Phyre2

Email	l.a.kelley@imperial.ac.uk
Description	P0A8A2
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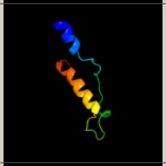
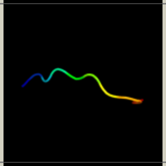
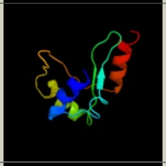
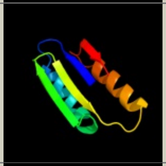
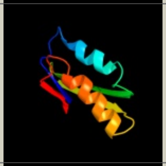
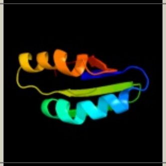
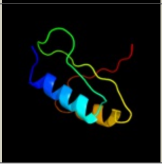
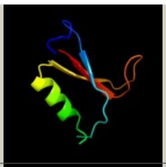
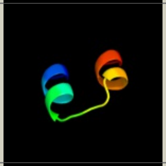
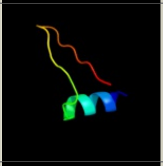
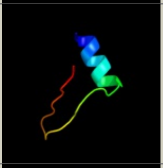
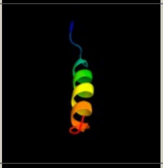
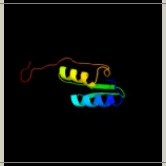
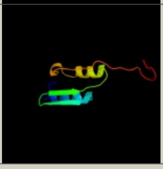
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1lfpa_	Alignment		100.0	36	**Fold:**YebC-like **Superfamily:**YebC-like **Family:**YebC-like
2	d1kona_	Alignment		100.0	39	**Fold:**YebC-like **Superfamily:**YebC-like **Family:**YebC-like
3	d1mw7a_	Alignment		100.0	32	**Fold:**YebC-like **Superfamily:**YebC-like **Family:**YebC-like
4	c2jsxA_	Alignment		58.9	18	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**protein napd; **PDBTitle:** solution structure of the e. coli tat proofreading2 chaperone protein napd
5	c2zf8A_	Alignment		43.0	13	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**component of sodium-driven polar flagellar motor; **PDBTitle:** crystal structure of moty
6	c2vsaA_	Alignment		35.3	55	**PDB header:**toxin **Chain:** A: **PDB Molecule:**mosquitocidal toxin; **PDBTitle:** structure and mode of action of a mosquitocidal holotoxin
7	c2dhaA_	Alignment		35.2	12	**PDB header:**rna binding protein **Chain:** A: **PDB Molecule:**flj20171 protein; **PDBTitle:** solution structure of the second rna recognition motif in2 hypothetical protein flj201171
8	d2cyya2	Alignment		33.9	10	**Fold:**Ferredoxin-like **Superfamily:**Dimeric alpha+beta barrel **Family:**Lrp/AsnC-like transcriptional regulator C-terminal domain
9	c3ibwA_	Alignment		32.7	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**gtp pyrophosphokinase; **PDBTitle:** crystal structure of the act domain from gtp2 pyrophosphokinase of chlorobium tepidum. northeast3 structural genomics consortium target ctr148a
10	c2zbcH_	Alignment		32.6	12	**PDB header:**transcription **Chain:** H: **PDB Molecule:**83aa long hypothetical transcriptional regulator asnc; **PDBTitle:** crystal structure of sts042, a stand-alone ram module protein, from2 hyperthermophilic archaeon sulfolobus tokodaii strain7.
11	d1kkha2	Alignment		31.9	14	**Fold:**Ferredoxin-like **Superfamily:**GHMP Kinase, C-terminal domain **Family:**Mevalonate kinase

12	c1fpqA_	Alignment		31.6	27	**PDB header:**transferase **Chain:** A: **PDB Molecule:**isoliquiritigenin 2'-o-methyltransferase; **PDBTitle:** crystal structure analysis of selenomethionine substituted chalcone o-2 methyltransferase
13	d1ewqa2	Alignment		31.4	39	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**ABC transporter ATPase domain-like
14	d1weya_	Alignment		31.3	17	**Fold:**Ferredoxin-like **Superfamily:**RNA-binding domain, RBD **Family:**Canonical RBD
15	c2nyiB_	Alignment		31.2	14	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**unknown protein; **PDBTitle:** crystal structure of an unknown protein from galdieria2 sulphuraria
16	d1p65a_	Alignment		31.0	26	**Fold:**Nucleocapsid protein dimerization domain **Superfamily:**Nucleocapsid protein dimerization domain **Family:**Arterivirus nucleocapsid protein
17	c1p65A_	Alignment		31.0	26	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**nucleocapsid protein; **PDBTitle:** crystal structure of the nucleocapsid protein of porcine reproductive2 and respiratory syndrome virus (prrsv)
18	c3k2qA_	Alignment		29.2	24	**PDB header:**transferase **Chain:** A: **PDB Molecule:**pyrophosphate-dependent phosphofructokinase; **PDBTitle:** crystal structure of pyrophosphate-dependent2 phosphofructokinase from marinobacter aquaeolei, northeast3 structural genomics consortium target mqr88
19	d2f1fa2	Alignment		26.5	14	**Fold:**Ferredoxin-like **Superfamily:**ACT-like **Family:**IlvH-like
20	d2pc6a1	Alignment		25.4	20	**Fold:**Ferredoxin-like **Superfamily:**ACT-like **Family:**IlvH-like
21	d2ex4a1	Alignment	not modelled	23.4	30	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**AD-003 protein-like
22	d1ub9a_	Alignment	not modelled	23.1	17	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**MarR-like transcriptional regulators
23	d1k47a2	Alignment	not modelled	22.9	10	**Fold:**Ferredoxin-like **Superfamily:**GHMP Kinase, C-terminal domain **Family:**Phosphomevalonate kinase (PMK)
24	c2b8kD_	Alignment	not modelled	22.9	21	**PDB header:**transferase **Chain:** D: **PDB Molecule:**dna-directed rna polymerase ii 32 kda **PDBTitle:** 12-subunit rna polymerase ii
25	c3l7pA_	Alignment	not modelled	22.3	23	**PDB header:**transcription **Chain:** A: **PDB Molecule:**putative nitrogen regulatory protein pii; **PDBTitle:** crystal structure of smu.1657c, putative nitrogen regulatory protein2 pii from streptococcus mutans
26	c3s01A_	Alignment	not modelled	22.2	14	**PDB header:**rna binding protein **Chain:** A: **PDB Molecule:**heterogeneous nuclear ribonucleoprotein l; **PDBTitle:** crystal structure of a heterogeneous nuclear ribonucleoprotein l2 (hnrpl) from mus musculus at 2.15 a resolution
27	d1kkca2	Alignment	not modelled	22.2	32	**Fold:**Fe,Mn superoxide dismutase (SOD), C-terminal domain **Superfamily:**Fe,Mn superoxide dismutase (SOD), C-terminal domain **Family:**Fe,Mn superoxide dismutase (SOD), C-terminal domain
28	d1gtra1	Alignment	not modelled	22.0	13	**Fold:**Ribosomal protein L25-like **Superfamily:**Ribosomal protein L25-like **Family:**Gln-tRNA synthetase (GlnRS), C-terminal (anticodon-binding) domain

29	c3lk7A_	Alignment	not modelled	21.2	18	**PDB header:**ligase **Chain:** A: **PDB Molecule:**udp-n-acetylmuramoylalanine--d-glutamate ligase; **PDBTitle:** the crystal structure of udp-n-acetylmuramoylalanine-d-2 glutamate (murd) ligase from streptococcus agalactiae to3 1.5a
30	d1wb9a2	Alignment	not modelled	21.1	44	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**ABC transporter ATPase domain-like
31	d2nzca1	Alignment	not modelled	20.9	11	**Fold:**Ferredoxin-like **Superfamily:**ACT-like **Family:**TM1266-like
32	d1jr3d2	Alignment	not modelled	20.7	7	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Extended AAA-ATPase domain
33	d1i1ga2	Alignment	not modelled	19.9	15	**Fold:**Ferredoxin-like **Superfamily:**Dimeric alpha+beta barrel **Family:**Lrp/AsnC-like transcriptional regulator C-terminal domain
34	d4pfka_	Alignment	not modelled	19.9	26	**Fold:**Phosphofructokinase **Superfamily:**Phosphofructokinase **Family:**Phosphofructokinase
35	c2e1cA_	Alignment	not modelled	19.5	10	**PDB header:**transcription/dna **Chain:** A: **PDB Molecule:**putative hth-type transcriptional regulator ph1519; **PDBTitle:** structure of putative hth-type transcriptional regulator ph1519/dna2 complex
36	d2ev0a2	Alignment	not modelled	19.1	28	**Fold:**Iron-dependent repressor protein, dimerization domain **Superfamily:**Iron-dependent repressor protein, dimerization domain **Family:**Iron-dependent repressor protein, dimerization domain
37	d1fima_	Alignment	not modelled	19.0	7	**Fold:**Tautomerase/MIF **Superfamily:**Tautomerase/MIF **Family:**MIF-related
38	d1y14a_	Alignment	not modelled	18.7	21	**Fold:**SAM domain-like **Superfamily:**HRDC-like **Family:**RNA polymerase II subunit RBP4 (RpoF)
39	c1kyzC_	Alignment	not modelled	18.7	30	**PDB header:**transferase **Chain:** C: **PDB Molecule:**caffeic acid 3-o-methyltransferase; **PDBTitle:** crystal structure analysis of caffeic acid/5-hydroxyferulic2 acid 3/5-o-methyltransferase ferulic acid complex
40	c3dx5A_	Alignment	not modelled	18.6	13	**PDB header:**lyase **Chain:** A: **PDB Molecule:**uncharacterized protein asbf; **PDBTitle:** crystal structure of the probable 3-dhs dehydratase asbf involved in2 the petrobactin synthesis from bacillus anthracis
41	c3canA_	Alignment	not modelled	18.4	22	**PDB header:**lyase activator **Chain:** A: **PDB Molecule:**pyruvate-formate lyase-activating enzyme; **PDBTitle:** crystal structure of a domain of pyruvate-formate lyase-activating2 enzyme from bacteroides vulgatus atcc 8482
42	d1p9qc2	Alignment	not modelled	18.2	13	**Fold:**FYSH domain **Superfamily:**FYSH domain **Family:**Hypothetical protein AF0491, N-terminal domain
43	d1ul3a_	Alignment	not modelled	17.9	19	**Fold:**Ferredoxin-like **Superfamily:**GlnB-like **Family:**Prokaryotic signal transducing protein
44	d2r9ga1	Alignment	not modelled	17.8	13	**Fold:**post-AAA+ oligomerization domain-like **Superfamily:**post-AAA+ oligomerization domain-like **Family:**MgsA/YrvN C-terminal domain-like
45	d2auna2	Alignment	not modelled	17.5	15	**Fold:**Flavodoxin-like **Superfamily:**Class I glutamine amidotransferase-like **Family:**LD-carboxypeptidase A N-terminal domain-like
46	c2cveA_	Alignment	not modelled	17.2	13	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein ttha1053; **PDBTitle:** crystal structure of a conserved hypothetical protein tt1547 from2 thermus thermophilus hb8
47	d1qmha1	Alignment	not modelled	16.7	29	**Fold:**Thioredoxin fold **Superfamily:**RNA 3'-terminal phosphate cyclase, RPTC, insert domain **Family:**RNA 3'-terminal phosphate cyclase, RPTC, insert domain
48	c1ewrA_	Alignment	not modelled	16.6	39	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**dna mismatch repair protein muts; **PDBTitle:** crystal structure of taq muts
49	d2cg4a2	Alignment	not modelled	16.4	13	**Fold:**Ferredoxin-like **Superfamily:**Dimeric alpha+beta barrel **Family:**Lrp/AsnC-like transcriptional regulator C-terminal domain
50	d3ctda1	Alignment	not modelled	16.2	13	**Fold:**post-AAA+ oligomerization domain-like **Superfamily:**post-AAA+ oligomerization domain-like **Family:**MgsA/YrvN C-terminal domain-like
51	c2k6xA_	Alignment	not modelled	15.8	28	**PDB header:**transcription **Chain:** A: **PDB Molecule:**rna polymerase sigma factor rpod; **PDBTitle:** autoregulation of a group 1 bacterial sigma factor involves2 the formation of a region 1.1- induced compacted structure
52	c1d1rA_	Alignment	not modelled	15.5	21	**PDB header:**structural genomics **Chain:** A: **PDB Molecule:**hypothetical 11.4 kd protein ycih in pyrf-osmb **PDBTitle:** nmr solution structure of the product of the e. coli ycih2 gene.
53	d1d1ra_	Alignment	not modelled	15.5	21	**Fold:**eIF1-like **Superfamily:**eIF1-like **Family:**eIF1-like
						Fold: Ferredoxin-like

54	d1cc8a_	Alignment	not modelled	15.4	23	**Superfamily:**HMA, heavy metal-associated domain **Family:**HMA, heavy metal-associated domain
55	c1zxxA_	Alignment	not modelled	15.4	22	**PDB header:**transferase **Chain:** A: **PDB Molecule:**6-phosphofructokinase; **PDBTitle:** the crystal structure of phosphofructokinase from lactobacillus2 delbrueckii
56	c1qr6A_	Alignment	not modelled	15.3	13	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**malic enzyme 2; **PDBTitle:** human mitochondrial nad(p)-dependent malic enzyme
57	d3bgea1	Alignment	not modelled	15.3	13	**Fold:**post-AAA+ oligomerization domain-like **Superfamily:**post-AAA+ oligomerization domain-like **Family:**MgsA/YrvN C-terminal domain-like
58	d1gd0a_	Alignment	not modelled	15.1	11	**Fold:**Tautomerase/MIF **Superfamily:**Tautomerase/MIF **Family:**MIF-related
59	c1o0sB_	Alignment	not modelled	15.1	14	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**nad-dependent malic enzyme; **PDBTitle:** crystal structure of ascaris suum malic enzyme complexed with nadh
60	c3thxB_	Alignment	not modelled	15.0	39	**PDB header:**dna binding protein/dna **Chain:** B: **PDB Molecule:**dna mismatch repair protein msh3; **PDBTitle:** human mutsbeta complexed with an idl of 3 bases (loop3) and adp
61	c1ewqA_	Alignment	not modelled	14.7	39	**PDB header:**replication/dna **Chain:** A: **PDB Molecule:**dna mismatch repair protein muts; **PDBTitle:** crystal structure taq muts complexed with a heteroduplex2 dna at 2.2 a resolution
62	d1pfka_	Alignment	not modelled	14.6	22	**Fold:**Phosphofructokinase **Superfamily:**Phosphofructokinase **Family:**Phosphofructokinase
63	c1b4aA_	Alignment	not modelled	14.3	15	**PDB header:**repressor **Chain:** A: **PDB Molecule:**arginine repressor; **PDBTitle:** structure of the arginine repressor from bacillus stearothermophilus
64	d2gdga1	Alignment	not modelled	14.2	7	**Fold:**Tautomerase/MIF **Superfamily:**Tautomerase/MIF **Family:**MIF-related
65	d2vv5a2	Alignment	not modelled	14.0	11	**Fold:**Ferredoxin-like **Superfamily:**Mechanosensitive channel protein MscS (YggB), C-terminal domain **Family:**Mechanosensitive channel protein MscS (YggB), C-terminal domain
66	c2o8dB_	Alignment	not modelled	14.0	35	**PDB header:**dna binding protein/dna **Chain:** B: **PDB Molecule:**dna mismatch repair protein msh6; **PDBTitle:** human mutsalpha (msh2/msh6) bound to adp and a g du mispair
67	c3ctdB_	Alignment	not modelled	13.9	13	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**putative atpase, aaa family; **PDBTitle:** crystal structure of a putative aaa family atpase from2 prochlorococcus marinus subsp. pastoris
68	c3iwcD_	Alignment	not modelled	13.7	20	**PDB header:**lyase **Chain:** D: **PDB Molecule:**s-adenosylmethionine decarboxylase; **PDBTitle:** t. maritima adometdc complex with s-adenosylmethionine2 methyl ester
69	c3fybA_	Alignment	not modelled	13.6	29	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**protein of unknown function (duf1244); **PDBTitle:** crystal structure of a protein of unknown function (duf1244) from2 alcanivorax borkumensis
70	c3b64A_	Alignment	not modelled	13.5	14	**PDB header:**cytokine **Chain:** A: **PDB Molecule:**macrophage migration inhibitory factor-like **PDBTitle:** macrophage migration inhibitory factor (mif) from2 /leishmania major
71	d2fgca1	Alignment	not modelled	13.4	20	**Fold:**Ferredoxin-like **Superfamily:**ACT-like **Family:**IlvH-like
72	d2f06a1	Alignment	not modelled	13.1	22	**Fold:**Ferredoxin-like **Superfamily:**ACT-like **Family:**BT0572-like
73	d2o35a1	Alignment	not modelled	13.0	29	**Fold:**SMc04008-like **Superfamily:**SMc04008-like **Family:**SMc04008-like
74	c2o35A_	Alignment	not modelled	13.0	29	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein duf1244; **PDBTitle:** protein of unknown function (duf1244) from sinorhizobium meliloti
75	c1i1gA_	Alignment	not modelled	12.7	15	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcriptional regulator lrpa; **PDBTitle:** crystal structure of the lrp-like transcriptional regulator from the2 archaeon pyrococcus furiosus
76	c3ereD_	Alignment	not modelled	12.5	18	**PDB header:**dna binding protein/dna **Chain:** D: **PDB Molecule:**arginine repressor; **PDBTitle:** crystal structure of the arginine repressor protein from mycobacterium2 tuberculosis in complex with the dna operator
77	d1xtpa_	Alignment	not modelled	12.5	24	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**AD-003 protein-like
78	c2pc6C_	Alignment	not modelled	12.4	20	**PDB header:**lyase **Chain:** C: **PDB Molecule:**probable acetolactate synthase isozyme iii (small subunit); **PDBTitle:** crystal structure of putative acetolactate synthase- small subunit2 from nitrosomonas europaea
79	d1pkxa1	Alignment	not modelled	12.2	14	**Fold:**Methylglyoxal synthase-like **Superfamily:**Methylglyoxal synthase-like **Family:**Inosicase

80	c2e1aD_	Alignment	not modelled	12.1	13	**PDB header:**transcription **Chain:** D: **PDB Molecule:**75aa long hypothetical regulatory protein asnc; **PDBTitle:** crystal structure of ffrp-dm1
81	c3k85B_	Alignment	not modelled	11.9	23	**PDB header:**transferase **Chain:** B: **PDB Molecule:**d-glycero-d-manno-heptose 1-phosphate kinase; **PDBTitle:** crystal structure of a d-glycero-d-manno-heptose 1-phosphate2 kinase from bacteriodes thetaiotaomicron
82	d2fxaa1	Alignment	not modelled	11.9	19	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**MarR-like transcriptional regulators
83	c3ia1A_	Alignment	not modelled	11.9	16	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**thio-disulfide isomerase/thioredoxin; **PDBTitle:** crystal structure of thio-disulfide isomerase from thermus2 thermophilus
84	d2adca1	Alignment	not modelled	11.9	14	**Fold:**Ferredoxin-like **Superfamily:**RNA-binding domain, RBD **Family:**Canonical RBD
85	c2w2uA_	Alignment	not modelled	11.9	25	**PDB header:**hydrolase/transport **Chain:** A: **PDB Molecule:**hypothetical p60 katanin; **PDBTitle:** structural insight into the interaction between archaeal2 escrt-iii and aaa-atpase
86	c2qt7B_	Alignment	not modelled	11.8	18	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**receptor-type tyrosine-protein phosphatase-like **PDBTitle:** crystallographic structure of the mature ectodomain of the2 human receptor-type protein-tyrosine phosphatase ia-2 at3 1.30 angstroms
87	c2i38A_	Alignment	not modelled	11.7	17	**PDB header:**rna binding protein/chimera **Chain:** A: **PDB Molecule:**fusion protein consists of immunoglobin g- **PDBTitle:** solution structure of the rrm of srp20
88	d2u1aa_	Alignment	not modelled	11.6	10	**Fold:**Ferredoxin-like **Superfamily:**RNA-binding domain, RBD **Family:**Canonical RBD
89	c2cb4D_	Alignment	not modelled	11.5	40	**PDB header:**toxin **Chain:** D: **PDB Molecule:**mosquitocidal toxin; **PDBTitle:** crystal structure of the catalytic domain of the2 mosquitocidal toxin from bacillus sphaericus, mutant e197q
90	d1vr7a1	Alignment	not modelled	11.4	20	**Fold:**S-adenosylmethionine decarboxylase **Superfamily:**S-adenosylmethionine decarboxylase **Family:**Bacterial S-adenosylmethionine decarboxylase
91	c3p6lA_	Alignment	not modelled	11.3	17	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**sugar phosphate isomerase/epimerase; **PDBTitle:** crystal structure of a sugar phosphate isomerase/epimerase (bdi_1903)2 from parabacteroides distasonis atcc 8503 at 1.85 a resolution
92	d1fp1d2	Alignment	not modelled	11.3	27	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**Plant O-methyltransferase, C-terminal domain
93	c3jz3B_	Alignment	not modelled	11.2	30	**PDB header:**transferase **Chain:** B: **PDB Molecule:**sensor protein qsec; **PDBTitle:** structure of the cytoplasmic segment of histidine kinase qsec
94	c2d9oA_	Alignment	not modelled	11.1	8	**PDB header:**rna binding protein **Chain:** A: **PDB Molecule:**dnaj (hsp40) homolog, subfamily c, member 17; **PDBTitle:** solution structure of rna binding domain in hypothetical2 protein flj10634
95	c2p6tH_	Alignment	not modelled	11.1	16	**PDB header:**transcription **Chain:** H: **PDB Molecule:**transcriptional regulator, lrp/asnc family; **PDBTitle:** crystal structure of transcriptional regulator nmb0573 and l-leucine2 complex from neisseria meningitidis
96	c2vxcA_	Alignment	not modelled	11.0	12	**PDB header:**cell cycle **Chain:** A: **PDB Molecule:**dna repair protein rhp9; **PDBTitle:** structure of the crb2-brct2 domain complex with2 phosphopeptide.
97	d1mwza_	Alignment	not modelled	10.9	17	**Fold:**Ferredoxin-like **Superfamily:**HMA, heavy metal-associated domain **Family:**HMA, heavy metal-associated domain
98	c2o8bA_	Alignment	not modelled	10.9	48	**PDB header:**dna binding protein/dna **Chain:** A: **PDB Molecule:**dna mismatch repair protein msh2; **PDBTitle:** human mutsalpha (msh2/msh6) bound to adp and a g t mispair
99	c1wbdA_	Alignment	not modelled	10.8	39	**PDB header:**dna-binding **Chain:** A: **PDB Molecule:**dna mismatch repair protein muts; **PDBTitle:** crystal structure of e. coli dna mismatch repair enzyme2 muts, e38q mutant, in complex with a g.t mismatch