
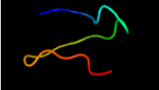









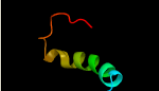

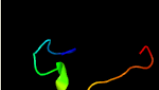








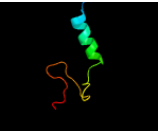
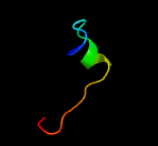
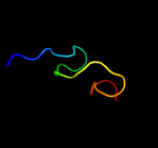
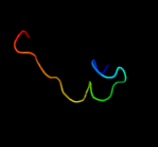

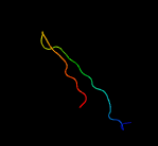
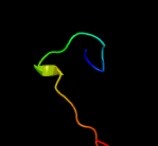
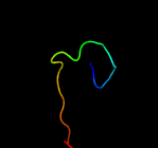
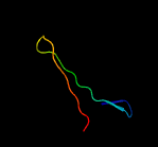


# Phyre2

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Date	Mon Aug 5 13:25:25 BST 2019
Unique Job ID	e9aac0a5300e70ca

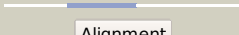

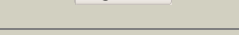
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c3w0fA_</a>	 Alignment		75.0	24	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> endonuclease 8-like 3; <b>PDBTitle:</b> crystal structure of mouse endonuclease viii-like 3 (mnei13)
2	<a href="#">c2f5qA_</a>	 Alignment		75.0	29	<b>PDB header:</b> hydrolase/dna <b>Chain:</b> A: <b>PDB Molecule:</b> formamidopyrimidine-dna glycosidase; <b>PDBTitle:</b> catalytically inactive (e3q) mutm crosslinked to oxog:c2 containing dna cc2
3	<a href="#">c6gjeA_</a>	 Alignment		70.8	35	<b>PDB header:</b> protein transport <b>Chain:</b> A: <b>PDB Molecule:</b> protein amnionless; <b>PDBTitle:</b> structure of the amnionless(20-357)-cubilin(36-135) complex
4	<a href="#">c2qgpA_</a>	 Alignment		66.7	35	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> hnh endonuclease; <b>PDBTitle:</b> x-ray structure of the hnh endonuclease from geobacter2 metallireducens. northeast structural genomics consortium target3 gmr87.
5	<a href="#">c1ee8A_</a>	 Alignment		65.7	45	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> mutm (fpg) protein; <b>PDBTitle:</b> crystal structure of mutm (fpg) protein from thermus thermophilus hb8
6	<a href="#">c4o6hA_</a>	 Alignment		63.5	26	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> nucleoprotein; <b>PDBTitle:</b> 2.8a crystal structure of lymphocytic choriomeningitis virus2 nucleoprotein c-terminal domain
7	<a href="#">c6em4u_</a>	 Alignment		57.9	30	<b>PDB header:</b> ribosome <b>Chain:</b> U: <b>PDB Molecule:</b> <b>PDBTitle:</b> state b architectural model (nsa1-tap flag-ytm1) - visualizing the2 assembly pathway of nucleolar pre-60s ribosomes
8	<a href="#">d2qam01</a>	 Alignment		57.5	35	<b>Fold:</b> Rubredoxin-like <b>Superfamily:</b> Zn-binding ribosomal proteins <b>Family:</b> Ribosomal protein L32p
9	<a href="#">c3j65p_</a>	 Alignment		57.4	29	<b>PDB header:</b> ribosome <b>Chain:</b> P: <b>PDB Molecule:</b> 60s ribosomal protein l5; <b>PDBTitle:</b> arx1 pre-60s particle. this entry contains the r-proteins and2 biogenesis factors.
10	<a href="#">c1s1iS_</a>	 Alignment		56.6	14	<b>PDB header:</b> ribosome <b>Chain:</b> S: <b>PDB Molecule:</b> 60s ribosomal protein l24-a; <b>PDBTitle:</b> structure of the ribosomal 80s-eef2-sordarin complex from yeast2 obtained by docking atomic models for rna and protein components into3 a 11.7 a cryo-em map. this file, 1s1i, contains 60s subunit. the 40s4 ribosomal subunit is in file 1s1h.
11	<a href="#">c5an9G_</a>	 Alignment		56.5	20	<b>PDB header:</b> translation <b>Chain:</b> G: <b>PDB Molecule:</b> 60s ribosomal protein l24; <b>PDBTitle:</b> mechanism of eif6 release from the nascent 60s ribosomal subunit

12	<a href="#">c6o3pA</a>	Alignment		56.3	29	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> peroxisomal nadh pyrophosphatase nudt12; <b>PDBTitle:</b> crystal structure of the catalytic domain of mouse nudt12 in complex2 with amp and 3 mg2+ ions
13	<a href="#">c3iz5Z</a>	Alignment		56.3	20	<b>PDB header:</b> ribosome <b>Chain:</b> Z: <b>PDB Molecule:</b> 60s ribosomal protein l24 (l24e); <b>PDBTitle:</b> localization of the large subunit ribosomal proteins into a 5.5 a2 cryo-em map of triticum aestivum translating 80s ribosome
14	<a href="#">c5ikfA</a>	Alignment		55.7	21	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> chromatin remodeling factor mit1; <b>PDBTitle:</b> crystal structure of the c-terminal domain of the mit1 nucleosome2 remodeler in complex with clr1
15	<a href="#">c3jz1V</a>	Alignment		54.9	33	<b>PDB header:</b> ribosome <b>Chain:</b> V: <b>PDB Molecule:</b> 50s ribosomal protein l24e; <b>PDBTitle:</b> promiscuous behavior of proteins in archaeal ribosomes revealed by2 cryo-em: implications for evolution of eukaryotic ribosomes (50s3 ribosomal proteins)
16	<a href="#">c3izcZ</a>	Alignment		54.8	15	<b>PDB header:</b> ribosome <b>Chain:</b> Z: <b>PDB Molecule:</b> 60s ribosomal protein rpl24 (l24e); <b>PDBTitle:</b> localization of the large subunit ribosomal proteins into a 6.1 a2 cryo-em map of saccharomyces cerevisiae translating 80s ribosome
17	<a href="#">d2c34a1</a>	Alignment		54.8	11	<b>Fold:</b> Immunoglobulin-like beta-sandwich <b>Superfamily:</b> ICP-like <b>Family:</b> ICP-like
18	<a href="#">d1vqou1</a>	Alignment		54.0	24	<b>Fold:</b> Glucocorticoid receptor-like (DNA-binding domain) <b>Superfamily:</b> Glucocorticoid receptor-like (DNA-binding domain) <b>Family:</b> Ribosomal protein L24e
19	<a href="#">c3ccjU</a>	Alignment		54.0	24	<b>PDB header:</b> ribosome <b>Chain:</b> U: <b>PDB Molecule:</b> 50s ribosomal protein l24e; <b>PDBTitle:</b> structure of anisomycin resistant 50s ribosomal subunit: 23s rrna2 mutation c2534u
20	<a href="#">c3m86B</a>	Alignment		53.9	11	<b>PDB header:</b> protein binding <b>Chain:</b> B: <b>PDB Molecule:</b> amoebiasin-2; <b>PDBTitle:</b> crystal structure of the cysteine protease inhibitor, ehicp2, from2 entamoeba histolytica
21	<a href="#">c2wgnB</a>	Alignment	not modelled	53.5	18	<b>PDB header:</b> hydrolase inhibitor <b>Chain:</b> B: <b>PDB Molecule:</b> inhibitor of cysteine peptidase compnd 3; <b>PDBTitle:</b> pseudomonas aeruginosa icp
22	<a href="#">c2zkru</a>	Alignment	not modelled	52.8	33	<b>PDB header:</b> ribosomal protein/rna <b>Chain:</b> U: <b>PDB Molecule:</b> rna expansion segment es41; <b>PDBTitle:</b> 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
23	<a href="#">c4a1eT</a>	Alignment	not modelled	52.5	25	<b>PDB header:</b> ribosome <b>Chain:</b> T: <b>PDB Molecule:</b> rpl24; <b>PDBTitle:</b> t.thermophila 60s ribosomal subunit in complex with2 initiation factor 6. this file contains 5s rrna, 5.8s rrna3 and proteins of molecule 1
24	<a href="#">c1k82D</a>	Alignment	not modelled	52.2	32	<b>PDB header:</b> hydrolase/dna <b>Chain:</b> D: <b>PDB Molecule:</b> formamidopyrimidine-dna glycosylase; <b>PDBTitle:</b> crystal structure of e.coli formamidopyrimidine-dna2 glycosylase (fpg) covalently trapped with dna
25	<a href="#">c2ecyA</a>	Alignment	not modelled	52.1	23	<b>PDB header:</b> apoptosis <b>Chain:</b> A: <b>PDB Molecule:</b> tnf receptor-associated factor 3; <b>PDBTitle:</b> solution structure of the zinc finger, c3hc4 type (ring2 finger)" domain of tnf receptor-associated factor 3
26	<a href="#">d1tdza3</a>	Alignment	not modelled	51.7	24	<b>Fold:</b> Glucocorticoid receptor-like (DNA-binding domain) <b>Superfamily:</b> Glucocorticoid receptor-like (DNA-binding domain) <b>Family:</b> C-terminal, Zn-finger domain of MutM-like DNA repair proteins
27	<a href="#">c1nnpjA</a>	Alignment	not modelled	49.9	26	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> formamidopyrimidine-dna glycosylase; <b>PDBTitle:</b> crystal structure complex between the lactococcus lactis fpg and an2 abasic site containing dna
28	<a href="#">c3zf7Y</a>	Alignment	not modelled	49.2	20	<b>PDB header:</b> ribosome <b>Chain:</b> Y: <b>PDB Molecule:</b> 60s ribosomal protein l24, putative; <b>PDBTitle:</b> high-resolution cryo-electron microscopy structure of the trypanosoma2 brucei ribosome

29	<a href="#">c3mkrB</a>	Alignment	not modelled	47.0	50	<b>PDB header:</b> transport protein <b>Chain:</b> B: <b>PDB Molecule:</b> coatomer subunit alpha; <b>PDBTitle:</b> crystal structure of yeast alpha/epsilon-cop subcomplex of the copi2 vesicular coat
30	<a href="#">c4v195</a>	Alignment	not modelled	45.9	24	<b>PDB header:</b> ribosome <b>Chain:</b> 5: <b>PDB Molecule:</b> mitoribosomal protein bl32m, mrpl32; <b>PDBTitle:</b> structure of the large subunit of the mammalian mitoribosome, part 12 of 2
31	<a href="#">c2opfA</a>	Alignment	not modelled	45.6	24	<b>PDB header:</b> hydrolase/dna <b>Chain:</b> A: <b>PDB Molecule:</b> endonuclease viii; <b>PDBTitle:</b> crystal structure of the dna repair enzyme endonuclease-viii (nei)2 from e. coli (r252a) in complex with ap-site containing dna substrate
32	<a href="#">d1r2za3</a>	Alignment	not modelled	45.6	43	<b>Fold:</b> Glucocorticoid receptor-like (DNA-binding domain) <b>Superfamily:</b> Glucocorticoid receptor-like (DNA-binding domain) <b>Family:</b> C-terminal, Zn-finger domain of MutM-like DNA repair proteins
33	<a href="#">c5dngA</a>	Alignment	not modelled	43.8	14	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> e3 ubiquitin-protein ligase bre1a; <b>PDBTitle:</b> crystal structure of the rnf20 ring domain
34	<a href="#">c5vgbA</a>	Alignment	not modelled	43.7	17	<b>PDB header:</b> hydrolase/hydrolase inhibitor <b>Chain:</b> A: <b>PDB Molecule:</b> crispr-associated endonuclease cas9; <b>PDBTitle:</b> crystal structure of nmecas9 hnh domain bound to anti-crispr acriic1
35	<a href="#">d1k82a3</a>	Alignment	not modelled	43.4	33	<b>Fold:</b> Glucocorticoid receptor-like (DNA-binding domain) <b>Superfamily:</b> Glucocorticoid receptor-like (DNA-binding domain) <b>Family:</b> C-terminal, Zn-finger domain of MutM-like DNA repair proteins
36	<a href="#">c2k5cA</a>	Alignment	not modelled	42.5	56	<b>PDB header:</b> metal binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein pf0385; <b>PDBTitle:</b> nmr structure for pf0385
37	<a href="#">c3pihA</a>	Alignment	not modelled	42.2	38	<b>PDB header:</b> hydrolase/dna <b>Chain:</b> A: <b>PDB Molecule:</b> uvrabc system protein a; <b>PDBTitle:</b> t. maritima uvra in complex with fluorescein-modified dna
38	<a href="#">c2qnfB</a>	Alignment	not modelled	41.2	21	<b>PDB header:</b> hydrolase/dna <b>Chain:</b> B: <b>PDB Molecule:</b> recombination endonuclease vii; <b>PDBTitle:</b> crystal structure of t4 endonuclease vii h43n mutant in2 complex with heteroduplex dna containing base mismatches
39	<a href="#">c4gveA</a>	Alignment	not modelled	40.9	31	<b>PDB header:</b> viral protein <b>Chain:</b> A: <b>PDB Molecule:</b> nucleoprotein; <b>PDBTitle:</b> tacaribe nucleoprotein structure
40	<a href="#">c2eciA</a>	Alignment	not modelled	40.4	23	<b>PDB header:</b> metal binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> tnf receptor-associated factor 6; <b>PDBTitle:</b> solution structure of the ring domain of the human tnf2 receptor-associated factor 6 protein
41	<a href="#">d2nqda1</a>	Alignment	not modelled	40.1	11	<b>Fold:</b> Immunoglobulin-like beta-sandwich <b>Superfamily:</b> ICP-like <b>Family:</b> ICP-like
42	<a href="#">c3zqjC</a>	Alignment	not modelled	39.9	43	<b>PDB header:</b> dna binding protein <b>Chain:</b> C: <b>PDB Molecule:</b> uvrabc system protein a; <b>PDBTitle:</b> mycobacterium tuberculosis uvra
43	<a href="#">c1yuzB</a>	Alignment	not modelled	39.6	44	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> nigerythrin; <b>PDBTitle:</b> partially reduced state of nigerythrin
44	<a href="#">d1rmda2</a>	Alignment	not modelled	39.4	27	<b>Fold:</b> RING/U-box <b>Superfamily:</b> RING/U-box <b>Family:</b> RING finger domain, C3HC4
45	<a href="#">c2f42A</a>	Alignment	not modelled	39.0	14	<b>PDB header:</b> chaperone <b>Chain:</b> A: <b>PDB Molecule:</b> stip1 homology and u-box containing protein 1; <b>PDBTitle:</b> dimerization and u-box domains of zebrafish c-terminal of hsp702 interacting protein
46	<a href="#">d1u5sb1</a>	Alignment	not modelled	38.7	38	<b>Fold:</b> Glucocorticoid receptor-like (DNA-binding domain) <b>Superfamily:</b> Glucocorticoid receptor-like (DNA-binding domain) <b>Family:</b> LIM domain
47	<a href="#">c3iz5i</a>	Alignment	not modelled	38.6	21	<b>PDB header:</b> ribosome <b>Chain:</b> I: <b>PDB Molecule:</b> 60s ribosomal protein l10 (l10e); <b>PDBTitle:</b> localization of the large subunit ribosomal proteins into a 5.5 a2 cryo-em map of triticum aestivum translating 80s ribosome
48	<a href="#">d1ee8a3</a>	Alignment	not modelled	38.4	43	<b>Fold:</b> Glucocorticoid receptor-like (DNA-binding domain) <b>Superfamily:</b> Glucocorticoid receptor-like (DNA-binding domain) <b>Family:</b> C-terminal, Zn-finger domain of MutM-like DNA repair proteins
49	<a href="#">c2cupA</a>	Alignment	not modelled	38.3	29	<b>PDB header:</b> metal binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> skeletal muscle lim-protein 1; <b>PDBTitle:</b> solution structure of the skeletal muscle lim-protein 1
50	<a href="#">c2kdxA</a>	Alignment	not modelled	36.9	15	<b>PDB header:</b> metal-binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> hydrogenase/urease nickel incorporation protein <b>PDBTitle:</b> solution structure of hypa protein
51	<a href="#">c2yurA</a>	Alignment	not modelled	36.3	15	<b>PDB header:</b> protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> retinoblastoma-binding protein 6; <b>PDBTitle:</b> solution structure of the ring finger of human2 retinoblastoma-binding protein 6
52	<a href="#">c1wyhA</a>	Alignment	not modelled	36.0	33	<b>PDB header:</b> metal binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> skeletal muscle lim-protein 2; <b>PDBTitle:</b> solution structure of the lim domain from human skeletal2 muscle lim-protein 2
53	<a href="#">c5a3aA</a>	Alignment	not modelled	35.9	42	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> sir2 family protein; <b>PDBTitle:</b> crystal structure of the adp-ribosylating sirtuin (sirtm)2 from streptococcus pyogenes (apo form)
54	<a href="#">c4ce45</a>	Alignment	not modelled	34.5	24	<b>PDB header:</b> ribosome <b>Chain:</b> 5: <b>PDB Molecule:</b> mrpl32; <b>PDBTitle:</b> 39s large subunit of the porcine mitochondrial ribosome

55	<a href="#">c2jmdA</a>	Alignment	not modelled	34.0	23	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> tnf receptor-associated factor 6; <b>PDBTitle:</b> solution structure of the ring domain of human traf6
56	<a href="#">c2daja</a>	Alignment	not modelled	33.4	27	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> kiaa0977 protein; <b>PDBTitle:</b> solution structure of the novel identified ubiquitin-like2 domain in the human cobl-like 1 protein
57	<a href="#">d1l1ta3</a>	Alignment	not modelled	33.3	50	<b>Fold:</b> Glucocorticoid receptor-like (DNA-binding domain) <b>Superfamily:</b> Glucocorticoid receptor-like (DNA-binding domain) <b>Family:</b> C-terminal, Zn-finger domain of MutM-like DNA repair proteins
58	<a href="#">c4bs9A</a>	Alignment	not modelled	33.1	22	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> trud; <b>PDBTitle:</b> structure of the heterocyclase trud
59	<a href="#">c4ogeA</a>	Alignment	not modelled	33.0	21	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> hnh endonuclease domain protein; <b>PDBTitle:</b> crystal structure of the type ii-c cas9 enzyme from actinomyces2 naeslundii
60	<a href="#">c3a46B</a>	Alignment	not modelled	32.9	13	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> formamidopyrimidine-dna glycosylase; <b>PDBTitle:</b> crystal structure of mvnei1/thf complex
61	<a href="#">d1cta1</a>	Alignment	not modelled	32.4	33	<b>Fold:</b> Glucocorticoid receptor-like (DNA-binding domain) <b>Superfamily:</b> Glucocorticoid receptor-like (DNA-binding domain) <b>Family:</b> LIM domain
62	<a href="#">c1z6uA</a>	Alignment	not modelled	32.4	22	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> np95-like ring finger protein isoform b; <b>PDBTitle:</b> np95-like ring finger protein isoform b [homo sapiens]
63	<a href="#">c6o9l3</a>	Alignment	not modelled	31.5	26	<b>PDB header:</b> transcription/dna <b>Chain:</b> 3: <b>PDB Molecule:</b> cdk-activating kinase assembly factor mat1; <b>PDBTitle:</b> human holo-pic in the closed state
64	<a href="#">c4i5iA</a>	Alignment	not modelled	31.4	29	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> nad-dependent protein deacetylase sirtuin-1; <b>PDBTitle:</b> crystal structure of the sirt1 catalytic domain bound to nad and an2 ex527 analog
65	<a href="#">c3hkzP</a>	Alignment	not modelled	31.4	33	<b>PDB header:</b> transferase <b>Chain:</b> P: <b>PDB Molecule:</b> dna-directed rna polymerase subunit p; <b>PDBTitle:</b> the x-ray crystal structure of rna polymerase from archaea
66	<a href="#">c1x4jA</a>	Alignment	not modelled	30.5	33	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> ring finger protein 38; <b>PDBTitle:</b> solution structure of ring finger in ring finger protein 38
67	<a href="#">c2gb5B</a>	Alignment	not modelled	30.5	18	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> nadh pyrophosphatase; <b>PDBTitle:</b> crystal structure of nadh pyrophosphatase (ec 3.6.1.22) (1790429) from2 escherichia coli k12 at 2.30 a resolution
68	<a href="#">c1g8jC</a>	Alignment	not modelled	30.2	30	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> arsenite oxidase; <b>PDBTitle:</b> crystal structure analysis of arsenite oxidase from2 alcaligenes faecalis
69	<a href="#">c3mv2A</a>	Alignment	not modelled	30.1	25	<b>PDB header:</b> protein transport <b>Chain:</b> A: <b>PDB Molecule:</b> coatomer subunit alpha; <b>PDBTitle:</b> crystal structure of a-cop in complex with e-cop
70	<a href="#">c2hr5B</a>	Alignment	not modelled	29.8	57	<b>PDB header:</b> metal binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> rubrerythrin; <b>PDBTitle:</b> pf1283- rubrerythrin from pyrococcus furiosus iron bound form
71	<a href="#">d2dara2</a>	Alignment	not modelled	29.5	29	<b>Fold:</b> Glucocorticoid receptor-like (DNA-binding domain) <b>Superfamily:</b> Glucocorticoid receptor-like (DNA-binding domain) <b>Family:</b> LIM domain
72	<a href="#">c2aklA</a>	Alignment	not modelled	29.0	39	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> phna-like protein pa0128; <b>PDBTitle:</b> solution structure for phn-a like protein pa0128 from2 pseudomonas aeruginosa
73	<a href="#">c2e72A</a>	Alignment	not modelled	28.6	38	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> pogo transposable element with znf domain; <b>PDBTitle:</b> solution structure of the zinc finger domain of human2 kiaa0461
74	<a href="#">d2akla2</a>	Alignment	not modelled	28.2	39	<b>Fold:</b> Rubredoxin-like <b>Superfamily:</b> Zinc beta-ribbon <b>Family:</b> PhnA zinc-binding domain
75	<a href="#">c6g5iy</a>	Alignment	not modelled	27.9	14	<b>PDB header:</b> ribosome <b>Chain:</b> Y: <b>PDB Molecule:</b> 40s ribosomal protein s24; <b>PDBTitle:</b> cryo-em structure of a late human pre-40s ribosomal subunit - state r
76	<a href="#">d1k3xa3</a>	Alignment	not modelled	27.7	33	<b>Fold:</b> Glucocorticoid receptor-like (DNA-binding domain) <b>Superfamily:</b> Glucocorticoid receptor-like (DNA-binding domain) <b>Family:</b> C-terminal, Zn-finger domain of MutM-like DNA repair proteins
77	<a href="#">c1x61A</a>	Alignment	not modelled	26.7	30	<b>PDB header:</b> cell adhesion <b>Chain:</b> A: <b>PDB Molecule:</b> thyroid receptor interacting protein 6; <b>PDBTitle:</b> solution structure of the first lim domain of thyroid2 receptor interacting protein 6 (trip6)
78	<a href="#">c3iynM</a>	Alignment	not modelled	26.6	24	<b>PDB header:</b> virus <b>Chain:</b> M: <b>PDB Molecule:</b> penton base protein; <b>PDBTitle:</b> 3.6-angstrom cryoem structure of human adenovirus type 5
79	<a href="#">c5mqfl</a>	Alignment	not modelled	26.1	31	<b>PDB header:</b> splicing <b>Chain:</b> I: <b>PDB Molecule:</b> pre-mrna-processing factor 19; <b>PDBTitle:</b> cryo-em structure of a human spliceosome activated for step 2 of2 splicing (c* complex)
80	<a href="#">c5ijlA</a>	Alignment	not modelled	26.0	31	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> dna polymerase ii large subunit; <b>PDBTitle:</b> d-family dna polymerase - dp2 subunit (catalytic subunit)

81	<a href="#">c2dkdA</a>	 Alignment	not modelled	26.0	14	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> phosphoacetylglucosamine mutase; <b>PDBTitle:</b> crystal structure of n-acetylglucosamine-phosphate mutase,2 a member of the alpha-d-phosphohexomutase superfamily, in3 the product complex
82	<a href="#">c4bjuB</a>	 Alignment	not modelled	25.8	10	<b>PDB header:</b> isomerase <b>Chain:</b> B: <b>PDB Molecule:</b> n-acetylglucosamine-phosphate mutase; <b>PDBTitle:</b> genetic and structural validation of aspergillus fumigatus2 n-acetylphosphoglucosamine mutase as an antifungal target
83	<a href="#">c3glsC</a>	 Alignment	not modelled	25.7	42	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> nad-dependent deacetylase sirtuin-3, <b>PDBTitle:</b> crystal structure of human sirt3
84	<a href="#">d1t1ha</a>	 Alignment	not modelled	25.6	27	<b>Fold:</b> RING/U-box <b>Superfamily:</b> RING/U-box <b>Family:</b> U-box
85	<a href="#">c2bldD</a>	 Alignment	not modelled	25.5	24	<b>PDB header:</b> virus <b>Chain:</b> D: <b>PDB Molecule:</b> penton protein; <b>PDBTitle:</b> the quasi-atomic model of human adenovirus type 52 capsid (part 1)
86	<a href="#">d1kfia2</a>	 Alignment	not modelled	25.2	21	<b>Fold:</b> Phosphoglucomutase, first 3 domains <b>Superfamily:</b> Phosphoglucomutase, first 3 domains <b>Family:</b> Phosphoglucomutase, first 3 domains
87	<a href="#">c5a1vK</a>	 Alignment	not modelled	25.2	44	<b>PDB header:</b> transport protein <b>Chain:</b> K: <b>PDB Molecule:</b> coatomer subunit alpha; <b>PDBTitle:</b> the structure of the copi coat linkage i
88	<a href="#">c2cu8A</a>	 Alignment	not modelled	24.5	29	<b>PDB header:</b> metal binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> cysteine-rich protein 2; <b>PDBTitle:</b> solution structure of the lim domain of human cysteine-rich2 protein 2
89	<a href="#">c2lcqA</a>	 Alignment	not modelled	24.5	27	<b>PDB header:</b> metal binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> putative toxin vpc6; <b>PDBTitle:</b> solution structure of the endonuclease nob1 from p.horikoshii
90	<a href="#">c4rgiA</a>	 Alignment	not modelled	24.3	14	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> crystal structure of ktsc domain protein ypo2434 from yersinia pestis
91	<a href="#">c2pziA</a>	 Alignment	not modelled	24.2	24	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> probable serine/threonine-protein kinase pkng; <b>PDBTitle:</b> crystal structure of protein kinase pkng from mycobacterium2 tuberculosis in complex with tetrahydrobenzothiophene ax20017
92	<a href="#">d1m2ka</a>	 Alignment	not modelled	24.2	42	<b>Fold:</b> DHS-like NAD/FAD-binding domain <b>Superfamily:</b> DHS-like NAD/FAD-binding domain <b>Family:</b> Sir2 family of transcriptional regulators
93	<a href="#">c5gtxA</a>	 Alignment	not modelled	23.5	12	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> buckwheat glutaredoxin; <b>PDBTitle:</b> crystal structure of mutated buckwheat glutaredoxin
94	<a href="#">c4aaqA</a>	 Alignment	not modelled	23.5	24	<b>PDB header:</b> viral protein <b>Chain:</b> A: <b>PDB Molecule:</b> l2 protein iii (penton base); <b>PDBTitle:</b> dodecahedron formed of penton base protein from adenovirus ad3
95	<a href="#">c5oj7A</a>	 Alignment	not modelled	23.4	42	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> nad-dependent protein deacylase; <b>PDBTitle:</b> sirtuin 4 orthologue from xenopus tropicalis in complex with adp-2 ribose
96	<a href="#">d2c2la2</a>	 Alignment	not modelled	23.2	18	<b>Fold:</b> RING/U-box <b>Superfamily:</b> RING/U-box <b>Family:</b> U-box
97	<a href="#">c5dkaA</a>	 Alignment	not modelled	23.1	26	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> e3 ubiquitin-protein ligase rnf125; <b>PDBTitle:</b> a c2hc zinc finger is essential for the activity of the ring ubiquitin2 ligase rnf125
98	<a href="#">c3f2cA</a>	 Alignment	not modelled	23.1	38	<b>PDB header:</b> transferase/dna <b>Chain:</b> A: <b>PDB Molecule:</b> geobacillus kaustophilus dna polc; <b>PDBTitle:</b> dna polymerase polc from geobacillus kaustophilus complex with dna,2 dgtp and mn
99	<a href="#">d1q1aa</a>	 Alignment	not modelled	23.0	33	<b>Fold:</b> DHS-like NAD/FAD-binding domain <b>Superfamily:</b> DHS-like NAD/FAD-binding domain <b>Family:</b> Sir2 family of transcriptional regulators
100	<a href="#">c6gc1A</a>	 Alignment	not modelled	23.0	13	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> nhl repeat-containing protein 2; <b>PDBTitle:</b> crystal structure of trx-like and nhl repeat containing domains of2 human nhlrc2
101	<a href="#">d1s5pa</a>	 Alignment	not modelled	22.9	21	<b>Fold:</b> DHS-like NAD/FAD-binding domain <b>Superfamily:</b> DHS-like NAD/FAD-binding domain <b>Family:</b> Sir2 family of transcriptional regulators
102	<a href="#">c3oheA</a>	 Alignment	not modelled	22.9	15	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> histidine triad (hit) protein; <b>PDBTitle:</b> crystal structure of a histidine triad protein (maqu_1709) from2 marinobacter aquaeolei vt8 at 1.20 a resolution
103	<a href="#">c2emcA</a>	 Alignment	not modelled	22.7	25	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> zinc finger protein 473; <b>PDBTitle:</b> solution structure of the c2h2 type zinc finger (region 641-2 673) of human zinc finger protein 473
104	<a href="#">c4r7eA</a>	 Alignment	not modelled	22.3	18	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> e3 ubiquitin-protein ligase bre1; <b>PDBTitle:</b> structure of bre1 ring domain
105	<a href="#">c4giwP</a>	 Alignment	not modelled	22.2	33	<b>PDB header:</b> transcription <b>Chain:</b> P: <b>PDB Molecule:</b> dna-directed rna polymerase subunit p; <b>PDBTitle:</b> crystal structure of euryarchaeal rna polymerase from thermococcus2 kodakarensis
106	<a href="#">c2kreA</a>	 Alignment	not modelled	22.0	23	<b>PDB header:</b> protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> ubiquitin conjugation factor e4 b; <b>PDBTitle:</b> solution structure of e4b/ufd2a u-box domain

107	<a href="#">c3zifM_</a>	Alignment	not modelled	22.0	22	<b>PDB header:</b> virus <b>Chain:</b> M: <b>PDB Molecule:</b> penton protein; <b>PDBTitle:</b> cryo-em structures of two intermediates provide insight into2 adenovirus assembly and disassembly
108	<a href="#">d1e7la2</a>	Alignment	not modelled	22.0	19	<b>Fold:</b> His-Me finger endonucleases <b>Superfamily:</b> His-Me finger endonucleases <b>Family:</b> Recombination endonuclease VII, N-terminal domain
109	<a href="#">c2l7xA_</a>	Alignment	not modelled	21.9	38	<b>PDB header:</b> viral protein <b>Chain:</b> A: <b>PDB Molecule:</b> envelope glycoprotein; <b>PDBTitle:</b> crimean congo hemorrhagic fever gn zinc finger
110	<a href="#">d1imla1</a>	Alignment	not modelled	21.9	56	<b>Fold:</b> Glucocorticoid receptor-like (DNA-binding domain) <b>Superfamily:</b> Glucocorticoid receptor-like (DNA-binding domain) <b>Family:</b> LIM domain
111	<a href="#">c5fywW_</a>	Alignment	not modelled	21.8	70	<b>PDB header:</b> transcription <b>Chain:</b> W: <b>PDB Molecule:</b> transcription initiation factor iie subunit alpha; <b>PDBTitle:</b> transcription initiation complex structures elucidate dna opening (oc)
112	<a href="#">c1dvbA_</a>	Alignment	not modelled	21.5	57	<b>PDB header:</b> electron transport <b>Chain:</b> A: <b>PDB Molecule:</b> rubrerythrin; <b>PDBTitle:</b> rubrerythrin
113	<a href="#">c3k1A_</a>	Alignment	not modelled	21.4	44	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> fancl; <b>PDBTitle:</b> crystal structure of fancl
114	<a href="#">d1yc5a1</a>	Alignment	not modelled	21.2	33	<b>Fold:</b> DHS-like NAD/FAD-binding domain <b>Superfamily:</b> DHS-like NAD/FAD-binding domain <b>Family:</b> Sir2 family of transcriptional regulators
115	<a href="#">c3a44D_</a>	Alignment	not modelled	20.9	21	<b>PDB header:</b> metal binding protein <b>Chain:</b> D: <b>PDB Molecule:</b> hydrogenase nickel incorporation protein hypa; <b>PDBTitle:</b> crystal structure of hypa in the dimeric form
116	<a href="#">c2iybG_</a>	Alignment	not modelled	20.8	38	<b>PDB header:</b> metal-binding <b>Chain:</b> G: <b>PDB Molecule:</b> testin; <b>PDBTitle:</b> structure of complex between the 3rd lim domain of tes and the evh12 domain of mena
117	<a href="#">c2bx9J_</a>	Alignment	not modelled	20.8	35	<b>PDB header:</b> transcription regulation <b>Chain:</b> J: <b>PDB Molecule:</b> tryptophan rna-binding attenuator protein-inhibitory <b>PDBTitle:</b> crystal structure of b.subtilis anti-trap protein, an2 antagonist of trap-rna interactions
118	<a href="#">c2lo2A_</a>	Alignment	not modelled	20.6	22	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> isaga-associated factor 11; <b>PDBTitle:</b> solution structure of sgf11(63-99) zinc finger domain
119	<a href="#">c5l9wC_</a>	Alignment	not modelled	20.1	43	<b>PDB header:</b> ligase <b>Chain:</b> C: <b>PDB Molecule:</b> acetophenone carboxylase beta subunit; <b>PDBTitle:</b> crystal structure of the apc core complex