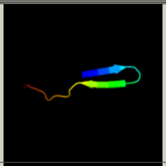
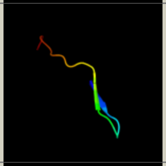
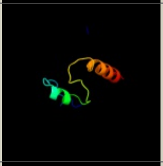
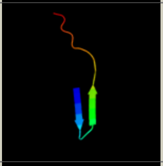
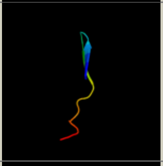
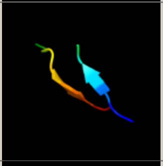
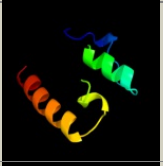
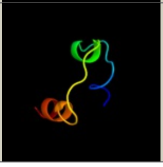
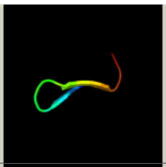
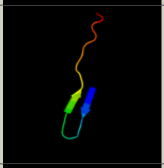
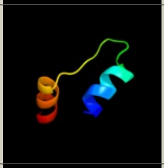
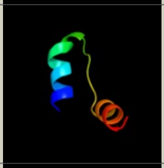
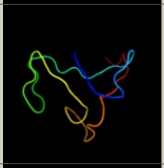
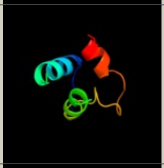
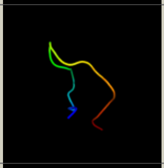
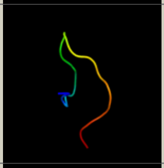
Email	l.a.kelley@imperial.ac.uk
Description	A1Z6I9
Date	Tue Jan 22 12:00:06 GMT 2013
Unique Job ID	e856bc3d2f8076dd

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2xr1B_	Alignment		43.6	25	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**cleavage and polyadenylation specificity factor 100 kd **PDBTitle:** dimeric archaeal cleavage and polyadenylation specificity2 factor with n-terminal kh domains (kh-cpsf) from methanosarcina3 mazei
2	c3af5A_	Alignment		41.0	30	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative uncharacterized protein ph1404; **PDBTitle:** the crystal structure of an archaeal cpsf subunit, ph1404 from2 pyrococcus horikoshii
3	d1ynha1	Alignment		40.0	100	**Fold:**Pentein, beta/alpha-propeller **Superfamily:**Pentein **Family:**Succinylarginine dihydrolase-like
4	d1v5ka_	Alignment		37.4	33	**Fold:**CH domain-like **Superfamily:**Calponin-homology domain, CH-domain **Family:**Calponin-homology domain, CH-domain
5	c2az4A_	Alignment		33.2	10	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein ef2904; **PDBTitle:** crystal structure of a protein of unknown function from enterococcus2 faecalis v583
6	d1ej2a_	Alignment		32.3	13	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Nucleotidylyl transferase **Family:**Adenylyltransferase
7	c2xr1A_	Alignment		30.9	25	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**cleavage and polyadenylation specificity factor 100 kd **PDBTitle:** dimeric archaeal cleavage and polyadenylation specificity2 factor with n-terminal kh domains (kh-cpsf) from methanosarcina3 mazei
8	c1w0pA_	Alignment		29.2	75	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**sialidase; **PDBTitle:** vibrio cholerae sialidase with alpha-2,6-sialyllactose
9	c1wyoA_	Alignment		22.9	28	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**microtubule-associated protein rp/eb family **PDBTitle:** solution structure of the ch domain of human microtubule-2 associated protein rp/eb family member 3
10	d2qjza1	Alignment		21.7	32	**Fold:**CH domain-like **Superfamily:**Calponin-homology domain, CH-domain **Family:**Calponin-homology domain, CH-domain
11	c3elkA_	Alignment		21.5	23	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**putative transcriptional regulator ta0346; **PDBTitle:** crystal structure of putative transcriptional regulator ta0346 from2 thermoplasma acidophilum

12	c2bibA_	Alignment		20.4	53	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**teichoic acid phosphorylcholine esterase/ choline binding **PDBTitle:** crystal structure of the complete modular teichioic acid2 phosphorylcholine esterase pce (cbpe) from streptococcus3 pneumoniae
13	c2ycbA_	Alignment		20.0	30	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**cleavage and polyadenylation specificity factor; **PDBTitle:** structure of the archaeal beta-casp protein with n-terminal2 kh domains from methanothermobacter thermautotrophicus
14	c2e1nA_	Alignment		18.5	19	**PDB header:**circadian clock protein **Chain:** A: **PDB Molecule:**pex; **PDBTitle:** crystal structure of the cyanobacterium circadian clock modifier pex
15	c2dqlA_	Alignment		17.8	15	**PDB header:**circadian clock protein **Chain:** A: **PDB Molecule:**pex protein; **PDBTitle:** crytal structure of the circadian clock associated protein2 pex from anabaena
16	d1jjcb3	Alignment		16.8	35	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Myf domain
17	c3l7wA_	Alignment		15.4	29	**PDB header:**transcription **Chain:** A: **PDB Molecule:**putative uncharacterized protein smu.1704; **PDBTitle:** the crystal structure of smu.1704 from streptococcus mutans ua159
18	d1ewsa_	Alignment		14.9	35	**Fold:**Defensin-like **Superfamily:**Defensin-like **Family:**Defensin
19	c1ewsA_	Alignment		14.9	35	**PDB header:**antimicrobial protein **Chain:** A: **PDB Molecule:**rk-1 defensin; **PDBTitle:** the three-dimensional solution structure of the rabbit2 kidney defensin, rk-1
20	c1tnuL_	Alignment		14.6	12	**PDB header:**transferase **Chain:** L: **PDB Molecule:**geranylgeranyl transferase type i beta subunit; **PDBTitle:** rat protein geranylgeranyltransferase type-i complexed with2 a ggpp analog and a gcincckvl peptide derived from rhob
21	d1n4qb_	Alignment	not modelled	14.6	12	**Fold:**alpha/alpha toroid **Superfamily:**Terpenoid cyclases/Protein prenyltransferases **Family:**Protein prenyltransferases
22	d2h6fb1	Alignment	not modelled	14.5	18	**Fold:**alpha/alpha toroid **Superfamily:**Terpenoid cyclases/Protein prenyltransferases **Family:**Protein prenyltransferases
23	d2i7xa1	Alignment	not modelled	14.3	24	**Fold:**Metallo-hydrolase/oxidoreductase **Superfamily:**Metallo-hydrolase/oxidoreductase **Family:**beta-CASP RNA-metabolising hydrolases
24	c2i7xA_	Alignment	not modelled	14.3	24	**PDB header:**rna binding protein, protein binding **Chain:** A: **PDB Molecule:**protein cft2; **PDBTitle:** structure of yeast cpsf-100 (ydh1p)
25	c1ztmC_	Alignment	not modelled	14.1	29	**PDB header:**viral protein **Chain:** C: **PDB Molecule:**fusion glycoprotein; **PDBTitle:** structure of the uncleaved paramyxovirus (hpiv3) fusion protein
26	d1u7na_	Alignment	not modelled	14.1	39	**Fold:**Isocitrate/Isopropylmalate dehydrogenase-like **Superfamily:**Isocitrate/Isopropylmalate dehydrogenase-like **Family:**PlsX-like
27	c3aygA_	Alignment	not modelled	13.8	31	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**nitric oxide reductase; **PDBTitle:** crystal structure of nitric oxide reductase complex with hqno
28	d2esha1	Alignment	not modelled	13.4	21	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**PadR-like
						PDB header:signaling protein **Chain:** A: **PDB Molecule:**sam pointed domain-containing ets

29	c2dkxA_	Alignment	not modelled	13.2	13	transcription **PDBTitle:** solution structure of the sam_pnt-domain of ets2 transcription factor pdef (prostate ets)
30	d1wraa1	Alignment	not modelled	12.3	53	**Fold:**Metallo-hydrolase/oxidoreductase **Superfamily:**Metallo-hydrolase/oxidoreductase **Family:**Pce catalytic domain-like
31	c3lq6A_	Alignment	not modelled	11.8	30	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**capsid protein; **PDBTitle:** crystal structure of murine norovirus protruding (p) domain
32	d1f9aa_	Alignment	not modelled	11.6	21	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Nucleotidylyl transferase **Family:**Adenylyltransferase
33	d2aq0a1	Alignment	not modelled	10.9	14	**Fold:**SAM domain-like **Superfamily:**RuvA domain 2-like **Family:**Hef domain-like
34	c3oirA_	Alignment	not modelled	10.9	14	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**sulfate transporter sulfate transporter family protein; **PDBTitle:** crystal structure of sulfate transporter family protein from wolinella2 succinogenes
35	c2h29A_	Alignment	not modelled	10.8	30	**PDB header:**transferase **Chain:** A: **PDB Molecule:**probable nicotinate-nucleotide **PDBTitle:** crystal structure of nicotinic acid mononucleotide2 adenylyltransferase from staphylococcus aureus: product3 bound form 1
36	c3hhhA_	Alignment	not modelled	10.7	38	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**transcriptional regulator, padr family; **PDBTitle:** crystal structure of transcriptional regulator, a member of padr2 family, from enterococcus faecalis v583
37	d2dkfa1	Alignment	not modelled	10.4	32	**Fold:**Metallo-hydrolase/oxidoreductase **Superfamily:**Metallo-hydrolase/oxidoreductase **Family:**beta-CASP RNA-metabolising hydrolases
38	c2f9jP_	Alignment	not modelled	10.1	64	**PDB header:**rna binding protein **Chain:** P: **PDB Molecule:**splicing factor 3b subunit 1; **PDBTitle:** 3.0 angstrom resolution structure of a y22m mutant of the spliceosomal2 protein p14 bound to a region of sf3b155
39	d2cbia3	Alignment	not modelled	9.8	23	**Fold:**Zincin-like **Superfamily:**beta-N-acetylhexosaminidase-like domain **Family:**Hyaluronidase N-terminal domain-like
40	c2rmsB_	Alignment	not modelled	9.8	35	**PDB header:**transcription **Chain:** B: **PDB Molecule:**msin3a-binding protein; **PDBTitle:** solution structure of the msin3a pah1-sap25 sid complex
41	c3ixxE_	Alignment	not modelled	9.5	33	**PDB header:**virus **Chain:** E: **PDB Molecule:**peptide pr; **PDBTitle:** the pseudo-atomic structure of west nile immature virus in2 complex with fab fragments of the anti-fusion loop antibody3 e53
42	c3f8fA_	Alignment	not modelled	9.5	25	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**transcriptional regulator, padr-like family; **PDBTitle:** crystal structure of multidrug binding transcriptional regulator lmrr2 complexed with daunomycin
43	d2co5a1	Alignment	not modelled	9.2	25	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**F93-like
44	c2p7vA_	Alignment	not modelled	9.1	23	**PDB header:**transcription **Chain:** A: **PDB Molecule:**regulator of sigma d; **PDBTitle:** crystal structure of the escherichia coli regulator of sigma 70, rsd,2 in complex with sigma 70 domain 4
45	c3hkzZ_	Alignment	not modelled	9.1	33	**PDB header:**transferase **Chain:** Z: **PDB Molecule:**dna-directed rna polymerase subunit 13; **PDBTitle:** the x-ray crystal structure of rna polymerase from archaea
46	d1xzpa3	Alignment	not modelled	9.1	64	**Fold:**Folate-binding domain **Superfamily:**Folate-binding domain **Family:**TrmE formyl-THF-binding domain
47	c1xzqB_	Alignment	not modelled	9.1	64	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**probable trna modification gtpase trme; **PDBTitle:** structure of the gtp-binding protein trme from thermotoga2 maritima complexed with 5-formyl-thf
48	d1hcra_	Alignment	not modelled	8.7	21	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Recombinase DNA-binding domain
49	d1ijwc_	Alignment	not modelled	8.6	21	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Recombinase DNA-binding domain
50	c3kzwD_	Alignment	not modelled	8.6	62	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**cytosol aminopeptidase; **PDBTitle:** crystal structure of cytosol aminopeptidase from staphylococcus aureus2 col
51	d1uptb_	Alignment	not modelled	8.6	35	**Fold:**GRIP domain **Superfamily:**GRIP domain **Family:**GRIP domain
52	d2i9wa3	Alignment	not modelled	8.5	55	**Fold:**Sec-C motif **Superfamily:**Sec-C motif **Family:**Sec-C motif
53	d1uptd_	Alignment	not modelled	8.2	35	**Fold:**GRIP domain **Superfamily:**GRIP domain **Family:**GRIP domain
54	c3ut2B_	Alignment	not modelled	8.1	15	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**catalase-peroxidase 2; **PDBTitle:** crystal structure of fungal magkatg2

55	c3tsjA_	Alignment	not modelled	8.0	18	**PDB header:**allergen, oxidoreductase **Chain:** A: **PDB Molecule:**pollen allergen phl p 4; **PDBTitle:** crystal structure of phl p 4, a grass pollen allergen with glucose2 dehydrogenase activity
56	d1mg7a1	Alignment	not modelled	7.9	60	**Fold:**Ribosomal protein S5 domain 2-like **Superfamily:**Ribosomal protein S5 domain 2-like **Family:**Early switch protein XOL-1, N-terminal domain
57	d3dssb1	Alignment	not modelled	7.9	19	**Fold:**alpha/alpha toroid **Superfamily:**Terpenoid cyclases/Protein prenyltransferases **Family:**Protein prenyltransferases
58	c3c6rE_	Alignment	not modelled	7.7	42	**PDB header:**virus **Chain:** E: **PDB Molecule:**peptide pr; **PDBTitle:** low ph immature dengue virus
59	d1sv0a_	Alignment	not modelled	7.7	18	**Fold:**SAM domain-like **Superfamily:**SAM/Pointed domain **Family:**Pointed domain
60	c3lvtA_	Alignment	not modelled	7.7	27	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**glycosyl hydrolase, family 38; **PDBTitle:** the crystal structure of a protein in the glycosyl hydrolase2 family 38 from enterococcus faecalis to 2.55a
61	c2wyhA_	Alignment	not modelled	7.7	33	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**alpha-mannosidase; **PDBTitle:** structure of the streptococcus pyogenes family gh38 alpha-2 mannosidase
62	c3peiA_	Alignment	not modelled	7.6	62	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**cytosol aminopeptidase; **PDBTitle:** crystal structure of cytosol aminopeptidase from francisella2 tularensis
63	c3c6eC_	Alignment	not modelled	7.6	42	**PDB header:**viral protein **Chain:** C: **PDB Molecule:**prm; **PDBTitle:** crystal structure of the precursor membrane protein-envelope protein2 heterodimer from the dengue 2 virus at neutral ph
64	c3ij3A_	Alignment	not modelled	7.6	54	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**cytosol aminopeptidase; **PDBTitle:** 1.8 angstrom resolution crystal structure of cytosol aminopeptidase2 from coxiella burnetii
65	c2e8pA_	Alignment	not modelled	7.4	22	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**elf3 protein; **PDBTitle:** solution structure of the n-terminal sam-domain of e74-like2 factor 3
66	c3bk2A_	Alignment	not modelled	7.3	22	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**metal dependent hydrolase; **PDBTitle:** crystal structure analysis of the rnase j/ump complex
67	d2c1ia2	Alignment	not modelled	7.3	18	**Fold:**Peptidoglycan deacetylase N-terminal noncatalytic region **Superfamily:**Peptidoglycan deacetylase N-terminal noncatalytic region **Family:**Peptidoglycan deacetylase N-terminal noncatalytic region
68	c3pqhB_	Alignment	not modelled	7.3	23	**PDB header:**viral protein **Chain:** B: **PDB Molecule:**gene product 138; **PDBTitle:** crystal structure of the c-terminal fragment of the bacteriophage2 phi92 membrane-piercing protein gp138
69	c4efdF_	Alignment	not modelled	7.3	54	**PDB header:**hydrolase **Chain:** F: **PDB Molecule:**aminopeptidase; **PDBTitle:** crystal structure of an m17 aminopeptidase from trypanosoma brucei,2 tb427tmp.02.4440
70	c3e37B_	Alignment	not modelled	7.2	18	**PDB header:**transferase **Chain:** B: **PDB Molecule:**protein farnesyltransferase subunit beta; **PDBTitle:** protein farnesyltransferase complexed with bisubstrate2 ethylenediamine scaffold inhibitor 5
71	c4b1oQ_	Alignment	not modelled	7.1	27	**PDB header:**transferase/dna **Chain:** Q: **PDB Molecule:**rna polymerase subunit 13; **PDBTitle:** archaeal rnap-dna binary complex at 4.32ang
72	c4esfA_	Alignment	not modelled	7.1	38	**PDB header:**transcription **Chain:** A: **PDB Molecule:**padr-like transcriptional regulator; **PDBTitle:** crystal structure of padr-like transcriptional regulator (bce3449)2 from bacillus cereus strain atcc 10987
73	c3h8gC_	Alignment	not modelled	7.1	62	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**cytosol aminopeptidase; **PDBTitle:** bestatin complex structure of leucine aminopeptidase from pseudomonas2 putida
74	d1mtxa_	Alignment	not modelled	7.1	100	**Fold:**Knottins (small inhibitors, toxins, lectins) **Superfamily:**Scorpion toxin-like **Family:**Short-chain scorpion toxins
75	c3hkzY_	Alignment	not modelled	7.0	33	**PDB header:**transferase **Chain:** Y: **PDB Molecule:**dna-directed rna polymerase subunit 13; **PDBTitle:** the x-ray crystal structure of rna polymerase from archaea
76	d1xmaa_	Alignment	not modelled	6.9	18	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**PadR-like
77	c1xmaA_	Alignment	not modelled	6.9	18	**PDB header:**transcription **Chain:** A: **PDB Molecule:**predicted transcriptional regulator; **PDBTitle:** structure of a transcriptional regulator from clostridium thermocellum2 cth-833
78	d1qwga_	Alignment	not modelled	6.9	28	**Fold:**TIM beta/alpha-barrel **Superfamily:**(2r)-phospho-3-sulfolactate synthase ComA **Family:**(2r)-phospho-3-sulfolactate synthase ComA
79	c4aclA_	Alignment	not modelled	6.8	12	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**tssl; **PDBTitle:** 3d structure of dotu from francisella novicida
80	d1h2tc3	Alignment	not modelled	6.8	28	**Fold:**alpha-alpha superhelix **Superfamily:**ARM repeat **Family:**MIF4G domain-like
						Fold: Nucleotidyltransferase

81	d2o5aa1	Alignment	not modelled	6.8	26	**Superfamily:**Nucleotidyltransferase **Family:**Iojap/YbeB-like
82	c2waqQ_	Alignment	not modelled	6.8	27	**PDB header:**transcription **Chain:** Q: **PDB Molecule:**dna-directed rna polymerase rpo13 subunit; **PDBTitle:** the complete structure of the archaeal 13-subunit dna-2 directed rna polymerase
83	c4esbA_	Alignment	not modelled	6.7	27	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcriptional regulator, padr family; **PDBTitle:** crystal structure of padr-like transcriptional regulator (bc4206) from2 bacillus cereus strain atcc 14579
84	d2nxya1	Alignment	not modelled	6.6	19	**Fold:**gp120 core **Superfamily:**gp120 core **Family:**gp120 core
85	c3ri2B_	Alignment	not modelled	6.5	22	**PDB header:**transcription regulator **Chain:** B: **PDB Molecule:**transcriptional regulator, padr-like family; **PDBTitle:** crystal structure of padr family transcriptional regulator from2 eggerthella lenta dsm 2243
86	c3pcoD_	Alignment	not modelled	6.5	29	**PDB header:**ligase **Chain:** D: **PDB Molecule:**phenylalanyl-trna synthetase, beta chain; **PDBTitle:** crystal structure of e. coli phenylalanine-trna synthetase complexed2 with phenylalanine and amp
87	c2qjxA_	Alignment	not modelled	6.4	23	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**protein bim1; **PDBTitle:** structural basis of microtubule plus end tracking by2 xmap215, clip-170 and eb1
88	c2kzhA_	Alignment	not modelled	6.4	36	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**tryptophan biosynthesis protein trpcf; **PDBTitle:** three-dimensional structure of a truncated phosphoribosylanthranilate2 isomerase (residues 255-384) from escherichia coli
89	c4aboI_	Alignment	not modelled	6.4	23	**PDB header:**structural protein **Chain:** I: **PDB Molecule:**microtubule integrity protein mal3; **PDBTitle:** mal3 ch domain homology model and mammalian tubulin (2xrp) docked2 into the 8.6-angstrom cryo-em map of mal3-gtpgammas-microtubules
90	c2p28A_	Alignment	not modelled	6.4	43	**PDB header:**cell adhesion **Chain:** A: **PDB Molecule:**integrin beta-2; **PDBTitle:** structure of the phe2 and phe3 fragments of the integrin beta2 subunit
91	c2kvsA_	Alignment	not modelled	6.4	24	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein mw0776; **PDBTitle:** nmr solution structure of q7a1e8 protein from staphylococcus2 aureus: northeast structural genomics consortium target:3 zr215
92	d1hcfa_	Alignment	not modelled	6.4	13	**Fold:**Cystine-knot cytokines **Superfamily:**Cystine-knot cytokines **Family:**Neurotrophin
93	c3kihC_	Alignment	not modelled	6.4	29	**PDB header:**sugar binding protein **Chain:** C: **PDB Molecule:**5-bladed -propeller lectin; **PDBTitle:** the crystal structures of two fragments truncated from 5-bladed -2 propeller lectin, tachylectin-2 (lib2-d2-15)
94	d1sxma_	Alignment	not modelled	6.3	100	**Fold:**Knottins (small inhibitors, toxins, lectins) **Superfamily:**Scorpion toxin-like **Family:**Short-chain scorpion toxins
95	c3qq5A_	Alignment	not modelled	6.2	60	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**small gtp-binding protein; **PDBTitle:** crystal structure of the [fefe]-hydrogenase maturation protein hydf
96	d1ok8a1	Alignment	not modelled	6.2	27	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**E set domains **Family:**Class II viral fusion proteins C-terminal domain
97	c4arpB_	Alignment	not modelled	6.1	35	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**pesticin; **PDBTitle:** structure of the inactive pesticin e178a mutant
98	c2hc9A_	Alignment	not modelled	6.1	69	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**leucine aminopeptidase 1; **PDBTitle:** structure of caenorhabditis elegans leucine aminopeptidase-zinc2 complex (lap1)
99	d1pjwa_	Alignment	not modelled	6.0	31	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**E set domains **Family:**Class II viral fusion proteins C-terminal domain