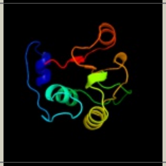
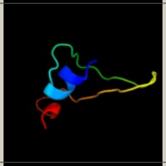
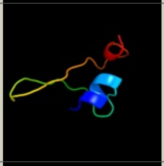
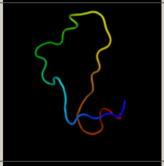
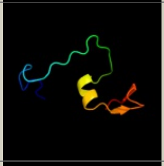
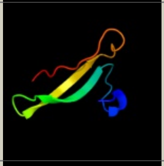
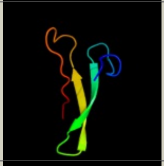
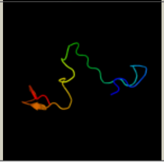
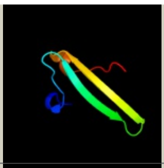
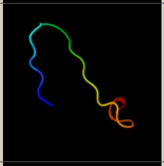
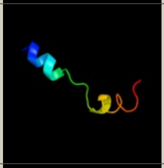
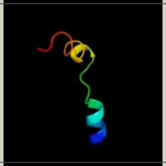
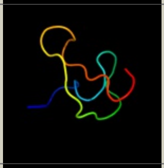
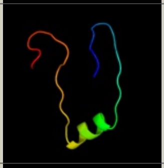
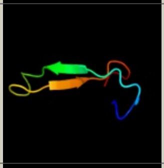
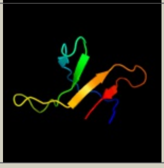
Phyre^2

Email	l.a.kelley@imperial.ac.uk
Description	P16688
Date	Wed Jan 25 15:20:39 GMT 2012
Unique Job ID	9eaafc199bce6c68

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d2fsua1	Alignment		83.2	18	**Fold:**PLP-dependent transferase-like **Superfamily:**PhnH-like **Family:**PhnH-like
2	c2fsuA_	Alignment		83.2	18	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**protein phnh; **PDBTitle:** crystal structure of the phnh protein from escherichia coli
3	d1jera_	Alignment		59.6	23	**Fold:**Cupredoxin-like **Superfamily:**Cupredoxins **Family:**Plastocyanin/azurin-like
4	c1jerA_	Alignment		59.6	23	**PDB header:**electron transport **Chain:** A: **PDB Molecule:**cucumber stellacyanin; **PDBTitle:** cucumber stellacyanin, cu2+, ph 7.0
5	c2l1uA_	Alignment		46.3	21	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**methionine-r-sulfoxide reductase b2, mitochondrial; **PDBTitle:** structure-functional analysis of mammalian msrb2 protein
6	d1ws8a_	Alignment		45.6	25	**Fold:**Cupredoxin-like **Superfamily:**Cupredoxins **Family:**Plastocyanin/azurin-like
7	c3eg9B_	Alignment		44.8	19	**PDB header:**protein transport **Chain:** B: **PDB Molecule:**sec24 related gene family, member d; **PDBTitle:** crystal structure of the mammalian copii-coat protein2 sec23/24 bound to the transport signal sequence of membrin
8	c1m2vB_	Alignment		40.0	23	**PDB header:**protein transport **Chain:** B: **PDB Molecule:**protein transport protein sec24; **PDBTitle:** crystal structure of the yeast sec23/24 heterodimer
9	c2jr7A_	Alignment		36.1	21	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**dph3 homolog; **PDBTitle:** solution structure of human desr1
10	d1ywsa1	Alignment		34.7	33	**Fold:**Rubredoxin-like **Superfamily:**CSL zinc finger **Family:**CSL zinc finger
11	c1pd0A_	Alignment		34.6	21	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**protein transport protein sec24; **PDBTitle:** crystal structure of the copii coat subunit, sec24,2 complexed with a peptide from the snare protein sed53 (yeast syntaxin-5)

12	d1wgea1	Alignment		34.3	21	**Fold:**Rubredoxin-like **Superfamily:**CSL zinc finger **Family:**CSL zinc finger
13	c1x9rA_	Alignment		34.2	26	**PDB header:**electron transport **Chain:** A: **PDB Molecule:**umecyanin; **PDBTitle:** umecyanin from horse raddish- crystal structure of the2 oxidised form
14	c2qkwA_	Alignment		30.7	20	**PDB header:**transferase **Chain:** A: **PDB Molecule:**avirulence protein; **PDBTitle:** structural basis for activation of plant immunity by2 bacterial effector protein avrpto
15	d2qkwa1	Alignment		30.7	20	**Fold:**immunoglobulin/albumin-binding domain-like **Superfamily:**Avirulence protein AvrPto **Family:**Avirulence protein AvrPto
16	c2fqhA_	Alignment		28.5	28	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein ta0938; **PDBTitle:** nmr structure of hypothetical protein ta0938 from2 termoplasma acidophilum
17	c3hm2G_	Alignment		26.6	22	**PDB header:**transferase **Chain:** G: **PDB Molecule:**precorrin-6y c5,15-methyltransferase; **PDBTitle:** crystal structure of putative precorrin-6y c5,15-2 methyltransferase targeted domain from corynebacterium3 diphtheriae
18	d3ehbb1	Alignment		23.6	29	**Fold:**Cupredoxin-like **Superfamily:**Cupredoxins **Family:**Periplasmic domain of cytochrome c oxidase subunit II
19	c2aklA_	Alignment		22.4	38	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**phna-like protein pa0128; **PDBTitle:** solution structure for phn-a like protein pa0128 from2 pseudomonas aeruginosa
20	c3cezA_	Alignment		20.4	21	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**methionine-r-sulfoxide reductase; **PDBTitle:** crystal structure of methionine-r-sulfoxide reductase from2 burkholderia pseudomallei
21	c3mb2J_	Alignment	not modelled	20.4	33	**PDB header:**isomerase **Chain:** J: **PDB Molecule:**4-oxalocrotonate tautomerase family enzyme - beta subunit; **PDBTitle:** kinetic and structural characterization of a heterohexamer 4-2 oxalocrotonate tautomerase from chloroflexus aurantiacus j-10-fl:3 implications for functional and structural diversity in the4 tautomerase superfamily
22	d1qypa_	Alignment	not modelled	20.3	20	**Fold:**Rubredoxin-like **Superfamily:**Zinc beta-ribbon **Family:**Transcriptional factor domain
23	d1l1da_	Alignment	not modelled	19.7	27	**Fold:**Mss4-like **Superfamily:**Mss4-like **Family:**SelR domain
24	c3hcjB_	Alignment	not modelled	19.2	19	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**peptide methionine sulfoxide reductase; **PDBTitle:** structure of msrb from xanthomonas campestris (oxidized2 form)
25	d1f56a_	Alignment	not modelled	19.1	19	**Fold:**Cupredoxin-like **Superfamily:**Cupredoxins **Family:**Plastocyanin/azurin-like
26	c4a02A_	Alignment	not modelled	19.0	17	**PDB header:**chitin binding protein **Chain:** A: **PDB Molecule:**chitin binding protein; **PDBTitle:** x-ray crystallographic structure of efcbm33a
27	c1ymzA_	Alignment	not modelled	19.0	71	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**cc45; **PDBTitle:** cc45, an artificial ww domain designed using statistical2 coupling analysis
28	c3uamD_	Alignment	not modelled	18.8	21	**PDB header:**protein binding **Chain:** D: **PDB Molecule:**chitin binding domain; **PDBTitle:** crystal structure of a chitin binding domain from

						burkholderia2 pseudomallei
29	c3l4hA_	Alignment	not modelled	18.4	33	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**e3 ubiquitin-protein ligase hecw1; **PDBTitle:** helical box domain and second ww domain of the human e3 ubiquitin-2 protein ligase hecw1
30	c3h87D_	Alignment	not modelled	18.4	40	**PDB header:**toxin/antitoxin **Chain:** D: **PDB Molecule:**putative uncharacterized protein; **PDBTitle:** rv0301 rv0300 toxin antitoxin complex from mycobacterium tuberculosis
31	d2fiya1	Alignment	not modelled	18.3	33	**Fold:**FdhE-like **Superfamily:**FdhE-like **Family:**FdhE-like
32	c2op8A_	Alignment	not modelled	18.2	13	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**probable tautomerase ywhb; **PDBTitle:** crystal structure of ywhb- homologue of 4-oxalocrotonate tautomerase
33	d1ok8a2	Alignment	not modelled	17.0	44	**Fold:**Viral glycoprotein, central and dimerisation domains **Superfamily:**Viral glycoprotein, central and dimerisation domains **Family:**Viral glycoprotein, central and dimerisation domains
34	d2bema_	Alignment	not modelled	16.7	21	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**E set domains **Family:**E-set domains of sugar-utilizing enzymes
35	c3l9vE_	Alignment	not modelled	16.3	32	**PDB header:**oxidoreductase **Chain:** E: **PDB Molecule:**putative thiol-disulfide isomerase or thioredoxin; **PDBTitle:** crystal structure of salmonella enterica serovar typhimurium srga
36	c3egxB_	Alignment	not modelled	15.8	21	**PDB header:**protein transport **Chain:** B: **PDB Molecule:**protein transport protein sec24a; **PDBTitle:** crystal structure of the mammalian copii-coat protein2 sec23a/24a complexed with the snare protein sec22b and3 bound to the transport signal sequence of the snare protein4 bet1
37	d1v54b1	Alignment	not modelled	15.7	29	**Fold:**Cupredoxin-like **Superfamily:**Cupredoxins **Family:**Periplasmic domain of cytochrome c oxidase subunit II
38	c3qwnC_	Alignment	not modelled	15.7	19	**PDB header:**antitoxin **Chain:** C: **PDB Molecule:**hypothetical nigd-like protein; **PDBTitle:** crystal structure of a hypothetical nigd-like protein (baccac_03262)2 from bacteroides caccae at 2.42 a resolution
39	c3abfB_	Alignment	not modelled	15.7	18	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**4-oxalocrotonate tautomerase; **PDBTitle:** crystal structure of a 4-oxalocrotonate tautomerase homologue2 (tthb242)
40	c3rrrM_	Alignment	not modelled	15.6	38	**PDB header:**viral protein **Chain:** M: **PDB Molecule:**fusion glycoprotein f0; **PDBTitle:** structure of the rsv f protein in the post-fusion conformation
41	d1svba2	Alignment	not modelled	15.6	33	**Fold:**Viral glycoprotein, central and dimerisation domains **Superfamily:**Viral glycoprotein, central and dimerisation domains **Family:**Viral glycoprotein, central and dimerisation domains
42	c2ormA_	Alignment	not modelled	15.5	13	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**probable tautomerase hp0924; **PDBTitle:** crystal structure of the 4-oxalocrotonate tautomerase homologue dmpi2 from helicobacter pylori.
43	d1otfa_	Alignment	not modelled	15.2	26	**Fold:**Tautomerase/MIF **Superfamily:**Tautomerase/MIF **Family:**4-oxalocrotonate tautomerase-like
44	c3c6dB_	Alignment	not modelled	14.9	44	**PDB header:**virus **Chain:** B: **PDB Molecule:**polyprotein; **PDBTitle:** the pseudo-atomic structure of dengue immature virus
45	c2bn5A_	Alignment	not modelled	14.9	14	**PDB header:**nuclear protein **Chain:** A: **PDB Molecule:**psi; **PDBTitle:** p-element somatic inhibitor protein complex with u1-70k2 proline-rich peptide
46	c3uajA_	Alignment	not modelled	14.8	44	**PDB header:**viral protein/immune system **Chain:** A: **PDB Molecule:**envelope protein; **PDBTitle:** crystal structure of the envelope glycoprotein ectodomain from dengue2 virus serotype 4 in complex with the fab fragment of the chimpanzee3 monoclonal antibody 5h2
47	d2cbpa_	Alignment	not modelled	14.7	19	**Fold:**Cupredoxin-like **Superfamily:**Cupredoxins **Family:**Plastocyanin/azurin-like
48	d3dtub1	Alignment	not modelled	14.2	23	**Fold:**Cupredoxin-like **Superfamily:**Cupredoxins **Family:**Periplasmic domain of cytochrome c oxidase subunit II
49	d1xm0a1	Alignment	not modelled	14.0	16	**Fold:**Mss4-like **Superfamily:**Mss4-like **Family:**SelR domain
50	c1urzC_	Alignment	not modelled	14.0	33	**PDB header:**virus/viral protein **Chain:** C: **PDB Molecule:**envelope protein; **PDBTitle:** low ph induced, membrane fusion conformation of the2 envelope protein of tick-borne encephalitis virus
51	c2x4iA_	Alignment	not modelled	13.7	15	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein 114; **PDBTitle:** orf 114a from sulfolobus islandicus rudivirus 1
52	c3e0mB_	Alignment	not modelled	13.5	13	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**peptide methionine sulfoxide reductase msra/msrb **PDBTitle:** crystal structure of fusion protein of msra and msrb
53	d1pd0a5	Alignment	not modelled	13.4	28	**Fold:**Rubredoxin-like **Superfamily:**Zn-finger domain of Sec23/24 **Family:**Zn-finger domain of Sec23/24
54	d1un2a_	Alignment	not modelled	13.3	23	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like

							Family: DsbA-like
55	d1rj9b1		Alignment	not modelled	12.6	50	**Fold:**Four-helical up-and-down bundle **Superfamily:**Domain of the SRP/SRP receptor G-proteins **Family:**Domain of the SRP/SRP receptor G-proteins
56	c3eg9A_		Alignment	not modelled	12.4	16	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**protein transport protein sec23a; **PDBTitle:** crystal structure of the mammalian copii-coat protein2 sec23/24 bound to the transport signal sequence of membrin
57	c1uzgA_		Alignment	not modelled	12.3	67	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**major envelope protein e; **PDBTitle:** crystal structure of the dengue type 3 virus envelope2 protein
58	d1qnta2		Alignment	not modelled	12.0	28	**Fold:**Ribonuclease H-like motif **Superfamily:**Methylated DNA-protein cysteine methyltransferase domain **Family:**Methylated DNA-protein cysteine methyltransferase domain
59	d2akla2		Alignment	not modelled	11.8	33	**Fold:**Rubredoxin-like **Superfamily:**Zinc beta-ribbon **Family:**PhnA zinc-binding domain
60	c2k8dA_		Alignment	not modelled	11.8	19	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**peptide methionine sulfoxide reductase msrb; **PDBTitle:** solution structure of a zinc-binding methionine sulfoxide reductase
61	d2vv5a2		Alignment	not modelled	11.6	11	**Fold:**Ferredoxin-like **Superfamily:**Mechanosensitive channel protein MscS (YggB), C-terminal domain **Family:**Mechanosensitive channel protein MscS (YggB), C-terminal domain
62	c3mv2A_		Alignment	not modelled	11.4	21	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**coatomer subunit alpha; **PDBTitle:** crystal structure of a-cop in complex with e-cop
63	c1vj7B_		Alignment	not modelled	11.2	44	**PDB header:**hydrolase, transferase **Chain:** B: **PDB Molecule:**bifunctional rela/spot; **PDBTitle:** crystal structure of the bifunctional catalytic fragment of relseq,2 the rela/spot homolog from streptococcus equisimilis.
64	d1fvka_		Alignment	not modelled	11.1	23	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**DsbA-like
65	c1v55B_		Alignment	not modelled	10.7	29	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**cytochrome c oxidase polypeptide ii; **PDBTitle:** bovine heart cytochrome c oxidase at the fully reduced state
66	d1utya_		Alignment	not modelled	10.6	31	**Fold:**BTV NS2-like ssRNA-binding domain **Superfamily:**BTV NS2-like ssRNA-binding domain **Family:**BTV NS2-like ssRNA-binding domain
67	c1utyA_		Alignment	not modelled	10.6	31	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**non-structural protein 2; **PDBTitle:** crystal structure of the rna binding domain of bluetongue2 virus non-structural protein 2(ns2)
68	c1m57H_		Alignment	not modelled	10.5	22	**PDB header:**oxidoreductase **Chain:** H: **PDB Molecule:**cytochrome c oxidase; **PDBTitle:** structure of cytochrome c oxidase from rhodobacter2 sphaeroides (eq(i-286) mutant))
69	c3nrtC_		Alignment	not modelled	10.5	26	**PDB header:**structural genomics, unknown function **Chain:** C: **PDB Molecule:**putative ryanodine receptor; **PDBTitle:** the crystal strucutre of putative ryanodine receptor from bacteroides2 thetaiotaomicron vpi-5482
70	c3mb2G_		Alignment	not modelled	10.5	32	**PDB header:**isomerase **Chain:** G: **PDB Molecule:**4-oxalocrotonate tautomerase family enzyme - alpha subunit; **PDBTitle:** kinetic and structural characterization of a heterohexamer 4-2 oxalocrotonate tautomerase from chloroflexus aurantiacus j-10-fl:3 implications for functional and structural diversity in the4 tautomerase superfamily
71	c1ar1B_		Alignment	not modelled	10.4	29	**PDB header:**complex (oxidoreductase/antibody) **Chain:** B: **PDB Molecule:**cytochrome c oxidase; **PDBTitle:** structure at 2.7 angstrom resolution of the paracoccus2 denitrificans two-subunit cytochrome c oxidase complexed3 with an antibody fv fragment
72	c1qleB_		Alignment	not modelled	10.4	29	**PDB header:**oxidoreductase/immune system **Chain:** B: **PDB Molecule:**cytochrome c oxidase polypeptide ii; **PDBTitle:** cryo-structure of the paracoccus denitrificans four-subunit2 cytochrome c oxidase in the completely oxidized state3 complexed with an antibody fv fragment
73	c2of6C_		Alignment	not modelled	10.1	44	**PDB header:**virus **Chain:** C: **PDB Molecule:**envelope glycoprotein e; **PDBTitle:** structure of immature west nile virus
74	c1m2oA_		Alignment	not modelled	9.8	23	**PDB header:**protein transport/signaling protein **Chain:** A: **PDB Molecule:**protein transport protein sec23; **PDBTitle:** crystal structure of the sec23-sar1 complex
75	d2qtva5		Alignment	not modelled	9.7	28	**Fold:**Rubredoxin-like **Superfamily:**Zn-finger domain of Sec23/24 **Family:**Zn-finger domain of Sec23/24
76	c2voyC_		Alignment	not modelled	9.6	35	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**sarcoplasmic/endoplasmic reticulum calcium **PDBTitle:** cryoem model of copa, the copper transporting atpase from2 archaeoglobus fulgidus
77	d1l1ta3		Alignment	not modelled	9.5	29	**Fold:**Glucocorticoid receptor-like (DNA-binding domain) **Superfamily:**Glucocorticoid receptor-like (DNA-binding domain) **Family:**C-terminal, Zn-finger domain of MutM-like DNA repair proteins
78	c3ry0A_		Alignment	not modelled	9.5	24	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**putative tautomerase; **PDBTitle:** crystal structure of tomn, a 4-oxalocrotonate tautomerase homologue in2 tomaymycin biosynthetic pathway

79	d1bjpa_	Alignment	not modelled	9.4	26	**Fold:**Tautomerase/MIF **Superfamily:**Tautomerase/MIF **Family:**4-oxalocrotonate tautomerase-like
80	c3m20A_	Alignment	not modelled	9.3	13	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**4-oxalocrotonate tautomerase, putative; **PDBTitle:** crystal structure of dmpi from archaeoglobus fulgidus determined to2 2.37 angstroms resolution
81	c2iwjA_	Alignment	not modelled	9.2	50	**PDB header:**transferase **Chain:** A: **PDB Molecule:**gag-pol polyprotein; **PDBTitle:** solution structure of the zn complex of hiv-2 ncp(23-49)2 peptide, encompassing protein cchc-linker, distal cchc zn-3 binding motif and c-terminal tail.
82	c2xwxB_	Alignment	not modelled	8.8	13	**PDB header:**chitin-binding protein **Chain:** B: **PDB Molecule:**glcnac-binding protein a; **PDBTitle:** vibrio cholerae colonization factor gbpa crystal structure
83	d1fftb1	Alignment	not modelled	8.8	23	**Fold:**Cupredoxin-like **Superfamily:**Cupredoxins **Family:**Periplasmic domain of cytochrome c oxidase subunit II
84	c2jq4A_	Alignment	not modelled	8.8	8	**PDB header:**structural genomics **Chain:** A: **PDB Molecule:**hypothetical protein atu2571; **PDBTitle:** complete resonance assignments and solution structure2 calculation of atc2521 (nesg id: att6) from agrobacterium3 tumefaciens
85	d2jq4a1	Alignment	not modelled	8.8	8	**Fold:**Acyl carrier protein-like **Superfamily:**ACP-like **Family:**Acyl-carrier protein (ACP)
86	c2kaoA_	Alignment	not modelled	8.7	25	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**methionine-r-sulfoxide reductase b1; **PDBTitle:** structure of reduced mouse methionine sulfoxide reductase b12 (sec95cys mutant)
87	c2ysbA_	Alignment	not modelled	8.5	45	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**salvador homolog 1 protein; **PDBTitle:** solution structure of the first ww domain from the mouse2 salvador homolog 1 protein (sav1)
88	d1k9ra_	Alignment	not modelled	8.5	50	**Fold:**WW domain-like **Superfamily:**WW domain **Family:**WW domain
89	c2hw2A_	Alignment	not modelled	8.3	54	**PDB header:**transferase **Chain:** A: **PDB Molecule:**rifampin adp-ribosyl transferase; **PDBTitle:** crystal structure of rifampin adp-ribosyl transferase in2 complex with rifampin
90	d1u5tb1	Alignment	not modelled	8.1	21	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Vacuolar sorting protein domain
91	c2x5cB_	Alignment	not modelled	8.1	29	**PDB header:**viral protein **Chain:** B: **PDB Molecule:**hypothetical protein orf131; **PDBTitle:** crystal structure of hypothetical protein orf131 from2 pyrobaculum spherical virus
92	d1tqza1	Alignment	not modelled	8.0	15	**Fold:**PH domain-like barrel **Superfamily:**PH domain-like **Family:**Necap1 N-terminal domain-like
93	d1nmva1	Alignment	not modelled	7.7	40	**Fold:**WW domain-like **Superfamily:**WW domain **Family:**WW domain
94	c1k82D_	Alignment	not modelled	7.7	25	**PDB header:**hydrolase/dna **Chain:** D: **PDB Molecule:**formamidopyrimidine-dna glycosylase; **PDBTitle:** crystal structure of e.coli formamidopyrimidine-dna2 glycosylase (fpg) covalently trapped with dna
95	d2joza1	Alignment	not modelled	7.7	31	**Fold:**Lipocalins **Superfamily:**Lipocalins **Family:**Retinol binding protein-like
96	c1p58C_	Alignment	not modelled	7.3	44	**PDB header:**virus **Chain:** C: **PDB Molecule:**major envelope protein e; **PDBTitle:** complex organization of dengue virus membrane proteins as revealed by2 9.5 angstrom cryo-em reconstruction
97	d1nuia2	Alignment	not modelled	7.3	27	**Fold:**Rubredoxin-like **Superfamily:**Zinc beta-ribbon **Family:**DNA primase zinc finger
98	c2wcuB_	Alignment	not modelled	7.3	17	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**protein fucu homolog; **PDBTitle:** crystal structure of mammalian fucu
99	c2x4kB_	Alignment	not modelled	7.1	20	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**4-oxalocrotonate tautomerase; **PDBTitle:** crystal structure of sar1376, a putative 4-oxalocrotonate2 tautomerase from the methicillin-resistant staphylococcus3 aureus (mrsa)