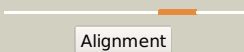

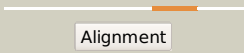

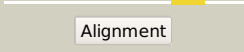


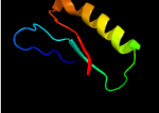


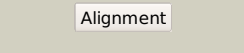
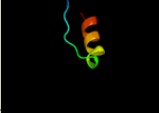
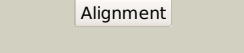
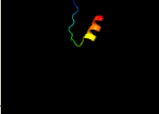

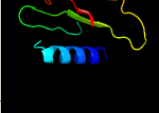
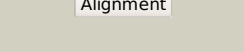
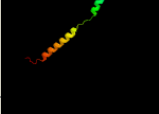
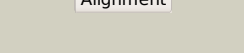

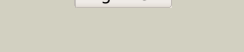
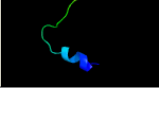


# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3190c_(-)_3555419_3556684
Date	Thu Aug 8 16:20:38 BST 2019
Unique Job ID	e27dd9017ff0c648

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c2vldA_</a>	 Alignment		88.0	19	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> endonuclease nucs; <b>PDBTitle:</b> crystal structure of a repair endonuclease from pyrococcus abyssi
2	<a href="#">c5gkeB_</a>	 Alignment		85.5	23	<b>PDB header:</b> hydrolase/dna <b>Chain:</b> B: <b>PDB Molecule:</b> endonuclease endoms; <b>PDBTitle:</b> structure of endoms-dsdna1 complex
3	<a href="#">c6hz9N_</a>	 Alignment		79.8	27	<b>PDB header:</b> dna binding protein <b>Chain:</b> N: <b>PDB Molecule:</b> protein mcrc; <b>PDBTitle:</b> structure of mcrcbc without dna binding domains (class 5)
4	<a href="#">d1y88a2</a>	 Alignment		64.4	15	<b>Fold:</b> Restriction endonuclease-like <b>Superfamily:</b> Restriction endonuclease-like <b>Family:</b> MRR-like
5	<a href="#">d1xmx_</a>	 Alignment		58.8	30	<b>Fold:</b> Restriction endonuclease-like <b>Superfamily:</b> Restriction endonuclease-like <b>Family:</b> Hypothetical protein VC1899
6	<a href="#">c5a08A_</a>	 Alignment		55.9	29	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> probable mannosyltransferase ktr4; <b>PDBTitle:</b> x-ray structure of the mannosyltransferase ktr4p from s. cerevisiae
7	<a href="#">c1s4pA_</a>	 Alignment		55.4	23	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> glycolipid 2-alpha-mannosyltransferase; <b>PDBTitle:</b> crystal structure of yeast alpha1,2-mannosyltransferase kre2p/mnt1p:2 ternary complex with gdp/mn and methyl-alpha-mannoside acceptor
8	<a href="#">c1y88A_</a>	 Alignment		54.0	20	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical protein af1548; <b>PDBTitle:</b> crystal structure of protein of unknown function af1548
9	<a href="#">c5xauD_</a>	 Alignment		48.4	15	<b>PDB header:</b> cell adhesion <b>Chain:</b> D: <b>PDB Molecule:</b> laminin subunit alpha-5; <b>PDBTitle:</b> crystal structure of integrin binding fragment of laminin-511
10	<a href="#">c3hxlA_</a>	 Alignment		48.2	20	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein dsy3957; <b>PDBTitle:</b> crystal structure of the sheath tail protein (dsy3957) from2 desulfitobacterium hafniense, northeast structural genomics3 consortium target dhr18
11	<a href="#">d1s4na_</a>	 Alignment		46.5	14	<b>Fold:</b> Nucleotide-diphospho-sugar transferases <b>Superfamily:</b> Nucleotide-diphospho-sugar transferases <b>Family:</b> Glycolipid 2-alpha-mannosyltransferase

12	<a href="#">c2ch0A_</a>	Alignment		38.0	18	<b>PDB header:</b> nuclear protein <b>Chain:</b> A; <b>PDB Molecule:</b> inner nuclear membrane protein man1; <b>PDBTitle:</b> solution structure of the human man1 c-terminal domain (residues 655-2 775)
13	<a href="#">c5t86A_</a>	Alignment		31.2	32	<b>PDB header:</b> toxin <b>Chain:</b> A; <b>PDB Molecule:</b> cdia toxin; <b>PDBTitle:</b> crystal structure of cdi complex from e. coli a0 34/86
14	<a href="#">c3h1tA_</a>	Alignment		30.1	21	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> type i site-specific restriction-modification <b>PDBTitle:</b> the fragment structure of a putative hsdR subunit of a type2 i restriction enzyme from vibrio vulnificus yj016
15	<a href="#">c3gybB_</a>	Alignment		29.4	16	<b>PDB header:</b> transcription regulator <b>Chain:</b> B; <b>PDB Molecule:</b> transcriptional regulators (laci-family <b>PDBTitle:</b> crystal structure of a laci-family transcriptional2 regulatory protein from corynebacterium glutamicum
16	<a href="#">c4ic1D_</a>	Alignment		29.1	24	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> D; <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> crystal structure of sso0001
17	<a href="#">c6gsiK_</a>	Alignment		26.3	20	<b>PDB header:</b> virus <b>Chain:</b> K; <b>PDB Molecule:</b> vp2; <b>PDBTitle:</b> feline calicivirus strain f9 bound to a soluble ectodomain fragment of f2 feline junctional adhesion molecule a - leading to assembly of a3 portal structure at a unique three-fold axis.
18	<a href="#">c6gsiL_</a>	Alignment		26.3	20	<b>PDB header:</b> virus <b>Chain:</b> I; <b>PDB Molecule:</b> vp2; <b>PDBTitle:</b> feline calicivirus strain f9 bound to a soluble ectodomain fragment of f2 feline junctional adhesion molecule a - leading to assembly of a3 portal structure at a unique three-fold axis.
19	<a href="#">c6emlr_</a>	Alignment		26.2	24	<b>PDB header:</b> ribosome <b>Chain:</b> R; <b>PDB Molecule:</b> 40s ribosomal protein s2; <b>PDBTitle:</b> cryo-em structure of a late pre-40s ribosomal subunit from2 saccharomyces cerevisiae
20	<a href="#">c3q66C_</a>	Alignment		25.5	27	<b>PDB header:</b> chaperone/transferase <b>Chain:</b> C; <b>PDB Molecule:</b> histone acetyltransferase rtt109; <b>PDBTitle:</b> structure of the vps75-rtt109 histone chaperone-lysine2 acetyltransferase complex (full-length proteins in space group p6122)
21	<a href="#">c2jqqa_</a>	Alignment	not modelled	24.1	6	<b>PDB header:</b> protein transport <b>Chain:</b> A; <b>PDB Molecule:</b> conserved oligomeric golgi complex subunit 2; <b>PDBTitle:</b> solution structure of saccharomyces cerevisiae conserved2 oligomeric golgi subunit 2 protein (cog2p)
22	<a href="#">c5w1hA_</a>	Alignment	not modelled	23.0	18	<b>PDB header:</b> rna binding protein/rna <b>Chain:</b> A; <b>PDB Molecule:</b> lbacas13a (c2c2); <b>PDBTitle:</b> crystal structure of lbacas13a (c2c2) bound to mature crrna (24-nt2 spacer)
23	<a href="#">c5mc9A_</a>	Alignment	not modelled	22.6	15	<b>PDB header:</b> cell adhesion <b>Chain:</b> A; <b>PDB Molecule:</b> laminin subunit alpha-1; <b>PDBTitle:</b> crystal structure of the heterotrimeric integrin-binding region of2 laminin-111
24	<a href="#">c4d8jD_</a>	Alignment	not modelled	20.8	23	<b>PDB header:</b> dna binding protein <b>Chain:</b> D; <b>PDB Molecule:</b> macrodomain ter protein; <b>PDBTitle:</b> structure of e. coli matp-mats complex
25	<a href="#">c5nv3P_</a>	Alignment	not modelled	20.0	15	<b>PDB header:</b> lyase <b>Chain:</b> P; <b>PDB Molecule:</b> ribulose biphosphate carboxylase small chain 1; <b>PDBTitle:</b> structure of rubisco from rhodobacter sphaeroides in complex with cabp
26	<a href="#">d1bxni_</a>	Alignment	not modelled	18.7	20	<b>Fold:</b> RuBisCO, small subunit <b>Superfamily:</b> RuBisCO, small subunit <b>Family:</b> RuBisCO, small subunit
27	<a href="#">c3eukC_</a>	Alignment	not modelled	17.7	8	<b>PDB header:</b> cell cycle <b>Chain:</b> C; <b>PDB Molecule:</b> chromosome partition protein mukb, linker; <b>PDBTitle:</b> crystal structure of muke-mukf(residues 292-443)-mukb(head domain)-2 atpgammas complex, asymmetric dimer
						<b>Fold:</b> RuBisCO, small subunit

28	<a href="#">dluzhc1</a>	Alignment	not modelled	17.4	25	<b>Superfamily:</b> RuBisCO, small subunit <b>Family:</b> RuBisCO, small subunit
29	<a href="#">dlgefa_</a>	Alignment	not modelled	17.3	17	<b>Fold:</b> Restriction endonuclease-like <b>Superfamily:</b> Restriction endonuclease-like <b>Family:</b> Hjc-like
30	<a href="#">d1rbli_</a>	Alignment	not modelled	17.0	15	<b>Fold:</b> RuBisCO, small subunit <b>Superfamily:</b> RuBisCO, small subunit <b>Family:</b> RuBisCO, small subunit
31	<a href="#">c6h3cC_</a>	Alignment	not modelled	16.5	12	<b>PDB header:</b> signaling protein <b>Chain:</b> C: <b>PDB Molecule:</b> brisc and brca1-a complex member 2; <b>PDBTitle:</b> cryo-em structure of the brisc complex bound to shmt2
32	<a href="#">c1mhmA_</a>	Alignment	not modelled	16.3	6	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> s-adenosylmethionine decarboxylase; <b>PDBTitle:</b> crystal structure of s-adenosylmethionine decarboxylase2 from potato
33	<a href="#">c6jx3B_</a>	Alignment	not modelled	16.1	28	<b>PDB header:</b> peptide binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> tfub1; <b>PDBTitle:</b> lasso peptide synthetase b1 complexed with the leader peptide
34	<a href="#">c6cb6A_</a>	Alignment	not modelled	15.8	31	<b>PDB header:</b> viral protein <b>Chain:</b> A: <b>PDB Molecule:</b> protein a6; <b>PDBTitle:</b> crystal structure of vaccinia virus a6 n-terminus (space group c2)
35	<a href="#">d1jloa_</a>	Alignment	not modelled	15.4	13	<b>Fold:</b> S-adenosylmethionine decarboxylase <b>Superfamily:</b> S-adenosylmethionine decarboxylase <b>Family:</b> S-adenosylmethionine decarboxylase
36	<a href="#">c2c5IT_</a>	Alignment	not modelled	15.3	10	<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 of2 vps51 in distorted conformation
37	<a href="#">c2zfnA_</a>	Alignment	not modelled	15.2	27	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> regulator of ty1 transposition protein 109; <b>PDBTitle:</b> self-acetylation mediated histone h3 lysine 56 acetylation by rtt109
38	<a href="#">d2j0id2</a>	Alignment	not modelled	15.1	18	<b>Fold:</b> OB-fold <b>Superfamily:</b> Nucleic acid-binding proteins <b>Family:</b> Cold shock DNA-binding domain-like
39	<a href="#">d1ir1s_</a>	Alignment	not modelled	15.1	30	<b>Fold:</b> RuBisCO, small subunit <b>Superfamily:</b> RuBisCO, small subunit <b>Family:</b> RuBisCO, small subunit
40	<a href="#">c2ybvN_</a>	Alignment	not modelled	15.0	20	<b>PDB header:</b> lyase <b>Chain:</b> N: <b>PDB Molecule:</b> ribulose bisphosphate carboxylase small subunit; <b>PDBTitle:</b> structure of rubisco from thermosynechococcus elongatus
41	<a href="#">c3rlcA_</a>	Alignment	not modelled	15.0	54	<b>PDB header:</b> structural protein <b>Chain:</b> A: <b>PDB Molecule:</b> a1 protein; <b>PDBTitle:</b> crystal structure of the read-through domain from bacteriophage qbeta2 a1 protein, hexagonal crystal form
42	<a href="#">c4eyyQ_</a>	Alignment	not modelled	14.7	25	<b>PDB header:</b> protein binding <b>Chain:</b> Q: <b>PDB Molecule:</b> icmq; <b>PDBTitle:</b> crystal structure of the icmr-icmq complex from legionella pneumophila
43	<a href="#">c6mr1A_</a>	Alignment	not modelled	14.7	17	<b>PDB header:</b> protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> carbon dioxide concentrating mechanism protein; <b>PDBTitle:</b> rbcs-like subdomain of cmm
44	<a href="#">d1svdm1</a>	Alignment	not modelled	14.6	25	<b>Fold:</b> RuBisCO, small subunit <b>Superfamily:</b> RuBisCO, small subunit <b>Family:</b> RuBisCO, small subunit
45	<a href="#">c5d3aA_</a>	Alignment	not modelled	14.4	6	<b>PDB header:</b> motor protein <b>Chain:</b> A: <b>PDB Molecule:</b> kinesin-like protein kif21a; <b>PDBTitle:</b> kif21a regulatory coiled coil
46	<a href="#">c6ah3D_</a>	Alignment	not modelled	14.0	15	<b>PDB header:</b> hydrolase/rna <b>Chain:</b> D: <b>PDB Molecule:</b> rnases mrp/p 32.9 kda subunit; <b>PDBTitle:</b> cryo-em structure of yeast ribonuclease p with pre-trna substrate
47	<a href="#">d1ywka1</a>	Alignment	not modelled	13.9	30	<b>Fold:</b> Double-stranded beta-helix <b>Superfamily:</b> RmlC-like cupins <b>Family:</b> Kdul-like
48	<a href="#">d1bwvs_</a>	Alignment	not modelled	13.7	15	<b>Fold:</b> RuBisCO, small subunit <b>Superfamily:</b> RuBisCO, small subunit <b>Family:</b> RuBisCO, small subunit
49	<a href="#">c3d35A_</a>	Alignment	not modelled	13.5	27	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> regulator of ty1 transposition protein 109; <b>PDBTitle:</b> crystal structure of rtt109-ac-coa complex
50	<a href="#">c5mz2l_</a>	Alignment	not modelled	13.1	16	<b>PDB header:</b> photosynthesis <b>Chain:</b> I: <b>PDB Molecule:</b> rubisco small subunit; <b>PDBTitle:</b> rubisco from thalassiosira antarctica
51	<a href="#">d1xoya_</a>	Alignment	not modelled	12.9	21	<b>Fold:</b> Galactose-binding domain-like <b>Superfamily:</b> Galactose-binding domain-like <b>Family:</b> Hypothetical protein AT3g04780/F7O18 27
52	<a href="#">c2hayD_</a>	Alignment	not modelled	12.8	20	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> putative nad(p)h-flavin oxidoreductase; <b>PDBTitle:</b> the crystal structure of the putative nad(p)h-flavin oxidoreductase2 from streptococcus pyogenes m1 gas
53	<a href="#">c1ywke_</a>	Alignment	not modelled	12.7	30	<b>PDB header:</b> isomerase <b>Chain:</b> E: <b>PDB Molecule:</b> 4-deoxy-l-threo-5-hexosulose-uronate ketol- <b>PDBTitle:</b> crystal structure of 4-deoxy-1-threo-5-hexosulose-uronate2 ketol-isomerase from enterococcus faecalis
54	<a href="#">c5v1uB_</a>	Alignment	not modelled	12.7	20	<b>PDB header:</b> protein binding <b>Chain:</b> B: <b>PDB Molecule:</b> tbib1;

						<b>PDBTitle:</b> tbib1 in complex with the tbia(beta) leader peptide
55	<a href="#">d2g8la1</a>	Alignment	not modelled	12.6	18	<b>Fold:</b> AF1104-like <b>Superfamily:</b> AF1104-like <b>Family:</b> AF1104-like
56	<a href="#">c2vkyB_</a>	Alignment	not modelled	12.3	20	<b>PDB header:</b> viral protein <b>Chain:</b> B: <b>PDB Molecule:</b> tail protein, piigcn4; <b>PDBTitle:</b> headbinding domain of phage p22 tailspike c-terminally fused to2 isoleucine zipper piigcn4 (chimera i)
57	<a href="#">c1w59B_</a>	Alignment	not modelled	12.1	10	<b>PDB header:</b> cell division <b>Chain:</b> B: <b>PDB Molecule:</b> cell division protein ftsz homolog 1; <b>PDBTitle:</b> ftsz dimer, empty (m. jannaschii)
58	<a href="#">c6hbbA_</a>	Alignment	not modelled	12.0	15	<b>PDB header:</b> protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> carbon dioxide concentrating mechanism protein ccmm; <b>PDBTitle:</b> crystal structure of the small subunit-like domain 1 of ccmm from2 synechococcus elongatus (strain pcc 7942)
59	<a href="#">d2uubm1</a>	Alignment	not modelled	12.0	26	<b>Fold:</b> S13-like H2TH domain <b>Superfamily:</b> S13-like H2TH domain <b>Family:</b> Ribosomal protein S13
60	<a href="#">c2wa0A_</a>	Alignment	not modelled	11.9	15	<b>PDB header:</b> immune system <b>Chain:</b> A: <b>PDB Molecule:</b> melanoma-associated antigen 4; <b>PDBTitle:</b> crystal structure of the human magea4
61	<a href="#">c5us5B_</a>	Alignment	not modelled	11.9	44	<b>PDB header:</b> structural genomics <b>Chain:</b> B: <b>PDB Molecule:</b> upf0297 protein ef_1202; <b>PDBTitle:</b> solution structure of the ireb homodimer
62	<a href="#">d1unda_</a>	Alignment	not modelled	11.7	17	<b>Fold:</b> VHP, Villin headpiece domain <b>Superfamily:</b> VHP, Villin headpiece domain <b>Family:</b> VHP, Villin headpiece domain
63	<a href="#">c1wwyA_</a>	Alignment	not modelled	11.6	21	<b>PDB header:</b> apoptosis <b>Chain:</b> A: <b>PDB Molecule:</b> thioredoxin-like protein 1; <b>PDBTitle:</b> solution structure of the duf1000 domain of a thioredoxin-like protein2 1
64	<a href="#">d1yu8x1</a>	Alignment	not modelled	11.5	25	<b>Fold:</b> VHP, Villin headpiece domain <b>Superfamily:</b> VHP, Villin headpiece domain <b>Family:</b> VHP, Villin headpiece domain
65	<a href="#">c5h64b_</a>	Alignment	not modelled	11.5	36	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> regulatory-associated protein of mtor; <b>PDBTitle:</b> cryo-em structure of mtorc1
66	<a href="#">c2wj0B_</a>	Alignment	not modelled	11.3	18	<b>PDB header:</b> hydrolase/dna <b>Chain:</b> B: <b>PDB Molecule:</b> archaeal hjc; <b>PDBTitle:</b> crystal structures of holliday junction resolvases from2 archaeoglobus fulgidus bound to dna substrate
67	<a href="#">d1vsra_</a>	Alignment	not modelled	11.1	20	<b>Fold:</b> Restriction endonuclease-like <b>Superfamily:</b> Restriction endonuclease-like <b>Family:</b> Very short patch repair (VSR) endonuclease
68	<a href="#">c3e66B_</a>	Alignment	not modelled	11.1	16	<b>PDB header:</b> splicing <b>Chain:</b> B: <b>PDB Molecule:</b> prp8; <b>PDBTitle:</b> crystal structure of the beta-finger domain of yeast prp8
69	<a href="#">c2eo0A_</a>	Alignment	not modelled	10.9	13	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical protein st1444; <b>PDBTitle:</b> crystal structure of holliday junction resolvase st1444
70	<a href="#">c2qieB_</a>	Alignment	not modelled	10.8	13	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> molybdopterin synthase small subunit; <b>PDBTitle:</b> staphylococcus aureus molybdopterin synthase in complex with precursor2 z
71	<a href="#">c6h2jB_</a>	Alignment	not modelled	10.6	18	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> type i restriction enzyme r protein; <b>PDBTitle:</b> crystal structure of the hsdR subunit of the ecor124i restriction2 enzyme with the c-terminal domain
72	<a href="#">c4ui9E_</a>	Alignment	not modelled	10.6	33	<b>PDB header:</b> cell cycle <b>Chain:</b> E: <b>PDB Molecule:</b> anaphase-promoting complex subunit 16; <b>PDBTitle:</b> atomic structure of the human anaphase-promoting complex
73	<a href="#">c2w74B_</a>	Alignment	not modelled	10.4	18	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> type i restriction enzyme ecor124ii r protein; <b>PDBTitle:</b> mutant (k220r) of the hsdR subunit of the ecor124i2 restriction enzyme in complex with atp
74	<a href="#">d1rl2a2</a>	Alignment	not modelled	10.4	13	<b>Fold:</b> OB-fold <b>Superfamily:</b> Nucleic acid-binding proteins <b>Family:</b> Cold shock DNA-binding domain-like
75	<a href="#">d1ejxc1</a>	Alignment	not modelled	10.4	26	<b>Fold:</b> Composite domain of metallo-dependent hydrolases <b>Superfamily:</b> Composite domain of metallo-dependent hydrolases <b>Family:</b> alpha-Subunit of urease
76	<a href="#">c6r7tB_</a>	Alignment	not modelled	10.2	26	<b>PDB header:</b> immune system <b>Chain:</b> B: <b>PDB Molecule:</b> melanoma-associated antigen b1; <b>PDBTitle:</b> crystal structure of human melanoma-associated antigen b1 (mageb1) in2 complex with nanobody
77	<a href="#">c2kjaA_</a>	Alignment	not modelled	10.2	8	<b>PDB header:</b> ribosomal protein <b>Chain:</b> A: <b>PDB Molecule:</b> 30s ribosomal protein s6; <b>PDBTitle:</b> solution structure and backbone dynamics of the permutant p54-55
78	<a href="#">c4rtbA_</a>	Alignment	not modelled	10.2	18	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> hydG protein; <b>PDBTitle:</b> x-ray structure of the fefe-hydrogenase maturase hydG from2 carboxydotherrmus hydrogeniformans
79	<a href="#">c5sxyA_</a>	Alignment	not modelled	10.0	12	<b>PDB header:</b> chaperone <b>Chain:</b> A: <b>PDB Molecule:</b> bifunctional coenzyme pqq synthesis protein c/d; <b>PDBTitle:</b> the solution nmr structure for the pqqd truncation of methylobacterium2 extorquens pqqcd representing a functional and stand-alone3 ribosomally synthesized and post-translational modified (ripp)4 recognition element (rre)
						<b>PDB header:</b> oxidoreductase

80	<a href="#">c2kw0A_</a>	Alignment	not modelled	9.8	16	<b>Chain:</b> A; <b>PDB Molecule:</b> ccmh protein; <b>PDBTitle:</b> solution structure of n-terminal domain of ccmh from escherichia.coli
81	<a href="#">c2w9yA_</a>	Alignment	not modelled	9.7	10	<b>PDB header:</b> lipid transport <b>Chain:</b> A; <b>PDB Molecule:</b> fatty acid/retinol binding protein protein 7, <b>PDBTitle:</b> the structure of the lipid binding protein ce-far-7 from 2 caenorhabditis elegans
82	<a href="#">d1vqoa2</a>	Alignment	not modelled	9.6	16	<b>Fold:</b> OB-fold <b>Superfamily:</b> Nucleic acid-binding proteins <b>Family:</b> Cold shock DNA-binding domain-like
83	<a href="#">c3cz7A_</a>	Alignment	not modelled	9.5	27	<b>PDB header:</b> replication <b>Chain:</b> A; <b>PDB Molecule:</b> regulator of ty1 transposition protein 109; <b>PDBTitle:</b> molecular basis for the autoregulation of the protein acetyl2 transferase rtt109
84	<a href="#">c2w00B_</a>	Alignment	not modelled	9.4	18	<b>PDB header:</b> hydrolase <b>Chain:</b> B; <b>PDB Molecule:</b> hsdr; <b>PDBTitle:</b> crystal structure of the hsdr subunit of the ecor124i restriction2 enzyme in complex with atp
85	<a href="#">d1unca_</a>	Alignment	not modelled	9.4	25	<b>Fold:</b> VHP, Villin headpiece domain <b>Superfamily:</b> VHP, Villin headpiece domain <b>Family:</b> VHP, Villin headpiece domain
86	<a href="#">c6jzbD_</a>	Alignment	not modelled	9.2	13	<b>PDB header:</b> transferase <b>Chain:</b> D; <b>PDB Molecule:</b> moad/this family protein; <b>PDBTitle:</b> structural analysis of molybdopterin synthases from two mycobacteria2 pathogens
87	<a href="#">d5csma_</a>	Alignment	not modelled	9.2	25	<b>Fold:</b> Chorismate mutase II <b>Superfamily:</b> Chorismate mutase II <b>Family:</b> Allosteric chorismate mutase
88	<a href="#">c5h7dI_</a>	Alignment	not modelled	9.2	11	<b>PDB header:</b> transferase, immune system/metal binding <b>Chain:</b> I; <b>PDB Molecule:</b> putrescine aminotransferase,immunoglobulin g-binding <b>PDBTitle:</b> crystal structure of the ygjg-protein a-zpa963-calmodulin complex
89	<a href="#">c3g2bA_</a>	Alignment	not modelled	9.1	8	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> A; <b>PDB Molecule:</b> coenzyme pqq synthesis protein d; <b>PDBTitle:</b> crystal structure of pqqd from xanthomonas campestris
90	<a href="#">d2zkmx1</a>	Alignment	not modelled	9.0	11	<b>Fold:</b> EF Hand-like <b>Superfamily:</b> EF-hand <b>Family:</b> EF-hand modules in multidomain proteins
91	<a href="#">d1cfra_</a>	Alignment	not modelled	8.9	20	<b>Fold:</b> Restriction endonuclease-like <b>Superfamily:</b> Restriction endonuclease-like <b>Family:</b> Cfr10I/Bse634I
92	<a href="#">c4wn5A_</a>	Alignment	not modelled	8.8	16	<b>PDB header:</b> transcription <b>Chain:</b> A; <b>PDB Molecule:</b> hypoxia-inducible factor 3-alpha; <b>PDBTitle:</b> crystal structure of the c-terminal per-arnt-sim (pasb) of human hif-2 3alpha9 bound to 18:1-1-monoacylglycerol
93	<a href="#">c6nrc6_</a>	Alignment	not modelled	8.7	16	<b>PDB header:</b> chaperone <b>Chain:</b> 6; <b>PDB Molecule:</b> prefoldin subunit 6; <b>PDBTitle:</b> htric-hpfd class3
94	<a href="#">c1u00A_</a>	Alignment	not modelled	8.7	18	<b>PDB header:</b> chaperone <b>Chain:</b> A; <b>PDB Molecule:</b> chaperone protein hsca; <b>PDBTitle:</b> hsca substrate binding domain complexed with the iscu2 recognition peptide elppvkih
95	<a href="#">c1jp3A_</a>	Alignment	not modelled	8.7	17	<b>PDB header:</b> transferase <b>Chain:</b> A; <b>PDB Molecule:</b> undecaprenyl pyrophosphate synthase; <b>PDBTitle:</b> structure of e.coli undecaprenyl pyrophosphate synthase
96	<a href="#">d1xrua1</a>	Alignment	not modelled	8.5	30	<b>Fold:</b> Double-stranded beta-helix <b>Superfamily:</b> RmIC-like cupins <b>Family:</b> Kdul-like
97	<a href="#">c4r0rA_</a>	Alignment	not modelled	8.5	19	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> A; <b>PDB Molecule:</b> eboizn21; <b>PDBTitle:</b> ebolavirus gp prehairpin intermediate mimic
98	<a href="#">c4oq2A_</a>	Alignment	not modelled	8.5	6	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> restriction endonuclease pvurts1 i; <b>PDBTitle:</b> 5hmc specific restriction endonuclease pvurts1i
99	<a href="#">c3i9oA_</a>	Alignment	not modelled	8.5	22	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> atp-dependent rna helicase dob1; <b>PDBTitle:</b> crystal structure of mtr4, a co-factor of the nuclear exosome