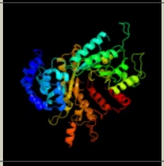
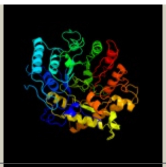
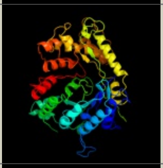
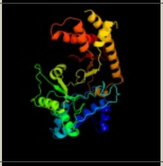
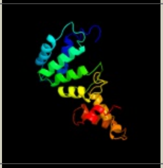
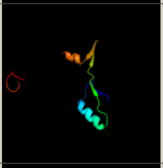
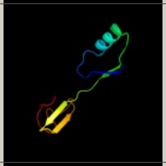
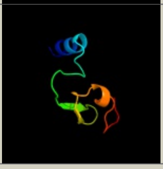
Phyre^2

Email	l.a.kelley@imperial.ac.uk
Description	P28903
Date	Thu Jan 5 11:45:16 GMT 2012
Unique Job ID	a3d84c41e8b53620

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1hk8A_	Alignment		100.0	57	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**anaerobic ribonucleotide-triphosphate reductase; **PDBTitle:** structural basis for allosteric substrate specificity2 regulation in class iii ribonucleotide reductases:3 nrdd in complex with dgtp
2	d1hk8a_	Alignment		100.0	57	**Fold:**PFL-like glycyl radical enzymes **Superfamily:**PFL-like glycyl radical enzymes **Family:**Class III anaerobic ribonucleotide reductase NRDD subunit
3	c3r1rB_	Alignment		99.9	13	**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
4	c3hnfA_	Alignment		99.8	14	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**ribonucleoside-diphosphate reductase large subunit; **PDBTitle:** crystal structure of human ribonucleotide reductase 1 bound to the2 effectors ttp and datp
5	c2cvuA_	Alignment		99.8	15	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**ribonucleoside-diphosphate reductase large chain **PDBTitle:** structures of yeast ribonucleotide reductase i
6	c2wghA_	Alignment		99.8	14	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**ribonucleoside-diphosphate reductase large **PDBTitle:** human ribonucleotide reductase r1 subunit (rrm1) in complex2 with datp and mg.
7	c1xjeA_	Alignment		99.7	14	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**ribonucleotide reductase, b12-dependent; **PDBTitle:** structural mechanism of allosteric substrate specificity in a2 ribonucleotide reductase: dttp-gdp complex
8	c1pemA_	Alignment		99.6	15	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**ribonucleoside-diphosphate reductase 2 alpha **PDBTitle:** ribonucleotide reductase protein r1e from salmonella2 typhimurium
9	d1r9da_	Alignment		99.5	18	**Fold:**PFL-like glycyl radical enzymes **Superfamily:**PFL-like glycyl radical enzymes **Family:**PFL-like
10	d1h16a_	Alignment		99.3	16	**Fold:**PFL-like glycyl radical enzymes **Superfamily:**PFL-like glycyl radical enzymes **Family:**PFL-like
11	c2f3oB_	Alignment		99.3	18	**PDB header:**unknown function **Chain:** B: **PDB Molecule:**pyruvate formate-lyase 2; **PDBTitle:** crystal structure of a glycyl radical enzyme from archaeoglobus2 fulgidus

12	d1l1la_	Alignment		99.3	13	**Fold:**PFL-like glycyl radical enzymes **Superfamily:**PFL-like glycyl radical enzymes **Family:**B12-dependent (class II) ribonucleotide reductase
13	d1peqa2	Alignment		99.1	14	**Fold:**PFL-like glycyl radical enzymes **Superfamily:**PFL-like glycyl radical enzymes **Family:**R1 subunit of ribonucleotide reductase, C-terminal domain
14	c2y8nC_	Alignment		98.9	16	**PDB header:**lyase **Chain:** C: **PDB Molecule:**4-hydroxyphenylacetate decarboxylase large subunit; **PDBTitle:** crystal structure of glycyl radical enzyme
15	d1rlra2	Alignment		98.8	15	**Fold:**PFL-like glycyl radical enzymes **Superfamily:**PFL-like glycyl radical enzymes **Family:**R1 subunit of ribonucleotide reductase, C-terminal domain
16	d1qhma_	Alignment		98.8	15	**Fold:**PFL-like glycyl radical enzymes **Superfamily:**PFL-like glycyl radical enzymes **Family:**PFL-like
17	d1rlra1	Alignment		98.7	12	**Fold:**R1 subunit of ribonucleotide reductase, N-terminal domain **Superfamily:**R1 subunit of ribonucleotide reductase, N-terminal domain **Family:**R1 subunit of ribonucleotide reductase, N-terminal domain
18	c3a44D_	Alignment		96.0	17	**PDB header:**metal binding protein **Chain:** D: **PDB Molecule:**hydrogenase nickel incorporation protein hypa; **PDBTitle:** crystal structure of hypa in the dimeric form
19	c2kdxA_	Alignment		95.9	11	**PDB header:**metal-binding protein **Chain:** A: **PDB Molecule:**hydrogenase/urease nickel incorporation protein **PDBTitle:** solution structure of hypa protein
20	c1dvbA_	Alignment		95.1	20	**PDB header:**electron transport **Chain:** A: **PDB Molecule:**rubrerythrin; **PDBTitle:** rubrerythrin
21	c1yuzB_	Alignment	not modelled	94.1	26	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**nigerythrin; **PDBTitle:** partially reduced state of nigerythrin
22	c2hr5B_	Alignment	not modelled	93.8	30	**PDB header:**metal binding protein **Chain:** B: **PDB Molecule:**rubrerythrin; **PDBTitle:** pf1283- rubrerythrin from pyrococcus furiosus iron bound form
23	d2gmga1	Alignment	not modelled	89.2	18	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**PF0610-like
24	c2lcqA_	Alignment	not modelled	88.3	38	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**putative toxin vapc6; **PDBTitle:** solution structure of the endonuclease nob1 from p.horikoshii
25	d1lkoa2	Alignment	not modelled	85.6	33	**Fold:**Rubredoxin-like **Superfamily:**Rubredoxin-like **Family:**Rubredoxin
26	d1yuza2	Alignment	not modelled	85.1	29	**Fold:**Rubredoxin-like **Superfamily:**Rubredoxin-like **Family:**Rubredoxin
27	c3lpeF_	Alignment	not modelled	84.8	27	**PDB header:**transferase **Chain:** F: **PDB Molecule:**dna-directed rna polymerase subunit e''; **PDBTitle:** crystal structure of spt4/5ngn heterodimer complex from methanococcus2 jannaschii
28	d1nnqa2	Alignment	not modelled	84.6	30	**Fold:**Rubredoxin-like **Superfamily:**Rubredoxin-like **Family:**Rubredoxin
						Fold: Rubredoxin-like

29	d1ryqa_	Alignment	not modelled	82.5	28	**Superfamily:**RNA polymerase subunits **Family:**RpoE2-like
30	d1dx8a_	Alignment	not modelled	82.2	40	**Fold:**Rubredoxin-like **Superfamily:**Rubredoxin-like **Family:**Rubredoxin
31	d2j0151	Alignment	not modelled	82.0	30	**Fold:**Rubredoxin-like **Superfamily:**Zn-binding ribosomal proteins **Family:**Ribosomal protein L32p
32	d2zjrz1	Alignment	not modelled	81.7	25	**Fold:**Rubredoxin-like **Superfamily:**Zn-binding ribosomal proteins **Family:**Ribosomal protein L32p
33	c1s24A_	Alignment	not modelled	81.6	38	**PDB header:**electron transport **Chain:** A: **PDB Molecule:**rubredoxin 2; **PDBTitle:** rubredoxin domain ii from pseudomonas oleovorans
34	d1s24a_	Alignment	not modelled	81.6	38	**Fold:**Rubredoxin-like **Superfamily:**Rubredoxin-like **Family:**Rubredoxin
35	d2apob1	Alignment	not modelled	81.5	45	**Fold:**Rubredoxin-like **Superfamily:**Nop10-like SnoRNP **Family:**Nucleolar RNA-binding protein Nop10-like
36	d4rxna_	Alignment	not modelled	81.3	32	**Fold:**Rubredoxin-like **Superfamily:**Rubredoxin-like **Family:**Rubredoxin
37	c2v3bB_	Alignment	not modelled	81.2	35	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**rubredoxin 2; **PDBTitle:** crystal structure of the electron transfer complex2 rubredoxin - rubredoxin reductase from pseudomonas3 aeruginosa.
38	d1iroa_	Alignment	not modelled	81.0	32	**Fold:**Rubredoxin-like **Superfamily:**Rubredoxin-like **Family:**Rubredoxin
39	d1rb9a_	Alignment	not modelled	80.8	32	**Fold:**Rubredoxin-like **Superfamily:**Rubredoxin-like **Family:**Rubredoxin
40	d2ey4e1	Alignment	not modelled	80.4	40	**Fold:**Rubredoxin-like **Superfamily:**Nop10-like SnoRNP **Family:**Nucleolar RNA-binding protein Nop10-like
41	c2gb5B_	Alignment	not modelled	80.4	20	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**nadh pyrophosphatase; **PDBTitle:** crystal structure of nadh pyrophosphatase (ec 3.6.1.22) (1790429) from2 escherichia coli k12 at 2.30 a resolution
42	d1h7va_	Alignment	not modelled	80.3	30	**Fold:**Rubredoxin-like **Superfamily:**Rubredoxin-like **Family:**Rubredoxin
43	d2gnra1	Alignment	not modelled	80.3	23	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**SSO2064-like
44	d1qcva_	Alignment	not modelled	80.3	19	**Fold:**Rubredoxin-like **Superfamily:**Rubredoxin-like **Family:**Rubredoxin
45	d1iu5a_	Alignment	not modelled	79.8	36	**Fold:**Rubredoxin-like **Superfamily:**Rubredoxin-like **Family:**Rubredoxin
46	c3axtA_	Alignment	not modelled	79.7	26	**PDB header:**transferase **Chain:** A: **PDB Molecule:**probable n(2),n(2)-dimethylguanosine trna methyltransferase **PDBTitle:** complex structure of trna methyltransferase trm1 from aquifex aeolicus2 with s-adenosyl-l-methionine
47	d2dsxa1	Alignment	not modelled	79.2	36	**Fold:**Rubredoxin-like **Superfamily:**Rubredoxin-like **Family:**Rubredoxin
48	c2k2dA_	Alignment	not modelled	78.4	20	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**ring finger and chy zinc finger domain- **PDBTitle:** solution nmr structure of c-terminal domain of human pirh2.2 northeast structural genomics consortium (nesg) target ht2c
49	d1brfa_	Alignment	not modelled	76.9	36	**Fold:**Rubredoxin-like **Superfamily:**Rubredoxin-like **Family:**Rubredoxin
50	c2ba1B_	Alignment	not modelled	76.9	25	**PDB header:**rna binding protein **Chain:** B: **PDB Molecule:**archaeal exosome rna binding protein csl4; **PDBTitle:** archaeal exosome core
51	d6rxna_	Alignment	not modelled	76.5	32	**Fold:**Rubredoxin-like **Superfamily:**Rubredoxin-like **Family:**Rubredoxin
52	d2cona1	Alignment	not modelled	73.9	35	**Fold:**Rubredoxin-like **Superfamily:**NOB1 zinc finger-like **Family:**NOB1 zinc finger-like
53	c2qkdA_	Alignment	not modelled	72.8	23	**PDB header:**signaling protein, cell cycle **Chain:** A: **PDB Molecule:**zinc finger protein zpr1; **PDBTitle:** crystal structure of tandem zpr1 domains
54	c2nn6I_	Alignment	not modelled	72.6	13	**PDB header:**hydrolase/transferase **Chain:** I: **PDB Molecule:**3'-5' exoribonuclease csl4 homolog; **PDBTitle:** structure of the human rna exosome composed of rrp41, rrp45,2 rrp46, rrp43, mtr3, rrp42, csl4, rrp4, and rrp40
55	d2rdva_	Alignment	not modelled	72.4	48	**Fold:**Rubredoxin-like **Superfamily:**Rubredoxin-like **Family:**Rubredoxin
						Fold: FdhE-like

56	d2fiya1	Alignment	not modelled	70.3	30	**Superfamily:**FdhE-like **Family:**FdhE-like
57	c2kn9A_	Alignment	not modelled	70.2	42	**PDB header:**electron transport **Chain:** A: **PDB Molecule:**rubredoxin; **PDBTitle:** solution structure of zinc-substituted rubredoxin b (rv3250c) from2 mycobacterium tuberculosis. seattle structural genomics center for3 infectious disease target mytud.01635.a
58	c2f9iD_	Alignment	not modelled	69.1	22	**PDB header:**transferase **Chain:** D: **PDB Molecule:**acetyl-coenzyme a carboxylase carboxyl **PDBTitle:** crystal structure of the carboxyltransferase subunit of acc2 from staphylococcus aureus
59	d2ct7a1	Alignment	not modelled	66.0	28	**Fold:**RING/U-box **Superfamily:**RING/U-box **Family:**IBR domain
60	d2qam01	Alignment	not modelled	65.2	23	**Fold:**Rubredoxin-like **Superfamily:**Zn-binding ribosomal proteins **Family:**Ribosomal protein L32p
61	c1u5kA_	Alignment	not modelled	65.0	19	**PDB header:**recombination,replication **Chain:** A: **PDB Molecule:**hypothetical protein; **PDBTitle:** recombinational repair protein reco
62	d2dkta1	Alignment	not modelled	63.6	24	**Fold:**CHY zinc finger-like **Superfamily:**CHY zinc finger-like **Family:**CHY zinc finger
63	d1pfva3	Alignment	not modelled	62.7	30	**Fold:**Rubredoxin-like **Superfamily:**Methionyl-tRNA synthetase (MetRS), Zn-domain **Family:**Methionyl-tRNA synthetase (MetRS), Zn-domain
64	c3ir9A_	Alignment	not modelled	62.2	35	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**peptide chain release factor subunit 1; **PDBTitle:** c-terminal domain of peptide chain release factor from2 methanosarcina mazei.
65	c2ktvA_	Alignment	not modelled	61.3	19	**PDB header:**translation **Chain:** A: **PDB Molecule:**eukaryotic peptide chain release factor subunit 1; **PDBTitle:** human erf1 c-domain, "open" conformer
66	d1nuia2	Alignment	not modelled	60.5	36	**Fold:**Rubredoxin-like **Superfamily:**Zinc beta-ribbon **Family:**DNA primase zinc finger
67	c2f9yB_	Alignment	not modelled	59.8	32	**PDB header:**ligase **Chain:** B: **PDB Molecule:**acetyl-coenzyme a carboxylase carboxyl transferase subunit **PDBTitle:** the crystal structure of the carboxyltransferase subunit of acc from2 escherichia coli
68	d2f9yb1	Alignment	not modelled	59.8	32	**Fold:**ClpP/crotonase **Superfamily:**ClpP/crotonase **Family:**Biotin dependent carboxylase carboxyltransferase domain
69	d1ltla_	Alignment	not modelled	59.6	22	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**DNA replication initiator (cdc21/cdc54) N-terminal domain
70	c2aklA_	Alignment	not modelled	56.1	21	**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
71	c3f2cA_	Alignment	not modelled	56.0	40	**PDB header:**transferase/dna **Chain:** A: **PDB Molecule:**geobacillus kaustophilus dna polc; **PDBTitle:** dna polymerase polc from geobacillus kaustophilus complex with dna,2 dgtp and mn
72	d2nn6i1	Alignment	not modelled	55.0	13	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
73	c3cngC_	Alignment	not modelled	54.5	29	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**nudix hydrolase; **PDBTitle:** crystal structure of nudix hydrolase from nitrosomonas europaea
74	c1ltlE_	Alignment	not modelled	54.1	22	**PDB header:**replication **Chain:** E: **PDB Molecule:**dna replication initiator (cdc21/cdc54); **PDBTitle:** the dodecamer structure of mcm from archaeal m.2 thermoautotrophicum
75	c3bjiA_	Alignment	not modelled	53.7	38	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**proto-oncogene vav; **PDBTitle:** structural basis of promiscuous guanine nucleotide exchange2 by the t-cell essential vav1
76	d2akla2	Alignment	not modelled	53.6	23	**Fold:**Rubredoxin-like **Superfamily:**Zinc beta-ribbon **Family:**PhnA zinc-binding domain
77	c1m2oA_	Alignment	not modelled	53.0	13	**PDB header:**protein transport/signaling protein **Chain:** A: **PDB Molecule:**protein transport protein sec23; **PDBTitle:** crystal structure of the sec23-sar1 complex
78	c2vl6C_	Alignment	not modelled	51.4	30	**PDB header:**dna binding protein **Chain:** C: **PDB Molecule:**minichromosome maintenance protein mcm; **PDBTitle:** structural analysis of the sulfolobus solfataricus mcm2 protein n-terminal domain
79	c1vddC_	Alignment	not modelled	51.4	19	**PDB header:**recombination **Chain:** C: **PDB Molecule:**recombination protein recr; **PDBTitle:** crystal structure of recombinational repair protein recr
80	d1pfta_	Alignment	not modelled	51.2	25	**Fold:**Rubredoxin-like **Superfamily:**Zinc beta-ribbon **Family:**Transcriptional factor domain
81	c2k5cA_	Alignment	not modelled	48.1	56	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**uncharacterized protein pf0385; **PDBTitle:** nmr structure for pf0385
						Fold: ArfGap/RecO-like zinc finger

82	d1u5ka2	Alignment	not modelled	48.0	19	**Superfamily:**ArfGap/RecO-like zinc finger **Family:**RecO C-terminal domain-like
83	d1dl6a_	Alignment	not modelled	47.9	29	**Fold:**Rubredoxin-like **Superfamily:**Zinc beta-ribbon **Family:**Transcriptional factor domain
84	d2dlqa2	Alignment	not modelled	47.0	75	**Fold:**beta-beta-alpha zinc fingers **Superfamily:**beta-beta-alpha zinc fingers **Family:**Classic zinc finger, C2H2
85	c3ky9B_	Alignment	not modelled	47.0	38	**PDB header:**apoptosis **Chain:** B: **PDB Molecule:**proto-oncogene vav; **PDBTitle:** autoinhibited vav1
86	d1ynjd1	Alignment	not modelled	44.9	35	**Fold:**beta and beta-prime subunits of DNA dependent RNA-polymerase **Superfamily:**beta and beta-prime subunits of DNA dependent RNA-polymerase **Family:**RNA-polymerase beta-prime
87	c3gn5B_	Alignment	not modelled	44.5	36	**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)
88	c3eswA_	Alignment	not modelled	43.4	23	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**peptide-n(4)-(n-acetyl-beta-glucosaminyl)asparagine **PDBTitle:** complex of yeast pngase with glcnac2-iac.
89	d2ctda2	Alignment	not modelled	43.3	50	**Fold:**beta-beta-alpha zinc fingers **Superfamily:**beta-beta-alpha zinc fingers **Family:**Classic zinc finger, C2H2
90	d1x6ma_	Alignment	not modelled	42.6	28	**Fold:**Mss4-like **Superfamily:**Mss4-like **Family:**Glutathione-dependent formaldehyde-activating enzyme, Gfa
91	c1ee8A_	Alignment	not modelled	42.5	26	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**mutm (fpg) protein; **PDBTitle:** crystal structure of mutm (fpg) protein from thermus thermophilus hb8
92	c3eh2B_	Alignment	not modelled	42.5	19	**PDB header:**protein transport **Chain:** B: **PDB Molecule:**protein transport protein sec24c; **PDBTitle:** crystal structure of the human copii-coat protein sec24c
93	c1m2vB_	Alignment	not modelled	42.2	20	**PDB header:**protein transport **Chain:** B: **PDB Molecule:**protein transport protein sec24; **PDBTitle:** crystal structure of the yeast sec23/24 heterodimer
94	c2owoA_	Alignment	not modelled	41.0	44	**PDB header:**ligase/dna **Chain:** A: **PDB Molecule:**dna ligase; **PDBTitle:** last stop on the road to repair: structure of e.coli dna ligase bound2 to nicked dna-adenylate
95	c3k7aM_	Alignment	not modelled	40.3	29	**PDB header:**transcription **Chain:** M: **PDB Molecule:**transcription initiation factor iib; **PDBTitle:** crystal structure of an rna polymerase ii-tfiib complex
96	c3h0gN_	Alignment	not modelled	40.0	21	**PDB header:**transcription **Chain:** N: **PDB Molecule:**dna-directed rna polymerase ii subunit rpb2; **PDBTitle:** rna polymerase ii from schizosaccharomyces pombe
97	c2ysaA_	Alignment	not modelled	39.7	21	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**retinoblastoma-binding protein 6; **PDBTitle:** solution structure of the zinc finger cchc domain from the2 human retinoblastoma-binding protein 6 (retinoblastoma-3 binding q protein 1, rbq-1)
98	c3cw2M_	Alignment	not modelled	39.2	22	**PDB header:**translation **Chain:** M: **PDB Molecule:**translation initiation factor 2 subunit beta; **PDBTitle:** crystal structure of the intact archaeal translation2 initiation factor 2 from sulfolobus solfataricus .
99	c1pd0A_	Alignment	not modelled	39.2	20	**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)
100	d1vdda_	Alignment	not modelled	39.1	23	**Fold:**Recombination protein RecR **Superfamily:**Recombination protein RecR **Family:**Recombination protein RecR
101	c2opfA_	Alignment	not modelled	38.5	33	**PDB header:**hydrolase/dna **Chain:** A: **PDB Molecule:**endonuclease viii; **PDBTitle:** crystal structure of the dna repair enzyme endonuclease-viii (nei)2 from e. coli (r252a) in complex with ap-site containing dna substrate
102	c3eg9B_	Alignment	not modelled	38.4	16	**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
103	c2yqqA_	Alignment	not modelled	38.1	29	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**zinc finger hit domain-containing protein 3; **PDBTitle:** solution structure of the zf-hit domain in zinc finger hit2 domain-containing protein 3 (trip-3)
104	d1j6wa_	Alignment	not modelled	38.1	57	**Fold:**LuxS/MPP-like metallohydrolase **Superfamily:**LuxS/MPP-like metallohydrolase **Family:**Autoinducer-2 production protein LuxS
105	c3h7hA_	Alignment	not modelled	38.1	19	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcription elongation factor spt4; **PDBTitle:** crystal structure of the human transcription elongation factor dsif,2 hspt4/hspt5 (176-273)
106	c2pmzB_	Alignment	not modelled	38.0	28	**PDB header:**translation, transferase **Chain:** B: **PDB Molecule:**dna-directed rna polymerase subunit b; **PDBTitle:** archaeal rna polymerase from sulfolobus solfataricus
						PDB header:transferase

107	c2ja6L_	Alignment	not modelled	37.7	21	**Chain:** L: **PDB Molecule:**dna-directed rna polymerases i, ii, and iii 7.7 **PDBTitle:** cpd lesion containing rna polymerase ii elongation complex2 b
108	c2bx9J_	Alignment	not modelled	37.3	35	**PDB header:**transcription regulation **Chain:** J: **PDB Molecule:**tryptophan rna-binding attenuator protein-inhibitory **PDBTitle:** crystal structure of b.subtilis anti-trap protein, an2 antagonist of trap-rna interactions
109	c3na7A_	Alignment	not modelled	37.3	20	**PDB header:**gene regulation, chaperone **Chain:** A: **PDB Molecule:**hp0958; **PDBTitle:** 2.2 angstrom structure of the hp0958 protein from helicobacter pylori2 ccug 17874
110	c3h0gL_	Alignment	not modelled	36.8	21	**PDB header:**transcription **Chain:** L: **PDB Molecule:**dna-directed rna polymerases i, ii, and iii **PDBTitle:** rna polymerase ii from schizosaccharomyces pombe
111	d1x3za1	Alignment	not modelled	36.7	22	**Fold:**Cysteine proteinases **Superfamily:**Cysteine proteinases **Family:**Transglutaminase core
112	c1nnjA_	Alignment	not modelled	36.6	24	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**formamidopyrimidine-dna glycosylase; **PDBTitle:** crystal structure complex between the lactococcus lactis fpg and an2 abasic site containing dna
113	c2f5qA_	Alignment	not modelled	35.9	32	**PDB header:**hydrolase/dna **Chain:** A: **PDB Molecule:**formamidopyrimidine-dna glycosidase; **PDBTitle:** catalytically inactive (e3q) mutm crosslinked to oxog:c2 containing dna cc2
114	c3pkiF_	Alignment	not modelled	35.5	28	**PDB header:**hydrolase **Chain:** F: **PDB Molecule:**nad-dependent deacetylase sirtuin-6; **PDBTitle:** human sirt6 crystal structure in complex with adp ribose
115	d1j6xa_	Alignment	not modelled	35.3	43	**Fold:**LuxS/MPP-like metallohydrolase **Superfamily:**LuxS/MPP-like metallohydrolase **Family:**Autoinducer-2 production protein LuxS
116	c1v9pB_	Alignment	not modelled	35.3	56	**PDB header:**ligase **Chain:** B: **PDB Molecule:**dna ligase; **PDBTitle:** crystal structure of nad+-dependent dna ligase
117	d2dula1	Alignment	not modelled	35.1	17	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**TRM1-like
118	d1srka_	Alignment	not modelled	35.0	33	**Fold:**beta-beta-alpha zinc fingers **Superfamily:**beta-beta-alpha zinc fingers **Family:**Classic zinc finger, C2H2
119	c3pfqA_	Alignment	not modelled	35.0	29	**PDB header:**transferase **Chain:** A: **PDB Molecule:**protein kinase c beta type; **PDBTitle:** crystal structure and allosteric activation of protein kinase c beta2 ii
120	c3f9vA_	Alignment	not modelled	34.9	30	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**minichromosome maintenance protein mcm; **PDBTitle:** crystal structure of a near full-length archaeal mcm: functional2 insights for an aaa+ hexameric helicase