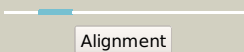
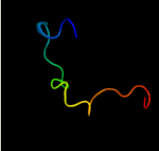
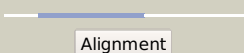

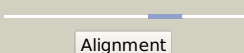

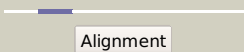
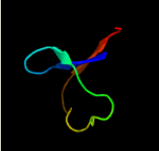
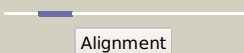
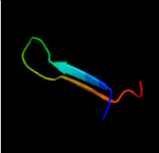
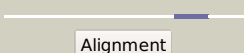


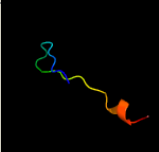
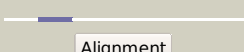
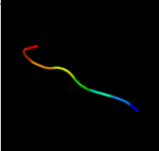
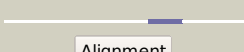

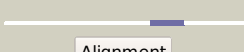

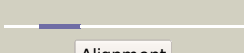

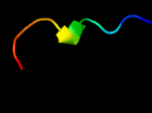
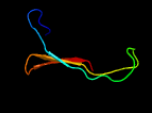
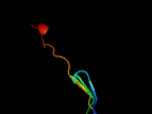




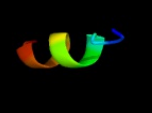
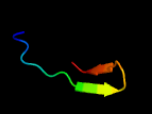


# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0349 (-) _418949_419608
Date	Tue Jul 23 14:50:42 BST 2019
Unique Job ID	0eb9ccc12b748bd0

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c5abvf_</a>	 Alignment		32.6	30	<b>PDB header:</b> translation <b>Chain:</b> F; <b>PDB Molecule:</b> gh11071p; <b>PDBTitle:</b> complex of d. melanogaster eif4e with the 4e-binding2 protein mexkli
2	<a href="#">c5wygC_</a>	 Alignment		23.5	17	<b>PDB header:</b> hydrolase <b>Chain:</b> C; <b>PDB Molecule:</b> probable endoribonuclease mazf7; <b>PDBTitle:</b> the crystal structure of the apo form of mtb mazf
3	<a href="#">c1sfeA_</a>	 Alignment		20.9	8	<b>PDB header:</b> dna-binding protein <b>Chain:</b> A; <b>PDB Molecule:</b> ada o6-methylguanine-dna methyltransferase; <b>PDBTitle:</b> ada o6-methylguanine-dna methyltransferase from escherichia coli
4	<a href="#">d1wxma1</a>	 Alignment		16.9	32	<b>Fold:</b> beta-Grasp (ubiquitin-like) <b>Superfamily:</b> Ubiquitin-like <b>Family:</b> Ras-binding domain, RBD
5	<a href="#">d1o12a1</a>	 Alignment		14.3	35	<b>Fold:</b> Composite domain of metallo-dependent hydrolases <b>Superfamily:</b> Composite domain of metallo-dependent hydrolases <b>Family:</b> N-acetylglucosamine-6-phosphate deacetylase, NagA
6	<a href="#">c4ng2E_</a>	 Alignment		13.5	24	<b>PDB header:</b> transcription regulator <b>Chain:</b> E; <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> crystal structure of lasr lbd-qsla complex from pseudomonas aeruginosa
7	<a href="#">c6ajrA_</a>	 Alignment		12.6	21	<b>PDB header:</b> dna binding protein <b>Chain:</b> A; <b>PDB Molecule:</b> uracil dna glycosylase superfamily protein; <b>PDBTitle:</b> complex form of uracil dna glycosylase x and uracil
8	<a href="#">c3g0kA_</a>	 Alignment		12.5	45	<b>PDB header:</b> ca-binding protein <b>Chain:</b> A; <b>PDB Molecule:</b> putative membrane protein; <b>PDBTitle:</b> crystal structure of a protein of unknown function with a cystatin-2 like fold (saro_2880) from novosphingobium aromaticivorans dsm at3 1.30 a resolution
9	<a href="#">c1t39A_</a>	 Alignment		12.4	28	<b>PDB header:</b> transferase/dna <b>Chain:</b> A; <b>PDB Molecule:</b> methylated-dna--protein-cysteine <b>PDBTitle:</b> human o6-alkylguanine-dna alkyltransferase covalently2 crosslinked to dna
10	<a href="#">c4bhcA_</a>	 Alignment		12.4	10	<b>PDB header:</b> transferase <b>Chain:</b> A; <b>PDB Molecule:</b> methylated-dna--protein-cysteine methyltransferase; <b>PDBTitle:</b> crystal structure of the m. tuberculosis o6-methylguanine2 methyltransferase r371 variant
11	<a href="#">c3dmqA_</a>	 Alignment		12.3	19	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> rna polymerase-associated protein rapa; <b>PDBTitle:</b> crystal structure of rapa, a swi2/snf2 protein that recycles rna2 polymerase during transcription

12	<a href="#">c2pnmA_</a>	Alignment		12.2	55	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> protease vp4; <b>PDBTitle:</b> crystal structure of vp4 protease from infectious pancreatic necrosis2 virus (ipnv) in space group p6122
13	<a href="#">c3hrqB_</a>	Alignment		11.9	19	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> B: <b>PDB Molecule:</b> aflatoxin biosynthesis polyketide synthase; <b>PDBTitle:</b> the product template domain from pksa with palmitate bound
14	<a href="#">c2v7sA_</a>	Alignment		11.6	23	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> probable conserved lipoprotein lppa; <b>PDBTitle:</b> crystal structure of the putative lipoprotein lppa from2 mycobacterium tuberculosis
15	<a href="#">c5vwxD_</a>	Alignment		11.3	36	<b>PDB header:</b> apoptosis <b>Chain:</b> D: <b>PDB Molecule:</b> bcl-2-like protein 11; <b>PDBTitle:</b> bak core latch dimer in complex with bim-h0-h3glt
16	<a href="#">c5vwxB_</a>	Alignment		11.3	36	<b>PDB header:</b> apoptosis <b>Chain:</b> B: <b>PDB Molecule:</b> bcl-2-like protein 11; <b>PDBTitle:</b> bak core latch dimer in complex with bim-h0-h3glt
17	<a href="#">c3j38V_</a>	Alignment		11.1	19	<b>PDB header:</b> ribosome <b>Chain:</b> V: <b>PDB Molecule:</b> 40s ribosomal protein s21; <b>PDBTitle:</b> structure of the d. melanogaster 40s ribosomal proteins
18	<a href="#">c5jnbG_</a>	Alignment		11.0	64	<b>PDB header:</b> transferase <b>Chain:</b> G: <b>PDB Molecule:</b> rnp (rrm rna binding domain) containing; <b>PDBTitle:</b> structure of gld-2/rnp-8 complex
19	<a href="#">c3qx3B_</a>	Alignment		10.6	29	<b>PDB header:</b> isomerase/dna/isomerase inhibitor <b>Chain:</b> B: <b>PDB Molecule:</b> dna topoisomerase 2-beta; <b>PDBTitle:</b> human topoisomerase iibeta in complex with dna and etoposide
20	<a href="#">c3l4gL_</a>	Alignment		10.3	20	<b>PDB header:</b> ligase <b>Chain:</b> L: <b>PDB Molecule:</b> phenylalanyl-trna synthetase beta chain; <b>PDBTitle:</b> crystal structure of homo sapiens cytoplasmic phenylalanyl-trna2 synthetase
21	<a href="#">d1sfea1</a>	Alignment	not modelled	10.3	8	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Methylated DNA-protein cysteine methyltransferase, C-terminal domain <b>Family:</b> Methylated DNA-protein cysteine methyltransferase, C-terminal domain
22	<a href="#">c5yhA_</a>	Alignment	not modelled	10.2	38	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized conserved protein yiim; <b>PDBTitle:</b> crystal structure of yiim from geobacillus stearothermophilus
23	<a href="#">c5jnbE_</a>	Alignment	not modelled	9.9	64	<b>PDB header:</b> transferase <b>Chain:</b> E: <b>PDB Molecule:</b> rnp (rrm rna binding domain) containing; <b>PDBTitle:</b> structure of gld-2/rnp-8 complex
24	<a href="#">c3izbT_</a>	Alignment	not modelled	9.6	22	<b>PDB header:</b> ribosome <b>Chain:</b> T: <b>PDB Molecule:</b> 40s ribosomal protein rps21 (s21e); <b>PDBTitle:</b> localization of the small subunit ribosomal proteins into a 6.1 a2 cryo-em map of saccharomyces cerevisiae translating 80s ribosome
25	<a href="#">c4xhcB_</a>	Alignment	not modelled	9.6	34	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> alpha-l-rhamnosidase; <b>PDBTitle:</b> rhamnosidase from klebsiella oxytoca with rhamnose bound
26	<a href="#">c4zyeA_</a>	Alignment	not modelled	9.6	16	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> methylated-dna--protein-cysteine methyltransferase; <b>PDBTitle:</b> crystal structure of sulfolobus solfataricus o6-methylguanine2 methyltransferase
27	<a href="#">c1wrjA_</a>	Alignment	not modelled	9.3	33	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> methylated-dna--protein-cysteine methyltransferase <b>PDBTitle:</b> crystal structure of o6-methylguanine methyltransferase2 from sulfolobus tokodaii
						<b>PDB header:</b> viral protein, rna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> non-structural protein 3 of replicase

28	<a href="#">c2k87A_</a>	Alignment	not modelled	9.0	20	polyprotein 1a; <b>PDBTitle:</b> nmr structure of a putative rna binding protein (sars1) from sars2 coronavirus <b>PDB header:</b> ribosome
29	<a href="#">c2xznZ_</a>	Alignment	not modelled	8.8	19	<b>PDBTitle:</b> crystal structure of the eukaryotic 40s ribosomal2 subunit in complex with initiation factor 1. this file3 contains the 40s subunit and initiation factor for4 molecule 2
30	<a href="#">d1o65a_</a>	Alignment	not modelled	8.7	36	<b>Fold:</b> PK beta-barrel domain-like <b>Superfamily:</b> PK beta-barrel domain-like <b>Family:</b> MOSCO (MOCO sulphurase C-terminal) domain
31	<a href="#">c2g7hA_</a>	Alignment	not modelled	8.6	14	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> methylated-dna--protein-cysteine <b>PDBTitle:</b> structure of an o6-methylguanine dna methyltransferase from2 methanococcus jannaschii (mj1529)
32	<a href="#">d2igsa1</a>	Alignment	not modelled	8.2	55	<b>Fold:</b> Lysozyme-like <b>Superfamily:</b> Lysozyme-like <b>Family:</b> PA2222-like
33	<a href="#">c3iz6T_</a>	Alignment	not modelled	8.2	25	<b>PDB header:</b> ribosome <b>Chain:</b> T: <b>PDB Molecule:</b> 40s ribosomal protein s21 (s21e); <b>PDBTitle:</b> localization of the small subunit ribosomal proteins into a 5.5 a2 cryo-em map of triticum aestivum translating 80s ribosome
34	<a href="#">c2qzbB_</a>	Alignment	not modelled	8.1	67	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> uncharacterized protein yfey; <b>PDBTitle:</b> crystal structure of the uncharacterized protein yfey from escherichia2 coli
35	<a href="#">c1mgtA_</a>	Alignment	not modelled	8.0	27	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> protein (o6-methylguanine-dna methyltransferase); <b>PDBTitle:</b> crystal structure of o6-methylguanine-dna methyltransferase from2 hyperthermophilic archaeon pyrococcus kodakaraensis strain kod1
36	<a href="#">c3fh1A_</a>	Alignment	not modelled	7.8	27	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized ntf2-like protein; <b>PDBTitle:</b> crystal structure of a ntf2-like protein of unknown function (mll8193)2 from mesorhizobium loti at 1.60 a resolution
37	<a href="#">c3zeyR_</a>	Alignment	not modelled	7.7	42	<b>PDB header:</b> ribosome <b>Chain:</b> R: <b>PDB Molecule:</b> 40s ribosomal protein s21, putative; <b>PDBTitle:</b> high-resolution cryo-electron microscopy structure of the trypanosoma2 brucei ribosome
38	<a href="#">c6fviA_</a>	Alignment	not modelled	7.5	50	<b>PDB header:</b> cell cycle <b>Chain:</b> A: <b>PDB Molecule:</b> centrosomal protein of 192 kda; <b>PDBTitle:</b> ash / papd-like domain of human cep192 (papd-like domain 7)
39	<a href="#">c5a9qB_</a>	Alignment	not modelled	7.3	13	<b>PDB header:</b> transport protein <b>Chain:</b> B: <b>PDB Molecule:</b> nuclear pore complex protein nup155; <b>PDBTitle:</b> human nuclear pore complex
40	<a href="#">c2wl2B_</a>	Alignment	not modelled	7.1	43	<b>PDB header:</b> isomerase <b>Chain:</b> B: <b>PDB Molecule:</b> dna gyrase subunit a; <b>PDBTitle:</b> crystal structure of n-terminal domain of gyra with the2 antibiotic simocyclinone d8
41	<a href="#">d1nosa_</a>	Alignment	not modelled	7.1	29	<b>Fold:</b> Nitric oxide (NO) synthase oxygenase domain <b>Superfamily:</b> Nitric oxide (NO) synthase oxygenase domain <b>Family:</b> Nitric oxide (NO) synthase oxygenase domain
42	<a href="#">d1a21a2</a>	Alignment	not modelled	7.1	15	<b>Fold:</b> Immunoglobulin-like beta-sandwich <b>Superfamily:</b> Fibronectin type III <b>Family:</b> Fibronectin type III
43	<a href="#">d2cg7a2</a>	Alignment	not modelled	7.0	55	<b>Fold:</b> Fnl-like domain <b>Superfamily:</b> Fnl-like domain <b>Family:</b> Fibronectin type I module
44	<a href="#">c4j7bC_</a>	Alignment	not modelled	6.9	20	<b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> 205 kda microtubule-associated protein; <b>PDBTitle:</b> crystal structure of polo-like kinase 1
45	<a href="#">c4j7bF_</a>	Alignment	not modelled	6.9	20	<b>PDB header:</b> transferase <b>Chain:</b> F: <b>PDB Molecule:</b> 205 kda microtubule-associated protein; <b>PDBTitle:</b> crystal structure of polo-like kinase 1
46	<a href="#">c5oqqD_</a>	Alignment	not modelled	6.9	40	<b>PDB header:</b> cell cycle <b>Chain:</b> D: <b>PDB Molecule:</b> condensin complex subunit 2; <b>PDBTitle:</b> crystal structure of the s. cerevisiae condensin ycg1-brn1 subcomplex
47	<a href="#">c5xyiV_</a>	Alignment	not modelled	6.8	19	<b>PDB header:</b> ribosome <b>Chain:</b> V: <b>PDB Molecule:</b> 40s ribosomal protein s21; <b>PDBTitle:</b> small subunit of trichomonas vaginalis ribosome
48	<a href="#">c3rafA_</a>	Alignment	not modelled	6.7	36	<b>PDB header:</b> isomerase/dna/antibiotic <b>Chain:</b> A: <b>PDB Molecule:</b> dna topoisomerase 4 subunit a; <b>PDBTitle:</b> quinazolinodione-dna cleavage complex of type iv topoisomerase from s.2 pneumoniae
49	<a href="#">d1vk8a_</a>	Alignment	not modelled	6.6	12	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> MTH1187/YkoF-like <b>Family:</b> MTH1187-like
50	<a href="#">d1pk8a1</a>	Alignment	not modelled	6.5	24	<b>Fold:</b> PreATP-grasp domain <b>Superfamily:</b> PreATP-grasp domain <b>Family:</b> Synapsin domain
51	<a href="#">c4hedA_</a>	Alignment	not modelled	6.5	67	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> zebrafish chemokine cx11
52	<a href="#">d2csua2</a>	Alignment	not modelled	6.4	22	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Succinyl-CoA synthetase domains <b>Family:</b> Succinyl-CoA synthetase domains
53	<a href="#">c3ifzA_</a>	Alignment	not modelled	6.4	36	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> dna gyrase subunit a; <b>PDBTitle:</b> crystal structure of the first part of the mycobacterium tuberculosis2 dna gyrase reaction core: the breakage and reunion domain at 2.7 a3 resolution

54	<a href="#">c2inrA_</a>	Alignment	not modelled	6.3	29	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> dna topoisomerase 4 subunit a; <b>PDBTitle:</b> crystal structure of a 59 kda fragment of topoisomerase iv subunit a2 (grla) from staphylococcus aureus
55	<a href="#">c3uepB_</a>	Alignment	not modelled	6.3	19	<b>PDB header:</b> protein transport <b>Chain:</b> B: <b>PDB Molecule:</b> yscq-c, type iii secretion protein; <b>PDBTitle:</b> crystal structure of yscq-c from yersinia pseudotuberculosis
56	<a href="#">c3smaD_</a>	Alignment	not modelled	6.3	17	<b>PDB header:</b> transferase <b>Chain:</b> D: <b>PDB Molecule:</b> frfbf; <b>PDBTitle:</b> a new n-acetyltransferase fold in the structure and mechanism of the2 phosphonate biosynthetic enzyme frfbf
57	<a href="#">c3r0bC_</a>	Alignment	not modelled	6.1	55	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> yav vp4; <b>PDBTitle:</b> crystal structure of yellowtail ascites virus vp4 protease with a2 wild-type active site reveals acyl-enzyme complexes and product3 complexes.
58	<a href="#">c4iikA_</a>	Alignment	not modelled	6.0	40	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> adenosine monophosphate-protein hydrolase sidd; <b>PDBTitle:</b> legionella pneumophila effector
59	<a href="#">d1qnta1</a>	Alignment	not modelled	6.0	27	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Methylated DNA-protein cysteine methyltransferase, C-terminal domain <b>Family:</b> Methylated DNA-protein cysteine methyltransferase, C-terminal domain
60	<a href="#">c3gx4X_</a>	Alignment	not modelled	6.0	36	<b>PDB header:</b> dna binding protein/dna <b>Chain:</b> X: <b>PDB Molecule:</b> alkyltransferase-like protein 1; <b>PDBTitle:</b> crystal structure analysis of s. pombe atl in complex with dna
61	<a href="#">c2kxqB_</a>	Alignment	not modelled	5.8	58	<b>PDB header:</b> protein binding <b>Chain:</b> B: <b>PDB Molecule:</b> smad7 py motif containing peptide; <b>PDBTitle:</b> solution structure of smurf2 ww2 and ww3 bound to smad7 py motif2 containing peptide
62	<a href="#">c2dijB_</a>	Alignment	not modelled	5.8	58	<b>PDB header:</b> ligase/signaling protein <b>Chain:</b> B: <b>PDB Molecule:</b> mothers against decapentaplegic homolog 7; <b>PDBTitle:</b> solution structure of smurf2 ww3 domain-smad7 py peptide2 complex
63	<a href="#">d1s28a_</a>	Alignment	not modelled	5.8	18	<b>Fold:</b> Secretion chaperone-like <b>Superfamily:</b> Type III secretory system chaperone-like <b>Family:</b> Type III secretory system chaperone
64	<a href="#">c2akwB_</a>	Alignment	not modelled	5.7	41	<b>PDB header:</b> ligase <b>Chain:</b> B: <b>PDB Molecule:</b> phenylalanyl-trna synthetase beta chain; <b>PDBTitle:</b> crystal structure of t.thermophilus phenylalanyl-trna synthetase2 complexed with p-cl-phenylalanine
65	<a href="#">d1ylxa1</a>	Alignment	not modelled	5.6	29	<b>Fold:</b> N domain of copper amine oxidase-like <b>Superfamily:</b> GK1464-like <b>Family:</b> GK1464-like
66	<a href="#">d2ix0a3</a>	Alignment	not modelled	5.6	48	<b>Fold:</b> OB-fold <b>Superfamily:</b> Nucleic acid-binding proteins <b>Family:</b> Cold shock DNA-binding domain-like
67	<a href="#">c5lc5a_</a>	Alignment	not modelled	5.6	56	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> snadh-ubiquinone oxidoreductase chain 3; <b>PDBTitle:</b> structure of mammalian respiratory complex i, class2
68	<a href="#">d1kkeal</a>	Alignment	not modelled	5.6	67	<b>Fold:</b> Triple beta-spiral <b>Superfamily:</b> Fibre shaft of virus attachment proteins <b>Family:</b> Reovirus attachment protein sigma 1
69	<a href="#">c5hk3B_</a>	Alignment	not modelled	5.5	16	<b>PDB header:</b> hydrolase/dna <b>Chain:</b> B: <b>PDB Molecule:</b> endoribonuclease mazf6; <b>PDBTitle:</b> crystal structure of m. tuberculosis mazf-mt3 t52d-f62d mutant in2 complex with dna
70	<a href="#">c6eg3A_</a>	Alignment	not modelled	5.5	28	<b>PDB header:</b> hydrolase/hydrolase inhibitor <b>Chain:</b> A: <b>PDB Molecule:</b> maltose/maltodextrin-binding periplasmic protein,probable <b>PDBTitle:</b> crystal structure of human brm in kplx with compound 15
71	<a href="#">d1ab4a_</a>	Alignment	not modelled	5.5	43	<b>Fold:</b> Type II DNA topoisomerase <b>Superfamily:</b> Type II DNA topoisomerase <b>Family:</b> Type II DNA topoisomerase
72	<a href="#">c3ue9A_</a>	Alignment	not modelled	5.4	32	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> adenylosuccinate synthetase; <b>PDBTitle:</b> crystal structure of adenylosuccinate synthetase (ampsase) (pura) from2 burkholderia thailandensis
73	<a href="#">c3hiuB_</a>	Alignment	not modelled	5.4	30	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> the crystal structure of protein (xcc3681) from xanthomonas2 campestris pv. campestris str. atcc 33913
74	<a href="#">c3e5aB_</a>	Alignment	not modelled	5.4	50	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> targeting protein for xklp2; <b>PDBTitle:</b> crystal structure of aurora a in complex with vx-680 and tpx2
75	<a href="#">d2nyqa1</a>	Alignment	not modelled	5.3	16	<b>Fold:</b> TTHA0583/YokD-like <b>Superfamily:</b> TTHA0583/YokD-like <b>Family:</b> Aminoglycoside 3-N-acetyltransferase-like
76	<a href="#">c3mwyW_</a>	Alignment	not modelled	5.3	26	<b>PDB header:</b> hydrolase <b>Chain:</b> W: <b>PDB Molecule:</b> chromo domain-containing protein 1; <b>PDBTitle:</b> crystal structure of the chromodomain-atpase portion of the yeast chd12 chromatin remodeler
77	<a href="#">c5hzrA_</a>	Alignment	not modelled	5.3	26	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> snf2-family atp dependent chromatin remodeling factor like <b>PDBTitle:</b> crystal structure of mtsnf2
78	<a href="#">d1jcb2</a>	Alignment	not modelled	5.2	40	<b>Fold:</b> Putative DNA-binding domain <b>Superfamily:</b> Putative DNA-binding domain <b>Family:</b> Domains B1 and B5 of PheRS-beta, PheT
						<b>PDB header:</b> motor protein/transport protein

79	<a href="#">c4l18A_</a>	Alignment	not modelled	5.2	18	<b>Chain:</b> A: <b>PDB Molecule:</b> myosin-4; <b>PDBTitle:</b> complex of carboxy terminal domain of myo4p and she3p middle fragment
80	<a href="#">c4z2cA_</a>	Alignment	not modelled	5.2	43	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> dna gyrase subunit a; <b>PDBTitle:</b> quinolone(moxifloxacin)-dna cleavage complex of gyrase from s.2 pneumoniae
81	<a href="#">d1z63a1</a>	Alignment	not modelled	5.1	26	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> Tandem AAA-ATPase domain