

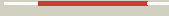









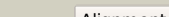









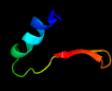

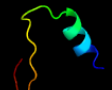
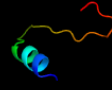
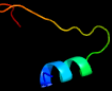

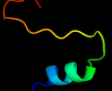
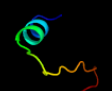
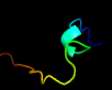


# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3385c_(- )_3799815_3800123
Date	Fri Aug 9 18:20:05 BST 2019
Unique Job ID	83ef391435da522a

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c2odkD_</a>	 Alignment		99.4	20	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> D; <b>PDB Molecule:</b> hypothetical protein; <b>PDBTitle:</b> putative prevent-host-death protein from nitrosomonas europaea
2	<a href="#">d2odka1</a>	 Alignment		99.3	20	<b>Fold:</b> YefM-like <b>Superfamily:</b> YefM-like <b>Family:</b> YefM-like
3	<a href="#">c3hryA_</a>	 Alignment		99.2	36	<b>PDB header:</b> antitoxin <b>Chain:</b> A; <b>PDB Molecule:</b> prevent host death protein; <b>PDBTitle:</b> crystal structure of phd in a trigonal space group and partially2 disordered
4	<a href="#">c3hs2H_</a>	 Alignment		99.1	39	<b>PDB header:</b> antitoxin <b>Chain:</b> H; <b>PDB Molecule:</b> prevent host death protein; <b>PDBTitle:</b> crystal structure of phd truncated to residue 57 in an orthorhombic2 space group
5	<a href="#">d2a6qb1</a>	 Alignment		98.7	23	<b>Fold:</b> YefM-like <b>Superfamily:</b> YefM-like <b>Family:</b> YefM-like
6	<a href="#">c3g5oA_</a>	 Alignment		98.6	20	<b>PDB header:</b> toxin/antitoxin <b>Chain:</b> A; <b>PDB Molecule:</b> uncharacterized protein rv2865; <b>PDBTitle:</b> the crystal structure of the toxin-antitoxin complex relbe2 (rv2865-2 2866) from mycobacterium tuberculosis
7	<a href="#">d2a6qa1</a>	 Alignment		98.4	23	<b>Fold:</b> YefM-like <b>Superfamily:</b> YefM-like <b>Family:</b> YefM-like
8	<a href="#">c3oeiB_</a>	 Alignment		97.7	24	<b>PDB header:</b> toxin, protein binding <b>Chain:</b> B; <b>PDB Molecule:</b> relj (antitoxin rv3357); <b>PDBTitle:</b> crystal structure of mycobacterium tuberculosis reljk (rv3357-rv3358-2 relbe3)
9	<a href="#">c3d55A_</a>	 Alignment		97.6	24	<b>PDB header:</b> toxin inhibitor <b>Chain:</b> A; <b>PDB Molecule:</b> uncharacterized protein rv3357/mt3465; <b>PDBTitle:</b> crystal structure of m. tuberculosis yefm antitoxin
10	<a href="#">c3k6qB_</a>	 Alignment		86.7	11	<b>PDB header:</b> ligand binding protein <b>Chain:</b> B; <b>PDB Molecule:</b> putative ligand binding protein; <b>PDBTitle:</b> crystal structure of an antitoxin part of a putative toxin/antitoxin2 system (swol_0700) from syntrophomonas wolfei subsp. wolfei at 1.80 a3 resolution
11	<a href="#">c1skoA_</a>	 Alignment		62.3	20	<b>PDB header:</b> signaling protein <b>Chain:</b> A; <b>PDB Molecule:</b> mitogen-activated protein kinase kinase 1 <b>PDBTitle:</b> mp1-p14 complex

12	<a href="#">d3cpta1</a>	Alignment		56.3	26	<b>Fold:</b> Profilin-like <b>Superfamily:</b> Roadblock/LC7 domain <b>Family:</b> Roadblock/LC7 domain
13	<a href="#">d2ns0a1</a>	Alignment		33.3	29	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> RHA1 ro06458-like
14	<a href="#">d1ogda_</a>	Alignment		19.4	30	<b>Fold:</b> RbsD-like <b>Superfamily:</b> RbsD-like <b>Family:</b> RbsD-like
15	<a href="#">c2wcvl_</a>	Alignment		18.9	19	<b>PDB header:</b> isomerase <b>Chain:</b> I; <b>PDB Molecule:</b> l-fucose mutarotase; <b>PDBTitle:</b> crystal structure of bacterial fucu
16	<a href="#">c3e7nB_</a>	Alignment		16.8	26	<b>PDB header:</b> transport protein <b>Chain:</b> B; <b>PDB Molecule:</b> d-ribose high-affinity transport system; <b>PDBTitle:</b> crystal structure of d-ribose high-affinity transport system from2 salmonella typhimurium lt2
17	<a href="#">c1gk7A_</a>	Alignment		16.5	19	<b>PDB header:</b> vimentin <b>Chain:</b> A; <b>PDB Molecule:</b> vimentin; <b>PDBTitle:</b> human vimentin coil 1a fragment (1a)
18	<a href="#">c3p13B_</a>	Alignment		16.1	22	<b>PDB header:</b> isomerase <b>Chain:</b> B; <b>PDB Molecule:</b> d-ribose pyranase; <b>PDBTitle:</b> complex structure of d-ribose pyranase sa240 with d-ribose
19	<a href="#">c4a34L_</a>	Alignment		14.9	19	<b>PDB header:</b> isomerase <b>Chain:</b> L; <b>PDB Molecule:</b> rbsd/fucu transport protein family protein; <b>PDBTitle:</b> crystal structure of the fucose mutarotase in complex with2 l-fucose from streptococcus pneumoniae
20	<a href="#">c3mvkA_</a>	Alignment		14.7	19	<b>PDB header:</b> isomerase <b>Chain:</b> A; <b>PDB Molecule:</b> protein fucu; <b>PDBTitle:</b> the crystal structure of fucu from bifidobacterium longum to 1.65a
21	<a href="#">c2wcuB_</a>	Alignment	not modelled	14.6	27	<b>PDB header:</b> isomerase <b>Chain:</b> B; <b>PDB Molecule:</b> protein fucu homolog; <b>PDBTitle:</b> crystal structure of mammalian fucu
22	<a href="#">d2ob5a1</a>	Alignment	not modelled	12.8	31	<b>Fold:</b> RbsD-like <b>Superfamily:</b> RbsD-like <b>Family:</b> RbsD-like
23	<a href="#">d1bifa2</a>	Alignment	not modelled	12.2	18	<b>Fold:</b> Phosphoglycerate mutase-like <b>Superfamily:</b> Phosphoglycerate mutase-like <b>Family:</b> 6-phosphofructo-2-kinase/fructose-2,6-bisphosphatase, phosphatase domain
24	<a href="#">c3s4rB_</a>	Alignment	not modelled	12.2	25	<b>PDB header:</b> structural protein <b>Chain:</b> B; <b>PDB Molecule:</b> vimentin; <b>PDBTitle:</b> crystal structure of vimentin coil1a/1b fragment with a stabilizing2 mutation
25	<a href="#">c2vm2C_</a>	Alignment	not modelled	11.6	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C; <b>PDB Molecule:</b> thioredoxin h isoform 1.; <b>PDBTitle:</b> crystal structure of barley thioredoxin h isoform 1 crystallized using2 peg as precipitant
26	<a href="#">d1k6ma2</a>	Alignment	not modelled	11.5	18	<b>Fold:</b> Phosphoglycerate mutase-like <b>Superfamily:</b> Phosphoglycerate mutase-like <b>Family:</b> 6-phosphofructo-2-kinase/fructose-2,6-bisphosphatase, phosphatase domain
27	<a href="#">d1tipa_</a>	Alignment	not modelled	11.1	18	<b>Fold:</b> Phosphoglycerate mutase-like <b>Superfamily:</b> Phosphoglycerate mutase-like <b>Family:</b> 6-phosphofructo-2-kinase/fructose-2,6-bisphosphatase, phosphatase domain
28	<a href="#">d1y8xb1</a>	Alignment	not modelled	10.4	21	<b>Fold:</b> Activating enzymes of the ubiquitin-like proteins <b>Superfamily:</b> Activating enzymes of the ubiquitin-like proteins <b>Family:</b> Ubiquitin activating enzymes (UBA)
						<b>PDB header:</b> oxidoreductase

29	<a href="#">c5zf2A_</a>	Alignment	not modelled	10.1	14	<b>Chain:</b> A: <b>PDB Molecule:</b> thioredoxin (h-type,trx-h); <b>PDBTitle:</b> crystal structure of trxp from edwardsiella tarda eib202
30	<a href="#">c4heoA_</a>	Alignment	not modelled	10.1	35	<b>PDB header:</b> viral protein <b>Chain:</b> A: <b>PDB Molecule:</b> phosphoprotein; <b>PDBTitle:</b> hendra virus phosphoprotein c terminal domain
31	<a href="#">d2hq7a1</a>	Alignment	not modelled	9.5	13	<b>Fold:</b> Split barrel-like <b>Superfamily:</b> FMN-binding split barrel <b>Family:</b> PNP-oxidase like
32	<a href="#">c2wtoB_</a>	Alignment	not modelled	9.3	33	<b>PDB header:</b> metal binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> orf131 protein; <b>PDBTitle:</b> crystal structure of apo-form czce from c. metallidurans ch34
33	<a href="#">d1x6va1</a>	Alignment	not modelled	8.9	27	<b>Fold:</b> PUA domain-like <b>Superfamily:</b> PUA domain-like <b>Family:</b> ATP sulfurylase N-terminal domain
34	<a href="#">c3jvoA_</a>	Alignment	not modelled	8.2	6	<b>PDB header:</b> viral protein <b>Chain:</b> A: <b>PDB Molecule:</b> gp6; <b>PDBTitle:</b> crystal structure of bacteriophage hk97 gp6
35	<a href="#">c2qsiB_</a>	Alignment	not modelled	8.0	9	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> putative hydrogenase expression/formation protein hupg; <b>PDBTitle:</b> crystal structure of putative hydrogenase expression/formation protein2 hupg from rhodospseudomonas palustris cga009
36	<a href="#">c3iprC_</a>	Alignment	not modelled	7.7	19	<b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> pts system, iia component; <b>PDBTitle:</b> crystal structure of the enterococcus faecalis gluconate2 specific eiaa phosphotransferase system component
37	<a href="#">c2pptA_</a>	Alignment	not modelled	7.5	10	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> thioredoxin-2; <b>PDBTitle:</b> crystal structure of thioredoxin-2
38	<a href="#">c5iddA_</a>	Alignment	not modelled	7.5	20	<b>PDB header:</b> protein transport <b>Chain:</b> A: <b>PDB Molecule:</b> mon1; <b>PDBTitle:</b> crystal structure of the heterodimeric gef mon1-ccz1 in complex with2 ypt7
39	<a href="#">c4ewvB_</a>	Alignment	not modelled	6.8	30	<b>PDB header:</b> ligase <b>Chain:</b> B: <b>PDB Molecule:</b> 4-substituted benzoates-glutamate ligase gh3.12; <b>PDBTitle:</b> crystal structure of gh3.12 in complex with ampcpp
40	<a href="#">c3v62F_</a>	Alignment	not modelled	6.3	50	<b>PDB header:</b> protein binding/dna binding protein <b>Chain:</b> F: <b>PDB Molecule:</b> atp-dependent dna helicase srs2; <b>PDBTitle:</b> structure of the s. cerevisiae srs2 c-terminal domain in complex with2 pcna conjugated to sumo on lysine 164
41	<a href="#">c3v62C_</a>	Alignment	not modelled	6.3	50	<b>PDB header:</b> protein binding/dna binding protein <b>Chain:</b> C: <b>PDB Molecule:</b> atp-dependent dna helicase srs2; <b>PDBTitle:</b> structure of the s. cerevisiae srs2 c-terminal domain in complex with2 pcna conjugated to sumo on lysine 164
42	<a href="#">c4jj0B_</a>	Alignment	not modelled	5.7	17	<b>PDB header:</b> electron transport <b>Chain:</b> B: <b>PDB Molecule:</b> mamp; <b>PDBTitle:</b> crystal structure of mamp
43	<a href="#">c4x3iA_</a>	Alignment	not modelled	5.7	30	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> activity-regulated cytoskeleton-associated protein; <b>PDBTitle:</b> the crystal structure of arc n-lobe complexed with camk2a fragment