Phyre2

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Description	A0AUZ9
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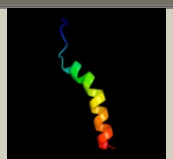
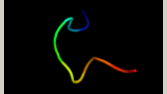
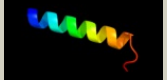
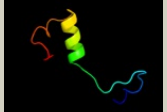
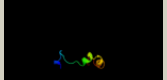
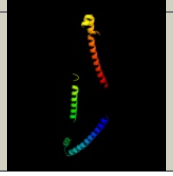
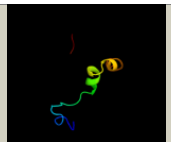
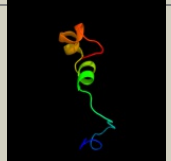
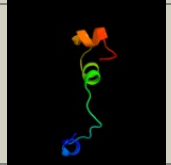
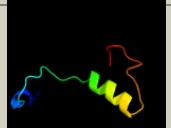
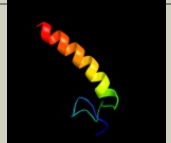
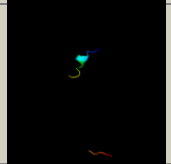
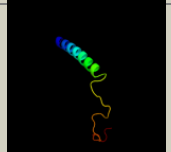
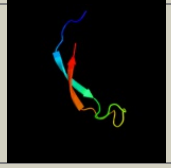
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2y0mB_	Alignment		89.8	43	**PDB header:**transcription **Chain:** B: **PDB Molecule:**male-specific lethal 1 homolog; **PDBTitle:** crystal structure of the complex between dosage2 compensation factors msl1 and mof
2	c2wb6A_	Alignment		53.5	70	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**afv1-102; **PDBTitle:** crystal structure of afv1-102, a protein from the acidianus2 filamentous virus 1
3	d2gykb1	Alignment		52.7	42	**Fold:**His-Me finger endonucleases **Superfamily:**His-Me finger endonucleases **Family:**HNH-motif
4	c7ceiB_	Alignment		50.7	42	**PDB header:**immune system **Chain:** B: **PDB Molecule:**protein (colicin e7 immunity protein); **PDBTitle:** the endonuclease domain of colicin e7 in complex with its inhibitor2 im7 protein
5	d2jb0b1	Alignment		47.5	50	**Fold:**His-Me finger endonucleases **Superfamily:**His-Me finger endonucleases **Family:**HNH-motif
6	d1r6ta1	Alignment		41.0	17	**Fold:**S15/NS1 RNA-binding domain **Superfamily:**S15/NS1 RNA-binding domain **Family:**a tRNA synthase domain
7	d1tafb_	Alignment		39.7	18	**Fold:**Histone-fold **Superfamily:**Histone-fold **Family:**TBP-associated factors, TAFs
8	c1zauA_	Alignment		34.9	32	**PDB header:**ligase **Chain:** A: **PDB Molecule:**dna ligase; **PDBTitle:** adenylation domain of nad+ dependent dna ligase from2 m.tuberculosis
9	d1v9pa3	Alignment		33.4	29	**Fold:**ATP-grasp **Superfamily:**DNA ligase/mRNA capping enzyme, catalytic domain **Family:**Adenylation domain of NAD+-dependent DNA ligase
10	d1b04a_	Alignment		30.6	40	**Fold:**ATP-grasp **Superfamily:**DNA ligase/mRNA capping enzyme, catalytic domain **Family:**Adenylation domain of NAD+-dependent DNA ligase
11	c3thfA_	Alignment		29.6	18	**PDB header:**actin-binding protein/protein binding **Chain:** A: **PDB Molecule:**protein shroom; **PDBTitle:** crystal structure of the sd2 domain from drosophila shroom

12	c3bacA_	Alignment		27.1	39	**PDB header:**ligase **Chain:** A: **PDB Molecule:**dna ligase; **PDBTitle:** structural basis for the inhibition of bacterial nad+2 dependent dna ligase
13	d1dgsa3	Alignment		25.4	29	**Fold:**ATP-grasp **Superfamily:**DNA ligase/mRNA capping enzyme, catalytic domain **Family:**Adenylation domain of NAD+-dependent DNA ligase
14	d1ta8a_	Alignment		24.8	42	**Fold:**ATP-grasp **Superfamily:**DNA ligase/mRNA capping enzyme, catalytic domain **Family:**Adenylation domain of NAD+-dependent DNA ligase
15	c2l5bA_	Alignment		22.6	55	**PDB header:**apoptosis **Chain:** A: **PDB Molecule:**activator of apoptosis harakiri; **PDBTitle:** solution structure of the transmembrane domain of bcl-2 member2 harakiri in micelles
16	c1dgsB_	Alignment		20.2	29	**PDB header:**ligase **Chain:** B: **PDB Molecule:**dna ligase; **PDBTitle:** crystal structure of nad+-dependent dna ligase from t.2 filiformis
17	c3m6wA_	Alignment		19.2	24	**PDB header:**transferase **Chain:** A: **PDB Molecule:**rrna methylase; **PDBTitle:** multi-site-specific 16s rrna methyltransferase rsmf from thermus2 thermophilus in space group p21212 in complex with s-adenosyl-l-3 methionine
18	c3v62F_	Alignment		18.6	41	**PDB header:**protein binding/dna binding protein **Chain:** F: **PDB Molecule:**atp-dependent dna helicase srs2; **PDBTitle:** structure of the s. cerevisiae srs2 c-terminal domain in complex with2 pcna conjugated to sumo on lysine 164
19	c1dipA_	Alignment		18.3	19	**PDB header:**acetylation **Chain:** A: **PDB Molecule:**delta-sleep-inducing peptide immunoreactive **PDBTitle:** the solution structure of porcine delta-sleep-inducing2 peptide immunoreactive peptide, nmr, 10 structures
20	c2fgtA_	Alignment		16.3	56	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**two-component system yycf/yycg regulatory **PDBTitle:** crystal structure of yych from bacillus subtilis
21	d1fyja_	Alignment	not modelled	16.1	22	**Fold:**S15/NS1 RNA-binding domain **Superfamily:**S15/NS1 RNA-binding domain **Family:**a tRNA synthase domain
22	c1mv4B_	Alignment	not modelled	15.9	36	**PDB header:**de novo protein **Chain:** B: **PDB Molecule:**tropomyosin 1 alpha chain; **PDBTitle:** tm9a251-284: a peptide model of the c-terminus of a rat2 striated alpha tropomyosin
23	c3eb8A_	Alignment	not modelled	15.8	78	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**cysteine protease-like vira; **PDBTitle:** vira
24	d1lg7a_	Alignment	not modelled	15.6	20	**Fold:**VSV matrix protein **Superfamily:**VSV matrix protein **Family:**VSV matrix protein
25	c3ee1A_	Alignment	not modelled	15.3	78	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**effector protein vira; **PDBTitle:** novel fold of vira, a type iii secretion system effector protein from2 shigella flexneri
26	c3m4xA_	Alignment	not modelled	13.3	24	**PDB header:**transferase **Chain:** A: **PDB Molecule:**nol1/nop2/sun family protein; **PDBTitle:** structure of a ribosomal methyltransferase
27	c3tweA_	Alignment	not modelled	13.3	31	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**alpha4h; **PDBTitle:** crystal structure of the de novo designed peptide alpha4h
28	c2l1qA_	Alignment	not modelled	13.0	36	**PDB header:**antimicrobial protein **Chain:** A: **PDB Molecule:**liver-expressed antimicrobial peptide 2; **PDBTitle:** solution structure of human liver expressed antimicrobial peptide 2
						PDB header:unknown function

29	c3tweB_	Alignment	not modelled	12.9	31	**Chain:** B: **PDB Molecule:**alpha4h; **PDBTitle:** crystal structure of the de novo designed peptide alpha4h
30	d1mzga_	Alignment	not modelled	12.9	19	**Fold:**SufE/NifU **Superfamily:**SufE/NifU **Family:**SufE-like
31	d1csca_	Alignment	not modelled	12.3	19	**Fold:**Citrate synthase **Superfamily:**Citrate synthase **Family:**Citrate synthase
32	c2qrlA_	Alignment	not modelled	12.2	18	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**saccharopine dehydrogenase, nad+, l-lysine- **PDBTitle:** crystal structure of oxalylglycine-bound saccharopine2 dehydrogenase (l-lys forming) from saccharomyces cerevisiae
33	d1fx7a3	Alignment	not modelled	11.7	28	**Fold:**SH3-like barrel **Superfamily:**C-terminal domain of transcriptional repressors **Family:**FeoA-like
34	d1fzya_	Alignment	not modelled	10.6	36	**Fold:**UBC-like **Superfamily:**UBC-like **Family:**UBC-related
35	d2ob5a1	Alignment	not modelled	10.6	13	**Fold:**RbsD-like **Superfamily:**RbsD-like **Family:**RbsD-like
36	c2yg8B_	Alignment	not modelled	10.4	19	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**dna-3-methyladenine glycosidase ii, putative; **PDBTitle:** structure of an unusual 3-methyladenine dna glycosylase ii (2 alka) from deinococcus radiodurans
37	c1nh1A_	Alignment	not modelled	10.2	13	**PDB header:**avirulence protein **Chain:** A: **PDB Molecule:**avirulence b protein; **PDBTitle:** crystal structure of the type iii effector avrb from2 pseudomonas syringae.
38	d1nh1a_	Alignment	not modelled	10.2	13	**Fold:**Antivirulence factor **Superfamily:**Antivirulence factor **Family:**Antivirulence factor
39	c1zg2A_	Alignment	not modelled	10.1	18	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical upf0213 protein bh0048; **PDBTitle:** solution nmr structure of the upf0213 protein bh0048 from2 bacillus halodurans. northeast structural genomics target3 bhr2.
40	c2djvA_	Alignment	not modelled	9.9	27	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**methionyl-trna synthetase; **PDBTitle:** solution structures of the whep-trs domain of human2 methionyl-trna synthetase
41	d2f76x1	Alignment	not modelled	9.3	27	**Fold:**Retroviral matrix proteins **Superfamily:**Retroviral matrix proteins **Family:**Mason-Pfizer monkey virus matrix protein
42	d1d2da_	Alignment	not modelled	9.3	24	**Fold:**S15/NS1 RNA-binding domain **Superfamily:**S15/NS1 RNA-binding domain **Family:**a tRNA synthase domain
43	c3bvhE_	Alignment	not modelled	9.2	21	**PDB header:**blood clotting **Chain:** E: **PDB Molecule:**fibrinogen beta chain; **PDBTitle:** crystal structure of recombinant gammad364a fibrinogen fragment d with2 the peptide ligand gly-pro-arg-pro-amide
44	c2hinA_	Alignment	not modelled	9.1	50	**PDB header:**transcription **Chain:** A: **PDB Molecule:**repressor protein; **PDBTitle:** structure of n15 cro at 1.05 a: an ortholog of lambda cro2 with a completely different but equally effective3 dimerization mechanism
45	c2frxD_	Alignment	not modelled	9.0	14	**PDB header:**transferase **Chain:** D: **PDB Molecule:**hypothetical protein yebu; **PDBTitle:** crystal structure of yebu, a m5c rna methyltransferase from e.coli
46	d1n7va_	Alignment	not modelled	8.8	29	**Fold:**Adsorption protein p2 **Superfamily:**Adsorption protein p2 **Family:**Adsorption protein p2
47	d1v1oa2	Alignment	not modelled	8.6	36	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**Superantigen toxins, C-terminal domain **Family:**Superantigen toxins, C-terminal domain
48	c3dxeB_	Alignment	not modelled	8.5	48	**PDB header:**protein binding **Chain:** B: **PDB Molecule:**amyloid beta a4 protein; **PDBTitle:** crystal structure of the intracellular domain of human app2 (t668a mutant) in complex with fe65-ptb2
49	c3fg9B_	Alignment	not modelled	8.3	45	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**protein of universal stress protein uspa family; **PDBTitle:** the crystal structure of an universal stress protein uspa2 family protein from lactobacillus plantarum wcfs1
50	c2cxiA_	Alignment	not modelled	8.3	26	**PDB header:**ligase **Chain:** A: **PDB Molecule:**phenylalanyl-trna synthetase beta chain; **PDBTitle:** crystal structure of an n-terminal fragment of the phenylalanyl-trna2 synthetase beta-subunit from pyrococcus horikoshii
51	d1uuja_	Alignment	not modelled	8.3	29	**Fold:**Lissencephaly-1 protein (Lis-1, PAF-AH alpha) N-terminal domain **Superfamily:**Lissencephaly-1 protein (Lis-1, PAF-AH alpha) N-terminal domain **Family:**Lissencephaly-1 protein (Lis-1, PAF-AH alpha) N-terminal domain
52	d1mwpa_	Alignment	not modelled	8.1	33	**Fold:**SRCR-like **Superfamily:**A heparin-binding domain **Family:**A heparin-binding domain
53	c1nh2C_	Alignment	not modelled	8.1	33	**PDB header:**transcription/dna **Chain:** C: **PDB Molecule:**transcription initiation factor iia large chain;

						PDBTitle: crystal structure of a yeast tfiia/tbp/dna complex
54	d1nh2c_	Alignment	not modelled	8.1	33	**Fold:**Transcription factor IIA (TFIIA), beta-barrel domain **Superfamily:**Transcription factor IIA (TFIIA), beta-barrel domain **Family:**Transcription factor IIA (TFIIA), beta-barrel domain
55	c3jslA_	Alignment	not modelled	8.0	14	**PDB header:**ligase **Chain:** A: **PDB Molecule:**dna ligase; **PDBTitle:** crystal structure of the adenylation domain of nad+-2 dependent dna ligase from staphylococcus aureus
56	c2x9oA_	Alignment	not modelled	7.8	25	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**15,16- dihydrobiliverdin-ferredoxin oxidoreductase; **PDBTitle:** structure of 15, 16- dihydrobiliverdin:ferredoxin2 oxidoreductase (peba)
57	c2g18K_	Alignment	not modelled	7.6	5	**PDB header:**oxidoreductase **Chain:** K: **PDB Molecule:**phycocyanobilin:ferredoxin oxidoreductase; **PDBTitle:** crystal structure of nostoc sp. 7120 phycocyanobilin:ferredoxin2 oxidoreductase (pcya) apoprotein
58	c3ktmB_	Alignment	not modelled	7.6	33	**PDB header:**cell adhesion, signaling protein **Chain:** B: **PDB Molecule:**amyloid beta a4 protein; **PDBTitle:** structure of the heparin-induced e1-dimer of the amyloid precursor2 protein (app)
59	c3ec8A_	Alignment	not modelled	7.1	42	**PDB header:**cell adhesion **Chain:** A: **PDB Molecule:**putative uncharacterized protein flj10324; **PDBTitle:** the crystal structure of the ra domain of flj10324 (radil)
60	c2w2rA_	Alignment	not modelled	7.0	14	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**matrix protein; **PDBTitle:** structure of the vesicular stomatitis virus matrix protein
61	c2jvhA_	Alignment	not modelled	7.0	19	**PDB header:**immune system **Chain:** A: **PDB Molecule:**igg-binding protein sbi; **PDBTitle:** structure of c3-binding domain 4 of s. aureus protein sbi
62	c2z5hB_	Alignment	not modelled	6.9	33	**PDB header:**contractile protein **Chain:** B: **PDB Molecule:**general control protein gcn4 and tropomyosin **PDBTitle:** crystal structure of the head-to-tail junction of2 tropomyosin complexed with a fragment of tnt
63	d2z8la2	Alignment	not modelled	6.6	27	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**Superantigen toxins, C-terminal domain **Family:**Superantigen toxins, C-terminal domain
64	c2ao9H_	Alignment	not modelled	6.6	16	**PDB header:**structural genomics, unknown function **Chain:** H: **PDB Molecule:**phage protein; **PDBTitle:** structural genomics, the crystal structure of a phage protein2 (phbc6a51) from bacillus cereus atcc 14579
65	c3d5jB_	Alignment	not modelled	6.6	26	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**glutaredoxin-2, mitochondrial; **PDBTitle:** structure of yeast grx2-c30s mutant with glutathionyl mixed disulfide
66	c3h0gA_	Alignment	not modelled	6.6	39	**PDB header:**transcription **Chain:** A: **PDB Molecule:**dna-directed rna polymerase ii subunit rpb1; **PDBTitle:** rna polymerase ii from schizosaccharomyces pombe
67	c3f2rA_	Alignment	not modelled	6.3	28	**PDB header:**transferase **Chain:** A: **PDB Molecule:**choline kinase alpha; **PDBTitle:** crystal structure of human choline kinase alpha in complex2 with hemicholinium-3
68	d2hrkb1	Alignment	not modelled	6.3	16	**Fold:**GST C-terminal domain-like **Superfamily:**GST C-terminal domain-like **Family:**Arc1p N-terminal domain-like
69	c2wjvE_	Alignment	not modelled	6.3	40	**PDB header:**hydrolase **Chain:** E: **PDB Molecule:**regulator of nonsense transcripts 2; **PDBTitle:** crystal structure of the complex between human nonsense2 mediated decay factors upf1 and upf2
70	c2v1lA_	Alignment	not modelled	6.2	57	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**hypothetical protein; **PDBTitle:** structure of the conserved hypothetical protein vc1805 from2 pathogenicity island vpi-2 of vibrio cholerae o1 biovar3 eltor str. n16961 shares structural homology with the4 human p32 protein
71	c2wcuB_	Alignment	not modelled	6.1	15	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**protein fucu homolog; **PDBTitle:** crystal structure of mammalian fucu
72	c3cuxA_	Alignment	not modelled	6.0	43	**PDB header:**transferase **Chain:** A: **PDB Molecule:**malate synthase; **PDBTitle:** atomic resolution structures of escherichia coli and2 bacillis anthracis malate synthase a: comparison with3 isoform g and implications for structure based drug design
73	c1ywlA_	Alignment	not modelled	6.0	8	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical upf0213 protein ef2693; **PDBTitle:** solution nmr structure of the protein ef2693 from e.2 faecalis: northeast structural genomics consortium target3 efr36
74	d1eg3a1	Alignment	not modelled	6.0	38	**Fold:**EF Hand-like **Superfamily:**EF-hand **Family:**EF-hand modules in multidomain proteins
75	c3lx6B_	Alignment	not modelled	6.0	20	**PDB header:**transferase **Chain:** B: **PDB Molecule:**cytosine-specific methyltransferase; **PDBTitle:** crystal structure of putative dna cytosine methylase from shigella2 flexneri 2a str. 2457t
76	c3iydD_	Alignment	not modelled	5.9	14	**PDB header:**transcription/dna **Chain:** D: **PDB Molecule:**dna-directed rna polymerase subunit beta; **PDBTitle:** three-dimensional em structure of an intact activator-dependent2 transcription initiation complex
77	c2q6qB_	Alignment	not modelled	5.9	67	**PDB header:**cell cycle **Chain:** B: **PDB Molecule:**spindle pole body component spc42; **PDBTitle:** crystal structure of spc42p, a critical component of spindle pole body2 in budding yeast
						Fold: Immunoglobulin-like beta-sandwich

78	d1axib1	Alignment	not modelled	5.8	43	**Superfamily:**Fibronectin type III **Family:**Fibronectin type III
79	d1nhpa3	Alignment	not modelled	5.8	15	**Fold:**CO dehydrogenase flavoprotein C-domain-like **Superfamily:**FAD/NAD-linked reductases, dimerisation (C-terminal) domain **Family:**FAD/NAD-linked reductases, dimerisation (C-terminal) domain
80	c2l1uA_	Alignment	not modelled	5.8	12	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**methionine-r-sulfoxide reductase b2, mitochondrial; **PDBTitle:** structure-functional analysis of mammalian msrb2 protein
81	c2w56B_	Alignment	not modelled	5.7	43	**PDB header:**unknown function **Chain:** B: **PDB Molecule:**vc0508; **PDBTitle:** structure of the hypothetical protein vc0508 from vibrio cholerae2 vsp-ii pathogenicity island
82	c2f9jP_	Alignment	not modelled	5.7	36	**PDB header:**rna binding protein **Chain:** P: **PDB Molecule:**splicing factor 3b subunit 1; **PDBTitle:** 3.0 angstrom resolution structure of a y22m mutant of the spliceosomal2 protein p14 bound to a region of sf3b155
83	c2k58B_	Alignment	not modelled	5.7	26	**PDB header:**transport protein **Chain:** B: **PDB Molecule:**neuronal acetylcholine receptor subunit beta-2; **PDBTitle:** nmr structures of the first transmembrane domain of the2 neuronal acetylcholine receptor beta 2 subunit
84	d1eita_	Alignment	not modelled	5.7	100	**Fold:**Knottins (small inhibitors, toxins, lectins) **Superfamily:**omega toxin-like **Family:**Spider toxins
85	d2qdyb1	Alignment	not modelled	5.7	25	**Fold:**SH3-like barrel **Superfamily:**Electron transport accessory proteins **Family:**Nitrile hydratase beta chain
86	c1z9vA_	Alignment	not modelled	5.5	30	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**conserved hypothetical protein mth0776; **PDBTitle:** solution structure of mth0776 from methanobacterium2 thermoautotrophicum (strain h)
87	c3ax1A_	Alignment	not modelled	5.5	9	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**serrate rna effector molecule; **PDBTitle:** molecular insights into mirna processing by arabidopsis serrate
88	d1yh2a1	Alignment	not modelled	5.5	36	**Fold:**UBC-like **Superfamily:**UBC-like **Family:**UBC-related
89	c1x4qA_	Alignment	not modelled	5.4	43	**PDB header:**rna binding protein **Chain:** A: **PDB Molecule:**u4/u6 small nuclear ribonucleoprotein prp3; **PDBTitle:** solution structure of pwi domain in u4/u6 small nuclear2 ribonucleoprotein prp3(hprp3)
90	d1qrjb1	Alignment	not modelled	5.3	16	**Fold:**Acyl carrier protein-like **Superfamily:**Retrovirus capsid dimerization domain-like **Family:**Retrovirus capsid protein C-terminal domain
91	c1v1oB_	Alignment	not modelled	5.3	36	**PDB header:**virulence factor **Chain:** B: **PDB Molecule:**exotoxin 1; **PDBTitle:** staphylococcal superantigen-like protein 7
92	c2k72A_	Alignment	not modelled	5.3	33	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**matrix metalloproteinase-23; **PDBTitle:** solution nmr structure of toxin-like potassium channel2 blocking domain in mmp23
93	d2etda1	Alignment	not modelled	5.3	14	**Fold:**Bromodomain-like **Superfamily:**LemA-like **Family:**LemA-like
94	d2tssa2	Alignment	not modelled	5.3	36	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**Superantigen toxins, C-terminal domain **Family:**Superantigen toxins, C-terminal domain
95	c4dzoA_	Alignment	not modelled	5.3	29	**PDB header:**cell cycle **Chain:** A: **PDB Molecule:**mitotic spindle assembly checkpoint protein mad1; **PDBTitle:** structure of human mad1 c-terminal domain reveals its involvement in2 kinetochore targeting
96	d2eiaa1	Alignment	not modelled	5.2	16	**Fold:**Acyl carrier protein-like **Superfamily:**Retrovirus capsid dimerization domain-like **Family:**Retrovirus capsid protein C-terminal domain
97	c2w4rB_	Alignment	not modelled	5.1	23	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**probable atp-dependent rna helicase dhx58; **PDBTitle:** crystal structure of the regulatory domain of human lgp2
98	c2b9sA_	Alignment	not modelled	5.1	8	**PDB header:**isomerase/dna **Chain:** A: **PDB Molecule:**topoisomerase i-like protein; **PDBTitle:** crystal structure of heterodimeric l. donovani2 topoisomerase i-vanadate-dna complex
99	c3l4nA_	Alignment	not modelled	5.1	20	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**monothiol glutaredoxin-6; **PDBTitle:** crystal structure of yeast monothiol glutaredoxin grx6