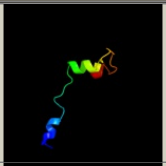
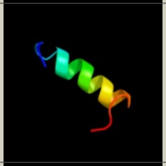
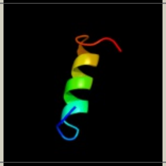
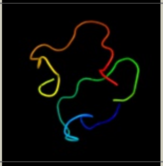
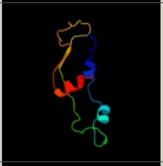
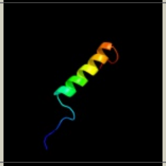
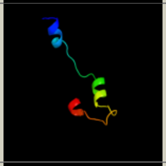
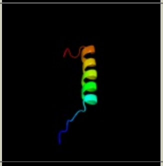
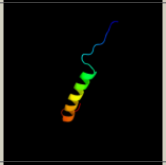
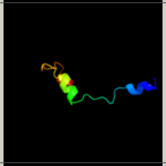
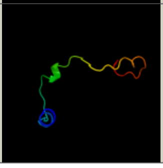
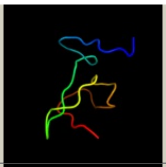
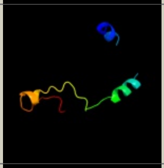
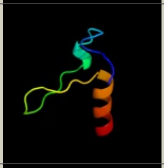
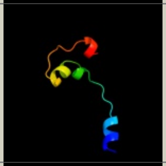
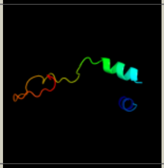
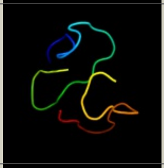
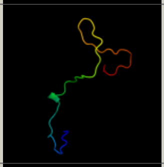
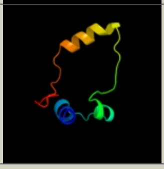
Phyre2

Email	l.a.kelley@imperial.ac.uk
Description	P76361
Date	Thu Jan 5 12:22:20 GMT 2012
Unique Job ID	6065ac5873f4750b

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1vlpa1	Alignment		61.7	26	**Fold:**alpha/beta-Hammerhead **Superfamily:**Nicotinate/Quinolinate PRTase N-terminal domain-like **Family:**Monomeric nicotinate phosphoribosyltransferase N-terminal domain-like
2	d1us7b_	Alignment		45.1	32	**Fold:**Hsp90 co-chaperone CDC37 **Superfamily:**Hsp90 co-chaperone CDC37 **Family:**Hsp90 co-chaperone CDC37
3	c1us7B_	Alignment		45.1	32	**PDB header:**chaperone **Chain:** B: **PDB Molecule:**hsp90 co-chaperone cdc37; **PDBTitle:** complex of hsp90 and p50
4	c2puyA_	Alignment		39.5	26	**PDB header:**transcription **Chain:** A: **PDB Molecule:**phd finger protein 21a; **PDBTitle:** crystal structure of the bhc80 phd finger
5	d2f7fa2	Alignment		35.7	25	**Fold:**alpha/beta-Hammerhead **Superfamily:**Nicotinate/Quinolinate PRTase N-terminal domain-like **Family:**NadC N-terminal domain-like
6	d1k0ga_	Alignment		33.6	17	**Fold:**ADC synthase **Superfamily:**ADC synthase **Family:**ADC synthase
7	d1ybea2	Alignment		33.2	26	**Fold:**alpha/beta-Hammerhead **Superfamily:**Nicotinate/Quinolinate PRTase N-terminal domain-like **Family:**Monomeric nicotinate phosphoribosyltransferase N-terminal domain-like
8	d1i7qa_	Alignment		32.7	17	**Fold:**ADC synthase **Superfamily:**ADC synthase **Family:**ADC synthase
9	d1i1qa_	Alignment		31.5	16	**Fold:**ADC synthase **Superfamily:**ADC synthase **Family:**ADC synthase
10	c1vlpA_	Alignment		30.0	26	**PDB header:**transferase **Chain:** A: **PDB Molecule:**nicotinate phosphoribosyltransferase; **PDBTitle:** crystal structure of a putative nicotinate phosphoribosyltransferase2 (yor209c, npt1) from saccharomyces cerevisiae at 1.75 a resolution
11	d1j96a_	Alignment		29.9	26	**Fold:**TIM beta/alpha-barrel **Superfamily:**NAD(P)-linked oxidoreductase **Family:**Aldo-keto reductases (NADP)

12	d1weqa_	Alignment		28.6	24	**Fold:**FYVE/PHD zinc finger **Superfamily:**FYVE/PHD zinc finger **Family:**PHD domain
13	d1q5ma_	Alignment		28.3	33	**Fold:**TIM beta/alpha-barrel **Superfamily:**NAD(P)-linked oxidoreductase **Family:**Aldo-keto reductases (NADP)
14	d1zbdb_	Alignment		26.9	26	**Fold:**FYVE/PHD zinc finger **Superfamily:**FYVE/PHD zinc finger **Family:**FYVE, a phosphatidylinositol-3-phosphate binding domain
15	d1yira2	Alignment		26.6	27	**Fold:**alpha/beta-Hammerhead **Superfamily:**Nicotinate/Quinolinate PRTase N-terminal domain-like **Family:**Monomeric nicotinate phosphoribosyltransferase N-terminal domain-like
16	d1ah4a_	Alignment		25.2	33	**Fold:**TIM beta/alpha-barrel **Superfamily:**NAD(P)-linked oxidoreductase **Family:**Aldo-keto reductases (NADP)
17	c3o37D_	Alignment		24.0	38	**PDB header:**transcription/protein binding **Chain:** D: **PDB Molecule:**transcription intermediary factor 1-alpha; **PDBTitle:** crystal structure of trim24 phd-bromo complexed with h3(1-10)k42 peptide
18	d2alra_	Alignment		22.6	29	**Fold:**TIM beta/alpha-barrel **Superfamily:**NAD(P)-linked oxidoreductase **Family:**Aldo-keto reductases (NADP)
19	d1hqta_	Alignment		21.8	32	**Fold:**TIM beta/alpha-barrel **Superfamily:**NAD(P)-linked oxidoreductase **Family:**Aldo-keto reductases (NADP)
20	d3ctaa2	Alignment		21.5	22	**Fold:**Reductase/isomerase/elongation factor common domain **Superfamily:**Riboflavin kinase-like **Family:**CTP-dependent riboflavin kinase-like
21	c2riqA_	Alignment	not modelled	20.6	28	**PDB header:**transferase **Chain:** A: **PDB Molecule:**poly [adp-ribose] polymerase 1; **PDBTitle:** crystal structure of the third zinc-binding domain of human parp-1
22	c3b4sA_	Alignment	not modelled	20.0	56	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**protein luxt; **PDBTitle:** crystal structure of a luxt domain from vibrio2 parahaemolyticus rimd 2210633
23	d1mn4a_	Alignment	not modelled	19.6	45	**Fold:**Common fold of diphtheria toxin/transcription factors/cytochrome f **Superfamily:**p53-like transcription factors **Family:**DNA-binding domain from NDT80
24	c1yj7A_	Alignment	not modelled	19.5	19	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**escj; **PDBTitle:** crystal structure of enteropathogenic e.coli (epec) type iii secretion2 system protein escj
25	c2obnA_	Alignment	not modelled	19.2	26	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**hypothetical protein; **PDBTitle:** crystal structure of a duf1611 family protein (ava_3511) from anabaena2 variabilis atcc 29413 at 2.30 a resolution
26	c1xwhA_	Alignment	not modelled	19.2	41	**PDB header:**transcription **Chain:** A: **PDB Molecule:**autoimmune regulator; **PDBTitle:** nmr structure of the first phd finger of autoimmune2 regulator protein (aire1): insights into apeced
27	c2jvnA_	Alignment	not modelled	18.7	30	**PDB header:**transferase **Chain:** A: **PDB Molecule:**poly [adp-ribose] polymerase 1; **PDBTitle:** domain c of human parp-1
28	d2g5fa1	Alignment	not modelled	16.8	10	**Fold:**ADC synthase **Superfamily:**ADC synthase **Family:**ADC synthase
						Fold: Inhibitor of apoptosis (IAP) repeat

29	d1q4qa_	Alignment	not modelled	15.6	21	**Superfamily:**Inhibitor of apoptosis (IAP) repeat **Family:**Inhibitor of apoptosis (IAP) repeat
30	d1iega_	Alignment	not modelled	15.2	39	**Fold:**Herpes virus serine proteinase, assemblin **Superfamily:**Herpes virus serine proteinase, assemblin **Family:**Herpes virus serine proteinase, assemblin
31	c3mhsE_	Alignment	not modelled	15.0	33	**PDB header:**hydrolase/transcription regulator/protei **Chain:** E: **PDB Molecule:**saga-associated factor 73; **PDBTitle:** structure of the saga ubp8/sgf11/sus1/sgf73 dub module bound to2 ubiquitin aldehyde
32	c3h9mA_	Alignment	not modelled	14.8	21	**PDB header:**lyase **Chain:** A: **PDB Molecule:**p-aminobenzoate synthetase, component i; **PDBTitle:** crystal structure of para-aminobenzoate synthetase,2 component i from cytophaga hutchinsonii
33	d2p6ra2	Alignment	not modelled	14.6	26	**Fold:**Sec63 N-terminal domain-like **Superfamily:**Sec63 N-terminal domain-like **Family:**Achaeal helicase C-terminal domain
34	d1afsa_	Alignment	not modelled	14.4	28	**Fold:**TIM beta/alpha-barrel **Superfamily:**NAD(P)-linked oxidoreductase **Family:**Aldo-keto reductases (NADP)
35	c2im5C_	Alignment	not modelled	14.3	26	**PDB header:**transferase **Chain:** C: **PDB Molecule:**nicotinate phosphoribosyltransferase; **PDBTitle:** crystal structure of nicotinate phosphoribosyltransferase2 from porphyromonas gingivalis
36	d1at3a_	Alignment	not modelled	14.0	19	**Fold:**Herpes virus serine proteinase, assemblin **Superfamily:**Herpes virus serine proteinase, assemblin **Family:**Herpes virus serine proteinase, assemblin
37	c2f6nA_	Alignment	not modelled	13.7	21	**PDB header:**transcription **Chain:** A: **PDB Molecule:**bromodomain phd finger transcription factor; **PDBTitle:** crystal structure of phd finger-linker-bromodomain fragment2 of human bptf in the free form
38	d2g0ta1	Alignment	not modelled	13.7	24	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Nitrogenase iron protein-like
39	d1us0a_	Alignment	not modelled	13.3	38	**Fold:**TIM beta/alpha-barrel **Superfamily:**NAD(P)-linked oxidoreductase **Family:**Aldo-keto reductases (NADP)
40	c2i6yA_	Alignment	not modelled	13.3	10	**PDB header:**lyase **Chain:** A: **PDB Molecule:**anthranilate synthase component i, putative; **PDBTitle:** structure and mechanism of mycobacterium tuberculosis salicylate2 synthase, mbti
41	c2fqxA_	Alignment	not modelled	13.3	22	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**membrane lipoprotein tmpc; **PDBTitle:** pnra from treponema pallidum complexed with guanosine
42	c2f7fA_	Alignment	not modelled	13.3	25	**PDB header:**transferase **Chain:** A: **PDB Molecule:**nicotinate phosphoribosyltransferase, putative; **PDBTitle:** crystal structure of enterococcus faecalis putative nicotinate2 phosphoribosyltransferase, new york structural genomics consortium
43	d2pbka1	Alignment	not modelled	13.1	32	**Fold:**Herpes virus serine proteinase, assemblin **Superfamily:**Herpes virus serine proteinase, assemblin **Family:**Herpes virus serine proteinase, assemblin
44	d1ubdc2	Alignment	not modelled	13.0	38	**Fold:**beta-beta-alpha zinc fingers **Superfamily:**beta-beta-alpha zinc fingers **Family:**Classic zinc finger, C2H2
45	c2l43A_	Alignment	not modelled	12.7	19	**PDB header:**transcription **Chain:** A: **PDB Molecule:**n-teminal domain from histone h3.3, linker, phd1 domain **PDBTitle:** structural basis for histone code recognition by brpf2-phd1 finger
46	c2bs5A_	Alignment	not modelled	12.5	47	**PDB header:**sugar binding protein **Chain:** A: **PDB Molecule:**fucose-binding lectin protein; **PDBTitle:** lectin from ralstonia solanacearum complexed with 2-2 fucosyllactose
47	d3efxd1	Alignment	not modelled	12.4	43	**Fold:**OB-fold **Superfamily:**Bacterial enterotoxins **Family:**Bacterial AB5 toxins, B-subunits
48	d1vzva_	Alignment	not modelled	12.4	21	**Fold:**Herpes virus serine proteinase, assemblin **Superfamily:**Herpes virus serine proteinase, assemblin **Family:**Herpes virus serine proteinase, assemblin
49	d1vqow1	Alignment	not modelled	12.4	13	**Fold:**Ribosomal protein L30p/L7e **Superfamily:**Ribosomal protein L30p/L7e **Family:**Ribosomal protein L30p/L7e
50	c3bu8B_	Alignment	not modelled	11.8	16	**PDB header:**dna binding protein **Chain:** B: **PDB Molecule:**telomeric repeat-binding factor 2; **PDBTitle:** crystal structure of trf2 trfh domain and tin2 peptide2 complex
51	d1qdla_	Alignment	not modelled	11.6	18	**Fold:**ADC synthase **Superfamily:**ADC synthase **Family:**ADC synthase
52	d1x3ha2	Alignment	not modelled	11.3	36	**Fold:**Glucocorticoid receptor-like (DNA-binding domain) **Superfamily:**Glucocorticoid receptor-like (DNA-binding domain) **Family:**LIM domain
53	c3pstA_	Alignment	not modelled	11.1	17	**PDB header:**nuclear protein **Chain:** A: **PDB Molecule:**protein doa1; **PDBTitle:** crystal structure of pul and pfu(mutate) domain
54	d1xg8a_	Alignment	not modelled	11.0	83	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like

						Family: YuzD-like
55	d2olua1	Alignment	not modelled	10.9	10	**Fold:**Lysozyme-like **Superfamily:**Lysozyme-like **Family:**PBP transglycosylase domain-like
56	c3d6zA_	Alignment	not modelled	10.6	33	**PDB header:**transcription regulator/dna **Chain:** A: **PDB Molecule:**multidrug-efflux transporter 1 regulator; **PDBTitle:** crystal structure of r275e mutant of bmrr bound to dna and rhodamine
57	c2euzA_	Alignment	not modelled	10.6	50	**PDB header:**cell cycle/dna **Chain:** A: **PDB Molecule:**ndt80 protein; **PDBTitle:** structure of a ndt80-dna complex (mse mutant mc5t)
58	d1mnna_	Alignment	not modelled	10.6	50	**Fold:**Common fold of diphtheria toxin/transcription factors/cytochrome f **Superfamily:**p53-like transcription factors **Family:**DNA-binding domain from NDT80
59	c3elfA_	Alignment	not modelled	10.5	20	**PDB header:**lyase **Chain:** A: **PDB Molecule:**fructose-bisphosphate aldolase; **PDBTitle:** structural characterization of tetrameric mycobacterium tuberculosis2 fructose 1,6-bisphosphate aldolase - substrate binding and catalysis3 mechanism of a class iia bacterial aldolase
60	d1o6ea_	Alignment	not modelled	10.0	29	**Fold:**Herpes virus serine proteinase, assemblin **Superfamily:**Herpes virus serine proteinase, assemblin **Family:**Herpes virus serine proteinase, assemblin
61	d3chbd_	Alignment	not modelled	10.0	44	**Fold:**OB-fold **Superfamily:**Bacterial enterotoxins **Family:**Bacterial AB5 toxins, B-subunits
62	c3ln3A_	Alignment	not modelled	10.0	39	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**dihydrodiol dehydrogenase; **PDBTitle:** crystal structure of putative reductase (np_038806.2) from2 mus musculus at 1.18 a resolution
63	c2krcA_	Alignment	not modelled	9.6	43	**PDB header:**transcription **Chain:** A: **PDB Molecule:**dna-directed rna polymerase subunit delta; **PDBTitle:** solution structure of the n-terminal domain of bacillus2 subtilis delta subunit of rna polymerase
64	c2ysmA_	Alignment	not modelled	9.5	23	**PDB header:**transferase **Chain:** A: **PDB Molecule:**myeloid/lymphoid or mixed-lineage leukemia **PDBTitle:** solution structure of the first and second phd domain from2 myeloid/lymphoid or mixed-lineage leukemia protein 33 homolog
65	c2w0tA_	Alignment	not modelled	9.4	31	**PDB header:**transcription **Chain:** A: **PDB Molecule:**lethal(3)malignant brain tumor-like 2 protein; **PDBTitle:** solution structure of the fcs zinc finger domain of human2 lmbl2
66	c2l7pA_	Alignment	not modelled	9.3	13	**PDB header:**transferase **Chain:** A: **PDB Molecule:**histone-lysine n-methyltransferase ashh2; **PDBTitle:** ashh2 a cw domain
67	c2a20A_	Alignment	not modelled	9.3	26	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**regulating synaptic membrane exocytosis protein **PDBTitle:** solution structure of rim2 zinc finger domain
68	c2e6rA_	Alignment	not modelled	9.3	24	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**jumonji/arid domain-containing protein 1d; **PDBTitle:** solution structure of the phd domain in smcy protein
69	d1npba_	Alignment	not modelled	9.0	31	**Fold:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase **Superfamily:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase **Family:**Antibiotic resistance proteins
70	c3os6A_	Alignment	not modelled	9.0	17	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**isochorismate synthase dhbc; **PDBTitle:** crystal structure of putative 2,3-dihydroxybenzoate-specific2 isochorismate synthase, dhbc from bacillus anthracis.
71	d1olma1	Alignment	not modelled	8.7	20	**Fold:**RuvA C-terminal domain-like **Superfamily:**CRAL/TRIO N-terminal domain **Family:**CRAL/TRIO N-terminal domain
72	d2af7a1	Alignment	not modelled	8.6	16	**Fold:**AhpD-like **Superfamily:**AhpD-like **Family:**CMD-like
73	d1kjna_	Alignment	not modelled	8.4	29	**Fold:**Hypothetical protein MTH777 (MT0777) **Superfamily:**Hypothetical protein MTH777 (MT0777) **Family:**Hypothetical protein MTH777 (MT0777)
74	d2h1ta1	Alignment	not modelled	8.3	27	**Fold:**Spiral beta-roll **Superfamily:**PA1994-like **Family:**PA1994-like
75	d1c8aa2	Alignment	not modelled	8.2	35	**Fold:**beta-clip **Superfamily:**AFP III-like domain **Family:**AFP III-like domain
76	d1l0nk_	Alignment	not modelled	8.2	33	**Fold:**Single transmembrane helix **Superfamily:**Subunit XI (6.4 kDa protein) of cytochrome bc1 complex (Ubiquinol-cytochrome c reductase) **Family:**Subunit XI (6.4 kDa protein) of cytochrome bc1 complex (Ubiquinol-cytochrome c reductase)
77	d1i8ta1	Alignment	not modelled	8.0	31	**Fold:**Nucleotide-binding domain **Superfamily:**Nucleotide-binding domain **Family:**UDP-galactopyranose mutase, N-terminal domain
78	d2bv3a5	Alignment	not modelled	7.9	17	**Fold:**Ferredoxin-like **Superfamily:**EF-G C-terminal domain-like **Family:**EF-G/eEF-2 domains III and V
						PDB header:oxidoreductase **Chain:** A: **PDB Molecule:**ribonucleoside-diphosphate reductase

79	c2wghA_	Alignment	not modelled	7.9	24	large **PDBTitle:** human ribonucleotide reductase r1 subunit (rrm1) in complex2 with datp and mg.
80	d2ezla_	Alignment	not modelled	7.8	36	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Recombinase DNA-binding domain
81	c4a1cV_	Alignment	not modelled	7.6	16	**PDB header:**ribosome **Chain:** V: **PDB Molecule:**60s ribosomal protein l7; **PDBTitle:** t.thermophila 60s ribosomal subunit in complex with2 initiation factor 6. this file contains 5s rrna,3 5.8s rrna and proteins of molecule 4.
82	c2zkr2_	Alignment	not modelled	7.6	60	**PDB header:**ribosomal protein/rna **Chain:** 2: **PDB Molecule:**60s ribosomal protein l37e; **PDBTitle:** structure of a mammalian ribosomal 60s subunit within an2 80s complex obtained by docking homology models of the rna3 and proteins into an 8.7 a cryo-em map
83	d2fyuk1	Alignment	not modelled	7.6	39	**Fold:**Single transmembrane helix **Superfamily:**Subunit XI (6.4 kDa protein) of cytochrome bc1 complex (Ubiquinol-cytochrome c reductase) **Family:**Subunit XI (6.4 kDa protein) of cytochrome bc1 complex (Ubiquinol-cytochrome c reductase)
84	c2cvuA_	Alignment	not modelled	7.6	32	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**ribonucleoside-diphosphate reductase large chain **PDBTitle:** structures of yeast ribonucleotide reductase i
85	c3p5rB_	Alignment	not modelled	7.4	23	**PDB header:**lyase **Chain:** B: **PDB Molecule:**taxadiene synthase; **PDBTitle:** crystal structure of taxadiene synthase from pacific yew (taxus2 brevifolia) in complex with mg2+ and 2-fluorogeranylgeranyl3 diphosphate
86	c3r1rB_	Alignment	not modelled	7.4	28	**PDB header:**complex (oxidoreductase/peptide) **Chain:** B: **PDB Molecule:**ribonucleotide reductase r1 protein; **PDBTitle:** ribonucleotide reductase r1 protein with amppnp occupying2 the activity site from escherichia coli
87	c3jueA_	Alignment	not modelled	7.4	32	**PDB header:**protein transport/endocytosis **Chain:** A: **PDB Molecule:**arfgap with coiled-coil, ank repeat and ph domain- **PDBTitle:** crystal structure of arfgap and ank repeat domain of acap1
88	d2yt9a1	Alignment	not modelled	7.3	63	**Fold:**beta-beta-alpha zinc fingers **Superfamily:**beta-beta-alpha zinc fingers **Family:**Classic zinc finger, C2H2
89	c1s1iY_	Alignment	not modelled	7.2	80	**PDB header:**ribosome **Chain:** Y: **PDB Molecule:**60s ribosomal protein l37-a; **PDBTitle:** structure of the ribosomal 80s-eef2-sordarin complex from2 yeast obtained by docking atomic models for rna and protein3 components into a 11.7 a cryo-em map. this file, 1s1i,4 contains 60s subunit. the 40s ribosomal subunit is in file5 1s1h.
90	c3jywY_	Alignment	not modelled	7.2	80	**PDB header:**ribosome **Chain:** Y: **PDB Molecule:**60s ribosomal protein l37(a); **PDBTitle:** structure of the 60s proteins for eukaryotic ribosome based on cryo-em2 map of thermomyces lanuginosus ribosome at 8.9a resolution
91	c2olvA_	Alignment	not modelled	7.1	9	**PDB header:**transferase **Chain:** A: **PDB Molecule:**penicillin-binding protein 2; **PDBTitle:** structural insight into the transglycosylation step of bacterial cell2 wall biosynthesis : donor ligand complex
92	d1b8da_	Alignment	not modelled	7.1	28	**Fold:**Globin-like **Superfamily:**Globin-like **Family:**Phycocyanin-like phycobilisome proteins
93	c3fehA_	Alignment	not modelled	7.1	38	**PDB header:**hydrolase activator **Chain:** A: **PDB Molecule:**centaurin-alpha-1; **PDBTitle:** crystal structure of full length centaurin alpha-1
94	c3k7bA_	Alignment	not modelled	7.0	36	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**protein a33; **PDBTitle:** the structure of the poxvirus a33 protein reveals a dimer of unique c-2 type lectin-like domains.
95	d1xp3a1	Alignment	not modelled	6.9	22	**Fold:**TIM beta/alpha-barrel **Superfamily:**Xylose isomerase-like **Family:**Endonuclease IV
96	d1mm2a_	Alignment	not modelled	6.9	31	**Fold:**FYVE/PHD zinc finger **Superfamily:**FYVE/PHD zinc finger **Family:**PHD domain
97	d1bb8a_	Alignment	not modelled	6.8	33	**Fold:**DNA-binding domain **Superfamily:**DNA-binding domain **Family:**DNA-binding domain from tn916 integrase
98	d1zina2	Alignment	not modelled	6.8	71	**Fold:**Rubredoxin-like **Superfamily:**Microbial and mitochondrial ADK, insert "zinc finger" domain **Family:**Microbial and mitochondrial ADK, insert "zinc finger" domain
99	c1ybeA_	Alignment	not modelled	6.7	23	**PDB header:**transferase **Chain:** A: **PDB Molecule:**nicotinate phosphoribosyltransferase; **PDBTitle:** crystal structure of a nicotinate phosphoribosyltransferase