
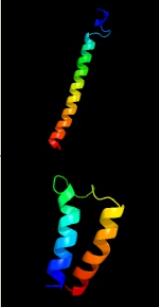

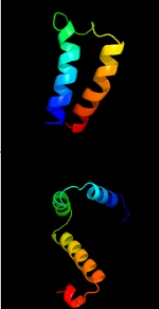
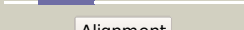
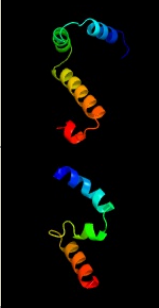
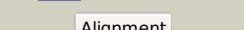
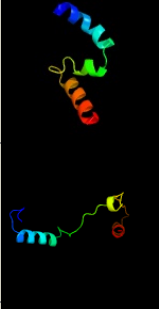
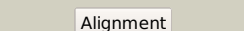
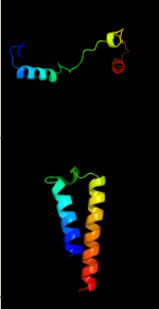
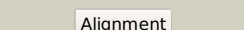
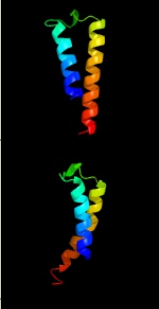
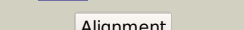
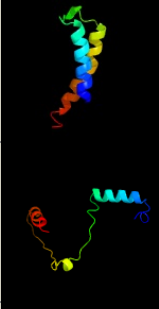
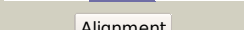
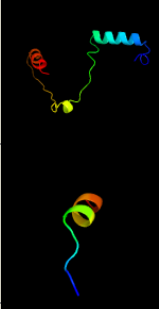
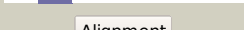
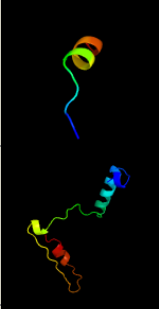

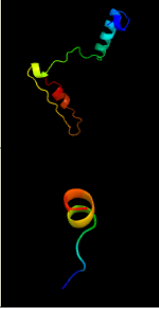





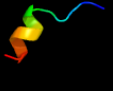
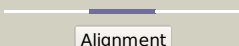
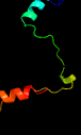
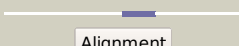

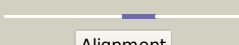

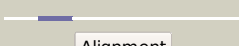


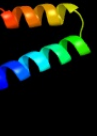





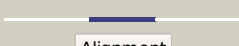

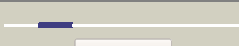






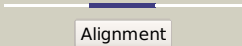

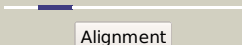
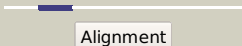

# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3466 (- )_3883704_3884372
Date	Fri Aug 9 18:20:14 BST 2019
Unique Job ID	e89252034132b509

Detailed template  
information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c2hv8D_</a>	 Alignment		22.5	12	<b>PDB header:</b> protein transport <b>Chain:</b> D; <b>PDB Molecule:</b> rab11 family-interacting protein 3; <b>PDBTitle:</b> crystal structure of gtp-bound rab11 in complex with fip3
2	<a href="#">c5tw9D_</a>	 Alignment		20.2	27	<b>PDB header:</b> lipid-binding protein <b>Chain:</b> D; <b>PDB Molecule:</b> iron uptake system component efeo; <b>PDBTitle:</b> 1.50 angstrom crystal structure of c-terminal fragment (residues 322-2 384) of iron uptake system component efeo from yersinia pestis.
3	<a href="#">c3frwF_</a>	 Alignment		19.7	15	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> F; <b>PDB Molecule:</b> putative trp repressor protein; <b>PDBTitle:</b> crystal structure of putative trpr protein from ruminococcus obeum
4	<a href="#">c3c4rC_</a>	 Alignment		19.3	20	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> C; <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> crystal structure of an uncharacterized protein encoded by2 cryptic prophage
5	<a href="#">c1i1gA_</a>	 Alignment		16.6	14	<b>PDB header:</b> transcription <b>Chain:</b> A; <b>PDB Molecule:</b> transcriptional regulator lrpA; <b>PDBTitle:</b> crystal structure of the lrp-like transcriptional regulator from the2 archaeon pyrococcus furiosus
6	<a href="#">c3at7B_</a>	 Alignment		16.4	18	<b>PDB header:</b> structural protein <b>Chain:</b> B; <b>PDB Molecule:</b> alginate-binding flagellin; <b>PDBTitle:</b> crystal structure of bacterial cell-surface alginate-binding protein2 algp7
7	<a href="#">c4bgoA_</a>	 Alignment		15.3	14	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> efem m75 peptidase; <b>PDBTitle:</b> structural and functional role of the imelysin-like protein2 efem from pseudomonas syringae pv. syringae and3 implications in bacterial iron transport
8	<a href="#">c2e1cA_</a>	 Alignment		15.1	14	<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
9	<a href="#">c5o8kB_</a>	 Alignment		13.4	38	<b>PDB header:</b> replication <b>Chain:</b> B; <b>PDB Molecule:</b> dna polymerase zeta catalytic subunit; <b>PDBTitle:</b> crystal structure of mammalian rev7 in complex with rev3 1875-1895
10	<a href="#">c2dbbA_</a>	 Alignment		12.6	27	<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
11	<a href="#">c4fjoD_</a>	 Alignment		12.1	46	<b>PDB header:</b> transferase/dna binding protein <b>Chain:</b> D; <b>PDB Molecule:</b> dna polymerase zeta catalytic subunit; <b>PDBTitle:</b> structure of the rev1 ctd-rev3/7-pol kappa rir complex

12	<a href="#">c3abdY_</a>		Alignment		12.0	38	<b>PDB header:</b> cell cycle/replication <b>Chain:</b> Y: <b>PDB Molecule:</b> dna polymerase zeta catalytic subunit; <b>PDBTitle:</b> structure of human rev7 in complex with a human rev3 fragment in a2 monoclinic crystal
13	<a href="#">c3abdX_</a>		Alignment		12.0	38	<b>PDB header:</b> cell cycle/replication <b>Chain:</b> X: <b>PDB Molecule:</b> dna polymerase zeta catalytic subunit; <b>PDBTitle:</b> structure of human rev7 in complex with a human rev3 fragment in a2 monoclinic crystal
14	<a href="#">c2cfxD_</a>		Alignment		11.8	14	<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
15	<a href="#">c6gymW_</a>		Alignment		11.1	18	<b>PDB header:</b> transcription <b>Chain:</b> W: <b>PDB Molecule:</b> transcription initiation factor iie subunit alpha, <b>PDBTitle:</b> structure of a yeast closed complex with distorted dna (ccdist)
16	<a href="#">c5oqjW_</a>		Alignment		11.1	18	<b>PDB header:</b> transcription <b>Chain:</b> W: <b>PDB Molecule:</b> transcription initiation factor iie subunit alpha; <b>PDBTitle:</b> structure of yeast transcription pre-initiation complex with tfiih
17	<a href="#">c2kq5A_</a>		Alignment		11.1	14	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> avirulence protein; <b>PDBTitle:</b> solution nmr structure of a section of the repeat domain of the type2 iii effector protein ptha
18	<a href="#">c5oqmW_</a>		Alignment		11.0	18	<b>PDB header:</b> transcription <b>Chain:</b> W: <b>PDB Molecule:</b> transcription factor tfiie subunit; <b>PDBTitle:</b> structure of yeast transcription pre-initiation complex with tfiih and2 core mediator
19	<a href="#">c3korD_</a>		Alignment		9.9	14	<b>PDB header:</b> transcription <b>Chain:</b> D: <b>PDB Molecule:</b> possible trp repressor; <b>PDBTitle:</b> crystal structure of a putative trp repressor from staphylococcus2 aureus
20	<a href="#">c3abeZ_</a>		Alignment		8.5	38	<b>PDB header:</b> cell cycle/replication <b>Chain:</b> Z: <b>PDB Molecule:</b> dna polymerase zeta catalytic subunit; <b>PDBTitle:</b> structure of human rev7 in complex with a human rev3 fragment in a2 tetragonal crystal
21	<a href="#">c3nufB_</a>		Alignment	not modelled	7.4	25	<b>PDB header:</b> transcription regulator <b>Chain:</b> B: <b>PDB Molecule:</b> prd-containing transcription regulator; <b>PDBTitle:</b> crystal structure of a prd-containing transcription regulator2 (lsei_2718) from lactobacillus casei atcc 334 at 1.38 a resolution
22	<a href="#">c4czdD_</a>		Alignment	not modelled	7.4	14	<b>PDB header:</b> lyase <b>Chain:</b> D: <b>PDB Molecule:</b> putative transcriptional regulator, asnc family; <b>PDBTitle:</b> sirohaem decarboxylase ahba/b - an enzyme with structural homology2 to the lrp/asnc transcription factor family that is part of the3 alternative haem biosynthesis pathway.
23	<a href="#">d2imja1</a>		Alignment	not modelled	6.8	20	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> NTF2-like <b>Family:</b> PFL3262-like
24	<a href="#">c4extB_</a>		Alignment	not modelled	6.2	38	<b>PDB header:</b> transferase/transcription <b>Chain:</b> B: <b>PDB Molecule:</b> peptide from dna polymerase zeta catalytic subunit; <b>PDBTitle:</b> structure of polymerase-interacting domain of human rev1 in complex2 with translesional synthesis polymerase zeta
25	<a href="#">c1y6iA_</a>		Alignment	not modelled	6.1	42	<b>PDB header:</b> ligand binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> mg-chelatase cofactor gun4; <b>PDBTitle:</b> synechocystis gun4
26	<a href="#">d1rcwa_</a>		Alignment	not modelled	6.1	13	<b>Fold:</b> Heme oxygenase-like <b>Superfamily:</b> Heme oxygenase-like <b>Family:</b> PqqC-like
27	<a href="#">c2rghA_</a>		Alignment	not modelled	5.7	14	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> alpha-glycerophosphate oxidase; <b>PDBTitle:</b> structure of alpha-glycerophosphate oxidase from2 streptococcus sp.: a template for the mitochondrial alpha-3 glycerophosphate dehydrogenase

28	<a href="#">c3iwkB_</a>	 Alignment	not modelled	5.7	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> aminoaldehyde dehydrogenase; <b>PDBTitle:</b> crystal structure of aminoaldehyde dehydrogenase 1 from pisum sativum2 (psamadh1)
29	<a href="#">c4czdA_</a>	 Alignment	not modelled	5.6	14	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> putative transcriptional regulator, asnc family; <b>PDBTitle:</b> sirohaem decarboxylase ahba/b - an enzyme with structural homology2 to the lrp/asnc transcription factor family that is part of the3 alternative haem biosynthesis pathway.
30	<a href="#">c2ldjA_</a>	 Alignment	not modelled	5.2	50	<b>PDB header:</b> de novo protein <b>Chain:</b> A: <b>PDB Molecule:</b> trp-cage mini-protein; <b>PDBTitle:</b> 1h chemical shift assignments and structure of trp-cage mini-protein2 with d-amino acid
31	<a href="#">c4gk5C_</a>	 Alignment	not modelled	5.1	36	<b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> dna polymerase zeta catalytic subunit; <b>PDBTitle:</b> crystal structure of human rev3-rev7-rev1-polkappa complex
32	<a href="#">c4gk0C_</a>	 Alignment	not modelled	5.1	36	<b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> dna polymerase zeta catalytic subunit; <b>PDBTitle:</b> crystal structure of human rev3-rev7-rev1 complex
33	<a href="#">c4gk0D_</a>	 Alignment	not modelled	5.1	36	<b>PDB header:</b> transferase <b>Chain:</b> D: <b>PDB Molecule:</b> dna polymerase zeta catalytic subunit; <b>PDBTitle:</b> crystal structure of human rev3-rev7-rev1 complex