Phyre^2

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Description	A2A6A1
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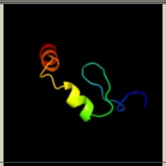
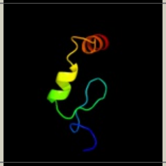
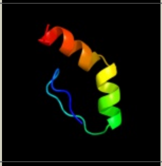
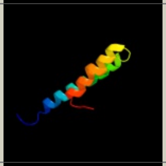
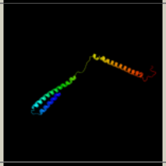
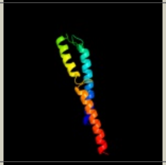
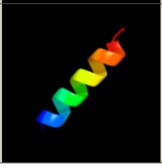
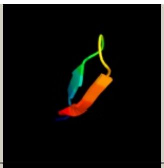
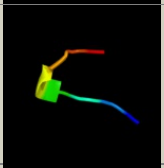
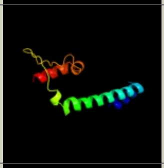
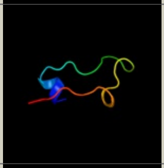
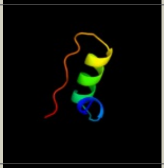
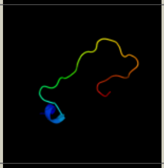
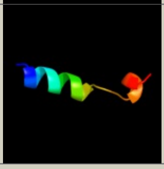
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1zr9a1	Alignment		97.8	33	**Fold:**beta-beta-alpha zinc fingers **Superfamily:**beta-beta-alpha zinc fingers **Family:**HkH motif-containing C2H2 finger
2	c1zr9A_	Alignment		97.8	33	**PDB header:**transcription **Chain:** A: **PDB Molecule:**zinc finger protein 593; **PDBTitle:** solution structure of a human c2h2-type zinc finger protein
3	c4dgwA_	Alignment		95.6	20	**PDB header:**splicing **Chain:** A: **PDB Molecule:**pre-mrna-splicing factor prp9; **PDBTitle:** crystal structure of the sf3a splicing factor complex of u2 snrnp
4	c1zu1A_	Alignment		93.2	18	**PDB header:**rna binding protein **Chain:** A: **PDB Molecule:**rna binding protein zfa; **PDBTitle:** solution structure of the n-terminal zinc fingers of the2 xenopus laevis double stranded rna binding protein zfa
5	c4f9aB_	Alignment		89.7	41	**PDB header:**transferase **Chain:** B: **PDB Molecule:**protein dbf4 homolog a; **PDBTitle:** human cdc7 kinase in complex with dbf4 and nucleotide
6	c4lctD_	Alignment		88.7	20	**PDB header:**signaling protein **Chain:** D: **PDB Molecule:**cop9 signalosome complex subunit 1; **PDBTitle:** crystal structure and versatile functional roles of the cop92 signalosome subunit 1
7	d2elba1	Alignment		86.3	18	**Fold:**BAR/IMD domain-like **Superfamily:**BAR/IMD domain-like **Family:**BAR domain
8	d1zu1a2	Alignment		76.6	18	**Fold:**beta-beta-alpha zinc fingers **Superfamily:**beta-beta-alpha zinc fingers **Family:**HkH motif-containing C2H2 finger
9	c1l8dB_	Alignment		70.9	19	**PDB header:**replication **Chain:** B: **PDB Molecule:**dna double-strand break repair rad50 atpase; **PDBTitle:** rad50 coiled-coil zn hook
10	c2rsiA_	Alignment		47.6	30	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**zinc finger protein zfat; **PDBTitle:** solution structures of the dna-binding domains of immune-related zinc-2 finger protein zfat
11	d1mr1c_	Alignment		47.5	18	**Fold:**SAND domain-like **Superfamily:**SAND domain-like **Family:**SMAD4-binding domain of oncoprotein Ski

12	c4esjA_	Alignment		46.5	42	**PDB header:**hydrolase/dna **Chain:** A: **PDB Molecule:**type-2 restriction enzyme dpni; **PDBTitle:** restriction endonuclease dpni in complex with target dna
13	d1fu9a_	Alignment		44.1	50	**Fold:**beta-beta-alpha zinc fingers **Superfamily:**beta-beta-alpha zinc fingers **Family:**C2HC finger
14	d2vrda1	Alignment		43.9	63	**Fold:**beta-beta-alpha zinc fingers **Superfamily:**beta-beta-alpha zinc fingers **Family:**HkH motif-containing C2H2 finger
15	c2vgqA_	Alignment		43.6	13	**PDB header:**immune system/transport **Chain:** A: **PDB Molecule:**maltose-binding periplasmic protein, **PDBTitle:** crystal structure of human ips-1 card
16	d1m9ma_	Alignment		43.0	36	**Fold:**Nitric oxide (NO) synthase oxygenase domain **Superfamily:**Nitric oxide (NO) synthase oxygenase domain **Family:**Nitric oxide (NO) synthase oxygenase domain
17	d1q2oa_	Alignment		42.0	36	**Fold:**Nitric oxide (NO) synthase oxygenase domain **Superfamily:**Nitric oxide (NO) synthase oxygenase domain **Family:**Nitric oxide (NO) synthase oxygenase domain
18	d1qusa_	Alignment		41.5	23	**Fold:**Lysozyme-like **Superfamily:**Lysozyme-like **Family:**Bacterial muramidase, catalytic domain
19	c1loiA_	Alignment		41.2	56	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**cyclic 3',5'-amp specific phosphodiesterase rd1; **PDBTitle:** n-terminal splice region of rat c-amp phosphodiesterase,2 nmr, 7 structures
20	d1ztda1	Alignment		41.0	32	**Fold:**RNase III domain-like **Superfamily:**RNase III domain-like **Family:**PF0609-like
21	c3eplA_	Alignment	not modelled	40.5	22	**PDB header:**transferase/rna **Chain:** A: **PDB Molecule:**trna isopentenyltransferase; **PDBTitle:** crystallographic snapshots of eukaryotic2 dimethylallyltransferase acting on trna: insight into trna3 recognition and reaction mechanism
22	c4anrA_	Alignment	not modelled	40.2	27	**PDB header:**lyase **Chain:** A: **PDB Molecule:**soluble lytic transglycosylase b; **PDBTitle:** crystal structure of soluble lytic transglycosylase sltb12 from pseudomonas aeruginosa
23	c3cw19_	Alignment	not modelled	39.3	63	**PDB header:**splicing **Chain:** 9: **PDB Molecule:**u1 small nuclear ribonucleoprotein c; **PDBTitle:** crystal structure of human spliceosomal u1 snrnp
24	d1qlma_	Alignment	not modelled	39.2	38	**Fold:**Methenyltetrahydromethanopterin cyclohydrolase **Superfamily:**Methenyltetrahydromethanopterin cyclohydrolase **Family:**Methenyltetrahydromethanopterin cyclohydrolase
25	d2atza1	Alignment	not modelled	38.9	28	**Fold:**Prim-pol domain **Superfamily:**Prim-pol domain **Family:**HP0184-like
26	d1nosa_	Alignment	not modelled	38.8	43	**Fold:**Nitric oxide (NO) synthase oxygenase domain **Superfamily:**Nitric oxide (NO) synthase oxygenase domain **Family:**Nitric oxide (NO) synthase oxygenase domain
27	c4fs9B_	Alignment	not modelled	38.6	13	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**broad specificity amino acid racemase; **PDBTitle:** complex structure of a broad specificity amino acid racemase (bar)2 within the reactive intermediate
28	c1fooA_	Alignment	not modelled	37.8	36	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**nitric-oxide synthase; **PDBTitle:** bovine endothelial nitric oxide synthase heme domain complexed with l-2 arg and no(h4b-free)

29	c2dmiA_	Alignment	not modelled	37.7	32	**PDB header:**transcription **Chain:** A: **PDB Molecule:**teashirt homolog 3; **PDBTitle:** solution structure of the first and the second zf-c2h2 like2 domains of human teashirt homolog 3
30	c1un6D_	Alignment	not modelled	37.5	10	**PDB header:**rna-binding protein/rna **Chain:** D: **PDB Molecule:**transcription factor iiia; **PDBTitle:** the crystal structure of a zinc finger - rna complex2 reveals two modes of molecular recognition
31	d1mjta_	Alignment	not modelled	36.5	43	**Fold:**Nitric oxide (NO) synthase oxygenase domain **Superfamily:**Nitric oxide (NO) synthase oxygenase domain **Family:**Nitric oxide (NO) synthase oxygenase domain
32	c3o4xE_	Alignment	not modelled	36.1	16	**PDB header:**protein binding **Chain:** E: **PDB Molecule:**protein diaphanous homolog 1; **PDBTitle:** crystal structure of complex between amino and carboxy terminal2 fragments of mdia1
33	c3o4xF_	Alignment	not modelled	36.1	16	**PDB header:**protein binding **Chain:** F: **PDB Molecule:**protein diaphanous homolog 1; **PDBTitle:** crystal structure of complex between amino and carboxy terminal2 fragments of mdia1
34	d3e7ga1	Alignment	not modelled	35.8	43	**Fold:**Nitric oxide (NO) synthase oxygenase domain **Superfamily:**Nitric oxide (NO) synthase oxygenase domain **Family:**Nitric oxide (NO) synthase oxygenase domain
35	d1fnna1	Alignment	not modelled	35.5	17	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Helicase DNA-binding domain
36	c1l7eC_	Alignment	not modelled	35.2	19	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**nicotinamide nucleotide transhydrogenase, **PDBTitle:** crystal structure of r. rubrum transhydrogenase domain i2 with bound nadh
37	d2dara1	Alignment	not modelled	35.0	38	**Fold:**Glucocorticoid receptor-like (DNA-binding domain) **Superfamily:**Glucocorticoid receptor-like (DNA-binding domain) **Family:**LIM domain
38	c2ctdA_	Alignment	not modelled	34.9	26	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**zinc finger protein 512; **PDBTitle:** solution structure of two zf-c2h2 domains from human zinc2 finger protein 512
39	c4gvsA_	Alignment	not modelled	34.7	30	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**methenyltetrahydromethanopterin cyclohydrolase; **PDBTitle:** x-ray structure of the archaeoglobus fulgidus methenyl-2 tetrahydromethanopterin cyclohydrolase in complex with n5-formyl-3 tetrahydromethanopterin
40	c2gqjA_	Alignment	not modelled	34.3	25	**PDB header:**gene regulation **Chain:** A: **PDB Molecule:**zinc finger protein kiaa1196; **PDBTitle:** solution structure of the two zf-c2h2 like domains(493-575)2 of human zinc finger protein kiaa1196
41	d1om4a_	Alignment	not modelled	34.3	32	**Fold:**Nitric oxide (NO) synthase oxygenase domain **Superfamily:**Nitric oxide (NO) synthase oxygenase domain **Family:**Nitric oxide (NO) synthase oxygenase domain
42	c4ijdA_	Alignment	not modelled	34.3	20	**PDB header:**transferase **Chain:** A: **PDB Molecule:**histone-lysine n-methyltransferase prdm9; **PDBTitle:** crystal structure of methyltransferase domain of human pr domain-2 containing protein 9
43	d3e7ma1	Alignment	not modelled	34.2	43	**Fold:**Nitric oxide (NO) synthase oxygenase domain **Superfamily:**Nitric oxide (NO) synthase oxygenase domain **Family:**Nitric oxide (NO) synthase oxygenase domain
44	d1p7aa_	Alignment	not modelled	33.9	25	**Fold:**beta-beta-alpha zinc fingers **Superfamily:**beta-beta-alpha zinc fingers **Family:**Classic zinc finger, C2H2
45	c2ct1A_	Alignment	not modelled	33.8	19	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcriptional repressor ctcf; **PDBTitle:** solution structure of the zinc finger domain of2 transcriptional repressor ctcf protein
46	c2ogfD_	Alignment	not modelled	33.0	28	**PDB header:**structural genomics, unknown function **Chain:** D: **PDB Molecule:**hypothetical protein mj0408; **PDBTitle:** crystal structure of protein mj0408 from methanococcus jannaschii,2 pfam duf372
47	c1bboA_	Alignment	not modelled	32.9	30	**PDB header:**dna-binding protein **Chain:** A: **PDB Molecule:**human enhancer-binding protein mbp-1; **PDBTitle:** high-resolution solution structure of the double cys2*his22 zinc finger from the human enhancer binding protein mbp-1
48	d3ebya1	Alignment	not modelled	32.4	36	**Fold:**Cystatin-like **Superfamily:**NTF2-like **Family:**Ring hydroxylating beta subunit
49	d1weva_	Alignment	not modelled	32.1	33	**Fold:**FYVE/PHD zinc finger **Superfamily:**FYVE/PHD zinc finger **Family:**PHD domain
50	d1h6ga2	Alignment	not modelled	31.9	33	**Fold:**Four-helical up-and-down bundle **Superfamily:**alpha-catenin/vinculin-like **Family:**alpha-catenin/vinculin
51	c2epqA_	Alignment	not modelled	31.2	15	**PDB header:**transcription **Chain:** A: **PDB Molecule:**poz-, at hook-, and zinc finger-containing **PDBTitle:** solution structure of the third zinc finger domain of zinc2 finger protein 278
52	c2elqA_	Alignment	not modelled	31.0	25	**PDB header:**transcription **Chain:** A: **PDB Molecule:**zinc finger protein 406; **PDBTitle:** solution structure of the 14th c2h2 zinc finger of human2 zinc finger protein 406
53	d2ieca1	Alignment	not modelled	30.6	31	**Fold:**MK0786-like **Superfamily:**MK0786-like **Family:**MK0786-like
54	d2a2na1	Alignment	not modelled	30.5	25	**Fold:**Cyclophilin-like **Superfamily:**Cyclophilin-like **Family:**Cyclophilin (peptidylprolyl isomerase)

55	c2rsjA_	Alignment	not modelled	30.5	26	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**zinc finger protein zfat; **PDBTitle:** solution structures of the dna-binding domains of immune-related zinc-2 finger protein zfat
56	c2zciD_	Alignment	not modelled	30.5	17	**PDB header:**signaling protein, lyase **Chain:** D: **PDB Molecule:**phosphoenolpyruvate carboxykinase [gtp]; **PDBTitle:** structure of a gtp-dependent bacterial pep-carboxykinase2 from corynebacterium glutamicum
57	d1zs8a2	Alignment	not modelled	30.3	9	**Fold:**MHC antigen-recognition domain **Superfamily:**MHC antigen-recognition domain **Family:**MHC antigen-recognition domain
58	c4gznC_	Alignment	not modelled	30.3	25	**PDB header:**transcription/dna **Chain:** C: **PDB Molecule:**zinc finger protein 57; **PDBTitle:** mouse zfp57 zinc fingers in complex with methylated dna
59	c2flqA_	Alignment	not modelled	29.4	41	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**nitric oxide synthase; **PDBTitle:** crystal structure of nitric oxide synthase from geobacillus2 stearothermophilus (atcc 12980) complexed with l-arginine
60	c2k7nA_	Alignment	not modelled	29.4	29	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**peptidyl-prolyl cis-trans isomerase-like 1; **PDBTitle:** solution structure of the ppil1 bound to a fragment of skip
61	c2yt9A_	Alignment	not modelled	29.3	25	**PDB header:**transcription **Chain:** A: **PDB Molecule:**zinc finger-containing protein 1; **PDBTitle:** solution structure of c2h2 type zinc finger domain 345 in2 zinc finger protein 278
62	c3p0kA_	Alignment	not modelled	29.2	46	**PDB header:**oxidoreductase, viral protein **Chain:** A: **PDB Molecule:**sulfhydryl oxidase; **PDBTitle:** structure of baculovirus sulfhydryl oxidase ac92
63	c2ee8A_	Alignment	not modelled	28.8	24	**PDB header:**gene regulation **Chain:** A: **PDB Molecule:**protein odd-skipped-related 2; **PDBTitle:** solution structure of three zf-c2h2 domains from mouse2 protein odd-skipped-related 2 splicing isoform 2
64	c3iufA_	Alignment	not modelled	28.5	40	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**zinc finger protein ubi-d4; **PDBTitle:** crystal structure of the c2h2-type zinc finger domain of human ubi-d4
65	c1x5wA_	Alignment	not modelled	28.4	15	**PDB header:**transcription **Chain:** A: **PDB Molecule:**zinc finger protein 64, isoforms 1; **PDBTitle:** solution structure of the c2h2 type zinc-binding domain of2 human zinc finger protein 64, isoforms 1 and 2
66	c1wjpA_	Alignment	not modelled	28.2	15	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**zinc finger protein 295; **PDBTitle:** solution structure of zf-c2h2 domains from human zinc2 finger protein 295
67	d1m7va_	Alignment	not modelled	27.9	24	**Fold:**Nitric oxide (NO) synthase oxygenase domain **Superfamily:**Nitric oxide (NO) synthase oxygenase domain **Family:**Nitric oxide (NO) synthase oxygenase domain
68	d2chca1	Alignment	not modelled	27.8	17	**Fold:**Cystatin-like **Superfamily:**NTF2-like **Family:**Rv3472-like
69	c3hizB_	Alignment	not modelled	27.8	9	**PDB header:**transferase/oncoprotein **Chain:** B: **PDB Molecule:**phosphatidylinositol 3-kinase regulatory subunit **PDBTitle:** crystal structure of p110alpha h1047r mutant in complex with2 nish2 of p85alpha
70	c1f2iI_	Alignment	not modelled	27.2	25	**PDB header:**transcription/dna **Chain:** I: **PDB Molecule:**fusion of n-terminal 17-mer peptide extension to **PDBTitle:** cocrystal structure of selected zinc finger dimer bound to2 dna
71	c2qeyA_	Alignment	not modelled	27.2	26	**PDB header:**lyase **Chain:** A: **PDB Molecule:**phosphoenolpyruvate carboxykinase, cytosolic [gtp]; **PDBTitle:** rat cytosolic pepck in complex with gtp
72	c2lv2A_	Alignment	not modelled	26.8	15	**PDB header:**transcription **Chain:** A: **PDB Molecule:**insulinoma-associated protein 1; **PDBTitle:** solution nmr structure of c2h2-type zinc-fingers 4 and 5 from human2 insulinoma-associated protein 1 (fragment 424-497), northeast3 structural genomics consortium target hr7614b
73	c3g6iA_	Alignment	not modelled	26.2	31	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**putative outer membrane protein, part of carbohydrate **PDBTitle:** crystal structure of an outer membrane protein, part of a putative2 carbohydrate binding complex (bt_1022) from bacteroides3 thetaiotaomicron vpi-5482 at 1.93 a resolution
74	d1wbxa2	Alignment	not modelled	25.4	20	**Fold:**MHC antigen-recognition domain **Superfamily:**MHC antigen-recognition domain **Family:**MHC antigen-recognition domain
75	c2lvuA_	Alignment	not modelled	25.2	33	**PDB header:**transcription **Chain:** A: **PDB Molecule:**zinc finger and btb domain-containing protein 17; **PDBTitle:** solution structure of miz-1 zinc finger 10
76	d1vlga_	Alignment	not modelled	25.1	23	**Fold:**Ferritin-like **Superfamily:**Ferritin-like **Family:**Ferritin
77	c2elvA_	Alignment	not modelled	25.0	22	**PDB header:**transcription **Chain:** A: **PDB Molecule:**zinc finger protein 406; **PDBTitle:** solution structure of the 6th c2h2 zinc finger of human2 zinc finger protein 406
78	d2dmda2	Alignment	not modelled	24.7	28	**Fold:**beta-beta-alpha zinc fingers **Superfamily:**beta-beta-alpha zinc fingers **Family:**Classic zinc finger, C2H2
79	c1tllA_	Alignment	not modelled	24.6	19	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**nitric-oxide synthase, brain; **PDBTitle:** crystal structure of rat neuronal nitric-oxide synthase2 reductase module at 2.3 a resolution.

80	c2eoxA_	Alignment	not modelled	24.2	20	**PDB header:**transcription **Chain:** A: **PDB Molecule:**zinc finger protein 473; **PDBTitle:** solution structure of the c2h2 type zinc finger (region 315-2 345) of human zinc finger protein 473
81	c1arfA_	Alignment	not modelled	24.2	25	**PDB header:**transcription regulation **Chain:** A: **PDB Molecule:**yeast transcription factor adr1; **PDBTitle:** structures of dna-binding mutant zinc finger domains:2 implications for dna binding
82	d1hcia4	Alignment	not modelled	24.1	17	**Fold:**Spectrin repeat-like **Superfamily:**Spectrin repeat **Family:**Spectrin repeat
83	d1c16a2	Alignment	not modelled	23.7	13	**Fold:**MHC antigen-recognition domain **Superfamily:**MHC antigen-recognition domain **Family:**MHC antigen-recognition domain
84	c3bo7D_	Alignment	not modelled	23.6	25	**PDB header:**isomerase/immunosuppressant **Chain:** D: **PDB Molecule:**peptidyl-prolyl cis-trans isomerase cyclophilin-type; **PDBTitle:** crystal structure of toxoplasma gondii peptidyl-prolyl cis-trans2 isomerase, 541.m00136
85	c3pe0B_	Alignment	not modelled	23.4	25	**PDB header:**structural protein **Chain:** B: **PDB Molecule:**plectin; **PDBTitle:** structure of the central region of the plakin domain of plectin
86	c3c85D_	Alignment	not modelled	23.1	43	**PDB header:**transport protein **Chain:** D: **PDB Molecule:**putative glutathione-regulated potassium-efflux system **PDBTitle:** crystal structure of trka domain of putative glutathione-regulated2 potassium-efflux kefb from vibrio parahaemolyticus
87	c1hx9A_	Alignment	not modelled	23.0	18	**PDB header:**lyase **Chain:** A: **PDB Molecule:**5-epi-aristolochene synthase; **PDBTitle:** crystal structure of teas w273s form 1
88	c2ig7A_	Alignment	not modelled	22.3	21	**PDB header:**transferase **Chain:** A: **PDB Molecule:**choline/ethanolamine kinase; **PDBTitle:** crystal structure of human choline kinase b
89	c3hl6B_	Alignment	not modelled	21.9	25	**PDB header:**unknown function **Chain:** B: **PDB Molecule:**pathogenicity island protein; **PDBTitle:** staphylococcus aureus pathogenicity island 3 orf9 protein
90	c2emcA_	Alignment	not modelled	21.8	25	**PDB header:**transcription **Chain:** A: **PDB Molecule:**zinc finger protein 473; **PDBTitle:** solution structure of the c2h2 type zinc finger (region 641-2 673) of human zinc finger protein 473
91	c1j9zB_	Alignment	not modelled	21.7	28	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**nadph-cytochrome p450 reductase; **PDBTitle:** cypor-w677g
92	c2drpD_	Alignment	not modelled	21.7	20	**PDB header:**transcription/dna **Chain:** D: **PDB Molecule:**protein (tramtrack dna-binding domain); **PDBTitle:** the crystal structure of a two zinc-finger peptide reveals2 an extension to the rules for zinc-finger/dna recognition
93	d1oaoc_	Alignment	not modelled	21.6	19	**Fold:**Prismane protein-like **Superfamily:**Prismane protein-like **Family:**Acetyl-CoA synthase
94	c1ei3C_	Alignment	not modelled	21.6	8	**PDB header:**blood clotting **Chain:** C: **PDB Molecule:**fibrinogen; **PDBTitle:** crystal structure of native chicken fibrinogen
95	c3ve5D_	Alignment	not modelled	21.5	23	**PDB header:**recombination **Chain:** D: **PDB Molecule:**recombination protein recr; **PDBTitle:** structure of recombination mediator protein recr16-196 deletion mutant
96	c3lvgF_	Alignment	not modelled	21.5	20	**PDB header:**structural protein **Chain:** F: **PDB Molecule:**clathrin light chain b; **PDBTitle:** crystal structure of a clathrin heavy chain and clathrin light chain2 complex
97	c2lceA_	Alignment	not modelled	21.4	20	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**b-cell lymphoma 6 protein; **PDBTitle:** chemical shift assignment of hr4436b from homo sapiens, northeast2 structural genomics consortium
98	c1llmC_	Alignment	not modelled	21.3	10	**PDB header:**transcription/dna **Chain:** C: **PDB Molecule:**chimera of zif23-gcn4; **PDBTitle:** crystal structure of a zif23-gcn4 chimera bound to dna
99	c2em5A_	Alignment	not modelled	21.2	14	**PDB header:**transcription **Chain:** A: **PDB Molecule:**zinc finger protein 95 homolog; **PDBTitle:** solution structure of the c2h2 type zinc finger (region 768-2 800) of human zinc finger protein 95 homolog
100	d1fpsa_	Alignment	not modelled	21.1	14	**Fold:**Terpenoid synthases **Superfamily:**Terpenoid synthases **Family:**Isoprenyl diphosphate synthases
101	c2d9hA_	Alignment	not modelled	21.1	20	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**zinc finger protein 692; **PDBTitle:** solution structure of the forth and fifth zf-c2h2 domains2 of zinc finger protein 692
102	d1zt1a2	Alignment	not modelled	20.9	18	**Fold:**MHC antigen-recognition domain **Superfamily:**MHC antigen-recognition domain **Family:**MHC antigen-recognition domain
103	c4euhA_	Alignment	not modelled	20.9	24	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**putative reductase ca_c0462; **PDBTitle:** crystal structure of clostridium acetobutulicum trans-2-enoyl-coa2 reductase apo form
104	c2rpcA_	Alignment	not modelled	20.9	20	**PDB header:**transcription **Chain:** A: **PDB Molecule:**zinc finger protein zic 3; **PDBTitle:** solution structure of the tandem zf-c2h2 domains from the2 human zinc finger protein zic 3
105	c2j1dG_	Alignment	not modelled	20.9	9	**PDB header:**protein binding **Chain:** G: **PDB Molecule:**disheveled-associated activator of morphogenesis 1; **PDBTitle:** crystallization of hdaam1 c-terminal fragment

106	c1m46B_	Alignment	not modelled	20.7	46	**PDB header:**cell cycle protein **Chain:** B: **PDB Molecule:**iq4 motif from myo2p, a class v myosin; **PDBTitle:** crystal structure of mlc1p bound to iq4 of myo2p, a class v2 myosin
107	d2oeea1	Alignment	not modelled	20.3	44	**Fold:**YheA-like **Superfamily:**YheA/YmcA-like **Family:**YheA-like
108	c2z6eC_	Alignment	not modelled	20.3	10	**PDB header:**protein fibril regulator **Chain:** C: **PDB Molecule:**disheveled-associated activator of morphogenesis **PDBTitle:** crystal structure of human daam1 fh2
109	c2ghfA_	Alignment	not modelled	20.2	26	**PDB header:**transcription, metal binding protein **Chain:** A: **PDB Molecule:**zinc fingers and homeoboxes protein 1; **PDBTitle:** solution structure of the complete zinc-finger region of2 human zinc-fingers and homeoboxes 1 (zhx1)