




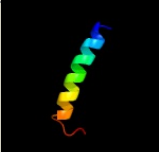





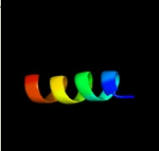



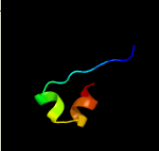
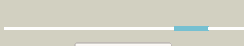
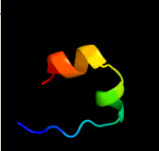



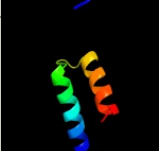


# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3195 (- )_3564361_3565779
Date	Thu Aug 8 16:20:38 BST 2019
Unique Job ID	68499f1137153a78

Detailed template  
information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c3cmnA_</a>	 Alignment		100.0	22	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> putative hydrolase; <b>PDBTitle:</b> crystal structure of a putative hydrolase with a novel fold2 from chloroflexus aurantiacus
2	<a href="#">d3cmna1</a>	 Alignment		100.0	23	<b>Fold:</b> Zincin-like <b>Superfamily:</b> Metalloproteases ("zincins"), catalytic domain <b>Family:</b> Caur0242-like
3	<a href="#">d1nkzb_</a>	 Alignment		61.1	36	<b>Fold:</b> Light-harvesting complex subunits <b>Superfamily:</b> Light-harvesting complex subunits <b>Family:</b> Light-harvesting complex subunits
4	<a href="#">c4clvB_</a>	 Alignment		54.7	16	<b>PDB header:</b> metal binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> nickel-cobalt-cadmium resistance protein nccx; <b>PDBTitle:</b> crystal structure of dodecylphosphocholine-solubilized nccx2 from cupriavidus metallidurans 31a
5	<a href="#">c4jiuA_</a>	 Alignment		48.4	26	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> proabylisin; <b>PDBTitle:</b> crystal structure of the metallopeptidase zymogen of pyrococcus abyssi2 abylysin
6	<a href="#">c4jixB_</a>	 Alignment		43.5	27	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> projannalysin; <b>PDBTitle:</b> crystal structure of the metallopeptidase zymogen of2 methanocaldococcus jannaschii jannalysin
7	<a href="#">c3opwA_</a>	 Alignment		37.4	20	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> dna damage-responsive transcriptional repressor rph1; <b>PDBTitle:</b> crystal structure of the rph1 catalytic core
8	<a href="#">c5a1fA_</a>	 Alignment		34.6	32	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> lysine-specific demethylase 5b, lysine-specific <b>PDBTitle:</b> crystal structure of the catalytic domain of plu1 in complex with2 n-oxalylglycine.
9	<a href="#">c2os2A_</a>	 Alignment		31.5	10	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> jmjc domain-containing histone demethylation protein 3a; <b>PDBTitle:</b> crystal structure of jmjd2a complexed with histone h3 peptide2 trimethylated at lys36
10	<a href="#">c2q8eB_</a>	 Alignment		30.0	10	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> jmjc domain-containing histone demethylation protein 3a; <b>PDBTitle:</b> specificity and mechanism of jmjd2a, a trimethyllysine-specific2 histone demethylase
11	<a href="#">c5xbvA_</a>	 Alignment		29.1	11	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> wss1p; <b>PDBTitle:</b> crystal structure of wss1 mutant from saccharomyces cerevisiae

12	<a href="#">c5yknA_</a>	Alignment		29.0	35	<b>PDB header:</b> gene regulation <b>Chain:</b> A: <b>PDB Molecule:</b> probable lysine-specific demethylase jmj14; <b>PDBTitle:</b> crystal structure of arabidopsis thaliana jmj14 catalytic domain
13	<a href="#">d1kn1b_</a>	Alignment		26.9	12	<b>Fold:</b> Globin-like <b>Superfamily:</b> Globin-like <b>Family:</b> Phycocyanin-like phycobilisome proteins
14	<a href="#">c6jp4A_</a>	Alignment		25.9	15	<b>PDB header:</b> gene regulation <b>Chain:</b> A: <b>PDB Molecule:</b> arabidopsis jmj13; <b>PDBTitle:</b> crystal structure of arabidopsis thaliana jmj13 catalytic domain in2 complex with nog and an h3k27me3 peptide
15	<a href="#">d2cwl1_</a>	Alignment		25.8	19	<b>Fold:</b> Ferritin-like <b>Superfamily:</b> Ferritin-like <b>Family:</b> Manganese catalase (T-catalase)
16	<a href="#">c4yk3B_</a>	Alignment		25.2	20	<b>PDB header:</b> protein binding <b>Chain:</b> B: <b>PDB Molecule:</b> bepe protein; <b>PDBTitle:</b> crystal structure of the bid domain of bepe from bartonella henselae
17	<a href="#">c5ldeB_</a>	Alignment		24.7	25	<b>PDB header:</b> viral protein <b>Chain:</b> B: <b>PDB Molecule:</b> immunoglobulin g-binding protein g,viral flce protein; <b>PDBTitle:</b> crystal structure of a vflip-ikkgamma stapled peptide dimer
18	<a href="#">c5cehA_</a>	Alignment		23.7	32	<b>PDB header:</b> oxidoreductase/inhibitor <b>Chain:</b> A: <b>PDB Molecule:</b> lysine-specific demethylase 5a; <b>PDBTitle:</b> structure of histone lysine demethylase kdm5a in complex with2 selective inhibitor
19	<a href="#">c6et5u_</a>	Alignment		23.5	29	<b>PDB header:</b> photosynthesis <b>Chain:</b> U: <b>PDB Molecule:</b> light-harvesting protein b-1015 gamma chain; <b>PDBTitle:</b> reaction centre light harvesting complex 1 from blc. viridis
20	<a href="#">c4igpA_</a>	Alignment		22.1	20	<b>PDB header:</b> structural protein <b>Chain:</b> A: <b>PDB Molecule:</b> os05g0196500 protein; <b>PDBTitle:</b> histone h3 lysine 4 demethylating rice jmj703 apo enzyme
21	<a href="#">d1e3oc2</a>	Alignment	not modelled	21.1	30	<b>Fold:</b> lambda repressor-like DNA-binding domains <b>Superfamily:</b> lambda repressor-like DNA-binding domains <b>Family:</b> POU-specific domain
22	<a href="#">d1jo5a_</a>	Alignment	not modelled	20.8	27	<b>Fold:</b> Light-harvesting complex subunits <b>Superfamily:</b> Light-harvesting complex subunits <b>Family:</b> Light-harvesting complex subunits
23	<a href="#">d1ngka_</a>	Alignment	not modelled	20.8	9	<b>Fold:</b> Globin-like <b>Superfamily:</b> Globin-like <b>Family:</b> Truncated hemoglobin
24	<a href="#">d1alb_</a>	Alignment	not modelled	19.8	10	<b>Fold:</b> Globin-like <b>Superfamily:</b> Globin-like <b>Family:</b> Phycocyanin-like phycobilisome proteins
25	<a href="#">c2p32B_</a>	Alignment	not modelled	19.8	15	<b>PDB header:</b> chaperone <b>Chain:</b> B: <b>PDB Molecule:</b> heat shock 70 kda protein a; <b>PDBTitle:</b> crystal structure of the c-terminal 10 kda subdomain from c. elegans2 hsp70
26	<a href="#">d1lmla_</a>	Alignment	not modelled	19.8	30	<b>Fold:</b> Zincin-like <b>Superfamily:</b> Metalloproteases ("zincins"), catalytic domain <b>Family:</b> Leishmanolysin
27	<a href="#">c3u1dA_</a>	Alignment	not modelled	19.5	18	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> the structure of a protein with a gntr superfamily winged-helix-turn-2 helix domain from halomicrobium mukohataei.
28	<a href="#">c6fqbe_</a>	Alignment	not modelled	19.3	21	<b>PDB header:</b> ligase <b>Chain:</b> E: <b>PDB Molecule:</b> cobryric acid synthase; <b>PDBTitle:</b> murt/gatd peptidoglycan amidotransferase complex from streptococcus2 pneumoniae r6
29	<a href="#">d1a2za_</a>	Alignment	not modelled	18.9	15	<b>Fold:</b> Phosphorylase/hydrolase-like <b>Superfamily:</b> Pyrrolidone carboxyl peptidase (pyroglutamate aminopeptidase)

						<b>Family:</b> Pyrrolidone carboxyl peptidase (pyroglutamate aminopeptidase)
30	<a href="#">c3zdoC_</a>	Alignment	not modelled	18.8	28	<b>PDB header:</b> viral protein <b>Chain:</b> C: <b>PDB Molecule:</b> phosphoprotein; <b>PDBTitle:</b> tetramerization domain of measles virus phosphoprotein
31	<a href="#">d1jkva_</a>	Alignment	not modelled	18.1	33	<b>Fold:</b> Ferritin-like <b>Superfamily:</b> Ferritin-like <b>Family:</b> Manganese catalase (T-catalase)
32	<a href="#">c5mtwD_</a>	Alignment	not modelled	17.5	16	<b>PDB header:</b> chaperone <b>Chain:</b> D: <b>PDB Molecule:</b> secb-like chaperone rv1957; <b>PDBTitle:</b> mycobacterium tuberculosis rv1957 secb-like chaperone in complex with2 a chad peptide from rv1956 higa1 antitoxin
33	<a href="#">c4yk2B_</a>	Alignment	not modelled	17.4	12	<b>PDB header:</b> protein binding <b>Chain:</b> B: <b>PDB Molecule:</b> bartonella effector protein (bep) substrate of virb t4ss; <b>PDBTitle:</b> crystal structure of the bid domain of bep9 from bartonella2 clarridgeiae
34	<a href="#">c5z8qA_</a>	Alignment	not modelled	17.3	15	<b>PDB header:</b> chaperone <b>Chain:</b> A: <b>PDB Molecule:</b> heat shock protein ssa1; <b>PDBTitle:</b> solution structure of the sbdalpha domain of yeast ssa1
35	<a href="#">c3bdnB_</a>	Alignment	not modelled	17.3	14	<b>PDB header:</b> transcription/dna <b>Chain:</b> B: <b>PDB Molecule:</b> lambda repressor; <b>PDBTitle:</b> crystal structure of the lambda repressor
36	<a href="#">c3eusB_</a>	Alignment	not modelled	16.8	24	<b>PDB header:</b> dna binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> dna-binding protein; <b>PDBTitle:</b> the crystal structure of the dna binding protein from silicibacter2 pomeroyi
37	<a href="#">d1b33b_</a>	Alignment	not modelled	16.6	10	<b>Fold:</b> Globin-like <b>Superfamily:</b> Globin-like <b>Family:</b> Phycocyanin-like phycobilisome proteins
38	<a href="#">c1mqrA_</a>	Alignment	not modelled	16.0	30	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> alpha-d-glucuronidase; <b>PDBTitle:</b> the crystal structure of alpha-d-glucuronidase (e386q) from bacillus2 stearothersophilus t-6
39	<a href="#">d1au7a2</a>	Alignment	not modelled	15.8	25	<b>Fold:</b> lambda repressor-like DNA-binding domains <b>Superfamily:</b> lambda repressor-like DNA-binding domains <b>Family:</b> POU-specific domain
40	<a href="#">d1l8na1</a>	Alignment	not modelled	15.1	30	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> (Trans)glycosidases <b>Family:</b> alpha-D-glucuronidase/Hyaluronidase catalytic domain
41	<a href="#">c6g7cF_</a>	Alignment	not modelled	14.7	16	<b>PDB header:</b> transport protein <b>Chain:</b> F: <b>PDB Molecule:</b> impa-related domain protein; <b>PDBTitle:</b> nt2-ctd domains of the tssa component from the type vi secretion2 system of aeromonas hydrophila.
42	<a href="#">c3qyxD_</a>	Alignment	not modelled	13.0	16	<b>PDB header:</b> transcription/dna <b>Chain:</b> D: <b>PDB Molecule:</b> esx-1 secretion-associated regulator espr; <b>PDBTitle:</b> crystal structure of mycobacterium tuberculosis espr in complex with a2 small dna fragment
43	<a href="#">c3cqxD_</a>	Alignment	not modelled	12.9	44	<b>PDB header:</b> chaperone <b>Chain:</b> D: <b>PDB Molecule:</b> bag family molecular chaperone regulator 2; <b>PDBTitle:</b> chaperone complex
44	<a href="#">d1iofa_</a>	Alignment	not modelled	12.4	15	<b>Fold:</b> Phosphorylase/hydrolase-like <b>Superfamily:</b> Pyrrolidone carboxyl peptidase (pyroglutamate aminopeptidase) <b>Family:</b> Pyrrolidone carboxyl peptidase (pyroglutamate aminopeptidase)
45	<a href="#">c2kvrA_</a>	Alignment	not modelled	12.3	20	<b>PDB header:</b> protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> ubiquitin carboxyl-terminal hydrolase 7; <b>PDBTitle:</b> solution nmr structure of human ubiquitin specific protease usp7 ubl2 domain (residues 537-664). nesg target hr4395c/sgc-toronto
46	<a href="#">c4ng7A_</a>	Alignment	not modelled	12.2	16	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> trap periplasmic solute binding protein; <b>PDBTitle:</b> crystal structure of a trap periplasmic solute binding protein from2 citrobacter koseri (cko_04899), target efi-510094, apo, open3 structure
47	<a href="#">d2ce7a1</a>	Alignment	not modelled	12.2	25	<b>Fold:</b> FtsH protease domain-like <b>Superfamily:</b> FtsH protease domain-like <b>Family:</b> FtsH protease domain-like
48	<a href="#">c2da4A_</a>	Alignment	not modelled	11.9	18	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical protein dkfzp686k21156; <b>PDBTitle:</b> solution structure of the homeobox domain of the2 hypothetical protein, dkfzp686k21156
49	<a href="#">c4ivvA_</a>	Alignment	not modelled	11.9	19	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> autolysin; <b>PDBTitle:</b> catalytic amidase domain of the major autolysin lyta from2 streptococcus pneumoniae
50	<a href="#">d2di4a1</a>	Alignment	not modelled	11.8	25	<b>Fold:</b> FtsH protease domain-like <b>Superfamily:</b> FtsH protease domain-like <b>Family:</b> FtsH protease domain-like
51	<a href="#">c4yk1A_</a>	Alignment	not modelled	11.7	14	<b>PDB header:</b> protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> bartonella effector protein (bep) substrate of virb t4ss; <b>PDBTitle:</b> crystal structure of the bid domain of bep6 from bartonella rochalimae
52	<a href="#">c2di4B_</a>	Alignment	not modelled	11.7	25	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> cell division protein ftsH homolog; <b>PDBTitle:</b> crystal structure of the ftsH protease domain
53	<a href="#">c1cqxB_</a>	Alignment	not modelled	11.0	22	<b>PDB header:</b> lipid binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> flavoheomprotein; <b>PDBTitle:</b> crystal structure of the flavohemoglobin from alcaligenes eutrophus at2 1.75 a resolution
54	<a href="#">c3qzCA_</a>	Alignment	not modelled	11.0	13	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> periplasmic protein cpxp; <b>PDBTitle:</b> structure of the periplasmic stress response protein cpxp

55	<a href="#">c4b24A</a>	Alignment	not modelled	10.8	10	<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
56	<a href="#">c3pvpA</a>	Alignment	not modelled	10.3	14	<b>PDB header:</b> dna binding protein/dna <b>Chain:</b> A: <b>PDB Molecule:</b> chromosomal replication initiator protein dnaa; <b>PDBTitle:</b> structure of mycobacterium tuberculosis dnaa-dbd in complex with box22 dna
57	<a href="#">c1sazA</a>	Alignment	not modelled	10.0	19	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> probable butyrate kinase 2; <b>PDBTitle:</b> membership in the askha superfamily: enzymological2 properties and crystal structure of butyrate kinase 2 from3 thermotoga maritima
58	<a href="#">d1xg0c</a>	Alignment	not modelled	9.9	10	<b>Fold:</b> Globin-like <b>Superfamily:</b> Globin-like <b>Family:</b> Phycocyanin-like phycobilisome proteins
59	<a href="#">c2vmlA</a>	Alignment	not modelled	9.9	6	<b>PDB header:</b> photosynthesis <b>Chain:</b> A: <b>PDB Molecule:</b> phycocyanin alpha chain; <b>PDBTitle:</b> the monoclinic structure of phycocyanin from gloeobacter violaceus
60	<a href="#">c6nu9A</a>	Alignment	not modelled	9.6	32	<b>PDB header:</b> viral protein <b>Chain:</b> A: <b>PDB Molecule:</b> zinc-binding non-structural protein; <b>PDBTitle:</b> crystal structure of a zinc-binding non-structural protein from the2 hepatitis e virus
61	<a href="#">c3c37B</a>	Alignment	not modelled	9.5	19	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> peptidase, m48 family; <b>PDBTitle:</b> x-ray structure of the putative zn-dependent peptidase q74d82 at the2 resolution 1.7 a. northeast structural genomics consortium target3 gsr143a
62	<a href="#">c4pyzA</a>	Alignment	not modelled	9.3	20	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> ubiquitin carboxyl-terminal hydrolase 7; <b>PDBTitle:</b> crystal structure of the first two ubl domains of deubiquitylase usp7
63	<a href="#">c3f6wE</a>	Alignment	not modelled	9.2	23	<b>PDB header:</b> dna binding protein <b>Chain:</b> E: <b>PDB Molecule:</b> xre-family like protein; <b>PDBTitle:</b> xre-family like protein from pseudomonas syringae pv. tomato str.2 dc3000
64	<a href="#">d1oqya2</a>	Alignment	not modelled	9.2	50	<b>Fold:</b> RuvA C-terminal domain-like <b>Superfamily:</b> UBA-like <b>Family:</b> UBA domain
65	<a href="#">c4nfuB</a>	Alignment	not modelled	8.7	9	<b>PDB header:</b> signaling protein <b>Chain:</b> B: <b>PDB Molecule:</b> senescence-associated carboxylesterase 101; <b>PDBTitle:</b> structure of the central plant immunity signaling node eds1 in complex2 with its interaction partner sag101
66	<a href="#">c2xsdC</a>	Alignment	not modelled	8.6	14	<b>PDB header:</b> transcription/dna <b>Chain:</b> C: <b>PDB Molecule:</b> pou domain, class 3, transcription factor 1; <b>PDBTitle:</b> crystal structure of the dimeric oct-6 (pou3f1) pou domain2 bound to palindromic more dna
67	<a href="#">c6mdxA</a>	Alignment	not modelled	8.6	26	<b>PDB header:</b> dna binding protein/dna <b>Chain:</b> A: <b>PDB Molecule:</b> sprt-like domain-containing protein spartan; <b>PDBTitle:</b> mechanism of protease dependent dpc repair
68	<a href="#">c3ckkA</a>	Alignment	not modelled	8.5	11	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> trna (guanine-n(7)-)-methyltransferase; <b>PDBTitle:</b> crystal structure of human methyltransferase-like protein 1
69	<a href="#">c2vqxA</a>	Alignment	not modelled	8.5	18	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> metalloproteinase; <b>PDBTitle:</b> precursor of protealysin, metalloproteinase from serratia2 proteamaculans.
70	<a href="#">d2fp1a1</a>	Alignment	not modelled	8.4	13	<b>Fold:</b> Chorismate mutase II <b>Superfamily:</b> Chorismate mutase II <b>Family:</b> Secreted chorismate mutase-like
71	<a href="#">c6eyyB</a>	Alignment	not modelled	8.0	27	<b>PDB header:</b> viral protein <b>Chain:</b> B: <b>PDB Molecule:</b> acrIIa6; <b>PDBTitle:</b> anti-crispr acrIIa6 cubic form
72	<a href="#">d1ud0a</a>	Alignment	not modelled	7.9	16	<b>Fold:</b> immunoglobulin/albumin-binding domain-like <b>Superfamily:</b> Heat shock protein 70kD (HSP70), C-terminal subdomain <b>Family:</b> Heat shock protein 70kD (HSP70), C-terminal subdomain
73	<a href="#">d1eyxb</a>	Alignment	not modelled	7.9	12	<b>Fold:</b> Globin-like <b>Superfamily:</b> Globin-like <b>Family:</b> Phycocyanin-like phycobilisome proteins
74	<a href="#">c4r42B</a>	Alignment	not modelled	7.7	33	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> alr3090 protein; <b>PDBTitle:</b> crystal structure of katb, a manganese catalase from anabaena pcc7120
75	<a href="#">c4pdnA</a>	Alignment	not modelled	7.7	43	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> crystal structure of e. coli yfcm
76	<a href="#">c3loff</a>	Alignment	not modelled	7.7	20	<b>PDB header:</b> chaperone <b>Chain:</b> F: <b>PDB Molecule:</b> heat shock 70 kda protein 1; <b>PDBTitle:</b> c-terminal domain of human heat shock 70kda protein 1b.
77	<a href="#">c1au7B</a>	Alignment	not modelled	7.6	14	<b>PDB header:</b> transcription/dna <b>Chain:</b> B: <b>PDB Molecule:</b> protein pit-1; <b>PDBTitle:</b> pit-1 mutant/dna complex
78	<a href="#">d1rioa</a>	Alignment	not modelled	7.6	14	<b>Fold:</b> lambda repressor-like DNA-binding domains <b>Superfamily:</b> lambda repressor-like DNA-binding domains <b>Family:</b> Phage repressors
79	<a href="#">d2o8ia1</a>	Alignment	not modelled	7.5	29	<b>Fold:</b> UraD-like <b>Superfamily:</b> UraD-Like <b>Family:</b> UraD-like

80	<a href="#">d1yuza1</a>	Alignment	not modelled	7.5	16	<b>Fold:</b> Ferritin-like <b>Superfamily:</b> Ferritin-like <b>Family:</b> Ferritin
81	<a href="#">d1alla_</a>	Alignment	not modelled	7.4	9	<b>Fold:</b> Globin-like <b>Superfamily:</b> Globin-like <b>Family:</b> Phycocyanin-like phycobilisome proteins
82	<a href="#">c3ee4A_</a>	Alignment	not modelled	7.2	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> probable ribonucleoside-diphosphate reductase; <b>PDBTitle:</b> r2-like ligand binding mn/fe oxidase from m. tuberculosis
83	<a href="#">d1lmb3_</a>	Alignment	not modelled	7.2	14	<b>Fold:</b> lambda repressor-like DNA-binding domains <b>Superfamily:</b> lambda repressor-like DNA-binding domains <b>Family:</b> Phage repressors
84	<a href="#">d1llib_</a>	Alignment	not modelled	7.0	14	<b>Fold:</b> lambda repressor-like DNA-binding domains <b>Superfamily:</b> lambda repressor-like DNA-binding domains <b>Family:</b> Phage repressors
85	<a href="#">c3b4rA_</a>	Alignment	not modelled	6.8	20	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> putative zinc metalloprotease mj0392; <b>PDBTitle:</b> site-2 protease from methanocaldococcus jannaschii
86	<a href="#">c3va9A_</a>	Alignment	not modelled	6.8	16	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> sensor histidine kinase; <b>PDBTitle:</b> crystal structure of the rhodopseudomonas palustris histidine kinase2 hk9 sensor domain
87	<a href="#">c3giuA_</a>	Alignment	not modelled	6.8	26	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> pyrrolidone-carboxylate peptidase; <b>PDBTitle:</b> 1.25 angstrom crystal structure of pyrrolidone-carboxylate peptidase2 (pcp) from staphylococcus aureus
88	<a href="#">c1hf0A_</a>	Alignment	not modelled	6.7	18	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> octamer-binding transcription factor 1; <b>PDBTitle:</b> crystal structure of the dna-binding domain of oct-1 bound to dna as a2 dimer
89	<a href="#">d1wh5a_</a>	Alignment	not modelled	6.7	18	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Homeodomain
90	<a href="#">d1phna_</a>	Alignment	not modelled	6.7	10	<b>Fold:</b> Globin-like <b>Superfamily:</b> Globin-like <b>Family:</b> Phycocyanin-like phycobilisome proteins
91	<a href="#">c5i44E_</a>	Alignment	not modelled	6.6	11	<b>PDB header:</b> dna binding protein/dna <b>Chain:</b> E: <b>PDB Molecule:</b> chromosome-anchoring protein raca; <b>PDBTitle:</b> structure of raca-dna complex; p21 form
92	<a href="#">d1rp3a1</a>	Alignment	not modelled	6.6	15	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Sigma3 and sigma4 domains of RNA polymerase sigma factors <b>Family:</b> Sigma3 domain
93	<a href="#">c2x7IP_</a>	Alignment	not modelled	6.6	22	<b>PDB header:</b> immune system <b>Chain:</b> P: <b>PDB Molecule:</b> protein rev; <b>PDBTitle:</b> implications of the hiv-1 rev dimer structure at 3.2a resolution for2 multimeric binding to the rev response element
94	<a href="#">c2rn7A_</a>	Alignment	not modelled	6.6	11	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> is629 orfa; <b>PDBTitle:</b> nmr solution structure of tnpe protein from shigella2 flexneri. northeast structural genomics target sfr125
95	<a href="#">c2qsfx_</a>	Alignment	not modelled	6.5	26	<b>PDB header:</b> dna binding protein <b>Chain:</b> X: <b>PDB Molecule:</b> uv excision repair protein rad23; <b>PDBTitle:</b> crystal structure of the rad4-rad23 complex
96	<a href="#">c1l0oC_</a>	Alignment	not modelled	6.5	14	<b>PDB header:</b> protein binding <b>Chain:</b> C: <b>PDB Molecule:</b> sigma factor; <b>PDBTitle:</b> crystal structure of the bacillus stearothermophilus anti-2 sigma factor spoiiab with the sporulation sigma factor3 sigmaf
97	<a href="#">d1l0oc_</a>	Alignment	not modelled	6.5	14	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Sigma3 and sigma4 domains of RNA polymerase sigma factors <b>Family:</b> Sigma4 domain
98	<a href="#">d1q5na_</a>	Alignment	not modelled	6.4	16	<b>Fold:</b> L-aspartase-like <b>Superfamily:</b> L-aspartase-like <b>Family:</b> L-aspartase/fumarase
99	<a href="#">c5vf3O_</a>	Alignment	not modelled	6.4	31	<b>PDB header:</b> virus <b>Chain:</b> O: <b>PDB Molecule:</b> small outer capsid protein; <b>PDBTitle:</b> bacteriophage t4 isometric capsid