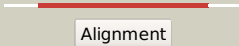

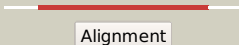

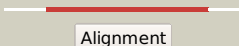



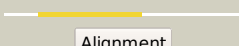
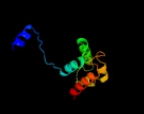
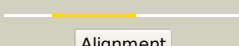
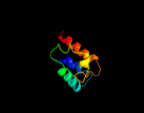
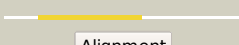

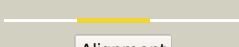

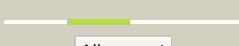

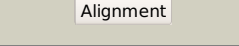


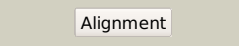
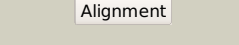
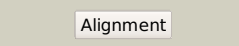
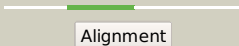
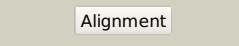



# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1210_(tagA)_1353528_1354142
Date	Wed Jul 31 22:05:30 BST 2019
Unique Job ID	9f6e9f90bb79595b

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">d1nkua_</a>	Alignment		100.0	45	<b>Fold:</b> DNA-glycosylase <b>Superfamily:</b> DNA-glycosylase <b>Family:</b> 3-Methyladenine DNA glycosylase I (Tag)
2	<a href="#">c2jg6A_</a>	Alignment		100.0	34	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> dna-3-methyladenine glycosidase; <b>PDBTitle:</b> crystal structure of a 3-methyladenine dna glycosylase i from2 staphylococcus aureus
3	<a href="#">d1keaa_</a>	Alignment		97.5	13	<b>Fold:</b> DNA-glycosylase <b>Superfamily:</b> DNA-glycosylase <b>Family:</b> Mismatch glycosylase
4	<a href="#">d1orna_</a>	Alignment		97.0	14	<b>Fold:</b> DNA-glycosylase <b>Superfamily:</b> DNA-glycosylase <b>Family:</b> Endonuclease III
5	<a href="#">c4uobA_</a>	Alignment		96.7	11	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> endonuclease iii-3; <b>PDBTitle:</b> crystal structure of deinococcus radiodurans endonuclease iii-3
6	<a href="#">d1pu6a_</a>	Alignment		96.6	17	<b>Fold:</b> DNA-glycosylase <b>Superfamily:</b> DNA-glycosylase <b>Family:</b> 3-Methyladenine DNA glycosylase III (MagIII)
7	<a href="#">d1rrqa1</a>	Alignment		96.1	16	<b>Fold:</b> DNA-glycosylase <b>Superfamily:</b> DNA-glycosylase <b>Family:</b> Mismatch glycosylase
8	<a href="#">d1kg2a_</a>	Alignment		96.0	18	<b>Fold:</b> DNA-glycosylase <b>Superfamily:</b> DNA-glycosylase <b>Family:</b> Mismatch glycosylase
9	<a href="#">c3fhgA_</a>	Alignment		95.9	18	<b>PDB header:</b> dna repair, hydrolase, lyase <b>Chain:</b> A: <b>PDB Molecule:</b> n-glycosylase/dna lyase; <b>PDBTitle:</b> crystal structure of sulfolobus solfataricus 8-oxoguanine dna2 glycosylase (ssogg)
10	<a href="#">c3n5nX_</a>	Alignment		95.7	18	<b>PDB header:</b> hydrolase <b>Chain:</b> X: <b>PDB Molecule:</b> a/g-specific adenine dna glycosylase; <b>PDBTitle:</b> crystal structure analysis of the catalytic domain and interdomain2 connector of human muty homologue
11	<a href="#">c4unfA_</a>	Alignment		93.5	14	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> endonuclease iii-1; <b>PDBTitle:</b> crystal structure of deinococcus radiodurans endonuclease iii-1

12	<a href="#">d2abka_</a>	 Alignment		93.0	15	<b>Fold:</b> DNA-glycosylase <b>Superfamily:</b> DNA-glycosylase <b>Family:</b> Endonuclease III
13	<a href="#">c3kntC_</a>	 Alignment		92.1	16	<b>PDB header:</b> hydrolase, lyase/dna <b>Chain:</b> C: <b>PDB Molecule:</b> n-glycosylase/dna lyase; <b>PDBTitle:</b> crystal structure of methanocaldococcus jannaschii 8-oxoguanine2 glycosylase/lyase in complex with 15mer dna containing 8-oxoguanine
14	<a href="#">c3n0uB_</a>	 Alignment		91.8	18	<b>PDB header:</b> hydrolase, lyase <b>Chain:</b> B: <b>PDB Molecule:</b> probable n-glycosylase/dna lyase; <b>PDBTitle:</b> crystal structure of tm1821, the 8-oxoguanine dna glycosylase of2 thermotoga maritima
15	<a href="#">d1ngna_</a>	 Alignment		89.6	13	<b>Fold:</b> DNA-glycosylase <b>Superfamily:</b> DNA-glycosylase <b>Family:</b> Mismatch glycosylase
16	<a href="#">c2yg8B_</a>	 Alignment		76.3	17	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> dna-3-methyladenine glycosidase ii, putative; <b>PDBTitle:</b> structure of an unusual 3-methyladenine dna glycosylase ii (alka) from2 deinococcus radiodurans
17	<a href="#">d1mpga1</a>	 Alignment		75.5	22	<b>Fold:</b> DNA-glycosylase <b>Superfamily:</b> DNA-glycosylase <b>Family:</b> DNA repair glycosylase, 2 C-terminal domains
18	<a href="#">c1rrqA_</a>	 Alignment		73.6	11	<b>PDB header:</b> hydrolase/dna <b>Chain:</b> A: <b>PDB Molecule:</b> muty; <b>PDBTitle:</b> muty adenine glycosylase in complex with dna containing an2 a:oxog pair
19	<a href="#">c2vtgA_</a>	 Alignment		72.2	15	<b>PDB header:</b> metal-binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> ionized calcium-binding adapter molecule 2; <b>PDBTitle:</b> crystal structure of human iba2, trigonal crystal form
20	<a href="#">c1oxjA_</a>	 Alignment		66.5	17	<b>PDB header:</b> rna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> rna-binding protein smaug; <b>PDBTitle:</b> crystal structure of the smaug rna binding domain
21	<a href="#">d1loxja1</a>	 Alignment	not modelled	59.3	12	<b>Fold:</b> SAM domain-like <b>Superfamily:</b> SAM/Pointed domain <b>Family:</b> SAM (sterile alpha motif) domain
22	<a href="#">c3hjzA_</a>	 Alignment	not modelled	58.6	21	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> transaldolase b; <b>PDBTitle:</b> the structure of an aldolase from prochlorococcus marinus
23	<a href="#">c3s6iA_</a>	 Alignment	not modelled	57.3	12	<b>PDB header:</b> hydrolase/dna <b>Chain:</b> A: <b>PDB Molecule:</b> dna-3-methyladenine glycosylase 1; <b>PDBTitle:</b> schizosaccharomyces pombe 3-methyladenine dna glycosylase (mag1) in2 complex with abasic-dna.
24	<a href="#">d2cs4a1</a>	 Alignment	not modelled	55.6	29	<b>Fold:</b> beta-Grasp (ubiquitin-like) <b>Superfamily:</b> Ubiquitin-like <b>Family:</b> Ras-binding domain, RBD
25	<a href="#">c2g2bA_</a>	 Alignment	not modelled	52.9	17	<b>PDB header:</b> immune system <b>Chain:</b> A: <b>PDB Molecule:</b> allograft inflammatory factor 1; <b>PDBTitle:</b> nmr structure of the human allograft inflammatory factor 1
26	<a href="#">c2fe9A_</a>	 Alignment	not modelled	52.4	18	<b>PDB header:</b> rna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> protein vts1; <b>PDBTitle:</b> solution structure of the vts1 sam domain in the presence2 of rna
27	<a href="#">c2eseA_</a>	 Alignment	not modelled	52.3	18	<b>PDB header:</b> protein/rna complex <b>Chain:</b> A: <b>PDB Molecule:</b> vts1p; <b>PDBTitle:</b> structure of the sam domain of vts1p in complex with rna
28	<a href="#">c2b6gA_</a>	 Alignment	not modelled	50.7	18	<b>PDB header:</b> rna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> vts1p; <b>PDBTitle:</b> rna recognition by the vts1 sam domain
		 Alignment				<b>PDB header:</b> metal binding protein

29	<a href="#">c2d58A_</a>	Alignment	not modelled	49.1	18	<b>Chain:</b> A: <b>PDB Molecule:</b> allograft inflammatory factor 1; <b>PDBTitle:</b> human microglia-specific protein iba1
30	<a href="#">d2noha1</a>	Alignment	not modelled	46.8	22	<b>Fold:</b> DNA-glycosylase <b>Superfamily:</b> DNA-glycosylase <b>Family:</b> DNA repair glycosylase, 2 C-terminal domains
31	<a href="#">c2hjwA_</a>	Alignment	not modelled	46.6	18	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> acetyl-coa carboxylase 2; <b>PDBTitle:</b> crystal structure of the bc domain of acc2
32	<a href="#">d1wg8a1</a>	Alignment	not modelled	45.2	22	<b>Fold:</b> SAM domain-like <b>Superfamily:</b> Putative methyltransferase TM0872, insert domain <b>Family:</b> Putative methyltransferase TM0872, insert domain
33	<a href="#">c2e8nA_</a>	Alignment	not modelled	41.3	23	<b>PDB header:</b> transferase, signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> ephrin type-a receptor 2; <b>PDBTitle:</b> solution structure of the c-terminal sam-domain of ephaa2:2 ephrin type-a receptor 2 precursor (ec 2.7.10.1)
34	<a href="#">c3m16A_</a>	Alignment	not modelled	39.1	23	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> transaldolase; <b>PDBTitle:</b> structure of a transaldolase from oleispira antarctica
35	<a href="#">c2remB_</a>	Alignment	not modelled	39.1	16	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> sulfide oxidoreductase; <b>PDBTitle:</b> crystal structure of oxidoreductase dsba from xylella fastidiosa
36	<a href="#">d1coka_</a>	Alignment	not modelled	38.6	19	<b>Fold:</b> SAM domain-like <b>Superfamily:</b> SAM/Pointed domain <b>Family:</b> SAM (sterile alpha motif) domain
37	<a href="#">c3k1rB_</a>	Alignment	not modelled	38.3	25	<b>PDB header:</b> structural protein <b>Chain:</b> B: <b>PDB Molecule:</b> usher syndrome type-1g protein; <b>PDBTitle:</b> structure of harmonin npd21 in complex with the sam-pbm of2 sans
38	<a href="#">c3igxA_</a>	Alignment	not modelled	38.3	20	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> transaldolase; <b>PDBTitle:</b> 1.85 angstrom resolution crystal structure of transaldolase b (tala)2 from francisella tularensis.
39	<a href="#">d1a9xa2</a>	Alignment	not modelled	34.9	14	<b>Fold:</b> Methylglyoxal synthase-like <b>Superfamily:</b> Methylglyoxal synthase-like <b>Family:</b> Carbamoyl phosphate synthetase, large subunit allosteric, C-terminal domain
40	<a href="#">d1kjna_</a>	Alignment	not modelled	34.1	36	<b>Fold:</b> Hypothetical protein MTH777 (MT0777) <b>Superfamily:</b> Hypothetical protein MTH777 (MT0777) <b>Family:</b> Hypothetical protein MTH777 (MT0777)
41	<a href="#">c3tkaA_</a>	Alignment	not modelled	33.6	17	<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
42	<a href="#">d1onra_</a>	Alignment	not modelled	33.6	20	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Aldolase <b>Family:</b> Class I aldolase
43	<a href="#">d1f05a_</a>	Alignment	not modelled	33.1	22	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Aldolase <b>Family:</b> Class I aldolase
44	<a href="#">c4b24A_</a>	Alignment	not modelled	31.7	19	<b>PDB header:</b> hydrolase/dna <b>Chain:</b> A: <b>PDB Molecule:</b> probable dna-3-methyladenine glycosylase 2; <b>PDBTitle:</b> unprecedented sculpting of dna at abasic sites by dna glycosylase2 homolog mag2
45	<a href="#">c2uv1B_</a>	Alignment	not modelled	31.1	40	<b>PDB header:</b> inhibitor <b>Chain:</b> B: <b>PDB Molecule:</b> host-nuclease inhibitor protein gam; <b>PDBTitle:</b> hexagonal crystal form of gams from bacteriophage lambda.
46	<a href="#">c3mwmA_</a>	Alignment	not modelled	30.0	33	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> putative metal uptake regulation protein; <b>PDBTitle:</b> graded expression of zinc-responsive genes through two regulatory2 zinc-binding sites in zur
47	<a href="#">c3r8rJ_</a>	Alignment	not modelled	29.9	24	<b>PDB header:</b> transferase <b>Chain:</b> J: <b>PDB Molecule:</b> transaldolase; <b>PDBTitle:</b> transaldolase from bacillus subtilis
48	<a href="#">c2yvqA_</a>	Alignment	not modelled	28.9	13	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> carbamoyl-phosphate synthase; <b>PDBTitle:</b> crystal structure of mgs domain of carbamoyl-phosphate2 synthetase from homo sapiens
49	<a href="#">c5udtD_</a>	Alignment	not modelled	28.2	26	<b>PDB header:</b> transferase <b>Chain:</b> D: <b>PDB Molecule:</b> lactate racemization operon protein lare; <b>PDBTitle:</b> lare, a sulfur transferase involved in synthesis of the cofactor for2 lactate racemase, in complex with amp
50	<a href="#">d1wlza1</a>	Alignment	not modelled	26.9	10	<b>Fold:</b> EF Hand-like <b>Superfamily:</b> EF-hand <b>Family:</b> EF-hand modules in multidomain proteins
51	<a href="#">c1vw4S_</a>	Alignment	not modelled	26.6	12	<b>PDB header:</b> ribosome <b>Chain:</b> S: <b>PDB Molecule:</b> 54s ribosomal protein l24, mitochondrial; <b>PDBTitle:</b> structure of the yeast mitochondrial large ribosomal subunit
52	<a href="#">c3cq0B_</a>	Alignment	not modelled	26.5	25	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> putative transaldolase ygr043c; <b>PDBTitle:</b> crystal structure of tal2_ yeast
53	<a href="#">c2m97A_</a>	Alignment	not modelled	26.5	13	<b>PDB header:</b> metal binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> optimized ratiometric calcium sensor; <b>PDBTitle:</b> optimized ratiometric calcium sensors for functional in vivo imaging2 of neurons and t-lymphocytes
54	<a href="#">d1vpXA_</a>	Alignment	not modelled	25.4	21	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Aldolase <b>Family:</b> Class I aldolase
						<b>PDB header:</b> apoptosis <b>Chain:</b> A: <b>PDB Molecule:</b> caspase recruitment domain-containing

55	<a href="#">c2nz7A_</a>	Alignment	not modelled	24.6	14	protein 4; <b>PDBTitle:</b> crystal structure analysis of caspase-recruitment domain2 (card) of nod1
56	<a href="#">c2l98A_</a>	Alignment	not modelled	24.4	16	<b>PDB header:</b> contractile protein <b>Chain:</b> A: <b>PDB Molecule:</b> troponin c, slow skeletal and cardiac muscles; <b>PDBTitle:</b> structure of trans-resveratrol in complex with the cardiac regulatory2 protein troponin c
57	<a href="#">c2dl0A_</a>	Alignment	not modelled	24.3	18	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> sam and sh3 domain-containing protein 1; <b>PDBTitle:</b> solution structure of the sam-domain of the sam and sh32 domain containing protein 1
58	<a href="#">c1wlzD_</a>	Alignment	not modelled	23.9	10	<b>PDB header:</b> unknown function <b>Chain:</b> D: <b>PDB Molecule:</b> cap-binding protein complex interacting protein <b>PDBTitle:</b> crystal structure of djbp fragment which was obtained by2 limited proteolysis
59	<a href="#">d2e1da1</a>	Alignment	not modelled	23.2	22	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Aldolase <b>Family:</b> Class I aldolase
60	<a href="#">c6j7aB_</a>	Alignment	not modelled	22.5	16	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> heme oxygenase 1,nadph--cytochrome p450 reductase; <b>PDBTitle:</b> fusion protein of heme oxygenase-1 and nadph cytochrome p450 reductase2 (17aa)
61	<a href="#">c1scvA_</a>	Alignment	not modelled	22.5	16	<b>PDB header:</b> contractile protein, structural protein <b>Chain:</b> A: <b>PDB Molecule:</b> troponin c, slow skeletal and cardiac muscles; <b>PDBTitle:</b> nmr structure of the c terminal domain of cardiac troponin2 c bound to the n terminal domain of cardiac troponin i
62	<a href="#">c2lc0A_</a>	Alignment	not modelled	21.8	9	<b>PDB header:</b> protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> putative uncharacterized protein tb39.8; <b>PDBTitle:</b> rv0020c_ nter structure
63	<a href="#">d1v38a_</a>	Alignment	not modelled	21.3	14	<b>Fold:</b> SAM domain-like <b>Superfamily:</b> SAM/Pointed domain <b>Family:</b> SAM (sterile alpha motif) domain
64	<a href="#">d1b0xa_</a>	Alignment	not modelled	21.0	18	<b>Fold:</b> SAM domain-like <b>Superfamily:</b> SAM/Pointed domain <b>Family:</b> SAM (sterile alpha motif) domain
65	<a href="#">c1b0xA_</a>	Alignment	not modelled	21.0	18	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> protein (epha4 receptor tyrosine kinase); <b>PDBTitle:</b> the crystal structure of an eph receptor sam domain reveals2 a mechanism for modular dimerization.
66	<a href="#">d1ulza2</a>	Alignment	not modelled	19.8	26	<b>Fold:</b> PreATP-grasp domain <b>Superfamily:</b> PreATP-grasp domain <b>Family:</b> BC N-terminal domain-like
67	<a href="#">c2k7bA_</a>	Alignment	not modelled	19.7	19	<b>PDB header:</b> metal binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> calcium-binding protein 1; <b>PDBTitle:</b> nmr structure of mg2+-bound cabp1 n-domain
68	<a href="#">c2ktgA_</a>	Alignment	not modelled	19.6	18	<b>PDB header:</b> ca-binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> calmodulin, putative; <b>PDBTitle:</b> calmodulin like protein from entamoeba histolytica: solution structure2 and calcium binding properties of a partially folded protein
69	<a href="#">c3s1vD_</a>	Alignment	not modelled	19.3	18	<b>PDB header:</b> transferase <b>Chain:</b> D: <b>PDB Molecule:</b> probable transaldolase; <b>PDBTitle:</b> transaldolase from thermoplasma acidophilum in complex with d-fructose2 6-phosphate schiff-base intermediate
70	<a href="#">c2eaoA_</a>	Alignment	not modelled	18.9	25	<b>PDB header:</b> signaling protein, transferase <b>Chain:</b> A: <b>PDB Molecule:</b> ephrin type-b receptor 1; <b>PDBTitle:</b> solution structure of the c-terminal sam-domain of mouse2 ephrin type-b receptor 1 precursor (ec 2.7.1.112)
71	<a href="#">d2j9ga2</a>	Alignment	not modelled	18.8	37	<b>Fold:</b> PreATP-grasp domain <b>Superfamily:</b> PreATP-grasp domain <b>Family:</b> BC N-terminal domain-like
72	<a href="#">c2jziB_</a>	Alignment	not modelled	18.8	36	<b>PDB header:</b> metal binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> serine/threonine-protein phosphatase 2b <b>PDBTitle:</b> structure of calmodulin complexed with the calmodulin2 binding domain of calcineurin
73	<a href="#">c2lweA_</a>	Alignment	not modelled	18.6	20	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> probable atp-dependent rna helicase ddx58; <b>PDBTitle:</b> solution structure of mutant (t170e) second card of human rig-i
74	<a href="#">c1eg4A_</a>	Alignment	not modelled	18.5	17	<b>PDB header:</b> structural protein <b>Chain:</b> A: <b>PDB Molecule:</b> dystrophin; <b>PDBTitle:</b> structure of a dystrophin ww domain fragment in complex2 with a beta-dystroglycan peptide
75	<a href="#">c2b1uA_</a>	Alignment	not modelled	18.4	30	<b>PDB header:</b> metal binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> calmodulin-like protein 5; <b>PDBTitle:</b> solution structure of calmodulin-like skin protein c2 terminal domain
76	<a href="#">c2ebuA_</a>	Alignment	not modelled	18.2	12	<b>PDB header:</b> replication <b>Chain:</b> A: <b>PDB Molecule:</b> replication factor c subunit 1; <b>PDBTitle:</b> solution structure of the brct domain from human2 replication factor c large subunit 1
77	<a href="#">c4q5uC_</a>	Alignment	not modelled	18.0	38	<b>PDB header:</b> calcium binding protein/protein binding <b>Chain:</b> C: <b>PDB Molecule:</b> serine/threonine-protein phosphatase 2b catalytic subunit <b>PDBTitle:</b> structure of calmodulin bound to its recognition site from calcineurin
78	<a href="#">c2obnA_</a>	Alignment	not modelled	18.0	23	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical protein; <b>PDBTitle:</b> crystal structure of a duf1611 family protein (ava_3511) from anaebacteria2 variabilis atcc 29413 at 2.30 a resolution
79	<a href="#">c5zrxB_</a>	Alignment	not modelled	17.6	16	<b>PDB header:</b> protein binding <b>Chain:</b> B: <b>PDB Molecule:</b> phosphatidylinositol 3,4,5-trisphosphate 5-phosphatase 2,

						<b>PDBTitle:</b> crystal structure of epha2/ship2 complex <b>PDB header:</b> ribosome <b>Chain:</b> 1: <b>PDB Molecule:</b> mitoribosomal protein bl28m, mrpl28; <b>PDBTitle:</b> structure of the large subunit of the mammalian mitoribosome, part 12 of 2
80	<a href="#">c4v191_</a>	Alignment	not modelled	17.6	6	
81	<a href="#">c1cjbB_</a>	Alignment	not modelled	17.2	21	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> protein (cytosolic phospholipase a2); <b>PDBTitle:</b> human cytosolic phospholipase a2
82	<a href="#">c2kdhA_</a>	Alignment	not modelled	17.1	16	<b>PDB header:</b> structural protein <b>Chain:</b> A: <b>PDB Molecule:</b> troponin c, slow skeletal and cardiac muscles; <b>PDBTitle:</b> the solution structure of human cardiac troponin c in2 complex with the green tea polyphenol; (-)-3 epigallocatechin-3-gallate
83	<a href="#">d1wi3a_</a>	Alignment	not modelled	16.8	14	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Homeodomain
84	<a href="#">c2o7pA_</a>	Alignment	not modelled	16.8	38	<b>PDB header:</b> hydrolase, oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> riboflavin biosynthesis protein ribd; <b>PDBTitle:</b> the crystal structure of ribd from escherichia coli in complex with2 the oxidised nadp+ cofactor in the active site of the reductase3 domain
85	<a href="#">c2jhnB_</a>	Alignment	not modelled	16.4	22	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> 3-methyladenine dna-glycosylase; <b>PDBTitle:</b> 3-methyladenine dna-glycosylase from archaeoglobus fulgidus
86	<a href="#">d1cja2</a>	Alignment	not modelled	15.9	21	<b>Fold:</b> FabD/lysophospholipase-like <b>Superfamily:</b> FabD/lysophospholipase-like <b>Family:</b> Lysophospholipase
87	<a href="#">c5eyvB_</a>	Alignment	not modelled	15.9	12	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> adenylosuccinate lyase; <b>PDBTitle:</b> crystal structure of adenylosuccinate lyase from schistosoma mansoni2 in apo form.
88	<a href="#">d2opoa1</a>	Alignment	not modelled	15.8	15	<b>Fold:</b> EF Hand-like <b>Superfamily:</b> EF-hand <b>Family:</b> Polcalcin
89	<a href="#">c5i2oA_</a>	Alignment	not modelled	15.7	9	<b>PDB header:</b> metal binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> ef-hand domain-containing protein d2; <b>PDBTitle:</b> structure of ef-hand containing protein
90	<a href="#">d1np8a_</a>	Alignment	not modelled	15.7	12	<b>Fold:</b> EF Hand-like <b>Superfamily:</b> EF-hand <b>Family:</b> Penta-EF-hand proteins
91	<a href="#">c2wtgA_</a>	Alignment	not modelled	15.7	14	<b>PDB header:</b> oxygen transport <b>Chain:</b> A: <b>PDB Molecule:</b> globin-like protein; <b>PDBTitle:</b> high resolution 3d structure of c.elegans globin-like2 protein glb-1
92	<a href="#">c4i2yB_</a>	Alignment	not modelled	15.5	22	<b>PDB header:</b> fluorescent protein <b>Chain:</b> B: <b>PDB Molecule:</b> rgeco1; <b>PDBTitle:</b> crystal structure of the genetically encoded calcium indicator rgeco1
93	<a href="#">d1wx0a1</a>	Alignment	not modelled	15.5	24	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Aldolase <b>Family:</b> Class I aldolase
94	<a href="#">c5izrC_</a>	Alignment	not modelled	15.4	28	<b>PDB header:</b> hydrolase/hydrolase inhibitor <b>Chain:</b> C: <b>PDB Molecule:</b> cytosolic phospholipase a2 delta; <b>PDBTitle:</b> human givd cytosolic phospholipase a2 in complex with methyl gamma-2 linolenyl fluorophosphonate inhibitor and terbium chloride
95	<a href="#">c2eeeA_</a>	Alignment	not modelled	15.3	23	<b>PDB header:</b> gene regulation <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein c6orf130; <b>PDBTitle:</b> solution structure of the a1pp domain from human protein2 c6orf130
96	<a href="#">d1l7ba_</a>	Alignment	not modelled	15.1	18	<b>Fold:</b> BRCT domain <b>Superfamily:</b> BRCT domain <b>Family:</b> DNA ligase
97	<a href="#">d1hlqa_</a>	Alignment	not modelled	15.0	29	<b>Fold:</b> HIPIP (high potential iron protein) <b>Superfamily:</b> HIPIP (high potential iron protein) <b>Family:</b> HIPIP (high potential iron protein)
98	<a href="#">c1ozsA_</a>	Alignment	not modelled	14.8	17	<b>PDB header:</b> structural protein <b>Chain:</b> A: <b>PDB Molecule:</b> troponin c, slow skeletal and cardiac muscles; <b>PDBTitle:</b> c-domain of human cardiac troponin c in complex with the2 inhibitory region of human cardiac troponin i
99	<a href="#">d1a77a1</a>	Alignment	not modelled	14.5	28	<b>Fold:</b> SAM domain-like <b>Superfamily:</b> 5' to 3' exonuclease, C-terminal subdomain <b>Family:</b> 5' to 3' exonuclease, C-terminal subdomain