
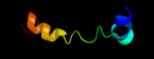
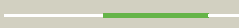
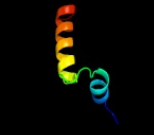
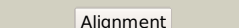

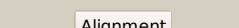

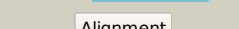

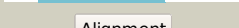

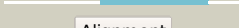











# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1584c_(-)_1786314_1786535
Date	Fri Aug 2 13:30:17 BST 2019
Unique Job ID	7e3fabce2271a99c

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c1gw4A_</a>	 Alignment		72.3	55	<b>PDB header:</b> high density lipoproteins <b>Chain:</b> A: <b>PDB Molecule:</b> apoa-i; <b>PDBTitle:</b> the helix-hinge-helix structural motif in human2 apolipoprotein a-i determined by nmr spectroscopy, 13 structure
2	<a href="#">d1u8va1</a>	 Alignment		57.0	30	<b>Fold:</b> Bromodomain-like <b>Superfamily:</b> Acyl-CoA dehydrogenase C-terminal domain-like <b>Family:</b> Medium chain acyl-CoA dehydrogenase-like, C-terminal domain
3	<a href="#">c4oo2D_</a>	 Alignment		50.1	20	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> chlorophenol-4-monooxygenase; <b>PDBTitle:</b> streptomyces globisporus c-1027 fad dependent (s)-3-chloro-β-2 tyrosine-s-sgcc2 c-5 hydroxylase sgcc apo form
4	<a href="#">c3hwcD_</a>	 Alignment		34.5	9	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> chlorophenol-4-monooxygenase component 2; <b>PDBTitle:</b> crystal structure of chlorophenol 4-monooxygenase (tftd) of2 burkholderia cepacia ac1100
5	<a href="#">c6eb0A_</a>	 Alignment		33.4	22	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> 4-hydroxyphenylacetate 3-monooxygenase, oxygenase subunit; <b>PDBTitle:</b> structure of 4-hydroxyphenylacetate 3-monooxygenase (hpab), oxygenase2 component from escherichia coli
6	<a href="#">d1mtyb_</a>	 Alignment		31.6	26	<b>Fold:</b> Ferritin-like <b>Superfamily:</b> Ferritin-like <b>Family:</b> Ribonucleotide reductase-like
7	<a href="#">d2q22a1</a>	 Alignment		31.3	18	<b>Fold:</b> Ava3019-like <b>Superfamily:</b> Ava3019-like <b>Family:</b> Ava3019-like
8	<a href="#">c1odrA_</a>	 Alignment		30.3	40	<b>PDB header:</b> lipid transport <b>Chain:</b> A: <b>PDB Molecule:</b> apoa-i peptide; <b>PDBTitle:</b> peptide of human apoa-i residues 166-185. nmr, 5 structures2 at ph 6.0, 37 degrees celsius and peptide:dpc mole ratio3 of 1:40
9	<a href="#">c1odpA_</a>	 Alignment		30.3	40	<b>PDB header:</b> lipid transport <b>Chain:</b> A: <b>PDB Molecule:</b> apoa-i peptide; <b>PDBTitle:</b> peptide of human apoa-i residues 166-185. nmr, 5 structures2 at ph 6.6, 37 degrees celsius and peptide:sds mole ratio3 of 1:40
10	<a href="#">c1odqA_</a>	 Alignment		30.3	40	<b>PDB header:</b> lipid transport <b>Chain:</b> A: <b>PDB Molecule:</b> apoa-i peptide; <b>PDBTitle:</b> peptide of human apoa-i residues 166-185. nmr, 5 structures2 at ph 3.7, 37 degrees celsius and peptide:sds mole ratio3 of 1:40
11	<a href="#">c1u8va_</a>	 Alignment		26.1	32	<b>PDB header:</b> lyase, isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> gamma-aminobutyrate metabolism dehydratase/isomerase; <b>PDBTitle:</b> crystal structure of 4-hydroxybutyryl-coa dehydratase from clostridium2 aminobutyricum: radical catalysis involving a [4fe-4s] cluster and3 flavin

12	<a href="#">c6ny5A_</a>	Alignment		25.3	14	<b>PDB header:</b> rna binding protein/rna <b>Chain:</b> A: <b>PDB Molecule:</b> pumilio domain-containing protein c56f2.08c; <b>PDBTitle:</b> crystal structure of the pum-hd domain of s. pombe puf1 in complex2 with rna
13	<a href="#">c4g5eD_</a>	Alignment		17.0	10	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> 2,4,6-trichlorophenol 4-monooxygenase; <b>PDBTitle:</b> 2,4,6-trichlorophenol 4-monooxygenase
14	<a href="#">d1hj3a1</a>	Alignment		16.2	20	<b>Fold:</b> Cytochrome c <b>Superfamily:</b> Cytochrome c <b>Family:</b> N-terminal (heme c) domain of cytochrome cd1-nitrite reductase
15	<a href="#">d1rbli_</a>	Alignment		16.1	50	<b>Fold:</b> RuBisCO, small subunit <b>Superfamily:</b> RuBisCO, small subunit <b>Family:</b> RuBisCO, small subunit
16	<a href="#">c2kz5A_</a>	Alignment		14.7	53	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> transcription factor nf-e2 45 kda subunit; <b>PDBTitle:</b> solution nmr structure of transcription factor nf-e2 subunit's dna2 binding domain from homo sapiens, northeast structural genomics3 consortium target hr4653b
17	<a href="#">d1svdm1</a>	Alignment		14.5	33	<b>Fold:</b> RuBisCO, small subunit <b>Superfamily:</b> RuBisCO, small subunit <b>Family:</b> RuBisCO, small subunit
18	<a href="#">c2yyjA_</a>	Alignment		14.5	23	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> 4-hydroxyphenylacetate-3-hydroxylase; <b>PDBTitle:</b> crystal structure of the oxygenase component (hpab) of 4-2 hydroxyphenylacetate 3-monooxygenase complexed with fad and 4-3 hydroxyphenylacetate
19	<a href="#">d2r40d1</a>	Alignment		14.3	47	<b>Fold:</b> Nuclear receptor ligand-binding domain <b>Superfamily:</b> Nuclear receptor ligand-binding domain <b>Family:</b> Nuclear receptor ligand-binding domain
20	<a href="#">d2csua3</a>	Alignment		14.1	24	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Succinyl-CoA synthetase domains <b>Family:</b> Succinyl-CoA synthetase domains
21	<a href="#">d1wdds_</a>	Alignment	not modelled	13.7	45	<b>Fold:</b> RuBisCO, small subunit <b>Superfamily:</b> RuBisCO, small subunit <b>Family:</b> RuBisCO, small subunit
22	<a href="#">d1gk8i_</a>	Alignment	not modelled	13.6	40	<b>Fold:</b> RuBisCO, small subunit <b>Superfamily:</b> RuBisCO, small subunit <b>Family:</b> RuBisCO, small subunit
23	<a href="#">c5mz2l_</a>	Alignment	not modelled	12.9	42	<b>PDB header:</b> photosynthesis <b>Chain:</b> I: <b>PDB Molecule:</b> rubisco small subunit; <b>PDBTitle:</b> rubisco from thalassiosira antarctica
24	<a href="#">d1bwvs_</a>	Alignment	not modelled	12.4	58	<b>Fold:</b> RuBisCO, small subunit <b>Superfamily:</b> RuBisCO, small subunit <b>Family:</b> RuBisCO, small subunit
25	<a href="#">c3oeoD_</a>	Alignment	not modelled	12.0	36	<b>PDB header:</b> signaling protein <b>Chain:</b> D: <b>PDB Molecule:</b> spheroplast protein y; <b>PDBTitle:</b> the crystal structure e. coli spy
26	<a href="#">c4a8xB_</a>	Alignment	not modelled	11.8	67	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> hook-like, isoform a; <b>PDBTitle:</b> structure of the core asap complex
27	<a href="#">d1bxni_</a>	Alignment	not modelled	11.6	58	<b>Fold:</b> RuBisCO, small subunit <b>Superfamily:</b> RuBisCO, small subunit <b>Family:</b> RuBisCO, small subunit
28	<a href="#">c6fkfd_</a>	Alignment	not modelled	11.5	12	<b>PDB header:</b> membrane protein <b>Chain:</b> D: <b>PDB Molecule:</b> atp synthase subunit beta, chloroplastic; <b>PDBTitle:</b> chloroplast f1fo conformation 1
29	<a href="#">c2ybvN_</a>	Alignment	not modelled	11.2	50	<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

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30	<a href="#">c5nv3P_</a>	Alignment	not modelled	11.0	50	<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
31	<a href="#">d3eaua1</a>	Alignment	not modelled	10.7	20	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> NAD(P)-linked oxidoreductase <b>Family:</b> Aldo-keto reductases (NADP)
32	<a href="#">d8rucj_</a>	Alignment	not modelled	10.7	45	<b>Fold:</b> RuBisCO, small subunit <b>Superfamily:</b> RuBisCO, small subunit <b>Family:</b> RuBisCO, small subunit
33	<a href="#">d1uzdc1</a>	Alignment	not modelled	10.5	40	<b>Fold:</b> RuBisCO, small subunit <b>Superfamily:</b> RuBisCO, small subunit <b>Family:</b> RuBisCO, small subunit
34	<a href="#">d2v6ai1</a>	Alignment	not modelled	10.4	40	<b>Fold:</b> RuBisCO, small subunit <b>Superfamily:</b> RuBisCO, small subunit <b>Family:</b> RuBisCO, small subunit
35	<a href="#">d1ej7s_</a>	Alignment	not modelled	10.2	40	<b>Fold:</b> RuBisCO, small subunit <b>Superfamily:</b> RuBisCO, small subunit <b>Family:</b> RuBisCO, small subunit
36	<a href="#">c2yclA_</a>	Alignment	not modelled	10.1	27	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> carbon monoxide dehydrogenase corrinoid/iron-sulfur <b>PDBTitle:</b> complete structure of the corrinoid,iron-sulfur protein including2 the n-terminal domain with a 4fe-4s cluster
37	<a href="#">c3bt5A_</a>	Alignment	not modelled	10.1	32	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein duf305; <b>PDBTitle:</b> crystal structure of duf305 fragment from deinococcus radiodurans
38	<a href="#">d1ru0a_</a>	Alignment	not modelled	9.8	33	<b>Fold:</b> DCoH-like <b>Superfamily:</b> PCD-like <b>Family:</b> PCD-like
39	<a href="#">d1gyxa_</a>	Alignment	not modelled	9.7	31	<b>Fold:</b> Tautomerase/MIF <b>Superfamily:</b> Tautomerase/MIF <b>Family:</b> 4-oxalocrotonate tautomerase-like
40	<a href="#">c3lutA_</a>	Alignment	not modelled	9.6	20	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> voltage-gated potassium channel subunit beta-2; <b>PDBTitle:</b> a structural model for the full-length shaker potassium channel kv1.2
41	<a href="#">c6rdlP_</a>	Alignment	not modelled	9.3	31	<b>PDB header:</b> proton transport <b>Chain:</b> P: <b>PDB Molecule:</b> mitochondrial atp synthase subunit oscp; <b>PDBTitle:</b> cryo-em structure of polytomella f-atp synthase, rotary substate 1b,2 monomer-masked refinement
42	<a href="#">d1fi3a_</a>	Alignment	not modelled	8.8	35	<b>Fold:</b> Cytochrome c <b>Superfamily:</b> Cytochrome c <b>Family:</b> monodomain cytochrome c
43	<a href="#">d1mhyb_</a>	Alignment	not modelled	8.8	29	<b>Fold:</b> Ferritin-like <b>Superfamily:</b> Ferritin-like <b>Family:</b> Ribonucleotide reductase-like
44	<a href="#">c3epvB_</a>	Alignment	not modelled	8.6	19	<b>PDB header:</b> metal binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> nickel and cobalt resistance protein cnrr; <b>PDBTitle:</b> x-ray structure of the metal-sensor cnrx in both the apo- and copper-2 bound forms
45	<a href="#">c3m20A_</a>	Alignment	not modelled	8.6	27	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> 4-oxalocrotonate tautomerase, putative; <b>PDBTitle:</b> crystal structure of dmpi from archaeoglobus fulgidus determined to2 2.37 angstroms resolution
46	<a href="#">c4kmfA_</a>	Alignment	not modelled	8.5	27	<b>PDB header:</b> transferase/dna <b>Chain:</b> A: <b>PDB Molecule:</b> interferon-inducible and double-stranded-dependent eif- <b>PDBTitle:</b> crystal structure of zalpha domain from carassius auratus pkz in2 complex with z-dna
47	<a href="#">c4lb6B_</a>	Alignment	not modelled	8.5	45	<b>PDB header:</b> transferase/dna <b>Chain:</b> B: <b>PDB Molecule:</b> protein kinase containing z-dna binding domains; <b>PDBTitle:</b> crystal structure of pkz zalpha in complex with ds(cg)6 (tetragonal2 form)
48	<a href="#">d2apla1</a>	Alignment	not modelled	8.4	25	<b>Fold:</b> PG0816-like <b>Superfamily:</b> PG0816-like <b>Family:</b> PG0816-like
49	<a href="#">c2lz1A_</a>	Alignment	not modelled	8.2	41	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> nuclear factor erythroid 2-related factor 2; <b>PDBTitle:</b> solution nmr structure of the dna-binding domain of human nf-e2-2 related factor 2, northeast structural genomics consortium (nesg)3 target hr3520o
50	<a href="#">c6b8ho_</a>	Alignment	not modelled	8.2	31	<b>PDB header:</b> membrane protein <b>Chain:</b> O: <b>PDB Molecule:</b> atp synthase subunit 5, mitochondrial; <b>PDBTitle:</b> mosaic model of yeast mitochondrial atp synthase monomer
51	<a href="#">c4uf6L_</a>	Alignment	not modelled	8.1	46	<b>PDB header:</b> hydrolase <b>Chain:</b> L: <b>PDB Molecule:</b> nuclear factor related to kappa-b-binding protein; <b>PDBTitle:</b> uch-15 in complex with ubiquitin-propargyl bound to an activating2 fragment of ino80g
52	<a href="#">c1q2iA_</a>	Alignment	not modelled	8.1	44	<b>PDB header:</b> antitumor protein <b>Chain:</b> A: <b>PDB Molecule:</b> pnc27; <b>PDBTitle:</b> nmr solution structure of a peptide from the mdm-2 binding2 domain of the p53 protein that is selectively cytotoxic to3 cancer cells
53	<a href="#">c5jffD_</a>	Alignment	not modelled	7.9	56	<b>PDB header:</b> transferase <b>Chain:</b> D: <b>PDB Molecule:</b> uncharacterized protein yhfg; <b>PDBTitle:</b> e. coli ecfct mutant g55r in complex with ecfca <b>PDB header:</b> transferase/vitamin-binding protein

54	<a href="#">c4djeE_</a>	Alignment	not modelled	7.6	24	<b>Chain:</b> E: <b>PDB Molecule:</b> corrinoïd/iron-sulfur protein large subunit; <b>PDBTitle:</b> crystal structure of folate-bound corrinoïd iron-sulfur protein2 (cfesp) in complex with its methyltransferase (metr), co-crystallized3 with folate
55	<a href="#">c4xdnA_</a>	Alignment	not modelled	7.6	47	<b>PDB header:</b> cell cycle <b>Chain:</b> A: <b>PDB Molecule:</b> mau2 chromatid cohesion factor homolog; <b>PDBTitle:</b> crystal structure of scc4 in complex with scc2n
56	<a href="#">d2bgxa2</a>	Alignment	not modelled	7.5	17	<b>Fold:</b> N-acetylmuramoyl-L-alanine amidase-like <b>Superfamily:</b> N-acetylmuramoyl-L-alanine amidase-like <b>Family:</b> N-acetylmuramoyl-L-alanine amidase-like
57	<a href="#">c4mqvD_</a>	Alignment	not modelled	7.4	55	<b>PDB header:</b> protein binding <b>Chain:</b> D: <b>PDB Molecule:</b> swi/snf-related matrix-associated actin-dependent regulator <b>PDBTitle:</b> crystal complex of rpa32c and smarc11 n-terminus
58	<a href="#">c4mqvB_</a>	Alignment	not modelled	7.4	55	<b>PDB header:</b> protein binding <b>Chain:</b> B: <b>PDB Molecule:</b> swi/snf-related matrix-associated actin-dependent regulator <b>PDBTitle:</b> crystal complex of rpa32c and smarc11 n-terminus
59	<a href="#">c5t4oL_</a>	Alignment	not modelled	7.2	19	<b>PDB header:</b> hydrolase <b>Chain:</b> L: <b>PDB Molecule:</b> atp synthase subunit delta; <b>PDBTitle:</b> autoinhibited e. coli atp synthase state 1
60	<a href="#">d1tm9a_</a>	Alignment	not modelled	7.0	64	<b>Fold:</b> Hypothetical protein MG354 <b>Superfamily:</b> Hypothetical protein MG354 <b>Family:</b> Hypothetical protein MG354
61	<a href="#">d1c75a_</a>	Alignment	not modelled	7.0	11	<b>Fold:</b> Cytochrome c <b>Superfamily:</b> Cytochrome c <b>Family:</b> monodomain cytochrome c
62	<a href="#">d351ca_</a>	Alignment	not modelled	7.0	18	<b>Fold:</b> Cytochrome c <b>Superfamily:</b> Cytochrome c <b>Family:</b> monodomain cytochrome c
63	<a href="#">c4u5pA_</a>	Alignment	not modelled	6.9	21	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> rhcc; <b>PDBTitle:</b> crystal structure of native rhcc (yp_702633.1) from rhodococcus jostii2 rha1 at 1.78 angstrom
64	<a href="#">c2lr4A_</a>	Alignment	not modelled	6.9	50	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> spbc2 prophage-derived uncharacterized protein yola; <b>PDBTitle:</b> nmr structure of the protein np_390037.1 from bacillus subtilis
65	<a href="#">c3nzzA_</a>	Alignment	not modelled	6.8	36	<b>PDB header:</b> cell invasion <b>Chain:</b> A: <b>PDB Molecule:</b> cell invasion protein sipd; <b>PDBTitle:</b> crystal structure of the salmonella type iii secretion system tip2 protein sipd
66	<a href="#">c3qzcA_</a>	Alignment	not modelled	6.4	19	<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
67	<a href="#">c3bdnB_</a>	Alignment	not modelled	6.4	36	<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
68	<a href="#">c3itfA_</a>	Alignment	not modelled	6.3	17	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> periplasmic adaptor protein cpxp; <b>PDBTitle:</b> structural basis for the inhibitory function of the cpxp adaptor2 protein
69	<a href="#">c2qw6A_</a>	Alignment	not modelled	6.2	25	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> aaa atpase, central region; <b>PDBTitle:</b> crystal structure of the c-terminal domain of an aaa atpase from2 enterococcus faecium do
70	<a href="#">d2qw6a1</a>	Alignment	not modelled	6.2	25	<b>Fold:</b> post-AAA+ oligomerization domain-like <b>Superfamily:</b> post-AAA+ oligomerization domain-like <b>Family:</b> MgsA/YrvN C-terminal domain-like
71	<a href="#">c5jzfF_</a>	Alignment	not modelled	5.9	57	<b>PDB header:</b> transferase <b>Chain:</b> F: <b>PDB Molecule:</b> uncharacterized protein yhfq; <b>PDBTitle:</b> e. coli ecfct in complex with ecfica mutant e28g
72	<a href="#">c5jzfB_</a>	Alignment	not modelled	5.9	57	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> uncharacterized protein yhfq; <b>PDBTitle:</b> e. coli ecfct in complex with ecfica mutant e28g
73	<a href="#">c3c6vB_</a>	Alignment	not modelled	5.8	36	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> probable tautomerase/dehalogenase au4130; <b>PDBTitle:</b> crystal structure of au4130/apc7354, a probable enzyme from the2 thermophilic fungus aspergillus fumigatus
74	<a href="#">c2l69A_</a>	Alignment	not modelled	5.8	50	<b>PDB header:</b> de novo protein <b>Chain:</b> A: <b>PDB Molecule:</b> rossmann 2x3 fold protein; <b>PDBTitle:</b> solution nmr structure of de novo designed protein, p-loop ntpase2 fold, northeast structural genomics consortium target or28
75	<a href="#">d1euva_</a>	Alignment	not modelled	5.7	19	<b>Fold:</b> Cysteine proteinases <b>Superfamily:</b> Cysteine proteinases <b>Family:</b> Adenain-like
76	<a href="#">c4l8iA_</a>	Alignment	not modelled	5.7	19	<b>PDB header:</b> immune system <b>Chain:</b> A: <b>PDB Molecule:</b> rsv epitope scaffold ffi_005; <b>PDBTitle:</b> crystal structure of rsv epitope scaffold ffi_005
77	<a href="#">d1k78a1</a>	Alignment	not modelled	5.6	54	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Paired domain
78	<a href="#">c2rrnA_</a>	Alignment	not modelled	5.5	53	<b>PDB header:</b> protein transport <b>Chain:</b> A: <b>PDB Molecule:</b> probable secdf protein-export membrane protein; <b>PDBTitle:</b> solution structure of secdf periplasmic domain p4
79	<a href="#">c4wlpB_</a>	Alignment	not modelled	5.5	46	<b>PDB header:</b> protein binding <b>Chain:</b> B: <b>PDB Molecule:</b> nuclear factor related to kappa-b-binding protein; <b>PDBTitle:</b> crystal structure of uch37-nfrkb inhibited deubiquitylating

						complex
80	<a href="#">c4bolA_</a>	Alignment	not modelled	5.4	26	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> ampdh2; <b>PDBTitle:</b> crystal structure of ampdh2 from pseudomonas aeruginosa in2 complex with pentapeptide
81	<a href="#">d1ynra1</a>	Alignment	not modelled	5.4	29	<b>Fold:</b> Cytochrome c <b>Superfamily:</b> Cytochrome c <b>Family:</b> monodomain cytochrome c
82	<a href="#">d1k0ia2</a>	Alignment	not modelled	5.4	50	<b>Fold:</b> FAD-linked reductases, C-terminal domain <b>Superfamily:</b> FAD-linked reductases, C-terminal domain <b>Family:</b> PHBH-like
83	<a href="#">c2yjfM_</a>	Alignment	not modelled	5.3	31	<b>PDB header:</b> motor protein <b>Chain:</b> M: <b>PDB Molecule:</b> mkl/myocardin-like protein 1; <b>PDBTitle:</b> oligomeric assembly of actin bound to mrtf-a
84	<a href="#">d1t2sa_</a>	Alignment	not modelled	5.3	16	<b>Fold:</b> SH3-like barrel <b>Superfamily:</b> PAZ domain <b>Family:</b> PAZ domain
85	<a href="#">d1sknp_</a>	Alignment	not modelled	5.2	44	<b>Fold:</b> A DNA-binding domain in eukaryotic transcription factors <b>Superfamily:</b> A DNA-binding domain in eukaryotic transcription factors <b>Family:</b> A DNA-binding domain in eukaryotic transcription factors
86	<a href="#">c2kktA_</a>	Alignment	not modelled	5.2	75	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> ataxin-7-like protein 3; <b>PDBTitle:</b> solution structure of the sca7 domain of human ataxin-7- l3 protein
87	<a href="#">c5u0pU_</a>	Alignment	not modelled	5.2	26	<b>PDB header:</b> transcription <b>Chain:</b> U: <b>PDB Molecule:</b> mediator complex subunit 21; <b>PDBTitle:</b> cryo-em structure of the transcriptional mediator
88	<a href="#">c1yybA_</a>	Alignment	not modelled	5.1	75	<b>PDB header:</b> apoptosis <b>Chain:</b> A: <b>PDB Molecule:</b> programmed cell death protein 5; <b>PDBTitle:</b> solution structure of 1-26 fragment of human programmed2 cell death 5 protein
89	<a href="#">c4clvB_</a>	Alignment	not modelled	5.1	19	<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
90	<a href="#">d2cqea1</a>	Alignment	not modelled	5.1	30	<b>Fold:</b> CCCH zinc finger <b>Superfamily:</b> CCCH zinc finger <b>Family:</b> CCCH zinc finger
91	<a href="#">c6h5lB_</a>	Alignment	not modelled	5.0	29	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> conserved hypothetical cytochrome protein; <b>PDBTitle:</b> kueningenia stuttgartiensis reducing hao-like protein complex2 kustc0457/kustc0458
92	<a href="#">c5lqzU_</a>	Alignment	not modelled	5.0	25	<b>PDB header:</b> hydrolase <b>Chain:</b> U: <b>PDB Molecule:</b> atp synthase oscp subunit; <b>PDBTitle:</b> structure of f-atpase from pichia angusta, state1