alignment	not modelled	6.3	50	**Fold:**S15/NS1 RNA-binding domain **Superfamily:**S15/NS1 RNA-binding domain **Family:**Ribosomal protein S15
60	d2tpta1	Alignment	not modelled	6.2	23	**Fold:**Methionine synthase domain-like **Superfamily:**Nucleoside phosphorylase/phosphoribosyltransferase N-terminal domain **Family:**Nucleoside phosphorylase/phosphoribosyltransferase N-terminal domain
61	c2f5xC_	Alignment	not modelled	6.2	20	**PDB header:**transport protein **Chain:** C: **PDB Molecule:**bugd; **PDBTitle:** structure of periplasmic binding protein bugd
62	d1vs5o1	Alignment	not modelled	5.6	42	**Fold:**S15/NS1 RNA-binding domain **Superfamily:**S15/NS1 RNA-binding domain **Family:**Ribosomal protein S15
63	d1chma1	Alignment	not modelled	5.5	6	**Fold:**Ribonuclease H-like motif **Superfamily:**Creatinase/prolidase N-terminal domain **Family:**Creatinase/prolidase N-terminal domain
64	c3ulwA_	Alignment	not modelled	5.4	25	**PDB header:**ribosomal protein **Chain:** A: **PDB Molecule:**30s ribosomal protein s15; **PDBTitle:** 30s ribosomal protein s15 from campylobacter jejuni
65	d1brwa1	Alignment	not modelled	5.2	27	**Fold:**Methionine synthase domain-like **Superfamily:**Nucleoside phosphorylase/phosphoribosyltransferase N-terminal domain **Family:**Nucleoside phosphorylase/phosphoribosyltransferase N-terminal domain
66	c3cqxD_	Alignment	not modelled	5.1	31	**PDB header:**chaperone **Chain:** D: **PDB Molecule:**bag family molecular chaperone regulator 2; **PDBTitle:** chaperone complex