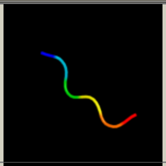
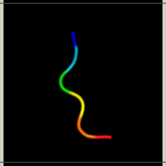
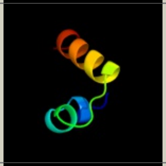
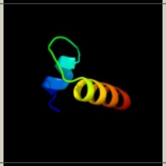
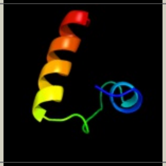
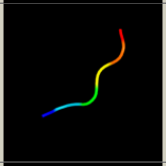
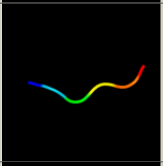
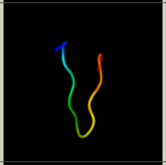
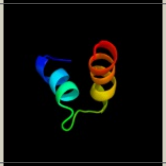
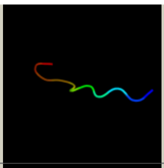
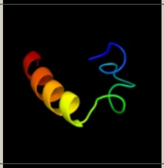
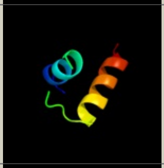
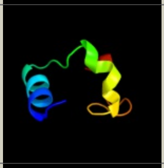
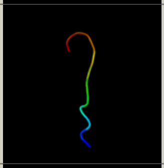
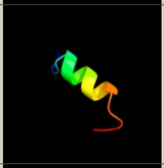
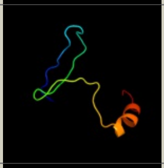
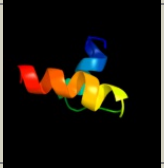
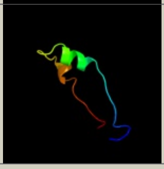
Email	l.a.kelley@imperial.ac.uk
Description	P0AAS0
Date	Thu Jan 5 11:13:38 GMT 2012
Unique Job ID	1e87f017522fc46f

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1df6a_	Alignment		61.5	100	**Fold:**Knottins (small inhibitors, toxins, lectins) **Superfamily:**Cyclotides **Family:**Cycloviolacin
2	c1df6A_	Alignment		61.5	100	**PDB header:**plant protein **Chain:** A: **PDB Molecule:**cycloviolacin o1; **PDBTitle:** 1h nmr solution structure of cycloviolacin o1
3	d2bjca1	Alignment		48.6	19	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**GalR/LacI-like bacterial regulator
4	d1lcda_	Alignment		48.5	16	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**GalR/LacI-like bacterial regulator
5	d1qpza1	Alignment		47.0	19	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**GalR/LacI-like bacterial regulator
6	c2l8nA_	Alignment		45.2	23	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**transcriptional repressor cytr; **PDBTitle:** nmr structure of the cytidine repressor dna binding domain in presence2 of operator half-site dna
7	d1nbja_	Alignment		43.9	100	**Fold:**Knottins (small inhibitors, toxins, lectins) **Superfamily:**Cyclotides **Family:**Cycloviolacin
8	c1nbjA_	Alignment		43.9	100	**PDB header:**plant protein **Chain:** A: **PDB Molecule:**cycloviolacin o1; **PDBTitle:** high-resolution solution structure of cycloviolacin o1
9	c2c3hC_	Alignment		41.0	36	**PDB header:**carbohydrate-binding module **Chain:** C: **PDB Molecule:**alpha-amylase g-6; **PDBTitle:** structure of cbm26 from bacillus halodurans amylase in2 complex with maltose
10	d1uxca_	Alignment		38.6	19	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**GalR/LacI-like bacterial regulator
11	c2b5kA_	Alignment		37.8	55	**PDB header:**antimicrobial protein **Chain:** A: **PDB Molecule:**polyphemusin-1; **PDBTitle:** pv5 nmr solution structure in dpc micelles

12	d2phcb1	Alignment		36.4	36	**Fold:**Cyclophilin-like **Superfamily:**Cyclophilin-like **Family:**PH0987 C-terminal domain-like
13	c2lcvA_	Alignment		31.9	23	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**hth-type transcriptional repressor cytr; **PDBTitle:** structure of the cytidine repressor dna-binding domain; an alternate2 calculation
14	d1efaa1	Alignment		29.6	16	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**GalR/LacI-like bacterial regulator
15	c3bd1B_	Alignment		24.4	14	**PDB header:**transcription **Chain:** B: **PDB Molecule:**cro protein; **PDBTitle:** structure of the cro protein from putative prophage element xfaso 1 in2 xylella fastidiosa strain ann-1
16	c2zp2B_	Alignment		22.1	42	**PDB header:**transferase inhibitor **Chain:** B: **PDB Molecule:**kinase a inhibitor; **PDBTitle:** c-terminal domain of kipi from bacillus subtilis
17	c2vt1A_	Alignment		22.0	22	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**surface presentation of antigens protein spas; **PDBTitle:** crystal structure of the cytoplasmic domain of spa40, the2 specificity switch for the shigella flexneri type iii3 secretion system
18	c3h9xB_	Alignment		20.8	28	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**uncharacterized protein pspto_3016; **PDBTitle:** crystal structure of the pspto_3016 protein from2 pseudomonas syringae, northeast structural genomics3 consortium target psr293
19	d1uxda_	Alignment		19.6	19	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**GalR/LacI-like bacterial regulator
20	c3hgtA_	Alignment		18.5	29	**PDB header:**transcription **Chain:** A: **PDB Molecule:**hda1 complex subunit 3; **PDBTitle:** structural and functional studies of the yeast class ii hda12 hdac complex
21	c2phcB_	Alignment	not modelled	16.6	33	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**uncharacterized protein ph0987; **PDBTitle:** crystal structure of conserved uncharacterized protein ph0987 from2 pyrococcus horikoshii
22	d2ptda_	Alignment	not modelled	16.4	10	**Fold:**TIM beta/alpha-barrel **Superfamily:**PLC-like phosphodiesterases **Family:**Bacterial PLC
23	d2duca1	Alignment	not modelled	16.2	37	**Fold:**Trypsin-like serine proteases **Superfamily:**Trypsin-like serine proteases **Family:**Viral cysteine protease of trypsin fold
24	d2hsga1	Alignment	not modelled	16.0	29	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**GalR/LacI-like bacterial regulator
25	d2elca1	Alignment	not modelled	15.5	20	**Fold:**Methionine synthase domain-like **Superfamily:**Nucleoside phosphorylase/phosphoribosyltransferase N-terminal domain **Family:**Nucleoside phosphorylase/phosphoribosyltransferase N-terminal domain
26	c2rp4C_	Alignment	not modelled	15.5	20	**PDB header:**transcription **Chain:** C: **PDB Molecule:**transcription factor p53; **PDBTitle:** solution structure of the oligomerization domain in dmp53
27	d1vb8a_	Alignment	not modelled	15.0	100	**Fold:**Knottins (small inhibitors, toxins, lectins) **Superfamily:**Cyclotides **Family:**Cycloviolacin
28	c1vb8A_	Alignment	not modelled	15.0	100	**PDB header:**plant protein **Chain:** A: **PDB Molecule:**viola hederacea root peptide 1; **PDBTitle:** solution structure of vhr1, the first cyclotide from root2 tissue

29	c1bdhA_	Alignment	not modelled	14.4	19	**PDB header:**transcription/dna **Chain:** A: **PDB Molecule:**protein (purine repressor); **PDBTitle:** purine repressor mutant-hypoxanthine-palindromic operator2 complex
30	c1bcrA_	Alignment	not modelled	13.2	15	**PDB header:**hydrolase/hydrolase inhibitor **Chain:** A: **PDB Molecule:**serine carboxypeptidase ii; **PDBTitle:** complex of the wheat serine carboxypeptidase, cpdw-ii, with the2 microbial peptide aldehyde inhibitor, antipain, and arginine at room3 temperature
31	d1us7b_	Alignment	not modelled	12.9	8	**Fold:**Hsp90 co-chaperone CDC37 **Superfamily:**Hsp90 co-chaperone CDC37 **Family:**Hsp90 co-chaperone CDC37
32	c1us7B_	Alignment	not modelled	12.9	8	**PDB header:**chaperone **Chain:** B: **PDB Molecule:**hsp90 co-chaperone cdc37; **PDBTitle:** complex of hsp90 and p50
33	c1t3jA_	Alignment	not modelled	12.0	18	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**mitofusin 1; **PDBTitle:** mitofusin domain hr2 v686m/i708m mutant
34	c3odnA_	Alignment	not modelled	11.7	25	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**dally-like protein; **PDBTitle:** the crystal structure of drosophila dally-like protein core domain
35	c2l27A_	Alignment	not modelled	11.3	50	**PDB header:**membrane protein, peptide binding protei **Chain:** A: **PDB Molecule:**seven transmembrane helix receptor; **PDBTitle:** nmr structure of the ecd1 of crf-r1 in complex with a peptide agonist
36	c3e90B_	Alignment	not modelled	11.2	63	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**ns3 protease; **PDBTitle:** west nile vi rus ns2b-ns3protease in complexed with2 inhibitor naph-kkr-h
37	d2ijob1	Alignment	not modelled	11.0	63	**Fold:**Trypsin-like serine proteases **Superfamily:**Trypsin-like serine proteases **Family:**Viral proteases
38	d2fp7b1	Alignment	not modelled	10.9	63	**Fold:**Trypsin-like serine proteases **Superfamily:**Trypsin-like serine proteases **Family:**Viral proteases
39	d1xp8a2	Alignment	not modelled	10.9	16	**Fold:**Anti-LPS factor/recA domain **Superfamily:**RecA protein, C-terminal domain **Family:**RecA protein, C-terminal domain
40	c3n7sB_	Alignment	not modelled	10.7	27	**PDB header:**membrane protein **Chain:** B: **PDB Molecule:**calcitonin gene-related peptide type 1 receptor; **PDBTitle:** crystal structure of the ectodomain complex of the cgrp receptor, a2 class-b gpcr, reveals the site of drug antagonism
41	d2ok5a4	Alignment	not modelled	10.6	50	**Fold:**Complement control module/SCR domain **Superfamily:**Complement control module/SCR domain **Family:**Complement control module/SCR domain
42	c3q7tB_	Alignment	not modelled	10.5	20	**PDB header:**transcription **Chain:** B: **PDB Molecule:**transcriptional regulatory protein; **PDBTitle:** 2.15a resolution structure (i41 form) of the chxr receiver domain from2 chlamydia trachomatis
43	d1f37b_	Alignment	not modelled	10.2	30	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Thioredoxin-like 2Fe-2S ferredoxin
44	c3d23A_	Alignment	not modelled	10.1	26	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**3c-like proteinase; **PDBTitle:** main protease of hcov-hku1
45	c2q6fB_	Alignment	not modelled	9.7	26	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**infectious bronchitis virus (ibv) main protease; **PDBTitle:** crystal structure of infectious bronchitis virus (ibv) main2 protease in complex with a michael acceptor inhibitor n3
46	d1lvoa_	Alignment	not modelled	9.6	26	**Fold:**Trypsin-like serine proteases **Superfamily:**Trypsin-like serine proteases **Family:**Viral cysteine protease of trypsin fold
47	d2vgna2	Alignment	not modelled	9.4	17	**Fold:**Ribonuclease H-like motif **Superfamily:**Translational machinery components **Family:**ERF1/Dom34 middle domain-like
48	c2re3A_	Alignment	not modelled	9.3	27	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of a duf1285 family protein (spo_0140) from2 silicibacter pomeroyi dss-3 at 2.50 a resolution
49	d1q0qa1	Alignment	not modelled	9.2	31	**Fold:**Left-handed superhelix **Superfamily:**1-deoxy-D-xylulose-5-phosphate reductoisomerase, C-terminal domain **Family:**1-deoxy-D-xylulose-5-phosphate reductoisomerase, C-terminal domain
50	d1hfia_	Alignment	not modelled	9.1	50	**Fold:**Complement control module/SCR domain **Superfamily:**Complement control module/SCR domain **Family:**Complement control module/SCR domain
51	d1mo6a2	Alignment	not modelled	8.9	14	**Fold:**Anti-LPS factor/recA domain **Superfamily:**RecA protein, C-terminal domain **Family:**RecA protein, C-terminal domain
52	d2fomb1	Alignment	not modelled	8.8	38	**Fold:**Trypsin-like serine proteases **Superfamily:**Trypsin-like serine proteases **Family:**Viral proteases
53	c2d56A_	Alignment	not modelled	8.6	57	**PDB header:**antibiotic **Chain:** A: **PDB Molecule:**asabf; **PDBTitle:** solution structure of asabf, antibacterial peptide isolated2 from a nematode, ascaris suum
54	d1dgna_	Alignment	not modelled	8.6	11	**Fold:**DEATH domain **Superfamily:**DEATH domain **Family:**Caspase recruitment domain, CARD

55	d1u94a2	Alignment	not modelled	8.5	17	**Fold:**Anti-LPS factor/recA domain **Superfamily:**RecA protein, C-terminal domain **Family:**RecA protein, C-terminal domain
56	d1p9sa_	Alignment	not modelled	8.4	26	**Fold:**Trypsin-like serine proteases **Superfamily:**Trypsin-like serine proteases **Family:**Viral cysteine protease of trypsin fold
57	d1v86a_	Alignment	not modelled	8.3	7	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**Ubiquitin-like **Family:**Ubiquitin-related
58	c1zvvA_	Alignment	not modelled	8.3	29	**PDB header:**transcription/dna **Chain:** A: **PDB Molecule:**glucose-resistance amylase regulator; **PDBTitle:** crystal structure of a ccpa-crh-dna complex
59	c2auvA_	Alignment	not modelled	8.3	29	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**potential nad-reducing hydrogenase subunit; **PDBTitle:** solution structure of hndac : a thioredoxin-like [2fe-2s]2 ferredoxin involved in the nadp-reducing hydrogenase3 complex
60	d1gx5a_	Alignment	not modelled	8.2	31	**Fold:**DNA/RNA polymerases **Superfamily:**DNA/RNA polymerases **Family:**RNA-dependent RNA-polymerase
61	d1r0ka1	Alignment	not modelled	8.1	23	**Fold:**Left-handed superhelix **Superfamily:**1-deoxy-D-xylulose-5-phosphate reductoisomerase, C-terminal domain **Family:**1-deoxy-D-xylulose-5-phosphate reductoisomerase, C-terminal domain
62	d2ffga1	Alignment	not modelled	8.0	38	**Fold:**YkuJ-like **Superfamily:**YkuJ-like **Family:**YkuJ-like
63	d1mdwa_	Alignment	not modelled	7.9	21	**Fold:**Cysteine proteinases **Superfamily:**Cysteine proteinases **Family:**Calpain large subunit, catalytic domain (domain II)
64	c3dl8D_	Alignment	not modelled	7.8	26	**PDB header:**protein transport **Chain:** D: **PDB Molecule:**sece; **PDBTitle:** structure of the complex of aquifex aeolicus secyeg and2 bacillus subtilis seca
65	d1ubea2	Alignment	not modelled	7.7	14	**Fold:**Anti-LPS factor/recA domain **Superfamily:**RecA protein, C-terminal domain **Family:**RecA protein, C-terminal domain
66	c2fgtA_	Alignment	not modelled	7.7	29	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**two-component system yycf/yycg regulatory **PDBTitle:** crystal structure of yych from bacillus subtilis
67	c3lkwA_	Alignment	not modelled	7.4	38	**PDB header:**viral protein,hydrolase **Chain:** A: **PDB Molecule:**fusion protein of nonstructural protein 2b and **PDBTitle:** crystal structure of dengue virus 1 ns2b/ns3 protease active2 site mutant
68	d2fbea1	Alignment	not modelled	7.4	22	**Fold:**Concanavalin A-like lectins/glucanases **Superfamily:**Concanavalin A-like lectins/glucanases **Family:**SPRY domain
69	c1ct9D_	Alignment	not modelled	7.4	30	**PDB header:**ligase **Chain:** D: **PDB Molecule:**asparagine synthetase b; **PDBTitle:** crystal structure of asparagine synthetase b from2 escherichia coli
70	d1nb4a_	Alignment	not modelled	7.3	31	**Fold:**DNA/RNA polymerases **Superfamily:**DNA/RNA polymerases **Family:**RNA-dependent RNA-polymerase
71	d1befa_	Alignment	not modelled	7.3	38	**Fold:**Trypsin-like serine proteases **Superfamily:**Trypsin-like serine proteases **Family:**Viral proteases
72	d1kgda_	Alignment	not modelled	7.2	16	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Nucleotide and nucleoside kinases
73	c2wl1A_	Alignment	not modelled	7.1	44	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**pyrin; **PDBTitle:** pyrin pryspry domain
74	d1jgta2	Alignment	not modelled	7.0	19	**Fold:**Ntn hydrolase-like **Superfamily:**N-terminal nucleophile aminohydrolases (Ntn hydrolases) **Family:**Class II glutamine amidotransferases
75	d1mj4a_	Alignment	not modelled	6.8	44	**Fold:**Cytochrome b5-like heme/steroid binding domain **Superfamily:**Cytochrome b5-like heme/steroid binding domain **Family:**Cytochrome b5
76	d2iwgb1	Alignment	not modelled	6.7	56	**Fold:**Concanavalin A-like lectins/glucanases **Superfamily:**Concanavalin A-like lectins/glucanases **Family:**SPRY domain
77	d1v4sa2	Alignment	not modelled	6.7	28	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**Hexokinase
78	c3rkoA_	Alignment	not modelled	6.5	16	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**nadh-quinone oxidoreductase subunit a; **PDBTitle:** crystal structure of the membrane domain of respiratory complex i from2 e. coli at 3.0 angstrom resolution
79	d1mhqa_	Alignment	not modelled	6.5	8	**Fold:**alpha-alpha superhelix **Superfamily:**ENTH/VHS domain **Family:**VHS domain
80	c3kjxD_	Alignment	not modelled	6.3	19	**PDB header:**transcription regulator **Chain:** D: **PDB Molecule:**transcriptional regulator, laci family; **PDBTitle:** crystal structure of a transcriptional regulator, lacl2 family protein from silicibacter pomeroyi

81	d1u34a_	Alignment	not modelled	6.3	63	**Fold:**Hormone receptor domain **Superfamily:**Hormone receptor domain **Family:**Hormone receptor domain
82	c3ba3A_	Alignment	not modelled	6.2	12	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**pyridoxamine 5'-phosphate oxidase-like protein; **PDBTitle:** crystal structure of pyridoxamine 5'-phosphate oxidase-like protein2 (np_783940.1) from lactobacillus plantarum at 1.55 a resolution
83	c3fotA_	Alignment	not modelled	6.2	24	**PDB header:**transferase **Chain:** A: **PDB Molecule:**15-o-acetyltransferase; **PDBTitle:** structural and functional characterization of tri3 trichothecene 15-o-2 acetyltransferase from fusarium sporotrichioides
84	c1q15A_	Alignment	not modelled	6.2	20	**PDB header:**biosynthetic protein **Chain:** A: **PDB Molecule:**cara; **PDBTitle:** carbapenam synthetase
85	c3cm8B_	Alignment	not modelled	6.0	30	**PDB header:**rna binding protein/transferase **Chain:** B: **PDB Molecule:**peptide from rna-directed rna polymerase **PDBTitle:** a rna polymerase subunit structure from virus
86	c2k50A_	Alignment	not modelled	6.0	21	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**replication factor a related protein; **PDBTitle:** solution nmr structure of the replication factor a related2 protein from methanobacterium thermoautotrophicum.3 northeast structural genomics target tr91a.
87	d1kxoa_	Alignment	not modelled	6.0	8	**Fold:**Lipocalins **Superfamily:**Lipocalins **Family:**Retinol binding protein-like
88	c2bsjB_	Alignment	not modelled	6.0	50	**PDB header:**chaperone **Chain:** B: **PDB Molecule:**chaperone protein syct; **PDBTitle:** native crystal structure of the type iii secretion2 chaperone syct from yersinia enterocolitica
89	d3c2wa2	Alignment	not modelled	5.9	17	**Fold:**Profilin-like **Superfamily:**GAF domain-like **Family:**Phytochrome-specific domain
90	c3kb5A_	Alignment	not modelled	5.8	67	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**tripartite motif-containing protein 72; **PDBTitle:** pry-spry domain of human trim72
91	d1q15a2	Alignment	not modelled	5.7	20	**Fold:**Ntn hydrolase-like **Superfamily:**N-terminal nucleophile aminohydrolases (Ntn hydrolases) **Family:**Class II glutamine amidotransferases
92	c3kzgB_	Alignment	not modelled	5.7	8	**PDB header:**transport protein **Chain:** B: **PDB Molecule:**arginine 3rd transport system periplasmic binding **PDBTitle:** crystal structure of an arginine 3rd transport system2 periplasmic binding protein from legionella pneumophila
93	c1htrP_	Alignment	not modelled	5.6	38	**PDB header:**aspartyl protease **Chain:** P: **PDB Molecule:**progastricsin (pro segment); **PDBTitle:** crystal and molecular structures of human progastricsin at 1.622 angstroms resolution
94	d1scjb_	Alignment	not modelled	5.6	16	**Fold:**Ferredoxin-like **Superfamily:**Protease propeptides/inhibitors **Family:**Subtilase propeptides/inhibitors
95	c1gxsC_	Alignment	not modelled	5.5	17	**PDB header:**lyase **Chain:** C: **PDB Molecule:**p-(s)-hydroxymandelonitrile lyase chain a; **PDBTitle:** crystal structure of hydroxynitrile lyase from sorghum2 bicolor in complex with inhibitor benzoic acid: a novel3 cyanogenic enzyme
96	c3jsrA_	Alignment	not modelled	5.5	21	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**all0216 protein; **PDBTitle:** x-ray structure of all0216 protein from nostoc sp. pcc 7120 at the2 resolution 1.8a. northeast structural genomics consortium target3 nsr236
97	c1m1zB_	Alignment	not modelled	5.5	44	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**beta-lactam synthetase; **PDBTitle:** beta-lactam synthetase apo enzyme
98	c3fcnA_	Alignment	not modelled	5.4	36	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**an alpha-helical protein of unknown function (pfam01724); **PDBTitle:** crystal structure of an alpha-helical protein of unknown function2 (rru_a3208) from rhodospirillum rubrum atcc 11170 at 1.45 a3 resolution
99	d1oqja_	Alignment	not modelled	5.1	14	**Fold:**SAND domain-like **Superfamily:**SAND domain-like **Family:**SAND domain