Phyre^2

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Description	P0A7H3
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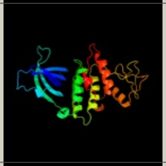
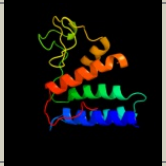
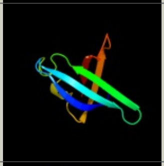
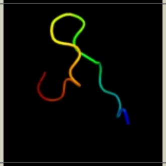
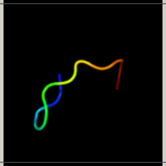
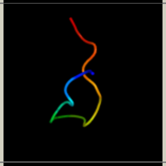
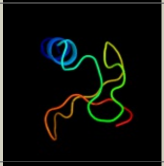
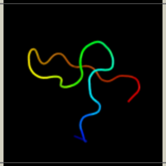
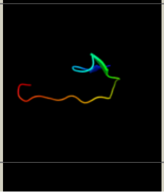
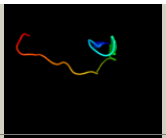
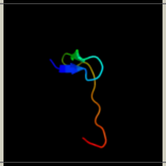
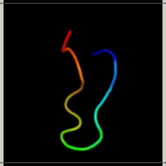
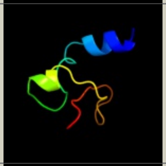
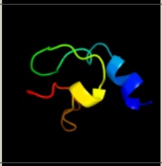
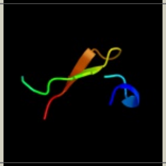
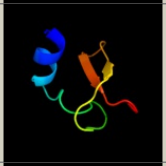
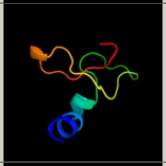
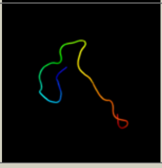
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3q8dB_	Alignment		100.0	100	**PDB header:**dna binding protein **Chain:** B: **PDB Molecule:**dna repair protein reco; **PDBTitle:** e. coli reco complex with ssb c-terminus
2	c1u5kA_	Alignment		100.0	17	**PDB header:**recombination,replication **Chain:** A: **PDB Molecule:**hypothetical protein; **PDBTitle:** recombinational repair protein reco
3	d1u5ka2	Alignment		99.9	16	**Fold:**ArfGap/RecO-like zinc finger **Superfamily:**ArfGap/RecO-like zinc finger **Family:**RecO C-terminal domain-like
4	d1u5ka1	Alignment		98.4	15	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**RecO N-terminal domain-like
5	d2dloa1	Alignment		30.9	26	**Fold:**Glucocorticoid receptor-like (DNA-binding domain) **Superfamily:**Glucocorticoid receptor-like (DNA-binding domain) **Family:**LIM domain
6	d1ibia2	Alignment		27.3	33	**Fold:**Glucocorticoid receptor-like (DNA-binding domain) **Superfamily:**Glucocorticoid receptor-like (DNA-binding domain) **Family:**LIM domain
7	d1rutx1	Alignment		26.2	33	**Fold:**Glucocorticoid receptor-like (DNA-binding domain) **Superfamily:**Glucocorticoid receptor-like (DNA-binding domain) **Family:**LIM domain
8	c2d9lA_	Alignment		25.7	15	**PDB header:**gene regulation **Chain:** A: **PDB Molecule:**nucleoporin-like protein rip; **PDBTitle:** solution structure of the arfgap domain of human rip
9	c2p57A_	Alignment		24.3	13	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**gtpase-activating protein znf289; **PDBTitle:** gap domain of znf289, an id1-regulated zinc finger protein
10	d1m3va1	Alignment		23.7	21	**Fold:**Glucocorticoid receptor-like (DNA-binding domain) **Superfamily:**Glucocorticoid receptor-like (DNA-binding domain) **Family:**LIM domain
11	c3iz5Z_	Alignment		23.5	17	**PDB header:**ribosome **Chain:** Z: **PDB Molecule:**60s ribosomal protein l24 (l24e); **PDBTitle:** localization of the large subunit ribosomal proteins into a 5.5 a2 cryo-em map of triticum aestivum translating 80s ribosome

12	c3izcZ_	Alignment		22.5	8	**PDB header:**ribosome **Chain:** Z: **PDB Molecule:**60s ribosomal protein rpl24 (l24e); **PDBTitle:** localization of the large subunit ribosomal proteins into a 6.1 a2 cryo-em map of saccharomyces cerevisiae translating 80s ribosome
13	c4a1eT_	Alignment		22.2	13	**PDB header:**ribosome **Chain:** T: **PDB Molecule:**rpl24; **PDBTitle:** t.thermophila 60s ribosomal subunit in complex with2 initiation factor 6. this file contains 5s rrna, 5.8s rrna3 and proteins of molecule 1
14	d1j2oa1	Alignment		22.0	20	**Fold:**Glucocorticoid receptor-like (DNA-binding domain) **Superfamily:**Glucocorticoid receptor-like (DNA-binding domain) **Family:**LIM domain
15	d1dcqa2	Alignment		21.4	11	**Fold:**ArfGap/RecO-like zinc finger **Superfamily:**ArfGap/RecO-like zinc finger **Family:**Pyk2-associated protein beta ARF-GAP domain
16	c2owaB_	Alignment		21.1	8	**PDB header:**protein transport **Chain:** B: **PDB Molecule:**arfgap-like finger domain containing protein; **PDBTitle:** crystal structure of putative gtpase activating protein for2 adp ribosylation factor from cryptosporidium parvum3 (cgd5_1040)
17	d1m4ma_	Alignment		20.8	9	**Fold:**Inhibitor of apoptosis (IAP) repeat **Superfamily:**Inhibitor of apoptosis (IAP) repeat **Family:**Inhibitor of apoptosis (IAP) repeat
18	c3o47A_	Alignment		20.3	11	**PDB header:**hydrolase, hydrolase activator **Chain:** A: **PDB Molecule:**adp-ribosylation factor gtpase-activating protein 1, adp- **PDBTitle:** crystal structure of arfgap1-arf1 fusion protein
19	c2iqjB_	Alignment		19.8	16	**PDB header:**protein transport **Chain:** B: **PDB Molecule:**stromal membrane-associated protein 1-like; **PDBTitle:** crystal structure of the gap domain of smap1l (loc64744)2 stromal membrane-associated protein 1-like
20	c2zkru_	Alignment		19.5	26	**PDB header:**ribosomal protein/rna **Chain:** U: **PDB Molecule:**rna expansion segment es41; **PDBTitle:** structure of a mammalian ribosomal 60s subunit within an2 80s complex obtained by docking homology models of the rna3 and proteins into an 8.7 a cryo-em map
21	c3lvrE_	Alignment	not modelled	19.4	13	**PDB header:**protein transport **Chain:** E: **PDB Molecule:**arf-gap with sh3 domain, ank repeat and ph domain- **PDBTitle:** the crystal structure of asap3 in complex with arf6 in transition2 state soaked with calcium
22	d2ds5a1	Alignment	not modelled	16.9	7	**Fold:**Glucocorticoid receptor-like (DNA-binding domain) **Superfamily:**Glucocorticoid receptor-like (DNA-binding domain) **Family:**ClpX chaperone zinc binding domain
23	c3mhsE_	Alignment	not modelled	16.3	25	**PDB header:**hydrolase/transcription regulator/protei **Chain:** E: **PDB Molecule:**saga-associated factor 73; **PDBTitle:** structure of the saga ubp8/sgf11/sus1/sgf73 dub module bound to2 ubiquitin aldehyde
24	c1ovxB_	Alignment	not modelled	16.3	7	**PDB header:**metal binding protein **Chain:** B: **PDB Molecule:**atp-dependent clp protease atp-binding subunit clpx; **PDBTitle:** nmr structure of the e. coli clpx chaperone zinc binding domain dimer
25	c3dwdB_	Alignment	not modelled	15.6	11	**PDB header:**transport protein **Chain:** B: **PDB Molecule:**adp-ribosylation factor gtpase-activating protein 1; **PDBTitle:** crystal structure of the arfgap domain of human arfgap1
26	c1s1iS_	Alignment	not modelled	15.0	9	**PDB header:**ribosome **Chain:** S: **PDB Molecule:**60s ribosomal protein l24-a; **PDBTitle:** structure of the ribosomal 80s-eef2-sordarin complex from2 yeast obtained by docking atomic models for rna and protein3 components into a 11.7 a cryo-em map. this file, 1s1i,4 contains 60s subunit. the 40s ribosomal subunit is in file5 1s1h.
27	d2cupa3	Alignment	not modelled	14.7	15	**Fold:**Glucocorticoid receptor-like (DNA-binding domain) **Superfamily:**Glucocorticoid receptor-like (DNA-binding domain) **Family:**LIM domain
28	c3k7aM_	Alignment	not modelled	14.4	15	**PDB header:**transcription **Chain:** M: **PDB Molecule:**transcription initiation factor iib;

						PDBTitle: crystal structure of an rna polymerase ii-tfiib complex
29	c2ds8A_	Alignment	not modelled	14.0	8	**PDB header:**metal binding protein, protein binding **Chain:** A: **PDB Molecule:**atp-dependent clp protease atp-binding subunit **PDBTitle:** structure of the zbd-xb complex
30	c3na7A_	Alignment	not modelled	13.9	12	**PDB header:**gene regulation, chaperone **Chain:** A: **PDB Molecule:**hp0958; **PDBTitle:** 2.2 angstrom structure of the hp0958 protein from helicobacter pylori2 ccug 17874
31	d1vqou1	Alignment	not modelled	13.9	14	**Fold:**Glucocorticoid receptor-like (DNA-binding domain) **Superfamily:**Glucocorticoid receptor-like (DNA-binding domain) **Family:**Ribosomal protein L24e
32	c3ccjU_	Alignment	not modelled	13.9	14	**PDB header:**ribosome **Chain:** U: **PDB Molecule:**50s ribosomal protein l24e; **PDBTitle:** structure of anisomycin resistant 50s ribosomal subunit: 23s rrna2 mutation c2534u
33	d2qfaa1	Alignment	not modelled	13.6	9	**Fold:**Inhibitor of apoptosis (IAP) repeat **Superfamily:**Inhibitor of apoptosis (IAP) repeat **Family:**Inhibitor of apoptosis (IAP) repeat
34	c1x6aA_	Alignment	not modelled	13.4	12	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**lim domain kinase 2; **PDBTitle:** solution structures of the second lim domain of human lim-2 kinase 2 (limk2)
35	d1vd4a_	Alignment	not modelled	13.0	9	**Fold:**Rubredoxin-like **Superfamily:**Zinc beta-ribbon **Family:**Transcriptional factor domain
36	d2raxa1	Alignment	not modelled	12.9	9	**Fold:**Inhibitor of apoptosis (IAP) repeat **Superfamily:**Inhibitor of apoptosis (IAP) repeat **Family:**Inhibitor of apoptosis (IAP) repeat
37	d2cora1	Alignment	not modelled	12.8	21	**Fold:**Glucocorticoid receptor-like (DNA-binding domain) **Superfamily:**Glucocorticoid receptor-like (DNA-binding domain) **Family:**LIM domain
38	d1xb0b_	Alignment	not modelled	12.4	23	**Fold:**Inhibitor of apoptosis (IAP) repeat **Superfamily:**Inhibitor of apoptosis (IAP) repeat **Family:**Inhibitor of apoptosis (IAP) repeat
39	c2b0oF_	Alignment	not modelled	11.9	13	**PDB header:**metal binding protein **Chain:** F: **PDB Molecule:**uplc1; **PDBTitle:** crystal structure of uplc1 gap domain
40	c1dcqA_	Alignment	not modelled	11.1	11	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**pyk2-associated protein beta; **PDBTitle:** crystal structure of the arf-gap domain and ankyrin repeats2 of papbeta.
41	c2dloA_	Alignment	not modelled	11.0	28	**PDB header:**cell adhesion **Chain:** A: **PDB Molecule:**thyroid receptor-interacting protein 6; **PDBTitle:** solution structure of the second lim domain of human2 thyroid receptor-interacting protein 6
42	c3fehA_	Alignment	not modelled	10.9	18	**PDB header:**hydrolase activator **Chain:** A: **PDB Molecule:**centaurin-alpha-1; **PDBTitle:** crystal structure of full length centaurin alpha-1
43	c2co8A_	Alignment	not modelled	10.8	10	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**nedd9 interacting protein with calponin homology **PDBTitle:** solution structures of the lim domain of human nedd92 interacting protein with calponin homology and lim domains
44	d2qam01	Alignment	not modelled	10.6	20	**Fold:**Rubredoxin-like **Superfamily:**Zn-binding ribosomal proteins **Family:**Ribosomal protein L32p
45	d1qbha_	Alignment	not modelled	9.9	23	**Fold:**Inhibitor of apoptosis (IAP) repeat **Superfamily:**Inhibitor of apoptosis (IAP) repeat **Family:**Inhibitor of apoptosis (IAP) repeat
46	d1tfqa_	Alignment	not modelled	9.9	27	**Fold:**Inhibitor of apoptosis (IAP) repeat **Superfamily:**Inhibitor of apoptosis (IAP) repeat **Family:**Inhibitor of apoptosis (IAP) repeat
47	d1q4qa_	Alignment	not modelled	9.9	27	**Fold:**Inhibitor of apoptosis (IAP) repeat **Superfamily:**Inhibitor of apoptosis (IAP) repeat **Family:**Inhibitor of apoptosis (IAP) repeat
48	d1x3ha1	Alignment	not modelled	9.8	33	**Fold:**Glucocorticoid receptor-like (DNA-binding domain) **Superfamily:**Glucocorticoid receptor-like (DNA-binding domain) **Family:**LIM domain
49	d2j0151	Alignment	not modelled	9.7	6	**Fold:**Rubredoxin-like **Superfamily:**Zn-binding ribosomal proteins **Family:**Ribosomal protein L32p
50	d2zjrz1	Alignment	not modelled	9.6	19	**Fold:**Rubredoxin-like **Superfamily:**Zn-binding ribosomal proteins **Family:**Ribosomal protein L32p
51	c2kgoA_	Alignment	not modelled	9.6	27	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein ybii; **PDBTitle:** solution nmr structure of zn finger protein ybil from escherichia2 coli. nesg target et107, ocsp target ec0402
52	d2vsla1	Alignment	not modelled	9.4	27	**Fold:**Inhibitor of apoptosis (IAP) repeat **Superfamily:**Inhibitor of apoptosis (IAP) repeat **Family:**Inhibitor of apoptosis (IAP) repeat
53	c3dzuD_	Alignment	not modelled	8.9	29	**PDB header:**transcription/dna **Chain:** D: **PDB Molecule:**peroxisome proliferator-activated receptor gamma; **PDBTitle:** intact ppar gamma - rxr alpha nuclear receptor complex on dna bound2 with bvt.13, 9-cis retinoic acid and ncoa2 peptide
54	c1oy7C_	Alignment	not modelled	8.9	14	**PDB header:**apoptosis/peptide **Chain:** C: **PDB Molecule:**baculoviral iap repeat-containing protein 7; **PDBTitle:** structure and function analysis of peptide antagonists of

						melanoma2 inhibitor of apoptosis (ml-iap)
55	d2aqaa1	Alignment	not modelled	8.8	17	**Fold:**Rubredoxin-like **Superfamily:**Nop10-like SnoRNP **Family:**Nucleolar RNA-binding protein Nop10-like
56	c2poiA_	Alignment	not modelled	8.7	27	**PDB header:**signaling protein/apoptosis **Chain:** A: **PDB Molecule:**baculoviral iap repeat-containing protein 4; **PDBTitle:** crystal structure of xiap bir1 domain (i222 form)
57	d1v4aa2	Alignment	not modelled	8.6	14	**Fold:**Nucleotidyltransferase **Superfamily:**Nucleotidyltransferase **Family:**GlnE-like domain
58	d1u5sb1	Alignment	not modelled	8.6	18	**Fold:**Glucocorticoid receptor-like (DNA-binding domain) **Superfamily:**Glucocorticoid receptor-like (DNA-binding domain) **Family:**LIM domain
59	c2joxA_	Alignment	not modelled	8.6	38	**PDB header:**transcription **Chain:** A: **PDB Molecule:**churchill protein; **PDBTitle:** embryonic neural inducing factor churchill is not a dna-2 binding zinc finger protein: solution structure reveals a3 solvent-exposed beta-sheet and zinc binuclear cluster
60	c2k5cA_	Alignment	not modelled	8.3	25	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**uncharacterized protein pf0385; **PDBTitle:** nmr structure for pf0385
61	c2vm5A_	Alignment	not modelled	8.3	18	**PDB header:**apoptosis **Chain:** A: **PDB Molecule:**baculoviral iap repeat-containing protein 1; **PDBTitle:** human bir2 domain of baculoviral inhibitor of apoptosis2 repeat-containing 1 (birc1)
62	c2p9lD_	Alignment	not modelled	8.2	21	**PDB header:**structural protein **Chain:** D: **PDB Molecule:**actin-related protein 2/3 complex subunit 2; **PDBTitle:** crystal structure of bovine arp2/3 complex
63	c2kaeA_	Alignment	not modelled	8.2	21	**PDB header:**transcription/dna **Chain:** A: **PDB Molecule:**gata-type transcription factor; **PDBTitle:** data-driven model of med1:dna complex
64	d1rutx3	Alignment	not modelled	8.0	17	**Fold:**Glucocorticoid receptor-like (DNA-binding domain) **Superfamily:**Glucocorticoid receptor-like (DNA-binding domain) **Family:**LIM domain
65	d2apob1	Alignment	not modelled	8.0	18	**Fold:**Rubredoxin-like **Superfamily:**Nop10-like SnoRNP **Family:**Nucleolar RNA-binding protein Nop10-like
66	d1u5sb2	Alignment	not modelled	7.9	30	**Fold:**Glucocorticoid receptor-like (DNA-binding domain) **Superfamily:**Glucocorticoid receptor-like (DNA-binding domain) **Family:**LIM domain
67	c3m0aD_	Alignment	not modelled	7.9	32	**PDB header:**signaling protein **Chain:** D: **PDB Molecule:**baculoviral iap repeat-containing protein 3; **PDBTitle:** crystal structure of traf2:ciap2 complex
68	d1osxa_	Alignment	not modelled	7.9	25	**Fold:**TNF receptor-like **Superfamily:**TNF receptor-like **Family:**BAFF receptor-like
69	d1g73d_	Alignment	not modelled	7.8	27	**Fold:**Inhibitor of apoptosis (IAP) repeat **Superfamily:**Inhibitor of apoptosis (IAP) repeat **Family:**Inhibitor of apoptosis (IAP) repeat
70	d1i3oe_	Alignment	not modelled	7.7	27	**Fold:**Inhibitor of apoptosis (IAP) repeat **Superfamily:**Inhibitor of apoptosis (IAP) repeat **Family:**Inhibitor of apoptosis (IAP) repeat
71	d1jd5a_	Alignment	not modelled	7.7	27	**Fold:**Inhibitor of apoptosis (IAP) repeat **Superfamily:**Inhibitor of apoptosis (IAP) repeat **Family:**Inhibitor of apoptosis (IAP) repeat
72	c1ibiA_	Alignment	not modelled	7.6	22	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**cysteine-rich protein 2; **PDBTitle:** quail cysteine and glycine-rich protein, nmr, 15 minimized2 model structures
73	c1x64A_	Alignment	not modelled	7.4	12	**PDB header:**contractile protein **Chain:** A: **PDB Molecule:**alpha-actinin-2 associated lim protein; **PDBTitle:** solution structure of the lim domain of alpha-actinin-22 associated lim protein
74	d1k8kd2	Alignment	not modelled	7.4	23	**Fold:**Secretion chaperone-like **Superfamily:**Arp2/3 complex subunits **Family:**Arp2/3 complex subunits
75	c2gviA_	Alignment	not modelled	7.2	16	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**conserved hypothetical protein; **PDBTitle:** crystal structure of a putative formylmethanofuran dehydrogenase2 subunit e (ta1109) from thermoplasma acidophilum at 1.87 a resolution
76	c1hk8A_	Alignment	not modelled	7.2	15	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**anaerobic ribonucleotide-triphosphate reductase; **PDBTitle:** structural basis for allosteric substrate specificity2 regulation in class iii ribonucleotide reductases:3 nrdd in complex with dgtp
77	d1hk8a_	Alignment	not modelled	7.2	15	**Fold:**PFL-like glycyl radical enzymes **Superfamily:**PFL-like glycyl radical enzymes **Family:**Class III anaerobic ribonucleotide reductase NRDD subunit
78	c1imlA_	Alignment	not modelled	7.0	11	**PDB header:**metal-binding protein **Chain:** A: **PDB Molecule:**cysteine rich intestinal protein; **PDBTitle:** cysteine rich intestinal protein, nmr, 48 structures
79	d2ey4e1	Alignment	not modelled	6.9	23	**Fold:**Rubredoxin-like **Superfamily:**Nop10-like SnoRNP **Family:**Nucleolar RNA-binding protein Nop10-like
80	c1p0tq	Alignment	not modelled	6.8	25	**PDB header:**protein binding **Chain:** Q: **PDB Molecule:**tumor necrosis factor receptor

80	c1potq_	Alignment	not modelled	6.8	25	superfamily **PDBTitle:** crystal structure of the baff-baff-r complex (part ii)
81	c3dwlI_	Alignment	not modelled	6.7	31	**PDB header:**structural protein **Chain:** I: **PDB Molecule:**actin-related protein 2/3 complex subunit 2; **PDBTitle:** crystal structure of fission yeast arp2/3 complex lacking the arp22 subunit
82	c2kq9A_	Alignment	not modelled	6.7	21	**PDB header:**transcription **Chain:** A: **PDB Molecule:**dnak suppressor protein; **PDBTitle:** solution structure of dnak suppressor protein from2 agrobacterium tumefaciens c58. northeast structural3 genomics consortium target att12/ontario center for4 structural proteomics target atc0888
83	d1oqen_	Alignment	not modelled	6.7	25	**Fold:**TNF receptor-like **Superfamily:**TNF receptor-like **Family:**BAFF receptor-like
84	d2dara2	Alignment	not modelled	6.7	18	**Fold:**Glucocorticoid receptor-like (DNA-binding domain) **Superfamily:**Glucocorticoid receptor-like (DNA-binding domain) **Family:**LIM domain
85	c1tjlD_	Alignment	not modelled	6.7	23	**PDB header:**transcription **Chain:** D: **PDB Molecule:**dnak suppressor protein; **PDBTitle:** crystal structure of transcription factor dksa from e. coli
86	d1xpaa2	Alignment	not modelled	6.4	14	**Fold:**Glucocorticoid receptor-like (DNA-binding domain) **Superfamily:**Glucocorticoid receptor-like (DNA-binding domain) **Family:**DNA repair factor XPA DNA- and RPA-binding domain, N-terminal subdomain
87	c3jueA_	Alignment	not modelled	6.4	10	**PDB header:**protein transport/endocytosis **Chain:** A: **PDB Molecule:**arfgap with coiled-coil, ank repeat and ph domain- **PDBTitle:** crystal structure of arfgap and ank repeat domain of acap1
88	d1oqek_	Alignment	not modelled	6.3	25	**Fold:**TNF receptor-like **Superfamily:**TNF receptor-like **Family:**BAFF receptor-like
89	d2dloa2	Alignment	not modelled	6.3	15	**Fold:**Glucocorticoid receptor-like (DNA-binding domain) **Superfamily:**Glucocorticoid receptor-like (DNA-binding domain) **Family:**LIM domain
90	d1te5a_	Alignment	not modelled	6.3	8	**Fold:**Ntn hydrolase-like **Superfamily:**N-terminal nucleophile aminohydrolases (Ntn hydrolases) **Family:**Class II glutamine amidotransferases
91	d1wyha1	Alignment	not modelled	6.2	24	**Fold:**Glucocorticoid receptor-like (DNA-binding domain) **Superfamily:**Glucocorticoid receptor-like (DNA-binding domain) **Family:**LIM domain
92	c2eheA_	Alignment	not modelled	6.1	9	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**four and a half lim domains 3; **PDBTitle:** solution structure of the first lim domain from human four2 and a half lim domains protein 3
93	c3d00A_	Alignment	not modelled	6.1	21	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**tungsten formylmethanofuran dehydrogenase subunit e; **PDBTitle:** crystal structure of a tungsten formylmethanofuran dehydrogenase2 subunit e (fmde)-like protein (syn_00638) from syntrophus3 aciditrophicus at 1.90 a resolution
94	d1xb0a_	Alignment	not modelled	6.0	24	**Fold:**Inhibitor of apoptosis (IAP) repeat **Superfamily:**Inhibitor of apoptosis (IAP) repeat **Family:**Inhibitor of apoptosis (IAP) repeat
95	c2yqpA_	Alignment	not modelled	5.8	33	**PDB header:**gene regulation, hydrolase **Chain:** A: **PDB Molecule:**probable atp-dependent rna helicase ddx59; **PDBTitle:** solution structure of the zf-hit domain in dead (asp-glu-2 ala-asp) box polypeptide 59
96	c3hvzB_	Alignment	not modelled	5.5	35	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of the tgs domain of the clolep_03100 protein from2 clostridium leptum, northeast structural genomics consortium target3 qlr13a
97	d2dara1	Alignment	not modelled	5.5	23	**Fold:**Glucocorticoid receptor-like (DNA-binding domain) **Superfamily:**Glucocorticoid receptor-like (DNA-binding domain) **Family:**LIM domain
98	c2o13A_	Alignment	not modelled	5.4	22	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**muscle lim protein; **PDBTitle:** solution structure of the c-terminal lim domain of mlp/crp3
99	c1nnjA_	Alignment	not modelled	5.4	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**formamidopyrimidine-dna glycosylase; **PDBTitle:** crystal structure complex between the lactococcus lactis fpg and an2 abasic site containing dna