




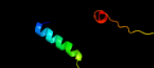

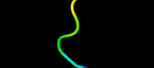

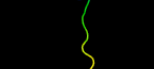

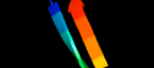

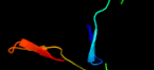

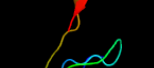

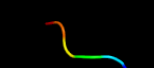






# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0122_(-)_148489_148857
Date	Tue Jul 23 14:50:16 BST 2019
Unique Job ID	65292ea3ca00bba6

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c2equA_</a>	 Alignment		46.5	30	<b>PDB header:</b> protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> phd finger protein 20-like 1; <b>PDBTitle:</b> solution structure of the tudor domain of phd finger2 protein 20-like 1
2	<a href="#">c2yf2C_</a>	 Alignment		39.9	29	<b>PDB header:</b> immune system <b>Chain:</b> C: <b>PDB Molecule:</b> c4b binding protein; <b>PDBTitle:</b> crystal structure of the oligomerisation domain of c4b-binding2 protein from gallus gallus
3	<a href="#">c3w0ID_</a>	 Alignment		27.1	43	<b>PDB header:</b> transferase/transferase inhibitor <b>Chain:</b> D: <b>PDB Molecule:</b> glucokinase regulatory protein; <b>PDBTitle:</b> the crystal structure of xenopus glucokinase and glucokinase2 regulatory protein complex
4	<a href="#">c1qfnB_</a>	 Alignment		26.8	78	<b>PDB header:</b> electron transport/oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> protein (ribonucleoside-diphosphate reductase 1); <b>PDBTitle:</b> glutaredoxin-1-ribonucleotide reductase b1 mixed disulfide2 bond
5	<a href="#">c4bbaA_</a>	 Alignment		26.2	24	<b>PDB header:</b> protein-binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> glucokinase regulatory protein; <b>PDBTitle:</b> crystal structure of glucokinase regulatory protein complexed to2 phosphate
6	<a href="#">c2kzba_</a>	 Alignment		24.8	46	<b>PDB header:</b> protein transport <b>Chain:</b> A: <b>PDB Molecule:</b> autophagy-related protein 19; <b>PDBTitle:</b> solution structure of alpha-mannosidase binding domain of atg19
7	<a href="#">d1npla_</a>	 Alignment		22.6	29	<b>Fold:</b> beta-Prism II <b>Superfamily:</b> alpha-D-mannose-specific plant lectins <b>Family:</b> alpha-D-mannose-specific plant lectins
8	<a href="#">c3r0eC_</a>	 Alignment		22.0	24	<b>PDB header:</b> sugar binding protein <b>Chain:</b> C: <b>PDB Molecule:</b> lectin; <b>PDBTitle:</b> structure of remusatia vivipara lectin
9	<a href="#">d1v54k_</a>	 Alignment		19.8	67	<b>Fold:</b> Single transmembrane helix <b>Superfamily:</b> Mitochondrial cytochrome c oxidase subunit VIIb <b>Family:</b> Mitochondrial cytochrome c oxidase subunit VIIb
10	<a href="#">c2y69X_</a>	 Alignment		19.8	67	<b>PDB header:</b> electron transport <b>Chain:</b> X: <b>PDB Molecule:</b> cytochrome c oxidase polypeptide 7b; <b>PDBTitle:</b> bovine heart cytochrome c oxidase re-refined with molecular oxygen
11	<a href="#">c2ov2O_</a>	 Alignment		18.5	11	<b>PDB header:</b> protein binding/transferase <b>Chain:</b> O: <b>PDB Molecule:</b> serine/threonine-protein kinase pak 4; <b>PDBTitle:</b> the crystal structure of the human rac3 in complex with the crib2 domain of human p21-activated kinase 4 (pak4)

12	<a href="#">c4lc9A_</a>	Alignment		17.7	20	<b>PDB header:</b> transferase/transferase regulator <b>Chain:</b> A: <b>PDB Molecule:</b> glucokinase regulatory protein; <b>PDBTitle:</b> structural basis for regulation of human glucokinase by glucokinase2 regulatory protein
13	<a href="#">c2kzkA_</a>	Alignment		16.4	46	<b>PDB header:</b> protein transport <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein yol083w; <b>PDBTitle:</b> solution structure of alpha-mannosidase binding domain of atg34
14	<a href="#">d1qw1a1</a>	Alignment		14.3	22	<b>Fold:</b> SH3-like barrel <b>Superfamily:</b> C-terminal domain of transcriptional repressors <b>Family:</b> FeoA-like
15	<a href="#">d1vqod1</a>	Alignment		14.1	31	<b>Fold:</b> RL5-like <b>Superfamily:</b> RL5-like <b>Family:</b> Ribosomal protein L5
16	<a href="#">c2ldmA_</a>	Alignment		13.8	24	<b>PDB header:</b> transcription/protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> solution structure of human phf20 tudor2 domain bound to a p53 segment2 containing a dimethyllysine analog p53k370me2
17	<a href="#">d1b2pa_</a>	Alignment		13.4	29	<b>Fold:</b> beta-Prism II <b>Superfamily:</b> alpha-D-mannose-specific plant lectins <b>Family:</b> alpha-D-mannose-specific plant lectins
18	<a href="#">c2odbB_</a>	Alignment		13.2	16	<b>PDB header:</b> protein binding <b>Chain:</b> B: <b>PDB Molecule:</b> serine/threonine-protein kinase pak 6; <b>PDBTitle:</b> the crystal structure of human cdc42 in complex with the crib domain2 of human p21-activated kinase 6 (pak6)
19	<a href="#">d1odha_</a>	Alignment		12.9	25	<b>Fold:</b> GCM domain <b>Superfamily:</b> GCM domain <b>Family:</b> GCM domain
20	<a href="#">c1vraB_</a>	Alignment		12.9	29	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> arginine biosynthesis bifunctional protein argj; <b>PDBTitle:</b> crystal structure of arginine biosynthesis bifunctional protein argj2 (10175521) from bacillus halodurans at 2.00 a resolution
21	<a href="#">c2w80E_</a>	Alignment	not modelled	12.8	21	<b>PDB header:</b> immune system <b>Chain:</b> E: <b>PDB Molecule:</b> complement factor h; <b>PDBTitle:</b> structure of a complex between neisseria meningitidis2 factor h binding protein and ccps 6-7 of human complement3 factor h
22	<a href="#">c4aydA_</a>	Alignment	not modelled	12.7	21	<b>PDB header:</b> immune system <b>Chain:</b> A: <b>PDB Molecule:</b> complement factor h; <b>PDBTitle:</b> structure of a complex between ccps 6 and 7 of human2 complement factor h and neisseria meningitidis fhbp3 variant 1 r106a mutant
23	<a href="#">c5gkeB_</a>	Alignment	not modelled	12.4	20	<b>PDB header:</b> hydrolase/dna <b>Chain:</b> B: <b>PDB Molecule:</b> endonuclease endoms; <b>PDBTitle:</b> structure of endoms-dsdna1 complex
24	<a href="#">c5d0bB_</a>	Alignment	not modelled	12.3	45	<b>PDB header:</b> oxidoreductase/rna <b>Chain:</b> B: <b>PDB Molecule:</b> epoxyqueuosine reductase; <b>PDBTitle:</b> crystal structure of epoxyqueuosine reductase with a trna-tyr2 epoxyqueuosine-modified trna stem loop
25	<a href="#">c5d6sB_</a>	Alignment	not modelled	12.2	54	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> epoxyqueuosine reductase; <b>PDBTitle:</b> structure of epoxyqueuosine reductase from streptococcus thermophilus.
26	<a href="#">c4jhnD_</a>	Alignment	not modelled	11.8	11	<b>PDB header:</b> unknown function <b>Chain:</b> D: <b>PDB Molecule:</b> x-linked retinitis pigmentosa gtpase regulator; <b>PDBTitle:</b> the crystal structure of the rpgr rcc1-like domain
27	<a href="#">c2kx2A_</a>	Alignment	not modelled	11.7	56	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> putative uncharacterized protein; <b>PDBTitle:</b> the solution structure of mth1821
28	<a href="#">c3faoA_</a>	Alignment	not modelled	11.6	58	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> non-structural protein; <b>PDBTitle:</b> crystal structure of s118a mutant 3clsp of prrsv

29	<a href="#">c2ra9A_</a>	Alignment	not modelled	11.5	36	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein duf1285; <b>PDBTitle:</b> crystal structure of a duf1285 family protein (sba1_2486) from2 shewanella baltica os155 at 1.40 a resolution
30	<a href="#">c1flIX_</a>	Alignment	not modelled	11.4	47	<b>PDB header:</b> apoptosis <b>Chain:</b> X: <b>PDB Molecule:</b> b-cell surface antigen cd40; <b>PDBTitle:</b> molecular basis for cd40 signaling mediated by traf3
31	<a href="#">c3qiiA_</a>	Alignment	not modelled	11.4	22	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> phd finger protein 20; <b>PDBTitle:</b> crystal structure of tudor domain 2 of human phd finger protein 20
32	<a href="#">c1flY_</a>	Alignment	not modelled	11.1	47	<b>PDB header:</b> apoptosis <b>Chain:</b> Y: <b>PDB Molecule:</b> b-cell surface antigen cd40; <b>PDBTitle:</b> molecular basis for cd40 signaling mediated by traf3
33	<a href="#">c3uaqB_</a>	Alignment	not modelled	10.5	44	<b>PDB header:</b> protein binding <b>Chain:</b> B: <b>PDB Molecule:</b> lbpb b-lobe; <b>PDBTitle:</b> crystal structure of the n-lobe domain of lactoferrin binding protein2 b (lbpb) of moraxella bovis
34	<a href="#">c1f3mB_</a>	Alignment	not modelled	10.4	42	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> serine/threonine-protein kinase pak-alpha; <b>PDBTitle:</b> crystal structure of human serine/threonine kinase pak1
35	<a href="#">c3en9B_</a>	Alignment	not modelled	10.4	22	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> o-sialoglycoprotein endopeptidase/protein kinase; <b>PDBTitle:</b> structure of the methanococcus jannaschii kae1-bud32 fusion2 protein
36	<a href="#">c1xnil_</a>	Alignment	not modelled	10.2	24	<b>PDB header:</b> cell cycle <b>Chain:</b> I: <b>PDB Molecule:</b> tumor suppressor p53-binding protein 1; <b>PDBTitle:</b> tandem tudor domain of 53bp1
37	<a href="#">c4a1cD_</a>	Alignment	not modelled	10.1	25	<b>PDB header:</b> ribosome <b>Chain:</b> D: <b>PDB Molecule:</b> 60s ribosomal protein l11; <b>PDBTitle:</b> t.thermophila 60s ribosomal subunit in complex with2 initiation factor 6. this file contains 5s rrna,3 5.8s rrna and proteins of molecule 4.
38	<a href="#">d2ed6a1</a>	Alignment	not modelled	10.1	35	<b>Fold:</b> WSSV envelope protein-like <b>Superfamily:</b> WSSV envelope protein-like <b>Family:</b> WSSV envelope protein-like
39	<a href="#">d1mbma_</a>	Alignment	not modelled	10.0	40	<b>Fold:</b> Trypsin-like serine proteases <b>Superfamily:</b> Trypsin-like serine proteases <b>Family:</b> Viral proteases
40	<a href="#">c3p8dB_</a>	Alignment	not modelled	9.7	21	<b>PDB header:</b> protein binding <b>Chain:</b> B: <b>PDB Molecule:</b> medulloblastoma antigen mu-mb-50.72; <b>PDBTitle:</b> crystal structure of the second tudor domain of human phf20 (homodimer2 form)
41	<a href="#">d2rb6a1</a>	Alignment	not modelled	9.2	28	<b>Fold:</b> Sm-like fold <b>Superfamily:</b> Sm-like ribonucleoproteins <b>Family:</b> YgdI/YgdR-like
42	<a href="#">d1i7na1</a>	Alignment	not modelled	9.1	20	<b>Fold:</b> PreATP-grasp domain <b>Superfamily:</b> PreATP-grasp domain <b>Family:</b> Synapsin domain
43	<a href="#">d2rd1a1</a>	Alignment	not modelled	8.8	22	<b>Fold:</b> Sm-like fold <b>Superfamily:</b> Sm-like ribonucleoproteins <b>Family:</b> YgdI/YgdR-like
44	<a href="#">d1vr3a1</a>	Alignment	not modelled	8.6	26	<b>Fold:</b> Double-stranded beta-helix <b>Superfamily:</b> RmlC-like cupins <b>Family:</b> Acireductone dioxygenase
45	<a href="#">c3c6fD_</a>	Alignment	not modelled	8.5	14	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> D: <b>PDB Molecule:</b> yetf protein; <b>PDBTitle:</b> crystal structure of protein bsu07140 from bacillus subtilis
46	<a href="#">c1s1ij_</a>	Alignment	not modelled	8.5	27	<b>PDB header:</b> ribosome <b>Chain:</b> J: <b>PDB Molecule:</b> 60s ribosomal protein l11; <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.
47	<a href="#">d3bdua1</a>	Alignment	not modelled	8.4	28	<b>Fold:</b> Sm-like fold <b>Superfamily:</b> Sm-like ribonucleoproteins <b>Family:</b> YgdI/YgdR-like
48	<a href="#">c2re3A_</a>	Alignment	not modelled	8.4	50	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> crystal structure of a duf1285 family protein (spo_0140) from2 silicibacter pomeroyi dss-3 at 2.50 a resolution
49	<a href="#">c1e0aB_</a>	Alignment	not modelled	8.2	37	<b>PDB header:</b> signalling protein/kinase <b>Chain:</b> B: <b>PDB Molecule:</b> serine/threonine-protein kinase pak-alpha; <b>PDBTitle:</b> cdc42 complexed with the gtpase binding domain of p212 activated kinase
50	<a href="#">c5gsmB_</a>	Alignment	not modelled	8.1	16	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> exo-beta-d-glucosaminidase; <b>PDBTitle:</b> glycoside hydrolase b with product
51	<a href="#">c4u9cA_</a>	Alignment	not modelled	8.1	47	<b>PDB header:</b> lactoferrin-binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> lactoferrin-binding protein b; <b>PDBTitle:</b> structure of the lbpb n-lobe from neisseria meningitidis
52	<a href="#">c4aydB_</a>	Alignment	not modelled	8.0	21	<b>PDB header:</b> immune system <b>Chain:</b> B: <b>PDB Molecule:</b> complement factor h; <b>PDBTitle:</b> structure of a complex between ccps 6 and 7 of human2 complement factor h and neisseria meningitidis fhbp3 variant 1 r106a mutant
53	<a href="#">c3it4B_</a>	Alignment	not modelled	7.9	21	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> arginine biosynthesis bifunctional protein argj <b>PDBTitle:</b> the crystal structure of ornithine acetyltransferase from2 mycobacterium tuberculosis (rv1653) at 1.7 a

54	<a href="#">d2ra2a1</a>	Alignment	not modelled	7.5	29	<b>Fold:</b> Sm-like fold <b>Superfamily:</b> Sm-like ribonucleoproteins <b>Family:</b> YgdI/YgdR-like
55	<a href="#">c3fetA</a>	Alignment	not modelled	7.1	13	<b>PDB header:</b> electron transport <b>Chain:</b> A; <b>PDB Molecule:</b> electron transfer flavoprotein subunit alpha related <b>PDBTitle:</b> crystal structure of the electron transfer flavoprotein subunit alpha2 related protein ta0212 from thermoplasma acidophilum
56	<a href="#">d1gesa3</a>	Alignment	not modelled	7.0	18	<b>Fold:</b> CO dehydrogenase flavoprotein C-domain-like <b>Superfamily:</b> FAD/NAD-linked reductases, dimerisation (C-terminal) domain <b>Family:</b> FAD/NAD-linked reductases, dimerisation (C-terminal) domain
57	<a href="#">c2eoyA</a>	Alignment	not modelled	6.8	86	<b>PDB header:</b> transcription <b>Chain:</b> A; <b>PDB Molecule:</b> zinc finger protein 473; <b>PDBTitle:</b> solution structure of the c2h2 type zinc finger (region 557-2 589) of human zinc finger protein 473
58	<a href="#">c2ybyA</a>	Alignment	not modelled	6.7	24	<b>PDB header:</b> immune system <b>Chain:</b> A; <b>PDB Molecule:</b> complement factor h; <b>PDBTitle:</b> structure of domains 6 and 7 of the mouse complement regulator2 factor h
59	<a href="#">d1l4db</a>	Alignment	not modelled	6.7	16	<b>Fold:</b> beta-Grasp (ubiquitin-like) <b>Superfamily:</b> Staphylokinase/streptokinase <b>Family:</b> Staphylokinase/streptokinase
60	<a href="#">c3zf7L</a>	Alignment	not modelled	6.6	29	<b>PDB header:</b> ribosome <b>Chain:</b> L; <b>PDB Molecule:</b> 60s ribosomal protein l11, putative; <b>PDBTitle:</b> high-resolution cryo-electron microscopy structure of the trypanosoma2 brucei ribosome
61	<a href="#">d2k57a1</a>	Alignment	not modelled	6.4	29	<b>Fold:</b> Sm-like fold <b>Superfamily:</b> Sm-like ribonucleoproteins <b>Family:</b> YgdI/YgdR-like
62	<a href="#">d1vlva1</a>	Alignment	not modelled	6.4	29	<b>Fold:</b> ATC-like <b>Superfamily:</b> Aspartate/ornithine carbamoyltransferase <b>Family:</b> Aspartate/ornithine carbamoyltransferase
63	<a href="#">c3c00B</a>	Alignment	not modelled	6.2	27	<b>PDB header:</b> membrane protein, protein transport <b>Chain:</b> B; <b>PDB Molecule:</b> rescu; <b>PDBTitle:</b> crystal structural of the mutated g247t escu/spas c-terminal domain
64	<a href="#">c4aaqA</a>	Alignment	not modelled	6.2	64	<b>PDB header:</b> viral protein <b>Chain:</b> A; <b>PDB Molecule:</b> l2 protein iii (penton base); <b>PDBTitle:</b> dodecahedron formed of penton base protein from adenovirus ad3
65	<a href="#">c4d77A</a>	Alignment	not modelled	6.0	33	<b>PDB header:</b> signaling protein <b>Chain:</b> A; <b>PDB Molecule:</b> gliomedin; <b>PDBTitle:</b> high-resolution structure of the extracellular olfactomedin2 domain from gliomedin
66	<a href="#">c1vgpA</a>	Alignment	not modelled	5.9	39	<b>PDB header:</b> transferase <b>Chain:</b> A; <b>PDB Molecule:</b> 373aa long hypothetical citrate synthase; <b>PDBTitle:</b> crystal structure of an isozyme of citrate synthase from sulfolobus2 tokodaii strain7
67	<a href="#">d1k7ka</a>	Alignment	not modelled	5.7	17	<b>Fold:</b> Anticodon-binding domain-like <b>Superfamily:</b> ITPase-like <b>Family:</b> ITPase (Ham1)
68	<a href="#">d1pk8a1</a>	Alignment	not modelled	5.7	23	<b>Fold:</b> PreATP-grasp domain <b>Superfamily:</b> PreATP-grasp domain <b>Family:</b> Synapsin domain
69	<a href="#">c4pdtA</a>	Alignment	not modelled	5.6	26	<b>PDB header:</b> sugar binding protein <b>Chain:</b> A; <b>PDB Molecule:</b> mannose recognizing lectin; <b>PDBTitle:</b> japanese marasmius oreades lectin
70	<a href="#">c2c6xA</a>	Alignment	not modelled	5.6	45	<b>PDB header:</b> transferase <b>Chain:</b> A; <b>PDB Molecule:</b> citrate synthase 1; <b>PDBTitle:</b> structure of bacillus subtilis citrate synthase
71	<a href="#">c5o7hE</a>	Alignment	not modelled	5.6	35	<b>PDB header:</b> antiviral protein <b>Chain:</b> E; <b>PDB Molecule:</b> cas7fv; <b>PDBTitle:</b> structure of the cascade-i-fv complex from shewanella putrefaciens
72	<a href="#">c2qqpD</a>	Alignment	not modelled	5.6	67	<b>PDB header:</b> virus <b>Chain:</b> D; <b>PDB Molecule:</b> small capsid protein; <b>PDBTitle:</b> crystal structure of authentic providence virus
73	<a href="#">d1aj8a</a>	Alignment	not modelled	5.3	33	<b>Fold:</b> Citrate synthase <b>Superfamily:</b> Citrate synthase <b>Family:</b> Citrate synthase
74	<a href="#">c1o94D</a>	Alignment	not modelled	5.3	30	<b>PDB header:</b> electron transport <b>Chain:</b> D; <b>PDB Molecule:</b> electron transfer flavoprotein alpha-subunit; <b>PDBTitle:</b> ternary complex between trimethylamine dehydrogenase and2 electron transferring flavoprotein
75	<a href="#">c4xi7A</a>	Alignment	not modelled	5.1	33	<b>PDB header:</b> ligase <b>Chain:</b> A; <b>PDB Molecule:</b> e3 ubiquitin-protein ligase mib1; <b>PDBTitle:</b> crystal structure of the mzm-rep domains of mind bomb 1 in complex2 with jagged1 n-box peptide
76	<a href="#">c2x0dA</a>	Alignment	not modelled	5.1	25	<b>PDB header:</b> transferase <b>Chain:</b> A; <b>PDB Molecule:</b> wsaf; <b>PDBTitle:</b> apo structure of wsaf
77	<a href="#">c2vzkD</a>	Alignment	not modelled	5.1	21	<b>PDB header:</b> transferase <b>Chain:</b> D; <b>PDB Molecule:</b> glutamate n-acetyltransferase 2 beta chain; <b>PDBTitle:</b> structure of the acyl-enzyme complex of an n-terminal nucleophile2 (ntn) hydrolase, oat2
78	<a href="#">d1jida</a>	Alignment	not modelled	5.0	29	<b>Fold:</b> SRP19 <b>Superfamily:</b> SRP19 <b>Family:</b> SRP19
						<b>PDB header:</b> translation <b>Chain:</b> G; <b>PDB Molecule:</b> protein ats1, diphthamide biosynthesis

79	<a href="#">c4d4pG</a>	Alignment	not modelled	5.0	32	protein 3; <b>PDBTitle:</b> crystal structure of the kti11 kti13 heterodimer spacegroup p65
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