Phyre^2

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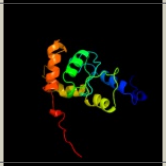
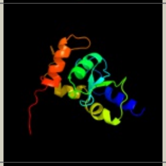
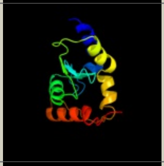
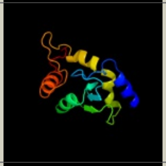
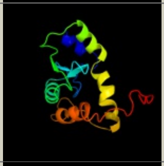
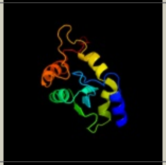
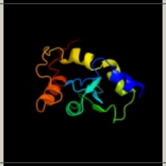
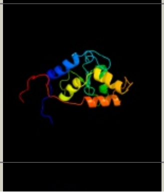
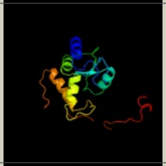
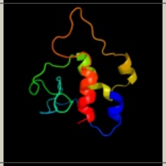
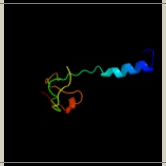
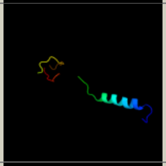
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2d9lA_	Alignment		100.0	95	**PDB header:**gene regulation **Chain:** A: **PDB Molecule:**nucleoporin-like protein rip; **PDBTitle:** solution structure of the arfgap domain of human rip
2	c2crrA_	Alignment		100.0	28	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**stromal membrane-associated protein smap1b; **PDBTitle:** solution structure of arfgap domain from human smap1
3	c3lvrE_	Alignment		100.0	19	**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
4	c2iqjB_	Alignment		100.0	28	**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
5	c3fehA_	Alignment		100.0	24	**PDB header:**hydrolase activator **Chain:** A: **PDB Molecule:**centaurin-alpha-1; **PDBTitle:** crystal structure of full length centaurin alpha-1
6	d1dcqa2	Alignment		100.0	21	**Fold:**ArfGap/RecO-like zinc finger **Superfamily:**ArfGap/RecO-like zinc finger **Family:**Pyk2-associated protein beta ARF-GAP domain
7	c3jueA_	Alignment		100.0	19	**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
8	c3t9kA_	Alignment		100.0	19	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**arf-gap with coiled-coil, ank repeat and ph domain- **PDBTitle:** crystal structure of acap1 c-portion mutant s554d fused with integrin2 beta1 peptide
9	c1dcqA_	Alignment		100.0	19	**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.
10	c2b0oF_	Alignment		100.0	19	**PDB header:**metal binding protein **Chain:** F: **PDB Molecule:**uplc1; **PDBTitle:** crystal structure of uplc1 gap domain
11	c2crwA_	Alignment		100.0	20	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**adp-ribosylation factor gtpase-activating **PDBTitle:** solution structure of the arfgap domain of adp-ribosylation2 factor gtpaseactivating protein 3 (arfgap 3)

12	c2owaB_	Alignment		100.0	21	**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)
13	c2p57A_	Alignment		100.0	20	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**gtpase-activating protein znf289; **PDBTitle:** gap domain of znf289, an id1-regulated zinc finger protein
14	c3o47A_	Alignment		100.0	21	**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
15	c3dwdB_	Alignment		100.0	23	**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
16	d1u5ka2	Alignment		96.1	18	**Fold:**ArfGap/RecO-like zinc finger **Superfamily:**ArfGap/RecO-like zinc finger **Family:**RecO C-terminal domain-like
17	c1u5kA_	Alignment		95.8	16	**PDB header:**recombination,replication **Chain:** A: **PDB Molecule:**hypothetical protein; **PDBTitle:** recombinational repair protein reco
18	c3bjiA_	Alignment		92.8	19	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**proto-oncogene vav; **PDBTitle:** structural basis of promiscuous guanine nucleotide exchange2 by the t-cell essential vav1
19	c1y1yS_	Alignment		67.8	16	**PDB header:**transferase/transcription/dna-rna hybrid **Chain:** S: **PDB Molecule:**transcription elongation factor s-ii; **PDBTitle:** rna polymerase ii-tfiis-dna/rna complex
20	d1y0ja1	Alignment		61.4	18	**Fold:**Glucocorticoid receptor-like (DNA-binding domain) **Superfamily:**Glucocorticoid receptor-like (DNA-binding domain) **Family:**Erythroid transcription factor GATA-1
21	c3a1bA_	Alignment	not modelled	59.3	14	**PDB header:**transferase **Chain:** A: **PDB Molecule:**dna (cytosine-5)-methyltransferase 3a, histone h3.1; **PDBTitle:** crystal structure of the dnmt3a add domain in complex with histone h3
22	c2zetD_	Alignment	not modelled	56.2	26	**PDB header:**signaling protein **Chain:** D: **PDB Molecule:**melanophilin; **PDBTitle:** crystal structure of the small gtpase rab27b complexed with2 the slp homology domain of slac2-a/melanophilin
23	d1pjua1	Alignment	not modelled	56.2	44	**Fold:**Plant proteinase inhibitors **Superfamily:**Plant proteinase inhibitors **Family:**Plant proteinase inhibitors
24	c3o3zB_	Alignment	not modelled	55.9	36	**PDB header:**viral protein **Chain:** B: **PDB Molecule:**chimeric alpha/beta peptide based on gp41 chr domain **PDBTitle:** complex of a chimeric alpha/beta-peptide based on the gp41 chr domain2 bound to a gp41 nhr domain peptide
25	c1kxuA_	Alignment	not modelled	54.6	16	**PDB header:**regulatory protein **Chain:** A: **PDB Molecule:**cyclin h; **PDBTitle:** cyclin h, a positive regulatory subunit of cdk activating kinase
26	d2bkra1	Alignment	not modelled	54.4	9	**Fold:**Cysteine proteinases **Superfamily:**Cysteine proteinases **Family:**Adenain-like
27	c1d4uA_	Alignment	not modelled	54.1	20	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**nucleotide excision repair protein xpa (xpa-mbd); **PDBTitle:** interactions of human nucleotide excision repair protein2 xpa with rpa70 and dna: chemical shift mapping and 15n nmr3 relaxation studies
28	c3h00A_	Alignment	not modelled	54.1	24	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**envelope glycoprotein gp160;

28	[illegible]	Alignment	not modelled	54.1	24	**PDBTitle:** structure of the c-terminal domain of a putative hiv-1 gp41 fusion2 intermediate
29	d2crga1	Alignment	not modelled	52.8	13	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Myb/SANT domain
30	c2egmA_	Alignment	not modelled	51.8	19	**PDB header:**transcription/metal binding protein **Chain:** A: **PDB Molecule:**tripartite motif-containing protein 41; **PDBTitle:** solution structure of the zf-b_box domain from human2 tripartite motif protein 41
31	c3f4yF_	Alignment	not modelled	51.8	36	**PDB header:**viral protein **Chain:** F: **PDB Molecule:**mutant peptide derived from hiv gp41 chr domain; **PDBTitle:** hiv gp41 six-helix bundle containing a mutant chr alpha-2 peptide sequence
32	c2yusA_	Alignment	not modelled	51.7	16	**PDB header:**transcription **Chain:** A: **PDB Molecule:**swi/snf-related matrix-associated actin- **PDBTitle:** solution structure of the sant domain of human swi/snf-2 related matrix-associated actin-dependent regulator of3 chromatin subfamily c member 1
33	c2i50A_	Alignment	not modelled	51.7	18	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**ubiquitin carboxyl-terminal hydrolase 16; **PDBTitle:** solution structure of ubp-m znf-ubp domain
34	c3ihpB_	Alignment	not modelled	51.3	30	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**ubiquitin carboxyl-terminal hydrolase 5; **PDBTitle:** covalent ubiquitin-usp5 complex
35	d1cjya2	Alignment	not modelled	50.9	19	**Fold:**FabD/lysophospholipase-like **Superfamily:**FabD/lysophospholipase-like **Family:**Lysophospholipase
36	c2junA_	Alignment	not modelled	50.7	20	**PDB header:**ligase **Chain:** A: **PDB Molecule:**midline-1; **PDBTitle:** structure of the mid1 tandem b-boxes reveals an interaction2 reminiscent of intermolecular ring heterodimers
37	c2kdxA_	Alignment	not modelled	50.2	21	**PDB header:**metal-binding protein **Chain:** A: **PDB Molecule:**hydrogenase/urease nickel incorporation protein **PDBTitle:** solution structure of hypa protein
38	d2br2b2	Alignment	not modelled	48.7	18	**Fold:**Ribonuclease PH domain 2-like **Superfamily:**Ribonuclease PH domain 2-like **Family:**Ribonuclease PH domain 2-like
39	d2je6b2	Alignment	not modelled	47.8	19	**Fold:**Ribonuclease PH domain 2-like **Superfamily:**Ribonuclease PH domain 2-like **Family:**Ribonuclease PH domain 2-like
40	c4a5bA_	Alignment	not modelled	47.7	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**nucleoside-triphosphatase 2; **PDBTitle:** crystal structure of the c258s/c268s variant of toxoplasma gondii2 nucleoside triphosphate diphosphohydrolase 1 (ntpdase1)
41	d2djaa1	Alignment	not modelled	46.9	23	**Fold:**B-box zinc-binding domain **Superfamily:**B-box zinc-binding domain **Family:**B-box zinc-binding domain
42	c2hr5B_	Alignment	not modelled	46.9	13	**PDB header:**metal binding protein **Chain:** B: **PDB Molecule:**rubrerythrin; **PDBTitle:** pf1283- rubrerythrin from pyrococcus furiosus iron bound form
43	d5gata_	Alignment	not modelled	46.1	23	**Fold:**Glucocorticoid receptor-like (DNA-binding domain) **Superfamily:**Glucocorticoid receptor-like (DNA-binding domain) **Family:**Erythroid transcription factor GATA-1
44	c1pqvS_	Alignment	not modelled	45.3	16	**PDB header:**transferase/transcription **Chain:** S: **PDB Molecule:**transcription elongation factor s-ii; **PDBTitle:** rna polymerase ii-tfiis complex
45	d2dq5a1	Alignment	not modelled	45.2	23	**Fold:**B-box zinc-binding domain **Superfamily:**B-box zinc-binding domain **Family:**B-box zinc-binding domain
46	d2ba0d2	Alignment	not modelled	44.9	14	**Fold:**Ribonuclease PH domain 2-like **Superfamily:**Ribonuclease PH domain 2-like **Family:**Ribonuclease PH domain 2-like
47	c2d8uA_	Alignment	not modelled	44.3	15	**PDB header:**ligase **Chain:** A: **PDB Molecule:**ubiquitin ligase trim63; **PDBTitle:** solution structure of the b-box domain of the human2 tripartite motif-containing 63 protein
48	d2vuti1	Alignment	not modelled	43.7	26	**Fold:**Glucocorticoid receptor-like (DNA-binding domain) **Superfamily:**Glucocorticoid receptor-like (DNA-binding domain) **Family:**Erythroid transcription factor GATA-1
49	d1zbdb_	Alignment	not modelled	43.3	18	**Fold:**FYVE/PHD zinc finger **Superfamily:**FYVE/PHD zinc finger **Family:**FYVE, a phosphatidylinositol-3-phosphate binding domain
50	d1fyba1	Alignment	not modelled	43.0	43	**Fold:**Plant proteinase inhibitors **Superfamily:**Plant proteinase inhibitors **Family:**Plant proteinase inhibitors
51	c3auoB_	Alignment	not modelled	42.9	10	**PDB header:**transferase/dna **Chain:** B: **PDB Molecule:**dna polymerase beta family (x family); **PDBTitle:** dna polymerase x from thermus thermophilus hb8 ternary complex with 1-2 nt gapped dna and ddgtp
52	d1gnfa_	Alignment	not modelled	42.3	18	**Fold:**Glucocorticoid receptor-like (DNA-binding domain) **Superfamily:**Glucocorticoid receptor-like (DNA-binding domain) **Family:**Erythroid transcription factor GATA-1
53	d1unld_	Alignment	not modelled	42.0	31	**Fold:**Cyclin-like **Superfamily:**Cyclin-like **Family:**Cyclin
54	d1ce3a_	Alignment	not modelled	41.9	38	**Fold:**Plant proteinase inhibitors **Superfamily:**Plant proteinase inhibitors **Family:**Plant proteinase inhibitors

55	c3c65A_	Alignment	not modelled	41.7	14	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**uvrabc system protein c; **PDBTitle:** crystal structure of bacillus stearothermophilus uvrc 5'2 endonuclease domain
56	c3w2zA_	Alignment	not modelled	41.4	17	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**methyl-accepting chemotaxis protein; **PDBTitle:** crystal structure of the cyanobacterial protein
57	c1unhD_	Alignment	not modelled	41.3	31	**PDB header:**cell cycle **Chain:** D: **PDB Molecule:**cyclin-dependent kinase 5 activator 1; **PDBTitle:** structural mechanism for the inhibition of cdk5-p25 by2 roscovitine, aloisine and indirubin.
58	c2kgoA_	Alignment	not modelled	41.3	13	**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
59	c2yumA_	Alignment	not modelled	41.2	15	**PDB header:**transcription **Chain:** A: **PDB Molecule:**zinc finger zz-type-containing protein 3; **PDBTitle:** solution structure of the myb-like dna-binding domain of2 human zzz3 protein
60	c3agrB_	Alignment	not modelled	40.4	13	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**nucleoside triphosphate hydrolase; **PDBTitle:** crystal structure of nucleoside triphosphate hydrolases from neospora2 caninum
61	c2p3xA_	Alignment	not modelled	40.4	21	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**polyphenol oxidase, chloroplast; **PDBTitle:** crystal structure of grenache (vitis vinifera) polyphenol2 oxidase
62	c1yuzB_	Alignment	not modelled	37.8	19	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**nigerythrin; **PDBTitle:** partially reduced state of nigerythrin
63	c2eqrA_	Alignment	not modelled	37.7	20	**PDB header:**transcription **Chain:** A: **PDB Molecule:**nuclear receptor corepressor 1; **PDBTitle:** solution structure of the first sant domain from human2 nuclear receptor corepressor 1
64	d1tiha_	Alignment	not modelled	37.6	43	**Fold:**Plant proteinase inhibitors **Superfamily:**Plant proteinase inhibitors **Family:**Plant proteinase inhibitors
65	d2k2na1	Alignment	not modelled	37.3	20	**Fold:**Profilin-like **Superfamily:**GAF domain-like **Family:**GAF domain
66	c1qh2B_	Alignment	not modelled	35.4	41	**PDB header:**hydrolase inhibitor **Chain:** B: **PDB Molecule:**protein (trypsin inhibitor c2); **PDBTitle:** chymotrypsin inhibitor (c2) from nicotiana alata
67	c4dzuB_	Alignment	not modelled	35.4	27	**PDB header:**de novo protein **Chain:** B: **PDB Molecule:**3-alpha; **PDBTitle:** complex of 3-alpha bound to gp41-5
68	c3a44D_	Alignment	not modelled	35.2	19	**PDB header:**metal binding protein **Chain:** D: **PDB Molecule:**hydrogenase nickel incorporation protein hypa; **PDBTitle:** crystal structure of hypa in the dimeric form
69	c3pihA_	Alignment	not modelled	34.9	15	**PDB header:**hydrolase/dna **Chain:** A: **PDB Molecule:**uvrabc system protein a; **PDBTitle:** t. maritima uvra in complex with fluorescein-modified dna
70	d2g45a1	Alignment	not modelled	34.8	42	**Fold:**RING/U-box **Superfamily:**RING/U-box **Family:**Zf-UBP
71	c1tjlD_	Alignment	not modelled	34.7	11	**PDB header:**transcription **Chain:** D: **PDB Molecule:**dnak suppressor protein; **PDBTitle:** crystal structure of transcription factor dksa from e. coli
72	c2w9mB_	Alignment	not modelled	34.7	7	**PDB header:**dna replication **Chain:** B: **PDB Molecule:**polymerase x; **PDBTitle:** structure of family x dna polymerase from deinococcus2 radiodurans
73	c2yrgA_	Alignment	not modelled	33.5	21	**PDB header:**ligase **Chain:** A: **PDB Molecule:**tripartite motif-containing protein 5; **PDBTitle:** solution structure of the b-box domain from tripartite2 motif-containing protein 5
74	d3gata_	Alignment	not modelled	33.5	16	**Fold:**Glucocorticoid receptor-like (DNA-binding domain) **Superfamily:**Glucocorticoid receptor-like (DNA-binding domain) **Family:**Erythroid transcription factor GATA-1
75	c3h01A_	Alignment	not modelled	33.5	24	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**envelope glycoprotein gp160; **PDBTitle:** structure of the c-terminal domain of a putative hiv-1 gp41 fusion2 intermediate
76	d1pfta_	Alignment	not modelled	33.2	21	**Fold:**Rubredoxin-like **Superfamily:**Zinc beta-ribbon **Family:**Transcriptional factor domain
77	c3j39p_	Alignment	not modelled	33.2	17	**PDB header:**ribosome **Chain:** P: **PDB Molecule:**60s ribosomal protein l17; **PDBTitle:** structure of the d. melanogaster 60s ribosomal proteins
78	d1v6za2	Alignment	not modelled	32.0	9	**Fold:**alpha/beta knot **Superfamily:**alpha/beta knot **Family:**YggJ C-terminal domain-like
79	c2difA_	Alignment	not modelled	31.8	23	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**tripartite motif protein 39; **PDBTitle:** one sequence two fold ? : miss fold of the zf-b-box domain2 from human tripartite motif protein 39
80	c2gb5B_	Alignment	not modelled	31.6	16	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**nadh pyrophosphatase; **PDBTitle:** crystal structure of nadh pyrophosphatase (ec 3.6.1.22) (1790429) from2 escherichia coli k12 at 2.30 a resolution
						PDB header:ribosome **Chain:** P: **PDB Molecule:**30s ribosomal protein s14p type z;

81	c3j20P_	Alignment	not modelled	31.6	35	**PDBTitle:** promiscuous behavior of proteins in archaeal ribosomes revealed by2 cryo-em: implications for evolution of eukaryotic ribosomes (30s3 ribosomal subunit)
82	c1fybA_	Alignment	not modelled	31.6	43	**PDB header:**hydrolase inhibitor **Chain:** A: **PDB Molecule:**proteinase inhibitor; **PDBTitle:** solution structure of c1-t1, a two-domain proteinase2 inhibitor derived from the circular precursor protein na-3 propi from nicotiana alata
83	c3o5aB_	Alignment	not modelled	31.3	36	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**diheme cytochrome c napb; **PDBTitle:** crystal structure of partially reduced periplasmic nitrate reductase2 from cupriavidus necator using ionic liquids
84	c3ky9B_	Alignment	not modelled	30.6	13	**PDB header:**apoptosis **Chain:** B: **PDB Molecule:**proto-oncogene vav; **PDBTitle:** autoinhibited vav1
85	d2cora1	Alignment	not modelled	30.0	17	**Fold:**Glucocorticoid receptor-like (DNA-binding domain) **Superfamily:**Glucocorticoid receptor-like (DNA-binding domain) **Family:**LIM domain
86	d1dl6a_	Alignment	not modelled	29.6	17	**Fold:**Rubredoxin-like **Superfamily:**Zinc beta-ribbon **Family:**Transcriptional factor domain
87	c1oahA_	Alignment	not modelled	29.6	17	**PDB header:**reductase **Chain:** A: **PDB Molecule:**cytochrome c nitrite reductase; **PDBTitle:** cytochrome c nitrite reductase from desulfovibrio2 desulfuricans atcc 27774: the relevance of the two3 calcium sites in the structure of the catalytic subunit4 (nrfa).
88	d1oaha_	Alignment	not modelled	29.6	17	**Fold:**Multiheme cytochromes **Superfamily:**Multiheme cytochromes **Family:**Di-heme elbow motif
89	c2qa4Z_	Alignment	not modelled	29.2	13	**PDB header:**ribosome **Chain:** Z: **PDB Molecule:**50s ribosomal protein l37ae; **PDBTitle:** a more complete structure of the the l7/l12 stalk of the2 haloarcula marismortui 50s large ribosomal subunit
90	c1l4aE_	Alignment	not modelled	29.2	21	**PDB header:**endocytosis/exocytosis **Chain:** E: **PDB Molecule:**synaphin a; **PDBTitle:** x-ray structure of the neuronal complexin/snare complex2 from the squid loligo pealei
91	d1jkwa1	Alignment	not modelled	29.2	14	**Fold:**Cyclin-like **Superfamily:**Cyclin-like **Family:**Cyclin
92	d1oyvi_	Alignment	not modelled	28.9	41	**Fold:**Plant proteinase inhibitors **Superfamily:**Plant proteinase inhibitors **Family:**Plant proteinase inhibitors
93	d1hcqa_	Alignment	not modelled	28.9	22	**Fold:**Glucocorticoid receptor-like (DNA-binding domain) **Superfamily:**Glucocorticoid receptor-like (DNA-binding domain) **Family:**Nuclear receptor
94	d1vqoz1	Alignment	not modelled	28.8	14	**Fold:**Rubredoxin-like **Superfamily:**Zn-binding ribosomal proteins **Family:**Ribosomal protein L37ae
95	c3k1fM_	Alignment	not modelled	28.7	28	**PDB header:**transcription **Chain:** M: **PDB Molecule:**transcription initiation factor iib; **PDBTitle:** crystal structure of rna polymerase ii in complex with tfiib
96	d1jj2y_	Alignment	not modelled	28.3	17	**Fold:**Rubredoxin-like **Superfamily:**Zn-binding ribosomal proteins **Family:**Ribosomal protein L37ae
97	c3f29A_	Alignment	not modelled	28.1	20	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**eight-heme nitrite reductase; **PDBTitle:** structure of the thioalkalivibrio nitratireducens2 cytochrome c nitrite reductase in complex with sulfite
98	c3zg6A_	Alignment	not modelled	27.9	20	**PDB header:**hydrolase/inhibitor **Chain:** A: **PDB Molecule:**nad-dependent protein deacetylase sirtuin-6; **PDBTitle:** the novel de-long chain fatty acid function of human sirt6
99	c4bkxA_	Alignment	not modelled	27.8	12	**PDB header:**transcription **Chain:** A: **PDB Molecule:**metastasis-associated protein mta1; **PDBTitle:** the structure of hdac1 in complex with the dimeric elm2-sant domain2 of mta1 from the nurd complex
100	c3k7aM_	Alignment	not modelled	27.7	32	**PDB header:**transcription **Chain:** M: **PDB Molecule:**transcription initiation factor iib; **PDBTitle:** crystal structure of an rna polymerase ii-tfiib complex
101	c3izrm_	Alignment	not modelled	27.6	17	**PDB header:**ribosome **Chain:** M: **PDB Molecule:**60s ribosomal protein l23 (l14p); **PDBTitle:** localization of the large subunit ribosomal proteins into a 5.5 a2 cryo-em map of triticum aestivum translating 80s ribosome
102	c1yshD_	Alignment	not modelled	27.6	16	**PDB header:**structural protein/rna **Chain:** D: **PDB Molecule:**ribosomal protein l37a; **PDBTitle:** localization and dynamic behavior of ribosomal protein l30e
103	d2dida1	Alignment	not modelled	27.4	19	**Fold:**B-box zinc-binding domain **Superfamily:**B-box zinc-binding domain **Family:**B-box zinc-binding domain
104	d1gefa_	Alignment	not modelled	27.4	6	**Fold:**Restriction endonuclease-like **Superfamily:**Restriction endonuclease-like **Family:**Hjc-like
105	d2d8ua1	Alignment	not modelled	27.3	18	**Fold:**B-box zinc-binding domain **Superfamily:**B-box zinc-binding domain **Family:**B-box zinc-binding domain
106	d1wkqa_	Alignment	not modelled	27.2	12	**Fold:**Cytidine deaminase-like **Superfamily:**Cytidine deaminase-like **Family:**Deoxycytidylate deaminase-like
107	c1favC_	Alignment	not modelled	27.2	27	**PDB header:**viral protein **Chain:** C: **PDB Molecule:**protein (transmembrane glycoprotein); **PDBTitle:** the structure of an hiv-1 specific cell entry inhibitor in

						complex2 with the hiv-1 gp41 trimeric core
108	c3eeaB_	Alignment	not modelled	27.2	11	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**gaf domain/hd domain protein; **PDBTitle:** the crystal structure of the gaf domain/hd domain protein2 from geobacter sulfurreducens
109	c2zkrz_	Alignment	not modelled	27.1	19	**PDB header:**ribosomal protein/rna **Chain:** Z: **PDB Molecule:**e site t-rna; **PDBTitle:** structure of a mammalian ribosomal 60s subunit within an 80s complex2 obtained by docking homology models of the rna and proteins into an3 8.7 a cryo-em map
110	c2lb5A_	Alignment	not modelled	26.4	20	**PDB header:**transferase **Chain:** A: **PDB Molecule:**sensor histidine kinase; **PDBTitle:** refined structural basis for the photoconversion of a phytochrome to2 the activated far-red light-absorbing form
111	c2kq9A_	Alignment	not modelled	26.4	6	**PDB header:**transcription **Chain:** A: **PDB Molecule:**dnak suppressor protein; **PDBTitle:** solution structure of dnak suppressor protein from agrobacterium2 tumefaciens c58. northeast structural genomics consortium target3 att12/ontario center for structural proteomics target atc0888
112	d1ffkw_	Alignment	not modelled	26.0	16	**Fold:**Rubredoxin-like **Superfamily:**Zn-binding ribosomal proteins **Family:**Ribosomal protein L37ae
113	c3s5bB_	Alignment	not modelled	26.0	18	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**endonuclease g; **PDBTitle:** crystal structure of ced-3 protease suppressor-6 (cps-6) from2 caenorhabditis elegans
114	c3j21i_	Alignment	not modelled	25.9	14	**PDB header:**ribosome **Chain:** I: **PDB Molecule:**50s ribosomal protein l13p; **PDBTitle:** promiscuous behavior of proteins in archaeal ribosomes revealed by2 cryo-em: implications for evolution of eukaryotic ribosomes (50s3 ribosomal proteins)
115	d2dipa1	Alignment	not modelled	25.5	22	**Fold:**RING/U-box **Superfamily:**RING/U-box **Family:**ZZ domain
116	d1p6oa_	Alignment	not modelled	25.0	24	**Fold:**Cytidine deaminase-like **Superfamily:**Cytidine deaminase-like **Family:**Deoxycytidylate deaminase-like
117	c3zey8_	Alignment	not modelled	24.8	26	**PDB header:**ribosome **Chain:** 8: **PDB Molecule:**ribosomal protein s29, putative; **PDBTitle:** high-resolution cryo-electron microscopy structure of the trypanosoma2 brucei ribosome
118	c4a17Y_	Alignment	not modelled	24.8	17	**PDB header:**ribosome **Chain:** Y: **PDB Molecule:**rpl37a; **PDBTitle:** t.thermophila 60s ribosomal subunit in complex with2 initiation factor 6. this file contains 5s rrna,3 5.8s rrna and proteins of molecule 2.
119	d1b8ta2	Alignment	not modelled	24.7	22	**Fold:**Glucocorticoid receptor-like (DNA-binding domain) **Superfamily:**Glucocorticoid receptor-like (DNA-binding domain) **Family:**LIM domain
120	d1euva_	Alignment	not modelled	24.6	16	**Fold:**Cysteine proteinases **Superfamily:**Cysteine proteinases **Family:**Adenain-like