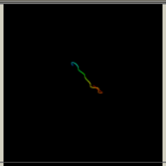
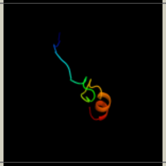
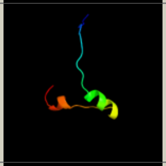
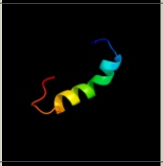
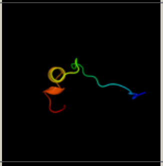
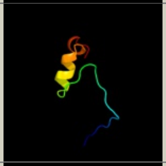
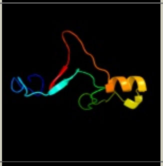
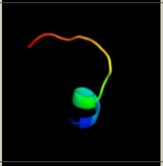
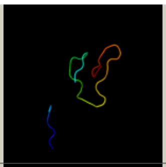
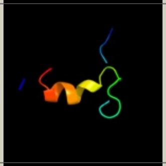
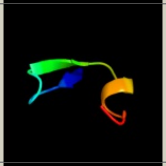
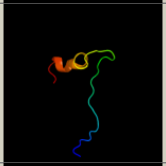
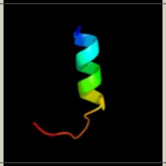
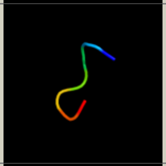
Email	l.a.kelley@imperial.ac.uk
Description	P31469
Date	Thu Jan 5 11:47:58 GMT 2012
Unique Job ID	abf5369e4615f039

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2v5iA_	Alignment		34.0	60	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**salmonella typhimurium db7155 bacteriophage det7 **PDBTitle:** structure of the receptor-binding protein of bacteriophage2 det7: a podoviral tailspike in a myovirus
2	d2gzoa1	Alignment		28.3	31	**Fold:**VC0467-like **Superfamily:**VC0467-like **Family:**VC0467-like
3	d2hafa1	Alignment		27.8	27	**Fold:**VC0467-like **Superfamily:**VC0467-like **Family:**VC0467-like
4	c3kzqE_	Alignment		26.0	37	**PDB header:**structural genomics, unknown function **Chain:** E: **PDB Molecule:**putative uncharacterized protein vp2116; **PDBTitle:** the crystal structure of the protein with unknown function from vibrio2 parahaemolyticus rimd 2210633
5	c2aj2A_	Alignment		25.0	27	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**hypothetical upf0301 protein vc0467; **PDBTitle:** x-ray crystal structure of protein vc0467 from vibrio2 cholerae. northeast structural genomics consortium target3 vcr8.
6	c2in3A_	Alignment		24.5	43	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**hypothetical protein; **PDBTitle:** crystal structure of a putative protein disulfide isomerase from2 nitrosomonas europaea
7	d2do8a1	Alignment		23.9	23	**Fold:**VC0467-like **Superfamily:**VC0467-like **Family:**VC0467-like
8	c1x31D_	Alignment		23.8	19	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**sarcosine oxidase delta subunit; **PDBTitle:** crystal structure of heterotetrameric sarcosine oxidase from2 corynebacterium sp. u-96
9	d2ct1a1	Alignment		21.6	36	**Fold:**beta-beta-alpha zinc fingers **Superfamily:**beta-beta-alpha zinc fingers **Family:**Classic zinc finger, C2H2
10	c2dvwB_	Alignment		21.1	31	**PDB header:**cell cycle/protein-binding **Chain:** B: **PDB Molecule:**26s protease regulatory subunit 6b; **PDBTitle:** structure of the oncoprotein gankyrin in complex with s62 atpase of the 26s proteasome
11	c3mjhD_	Alignment		20.9	53	**PDB header:**protein transport **Chain:** D: **PDB Molecule:**early endosome antigen 1; **PDBTitle:** crystal structure of human rab5a in complex with the c2h2 zinc finger2 of eea1

12	c2jm1A_	Alignment		20.7	26	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**transcriptional regulator atrx; **PDBTitle:** structures and chemical shift assignments for the add domain of the2 atrx protein
13	c2dzoD_	Alignment		20.5	31	**PDB header:**protein binding **Chain:** D: **PDB Molecule:**26s protease regulatory subunit 6b homolog; **PDBTitle:** crystal structure analysis of yeast nas6p complexed with2 the proteasome subunit, rpt3
14	d2gs5a1	Alignment		19.5	29	**Fold:**VC0467-like **Superfamily:**VC0467-like **Family:**VC0467-like
15	d2dida1	Alignment		19.1	21	**Fold:**B-box zinc-binding domain **Superfamily:**B-box zinc-binding domain **Family:**B-box zinc-binding domain
16	d2ew0a1	Alignment		19.0	23	**Fold:**VC0467-like **Superfamily:**VC0467-like **Family:**VC0467-like
17	c3mhvC_	Alignment		16.7	33	**PDB header:**protein transport **Chain:** C: **PDB Molecule:**vacuolar protein sorting-associated protein 4; **PDBTitle:** crystal structure of vps4 and vta1
18	c2yrgA_	Alignment		15.9	16	**PDB header:**ligase **Chain:** A: **PDB Molecule:**tripartite motif-containing protein 5; **PDBTitle:** solution structure of the b-box domain from tripartite2 motif-containing protein 5
19	c3gl5A_	Alignment		15.2	57	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**putative dsba oxidoreductase sco1869; **PDBTitle:** crystal structure of probable dsba oxidoreductase sco1869 from2 streptomyces coelicolor
20	d2ctda2	Alignment		14.1	67	**Fold:**beta-beta-alpha zinc fingers **Superfamily:**beta-beta-alpha zinc fingers **Family:**Classic zinc finger, C2H2
21	d2ct7a1	Alignment	not modelled	13.5	17	**Fold:**RING/U-box **Superfamily:**RING/U-box **Family:**IBR domain
22	c2e5rA_	Alignment	not modelled	13.2	26	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**dystrobrevin alpha; **PDBTitle:** solution structure of the zz domain of dystrobrevin alpha2 (dystrobrevin-alpha)
23	c1rimA_	Alignment	not modelled	13.1	50	**PDB header:**de novo protein **Chain:** A: **PDB Molecule:**e6apc2 peptide; **PDBTitle:** e6-binding zinc finger (e6apc2)
24	c1x4jA_	Alignment	not modelled	13.0	24	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**ring finger protein 38; **PDBTitle:** solution structure of ring finger in ring finger protein 38
25	c3bciA_	Alignment	not modelled	12.1	38	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**disulfide bond protein a; **PDBTitle:** crystal structure of staphylococcus aureus dsba
26	c1rikA_	Alignment	not modelled	12.0	50	**PDB header:**de novo protein **Chain:** A: **PDB Molecule:**e6apc1 peptide; **PDBTitle:** e6-binding zinc finger (e6apc1)
27	d1ibia2	Alignment	not modelled	11.9	75	**Fold:**Glucocorticoid receptor-like (DNA-binding domain) **Superfamily:**Glucocorticoid receptor-like (DNA-binding domain) **Family:**LIM domain
28	c2egmA_	Alignment	not modelled	11.9	26	**PDB header:**transcription/metal binding protein **Chain:** A: **PDB Molecule:**tripartite motif-containing protein 41; **PDBTitle:** solution structure of the zf-b_box domain from human2 tripartite motif protein 41
29	d2yt9a2	Alignment	not modelled	11.7	33	**Fold:**beta-beta-alpha zinc fingers **Superfamily:**beta-beta-alpha zinc fingers

						Family: Classic zinc finger, C2H2
30	c2hr5B_	Alignment	not modelled	11.7	13	**PDB header:**metal binding protein **Chain:** B: **PDB Molecule:**rubrerythrin; **PDBTitle:** pf1283- rubrerythrin from pyrococcus furiosus iron bound form
31	d2djaa1	Alignment	not modelled	11.6	30	**Fold:**B-box zinc-binding domain **Superfamily:**B-box zinc-binding domain **Family:**B-box zinc-binding domain
32	c1yzxB_	Alignment	not modelled	11.5	29	**PDB header:**transferase **Chain:** B: **PDB Molecule:**glutathione s-transferase kappa 1; **PDBTitle:** crystal structure of human kappa class glutathione2 transferase
33	c2imeA_	Alignment	not modelled	11.4	29	**PDB header:**transferase **Chain:** A: **PDB Molecule:**2-hydroxychromene-2-carboxylate isomerase; **PDBTitle:** 2-hydroxychromene-2-carboxylate isomerase: a kappa class glutathione-2 s-transferase from pseudomonas putida
34	d2fc7a1	Alignment	not modelled	11.3	23	**Fold:**RING/U-box **Superfamily:**RING/U-box **Family:**ZZ domain
35	d1xpna_	Alignment	not modelled	11.2	43	**Fold:**Prealbumin-like **Superfamily:**Hypothetical protein PA1324 **Family:**Hypothetical protein PA1324
36	d2d8ua1	Alignment	not modelled	11.2	26	**Fold:**B-box zinc-binding domain **Superfamily:**B-box zinc-binding domain **Family:**B-box zinc-binding domain
37	c2d8uA_	Alignment	not modelled	10.9	26	**PDB header:**ligase **Chain:** A: **PDB Molecule:**ubiquitin ligase trim63; **PDBTitle:** solution structure of the b-box domain of the human2 tripartite motif-containing 63 protein
38	d2ds5a1	Alignment	not modelled	10.7	15	**Fold:**Glucocorticoid receptor-like (DNA-binding domain) **Superfamily:**Glucocorticoid receptor-like (DNA-binding domain) **Family:**ClpX chaperone zinc binding domain
39	c1ovxB_	Alignment	not modelled	10.7	15	**PDB header:**metal binding protein **Chain:** B: **PDB Molecule:**atp-dependent clp protease atp-binding subunit clpx; **PDBTitle:** nmr structure of the e. coli clpx chaperone zinc binding domain dimer
40	c2yt5A_	Alignment	not modelled	10.6	26	**PDB header:**transcription **Chain:** A: **PDB Molecule:**metal-response element-binding transcription **PDBTitle:** solution structure of the phd domain of metal-response2 element-binding transcription factor 2
41	c3gmfA_	Alignment	not modelled	10.6	43	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**protein-disulfide isomerase; **PDBTitle:** crystal structure of protein-disulfide isomerase from novosphingobium2 aromaticivorans
42	c2wwaJ_	Alignment	not modelled	10.4	36	**PDB header:**ribosome **Chain:** J: **PDB Molecule:**60s ribosomal protein l19; **PDBTitle:** cryo-em structure of idle yeast ssh1 complex bound to the2 yeast 80s ribosome
43	d6rxna_	Alignment	not modelled	10.3	23	**Fold:**Rubredoxin-like **Superfamily:**Rubredoxin-like **Family:**Rubredoxin
44	d1dfxa2	Alignment	not modelled	10.1	36	**Fold:**Rubredoxin-like **Superfamily:**Rubredoxin-like **Family:**Desulforedoxin
45	d1r4wa_	Alignment	not modelled	9.9	29	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**DsbA-like
46	d1x68a1	Alignment	not modelled	9.4	23	**Fold:**Glucocorticoid receptor-like (DNA-binding domain) **Superfamily:**Glucocorticoid receptor-like (DNA-binding domain) **Family:**LIM domain
47	d1iiza_	Alignment	not modelled	9.4	21	**Fold:**Lysozyme-like **Superfamily:**Lysozyme-like **Family:**C-type lysozyme
48	c3alrA_	Alignment	not modelled	9.3	43	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**nanos protein; **PDBTitle:** crystal structure of nanos
49	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
50	c2difA_	Alignment	not modelled	9.3	21	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**tripartite motif protein 39; **PDBTitle:** one sequence two fold ? : miss fold of the zf-b-box domain2 from human tripartite motif protein 39
51	c2csvA_	Alignment	not modelled	9.1	20	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**tripartite motif protein 29; **PDBTitle:** solution structure of the zf-b_box type2 domain of human2 tripartite motif protein trim29 isoform alpha
52	c3fz5C_	Alignment	not modelled	9.1	0	**PDB header:**isomerase **Chain:** C: **PDB Molecule:**possible 2-hydroxychromene-2-carboxylate isomerase; **PDBTitle:** crystal structure of possible 2-hydroxychromene-2-carboxylate2 isomerase from rhodobacter sphaeroides
53	c3kp9A_	Alignment	not modelled	8.8	18	**PDB header:**blood coagulation,oxidoreductase **Chain:** A: **PDB Molecule:**vkorc1/thioredoxin domain protein; **PDBTitle:** structure of a bacterial homolog of vitamin k epoxide reductase
54	c3c7mB_	Alignment	not modelled	8.8	43	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**thiol:disulfide interchange protein dsba-like; **PDBTitle:** crystal structure of reduced dsbl
						PDB header:transferase

55	c2e6iA_	Alignment	not modelled	8.8	44	**Chain:** A: **PDB Molecule:**tyrosine-protein kinase itk/tsk; **PDBTitle:** solution structure of the btk motif of tyrosine-protein2 kinase itk from human
56	d1gd6a_	Alignment	not modelled	8.7	21	**Fold:**Lysozyme-like **Superfamily:**Lysozyme-like **Family:**C-type lysozyme
57	c2ds8A_	Alignment	not modelled	8.5	15	**PDB header:**metal binding protein, protein binding **Chain:** A: **PDB Molecule:**atp-dependent clp protease atp-binding subunit **PDBTitle:** structure of the zbd-xb complex
58	d1i9za_	Alignment	not modelled	8.5	17	**Fold:**DNase I-like **Superfamily:**DNase I-like **Family:**Inositol polyphosphate 5-phosphatase (IPP5)
59	c2k5cA_	Alignment	not modelled	8.4	28	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**uncharacterized protein pf0385; **PDBTitle:** nmr structure for pf0385
60	d2nwia1	Alignment	not modelled	8.4	23	**Fold:**Chorismate lyase-like **Superfamily:**Chorismate lyase-like **Family:**AF1396-like
61	c3gn3B_	Alignment	not modelled	8.4	43	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**putative protein-disulfide isomerase; **PDBTitle:** crystal structure of a putative protein-disulfide isomerase from2 pseudomonas syringae to 2.5a resolution.
62	d1x6fa1	Alignment	not modelled	8.4	33	**Fold:**beta-beta-alpha zinc fingers **Superfamily:**beta-beta-alpha zinc fingers **Family:**Classic zinc finger, C2H2
63	d1dx8a_	Alignment	not modelled	8.3	31	**Fold:**Rubredoxin-like **Superfamily:**Rubredoxin-like **Family:**Rubredoxin
64	d1vq0a2	Alignment	not modelled	8.2	30	**Fold:**HSP33 redox switch-like **Superfamily:**HSP33 redox switch-like **Family:**HSP33 redox switch-like
65	d1wena_	Alignment	not modelled	8.2	15	**Fold:**FYVE/PHD zinc finger **Superfamily:**FYVE/PHD zinc finger **Family:**PHD domain
66	c3ld0Q_	Alignment	not modelled	7.9	30	**PDB header:**gene regulation **Chain:** Q: **PDB Molecule:**inhibitor of trap, regulated by t-box (trp) sequence rtpa; **PDBTitle:** crystal structure of b.licheniformis anti-trap protein, an antagonist2 of trap-rna interactions
67	d2csva1	Alignment	not modelled	7.8	20	**Fold:**B-box zinc-binding domain **Superfamily:**B-box zinc-binding domain **Family:**B-box zinc-binding domain
68	d1fkqa_	Alignment	not modelled	7.8	20	**Fold:**Lysozyme-like **Superfamily:**Lysozyme-like **Family:**C-type lysozyme
69	c1ij2C_	Alignment	not modelled	7.8	27	**PDB header:**transcription **Chain:** C: **PDB Molecule:**general control protein gcn4; **PDBTitle:** gcn4-pvtl coiled-coil trimer with threonine at the a(16)2 position
70	d1iu5a_	Alignment	not modelled	7.7	27	**Fold:**Rubredoxin-like **Superfamily:**Rubredoxin-like **Family:**Rubredoxin
71	d1vzya2	Alignment	not modelled	7.6	20	**Fold:**HSP33 redox switch-like **Superfamily:**HSP33 redox switch-like **Family:**HSP33 redox switch-like
72	d2dq5a1	Alignment	not modelled	7.5	32	**Fold:**B-box zinc-binding domain **Superfamily:**B-box zinc-binding domain **Family:**B-box zinc-binding domain
73	d1xjha_	Alignment	not modelled	7.5	30	**Fold:**HSP33 redox switch-like **Superfamily:**HSP33 redox switch-like **Family:**HSP33 redox switch-like
74	c2krkA_	Alignment	not modelled	7.5	38	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**26s protease regulatory subunit 8; **PDBTitle:** solution nmr structure of 26s protease regulatory subunit 82 from h.sapiens, northeast structural genomics consortium3 target target hr3102a
75	d2rdva_	Alignment	not modelled	7.4	27	**Fold:**Rubredoxin-like **Superfamily:**Rubredoxin-like **Family:**Rubredoxin
76	c3cegA_	Alignment	not modelled	7.4	12	**PDB header:**ligase **Chain:** A: **PDB Molecule:**baculoviral iap repeat-containing protein 6; **PDBTitle:** crystal structure of the ubc domain of baculoviral iap2 repeat-containing protein 6
77	c3ghaA_	Alignment	not modelled	7.3	43	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**disulfide bond formation protein d; **PDBTitle:** crystal structure of etda-treated bdbd (reduced)
78	c1ij2B_	Alignment	not modelled	7.3	27	**PDB header:**transcription **Chain:** B: **PDB Molecule:**general control protein gcn4; **PDBTitle:** gcn4-pvtl coiled-coil trimer with threonine at the a(16)2 position
79	c3a44D_	Alignment	not modelled	7.2	33	**PDB header:**metal binding protein **Chain:** D: **PDB Molecule:**hydrogenase nickel incorporation protein hypa; **PDBTitle:** crystal structure of hypa in the dimeric form
80	c2h51B_	Alignment	not modelled	7.1	27	**PDB header:**hydrolase/hydrolase inhibitor **Chain:** B: **PDB Molecule:**caspase-1; **PDBTitle:** crystal structure of human caspase-1 (glu390->asp and arg286->lys) in2 complex with 3-[2-(2-benzyloxycarbonylamino-3-methyl-butyrylamino)-3 propionylamino]-4-oxo-pentanoic acid (z-vad-fmk)

81	d1m4ma_	Alignment	not modelled	7.1	11	**Fold:**Inhibitor of apoptosis (IAP) repeat **Superfamily:**Inhibitor of apoptosis (IAP) repeat **Family:**Inhibitor of apoptosis (IAP) repeat
82	c3gn5B_	Alignment	not modelled	7.0	21	**PDB header:**dna binding protein **Chain:** B: **PDB Molecule:**hth-type transcriptional regulator mqsa (ygit/b3021); **PDBTitle:** structure of the e. coli protein mqsa (ygit/b3021)
83	d2dipa1	Alignment	not modelled	7.0	24	**Fold:**RING/U-box **Superfamily:**RING/U-box **Family:**ZZ domain
84	d1ypze2	Alignment	not modelled	6.9	17	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**Immunoglobulin **Family:**C1 set domains (antibody constant domain-like)
85	d1h7va_	Alignment	not modelled	6.8	31	**Fold:**Rubredoxin-like **Superfamily:**Rubredoxin-like **Family:**Rubredoxin
86	d2gvia2	Alignment	not modelled	6.6	33	**Fold:**Glucocorticoid receptor-like (DNA-binding domain) **Superfamily:**Glucocorticoid receptor-like (DNA-binding domain) **Family:**FwdE C-terminal domain-like
87	c2c2zB_	Alignment	not modelled	6.5	0	**PDB header:**hydrolase/hydrolase inhibitor **Chain:** B: **PDB Molecule:**caspase-8 p10 subunit; **PDBTitle:** crystal structure of caspase-8 in complex with aza-peptide michael2 acceptor inhibitor
88	d2cota1	Alignment	not modelled	6.5	50	**Fold:**beta-beta-alpha zinc fingers **Superfamily:**beta-beta-alpha zinc fingers **Family:**Classic zinc finger, C2H2
89	d1lv3a_	Alignment	not modelled	6.5	26	**Fold:**Glucocorticoid receptor-like (DNA-binding domain) **Superfamily:**Glucocorticoid receptor-like (DNA-binding domain) **Family:**Hypothetical zinc finger protein YacG
90	d2ewla1	Alignment	not modelled	6.4	40	**Fold:**E7 C-terminal domain-like **Superfamily:**E7 C-terminal domain-like **Family:**E7 C-terminal domain-like
91	d1hxma2	Alignment	not modelled	6.4	22	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**Immunoglobulin **Family:**C1 set domains (antibody constant domain-like)
92	d1f6sa_	Alignment	not modelled	6.3	17	**Fold:**Lysozyme-like **Superfamily:**Lysozyme-like **Family:**C-type lysozyme
93	d1rb9a_	Alignment	not modelled	6.3	28	**Fold:**Rubredoxin-like **Superfamily:**Rubredoxin-like **Family:**Rubredoxin
94	c2bsjB_	Alignment	not modelled	5.9	57	**PDB header:**chaperone **Chain:** B: **PDB Molecule:**chaperone protein syct; **PDBTitle:** native crystal structure of the type iii secretion2 chaperone syct from yersinia enterocolitica
95	d1llmc2	Alignment	not modelled	5.9	50	**Fold:**beta-beta-alpha zinc fingers **Superfamily:**beta-beta-alpha zinc fingers **Family:**Classic zinc finger, C2H2
96	d1nh8a2	Alignment	not modelled	5.9	32	**Fold:**Ferredoxin-like **Superfamily:**GlnB-like **Family:**ATP phosphoribosyltransferase (ATP-PRTase, HisG), regulatory C-terminal domain
97	c2ei5B_	Alignment	not modelled	5.8	27	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**hypothetical protein ttha0061; **PDBTitle:** crystal structure of hypothetical protein(ttha0061) from thermus2 thermophilus
98	d1paaa_	Alignment	not modelled	5.8	25	**Fold:**beta-beta-alpha zinc fingers **Superfamily:**beta-beta-alpha zinc fingers **Family:**Classic zinc finger, C2H2
99	d1x6ea2	Alignment	not modelled	5.8	63	**Fold:**beta-beta-alpha zinc fingers **Superfamily:**beta-beta-alpha zinc fingers **Family:**Classic zinc finger, C2H2