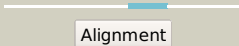
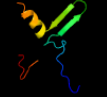


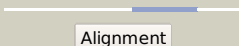

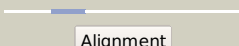

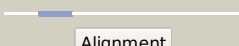

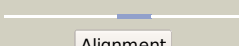

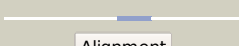

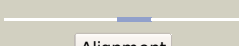









# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1574_(-)_1779797_1780660
Date	Fri Aug 2 13:30:16 BST 2019
Unique Job ID	e013c4017efca0bf

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c2kxgA_</a>	 Alignment		31.2	41	<b>PDB header:</b> hydrolase inhibitor <b>Chain:</b> A: <b>PDB Molecule:</b> aspartic protease inhibitor; <b>PDBTitle:</b> the solution structure of the squash aspartic acid proteinase2 inhibitor (sqapi)
2	<a href="#">c1psvA_</a>	 Alignment		28.6	50	<b>PDB header:</b> designed peptide <b>Chain:</b> A: <b>PDB Molecule:</b> pda8d; <b>PDBTitle:</b> computationally designed peptide with a beta-beta-alpha2 fold selection, nmr, 32 structures
3	<a href="#">c5xyiX_</a>	 Alignment		26.0	23	<b>PDB header:</b> ribosome <b>Chain:</b> X: <b>PDB Molecule:</b> 40s ribosomal protein s23, putative; <b>PDBTitle:</b> small subunit of trichomonas vaginalis ribosome
4	<a href="#">c2kqeA_</a>	 Alignment		23.7	45	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> aprataxin and pnk-like factor; <b>PDBTitle:</b> second pbz domain of human aplf protein in complex with2 ribofuranosyladenosine
5	<a href="#">c1cffB_</a>	 Alignment		23.2	36	<b>PDB header:</b> calmodulin <b>Chain:</b> B: <b>PDB Molecule:</b> calcium pump; <b>PDBTitle:</b> nmr solution structure of a complex of calmodulin with a binding2 peptide of the ca2+-pump
6	<a href="#">c2vzbA_</a>	 Alignment		21.2	26	<b>PDB header:</b> dna-binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulatory protein; <b>PDBTitle:</b> feast or famine regulatory protein (rv3291c)from m.2 tuberculosis complexed with l-tryptophan
7	<a href="#">c1g2hA_</a>	 Alignment		20.3	24	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulatory protein tyrr homolog; <b>PDBTitle:</b> solution structure of the dna-binding domain of the tyrr2 protein of haemophilus influenzae
8	<a href="#">d1g2ha_</a>	 Alignment		20.3	24	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> FIS-like
9	<a href="#">c2zkrx_</a>	 Alignment		20.3	73	<b>PDB header:</b> ribosomal protein/rna <b>Chain:</b> X: <b>PDB Molecule:</b> rna helices; <b>PDBTitle:</b> structure of a mammalian ribosomal 60s subunit within an 80s complex2 obtained by docking homology models of the rna and proteins into an3 8.7 a cryo-em map
10	<a href="#">c1ojlD_</a>	 Alignment		20.1	37	<b>PDB header:</b> response regulator <b>Chain:</b> D: <b>PDB Molecule:</b> transcriptional regulatory protein zrar; <b>PDBTitle:</b> crystal structure of a sigma54-activator suggests the mechanism for2 the conformational switch necessary for sigma54 binding
11	<a href="#">c2j376_</a>	 Alignment		19.5	73	<b>PDB header:</b> ribosome <b>Chain:</b> 6: <b>PDB Molecule:</b> ribosomal protein l31; <b>PDBTitle:</b> model of mammalian srp bound to 80s rncs

12	<a href="#">c2kqdA_</a>	Alignment		16.9	45	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> aprataxin and pnk-like factor; <b>PDBTitle:</b> first pbz domain of human ap1f protein in complex with2 ribofuranosyladenosine
13	<a href="#">d2p7vb1</a>	Alignment		15.8	17	<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
14	<a href="#">c3jywW_</a>	Alignment		15.7	55	<b>PDB header:</b> ribosome <b>Chain:</b> W: <b>PDB Molecule:</b> 60s ribosomal protein l31(a); <b>PDBTitle:</b> structure of the 60s proteins for eukaryotic ribosome based on cryo-em2 map of thermomyces lanuginosus ribosome at 8.9a resolution
15	<a href="#">d1ku3a_</a>	Alignment		13.8	29	<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
16	<a href="#">d1ntca_</a>	Alignment		13.3	35	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> FIS-like
17	<a href="#">d1etxa_</a>	Alignment		12.4	33	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> FIS-like
18	<a href="#">c5lnkt_</a>	Alignment		12.1	42	<b>PDB header:</b> oxidoreductase <b>Chain:</b> T: <b>PDB Molecule:</b> <b>PDBTitle:</b> entire ovine respiratory complex i
19	<a href="#">c2dbbA_</a>	Alignment		12.0	19	<b>PDB header:</b> transcriptional regulator <b>Chain:</b> A: <b>PDB Molecule:</b> putative hth-type transcriptional regulator ph0061; <b>PDBTitle:</b> crystal structure of ph0061
20	<a href="#">c2cfxD_</a>	Alignment		11.5	19	<b>PDB header:</b> transcription <b>Chain:</b> D: <b>PDB Molecule:</b> hth-type transcriptional regulator lrpc; <b>PDBTitle:</b> structure of b.subtilis lrpc
21	<a href="#">c5ldwn_</a>	Alignment	not modelled	11.3	42	<b>PDB header:</b> oxidoreductase <b>Chain:</b> N: <b>PDB Molecule:</b> nadh-ubiquinone oxidoreductase chain 2; <b>PDBTitle:</b> structure of mammalian respiratory complex i, class1
22	<a href="#">c5lc5n_</a>	Alignment	not modelled	11.3	42	<b>PDB header:</b> oxidoreductase <b>Chain:</b> N: <b>PDB Molecule:</b> nadh-ubiquinone oxidoreductase chain 2; <b>PDBTitle:</b> structure of mammalian respiratory complex i, class2
23	<a href="#">c5ldxn_</a>	Alignment	not modelled	11.3	42	<b>PDB header:</b> oxidoreductase <b>Chain:</b> N: <b>PDB Molecule:</b> nadh-ubiquinone oxidoreductase chain 2; <b>PDBTitle:</b> structure of mammalian respiratory complex i, class3.
24	<a href="#">c4ds7G_</a>	Alignment	not modelled	11.2	41	<b>PDB header:</b> protein binding <b>Chain:</b> G: <b>PDB Molecule:</b> spindle pole body component 110; <b>PDBTitle:</b> crystal structure of yeast calmodulin bound to the c-terminal fragment2 of spindle pole body protein spc110
25	<a href="#">c5m7nA_</a>	Alignment	not modelled	11.2	14	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> nitrogen assimilation regulatory protein; <b>PDBTitle:</b> crystal structure of ntrx from brucella abortus in complex with atp2 processed with the crystalldirect automated mounting and cryo-cooling3 technology
26	<a href="#">d1ttva_</a>	Alignment	not modelled	11.1	17	<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
27	<a href="#">d1fipa_</a>	Alignment	not modelled	10.7	33	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> FIS-like
28	<a href="#">c4a1eW_</a>	Alignment	not modelled	10.2	45	<b>PDB header:</b> ribosome <b>Chain:</b> W: <b>PDB Molecule:</b> 60s ribosomal protein l31; <b>PDBTitle:</b> t.thermophila 60s ribosomal subunit in complex with2 initiation factor 6. this file contains 5s rrna, 5.8s rrna3 and proteins of molecule 1

29	<a href="#">c4b6ad</a>	Alignment	not modelled	10.1	55	<b>PDB header:</b> ribosome <b>Chain:</b> D: <b>PDB Molecule:</b> 60s ribosomal protein l5; <b>PDBTitle:</b> cryo-em structure of the 60s ribosomal subunit in complex2 with arx1 and rei1
30	<a href="#">c2xzmL</a>	Alignment	not modelled	10.0	27	<b>PDB header:</b> ribosome <b>Chain:</b> L: <b>PDB Molecule:</b> 40s ribosomal protein s12; <b>PDBTitle:</b> crystal structure of the eukaryotic 40s ribosomal2 subunit in complex with initiation factor 1. this file3 contains the 40s subunit and initiation factor for4 molecule 1
31	<a href="#">d1nx4a</a>	Alignment	not modelled	10.0	23	<b>Fold:</b> Double-stranded beta-helix <b>Superfamily:</b> Clavaminatase synthase-like <b>Family:</b> gamma-Butyrobetaine hydroxylase
32	<a href="#">c6gcsR</a>	Alignment	not modelled	9.7	42	<b>PDB header:</b> oxidoreductase <b>Chain:</b> R: <b>PDB Molecule:</b> ni2m subunit; <b>PDBTitle:</b> cryo-em structure of respiratory complex i from yarrowia lipolytica
33	<a href="#">c5fiyE</a>	Alignment	not modelled	9.7	37	<b>PDB header:</b> apoptosis <b>Chain:</b> E: <b>PDB Molecule:</b> prkc apoptosis wt1 regulator protein; <b>PDBTitle:</b> crystal structure of coiled coil domain of pawr
34	<a href="#">c3j21a</a>	Alignment	not modelled	9.7	27	<b>PDB header:</b> ribosome <b>Chain:</b> A: <b>PDB Molecule:</b> 50s ribosomal protein l1p; <b>PDBTitle:</b> promiscuous behavior of proteins in archaeal ribosomes revealed by2 cryo-em: implications for evolution of eukaryotic ribosomes (50s3 ribosomal proteins)
35	<a href="#">c2e7xA</a>	Alignment	not modelled	9.4	19	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> 150aa long hypothetical transcriptional regulator; <b>PDBTitle:</b> structure of the lrp/asnc like transcriptional regulator from2 sulfobolus tokodaii 7 complexed with its cognate ligand
36	<a href="#">c2k6rA</a>	Alignment	not modelled	9.2	44	<b>PDB header:</b> de novo protein <b>Chain:</b> A: <b>PDB Molecule:</b> full sequence design 1 synthetic superstable; <b>PDBTitle:</b> protein folding on a highly rugged landscape: experimental observation2 of glassy dynamics and structural frustration
37	<a href="#">c4l5eA</a>	Alignment	not modelled	9.2	48	<b>PDB header:</b> protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulator (ntrc family); <b>PDBTitle:</b> crystal structure of a. aeolicus ntrc1 dna binding domain
38	<a href="#">c3zf7h</a>	Alignment	not modelled	9.1	55	<b>PDB header:</b> ribosome <b>Chain:</b> H: <b>PDB Molecule:</b> <b>PDBTitle:</b> high-resolution cryo-electron microscopy structure of the trypanosoma2 brucei ribosome
39	<a href="#">c3u5gX</a>	Alignment	not modelled	8.4	22	<b>PDB header:</b> ribosome <b>Chain:</b> X: <b>PDB Molecule:</b> 40s ribosomal protein s23-a; <b>PDBTitle:</b> the structure of the eukaryotic ribosome at 3.0 a resolution. this2 entry contains proteins of the 40s subunit, ribosome b
40	<a href="#">d1r69a</a>	Alignment	not modelled	8.3	13	<b>Fold:</b> lambda repressor-like DNA-binding domains <b>Superfamily:</b> lambda repressor-like DNA-binding domains <b>Family:</b> Phage repressors
41	<a href="#">c2kuoA</a>	Alignment	not modelled	8.3	45	<b>PDB header:</b> metal binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> aprataxin and pnk-like factor; <b>PDBTitle:</b> structure and identification of adp-ribose recognition motifs of aplf2 and role in the dna damage response
42	<a href="#">c1fsvA</a>	Alignment	not modelled	8.1	44	<b>PDB header:</b> beta beta alpha motif <b>Chain:</b> A: <b>PDB Molecule:</b> full sequence design 1 of beta beta alpha motif; <b>PDBTitle:</b> full sequence design 1 (fsd-1) of beta beta alpha motif,2 nmr, minimized average structure
43	<a href="#">c1fsdA</a>	Alignment	not modelled	8.1	44	<b>PDB header:</b> novel sequence <b>Chain:</b> A: <b>PDB Molecule:</b> full sequence design 1 of beta beta alpha motif; <b>PDBTitle:</b> full sequence design 1 (fsd-1) of beta beta alpha motif,2 nmr, 41 structures
44	<a href="#">c2fjrB</a>	Alignment	not modelled	7.9	5	<b>PDB header:</b> transcription regulator <b>Chain:</b> B: <b>PDB Molecule:</b> repressor protein ci; <b>PDBTitle:</b> crystal structure of bacteriophage 186
45	<a href="#">c1s1iW</a>	Alignment	not modelled	7.8	55	<b>PDB header:</b> ribosome <b>Chain:</b> W: <b>PDB Molecule:</b> 60s ribosomal protein l31; <b>PDBTitle:</b> structure of the ribosomal 80s-eef2-sordarin complex from yeast2 obtained by docking atomic models for rna and protein components into3 a 11.7 a cryo-em map. this file, 1s1i, contains 60s subunit. the 40s4 ribosomal subunit is in file 1s1h.
46	<a href="#">c6fkqC</a>	Alignment	not modelled	7.7	22	<b>PDB header:</b> toxin <b>Chain:</b> C: <b>PDB Molecule:</b> rv1990c (mbca); <b>PDBTitle:</b> crystal structure of the m.tuberculosis mbct-mbca toxin-antitoxin2 complex.
47	<a href="#">c2kneB</a>	Alignment	not modelled	7.6	50	<b>PDB header:</b> metal transport <b>Chain:</b> B: <b>PDB Molecule:</b> atpase, ca++ transporting, plasma membrane 4; <b>PDBTitle:</b> calmodulin wraps around its binding domain in the plasma2 membrane ca2+ pump anchored by a novel 18-1 motif
48	<a href="#">c3izrg</a>	Alignment	not modelled	7.6	73	<b>PDB header:</b> ribosome <b>Chain:</b> G: <b>PDB Molecule:</b> 60s ribosomal protein l6 (l6e); <b>PDBTitle:</b> localization of the large subunit ribosomal proteins into a 5.5 a2 cryo-em map of triticum aestivum translating 80s ribosome
49	<a href="#">d1vqox1</a>	Alignment	not modelled	7.5	27	<b>Fold:</b> Ribosomal protein L31e <b>Superfamily:</b> Ribosomal protein L31e <b>Family:</b> Ribosomal protein L31e
50	<a href="#">c3qp5C</a>	Alignment	not modelled	7.4	27	<b>PDB header:</b> transcription <b>Chain:</b> C: <b>PDB Molecule:</b> cvir transcriptional regulator; <b>PDBTitle:</b> crystal structure of cvir bound to antagonist chlorolactone (cl)
51	<a href="#">c2l4aA</a>	Alignment	not modelled	7.4	22	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> leucine responsive regulatory protein; <b>PDBTitle:</b> nmr structure of the dna-binding domain of e.coli lrp
52	<a href="#">d1trra</a>	Alianment	not modelled	7.3	24	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> TrpR-like

						<b>Family:</b> Trp repressor, TrpR
53	<a href="#">d1ku7a_</a>	Alignment	not modelled	7.2	29	<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 <b>PDB header:</b> hydrolase/rna
54	<a href="#">c6ah3B_</a>	Alignment	not modelled	7.1	34	<b>Chain:</b> B: <b>PDB Molecule:</b> ribonucleases p/mrp protein subunit pop1; <b>PDBTitle:</b> cryo-em structure of yeast ribonuclease p with pre-trna substrate
55	<a href="#">c6ahrB_</a>	Alignment	not modelled	7.0	41	<b>PDB header:</b> hydrolase/rna <b>Chain:</b> B: <b>PDB Molecule:</b> ribonucleases p/mrp protein subunit pop1; <b>PDBTitle:</b> cryo-em structure of human ribonuclease p
56	<a href="#">c3j3bd_</a>	Alignment	not modelled	7.0	73	<b>PDB header:</b> ribosome <b>Chain:</b> D: <b>PDB Molecule:</b> 60s ribosomal protein l5; <b>PDBTitle:</b> structure of the human 60s ribosomal proteins
57	<a href="#">c3t0yA_</a>	Alignment	not modelled	6.8	29	<b>PDB header:</b> transcription regulator/protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> response regulator; <b>PDBTitle:</b> structure of the phyr anti-anti-sigma domain bound to the anti-sigma2 factor, nepr
58	<a href="#">c2r0qF_</a>	Alignment	not modelled	6.8	21	<b>PDB header:</b> recombination/dna <b>Chain:</b> F: <b>PDB Molecule:</b> putative transposon tn552 dna-invertase bin3; <b>PDBTitle:</b> crystal structure of a serine recombinase- dna regulatory2 complex
59	<a href="#">c1wqkA_</a>	Alignment	not modelled	6.7	80	<b>PDB header:</b> toxin <b>Chain:</b> A: <b>PDB Molecule:</b> toxin apetx1; <b>PDBTitle:</b> solution structure of apetx1, a specific peptide inhibitor2 of human ether-a-go-go-related gene potassium channels3 from the venom of the sea anemone anthopleura4 elegantissima: a new fold for an herg toxin
60	<a href="#">c3t72o_</a>	Alignment	not modelled	6.3	17	<b>PDB header:</b> transcription/dna <b>Chain:</b> O: <b>PDB Molecule:</b> pho box dna (strand 1); <b>PDBTitle:</b> phob(e)-sigma70(4)-(rnap-beta-flap-tip-helix)-dna transcription2 activation sub-complex
61	<a href="#">d1jxa2</a>	Alignment	not modelled	6.3	43	<b>Fold:</b> beta-Trefoil <b>Superfamily:</b> Agglutinin <b>Family:</b> Agglutinin
62	<a href="#">c2e1cA_</a>	Alignment	not modelled	6.1	15	<b>PDB header:</b> transcription/dna <b>Chain:</b> A: <b>PDB Molecule:</b> putative hth-type transcriptional regulator ph1519; <b>PDBTitle:</b> structure of putative hth-type transcriptional regulator ph1519/dna2 complex
63	<a href="#">d1zrua1</a>	Alignment	not modelled	6.0	70	<b>Fold:</b> Virus attachment protein globular domain <b>Superfamily:</b> Virus attachment protein globular domain <b>Family:</b> Lactophage receptor-binding protein head domain
64	<a href="#">c2n64B_</a>	Alignment	not modelled	5.7	38	<b>PDB header:</b> signaling protein <b>Chain:</b> B: <b>PDB Molecule:</b> sh3 domain-containing kinase-binding protein 1; <b>PDBTitle:</b> nmr structure of the c-terminal coiled-coil domain of cin85
65	<a href="#">c2cmyB_</a>	Alignment	not modelled	5.6	69	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> veronica hederifolia trypsin inhibitor; <b>PDBTitle:</b> crystal complex between bovine trypsin and veronica2 hederifolia trypsin inhibitor
66	<a href="#">d2cmyb1</a>	Alignment	not modelled	5.6	69	<b>Fold:</b> Toxic hairpin <b>Superfamily:</b> VhTI-like <b>Family:</b> VhTI-like
67	<a href="#">c4tvxT_</a>	Alignment	not modelled	5.6	33	<b>PDB header:</b> <b>PDB COMPND:</b>
68	<a href="#">c3ieiD_</a>	Alignment	not modelled	5.5	35	<b>PDB header:</b> transferase <b>Chain:</b> D: <b>PDB Molecule:</b> leucine carboxyl methyltransferase 1; <b>PDBTitle:</b> crystal structure of human leucine carboxylmethyltransferase-1 in2 complex with s-adenosyl homocysteine
69	<a href="#">c2ln3A_</a>	Alignment	not modelled	5.5	59	<b>PDB header:</b> de novo protein <b>Chain:</b> A: <b>PDB Molecule:</b> de novo designed protein or135; <b>PDBTitle:</b> solution nmr structure of de novo designed protein, if3-like fold,2 northeast structural genomics consortium target or135 (casd target)
70	<a href="#">c3da0C_</a>	Alignment	not modelled	5.4	70	<b>PDB header:</b> viral protein <b>Chain:</b> C: <b>PDB Molecule:</b> cleaved chimeric receptor binding protein from <b>PDBTitle:</b> crystal structure of a cleaved form of a chimeric receptor binding2 protein from lactococcal phages subspecies tp901-1 and p2
71	<a href="#">c2lsqA_</a>	Alignment	not modelled	5.3	64	<b>PDB header:</b> immune system <b>Chain:</b> A: <b>PDB Molecule:</b> analog of the fragment 197-221 of beta-1 adrenoreceptor; <b>PDBTitle:</b> analog of the fragment 197-221 of beta-1 adrenoreceptor
72	<a href="#">c3d8mA_</a>	Alignment	not modelled	5.3	70	<b>PDB header:</b> virus/viral protein <b>Chain:</b> A: <b>PDB Molecule:</b> baseplate protein, receptor binding protein; <b>PDBTitle:</b> crystal structure of a chimeric receptor binding protein from2 lactococcal phages subspecies tp901-1 and p2
73	<a href="#">c2zwaA_</a>	Alignment	not modelled	5.3	35	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> leucine carboxyl methyltransferase 2; <b>PDBTitle:</b> crystal structure of trna wybutosine synthesizing enzyme2 tyw4
74	<a href="#">c3e7ID_</a>	Alignment	not modelled	5.2	22	<b>PDB header:</b> transcription regulator <b>Chain:</b> D: <b>PDB Molecule:</b> transcriptional regulator (ntrc family); <b>PDBTitle:</b> crystal structure of sigma54 activator ntrc4's dna binding2 domain
75	<a href="#">c2gqgB_</a>	Alignment	not modelled	5.1	22	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> leucine-responsive regulatory protein; <b>PDBTitle:</b> crystal structure of e. coli leucine-responsive regulatory protein2 (lrp)
76	<a href="#">d2cg4a1</a>	Alignment	not modelled	5.1	25	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain

