Email	l.a.kelley@imperial.ac.uk
Description	P13959
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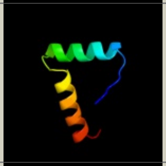
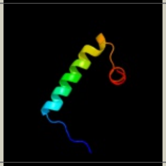
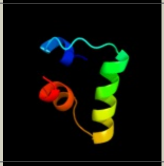
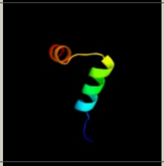
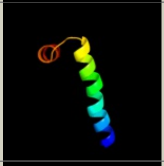
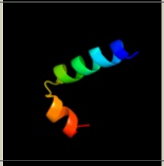
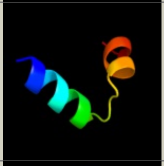
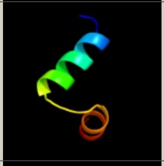
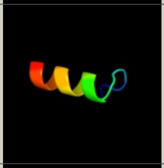
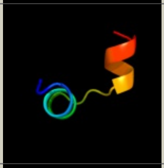
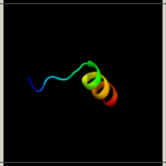
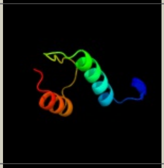
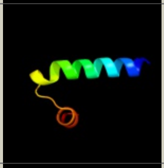
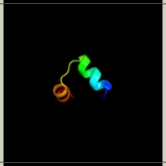
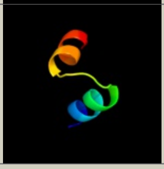
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2kelB_	Alignment		78.8	25	**PDB header:**transcription repressor **Chain:** B: **PDB Molecule:**uncharacterized protein 56b; **PDBTitle:** structure of the transcription regulator svtr from the2 hyperthermophilic archaeal virus sirv1
2	c2k29A_	Alignment		71.4	20	**PDB header:**transcription **Chain:** A: **PDB Molecule:**antitoxin relb; **PDBTitle:** structure of the dbd domain of e. coli antitoxin relb
3	d1rioa_	Alignment		65.0	34	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**Phage repressors
4	c2kebA_	Alignment		62.1	24	**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
5	c3op9A_	Alignment		51.6	37	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**pli0006 protein; **PDBTitle:** crystal structure of transcriptional regulator from listeria innocua
6	d1r69a_	Alignment		45.3	22	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**Phage repressors
7	c3f6wE_	Alignment		44.9	33	**PDB header:**dna binding protein **Chain:** E: **PDB Molecule:**xre-family like protein; **PDBTitle:** xre-family like protein from pseudomonas syringae pv. tomato str.2 dc3000
8	d1y9qa1	Alignment		43.6	10	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**Probable transcriptional regulator VC1968, N-terminal domain
9	d1b0na2	Alignment		43.1	22	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**SinR domain-like
10	c2xcjB_	Alignment		42.9	8	**PDB header:**viral protein **Chain:** B: **PDB Molecule:**c protein; **PDBTitle:** crystal structure of p2 c, the immunity repressor of2 temperate e. coli phage p2
11	d1sq8a_	Alignment		39.9	22	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**Phage repressors

12	c3cecA_	Alignment		39.7	24	**PDB header:**transcription **Chain:** A: **PDB Molecule:**putative antidote protein of plasmid maintenance system; **PDBTitle:** crystal structure of a putative antidote protein of plasmid2 maintenance system (npun_f2943) from nostoc punctiforme pcc 73102 at3 1.60 a resolution
13	c2hydB_	Alignment		39.6	35	**PDB header:**transport protein **Chain:** B: **PDB Molecule:**abc transporter homolog; **PDBTitle:** multidrug abc transporter sav1866
14	c3bs3A_	Alignment		38.3	19	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**putative dna-binding protein; **PDBTitle:** crystal structure of a putative dna-binding protein from bacteroides2 fragilis
15	c2yl4A_	Alignment		37.8	35	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**atp-binding cassette sub-family b member 10, **PDBTitle:** structure of the human mitochondrial abc transporter, abcb10
16	c3b7hA_	Alignment		37.0	17	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**prophage lp1 protein 11; **PDBTitle:** crystal structure of the prophage lp1 protein 11
17	c2yyzA_	Alignment		36.9	25	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**sugar abc transporter, atp-binding protein; **PDBTitle:** crystal structure of sugar abc transporter, atp-binding protein
18	d1lmb3_	Alignment		36.9	22	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**Phage repressors
19	d1adra_	Alignment		35.9	17	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**Phage repressors
20	c3fmyA_	Alignment		35.2	14	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**hth-type transcriptional regulator mqsa **PDBTitle:** structure of the c-terminal domain of the e. coli protein2 mqsa (ygit/b3021)
21	c2kpjA_	Alignment	not modelled	34.7	15	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**sos-response transcriptional repressor, lexa; **PDBTitle:** solution structure of protein sos-response transcriptional2 repressor, lexa from eubacterium rectale. northeast3 structural genomics consortium target err9a
22	c2ewtA_	Alignment	not modelled	34.4	21	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**putative dna-binding protein; **PDBTitle:** crystal structure of the dna-binding domain of bldd
23	d1y7ya1	Alignment	not modelled	34.3	25	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**SinR domain-like
24	c3t76A_	Alignment	not modelled	34.0	14	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**transcriptional regulator vanug; **PDBTitle:** crystal structure of transcriptional regulator vanug, form ii
25	d1h1js_	Alignment	not modelled	33.6	13	**Fold:**LEM/SAP HeH motif **Superfamily:**SAP domain **Family:**SAP domain
26	c3b5xB_	Alignment	not modelled	33.6	35	**PDB header:**membrane protein **Chain:** B: **PDB Molecule:**lipid a export atp-binding/permease protein msba; **PDBTitle:** crystal structure of msba from vibrio cholerae
27	d2hzab1	Alignment	not modelled	33.3	16	**Fold:**Ribbon-helix-helix **Superfamily:**Ribbon-helix-helix **Family:**CopG-like
28	c3b5wE_	Alignment	not modelled	31.8	35	**PDB header:**membrane protein **Chain:** E: **PDB Molecule:**lipid a export atp-binding/permease protein msba; **PDBTitle:** crystal structure of eschericia coli msba

29	c2ef8A_	Alignment	not modelled	30.7	27	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**putative transcription factor; **PDBTitle:** crystal structure of c.ecot38is
30	c3omtA_	Alignment	not modelled	29.9	33	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** putative antitoxin component, chu_2935 protein, from xre family from2 prevotella buccae.
31	c2kslA_	Alignment	not modelled	27.8	42	**PDB header:**toxin **Chain:** A: **PDB Molecule:**u1-agatoxin-ta1a; **PDBTitle:** structure of the insecticidal toxin taitx-1
32	c3kk4B_	Alignment	not modelled	27.6	24	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**uncharacterized protein bp1543; **PDBTitle:** uncharacterized protein bp1543 from bordetella pertussis tohama i
33	c3h8kB_	Alignment	not modelled	26.1	40	**PDB header:**ligase **Chain:** B: **PDB Molecule:**autocrine motility factor receptor, isoform 2; **PDBTitle:** crystal structure of ube2g2 complxed with the g2br domain of2 gp78 at 1.8-a resolution
34	d2b5aa1	Alignment	not modelled	25.7	13	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**SinR domain-like
35	c3lisB_	Alignment	not modelled	24.5	24	**PDB header:**transcription **Chain:** B: **PDB Molecule:**csp231i c protein; **PDBTitle:** crystal structure of the restriction-modification controller protein2 c.csp231i (monoclinic form)
36	d2bj7a1	Alignment	not modelled	23.7	21	**Fold:**Ribbon-helix-helix **Superfamily:**Ribbon-helix-helix **Family:**CopG-like
37	c1y9qA_	Alignment	not modelled	23.6	11	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**transcriptional regulator, hth_3 family; **PDBTitle:** crystal structure of hth_3 family transcriptional regulator2 from vibrio cholerae
38	d2hzaa1	Alignment	not modelled	22.9	18	**Fold:**Ribbon-helix-helix **Superfamily:**Ribbon-helix-helix **Family:**CopG-like
39	d2croa_	Alignment	not modelled	21.6	26	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**Phage repressors
40	c2k5jB_	Alignment	not modelled	20.6	13	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**uncharacterized protein yiif; **PDBTitle:** solution structure of protein yiif from shigella flexneri2 serotype 5b (strain 8401) . northeast structural genomics3 consortium target sft1
41	c3dnvB_	Alignment	not modelled	19.9	22	**PDB header:**transcription/dna **Chain:** B: **PDB Molecule:**hth-type transcriptional regulator hipb; **PDBTitle:** mdt protein
42	d1ehia2	Alignment	not modelled	19.9	25	**Fold:**ATP-grasp **Superfamily:**Glutathione synthetase ATP-binding domain-like **Family:**ATP-binding domain of peptide synthetases
43	d1x57a1	Alignment	not modelled	19.7	15	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**EDF1-like
44	c1kcfB_	Alignment	not modelled	19.6	15	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**hypothetical 30.2 kd protein c25g10.02 in **PDBTitle:** crystal structure of the yeast mitochondrial holliday2 junction resolvase, ydc2
45	d1jj7a_	Alignment	not modelled	19.3	23	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**ABC transporter ATPase domain-like
46	c1q5vB_	Alignment	not modelled	19.0	18	**PDB header:**transcription **Chain:** B: **PDB Molecule:**nickel responsive regulator; **PDBTitle:** apo-nikr
47	c1oxtB_	Alignment	not modelled	18.1	19	**PDB header:**transport protein **Chain:** B: **PDB Molecule:**abc transporter, atp binding protein; **PDBTitle:** crystal structure of glcv, the abc-atpase of the glucose abc2 transporter from sulfolobus solfataricus
48	c3eusB_	Alignment	not modelled	18.0	39	**PDB header:**dna binding protein **Chain:** B: **PDB Molecule:**dna-binding protein; **PDBTitle:** the crystal structure of the dna binding protein from silicibacter2 pomeroyi
49	c2fjrB_	Alignment	not modelled	17.6	18	**PDB header:**transcription regulator **Chain:** B: **PDB Molecule:**repressor protein ci; **PDBTitle:** crystal structure of bacteriophage 186
50	c2ca9B_	Alignment	not modelled	17.5	21	**PDB header:**transcriptional regulation **Chain:** B: **PDB Molecule:**putative nickel-responsive regulator; **PDBTitle:** apo-nikr from helicobacter pylori in closed trans-2 conformation
51	c3trbA_	Alignment	not modelled	17.4	29	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**virulence-associated protein i; **PDBTitle:** structure of an addiction module antidote protein of a higa (higa)2 family from coxiella burnetii
52	c2uwjG_	Alignment	not modelled	17.1	36	**PDB header:**chaperone **Chain:** G: **PDB Molecule:**type iii export protein pscg; **PDBTitle:** structure of the heterotrimeric complex which regulates2 type iii secretion needle formation
53	c2ebyA_	Alignment	not modelled	16.7	21	**PDB header:**transcription **Chain:** A: **PDB Molecule:**putative hth-type transcriptional regulator ybaq; **PDBTitle:** crystal structure of a hypothetical protein from e. coli
54	c2it1B_	Alignment	not modelled	15.8	23	**PDB header:**transport protein **Chain:** B: **PDB Molecule:**362aa long hypothetical maltose/maltodextrin

						PDBTitle: structure of ph0203 protein from pyrococcus horikoshii
55	d1g2912	Alignment	not modelled	15.6	27	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**ABC transporter ATPase domain-like
56	c2kvuA_	Alignment	not modelled	15.3	13	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**mkl/myocardin-like protein 1; **PDBTitle:** solution nmr structure of sap domain of mkl/myocardin-like2 protein 1 from h.sapiens, northeast structural genomics3 consortium target target hr4547e
57	d2a6ca1	Alignment	not modelled	14.9	32	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**NE1354
58	d1utxa_	Alignment	not modelled	14.8	19	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**SinR domain-like
59	c3fvqB_	Alignment	not modelled	14.7	19	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**fe(3+) ions import atp-binding protein fbpc; **PDBTitle:** crystal structure of the nucleotide binding domain fbpc2 complexed with atp
60	c3clcC_	Alignment	not modelled	14.7	18	**PDB header:**transcription regulator/dna **Chain:** C: **PDB Molecule:**regulatory protein; **PDBTitle:** crystal structure of the restriction-modification controller protein2 c.esp1396i tetramer in complex with its natural 35 base-pair operator
61	d1e4ea2	Alignment	not modelled	14.3	24	**Fold:**ATP-grasp **Superfamily:**Glutathione synthetase ATP-binding domain-like **Family:**ATP-binding domain of peptide synthetases
62	c1s16B_	Alignment	not modelled	13.8	15	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**topoisomerase iv subunit b; **PDBTitle:** crystal structure of e. coli topoisomerase iv pare 43kda subunit2 complexed with adpnp
63	c3mlfC_	Alignment	not modelled	13.6	23	**PDB header:**transcription regulator **Chain:** C: **PDB Molecule:**transcriptional regulator; **PDBTitle:** putative transcriptional regulator from staphylococcus aureus.
64	c1z47B_	Alignment	not modelled	13.6	25	**PDB header:**ligand binding protein **Chain:** B: **PDB Molecule:**putative abc-transporter atp-binding protein; **PDBTitle:** structure of the atpase subunit cysa of the putative2 sulfate atp-binding cassette (abc) transporter from3 alicyclobacillus acidocaldarius
65	c3bdnB_	Alignment	not modelled	13.2	29	**PDB header:**transcription/dna **Chain:** B: **PDB Molecule:**lambda repressor; **PDBTitle:** crystal structure of the lambda repressor
66	d1llib_	Alignment	not modelled	13.0	21	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**Phage repressors
67	c2d62A_	Alignment	not modelled	12.6	21	**PDB header:**sugar binding protein **Chain:** A: **PDB Molecule:**multiple sugar-binding transport atp-binding **PDBTitle:** crystal structure of multiple sugar binding transport atp-2 binding protein
68	c3ivpD_	Alignment	not modelled	12.5	18	**PDB header:**dna binding protein **Chain:** D: **PDB Molecule:**putative transposon-related dna-binding protein; **PDBTitle:** the structure of a possible transposon-related dna-binding protein2 from clostridium difficile 630.
69	c2o38A_	Alignment	not modelled	12.1	26	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein; **PDBTitle:** putative xre family transcriptional regulator
70	d2o38a1	Alignment	not modelled	12.1	26	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**NE1354
71	d2r1jl1	Alignment	not modelled	11.9	17	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**Phage repressors
72	c3g5uB_	Alignment	not modelled	11.7	35	**PDB header:**membrane protein **Chain:** B: **PDB Molecule:**multidrug resistance protein 1a; **PDBTitle:** structure of p-glycoprotein reveals a molecular basis for2 poly-specific drug binding
73	c1b0nA_	Alignment	not modelled	11.7	22	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**protein (sinr protein); **PDBTitle:** sinr protein/sini protein complex
74	c3f52A_	Alignment	not modelled	11.4	22	**PDB header:**transcription activator **Chain:** A: **PDB Molecule:**clp gene regulator (clgr); **PDBTitle:** crystal structure of the clp gene regulator clgr from c. glutamicum
75	c2bj3D_	Alignment	not modelled	11.1	21	**PDB header:**transcription **Chain:** D: **PDB Molecule:**nickel responsive regulator; **PDBTitle:** nikr-apo
76	c3kxaD_	Alignment	not modelled	10.9	14	**PDB header:**structural genomics, unknown function **Chain:** D: **PDB Molecule:**putative uncharacterized protein; **PDBTitle:** crystal structure of ngo0477 from neisseria gonorrhoeae
77	c1vciA_	Alignment	not modelled	10.9	19	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**sugar-binding transport atp-binding protein; **PDBTitle:** crystal structure of the atp-binding cassette of multisugar2 transporter from pyrococcus horikoshii ot3 complexed with3 atp
78	d1wgna_	Alignment	not modelled	10.6	33	**Fold:**RuvA C-terminal domain-like **Superfamily:**UBA-like **Family:**UBA domain

79	d2icta1	Alignment	not modelled	9.9	19	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**SinR domain-like
80	c1e4eB_	Alignment	not modelled	9.8	23	**PDB header:**ligase **Chain:** B: **PDB Molecule:**vancomycin/teicoplanin a-type resistance protein vana; **PDBTitle:** d-alanyl-d-lacate ligase
81	c3tqtB_	Alignment	not modelled	9.5	22	**PDB header:**ligase **Chain:** B: **PDB Molecule:**d-alanine--d-alanine ligase; **PDBTitle:** structure of the d-alanine-d-alanine ligase from coxiella burnetii
82	c3i12A_	Alignment	not modelled	9.5	26	**PDB header:**ligase **Chain:** A: **PDB Molecule:**d-alanine-d-alanine ligase a; **PDBTitle:** the crystal structure of the d-alanyl-alanine synthetase a from2 salmonella enterica subsp. enterica serovar typhimurium str. lt2
83	c3adjA_	Alignment	not modelled	9.3	22	**PDB header:**gene regulation **Chain:** A: **PDB Molecule:**f21m12.9 protein; **PDBTitle:** structure of arabidopsis hyl1 and its molecular implications for mirna2 processing
84	c2i80B_	Alignment	not modelled	9.2	26	**PDB header:**ligase **Chain:** B: **PDB Molecule:**d-alanine-d-alanine ligase; **PDBTitle:** allosteric inhibition of staphylococcus aureus d-alanine:d-alanine2 ligase revealed by crystallographic studies
85	c3gm8A_	Alignment	not modelled	8.2	18	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**glycoside hydrolase family 2, candidate beta-glycosidase; **PDBTitle:** crystal structure of a beta-glycosidase from bacteroides vulgatus
86	c2w62A_	Alignment	not modelled	8.1	16	**PDB header:**transferase **Chain:** A: **PDB Molecule:**glycolipid-anchored surface protein 2; **PDBTitle:** saccharomyces cerevisiae gas2p in complex with2 laminaripentaose
87	d1u5ta2	Alignment	not modelled	8.1	14	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Vacuolar sorting protein domain
88	c3se7A_	Alignment	not modelled	8.1	16	**PDB header:**ligase **Chain:** A: **PDB Molecule:**vana; **PDBTitle:** ancient vana
89	c1wwuA_	Alignment	not modelled	7.8	38	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein flj21935; **PDBTitle:** solution structure of the sam_pnt domain of human protein2 flj21935
90	d1tc3c_	Alignment	not modelled	7.7	21	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Recombinase DNA-binding domain
91	d3d31a2	Alignment	not modelled	7.7	27	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**ABC transporter ATPase domain-like
92	d1ayea2	Alignment	not modelled	7.4	10	**Fold:**Ferredoxin-like **Superfamily:**Protease propeptides/inhibitors **Family:**Pancreatic carboxypeptidase, activation domain
93	c2krfB_	Alignment	not modelled	6.9	13	**PDB header:**transcription **Chain:** B: **PDB Molecule:**transcriptional regulatory protein coma; **PDBTitle:** nmr solution structure of the dna binding domain of competence protein2 a
94	d1pcaa1	Alignment	not modelled	6.9	7	**Fold:**Ferredoxin-like **Superfamily:**Protease propeptides/inhibitors **Family:**Pancreatic carboxypeptidase, activation domain
95	d1pf4a1	Alignment	not modelled	6.8	33	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**ABC transporter ATPase domain-like
96	d1rfza_	Alignment	not modelled	6.7	23	**Fold:**YutG-like **Superfamily:**YutG-like **Family:**YutG-like
97	d1v43a3	Alignment	not modelled	6.7	19	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**ABC transporter ATPase domain-like
98	c2k9iB_	Alignment	not modelled	6.5	28	**PDB header:**dna binding protein **Chain:** B: **PDB Molecule:**plasmid prn1, complete sequence; **PDBTitle:** nmr structure of plasmid copy control protein orf56 from2 sulfolobus islandicus
99	c2pzfB_	Alignment	not modelled	6.4	33	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**cystic fibrosis transmembrane conductance regulator; **PDBTitle:** minimal human cftr first nucleotide binding domain as a head-to-tail2 dimer with delta f508