
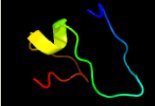

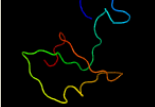
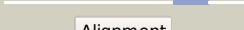










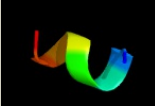
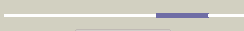




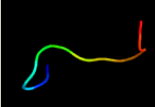

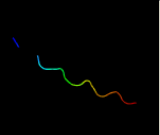
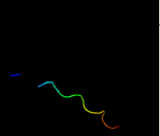
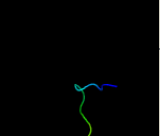
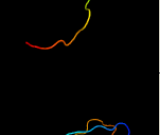



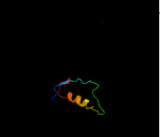


# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3572_(-)_4013690_4014220
Date	Fri Aug 9 18:20:25 BST 2019
Unique Job ID	2d8cbc88fc27997a

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">d1h3ga1</a>	 Alignment		37.9	26	<b>Fold:</b> Immunoglobulin-like beta-sandwich <b>Superfamily:</b> E set domains <b>Family:</b> E-set domains of sugar-utilizing enzymes
2	<a href="#">c5a7yA_</a>	 Alignment		37.9	12	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> trna (adenine(9)-n1)-methyltransferase; <b>PDBTitle:</b> crystal structure of sulfobolus acidocaldarius trm10 in2 complex with s-adenosylhomocysteine
3	<a href="#">d1gtfa_</a>	 Alignment		28.3	23	<b>Fold:</b> Double-stranded beta-helix <b>Superfamily:</b> TRAP-like <b>Family:</b> Trp RNA-binding attenuation protein (TRAP)
4	<a href="#">c5oevB_</a>	 Alignment		19.6	11	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> glutathione synthetase-like effector 22 (gpa-gss22-apo); <b>PDBTitle:</b> the structure of a glutathione synthetase like-effector (gss22) from2 globodera pallida in apoform.
5	<a href="#">c2hu9B_</a>	 Alignment		19.0	23	<b>PDB header:</b> metal transport <b>Chain:</b> B: <b>PDB Molecule:</b> mercuric transport protein periplasmic component; <b>PDBTitle:</b> x-ray structure of the archaeoglobus fulgidus copz n-2 terminal domain
6	<a href="#">c1mzwB_</a>	 Alignment		18.6	50	<b>PDB header:</b> isomerase <b>Chain:</b> B: <b>PDB Molecule:</b> u4/u6 snrnp 60kda protein; <b>PDBTitle:</b> crystal structure of a u4/u6 snrnp complex between human2 spliceosomal cyclophilin h and a u4/u6-60k peptide
7	<a href="#">d1olta_</a>	 Alignment		17.3	13	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Radical SAM enzymes <b>Family:</b> Oxygen-independent coproporphyrinogen III oxidase HemN
8	<a href="#">c2bzwB_</a>	 Alignment		15.6	75	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> bcl2-antagonist of cell death; <b>PDBTitle:</b> the crystal structure of bcl-xl in complex with full-length bad
9	<a href="#">c5oevD_</a>	 Alignment		14.9	14	<b>PDB header:</b> transferase <b>Chain:</b> D: <b>PDB Molecule:</b> glutathione synthetase-like effector 22 (gpa-gss22-apo); <b>PDBTitle:</b> the structure of a glutathione synthetase like-effector (gss22) from2 globodera pallida in apoform.
10	<a href="#">c6a0cB_</a>	 Alignment		14.3	47	<b>PDB header:</b> structural protein <b>Chain:</b> B: <b>PDB Molecule:</b> collagen type iii peptide; <b>PDBTitle:</b> structure of a triple-helix region of human collagen type iii
11	<a href="#">c4mitE_</a>	 Alignment		13.9	50	<b>PDB header:</b> signaling protein <b>Chain:</b> E: <b>PDB Molecule:</b> serine/threonine protein kinase pak, putative; <b>PDBTitle:</b> crystal structure of e. histolytica racc bound to the ehpak4 pbd

12	<a href="#">c4mitG_</a>	Alignment		13.8	50	<b>PDB header:</b> signaling protein <b>Chain:</b> G: <b>PDB Molecule:</b> serine/threonine protein kinase pak, putative; <b>PDBTitle:</b> crystal structure of e. histolytica racc bound to the ehpak4 pbd
13	<a href="#">c6a0cA_</a>	Alignment		13.5	47	<b>PDB header:</b> structural protein <b>Chain:</b> A: <b>PDB Molecule:</b> collagen type iii peptide; <b>PDBTitle:</b> structure of a triple-helix region of human collagen type iii
14	<a href="#">c6a0cC_</a>	Alignment		13.5	47	<b>PDB header:</b> structural protein <b>Chain:</b> C: <b>PDB Molecule:</b> collagen type iii peptide; <b>PDBTitle:</b> structure of a triple-helix region of human collagen type iii
15	<a href="#">c5ancC_</a>	Alignment		13.1	37	<b>PDB header:</b> translation <b>Chain:</b> C: <b>PDB Molecule:</b> 60s acidic ribosomal protein p0; <b>PDBTitle:</b> mechanism of eif6 release from the nascent 60s ribosomal subunit
16	<a href="#">c2jwyA_</a>	Alignment		13.1	10	<b>PDB header:</b> lipoprotein <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized lipoprotein yaji; <b>PDBTitle:</b> solution nmr structure of uncharacterized lipoprotein yaji from 2 escherichia coli. northeast structural genomics target er540
17	<a href="#">d1gyva_</a>	Alignment		12.7	44	<b>Fold:</b> Immunoglobulin-like beta-sandwich <b>Superfamily:</b> Clathrin adaptor appendage domain <b>Family:</b> gamma-adaptin C-terminal appendage domain-like
18	<a href="#">c2mcaA_</a>	Alignment		12.1	24	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> nmr structure of the protein yp_002937094.1 from eubacterium rectale
19	<a href="#">c2wyoC_</a>	Alignment		12.0	26	<b>PDB header:</b> ligase <b>Chain:</b> C: <b>PDB Molecule:</b> glutathione synthetase; <b>PDBTitle:</b> trypanosoma brucei glutathione synthetase
20	<a href="#">c3iz5s_</a>	Alignment		11.9	37	<b>PDB header:</b> ribosome <b>Chain:</b> S: <b>PDB Molecule:</b> 60s ribosomal protein l18a (l18ae); <b>PDBTitle:</b> localization of the large subunit ribosomal proteins into a 5.5 a2 cryo-em map of triticum aestivum translating 80s ribosome
21	<a href="#">d1m0wa1</a>	Alignment	not modelled	11.4	23	<b>Fold:</b> PreATP-grasp domain <b>Superfamily:</b> PreATP-grasp domain <b>Family:</b> Eukaryotic glutathione synthetase, substrate-binding domain
22	<a href="#">c3kvhA_</a>	Alignment	not modelled	11.4	60	<b>PDB header:</b> rna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> protein syndesmos; <b>PDBTitle:</b> crystal structure of human protein syndesmos (nudt16-like protein)
23	<a href="#">d1wapa_</a>	Alignment	not modelled	11.1	24	<b>Fold:</b> Double-stranded beta-helix <b>Superfamily:</b> TRAP-like <b>Family:</b> Trp RNA-binding attenuation protein (TRAP)
24	<a href="#">c1zzaA_</a>	Alignment	not modelled	10.8	60	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> stannin; <b>PDBTitle:</b> solution nmr structure of the membrane protein stannin
25	<a href="#">c3izcs_</a>	Alignment	not modelled	10.8	32	<b>PDB header:</b> ribosome <b>Chain:</b> S: <b>PDB Molecule:</b> 60s ribosomal protein rpl20 (l18ae); <b>PDBTitle:</b> localization of the large subunit ribosomal proteins into a 6.1 a2 cryo-em map of saccharomyces cerevisiae translating 80s ribosome
26	<a href="#">c3j3bq_</a>	Alignment	not modelled	10.4	26	<b>PDB header:</b> ribosome <b>Chain:</b> Q: <b>PDB Molecule:</b> 60s ribosomal protein l18; <b>PDBTitle:</b> structure of the human 60s ribosomal proteins
27	<a href="#">d1d2sa_</a>	Alignment	not modelled	10.1	9	<b>Fold:</b> Concanavalin A-like lectins/glucanases <b>Superfamily:</b> Concanavalin A-like lectins/glucanases <b>Family:</b> Laminin G-like module
28	<a href="#">d1gywb_</a>	Alignment	not modelled	9.7	44	<b>Fold:</b> Immunoglobulin-like beta-sandwich <b>Superfamily:</b> Clathrin adaptor appendage domain <b>Family:</b> gamma-adaptin C-terminal appendage domain-like
29	<a href="#">d1ng0a_</a>	Alignment	not modelled	9.0	19	<b>Fold:</b> Nucleoplasmin-like/VP (viral coat and capsid proteins) <b>Superfamily:</b> Positive stranded ssRNA viruses

						Family:Tombusviridae-like VP
30	<a href="#">c1ng0A</a>	Alignment	not modelled	9.0	19	<b>PDB header:</b> virus <b>Chain:</b> A: <b>PDB Molecule:</b> coat protein; <b>PDBTitle:</b> the three-dimensional structure of cocksfoot mottle virus at 2.7a2 resolution
31	<a href="#">c3couA</a>	Alignment	not modelled	8.8	60	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> nucleoside diphosphate-linked moiety x motif 16; <b>PDBTitle:</b> crystal structure of human nudix motif 16 (nudt16)
32	<a href="#">c3kp9A</a>	Alignment	not modelled	8.7	43	<b>PDB header:</b> blood coagulation,oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> vkorc1/thioredoxin domain protein; <b>PDBTitle:</b> structure of a bacterial homolog of vitamin k epoxide reductase
33	<a href="#">c4jw1A</a>	Alignment	not modelled	8.5	33	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> trna (guanine(9)-n1)-methyltransferase; <b>PDBTitle:</b> crystal structure of sctrm10(84)-sah complex
34	<a href="#">c2e9gA</a>	Alignment	not modelled	8.3	10	<b>PDB header:</b> protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> ap-1 complex subunit gamma-2; <b>PDBTitle:</b> solution structure of the alpha adaptinc2 domain from human2 adapter-related protein complex 1 gamma 2 subunit
35	<a href="#">c4jwhB</a>	Alignment	not modelled	8.1	23	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> trna (guanine(9)-n1)-methyltransferase; <b>PDBTitle:</b> crystal structure of sptrm10(full length)-sah complex
36	<a href="#">c6emsA</a>	Alignment	not modelled	8.1	16	<b>PDB header:</b> rna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> trna (guanine(9)-adenine(9)-n1)-methyltransferase; <b>PDBTitle:</b> crystal structure of dual specific trm10 construct from thermococcus2 kodakaraensis.
37	<a href="#">c1m0tB</a>	Alignment	not modelled	8.1	23	<b>PDB header:</b> ligase <b>Chain:</b> B: <b>PDB Molecule:</b> glutathione synthetase; <b>PDBTitle:</b> yeast glutathione synthase
38	<a href="#">c6emvA</a>	Alignment	not modelled	8.0	16	<b>PDB header:</b> rna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> trna (guanine(9)-adenine(9)-n1)-methyltransferase; <b>PDBTitle:</b> crystal structure of dual specific trm10 construct from thermococcus2 kodakaraensis.
39	<a href="#">c3ej9D</a>	Alignment	not modelled	7.6	32	<b>PDB header:</b> hydrolase <b>Chain:</b> D: <b>PDB Molecule:</b> beta-subunit of trans-3-chloroacrylic acid dehalogenase; <b>PDBTitle:</b> structural and mechanistic analysis of trans-3-chloroacrylic acid2 dehalogenase activity
40	<a href="#">c4v19P</a>	Alignment	not modelled	7.2	40	<b>PDB header:</b> ribosome <b>Chain:</b> P: <b>PDB Molecule:</b> mitoribosomal protein ul15m, mrp15; <b>PDBTitle:</b> structure of the large subunit of the mammalian mitoribosome, part 12 of 2
41	<a href="#">c4hubG</a>	Alignment	not modelled	7.1	42	<b>PDB header:</b> ribosome <b>Chain:</b> G: <b>PDB Molecule:</b> 50s ribosomal protein l10e; <b>PDBTitle:</b> the re-refined crystal structure of the haloarcula marismortui large2 ribosomal subunit at 2.4 angstrom resolution: more complete structure3 of the l7/l12 and l1 stalk, l5 and lx proteins
42	<a href="#">c1z45A</a>	Alignment	not modelled	7.0	22	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> gal10 bifunctional protein; <b>PDBTitle:</b> crystal structure of the gal10 fusion protein galactose2 mutarotase/udp-galactose 4-epimerase from saccharomyces cerevisiae3 complexed with nad, udp-glucose, and galactose
43	<a href="#">c2k8jX</a>	Alignment	not modelled	6.9	46	<b>PDB header:</b> viral protein <b>Chain:</b> X: <b>PDB Molecule:</b> p7tm2; <b>PDBTitle:</b> solution structure of hcv p7 tm2
44	<a href="#">c5nfjA</a>	Alignment	not modelled	6.9	26	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> mitochondrial ribonuclease p protein 1; <b>PDBTitle:</b> crystal structure of the methyltransferase subunit of human2 mitochondrial ribonuclease p (mrpp1) bound to s-adenosyl-methionine3 (sam)
45	<a href="#">d1x6ha1</a>	Alignment	not modelled	6.7	50	<b>Fold:</b> beta-beta-alpha zinc fingers <b>Superfamily:</b> beta-beta-alpha zinc fingers <b>Family:</b> Classic zinc finger, C2H2
46	<a href="#">c4ebjB</a>	Alignment	not modelled	6.6	42	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> aminoglycoside nucleotidyltransferase; <b>PDBTitle:</b> crystal structure of aminoglycoside 4'-o-adenylyltransferase ant(4)-2 iib, apo
47	<a href="#">d1ii7a</a>	Alignment	not modelled	6.5	11	<b>Fold:</b> Metallo-dependent phosphatases <b>Superfamily:</b> Metallo-dependent phosphatases <b>Family:</b> DNA double-strand break repair nuclease
48	<a href="#">c1bqfA</a>	Alignment	not modelled	6.5	83	<b>PDB header:</b> hormone/growth factor <b>Chain:</b> A: <b>PDB Molecule:</b> protein (growth-blocking peptide); <b>PDBTitle:</b> growth-blocking peptide (gbp) from pseudaletia separata
49	<a href="#">d1o75a2</a>	Alignment	not modelled	6.3	33	<b>Fold:</b> Immunoglobulin-like beta-sandwich <b>Superfamily:</b> Tp47 lipoprotein, middle and C-terminal domains <b>Family:</b> Tp47 lipoprotein, middle and C-terminal domains
50	<a href="#">d2j7ja3</a>	Alignment	not modelled	6.3	50	<b>Fold:</b> beta-beta-alpha zinc fingers <b>Superfamily:</b> beta-beta-alpha zinc fingers <b>Family:</b> Classic zinc finger, C2H2
51	<a href="#">c4jcbD</a>	Alignment	not modelled	6.2	31	<b>PDB header:</b> photosynthesis <b>Chain:</b> D: <b>PDB Molecule:</b> light-harvesting protein b-875 alpha chain; <b>PDBTitle:</b> rc-lh1-pufx dimer complex from rhodobacter sphaeroides
52	<a href="#">c6focB</a>	Alignment	not modelled	6.1	31	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> atp synthase subunit alpha,atp synthase subunit alpha,atp <b>PDBTitle:</b> f1-atpase from mycobacterium smegmatis
53	<a href="#">d2hw4a1</a>	Alignment	not modelled	5.9	14	<b>Fold:</b> PHP14-like <b>Superfamily:</b> PHP14-like <b>Family:</b> janus/Ocnus
54	<a href="#">c1pdlC</a>	Alignment	not modelled	5.9	67	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> tail-associated lysozyme; <b>PDBTitle:</b> fitting of gp5 in the cryoem reconstruction of the

					bacteriophage t42 baseplate
55	<a href="#">c4fmwA_</a>	Alignment	not modelled	5.8	23 <b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> rna (guanine-9-)-methyltransferase domain-containing <b>PDBTitle:</b> crystal structure of methyltransferase domain of human rna (guanine-9-2 ) methyltransferase domain containing protein 2
56	<a href="#">c6ht4A_</a>	Alignment	not modelled	5.7	78 <b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> ns5a; <b>PDBTitle:</b> nmr structure of ns5a-d2 (jfh1) peptide (304-323)
57	<a href="#">c2hw4A_</a>	Alignment	not modelled	5.5	14 <b>PDB header:</b> structural genomics, hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> 14 kda phosphohistidine phosphatase; <b>PDBTitle:</b> crystal structure of human phosphohistidine phosphatase
58	<a href="#">d1b78a_</a>	Alignment	not modelled	5.4	24 <b>Fold:</b> Anticodon-binding domain-like <b>Superfamily:</b> ITPase-like <b>Family:</b> ITPase (Ham1)
59	<a href="#">c6nm9A_</a>	Alignment	not modelled	5.1	27 <b>PDB header:</b> unknown function/rna <b>Chain:</b> A: <b>PDB Molecule:</b> acrva4; <b>PDBTitle:</b> cryoem structure of the lbcas12a-crrna-acrva4 dimer
60	<a href="#">c3djcA_</a>	Alignment	not modelled	5.1	12 <b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> type iii pantothenate kinase; <b>PDBTitle:</b> crystal structure of pantothenate kinase from legionella pneumophila
61	<a href="#">c6dx5B_</a>	Alignment	not modelled	5.1	26 <b>PDB header:</b> hydrolase, protein binding <b>Chain:</b> B: <b>PDB Molecule:</b> rna-dependent rna polymerase; <b>PDBTitle:</b> crystal structure of the viral otu domain protease from farallon virus