Phyre^2

Email	l.a.kelley@imperial.ac.uk
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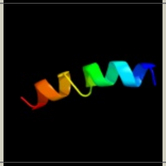
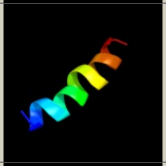
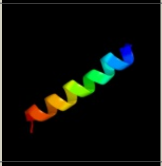
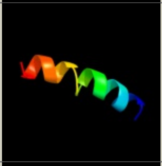
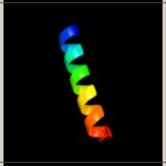
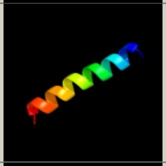
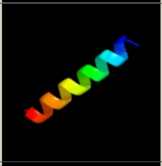
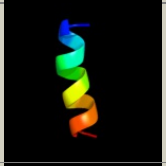
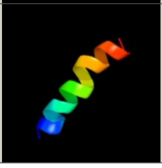
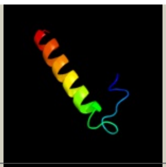
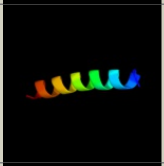
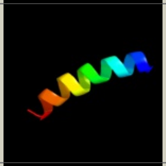
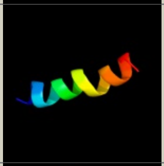
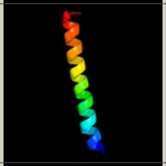
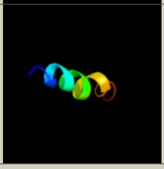
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2e76H_	Alignment		46.4	30	**PDB header:**photosynthesis **Chain:** H: **PDB Molecule:**cytochrome b6-f complex subunit 8; **PDBTitle:** crystal structure of the cytochrome b6f complex with tridecyl-2 stigmatellin (tds) from m.laminosus
2	c2e74H_	Alignment		46.4	30	**PDB header:**photosynthesis **Chain:** H: **PDB Molecule:**cytochrome b6-f complex subunit 8; **PDBTitle:** crystal structure of the cytochrome b6f complex from m.laminosus
3	c2e75H_	Alignment		46.4	30	**PDB header:**photosynthesis **Chain:** H: **PDB Molecule:**cytochrome b6-f complex subunit 8; **PDBTitle:** crystal structure of the cytochrome b6f complex with 2-nonyl-4-2 hydroxyquinoline n-oxide (nqno) from m.laminosus
4	c1u0iA_	Alignment		42.4	42	**PDB header:**de novo protein **Chain:** A: **PDB Molecule:**iaal-e3; **PDBTitle:** iaal-e3/k3 heterodimer
5	d2e74h1	Alignment		41.9	30	**Fold:**Single transmembrane helix **Superfamily:**PetN subunit of the cytochrome b6f complex **Family:**PetN subunit of the cytochrome b6f complex
6	c1ce0B_	Alignment		37.8	29	**PDB header:**hiv-1 envelope protein **Chain:** B: **PDB Molecule:**protein (leucine zipper model h38-p1); **PDBTitle:** trimerization specificity in hiv-1 gp41: analysis with a2 gcn4 leucine zipper model
7	c3he5A_	Alignment		37.6	26	**PDB header:**de novo protein **Chain:** A: **PDB Molecule:**synzip1; **PDBTitle:** heterospecific coiled-coil pair synzip2:synzip1
8	c3g9rF_	Alignment		37.5	33	**PDB header:**viral protein **Chain:** F: **PDB Molecule:**fusion complex of hiv-1 envelope glycoprotein **PDBTitle:** structure of the hiv-1 gp41 membrane-proximal ectodomain2 region in a putative prefusion conformation
9	c3lt7D_	Alignment		36.7	32	**PDB header:**cell adhesion **Chain:** D: **PDB Molecule:**adhesin yada; **PDBTitle:** a transition from strong right-handed to canonical left-handed2 supercoiling in a conserved coiled coil segment of trimeric3 autotransporter adhesins - the m3 mutant structure
10	c1u2uA_	Alignment		36.3	33	**PDB header:**transcription **Chain:** A: **PDB Molecule:**general control protein gcn4; **PDBTitle:** nmr solution structure of a designed heterodimeric leucine2 zipper
11	c1vf5H_	Alignment		33.9	30	**PDB header:**photosynthesis **Chain:** H: **PDB Molecule:**protein pet n; **PDBTitle:** crystal structure of cytochrome b6f complex from m.laminosus

12	c2lf0A_	Alignment		32.8	15	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein yibl; **PDBTitle:** solution structure of sf3636, a two-domain unknown function protein2 from shigella flexneri 2a, determined by joint refinement of nmr,3 residual dipolar couplings and small-angle x-ray scatting, nesg4 target sfr339/ocsp target sf3636
13	c3ci9B_	Alignment		32.5	30	**PDB header:**transcription **Chain:** B: **PDB Molecule:**heat shock factor-binding protein 1; **PDBTitle:** crystal structure of the human hsbp1
14	c2zt9H_	Alignment		32.2	43	**PDB header:**photosynthesis **Chain:** H: **PDB Molecule:**cytochrome b6-f complex subunit 8; **PDBTitle:** crystal structure of the cytochrome b6f complex from nostoc sp. pcc2 7120
15	c1hf9B_	Alignment		31.3	19	**PDB header:**atpase inhibitor **Chain:** B: **PDB Molecule:**atpase inhibitor (mitochondrial); **PDBTitle:** c-terminal coiled-coil domain from bovine if1
16	c1vf5U_	Alignment		30.7	30	**PDB header:**photosynthesis **Chain:** U: **PDB Molecule:**protein pet n; **PDBTitle:** crystal structure of cytochrome b6f complex from m.laminosus
17	c1aq5C_	Alignment		28.8	23	**PDB header:**coiled-coil **Chain:** C: **PDB Molecule:**cartilage matrix protein; **PDBTitle:** high-resolution solution nmr structure of the trimeric coiled-coil2 domain of chicken cartilage matrix protein, 20 structures
18	d1v54m_	Alignment		27.9	25	**Fold:**Single transmembrane helix **Superfamily:**Mitochondrial cytochrome c oxidase subunit VIIIb (aka IX) **Family:**Mitochondrial cytochrome c oxidase subunit VIIIb (aka IX)
19	c2y69Z_	Alignment		26.9	25	**PDB header:**electron transport **Chain:** Z: **PDB Molecule:**cytochrome c oxidase polypeptide 8h; **PDBTitle:** bovine heart cytochrome c oxidase re-refined with molecular2 oxygen
20	c2d2cH_	Alignment		26.5	30	**PDB header:**photosynthesis **Chain:** H: **PDB Molecule:**cytochrome b6-f complex subunit viii; **PDBTitle:** crystal structure of cytochrome b6f complex with dbmib from2 m. laminosus
21	c2d2cU_	Alignment	not modelled	26.5	30	**PDB header:**photosynthesis **Chain:** U: **PDB Molecule:**cytochrome b6-f complex subunit viii; **PDBTitle:** crystal structure of cytochrome b6f complex with dbmib from2 m. laminosus
22	c2ke4A_	Alignment	not modelled	25.7	12	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**cdc42-interacting protein 4; **PDBTitle:** the nmr structure of the tc10 and cdc42 interacting domain2 of cip4
23	c3m9hB_	Alignment	not modelled	23.9	24	**PDB header:**chaperone **Chain:** B: **PDB Molecule:**proteasome-associated atpase; **PDBTitle:** crystal structure of the amino terminal coiled coil domain of the2 mycobacterium tuberculosis proteasomal atpase mpa
24	c2qa7B_	Alignment	not modelled	23.6	27	**PDB header:**actin binding **Chain:** B: **PDB Molecule:**huntingtin-interacting protein 1; **PDBTitle:** crystal structure of huntingtin-interacting protein 12 (hip1) coiled-coil domain with a basic surface suitable3 for hip-protein interactor (hippi)
25	c3rylB_	Alignment	not modelled	22.3	42	**PDB header:**protein binding **Chain:** B: **PDB Molecule:**protein vpa1370; **PDBTitle:** dimerization domain of vibrio parahemolyticus vopl
26	d2gr7a1	Alignment	not modelled	19.7	20	**Fold:**Pili subunits **Superfamily:**Pili subunits **Family:**YadA C-terminal domain-like
27	c2gr7C_	Alignment	not modelled	19.7	20	**PDB header:**membrane protein **Chain:** C: **PDB Molecule:**adhesin; **PDBTitle:** hia 992-1098
28	c3p8cE_	Alignment	not modelled	19.5	21	**PDB header:**protein binding **Chain:** E: **PDB Molecule:**probable protein brick1; **PDBTitle:** structure and control of the actin regulatory wave

						complex
29	c1hwtC_	Alignment	not modelled	18.4	26	**PDB header:**gene regulation/dna **Chain:** C: **PDB Molecule:**protein (heme activator protein); **PDBTitle:** structure of a hap1/dna complex reveals dramatically2 asymmetric dna binding by a homodimeric protein
30	c1ij2C_	Alignment	not modelled	17.7	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
31	c3k7zA_	Alignment	not modelled	17.4	27	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**general control protein gcn4; **PDBTitle:** gcn4-leucine zipper core mutant as n16a trigonal automatic2 solution
32	c1rb6C_	Alignment	not modelled	17.4	27	**PDB header:**dna binding protein **Chain:** C: **PDB Molecule:**general control protein gcn4; **PDBTitle:** antiparallel trimer of gcn4-leucine zipper core mutant as2 n16a tetragonal form
33	c1swiA_	Alignment	not modelled	17.4	27	**PDB header:**leucine zipper **Chain:** A: **PDB Molecule:**gcn4p1; **PDBTitle:** gcn4-leucine zipper core mutant as n16a complexed with2 benzene
34	c1rb1A_	Alignment	not modelled	17.4	27	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**general control protein gcn4; **PDBTitle:** gcn4-leucine zipper core mutant as n16a trigonal automatic2 solution
35	c1rb1B_	Alignment	not modelled	17.4	27	**PDB header:**dna binding protein **Chain:** B: **PDB Molecule:**general control protein gcn4; **PDBTitle:** gcn4-leucine zipper core mutant as n16a trigonal automatic2 solution
36	c3k7zB_	Alignment	not modelled	17.4	27	**PDB header:**dna binding protein **Chain:** B: **PDB Molecule:**general control protein gcn4; **PDBTitle:** gcn4-leucine zipper core mutant as n16a trigonal automatic2 solution
37	d1vl2a2	Alignment	not modelled	16.8	21	**Fold:**Argininosuccinate synthetase, C-terminal domain **Superfamily:**Argininosuccinate synthetase, C-terminal domain **Family:**Argininosuccinate synthetase, C-terminal domain
38	c1ij3C_	Alignment	not modelled	16.6	27	**PDB header:**transcription **Chain:** C: **PDB Molecule:**general control protein gcn4; **PDBTitle:** gcn4-pvsl coiled-coil trimer with serine at the a(16)2 position
39	c1ij3B_	Alignment	not modelled	16.6	27	**PDB header:**transcription **Chain:** B: **PDB Molecule:**general control protein gcn4; **PDBTitle:** gcn4-pvsl coiled-coil trimer with serine at the a(16)2 position
40	d1slqa_	Alignment	not modelled	16.2	8	**Fold:**VP4 membrane interaction domain **Superfamily:**VP4 membrane interaction domain **Family:**VP4 membrane interaction domain
41	d1ioka2	Alignment	not modelled	15.9	32	**Fold:**The "swivelling" beta/beta/alpha domain **Superfamily:**GroEL apical domain-like **Family:**GroEL-like chaperone, apical domain
42	d1ta8a_	Alignment	not modelled	15.9	18	**Fold:**ATP-grasp **Superfamily:**DNA ligase/mRNA capping enzyme, catalytic domain **Family:**Adenylation domain of NAD+-dependent DNA ligase
43	c1ztaA_	Alignment	not modelled	15.8	29	**PDB header:**dna-binding motif **Chain:** A: **PDB Molecule:**leucine zipper monomer; **PDBTitle:** the solution structure of a leucine-zipper motif peptide
44	c1ij2B_	Alignment	not modelled	15.6	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
45	c3pn1A_	Alignment	not modelled	15.4	21	**PDB header:**ligase/ligase inhibitor **Chain:** A: **PDB Molecule:**dna ligase; **PDBTitle:** novel bacterial nad+-dependent dna ligase inhibitors with broad2 spectrum potency and antibacterial efficacy in vivo
46	c2ergA_	Alignment	not modelled	14.1	21	**PDB header:**transcription activator/dna **Chain:** A: **PDB Molecule:**regulatory protein leu3; **PDBTitle:** crystal structure of leu3 dna-binding domain with a single2 h50c mutation complexed with a 15mer dna duplex
47	c2xzrA_	Alignment	not modelled	12.3	13	**PDB header:**cell adhesion **Chain:** A: **PDB Molecule:**immunoglobulin-binding protein eibd; **PDBTitle:** escherichia coli immunoglobulin-binding protein eibd 391-438 fused2 to gcn4 adaptors
48	c2yy0D_	Alignment	not modelled	12.1	11	**PDB header:**transcription **Chain:** D: **PDB Molecule:**c-myc-binding protein; **PDBTitle:** crystal structure of ms0802, c-myc-1 binding protein domain2 from homo sapiens
49	c2zt9E_	Alignment	not modelled	12.0	27	**PDB header:**photosynthesis **Chain:** E: **PDB Molecule:**cytochrome b6-f complex subunit 6; **PDBTitle:** crystal structure of the cytochrome b6f complex from nostoc sp. pcc2 7120
50	c1kddC_	Alignment	not modelled	12.0	25	**PDB header:**de novo protein **Chain:** C: **PDB Molecule:**gcn4 acid base heterodimer acid-d12la16i; **PDBTitle:** x-ray structure of the coiled coil gcn4 acid base2 heterodimer acid-d12la16i base-d12la16l
51	d1b04a_	Alignment	not modelled	12.0	24	**Fold:**ATP-grasp **Superfamily:**DNA ligase/mRNA capping enzyme, catalytic domain **Family:**Adenylation domain of NAD+-dependent DNA ligase
52	c1kddA_	Alignment	not modelled	11.7	25	**PDB header:**de novo protein **Chain:** A: **PDB Molecule:**gcn4 acid base heterodimer acid-d12la16i; **PDBTitle:** x-ray structure of the coiled coil gcn4 acid base2 heterodimer acid-d12la16i base-d12la16l
53	c1kddF_	Alignment	not modelled	11.7	25	**PDB header:**de novo protein **Chain:** F: **PDB Molecule:**gcn4 acid base heterodimer acid-d12la16i; **PDBTitle:** x-ray structure of the coiled coil gcn4 acid base2 heterodimer acid-d12la16i base-d12la16l
						PDB header:ligase

54	c1zauA_	Alignment	not modelled	11.1	30	**Chain:** A: **PDB Molecule:**dna ligase; **PDBTitle:** adenylation domain of nad+ dependent dna ligase from2 m.tuberculosis
55	c2owoA_	Alignment	not modelled	11.1	21	**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
56	d1uuja_	Alignment	not modelled	10.6	25	**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
57	c3hroA_	Alignment	not modelled	10.2	33	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**transient receptor potential (trp) channel **PDBTitle:** crystal structure of a c-terminal coiled coil domain of2 transient receptor potential (trp) channel subfamily p3 member 2 (trpp2, polycystic kidney disease 2)
58	c1kd9A_	Alignment	not modelled	10.0	31	**PDB header:**de novo protein **Chain:** A: **PDB Molecule:**gcn4 acid base heterodimer acid-d12la16l; **PDBTitle:** x-ray structure of the coiled coil gcn4 acid base2 heterodimer acid-d12la16l base-d12la16l
59	c1kd9F_	Alignment	not modelled	10.0	31	**PDB header:**de novo protein **Chain:** F: **PDB Molecule:**gcn4 acid base heterodimer acid-d12la16l; **PDBTitle:** x-ray structure of the coiled coil gcn4 acid base2 heterodimer acid-d12la16l base-d12la16l
60	c1kd9C_	Alignment	not modelled	10.0	31	**PDB header:**de novo protein **Chain:** C: **PDB Molecule:**gcn4 acid base heterodimer acid-d12la16l; **PDBTitle:** x-ray structure of the coiled coil gcn4 acid base2 heterodimer acid-d12la16l base-d12la16l
61	c3gw6F_	Alignment	not modelled	10.0	27	**PDB header:**chaperone **Chain:** F: **PDB Molecule:**endo-n-acetylneuraminidase; **PDBTitle:** intramolecular chaperone
62	c3h5fB_	Alignment	not modelled	9.9	43	**PDB header:**de novo protein **Chain:** B: **PDB Molecule:**coil ser l16l-pen; **PDBTitle:** switching the chirality of the metal environment alters the2 coordination mode in designed peptides.
63	c3h5fC_	Alignment	not modelled	9.9	43	**PDB header:**de novo protein **Chain:** C: **PDB Molecule:**coil ser l16l-pen; **PDBTitle:** switching the chirality of the metal environment alters the2 coordination mode in designed peptides.
64	c3h5gA_	Alignment	not modelled	9.9	43	**PDB header:**de novo protein **Chain:** A: **PDB Molecule:**coil ser l16d-pen; **PDBTitle:** switching the chirality of the metal environment alters the2 coordination mode in designed peptides.
65	c3h5gB_	Alignment	not modelled	9.9	43	**PDB header:**de novo protein **Chain:** B: **PDB Molecule:**coil ser l16d-pen; **PDBTitle:** switching the chirality of the metal environment alters the2 coordination mode in designed peptides.
66	c3h5gC_	Alignment	not modelled	9.9	43	**PDB header:**de novo protein **Chain:** C: **PDB Molecule:**coil ser l16d-pen; **PDBTitle:** switching the chirality of the metal environment alters the2 coordination mode in designed peptides.
67	c3h5fA_	Alignment	not modelled	9.9	43	**PDB header:**de novo protein **Chain:** A: **PDB Molecule:**coil ser l16l-pen; **PDBTitle:** switching the chirality of the metal environment alters the2 coordination mode in designed peptides.
68	c2xv5A_	Alignment	not modelled	9.9	13	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**lamin-a/c; **PDBTitle:** human lamin a coil 2b fragment
69	c2p4vA_	Alignment	not modelled	9.8	21	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcription elongation factor greb; **PDBTitle:** crystal structure of the transcript cleavage factor, greb2 at 2.6a resolution
70	c1fmhA_	Alignment	not modelled	9.6	28	**PDB header:**transcription **Chain:** A: **PDB Molecule:**general control protein gcn4; **PDBTitle:** nmr solution structure of a designed heterodimeric leucine2 zipper
71	c1t3jA_	Alignment	not modelled	9.6	38	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**mitofusin 1; **PDBTitle:** mitofusin domain hr2 v686m/i708m mutant
72	c3jslA_	Alignment	not modelled	9.5	21	**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
73	c1ci6B_	Alignment	not modelled	9.1	17	**PDB header:**transcription **Chain:** B: **PDB Molecule:**transcription factor c/ebp beta; **PDBTitle:** transcription factor atf4-c/ebp beta bzip heterodimer
74	d1lrza1	Alignment	not modelled	8.8	14	**Fold:**Long alpha-hairpin **Superfamily:**tRNA-binding arm **Family:**Methicillin resistance protein FemA probable tRNA-binding arm
75	d1oela2	Alignment	not modelled	8.7	27	**Fold:**The "swivelling" beta/beta/alpha domain **Superfamily:**GroEL apical domain-like **Family:**GroEL-like chaperone, apical domain
76	c1grjA_	Alignment	not modelled	8.4	21	**PDB header:**transcription regulation **Chain:** A: **PDB Molecule:**grea protein; **PDBTitle:** grea transcript cleavage factor from escherichia coli
77	c3swfA_	Alignment	not modelled	8.3	26	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**cgmp-gated cation channel alpha-1; **PDBTitle:** cnga1 621-690 containing clz domain
78	c2o7hF_	Alignment	not modelled	8.1	22	**PDB header:**transcription **Chain:** F: **PDB Molecule:**general control protein gcn4; **PDBTitle:** crystal structure of trimeric coiled coil gcn4 leucine zipper

79	c2dl1A_	Alignment	not modelled	8.1	15	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**spartin; **PDBTitle:** solution structure of the mit domain from human spartin
80	c2rkhA_	Alignment	not modelled	7.4	38	**PDB header:**transcription **Chain:** A: **PDB Molecule:**putative apha-like transcription factor; **PDBTitle:** crystal structure of a putative apha-like transcription factor2 (zp_00208345.1) from magnetospirillum magnetotacticum ms-1 at 2.00 a3 resolution
81	d1vlia2	Alignment	not modelled	7.4	21	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**NeuB-like
82	c3hlsE_	Alignment	not modelled	7.3	18	**PDB header:**signaling protein **Chain:** E: **PDB Molecule:**guanylate cyclase soluble subunit beta-1; **PDBTitle:** crystal structure of the signaling helix coiled-coil doimain2 of the beta-1 subunit of the soluble guanylyl cyclase
83	c1gk6B_	Alignment	not modelled	7.2	17	**PDB header:**vimentin **Chain:** B: **PDB Molecule:**vimentin; **PDBTitle:** human vimentin coil 2b fragment linked to gcn4 leucine2 zipper (z2b)
84	d1seta1	Alignment	not modelled	7.1	0	**Fold:**Long alpha-hairpin **Superfamily:**tRNA-binding arm **Family:**Seryl-tRNA synthetase (SerRS)
85	c1yjgE_	Alignment	not modelled	7.1	14	**PDB header:**immune system **Chain:** E: **PDB Molecule:**surface protein vspa; **PDBTitle:** variable small protein 1 of borrelia turicatae (vspa or vsp1)
86	d2zdra2	Alignment	not modelled	7.0	18	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**NeuB-like
87	c2akfA_	Alignment	not modelled	6.9	36	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**coronin-1a; **PDBTitle:** crystal structure of the coiled-coil domain of coronin 1
88	c2akfB_	Alignment	not modelled	6.9	36	**PDB header:**protein binding **Chain:** B: **PDB Molecule:**coronin-1a; **PDBTitle:** crystal structure of the coiled-coil domain of coronin 1
89	c2akfC_	Alignment	not modelled	6.9	36	**PDB header:**protein binding **Chain:** C: **PDB Molecule:**coronin-1a; **PDBTitle:** crystal structure of the coiled-coil domain of coronin 1
90	c3nmdA_	Alignment	not modelled	6.9	21	**PDB header:**transferase **Chain:** A: **PDB Molecule:**cgmp dependent protein kinase; **PDBTitle:** crystal structure of the leucine zipper domain of cgmp dependent2 protein kinase i beta
91	c2wl2B_	Alignment	not modelled	6.8	19	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**dna gyrase subunit a; **PDBTitle:** crystal structure of n-terminal domain of gyra with the2 antibiotic simocyclinone d8
92	d1v9pa3	Alignment	not modelled	6.7	24	**Fold:**ATP-grasp **Superfamily:**DNA ligase/mRNA capping enzyme, catalytic domain **Family:**Adenylation domain of NAD+-dependent DNA ligase
93	c3o3nA_	Alignment	not modelled	6.6	21	**PDB header:**lyase **Chain:** A: **PDB Molecule:**alpha-subunit 2-hydroxyisocaproyl-coa dehydratase; **PDBTitle:** (r)-2-hydroxyisocaproyl-coa dehydratase in complex with its substrate2 (r)-2-hydroxyisocaproyl-coa
94	c2w6bA_	Alignment	not modelled	6.6	25	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**rho guanine nucleotide exchange factor 7; **PDBTitle:** crystal structure of the trimeric beta-pix coiled-coil2 domain
95	d1sjpa2	Alignment	not modelled	6.5	18	**Fold:**The "swivelling" beta/beta/alpha domain **Superfamily:**GroEL apical domain-like **Family:**GroEL-like chaperone, apical domain
96	d1kida_	Alignment	not modelled	6.5	32	**Fold:**The "swivelling" beta/beta/alpha domain **Superfamily:**GroEL apical domain-like **Family:**GroEL-like chaperone, apical domain
97	c3m0dC_	Alignment	not modelled	6.5	26	**PDB header:**signaling protein **Chain:** C: **PDB Molecule:**tnf receptor-associated factor 1; **PDBTitle:** crystal structure of the traf1:traf2:ciap2 complex
98	c2pnvA_	Alignment	not modelled	6.5	23	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**small conductance calcium-activated potassium **PDBTitle:** crystal structure of the leucine zipper domain of small-2 conductance ca2+-activated k+ (skca) channel from rattus3 norvegicus
99	c2zfcB_	Alignment	not modelled	6.4	25	**PDB header:**viral protein **Chain:** B: **PDB Molecule:**hiv-1 gp41; **PDBTitle:** x-ray crystal structure of an engineered n-terminal hiv-12 gp41 trimer with enhanced stability and potency