



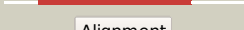

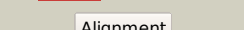

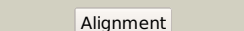





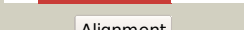

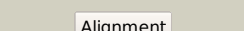

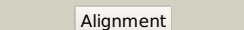


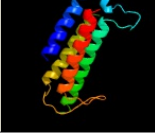


# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0738 (- )_830065_830613
Date	Fri Jul 26 01:50:31 BST 2019
Unique Job ID	885444544613d98b

Detailed template  
information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c2nsfA_</a>	 Alignment		100.0	19	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical protein cgl3021; <b>PDBTitle:</b> crystal structure of the mycothiol-dependent maleylpyruvate isomerase
2	<a href="#">d2nsfa1</a>	 Alignment		100.0	21	<b>Fold:</b> DinB/YfiT-like putative metalloenzymes <b>Superfamily:</b> DinB/YfiT-like putative metalloenzymes <b>Family:</b> Maleylpyruvate isomerase-like
3	<a href="#">c2rd9C_</a>	 Alignment		98.6	13	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> bh0186 protein; <b>PDBTitle:</b> crystal structure of a putative yfiT-like metal-dependent hydrolase2 (bh0186) from bacillus halodurans c-125 at 2.30 a resolution
4	<a href="#">c5cogB_</a>	 Alignment		98.4	9	<b>PDB header:</b> unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> irc4; <b>PDBTitle:</b> crystal structure of yeast irc4
5	<a href="#">c6iz2A_</a>	 Alignment		98.4	10	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> dinb/yfiT family protein; <b>PDBTitle:</b> crystal structure of dinb/yfiT protein dr0053 from d. radiodurans r1
6	<a href="#">d1rxqa_</a>	 Alignment		98.2	14	<b>Fold:</b> DinB/YfiT-like putative metalloenzymes <b>Superfamily:</b> DinB/YfiT-like putative metalloenzymes <b>Family:</b> YfiT-like putative metal-dependent hydrolases
7	<a href="#">c5civA_</a>	 Alignment		98.2	13	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> sibling bacteriocin; <b>PDBTitle:</b> sibling lethal factor precursor - dfsb
8	<a href="#">d2ou6a1</a>	 Alignment		98.0	19	<b>Fold:</b> DinB/YfiT-like putative metalloenzymes <b>Superfamily:</b> DinB/YfiT-like putative metalloenzymes <b>Family:</b> DinB-like
9	<a href="#">c3cexB_</a>	 Alignment		97.9	18	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> crystal structure of the conserved protein of locus ef_3021 from2 enterococcus faecalis
10	<a href="#">c4n6cB_</a>	 Alignment		97.9	10	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> crystal structure of the b1rzq2 protein from streptococcus pneumoniae.2 northeast structural genomics consortium (nesg) target spr36.
11	<a href="#">c2yqyB_</a>	 Alignment		97.9	22	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> hypothetical protein ttha0303; <b>PDBTitle:</b> crystal structure of tt2238, a four-helix bundle protein

12	<a href="#">c3di5A_</a>	Alignment		97.8	13	<b>PDB header:</b> metal binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> dinb-like protein; <b>PDBTitle:</b> crystal structure of a dinb-like protein (bce_4655) from bacillus2 cereus atcc 10987 at 2.01 a resolution
13	<a href="#">c3dkaA_</a>	Alignment		97.8	9	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> dinb-like protein; <b>PDBTitle:</b> crystal structure of a dinb-like protein (yjoa, bsu12410) from2 bacillus subtilis at 2.30 a resolution
14	<a href="#">d2p1aa1</a>	Alignment		97.6	10	<b>Fold:</b> DinB/YfiT-like putative metalloenzymes <b>Superfamily:</b> DinB/YfiT-like putative metalloenzymes <b>Family:</b> DinB-like
15	<a href="#">c2qe9B_</a>	Alignment		97.4	7	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> uncharacterized protein yiza; <b>PDBTitle:</b> crystal structure of a putative metal-dependent hydrolase (yiza,2 bsu10800) from bacillus subtilis at 1.90 a resolution
16	<a href="#">c3e4xB_</a>	Alignment		97.3	9	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> apc36150; <b>PDBTitle:</b> crystal structure of putative metal-dependent hydrolases2 apc36150
17	<a href="#">c5cofA_</a>	Alignment		97.2	17	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> crystal structure of uncharacterised protein q1r1x2 from escherichia2 coli uti89
18	<a href="#">c5cqVB_</a>	Alignment		97.1	8	<b>PDB header:</b> unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> crystal structure of uncharacterized protein q8dvw2 from streptococcus2 agalactiae
19	<a href="#">d2hkva1</a>	Alignment		97.0	13	<b>Fold:</b> DinB/YfiT-like putative metalloenzymes <b>Superfamily:</b> DinB/YfiT-like putative metalloenzymes <b>Family:</b> DinB-like
20	<a href="#">c6anrA_</a>	Alignment		96.9	13	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> colibactin self-protection protein clbs; <b>PDBTitle:</b> crystal structure of a self resistance protein clbs from colibactin2 biosynthetic gene cluster
21	<a href="#">c5wk0A_</a>	Alignment	not modelled	63.1	12	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> damage-inducible protein dinb; <b>PDBTitle:</b> crystal structure of the bacillithiol transferase bsta from2 staphylococcus aureus.
22	<a href="#">c2jobA_</a>	Alignment	not modelled	21.8	60	<b>PDB header:</b> lipid binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> antilipopolsaccharide factor; <b>PDBTitle:</b> solution structure of an antilipopolsaccharide factor from2 shrimp and its possible lipid a binding site
23	<a href="#">c4idiA_</a>	Alignment	not modelled	10.2	16	<b>PDB header:</b> protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> oryza sativa rum1-related; <b>PDBTitle:</b> crystal structure of rum1-related protein from plasmodium yoelii,2 py06420
24	<a href="#">c2dkzA_</a>	Alignment	not modelled	7.9	16	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical protein loc64762; <b>PDBTitle:</b> solution structure of the sam_pnt-domain of the2 hypothetical protein loc64762
25	<a href="#">c2k9xA_</a>	Alignment	not modelled	7.4	13	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> solution structure of urm1 from trypanosoma brucei
26	<a href="#">d1lbaa_</a>	Alignment	not modelled	7.1	20	<b>Fold:</b> N-acetylmuramoyl-L-alanine amidase-like <b>Superfamily:</b> N-acetylmuramoyl-L-alanine amidase-like <b>Family:</b> N-acetylmuramoyl-L-alanine amidase-like
27	<a href="#">c5uxtA_</a>	Alignment	not modelled	6.0	44	<b>PDB header:</b> de novo protein <b>Chain:</b> A: <b>PDB Molecule:</b> coiled-coil trimer with glu:trp:lys triad; <b>PDBTitle:</b> coiled-coil trimer with glu:trp:lys triad
28	<a href="#">c5uxtC_</a>	Alignment	not modelled	5.3	44	<b>PDB header:</b> de novo protein <b>Chain:</b> C: <b>PDB Molecule:</b> coiled-coil trimer with glu:trp:lys triad; <b>PDBTitle:</b> coiled-coil trimer with glu:trp:lys triad
						<b>Fold:</b> DNA/RNA-binding 3-helical bundle

29	<a href="#">d2od5a1</a>	Alignment	not modelled	5.1	80	<b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> Marine metagenome family WH1
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