Phyre^2

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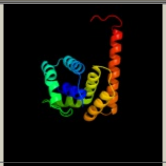
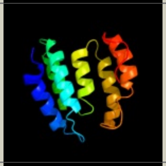
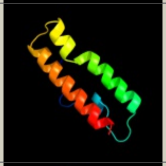
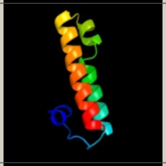
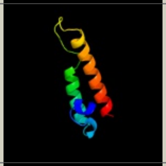
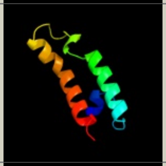
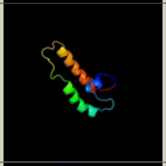
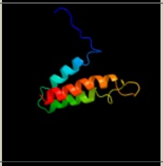
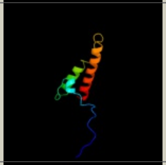
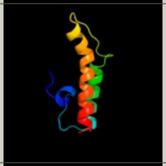
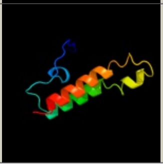
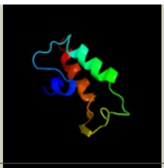
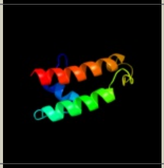
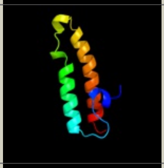
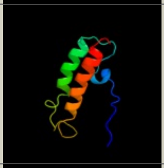
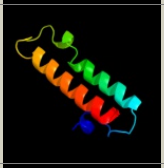
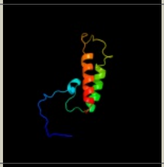
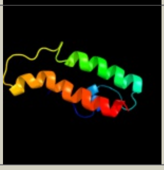
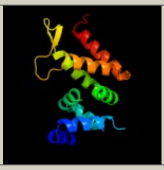
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d2ou3a1	Alignment		99.7	17	**Fold:**TerB-like **Superfamily:**TerB-like **Family:**COG3793-like
2	c2jxuA_	Alignment		99.7	15	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**terb; **PDBTitle:** nmr solution structure of kp-terb, a tellurite resistance2 protein from klebsiella pneumoniae
3	c3bvoA_	Alignment		99.5	14	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**co-chaperone protein hscb, mitochondrial precursor; **PDBTitle:** crystal structure of human co-chaperone protein hscb
4	c1fpoA_	Alignment		99.5	22	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**chaperone protein hscb; **PDBTitle:** hsc20 (hscb), a j-type co-chaperone from e. coli
5	c3hhoA_	Alignment		99.5	23	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**co-chaperone protein hscb homolog; **PDBTitle:** chaperone hscb from vibrio cholerae
6	c3apqB_	Alignment		99.5	31	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**dnaj homolog subfamily c member 10; **PDBTitle:** crystal structure of j-trx1 fragment of erdj5
7	c2l6lA_	Alignment		99.5	30	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**dnaj homolog subfamily c member 24; **PDBTitle:** solution structure of human j-protein co-chaperone, dph4
8	d1iura_	Alignment		99.5	20	**Fold:**Long alpha-hairpin **Superfamily:**Chaperone J-domain **Family:**Chaperone J-domain
9	d1wjza_	Alignment		99.4	32	**Fold:**Long alpha-hairpin **Superfamily:**Chaperone J-domain **Family:**Chaperone J-domain
10	c2ys8A_	Alignment		99.4	33	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**rab-related gtp-binding protein rabj; **PDBTitle:** solution structure of the dnaj-like domain from human ras-2 associated protein rap1
11	c2ctqA_	Alignment		99.3	28	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**dnaj homolog subfamily c member 12; **PDBTitle:** solution structure of j-domain from human dnaj subfamily c2 menber 12

12	d1gh6a_	Alignment		99.3	22	**Fold:**Long alpha-hairpin **Superfamily:**Chaperone J-domain **Family:**Chaperone J-domain
13	c2guzO_	Alignment		99.3	22	**PDB header:**chaperone, protein transport **Chain:** O: **PDB Molecule:**mitochondrial import inner membrane translocase **PDBTitle:** structure of the tim14-tim16 complex of the mitochondrial2 protein import motor
14	c2yuaA_	Alignment		99.3	26	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**williams-beuren syndrome chromosome region 18 **PDBTitle:** solution structure of the dnaj domain from human williams-2 beuren syndrome chromosome region 18 protein
15	c2qsaA_	Alignment		99.3	33	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**dnaj homolog dnj-2; **PDBTitle:** crystal structure of j-domain of dnaj homolog dnj-2 precursor from2 c.elegans.
16	c2dmxA_	Alignment		99.3	33	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**dnaj homolog subfamily b member 8; **PDBTitle:** solution structure of the j domain of dnaj homolog2 subfamily b member 8
17	c3ag7A_	Alignment		99.3	25	**PDB header:**plant protein **Chain:** A: **PDB Molecule:**putative uncharacterized protein f9e10.5; **PDBTitle:** an auxilin-like j-domain containing protein, jac1 j-domain
18	d1fpoa1	Alignment		99.3	22	**Fold:**Long alpha-hairpin **Superfamily:**Chaperone J-domain **Family:**Chaperone J-domain
19	c2ctwA_	Alignment		99.3	30	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**dnaj homolog subfamily c member 5; **PDBTitle:** solution structure of j-domain from mouse dnaj subfamily c2 member 5
20	c2ctrA_	Alignment		99.3	32	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**dnaj homolog subfamily b member 9; **PDBTitle:** solution structure of j-domain from human dnaj subfamily b2 member 9
21	c2lgwA_	Alignment	not modelled	99.2	32	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**dnaj homolog subfamily b member 2; **PDBTitle:** solution structure of the j domain of hsj1a
22	c2kqxA_	Alignment	not modelled	99.2	40	**PDB header:**chaperone binding protein **Chain:** A: **PDB Molecule:**curved dna-binding protein; **PDBTitle:** nmr structure of the j-domain (residues 2-72) in the2 escherichia coli cbpa
23	c2cugA_	Alignment	not modelled	99.2	38	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**mkiaa0962 protein; **PDBTitle:** solution structure of the j domain of the pseudo dnaj2 protein, mouse hypothetical mkiaa0962
24	d1fafa_	Alignment	not modelled	99.2	23	**Fold:**Long alpha-hairpin **Superfamily:**Chaperone J-domain **Family:**Chaperone J-domain
25	c2ctpA_	Alignment	not modelled	99.2	29	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**dnaj homolog subfamily b member 12; **PDBTitle:** solution structure of j-domain from human dnaj subfamily b2 menber 12
26	c2dn9A_	Alignment	not modelled	99.2	30	**PDB header:**apoptosis, chaperone **Chain:** A: **PDB Molecule:**dnaj homolog subfamily a member 3; **PDBTitle:** solution structure of j-domain from the dnaj homolog, human2 tid1 protein
27	d1n4ca_	Alignment	not modelled	99.2	27	**Fold:**Long alpha-hairpin **Superfamily:**Chaperone J-domain **Family:**Chaperone J-domain
28	d1nz6a_	Alignment	not modelled	99.1	26	**Fold:**Long alpha-hairpin **Superfamily:**Chaperone J-domain **Family:**Chaperone J-domain
						PDB header:hydrolase regulator/viral protein

29	c2pf4E_	Alignment	not modelled	99.1	21	**Chain:** E: **PDB Molecule:**small t antigen; **PDBTitle:** crystal structure of the full-length simian virus 40 small t antigen2 complexed with the protein phosphatase 2a aalpha subunit
30	d1hdja_	Alignment	not modelled	99.1	35	**Fold:**Long alpha-hairpin **Superfamily:**Chaperone J-domain **Family:**Chaperone J-domain
31	d1xbla_	Alignment	not modelled	99.1	33	**Fold:**Long alpha-hairpin **Superfamily:**Chaperone J-domain **Family:**Chaperone J-domain
32	c2o37A_	Alignment	not modelled	99.1	31	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**protein sis1; **PDBTitle:** j-domain of sis1 protein, hsp40 co-chaperone from2 saccharomyces cerevisiae.
33	c2ochA_	Alignment	not modelled	99.1	38	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**hypothetical protein dnj-12; **PDBTitle:** j-domain of dnj-12 from caenorhabditis elegans
34	c2guzD_	Alignment	not modelled	99.0	18	**PDB header:**chaperone, protein transport **Chain:** D: **PDB Molecule:**mitochondrial import inner membrane translocase **PDBTitle:** structure of the tim14-tim16 complex of the mitochondrial2 protein import motor
35	c1bq0A_	Alignment	not modelled	99.0	34	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**dnaj; **PDBTitle:** j-domain (residues 1-77) of the escherichia coli n-terminal2 fragment (residues 1-104) of the molecular chaperone dnaj,3 nmr, 20 structures
36	c2y4tA_	Alignment	not modelled	98.8	16	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**dnaj homolog subfamily c member 3; **PDBTitle:** crystal structure of the human co-chaperone p58(ipk)
37	c3uo2A_	Alignment	not modelled	97.5	23	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**j-type co-chaperone jac1, mitochondrial; **PDBTitle:** jac1 co-chaperone from saccharomyces cerevisiae
38	d2h5na1	Alignment	not modelled	97.2	11	**Fold:**TerB-like **Superfamily:**TerB-like **Family:**PG1108-like
39	c3apoA_	Alignment	not modelled	95.2	32	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**dnaj homolog subfamily c member 10; **PDBTitle:** crystal structure of full-length erdj5
40	d1ug2a_	Alignment	not modelled	92.3	18	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Myb/SANT domain
41	c3evrA_	Alignment	not modelled	77.9	10	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**myosin light chain kinase, green fluorescent **PDBTitle:** crystal structure of calcium bound monomeric gcamp2
42	d2ouwa1	Alignment	not modelled	75.9	20	**Fold:**AhpD-like **Superfamily:**AhpD-like **Family:**TTHA0727-like
43	d1aisb2	Alignment	not modelled	73.1	17	**Fold:**Cyclin-like **Superfamily:**Cyclin-like **Family:**Transcription factor IIB (TFIIB), core domain
44	c2hpkA_	Alignment	not modelled	69.3	13	**PDB header:**luminescent protein **Chain:** A: **PDB Molecule:**photoprotein berovin; **PDBTitle:** crystal structure of photoprotein berovin from beroe2 abyssicola
45	d2jxca1	Alignment	not modelled	67.1	7	**Fold:**EF Hand-like **Superfamily:**EF-hand **Family:**Eps15 homology domain (EH domain)
46	d1vola2	Alignment	not modelled	62.7	12	**Fold:**Cyclin-like **Superfamily:**Cyclin-like **Family:**Transcription factor IIB (TFIIB), core domain
47	c2iqcA_	Alignment		59.6	15	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**fanconi anemia group f protein; **PDBTitle:** crystal structure of human fancf protein that functions in2 the assembly of a dna damage signaling complex
48	c2aucC_	Alignment	not modelled	59.5	13	**PDB header:**membrane protein **Chain:** C: **PDB Molecule:**myosin a tail interacting protein; **PDBTitle:** structure of the plasmodium mtip-myoa complex, a key component of the2 parasite invasion motor
49	d1vola1	Alignment	not modelled	53.9	12	**Fold:**Cyclin-like **Superfamily:**Cyclin-like **Family:**Transcription factor IIB (TFIIB), core domain
50	d1a04a1	Alignment	not modelled	49.6	30	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**C-terminal effector domain of the bipartite response regulators **Family:**GerE-like (LuxR/UhpA family of transcriptional regulators)
51	c2q0oA_	Alignment	not modelled	46.5	23	**PDB header:**transcription **Chain:** A: **PDB Molecule:**probable transcriptional activator protein trar; **PDBTitle:** crystal structure of an anti-activation complex in bacterial quorum2 sensing
52	c3k7aM_	Alignment	not modelled	44.5	5	**PDB header:**transcription **Chain:** M: **PDB Molecule:**transcription initiation factor iib; **PDBTitle:** crystal structure of an rna polymerase ii-tfiib complex
53	c2kxaA_	Alignment	not modelled	44.0	32	**PDB header:**viral protein, immune system **Chain:** A: **PDB Molecule:**haemagglutinin ha2 chain peptide; **PDBTitle:** the hemagglutinin fusion peptide (h1 subtype) at ph 7.4
						PDB header:transcription/dna

54	c1h0mD_	Alignment	not modelled	42.2	27	**Chain:** D: **PDB Molecule:**transcriptional activator protein trar; **PDBTitle:** three-dimensional structure of the quorum sensing protein2 trar bound to its autoinducer and to its target dna
55	c2ggzB_	Alignment	not modelled	41.2	13	**PDB header:**lyase activator **Chain:** B: **PDB Molecule:**guanylyl cyclase-activating protein 3; **PDBTitle:** crystal structure of human guanylate cyclase activating2 protein-3
56	c2kfhA_	Alignment	not modelled	39.7	18	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**eh domain-containing protein 1; **PDBTitle:** structure of the c-terminal domain of ehd1 with fnyestgpftak
57	d1aisb1	Alignment	not modelled	39.4	18	**Fold:**Cyclin-like **Superfamily:**Cyclin-like **Family:**Transcription factor IIB (TFIIB), core domain
58	c2in3A_	Alignment	not modelled	38.9	14	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**hypothetical protein; **PDBTitle:** crystal structure of a putative protein disulfide isomerase from2 nitrosomonas europaea
59	c3hugJ_	Alignment	not modelled	38.7	25	**PDB header:**transcription/membrane protein **Chain:** J: **PDB Molecule:**probable conserved membrane protein; **PDBTitle:** crystal structure of mycobacterium tuberculosis anti-sigma factor rsla2 in complex with -35 promoter binding domain of sigl
60	c1yzxB_	Alignment	not modelled	38.5	13	**PDB header:**transferase **Chain:** B: **PDB Molecule:**glutathione s-transferase kappa 1; **PDBTitle:** crystal structure of human kappa class glutathione2 transferase
61	d1fi6a_	Alignment	not modelled	37.1	16	**Fold:**EF Hand-like **Superfamily:**EF-hand **Family:**Eps15 homology domain (EH domain)
62	c3fiaA_	Alignment	not modelled	37.0	9	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**intersectin-1; **PDBTitle:** crystal structure of the eh 1 domain from human intersectin-2 1 protein. northeast structural genomics consortium target3 hr3646e.
63	d1rioa_	Alignment	not modelled	36.6	15	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**Phage repressors
64	d1c07a_	Alignment	not modelled	36.5	7	**Fold:**EF Hand-like **Superfamily:**EF-hand **Family:**Eps15 homology domain (EH domain)
65	c3kzqE_	Alignment	not modelled	35.1	19	**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
66	d1vkea_	Alignment	not modelled	34.4	17	**Fold:**AhpD-like **Superfamily:**AhpD-like **Family:**CMD-like
67	c3oouA_	Alignment	not modelled	34.3	10	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**lin2118 protein; **PDBTitle:** the structure of a protein with unkown function from listeria innocua
68	d1p4wa_	Alignment	not modelled	34.2	23	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**C-terminal effector domain of the bipartite response regulators **Family:**GerE-like (LuxR/UhpA family of transcriptional regulators)
69	d1r4wa_	Alignment	not modelled	34.2	14	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**DsbA-like
70	d2mysb_	Alignment	not modelled	34.0	10	**Fold:**EF Hand-like **Superfamily:**EF-hand **Family:**Calmodulin-like
71	c2pmyB_	Alignment	not modelled	33.9	18	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**ras and ef-hand domain-containing protein; **PDBTitle:** ef-hand domain of human rasef
72	d1v4wa_	Alignment	not modelled	33.1	9	**Fold:**Globin-like **Superfamily:**Globin-like **Family:**Globins
73	c3ek7A_	Alignment	not modelled	32.2	13	**PDB header:**fluorescent protein **Chain:** A: **PDB Molecule:**myosin light chain kinase, green fluorescent **PDBTitle:** calcium-saturated gcamp2 dimer
74	c1w8jD_	Alignment	not modelled	32.0	19	**PDB header:**motor protein **Chain:** D: **PDB Molecule:**myosin va; **PDBTitle:** crystal structure of myosin v motor domain -2 nucleotide-free
75	c2hg5D_	Alignment	not modelled	32.0	24	**PDB header:**membrane protein **Chain:** D: **PDB Molecule:**kcsa channel; **PDBTitle:** cs+ complex of a k channel with an amide to ester substitution in the2 selectivity filter
76	c1o17A_	Alignment	not modelled	30.9	16	**PDB header:**transferase **Chain:** A: **PDB Molecule:**anthranilate phosphoribosyltransferase; **PDBTitle:** anthranilate phosphoribosyl-transferase (trpd)
77	c3mseB_	Alignment	not modelled	30.4	11	**PDB header:**transferase **Chain:** B: **PDB Molecule:**calcium-dependent protein kinase, putative; **PDBTitle:** crystal structure of c-terminal domain of pf110239.
78	c3ivpD_	Alignment	not modelled	30.0	17	**PDB header:**dna binding protein **Chain:** D: **PDB Molecule:**putative transposon-related dna-binding protein; **PDBTitle:** the structure of a possible transposon-related dna-binding protein2 from clostridium difficile 630.
79	d3e11a1	Alignment	not modelled	29.1	26	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**TTHA0227-like

80	c3j04A_	Alignment	not modelled	29.1	10	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**myosin-11; **PDBTitle:** em structure of the heavy meromyosin subfragment of chick smooth2 muscle myosin with regulatory light chain in phosphorylated state
81	c2doqA_	Alignment	not modelled	29.0	7	**PDB header:**cell cycle **Chain:** A: **PDB Molecule:**cell division control protein 31; **PDBTitle:** crystal structure of sfi1p/cdc31p complex
82	c3t76A_	Alignment	not modelled	28.9	20	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**transcriptional regulator vanug; **PDBTitle:** crystal structure of transcriptional regulator vanug, form ii
83	c2rmrA_	Alignment	not modelled	28.7	15	**PDB header:**transcription **Chain:** A: **PDB Molecule:**paired amphipathic helix protein sin3a; **PDBTitle:** solution structure of msin3a pah1 domain
84	c2otgA_	Alignment	not modelled	28.3	11	**PDB header:**contractile protein **Chain:** A: **PDB Molecule:**myosin heavy chain; **PDBTitle:** rigor-like structures of muscle myosins reveal key2 mechanical elements in the transduction pathways of this3 allosteric motor
85	c1p8cD_	Alignment	not modelled	28.2	16	**PDB header:**structural genomics, unknown function **Chain:** D: **PDB Molecule:**conserved hypothetical protein; **PDBTitle:** crystal structure of tm1620 (apc4843) from thermotoga2 maritima
86	c1eg4A_	Alignment	not modelled	27.0	14	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**dystrophin; **PDBTitle:** structure of a dystrophin ww domain fragment in complex2 with a beta-dystroglycan peptide
87	d1qjta_	Alignment	not modelled	26.7	18	**Fold:**EF Hand-like **Superfamily:**EF-hand **Family:**Eps15 homology domain (EH domain)
88	c3eusB_	Alignment	not modelled	25.7	10	**PDB header:**dna binding protein **Chain:** B: **PDB Molecule:**dna-binding protein; **PDBTitle:** the crystal structure of the dna binding protein from silicibacter2 pomeroyi
89	c2bl0C_	Alignment	not modelled	25.3	9	**PDB header:**muscle protein **Chain:** C: **PDB Molecule:**myosin regulatory light chain; **PDBTitle:** physarum polycephalum myosin ii regulatory domain
90	c2kvcA_	Alignment	not modelled	25.1	7	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**putative uncharacterized protein; **PDBTitle:** solution structure of the mycobacterium tuberculosis protein rv0543c,2 a member of the duf3349 superfamily. seattle structural genomics3 center for infectious disease target mytud.17112.a
91	d1sq8a_	Alignment	not modelled	25.1	41	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**Phage repressors
92	d1ha7a_	Alignment	not modelled	24.8	12	**Fold:**Globin-like **Superfamily:**Globin-like **Family:**Phycocyanin-like phycobilisome proteins
93	d1b33b_	Alignment	not modelled	24.6	14	**Fold:**Globin-like **Superfamily:**Globin-like **Family:**Phycocyanin-like phycobilisome proteins
94	c2kgrA_	Alignment	not modelled	24.6	12	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**intersectin-1; **PDBTitle:** solution structure of protein itsn1 from homo sapiens.2 northeast structural genomics consortium target hr5524a
95	d1allb_	Alignment	not modelled	24.4	15	**Fold:**Globin-like **Superfamily:**Globin-like **Family:**Phycocyanin-like phycobilisome proteins
96	c2dfsA_	Alignment	not modelled	24.4	19	**PDB header:**contractile protein/transport protein **Chain:** A: **PDB Molecule:**myosin-5a; **PDBTitle:** 3-d structure of myosin-v inhibited state
97	c3f6wE_	Alignment	not modelled	23.9	16	**PDB header:**dna binding protein **Chain:** E: **PDB Molecule:**xre-family like protein; **PDBTitle:** xre-family like protein from pseudomonas syringae pv. tomato str.2 dc3000
98	c1i84V_	Alignment	not modelled	22.9	10	**PDB header:**contractile protein **Chain:** V: **PDB Molecule:**smooth muscle myosin heavy chain; **PDBTitle:** cryo-em structure of the heavy meromyosin subfragment of2 chicken gizzard smooth muscle myosin with regulatory light3 chain in the dephosphorylated state. only c alphas4 provided for regulatory light chain. only backbone atoms5 provided for s2 fragment.
99	d2croa_	Alignment	not modelled	22.8	34	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**Phage repressors
100	d1jeba_	Alignment	not modelled	22.2	11	**Fold:**Globin-like **Superfamily:**Globin-like **Family:**Globins
101	c3d7iB_	Alignment	not modelled	21.7	21	**PDB header:**lyase **Chain:** B: **PDB Molecule:**carboxymuconolactone decarboxylase family protein; **PDBTitle:** crystal structure of carboxymuconolactone decarboxylase family protein2 possibly involved in oxygen detoxification (1591455) from3 methanococcus jannaschii at 1.75 a resolution
102	c3k69A_	Alignment	not modelled	21.6	15	**PDB header:**transcription **Chain:** A: **PDB Molecule:**putative transcription regulator; **PDBTitle:** crystal structure of a putative transcriptional regulator (lp_0360)2 from lactobacillus plantarum at 1.95 a resolution
103	d2gqba1	Alignment	not modelled	21.6	31	**Fold:**RPA2825-like **Superfamily:**RPA2825-like **Family:**RPA2825-like
						PDB header:transcription regulator

104	c3op9A_	Alignment	not modelled	21.5	11	**Chain:** A: **PDB Molecule:**pli0006 protein; **PDBTitle:** crystal structure of transcriptional regulator from listeria innocua
105	c3trbA_	Alignment	not modelled	21.4	19	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**virulence-associated protein i; **PDBTitle:** structure of an addiction module antidote protein of a higa (higa)2 family from coxiella burnetii
106	d1wdcb_	Alignment	not modelled	21.4	8	**Fold:**EF Hand-like **Superfamily:**EF-hand **Family:**Calmodulin-like
107	d1ffva1	Alignment	not modelled	21.3	21	**Fold:**CO dehydrogenase ISP C-domain like **Superfamily:**CO dehydrogenase ISP C-domain like **Family:**CO dehydrogenase ISP C-domain like
108	c3sibA_	Alignment	not modelled	21.3	11	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**ure3-bp sequence specific dna binding protein; **PDBTitle:** crystal structure of ure3-binding protein, wild-type
109	c2gbbA_	Alignment	not modelled	21.2	16	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**putative chorismate mutase; **PDBTitle:** crystal structure of secreted chorismate mutase from2 yersinia pestis
110	d1n62a1	Alignment	not modelled	20.7	18	**Fold:**CO dehydrogenase ISP C-domain like **Superfamily:**CO dehydrogenase ISP C-domain like **Family:**CO dehydrogenase ISP C-domain like
111	c2ebyA_	Alignment	not modelled	20.7	14	**PDB header:**transcription **Chain:** A: **PDB Molecule:**putative hth-type transcriptional regulator ybaq; **PDBTitle:** crystal structure of a hypothetical protein from e. coli
112	c1br4E_	Alignment	not modelled	20.2	10	**PDB header:**muscle protein **Chain:** E: **PDB Molecule:**myosin; **PDBTitle:** smooth muscle myosin motor domain-essential light chain2 complex with mgadp.bef3 bound at the active site
113	d1b8da_	Alignment	not modelled	20.1	8	**Fold:**Globin-like **Superfamily:**Globin-like **Family:**Phycocyanin-like phycobilisome proteins
114	d1f99a_	Alignment	not modelled	20.0	12	**Fold:**Globin-like **Superfamily:**Globin-like **Family:**Phycocyanin-like phycobilisome proteins