













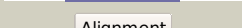

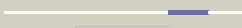
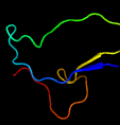


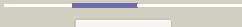

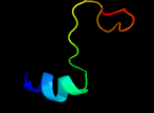

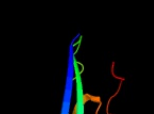
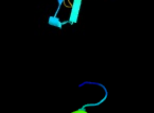
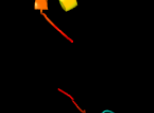



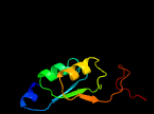


# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0394c (-)_474125_474844
Date	Tue Jul 23 14:50:46 BST 2019
Unique Job ID	7c1f5a14da9dd792

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c3x0uB_</a>	 Alignment		65.4	39	<b>PDB header:</b> toxin <b>Chain:</b> B: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> crystal structure of pirb
2	<a href="#">d1jhfa1</a>	 Alignment		30.3	33	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> LexA repressor, N-terminal DNA-binding domain
3	<a href="#">c2e11B_</a>	 Alignment		28.7	27	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> hydrolase; <b>PDBTitle:</b> the crystal structure of xc1258 from xanthomonas campestris: a cn-2 hydrolase superfamily protein with an arsenic adduct in the active3 site
4	<a href="#">c5zhbB_</a>	 Alignment		22.5	35	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> inositol-1-monophosphatase; <b>PDBTitle:</b> structure of inositol monophosphatase from anabaena (nostoc) sp. pcc2 7120
5	<a href="#">c3a5iB_</a>	 Alignment		19.2	25	<b>PDB header:</b> protein transport <b>Chain:</b> B: <b>PDB Molecule:</b> flagellar biosynthesis protein flha; <b>PDBTitle:</b> structure of the cytoplasmic domain of flha
6	<a href="#">c5z2wB_</a>	 Alignment		16.5	56	<b>PDB header:</b> cell cycle <b>Chain:</b> B: <b>PDB Molecule:</b> cell division protein ftsb; <b>PDBTitle:</b> crystal structure of the bacterial cell division protein ftsq and ftsb
7	<a href="#">d1jlia_</a>	 Alignment		15.7	29	<b>Fold:</b> 4-helical cytokines <b>Superfamily:</b> 4-helical cytokines <b>Family:</b> Short-chain cytokines
8	<a href="#">c6ohzA_</a>	 Alignment		15.2	24	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> structure of an uncharacterized protein from leptospira borgpetersenii2 serovar hardjo-bovis (strain jb197)
9	<a href="#">c4k05B_</a>	 Alignment		15.2	38	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> conserved hypothetical exported protein; <b>PDBTitle:</b> crystal structure of a duf1343 family protein (bf0371) from2 bacteroides fragilis nctc 9343 at 1.65 a resolution
10	<a href="#">c4jjaA_</a>	 Alignment		13.5	47	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical protein; <b>PDBTitle:</b> crystal structure of a duf1343 family protein (bf0379) from2 bacteroides fragilis nctc 9343 at 1.30 a resolution
11	<a href="#">c5j84A_</a>	 Alignment		13.0	27	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> dihydroxy-acid dehydratase; <b>PDBTitle:</b> crystal structure of l-arabinonate dehydratase in holo-form

12	<a href="#">c5fb5B_</a>	Alignment		12.1	28	<b>PDB header:</b> viral protein <b>Chain:</b> B: <b>PDB Molecule:</b> distal tube protein; <b>PDBTitle:</b> crystal structure of the bacteriophage phi29 tail knob protein gp9
13	<a href="#">d1mabg_</a>	Alignment		11.5	29	<b>Fold:</b> Pyruvate kinase C-terminal domain-like <b>Superfamily:</b> ATP synthase (F1-ATPase), gamma subunit <b>Family:</b> ATP synthase (F1-ATPase), gamma subunit
14	<a href="#">c3cjeA_</a>	Alignment		10.5	29	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> osmc-like protein; <b>PDBTitle:</b> crystal structure of an osmc-like hydroperoxide resistance protein2 (jann_2040) from jannaschia sp. ccs1 at 1.70 a resolution
15	<a href="#">d1seda_</a>	Alignment		9.3	38	<b>Fold:</b> Hypothetical protein YhaI <b>Superfamily:</b> Hypothetical protein YhaI <b>Family:</b> Hypothetical protein YhaI
16	<a href="#">d1bjja2</a>	Alignment		8.9	33	<b>Fold:</b> Immunoglobulin-like beta-sandwich <b>Superfamily:</b> Immunoglobulin <b>Family:</b> I set domains
17	<a href="#">c2dxbR_</a>	Alignment		8.7	19	<b>PDB header:</b> hydrolase <b>Chain:</b> R: <b>PDB Molecule:</b> thiocyanate hydrolase subunit gamma; <b>PDBTitle:</b> recombinant thiocyanate hydrolase comprising partially-modified cobalt2 centers
18	<a href="#">c3mixA_</a>	Alignment		8.4	16	<b>PDB header:</b> protein transport <b>Chain:</b> A: <b>PDB Molecule:</b> flagellar biosynthesis protein filha; <b>PDBTitle:</b> crystal structure of the cytosolic domain of b. subtilis filha
19	<a href="#">c6omzA_</a>	Alignment		8.3	21	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> dihydropteroate synthase; <b>PDBTitle:</b> crystal structure of dihydropteroate synthase from mycobacterium2 smegmatis with bound 6-hydroxymethylpterin-monophosphate
20	<a href="#">d1ppjc2</a>	Alignment		8.2	45	<b>Fold:</b> Heme-binding four-helical bundle <b>Superfamily:</b> Transmembrane di-heme cytochromes <b>Family:</b> Cytochrome b of cytochrome bc1 complex (Ubiquinol-cytochrome c reductase)
21	<a href="#">c5zmmD_</a>	Alignment	not modelled	8.2	34	<b>PDB header:</b> dna binding protein <b>Chain:</b> D: <b>PDB Molecule:</b> uncharacterized protein mcra; <b>PDBTitle:</b> structure of the type iv phosphorothioation-dependent restriction2 endonuclease scomcra
22	<a href="#">c3o4zD_</a>	Alignment	not modelled	8.1	14	<b>PDB header:</b> protein binding <b>Chain:</b> D: <b>PDB Molecule:</b> telomere length regulation protein tel2; <b>PDBTitle:</b> tel2 structure and function in the hsp90-dependent maturation of mtor2 and atr complexes
23	<a href="#">d2v9va1</a>	Alignment	not modelled	8.0	53	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> C-terminal fragment of elongation factor SelB
24	<a href="#">c2y5sA_</a>	Alignment	not modelled	8.0	21	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> dihydropteroate synthase; <b>PDBTitle:</b> crystal structure of burkholderia cenocepacia dihydropteroate2 synthase complexed with 7,8-dihydropteroate.
25	<a href="#">c5uz9K_</a>	Alignment	not modelled	7.8	31	<b>PDB header:</b> immune system/rna <b>Chain:</b> K: <b>PDB Molecule:</b> anti-crispr protein 30; <b>PDBTitle:</b> cryo em structure of anti-crisprs, acrf1 and acrf2, bound to type i-f2 crrna-guided crispr surveillance complex
26	<a href="#">d1ox0a2</a>	Alignment	not modelled	7.7	26	<b>Fold:</b> Thiolase-like <b>Superfamily:</b> Thiolase-like <b>Family:</b> Thiolase-related
27	<a href="#">d2e74a1</a>	Alignment	not modelled	7.6	27	<b>Fold:</b> Heme-binding four-helical bundle <b>Superfamily:</b> Transmembrane di-heme cytochromes <b>Family:</b> Cytochrome b of cytochrome bc1 complex (Ubiquinol-cytochrome c reductase)
28	<a href="#">c2g7rA_</a>	Alignment	not modelled	7.5	38	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> mucosa-associated lymphoid tissue lymphoma translocation <b>PDBTitle:</b> x-ray structure of the death domain of the human mucosa associated2 lymphoid tissue lymphoma translocation protein

					1	
29	<a href="#">c2ht9A_</a>	Alignment	not modelled	7.5	40	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> glutaredoxin-2; <b>PDBTitle:</b> the structure of dimeric human glutaredoxin 2
30	<a href="#">d3cx5c2</a>	Alignment	not modelled	7.3	41	<b>Fold:</b> Heme-binding four-helical bundle <b>Superfamily:</b> Transmembrane di-heme cytochromes <b>Family:</b> Cytochrome b of cytochrome bc1 complex (Ubiquinol-cytochrome c reductase)
31	<a href="#">d2cfua2</a>	Alignment	not modelled	7.3	23	<b>Fold:</b> Metallo-hydrolase/oxidoreductase <b>Superfamily:</b> Metallo-hydrolase/oxidoreductase <b>Family:</b> Alkylsulfatase-like
32	<a href="#">c2e2kC_</a>	Alignment	not modelled	7.1	35	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> formamidase; <b>PDBTitle:</b> helicobacter pylori formamidase amif contains a fine-tuned cysteine-2 glutamate-lysine catalytic triad
33	<a href="#">c5td7A_</a>	Alignment	not modelled	7.1	24	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> zgc:55652; <b>PDBTitle:</b> crystal structure of histone deacetylase 10
34	<a href="#">c1jbiA_</a>	Alignment	not modelled	6.9	33	<b>PDB header:</b> immune system <b>Chain:</b> A: <b>PDB Molecule:</b> cd3 epsilon and gamma ectodomain fragment <b>PDBTitle:</b> cd3 epsilon and gamma ectodomain fragment complex in single-2 chain construct
35	<a href="#">d2zjrn1</a>	Alignment	not modelled	6.9	25	<b>Fold:</b> PABP domain-like <b>Superfamily:</b> Ribosomal protein L20 <b>Family:</b> Ribosomal protein L20
36	<a href="#">c3jx9B_</a>	Alignment	not modelled	6.8	30	<b>PDB header:</b> isomerase <b>Chain:</b> B: <b>PDB Molecule:</b> putative phosphoheptose isomerase; <b>PDBTitle:</b> crystal structure of putative phosphoheptose isomerase2 (yp_001815198.1) from exiguobacterium sp. 255-15 at 1.95 a resolution
37	<a href="#">d1q90b_</a>	Alignment	not modelled	6.6	27	<b>Fold:</b> Heme-binding four-helical bundle <b>Superfamily:</b> Transmembrane di-heme cytochromes <b>Family:</b> Cytochrome b of cytochrome bc1 complex (Ubiquinol-cytochrome c reductase)
38	<a href="#">d1bccc3</a>	Alignment	not modelled	6.5	41	<b>Fold:</b> Heme-binding four-helical bundle <b>Superfamily:</b> Transmembrane di-heme cytochromes <b>Family:</b> Cytochrome b of cytochrome bc1 complex (Ubiquinol-cytochrome c reductase)
39	<a href="#">d1p5dx3</a>	Alignment	not modelled	6.4	22	<b>Fold:</b> Phosphoglucomutase, first 3 domains <b>Superfamily:</b> Phosphoglucomutase, first 3 domains <b>Family:</b> Phosphoglucomutase, first 3 domains
40	<a href="#">c2kubA_</a>	Alignment	not modelled	6.3	38	<b>PDB header:</b> structural protein <b>Chain:</b> A: <b>PDB Molecule:</b> fimbriae-associated protein fap1; <b>PDBTitle:</b> solution structure of the alpha subdomain of the major non-repeat unit2 of fap1 fimbriae of streptococcus parasanguis
41	<a href="#">d2j01u1</a>	Alignment	not modelled	6.2	29	<b>Fold:</b> PABP domain-like <b>Superfamily:</b> Ribosomal protein L20 <b>Family:</b> Ribosomal protein L20
42	<a href="#">c2e1mB_</a>	Alignment	not modelled	6.1	14	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> l-glutamate oxidase; <b>PDBTitle:</b> crystal structure of l-glutamate oxidase from streptomyces sp. x-119-6
43	<a href="#">c3ebjD_</a>	Alignment	not modelled	6.0	43	<b>PDB header:</b> transferase <b>Chain:</b> D: <b>PDB Molecule:</b> polymerase acidic protein; <b>PDBTitle:</b> crystal structure of an avian influenza virus protein
44	<a href="#">c3rguA_</a>	Alignment	not modelled	5.9	38	<b>PDB header:</b> structural protein <b>Chain:</b> A: <b>PDB Molecule:</b> fimbriae-associated protein fap1; <b>PDBTitle:</b> structure of fap-nra at ph 5.0
45	<a href="#">c4v19U_</a>	Alignment	not modelled	5.8	25	<b>PDB header:</b> ribosome <b>Chain:</b> U: <b>PDB Molecule:</b> mitoribosomal protein bl20m, mrpl20; <b>PDBTitle:</b> structure of the large subunit of the mammalian mitoribosome, part 12 of 2
46	<a href="#">c4e5gB_</a>	Alignment	not modelled	5.7	43	<b>PDB header:</b> viral protein, transcription <b>Chain:</b> B: <b>PDB Molecule:</b> polymerase protein pa; <b>PDBTitle:</b> crystal structure of avian influenza virus pan bound to compound 2
47	<a href="#">c3gx1A_</a>	Alignment	not modelled	5.7	23	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> lin1832 protein; <b>PDBTitle:</b> crystal structure of a domain of lin1832 from listeria innocua
48	<a href="#">c3fzaA_</a>	Alignment	not modelled	5.6	40	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> glutaredoxin; <b>PDBTitle:</b> crystal structure of poplar glutaredoxin s12 in complex with2 glutathione and beta-mercaptoethanol
49	<a href="#">c4i2uA_</a>	Alignment	not modelled	5.6	32	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> glutaredoxin; <b>PDBTitle:</b> crystal structure of the reduced glutaredoxin from chlorella2 sorokiniana t-89 in complex with glutathione
50	<a href="#">d2b8na1</a>	Alignment	not modelled	5.6	29	<b>Fold:</b> GckA/TtuD-like <b>Superfamily:</b> GckA/TtuD-like <b>Family:</b> GckA/TtuD-like
51	<a href="#">d1jhba_</a>	Alignment	not modelled	5.3	30	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> Thioltransferase
52	<a href="#">c2w69B_</a>	Alignment	not modelled	5.2	43	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> polymerase acidic protein; <b>PDBTitle:</b> influenza polymerase fragment
53	<a href="#">c1x3IA_</a>	Alignment	not modelled	5.2	33	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical protein ph0495; <b>PDBTitle:</b> crystal structure of the ph0495 protein from pyrococcus horikoshii2 ot3
54	<a href="#">c5oynB_</a>	Alignment	not modelled	5.2	18	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> dehydratase, ilvd/edd family; <b>PDBTitle:</b> crystal structure of d-xylonate dehydratase in holo-form

55	<a href="#">dluj4a1</a>	Alignment	not modelled	5.2	30	<b>Fold:</b> NagB/RpiA/CoA transferase-like <b>Superfamily:</b> NagB/RpiA/CoA transferase-like <b>Family:</b> D-ribose-5-phosphate isomerase (RpiA), catalytic domain
----	-------------------------	-----------	--------------	-----	----	---