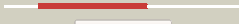
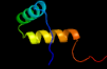











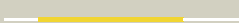

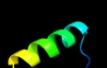






# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2104c (- )_2364535_2364789
Date	Mon Aug 5 13:25:22 BST 2019
Unique Job ID	dcff93639e4bbe10

Detailed template  
information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c5x3tA_</a>	 Alignment		95.0	31	<b>PDB header:</b> antitoxin/toxin <b>Chain:</b> A: <b>PDB Molecule:</b> antitoxin vapb26; <b>PDBTitle:</b> vapbc from mycobacterium tuberculosis
2	<a href="#">c2bj3D_</a>	 Alignment		92.3	19	<b>PDB header:</b> transcription <b>Chain:</b> D: <b>PDB Molecule:</b> nickel responsive regulator; <b>PDBTitle:</b> nikt-apo
3	<a href="#">c1q5vB_</a>	 Alignment		89.8	31	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> nickel responsive regulator; <b>PDBTitle:</b> apo-nikt
4	<a href="#">d2bj7a1</a>	 Alignment		88.5	19	<b>Fold:</b> Ribbon-helix-helix <b>Superfamily:</b> Ribbon-helix-helix <b>Family:</b> CopG-like
5	<a href="#">c2ca9B_</a>	 Alignment		87.5	22	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> putative nickel-responsive regulator; <b>PDBTitle:</b> apo-nikt from helicobacter pylori in closed trans-2 conformation
6	<a href="#">d2hzaa1</a>	 Alignment		86.6	30	<b>Fold:</b> Ribbon-helix-helix <b>Superfamily:</b> Ribbon-helix-helix <b>Family:</b> CopG-like
7	<a href="#">d2hza1</a>	 Alignment		85.5	30	<b>Fold:</b> Ribbon-helix-helix <b>Superfamily:</b> Ribbon-helix-helix <b>Family:</b> CopG-like
8	<a href="#">d2bsqe1</a>	 Alignment		76.4	15	<b>Fold:</b> Ribbon-helix-helix <b>Superfamily:</b> Ribbon-helix-helix <b>Family:</b> Trafficking protein A-like
9	<a href="#">d1p94a_</a>	 Alignment		76.3	18	<b>Fold:</b> Ribbon-helix-helix <b>Superfamily:</b> Ribbon-helix-helix <b>Family:</b> CopG-like
10	<a href="#">c2h1oH_</a>	 Alignment		71.9	15	<b>PDB header:</b> gene regulation/dna complex <b>Chain:</b> H: <b>PDB Molecule:</b> trafficking protein a; <b>PDBTitle:</b> structure of fitab bound to ir36 dna fragment
11	<a href="#">c6noyB_</a>	 Alignment		70.4	22	<b>PDB header:</b> structural protein <b>Chain:</b> B: <b>PDB Molecule:</b> maintenance of carboxysome positioning b protein, mcsb; <b>PDBTitle:</b> structure of cyanothecce mcdb

12	<a href="#">c2k5jB_</a>	Alignment		69.8	17	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> uncharacterized protein yiif; <b>PDBTitle:</b> solution structure of protein yiif from shigella flexneri2 serotype 5b (strain 8401) . northeast structural genomics3 consortium target sft1
13	<a href="#">c5yrzC_</a>	Alignment		54.8	29	<b>PDB header:</b> antitoxin/hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> hicb; <b>PDBTitle:</b> toxin-antitoxin complex from streptococcus pneumoniae
14	<a href="#">c6a7vU_</a>	Alignment		53.4	28	<b>PDB header:</b> toxin/antitoxin <b>Chain:</b> U: <b>PDB Molecule:</b> antitoxin vapp11; <b>PDBTitle:</b> crystal structure of mycobacterium tuberculosis vapbc11 toxin-2 antitoxin complex
15	<a href="#">c6g1nB_</a>	Alignment		53.3	18	<b>PDB header:</b> antitoxin <b>Chain:</b> B: <b>PDB Molecule:</b> antitoxin hicb; <b>PDBTitle:</b> crystal structure of the burkholderia pseudomallei antitoxin hicb
16	<a href="#">c3kk4B_</a>	Alignment		46.3	13	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> uncharacterized protein bp1543; <b>PDBTitle:</b> uncharacterized protein bp1543 from bordetella pertussis tohama i
17	<a href="#">c2k29A_</a>	Alignment		41.6	16	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> antitoxin relb; <b>PDBTitle:</b> structure of the dbd domain of e. coli antitoxin relb
18	<a href="#">c4p7dA_</a>	Alignment		38.7	9	<b>PDB header:</b> toxin <b>Chain:</b> A: <b>PDB Molecule:</b> antitoxin hicb3; <b>PDBTitle:</b> antitoxin hicb3 crystal structure
19	<a href="#">d2cpga_</a>	Alignment		33.2	24	<b>Fold:</b> Ribbon-helix-helix <b>Superfamily:</b> Ribbon-helix-helix <b>Family:</b> CopG-like
20	<a href="#">c1ea4K_</a>	Alignment		33.2	24	<b>PDB header:</b> gene regulation/dna <b>Chain:</b> K: <b>PDB Molecule:</b> transcriptional repressor copg; <b>PDBTitle:</b> transcriptional repressor copg/22bp dsdna complex
21	<a href="#">c6iyaD_</a>	Alignment	not modelled	30.2	28	<b>PDB header:</b> antitoxin <b>Chain:</b> D: <b>PDB Molecule:</b> transcriptional regulator copg family; <b>PDBTitle:</b> structure of the dna binding domain of antitoxin copaso
22	<a href="#">c4wyhA_</a>	Alignment	not modelled	25.2	21	<b>PDB header:</b> replication <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> crystal structure of prfx from the hyperthermophilic archaeon2 sulfolobus solfataricus
23	<a href="#">d2b4jc1</a>	Alignment	not modelled	22.4	16	<b>Fold:</b> N-cbl like <b>Superfamily:</b> HIV integrase-binding domain <b>Family:</b> HIV integrase-binding domain
24	<a href="#">c1z9eA_</a>	Alignment	not modelled	22.2	16	<b>PDB header:</b> protein binding/transcription <b>Chain:</b> A: <b>PDB Molecule:</b> pc4 and sfrs1 interacting protein 2; <b>PDBTitle:</b> solution structure of the hiv-1 integrase-binding domain in2 ledgf/p75
25	<a href="#">c6bwqB_</a>	Alignment	not modelled	22.1	9	<b>PDB header:</b> metal binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> pyridinium-3,5-bisthiocarboxylic acid mononucleotide nickel <b>PDBTitle:</b> larc2, the c-terminal domain of a cyclometallase involved in the2 synthesis of the npn cofactor of lactate racemase, in complex with3 mnctp
26	<a href="#">c4pg8B_</a>	Alignment	not modelled	21.1	42	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> homoserine dehydrogenase; <b>PDBTitle:</b> crystal structure of s. aureus homoserine dehydrogenase at ph8.5
27	<a href="#">c5ux1D_</a>	Alignment	not modelled	19.9	20	<b>PDB header:</b> lyase <b>Chain:</b> D: <b>PDB Molecule:</b> trna-(ms(2)io(6)a)-hydroxylase-like; <b>PDBTitle:</b> protein 43 with aldehyde deformylating oxygenase activity from2 synechococcus
28	<a href="#">d1vhib_</a>	Alignment	not modelled	19.6	38	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> Viral DNA-binding domain <b>Family:</b> Viral DNA-binding domain

29	<a href="#">c6qeqD</a>	Alignment	not modelled	18.3	18	<b>PDB header:</b> dna binding protein <b>Chain:</b> D: <b>PDB Molecule:</b> pcff; <b>PDBTitle:</b> pcff from enterococcus faecalis pcf10
30	<a href="#">c2mntA</a>	Alignment	not modelled	18.0	16	<b>PDB header:</b> transferase/protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> histone-lysine n-methyltransferase 2a, pc4 and sfrs1- <b>PDBTitle:</b> solution structure of mll-ibd complex
31	<a href="#">d1b3ta</a>	Alignment	not modelled	16.7	38	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> Viral DNA-binding domain <b>Family:</b> Viral DNA-binding domain
32	<a href="#">c6emoA</a>	Alignment	not modelled	16.6	16	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> pc4 and sfrs1-interacting protein,ledgf/p75 ibd-jpo2 m1; <b>PDBTitle:</b> solution structure of the ledgf/p75 ibd - jpo2 (aa 1-32) complex
33	<a href="#">c6emqA</a>	Alignment	not modelled	16.4	16	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> pc4 and sfrs1-interacting protein,histone-lysine n- <b>PDBTitle:</b> solution structure of the ledgf/p75 ibd - mll1 (aa 111-160) complex
34	<a href="#">c2mdvB</a>	Alignment	not modelled	13.9	16	<b>PDB header:</b> de novo protein <b>Chain:</b> B: <b>PDB Molecule:</b> designed protein; <b>PDBTitle:</b> nmr structure of beta alpha alpha 38
35	<a href="#">c3kxeD</a>	Alignment	not modelled	13.7	21	<b>PDB header:</b> protein binding <b>Chain:</b> D: <b>PDB Molecule:</b> antitoxin protein pard-1; <b>PDBTitle:</b> a conserved mode of protein recognition and binding in a2 pard-pare toxin-antitoxin complex
36	<a href="#">c3qf7D</a>	Alignment	not modelled	13.0	33	<b>PDB header:</b> hydrolase <b>Chain:</b> D: <b>PDB Molecule:</b> mre11; <b>PDBTitle:</b> the mre11:rad50 complex forms an atp dependent molecular clamp in dna2 double-strand break repair
37	<a href="#">c3do5A</a>	Alignment	not modelled	12.9	24	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> homoserine dehydrogenase; <b>PDBTitle:</b> crystal structure of putative homoserine dehydrogenase (np_069768.1)2 from archaeoglobus fulgidus at 2.20 a resolution
38	<a href="#">c3fxeA</a>	Alignment	not modelled	12.7	80	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> protein icmq; <b>PDBTitle:</b> crystal structure of interacting domains of icmr and icmq (seleno-2 derivative)
39	<a href="#">c4kmaA</a>	Alignment	not modelled	12.7	27	<b>PDB header:</b> protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> gm14141p; <b>PDBTitle:</b> crystal structure of drosophila suppressor of fused
40	<a href="#">c4fxeB</a>	Alignment	not modelled	12.5	16	<b>PDB header:</b> toxin/toxin inhibitor <b>Chain:</b> B: <b>PDB Molecule:</b> antitoxin relb; <b>PDBTitle:</b> crystal structure of the intact e. coli relbe toxin-antitoxin complex
41	<a href="#">c3ai9X</a>	Alignment	not modelled	12.3	17	<b>PDB header:</b> transferase <b>Chain:</b> X: <b>PDB Molecule:</b> upf0217 protein mj1640; <b>PDBTitle:</b> crystal structure of duf358 protein reveals a putative spout-class2 rrna methyltransferase
42	<a href="#">c2ejwB</a>	Alignment	not modelled	11.9	35	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> homoserine dehydrogenase; <b>PDBTitle:</b> homoserine dehydrogenase from thermus thermophilus hb8
43	<a href="#">c3mtjA</a>	Alignment	not modelled	11.2	26	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> homoserine dehydrogenase; <b>PDBTitle:</b> the crystal structure of a homoserine dehydrogenase from thiobacillus2 denitrificans to 2.15a
44	<a href="#">c6emrA</a>	Alignment	not modelled	11.2	16	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> pc4 and sfrs1-interacting protein,protein iws1 homolog; <b>PDBTitle:</b> solution structure of the ledgf/p75 ibd - iws1 (aa 446-548) complex
45	<a href="#">c4b1vM</a>	Alignment	not modelled	10.8	24	<b>PDB header:</b> structural protein <b>Chain:</b> M: <b>PDB Molecule:</b> phosphatase and actin regulator 1; <b>PDBTitle:</b> structure of the phactr1 rpel-n domain bound to g-actin
46	<a href="#">c4b1vN</a>	Alignment	not modelled	10.8	24	<b>PDB header:</b> structural protein <b>Chain:</b> N: <b>PDB Molecule:</b> phosphatase and actin regulator 1; <b>PDBTitle:</b> structure of the phactr1 rpel-n domain bound to g-actin
47	<a href="#">c2an7A</a>	Alignment	not modelled	10.8	18	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> protein pard; <b>PDBTitle:</b> solution structure of the bacterial antidote pard
48	<a href="#">c2r8rB</a>	Alignment	not modelled	10.4	48	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> sensor protein; <b>PDBTitle:</b> crystal structure of the n-terminal region (19..243) of sensor protein2 kdpp from pseudomonas syringae pv. tomato str. dc3000
49	<a href="#">c6a6xC</a>	Alignment	not modelled	10.2	19	<b>PDB header:</b> toxin <b>Chain:</b> C: <b>PDB Molecule:</b> antitoxin maze7; <b>PDBTitle:</b> the crystal structure of the mtb maze-mazf-mt9 complex
50	<a href="#">c5mwwA</a>	Alignment	not modelled	10.1	14	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> rna polymerase sigma factor siga; <b>PDBTitle:</b> sigma1.1 domain of sigmaa from bacillus subtilis
51	<a href="#">c2b0tA</a>	Alignment	not modelled	10.1	21	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> nadp isocitrate dehydrogenase; <b>PDBTitle:</b> structure of monomeric nadp isocitrate dehydrogenase
52	<a href="#">d2outa1</a>	Alignment	not modelled	10.0	24	<b>Fold:</b> LEM/SAP HeH motif <b>Superfamily:</b> Rho N-terminal domain-like <b>Family:</b> YqbF C-terminal domain-like
53	<a href="#">c2rbfB</a>	Alignment	not modelled	9.6	19	<b>PDB header:</b> oxidoreductase/dna <b>Chain:</b> B: <b>PDB Molecule:</b> bifunctional protein puta; <b>PDBTitle:</b> structure of the ribbon-helix-helix domain of escherichia coli puta2 (puta52) complexed with operator dna (o2)
54	<a href="#">d1rfma</a>	Alignment	not modelled	9.4	7	<b>Fold:</b> L-sulfolactate dehydrogenase-like <b>Superfamily:</b> L-sulfolactate dehydrogenase-like

						Family:L-sulfolactate dehydrogenase-like
55	<a href="#">d2i10a2</a>	Alignment	not modelled	9.2	11	<b>Fold:</b> Tetracyclin repressor-like, C-terminal domain <b>Superfamily:</b> Tetracyclin repressor-like, C-terminal domain <b>Family:</b> Tetracyclin repressor-like, C-terminal domain
56	<a href="#">c2c5iT</a>	Alignment	not modelled	9.0	22	<b>PDB header:</b> protein transport <b>Chain:</b> T: <b>PDB Molecule:</b> t-snare affecting a late golgi compartment <b>PDBTitle:</b> n-terminal domain of tlg1 complexed with n-terminus of 2 vps51 in distorted conformation
57	<a href="#">c6g3uA</a>	Alignment	not modelled	8.7	23	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> isocitrate dehydrogenase; <b>PDBTitle:</b> structure of pseudomonas aeruginosa isocitrate dehydrogenase, idh
58	<a href="#">d1qs0b1</a>	Alignment	not modelled	8.6	19	<b>Fold:</b> Thiamin diphosphate-binding fold (THDP-binding) <b>Superfamily:</b> Thiamin diphosphate-binding fold (THDP-binding) <b>Family:</b> Branched-chain alpha-keto acid dehydrogenase Pyr module
59	<a href="#">c6dzsD</a>	Alignment	not modelled	8.5	26	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> homoserine dehydrogenase; <b>PDBTitle:</b> mycobacterial homoserine dehydrogenase thra in complex with nadp
60	<a href="#">d1tafb</a>	Alignment	not modelled	8.4	35	<b>Fold:</b> Histone-fold <b>Superfamily:</b> Histone-fold <b>Family:</b> TBP-associated factors, TAFs
61	<a href="#">d1vkeb</a>	Alignment	not modelled	8.2	20	<b>Fold:</b> AhpD-like <b>Superfamily:</b> AhpD-like <b>Family:</b> CMD-like
62	<a href="#">c5x56A</a>	Alignment	not modelled	7.5	20	<b>PDB header:</b> photosynthesis <b>Chain:</b> A: <b>PDB Molecule:</b> photosystem ii repair protein psb27-h1, chloroplastic; <b>PDBTitle:</b> crystal structure of psb27 from arabidopsis thaliana
63	<a href="#">d1w85b1</a>	Alignment	not modelled	7.2	33	<b>Fold:</b> Thiamin diphosphate-binding fold (THDP-binding) <b>Superfamily:</b> Thiamin diphosphate-binding fold (THDP-binding) <b>Family:</b> Branched-chain alpha-keto acid dehydrogenase Pyr module
64	<a href="#">c4b1uM</a>	Alignment	not modelled	7.2	24	<b>PDB header:</b> structural protein <b>Chain:</b> M: <b>PDB Molecule:</b> phosphatase and actin regulator 1; <b>PDBTitle:</b> structure of the phacr1 rpe1 domain and rpe1 motif directed2 assemblies with g-actin reveal the molecular basis for actin binding3 cooperativity.
65	<a href="#">d1y88a1</a>	Alignment	not modelled	6.8	33	<b>Fold:</b> SAM domain-like <b>Superfamily:</b> Rad51 N-terminal domain-like <b>Family:</b> Hypothetical protein AF1548, C-terminal domain
66	<a href="#">c1rgxC</a>	Alignment	not modelled	6.7	13	<b>PDB header:</b> hormone/growth factor <b>Chain:</b> C: <b>PDB Molecule:</b> resistin; <b>PDBTitle:</b> crystal structure of resistin
67	<a href="#">c2kmfA</a>	Alignment	not modelled	6.7	26	<b>PDB header:</b> photosynthesis <b>Chain:</b> A: <b>PDB Molecule:</b> photosystem ii 11 kda protein; <b>PDBTitle:</b> solution structure of psb27 from cyanobacterial photosystem2 ii
68	<a href="#">c2n8jB</a>	Alignment	not modelled	6.6	40	<b>PDB header:</b> protein binding <b>Chain:</b> B: <b>PDB Molecule:</b> nitric oxide synthase, endothelial; <b>PDBTitle:</b> structure and 15n relaxation data of calmodulin bound to the2 endothelial nitric oxide synthase calmodulin binding domain peptide3 at physiological calcium concentration
69	<a href="#">c3c8mA</a>	Alignment	not modelled	6.5	21	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> homoserine dehydrogenase; <b>PDBTitle:</b> crystal structure of homoserine dehydrogenase from thermoplasma2 volcanium
70	<a href="#">c1niwB</a>	Alignment	not modelled	6.4	33	<b>PDB header:</b> signaling protein/oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> nitric-oxide synthase, endothelial; <b>PDBTitle:</b> crystal structure of endothelial nitric oxide synthase2 peptide bound to calmodulin
71	<a href="#">c1niwF</a>	Alignment	not modelled	6.4	33	<b>PDB header:</b> signaling protein/oxidoreductase <b>Chain:</b> F: <b>PDB Molecule:</b> nitric-oxide synthase, endothelial; <b>PDBTitle:</b> crystal structure of endothelial nitric oxide synthase2 peptide bound to calmodulin
72	<a href="#">c1niwH</a>	Alignment	not modelled	6.4	33	<b>PDB header:</b> signaling protein/oxidoreductase <b>Chain:</b> H: <b>PDB Molecule:</b> nitric-oxide synthase, endothelial; <b>PDBTitle:</b> crystal structure of endothelial nitric oxide synthase2 peptide bound to calmodulin
73	<a href="#">c1niwD</a>	Alignment	not modelled	6.4	33	<b>PDB header:</b> signaling protein/oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> nitric-oxide synthase, endothelial; <b>PDBTitle:</b> crystal structure of endothelial nitric oxide synthase2 peptide bound to calmodulin
74	<a href="#">c5zwo9</a>	Alignment	not modelled	6.3	47	<b>PDB header:</b> splicing <b>Chain:</b> 9: <b>PDB Molecule:</b> pre-mrna-splicing factor spp381; <b>PDBTitle:</b> cryo-em structure of the yeast b complex at average resolution of 3.92 angstrom
75	<a href="#">c6hs6E</a>	Alignment	not modelled	6.2	19	<b>PDB header:</b> transport protein <b>Chain:</b> E: <b>PDB Molecule:</b> type vi secretion protein impa; <b>PDBTitle:</b> c-terminal domain of the tssa component of the type vi secretion2 system from burkholderia cenocepacia
76	<a href="#">d2csba3</a>	Alignment	not modelled	6.2	44	<b>Fold:</b> SAM domain-like <b>Superfamily:</b> RuvA domain 2-like <b>Family:</b> Topoisomerase V repeat domain
77	<a href="#">c5t9jB</a>	Alignment	not modelled	6.2	39	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> flap endonuclease gen homolog 1; <b>PDBTitle:</b> crystal structure of human gen1 in complex with holliday junction dna2 in the upper interface
78	<a href="#">c4d7xA</a>	Alignment	not modelled	6.1	16	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> mediator of rna polymerase ii transcription subunit 15; <b>PDBTitle:</b> solution structure of the mediator gall11 kix domain of c.2 glabrata
79	<a href="#">c6h3pB</a>	Alignment	not modelled	6.0	18	<b>PDB header:</b> plant protein <b>Chain:</b> B: <b>PDB Molecule:</b> chorismate mutase; <b>PDBTitle:</b> crystal structure of the cytoplasmic chorismate mutase from zea mays <b>PDB header:</b> cell invasion

80	<a href="#">c6fpgG_</a>	Alignment	not modelled	6.0	14	<b>Chain:</b> G: <b>PDB Molecule:</b> chromosome 16, whole genome shotgun sequence; <b>PDBTitle:</b> structure of the ustilago maydis chorismate mutase 1 in complex with a2 zea mays kiwellin
81	<a href="#">c5avoA_</a>	Alignment	not modelled	5.9	47	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> homoserine dehydrogenase; <b>PDBTitle:</b> crystal structure of the reduced form of homoserine dehydrogenase from2 sulfolobus tokodaii.
82	<a href="#">c6m7fB_</a>	Alignment	not modelled	5.7	28	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> cucumene synthase; <b>PDBTitle:</b> wild-type cucumene synthase
83	<a href="#">c3mkqB_</a>	Alignment	not modelled	5.6	39	<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/betaprime-cop subcomplex of the copi2 vesicular coat
84	<a href="#">d2id3a2</a>	Alignment	not modelled	5.6	20	<b>Fold:</b> Tetracyclin repressor-like, C-terminal domain <b>Superfamily:</b> Tetracyclin repressor-like, C-terminal domain <b>Family:</b> Tetracyclin repressor-like, C-terminal domain
85	<a href="#">d1ebfa2</a>	Alignment	not modelled	5.6	25	<b>Fold:</b> FwdE/GAPDH domain-like <b>Superfamily:</b> Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain <b>Family:</b> Homoserine dehydrogenase-like
86	<a href="#">c3wa8B_</a>	Alignment	not modelled	5.6	6	<b>PDB header:</b> rna binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> crispr-associated protein, cse2 family; <b>PDBTitle:</b> crystal structure of m. ruber casb
87	<a href="#">c4aaiB_</a>	Alignment	not modelled	5.6	18	<b>PDB header:</b> viral protein <b>Chain:</b> B: <b>PDB Molecule:</b> orf e73; <b>PDBTitle:</b> thermostable protein from hyperthermophilic virus ssv-rh
88	<a href="#">c4a1qB_</a>	Alignment	not modelled	5.6	18	<b>PDB header:</b> viral protein <b>Chain:</b> B: <b>PDB Molecule:</b> orf e73; <b>PDBTitle:</b> solution structure of e73 protein from sulfolobus spindle-2 shaped virus ragged hills, a hyperthermophilic3 crenarchaeal virus from yellowstone national park
89	<a href="#">d1q9ja2</a>	Alignment	not modelled	5.4	19	<b>Fold:</b> CoA-dependent acyltransferases <b>Superfamily:</b> CoA-dependent acyltransferases <b>Family:</b> NRPS condensation domain (amide synthase)
90	<a href="#">d2ve8a1</a>	Alignment	not modelled	5.4	17	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> FtsK C-terminal domain-like
91	<a href="#">c1rrbA_</a>	Alignment	not modelled	5.3	21	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> raf proto-oncogene serine/threonine-protein <b>PDBTitle:</b> the ras-binding domain of raf-1 from rat, nmr, 1 structure
92	<a href="#">d1rfa_</a>	Alignment	not modelled	5.2	13	<b>Fold:</b> Resistin <b>Superfamily:</b> Resistin <b>Family:</b> Resistin