


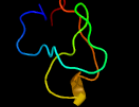
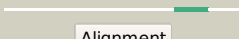
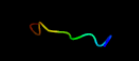



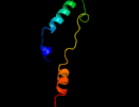

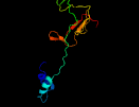

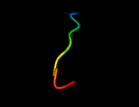

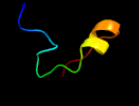

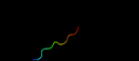



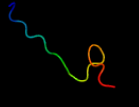
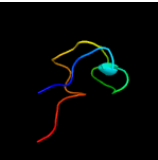
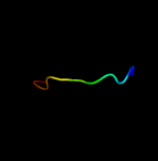
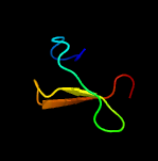


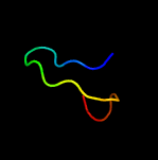


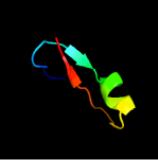


# Phyre2

Email	mdejesus@rockefeller.edu
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Date	Fri Jul 26 01:50:46 BST 2019
Unique Job ID	451e6f3d5362cc95

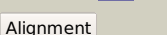

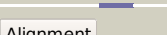
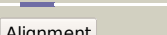



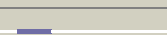
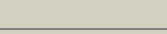
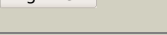
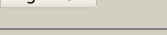
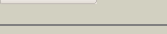




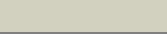
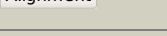
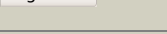
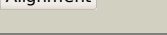
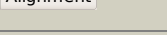
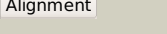
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c3d0fA_</a>	 Alignment		56.4	27	<b>PDB header:</b> transferase <b>Chain:</b> A; <b>PDB Molecule:</b> penicillin-binding 1 transmembrane protein mrca; <b>PDBTitle:</b> structure of the big_1156.2 domain of putative penicillin-binding2 protein mrca from nitrosomonas europaea atcc 19718
2	<a href="#">d1js2a_</a>	 Alignment		50.0	17	<b>Fold:</b> HIPIP (high potential iron protein) <b>Superfamily:</b> HIPIP (high potential iron protein) <b>Family:</b> HIPIP (high potential iron protein)
3	<a href="#">c4d0mW_</a>	 Alignment		41.7	27	<b>PDB header:</b> signaling protein <b>Chain:</b> W; <b>PDB Molecule:</b> phosphatidylinositol 4-kinase beta; <b>PDBTitle:</b> phosphatidylinositol 4-kinase iii beta in a complex with rab11a-gtp-2 gamma-s and the rab-binding domain of fip3
4	<a href="#">d1b0ya_</a>	 Alignment		40.2	22	<b>Fold:</b> HIPIP (high potential iron protein) <b>Superfamily:</b> HIPIP (high potential iron protein) <b>Family:</b> HIPIP (high potential iron protein)
5	<a href="#">c6e7aY_</a>	 Alignment		38.2	17	<b>PDB header:</b> dna binding protein/dna/rna <b>Chain:</b> Y; <b>PDB Molecule:</b> casx; <b>PDBTitle:</b> casx-grna-dna(30bp) state ii
6	<a href="#">c3csqC_</a>	 Alignment		32.9	14	<b>PDB header:</b> hydrolase <b>Chain:</b> C; <b>PDB Molecule:</b> morphogenesis protein 1; <b>PDBTitle:</b> crystal and cryoem structural studies of a cell wall2 degrading enzyme in the bacteriophage phi29 tail
7	<a href="#">c3ls8A_</a>	 Alignment		30.1	18	<b>PDB header:</b> transferase <b>Chain:</b> A; <b>PDB Molecule:</b> phosphatidylinositol 3-kinase catalytic subunit <b>PDBTitle:</b> crystal structure of human pik3c3 in complex with 3-[4-(4-2 morpholinyl)thieno[3,2-d]pyrimidin-2-yl]-phenol
8	<a href="#">c3h31A_</a>	 Alignment		30.0	20	<b>PDB header:</b> electron transport <b>Chain:</b> A; <b>PDB Molecule:</b> high potential iron-sulfur protein; <b>PDBTitle:</b> structure of rhodothermus marinus hipip at 1.0 a resolution
9	<a href="#">d1e7ua4</a>	 Alignment		29.7	18	<b>Fold:</b> Protein kinase-like (PK-like) <b>Superfamily:</b> Protein kinase-like (PK-like) <b>Family:</b> Phosphoinositide 3-kinase (PI3K), catalytic domain
10	<a href="#">d1hlqa_</a>	 Alignment		28.9	24	<b>Fold:</b> HIPIP (high potential iron protein) <b>Superfamily:</b> HIPIP (high potential iron protein) <b>Family:</b> HIPIP (high potential iron protein)
11	<a href="#">d1ckqa_</a>	 Alignment		28.2	32	<b>Fold:</b> Restriction endonuclease-like <b>Superfamily:</b> Restriction endonuclease-like <b>Family:</b> Restriction endonuclease EcoRI

12	<a href="#">c2wanA_</a>	Alignment		28.2	25	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> pullulanase; <b>PDBTitle:</b> pullulanase from bacillus acidopullulyticus
13	<a href="#">c2x6kB_</a>	Alignment		27.7	18	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> phosphatidylinositol 3 kinase 59f; <b>PDBTitle:</b> the crystal structure of the drosophila class iii pi3-kinase vps34 in2 complex with pi-103
14	<a href="#">c2akfA_</a>	Alignment		26.6	17	<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
15	<a href="#">d4znfa_</a>	Alignment		25.8	29	<b>Fold:</b> beta-beta-alpha zinc fingers <b>Superfamily:</b> beta-beta-alpha zinc fingers <b>Family:</b> Classic zinc finger, C2H2
16	<a href="#">c3znfA_</a>	Alignment		25.8	29	<b>PDB header:</b> zinc finger dna binding domain <b>Chain:</b> A: <b>PDB Molecule:</b> zinc finger; <b>PDBTitle:</b> high-resolution three-dimensional structure of a single2 zinc finger from a human enhancer binding protein in3 solution
17	<a href="#">c4znfA_</a>	Alignment		25.8	29	<b>PDB header:</b> zinc finger dna binding domain <b>Chain:</b> A: <b>PDB Molecule:</b> zinc finger; <b>PDBTitle:</b> high-resolution three-dimensional structure of a single2 zinc finger from a human enhancer binding protein in3 solution
18	<a href="#">d3hipa_</a>	Alignment		25.0	19	<b>Fold:</b> HIPIP (high potential iron protein) <b>Superfamily:</b> HIPIP (high potential iron protein) <b>Family:</b> HIPIP (high potential iron protein)
19	<a href="#">c2lxwA_</a>	Alignment		23.8	60	<b>PDB header:</b> apoptosis <b>Chain:</b> A: <b>PDB Molecule:</b> xiap-associated factor 1; <b>PDBTitle:</b> the solution structure of xiap(ring)-binding domain of human xaf1
20	<a href="#">d1dkca_</a>	Alignment		23.6	36	<b>Fold:</b> Knottins (small inhibitors, toxins, lectins) <b>Superfamily:</b> Gurmarin-like <b>Family:</b> Antifungal peptide
21	<a href="#">c5dfzC_</a>	Alignment	not modelled	22.9	27	<b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> phosphatidylinositol 3-kinase vps34; <b>PDBTitle:</b> structure of vps34 complex ii from s. cerevisiae.
22	<a href="#">d2akla2</a>	Alignment	not modelled	22.2	17	<b>Fold:</b> Rubredoxin-like <b>Superfamily:</b> Zinc beta-ribbon <b>Family:</b> PhnA zinc-binding domain
23	<a href="#">d2gmga1</a>	Alignment	not modelled	22.0	50	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> PF0610-like
24	<a href="#">c4av1C_</a>	Alignment	not modelled	19.9	27	<b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> poly [adp-ribose] polymerase 1; <b>PDBTitle:</b> crystal structure of the human parp-1 dna binding domain in2 complex with dna
25	<a href="#">c1vzhB_</a>	Alignment	not modelled	19.2	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> desulfoferrodoxin; <b>PDBTitle:</b> structure of superoxide reductase bound to ferrocyanide and active2 site expansion upon x-ray induced photoreduction
26	<a href="#">c3j3v0_</a>	Alignment	not modelled	19.0	32	<b>PDB header:</b> ribosome <b>Chain:</b> 0: <b>PDB Molecule:</b> 50s ribosomal protein l32; <b>PDBTitle:</b> atomic model of the immature 50s subunit from bacillus subtilis (state2 i-a)
27	<a href="#">d1hpia_</a>	Alignment	not modelled	19.0	20	<b>Fold:</b> HIPIP (high potential iron protein) <b>Superfamily:</b> HIPIP (high potential iron protein) <b>Family:</b> HIPIP (high potential iron protein)
28	<a href="#">d2j0151</a>	Alignment	not modelled	18.5	26	<b>Fold:</b> Rubredoxin-like <b>Superfamily:</b> Zn-binding ribosomal proteins <b>Family:</b> Ribosomal protein L32p
						<b>Fold:</b> Rubredoxin-like

29	<a href="#">d2zjrz1</a>	Alignment	not modelled	17.9	21	<b>Superfamily:</b> Zn-binding ribosomal proteins <b>Family:</b> Ribosomal protein L32p
30	<a href="#">d1isua</a>	Alignment	not modelled	17.9	40	<b>Fold:</b> HIPIP (high potential iron protein) <b>Superfamily:</b> HIPIP (high potential iron protein) <b>Family:</b> HIPIP (high potential iron protein)
31	<a href="#">c2y3aA</a>	Alignment	not modelled	17.9	14	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> phosphatidylinositol-4,5-bisphosphate 3-kinase catalytic <b>PDBTitle:</b> crystal structure of p110beta in complex with icsh2 of p85beta and the2 drug gdc-0941
32	<a href="#">c3rx9A</a>	Alignment	not modelled	17.3	22	<b>PDB header:</b> lipid binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> putative uncharacterized protein; <b>PDBTitle:</b> 3d structure of scin from an escherichia coli patotype
33	<a href="#">c5yz0A</a>	Alignment	not modelled	17.3	30	<b>PDB header:</b> cell cycle <b>Chain:</b> A: <b>PDB Molecule:</b> serine/threonine-protein kinase atr; <b>PDBTitle:</b> cryo-em structure of human atr-atrip complex
34	<a href="#">d2k4xa1</a>	Alignment	not modelled	17.3	42	<b>Fold:</b> Rubredoxin-like <b>Superfamily:</b> Zn-binding ribosomal proteins <b>Family:</b> Ribosomal protein S27a
35	<a href="#">c1sxbB</a>	Alignment	not modelled	17.1	42	<b>PDB header:</b> replication <b>Chain:</b> B: <b>PDB Molecule:</b> activator 1 37 kda subunit; <b>PDBTitle:</b> crystal structure of the eukaryotic clamp loader (replication factor2 c, rfc) bound to the dna sliding clamp (proliferating cell nuclear3 antigen, pcna)
36	<a href="#">c4jspA</a>	Alignment	not modelled	17.0	20	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> serine/threonine-protein kinase mtor; <b>PDBTitle:</b> structure of mtordeltan-mlst8-atpgammas-mg complex
37	<a href="#">c3tkaA</a>	Alignment	not modelled	16.9	44	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> ribosomal rna small subunit methyltransferase h; <b>PDBTitle:</b> crystal structure and solution saxs of methyltransferase rsmh from2 e.coli
38	<a href="#">c2wxoA</a>	Alignment	not modelled	16.9	13	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> phosphatidylinositol-4,5-bisphosphate 3-kinase catalytic <b>PDBTitle:</b> the crystal structure of the murine class ia pi 3-kinase p110delta in2 complex with as5.
39	<a href="#">c3tu8A</a>	Alignment	not modelled	16.7	53	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> burkholderia lethal factor 1 (blf1); <b>PDBTitle:</b> crystal structure of the burkholderia lethal factor 1 (blf1)
40	<a href="#">c3fhdA</a>	Alignment	not modelled	16.6	25	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> orf 37; <b>PDBTitle:</b> crystal structure of the shutoff and exonuclease protein from kaposi2 sarcoma associated herpesvirus
41	<a href="#">c5h64a</a>	Alignment	not modelled	16.2	20	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> serine/threonine-protein kinase mtor; <b>PDBTitle:</b> cryo-em structure of mtorc1
42	<a href="#">c1wg8B</a>	Alignment	not modelled	16.1	31	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> predicted s-adenosylmethionine-dependent <b>PDBTitle:</b> crystal structure of a predicted s-adenosylmethionine-2 dependent methyltransferase tt1512 from thermus3 thermophilus hb8.
43	<a href="#">d1qf8a</a>	Alignment	not modelled	16.1	32	<b>Fold:</b> Rubredoxin-like <b>Superfamily:</b> Casein kinase II beta subunit <b>Family:</b> Casein kinase II beta subunit
44	<a href="#">d1iuaa</a>	Alignment	not modelled	15.9	19	<b>Fold:</b> HIPIP (high potential iron protein) <b>Superfamily:</b> HIPIP (high potential iron protein) <b>Family:</b> HIPIP (high potential iron protein)
45	<a href="#">d2hipa</a>	Alignment	not modelled	15.7	18	<b>Fold:</b> HIPIP (high potential iron protein) <b>Superfamily:</b> HIPIP (high potential iron protein) <b>Family:</b> HIPIP (high potential iron protein)
46	<a href="#">c5x51X</a>	Alignment	not modelled	15.1	21	<b>PDB header:</b> transferase <b>Chain:</b> X: <b>PDB Molecule:</b> rna polymerase subunit, found in rna polymerase complexes <b>PDBTitle:</b> rna polymerase ii from komagataella pastoris (type-3 crystal)
47	<a href="#">c2ja6L</a>	Alignment	not modelled	15.1	21	<b>PDB header:</b> transferase <b>Chain:</b> L: <b>PDB Molecule:</b> dna-directed rna polymerases i, ii, and iii 7.7 kda <b>PDBTitle:</b> cpd lesion containing rna polymerase ii elongation complex b
48	<a href="#">c5cm2Z</a>	Alignment	not modelled	15.0	20	<b>PDB header:</b> transferase <b>Chain:</b> Z: <b>PDB Molecule:</b> trna methyltransferase; <b>PDBTitle:</b> insights into molecular plasticity in protein complexes from trm9-2 trm112 trna modifying enzyme crystal structure
49	<a href="#">d2d8xa2</a>	Alignment	not modelled	14.9	27	<b>Fold:</b> Glucocorticoid receptor-like (DNA-binding domain) <b>Superfamily:</b> Glucocorticoid receptor-like (DNA-binding domain) <b>Family:</b> LIM domain
50	<a href="#">c5is5A</a>	Alignment	not modelled	14.8	18	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> phosphatidylinositol 4,5-bisphosphate 3-kinase catalytic <b>PDBTitle:</b> discovery and pharmacological characterization of novel quinazoline-2 based pi3k delta-selective inhibitors
51	<a href="#">c2uzhB</a>	Alignment	not modelled	14.7	20	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> 2c-methyl-d-erythritol 2,4-cyclodiphosphate <b>PDBTitle:</b> mycobacterium smegmatis 2c-methyl-d-erythritol-2,4-2 cyclodiphosphate synthase (ispf)
52	<a href="#">c5dxuA</a>	Alignment	not modelled	14.7	14	<b>PDB header:</b> transferase/inhibitor <b>Chain:</b> A: <b>PDB Molecule:</b> phosphatidylinositol 4,5-bisphosphate 3-kinase catalytic <b>PDBTitle:</b> p110delta/p85alpha with gdc-0326
53	<a href="#">c3h0nl</a>	Alignment	not modelled	14.4	27	<b>PDB header:</b> transcription <b>Chain:</b> L: <b>PDB Molecule:</b> dna-directed rna polymerases i, ii, and iii

53	<a href="#">c1rv9L</a>	Alignment	not modelled	14.4	27	subunit rpabc4; <b>PDBTitle:</b> rna polymerase ii from schizosaccharomyces pombe
54	<a href="#">c5zcsB</a>	Alignment	not modelled	14.3	20	<b>PDB header:</b> gene regulation <b>Chain:</b> B: <b>PDB Molecule:</b> serine/threonine-protein kinase mtor; <b>PDBTitle:</b> 4.9 angstrom cryo-em structure of human mtor complex 2
55	<a href="#">d1twfj</a>	Alignment	not modelled	14.3	15	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> RNA polymerase subunit RPB10 <b>Family:</b> RNA polymerase subunit RPB10
56	<a href="#">c3odeA</a>	Alignment	not modelled	14.1	19	<b>PDB header:</b> dna binding protein/dna <b>Chain:</b> A: <b>PDB Molecule:</b> poly [adp-ribose] polymerase 1; <b>PDBTitle:</b> human parp-1 zinc finger 2 (zn2) bound to dna
57	<a href="#">d2j4wd1</a>	Alignment	not modelled	14.0	29	<b>Fold:</b> Apical membrane antigen 1 <b>Superfamily:</b> Apical membrane antigen 1 <b>Family:</b> Apical membrane antigen 1
58	<a href="#">c2j4wD</a>	Alignment	not modelled	14.0	29	<b>PDB header:</b> immune system <b>Chain:</b> D: <b>PDB Molecule:</b> apical membrane antigen 1; <b>PDBTitle:</b> structure of a plasmodium vivax apical membrane antigen 1-2 fab f8.12.19 complex
59	<a href="#">c3vpbF</a>	Alignment	not modelled	13.9	35	<b>PDB header:</b> ligase <b>Chain:</b> F: <b>PDB Molecule:</b> alpha-aminoadipate carrier protein lysw; <b>PDBTitle:</b> argx from sulfolobus tokodaii complexed with2 lysw/glu/adp/mg/zn/sulfate
60	<a href="#">c2rd0A</a>	Alignment	not modelled	13.9	21	<b>PDB header:</b> transferase/oncoprotein <b>Chain:</b> A: <b>PDB Molecule:</b> phosphatidylinositol-4,5-bisphosphate 3-kinase catalytic <b>PDBTitle:</b> structure of a human p110alpha/p85alpha complex
61	<a href="#">c2w45A</a>	Alignment	not modelled	13.8	27	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> alkaline exonuclease; <b>PDBTitle:</b> epstein-barr virus alkaline nuclease
62	<a href="#">c4yknA</a>	Alignment	not modelled	13.6	21	<b>PDB header:</b> transferase/transferase inhibitor <b>Chain:</b> A: <b>PDB Molecule:</b> phosphatidylinositol 3-kinase regulatory subunit alpha, <b>PDBTitle:</b> pi3k alpha lipid kinase with active site inhibitor
63	<a href="#">d1yzha1</a>	Alignment	not modelled	13.5	19	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> TrmB-like
64	<a href="#">d1iqca2</a>	Alignment	not modelled	13.5	20	<b>Fold:</b> Cytochrome c <b>Superfamily:</b> Cytochrome c <b>Family:</b> Di-heme cytochrome c peroxidase
65	<a href="#">c2zkr2</a>	Alignment	not modelled	13.4	36	<b>PDB header:</b> ribosomal protein/rna <b>Chain:</b> 2: <b>PDB Molecule:</b> 60s ribosomal protein l37e; <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
66	<a href="#">c3jvwY</a>	Alignment	not modelled	13.4	36	<b>PDB header:</b> ribosome <b>Chain:</b> Y: <b>PDB Molecule:</b> 60s ribosomal protein l37(a); <b>PDBTitle:</b> structure of the 60s proteins for eukaryotic ribosome based on cryo-em2 map of thermomyces lanuginosus ribosome at 8.9a resolution
67	<a href="#">c1s1iY</a>	Alignment	not modelled	13.0	36	<b>PDB header:</b> ribosome <b>Chain:</b> Y: <b>PDB Molecule:</b> 60s ribosomal protein l37-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.
68	<a href="#">c5flmL</a>	Alignment	not modelled	12.6	21	<b>PDB header:</b> transcription <b>Chain:</b> L: <b>PDB Molecule:</b> dna-directed rna polymerases i, ii, and iii subunit rpabc4; <b>PDBTitle:</b> structure of transcribing mammalian rna polymerase ii
69	<a href="#">d1jwhc</a>	Alignment	not modelled	12.5	32	<b>Fold:</b> Rubredoxin-like <b>Superfamily:</b> Casein kinase II beta subunit <b>Family:</b> Casein kinase II beta subunit
70	<a href="#">c1m6yA</a>	Alignment	not modelled	12.5	31	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> s-adenosyl-methyltransferase mraw; <b>PDBTitle:</b> crystal structure analysis of tm0872, a putative sam-dependent2 methyltransferase, complexed with sah
71	<a href="#">c6ba3A</a>	Alignment	not modelled	12.4	32	<b>PDB header:</b> toxin <b>Chain:</b> A: <b>PDB Molecule:</b> u21-hexatoxin-hi1a; <b>PDBTitle:</b> nmr structure of u21-hexatoxin-hi1a toxin from australian funnel-web2 spider hadronyche infensa
72	<a href="#">c5ivaB</a>	Alignment	not modelled	12.4	31	<b>PDB header:</b> transport protein <b>Chain:</b> B: <b>PDB Molecule:</b> lps-assembly lipoprotein lpte; <b>PDBTitle:</b> the lps transporter lptde from pseudomonas aeruginosa, core complex
73	<a href="#">c2kaeA</a>	Alignment	not modelled	12.3	15	<b>PDB header:</b> transcription/dna <b>Chain:</b> A: <b>PDB Molecule:</b> gata-type transcription factor; <b>PDBTitle:</b> data-driven model of med1:dna complex
74	<a href="#">c2dmjA</a>	Alignment	not modelled	12.3	27	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> poly (adp-ribose) polymerase family, member 1; <b>PDBTitle:</b> solution structure of the first zf-parp domain of human2 poly(adp-ribose)polymerase-1
75	<a href="#">c1e8zA</a>	Alignment	not modelled	12.3	14	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> phosphatidylinositol 3-kinase catalytic subunit; <b>PDBTitle:</b> structure determinants of phosphoinositide 3-kinase2 inhibition by wortmannin, ly294002, quercetin, myricetin3 and staurosporine
76	<a href="#">c5np1A</a>	Alignment	not modelled	12.2	20	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> serine-protein kinase atm; <b>PDBTitle:</b> open protomer of human atm (ataxia telangiectasia mutated)
77	<a href="#">c2hntC</a>	Alignment	not modelled	12.2	26	<b>PDB header:</b> serine protease <b>Chain:</b> C: <b>PDB Molecule:</b> gamma-thrombin; <b>PDBTitle:</b> crystallographic structure of human gamma-thrombin

78	<a href="#">c2f9iD</a>	 Alignment	not modelled	12.1	31	<b>PDB header:</b> transferase <b>Chain:</b> D: <b>PDB Molecule:</b> acetyl-coenzyme a carboxylase carboxyl transferase subunit <b>PDBTitle:</b> crystal structure of the carboxyltransferase subunit of acc from 2 staphylococcus aureus
79	<a href="#">c2lzoA</a>	 Alignment	not modelled	11.7	58	<b>PDB header:</b> toxin <b>Chain:</b> A: <b>PDB Molecule:</b> ugtX; <b>PDBTitle:</b> spatial structure of pi-anmtX ugr 9a-1
80	<a href="#">c5fvmB</a>	 Alignment	not modelled	11.7	40	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> serine/threonine-protein kinase tor2; <b>PDBTitle:</b> cryo electron microscopy of a complex of tor and Ist8
81	<a href="#">c1e2xA</a>	 Alignment	not modelled	11.5	18	<b>PDB header:</b> transcriptional regulation <b>Chain:</b> A: <b>PDB Molecule:</b> fatty acid metabolism regulator protein; <b>PDBTitle:</b> fadr, fatty acid responsive transcription factor from e.2 coli
82	<a href="#">c3j21e</a>	 Alignment	not modelled	11.5	45	<b>PDB header:</b> ribosome <b>Chain:</b> E: <b>PDB Molecule:</b> 50s ribosomal protein l5p; <b>PDBTitle:</b> promiscuous behavior of proteins in archaeal ribosomes revealed by 2 cryo-em: implications for evolution of eukaryotic ribosomes (50s3 ribosomal proteins)
83	<a href="#">d1vqo11</a>	 Alignment	not modelled	11.4	55	<b>Fold:</b> Rubredoxin-like <b>Superfamily:</b> Zn-binding ribosomal proteins <b>Family:</b> Ribosomal protein L37e
84	<a href="#">d1nmla2</a>	 Alignment	not modelled	11.4	20	<b>Fold:</b> Cytochrome c <b>Superfamily:</b> Cytochrome c <b>Family:</b> Di-heme cytochrome c peroxidase
85	<a href="#">c1sxD</a>	 Alignment	not modelled	11.1	45	<b>PDB header:</b> replication <b>Chain:</b> D: <b>PDB Molecule:</b> activator 1 41 kda subunit; <b>PDBTitle:</b> crystal structure of the eukaryotic clamp loader (replication factor 2 c, rfc) bound to the dna sliding clamp (proliferating cell nuclear 3 antigen, pcna)
86	<a href="#">c3ongA</a>	 Alignment	not modelled	11.1	29	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> ubiquitin-activating enzyme e1-like; <b>PDBTitle:</b> crystal structure of uba2ufd-ubc9: insights into e1-e2 interactions in 2 sumo pathways
87	<a href="#">c5x6oC</a>	 Alignment	not modelled	11.0	30	<b>PDB header:</b> transferase/dna binding protein <b>Chain:</b> C: <b>PDB Molecule:</b> serine/threonine-protein kinase mec1; <b>PDBTitle:</b> intact atr/mec1-atrip/ddc2 complex
88	<a href="#">d1zwyA1</a>	 Alignment	not modelled	10.9	34	<b>Fold:</b> Anticodon-binding domain-like <b>Superfamily:</b> TPase-like <b>Family:</b> YjyX-like
89	<a href="#">d1gnfa</a>	 Alignment	not modelled	10.8	22	<b>Fold:</b> Glucocorticoid receptor-like (DNA-binding domain) <b>Superfamily:</b> Glucocorticoid receptor-like (DNA-binding domain) <b>Family:</b> Erythroid transcription factor GATA-1
90	<a href="#">d2vuti1</a>	 Alignment	not modelled	10.6	36	<b>Fold:</b> Glucocorticoid receptor-like (DNA-binding domain) <b>Superfamily:</b> Glucocorticoid receptor-like (DNA-binding domain) <b>Family:</b> Erythroid transcription factor GATA-1
91	<a href="#">d1gk8a1</a>	 Alignment	not modelled	10.5	12	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> RuBisCo, C-terminal domain <b>Family:</b> RuBisCo, large subunit, C-terminal domain
92	<a href="#">d2f9yb1</a>	 Alignment	not modelled	10.3	33	<b>Fold:</b> ClpP/crotonase <b>Superfamily:</b> ClpP/crotonase <b>Family:</b> Biotin dependent carboxylase carboxyltransferase domain
93	<a href="#">c2f9yB</a>	 Alignment	not modelled	10.3	33	<b>PDB header:</b> ligase <b>Chain:</b> B: <b>PDB Molecule:</b> acetyl-coenzyme a carboxylase carboxyl transferase subunit <b>PDBTitle:</b> the crystal structure of the carboxyltransferase subunit of acc from 2 escherichia coli
94	<a href="#">d1vhib</a>	 Alignment	not modelled	10.3	23	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> Viral DNA-binding domain <b>Family:</b> Viral DNA-binding domain
95	<a href="#">c3zf7n</a>	 Alignment	not modelled	10.3	18	<b>PDB header:</b> ribosome <b>Chain:</b> N: <b>PDB Molecule:</b> 60s ribosomal protein l13; <b>PDBTitle:</b> high-resolution cryo-electron microscopy structure of the trypanosoma 2 brucei ribosome
96	<a href="#">c2kzyA</a>	 Alignment	not modelled	10.3	33	<b>PDB header:</b> metal binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> zfn5 protein (zinc finger protein 216 (predicted), <b>PDBTitle:</b> solution nmr structure of the znf216 a20 zinc finger
97	<a href="#">d1yuja</a>	 Alignment	not modelled	10.2	19	<b>Fold:</b> beta-beta-alpha zinc fingers <b>Superfamily:</b> beta-beta-alpha zinc fingers <b>Family:</b> Classic zinc finger, C2H2
98	<a href="#">c6ghcA</a>	 Alignment	not modelled	10.1	25	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> 5-methylcytosine-specific restriction enzyme a; <b>PDBTitle:</b> modification dependent ecomcra restriction endonuclease
99	<a href="#">d1vlma</a>	 Alignment	not modelled	10.0	27	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> UbiE/COQ5-like