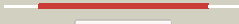



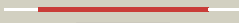



















# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0443 (- )_532399_532914
Date	Tue Jul 23 14:50:52 BST 2019
Unique Job ID	aecebf9238a891a

Detailed template  
information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c3cexB_</a>	 Alignment		100.0	37	<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
2	<a href="#">d2ou6a1</a>	 Alignment		100.0	20	<b>Fold:</b> DinB/YfiT-like putative metalloenzymes <b>Superfamily:</b> DinB/YfiT-like putative metalloenzymes <b>Family:</b> DinB-like
3	<a href="#">d2p1aa1</a>	 Alignment		100.0	14	<b>Fold:</b> DinB/YfiT-like putative metalloenzymes <b>Superfamily:</b> DinB/YfiT-like putative metalloenzymes <b>Family:</b> DinB-like
4	<a href="#">d1rxqa_</a>	 Alignment		100.0	11	<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
5	<a href="#">c6iz2A_</a>	 Alignment		100.0	10	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> dinb-like protein; <b>PDBTitle:</b> crystal structure of dinb/yfiT protein dr0053 from d. radiodurans r1
6	<a href="#">c3dkaA_</a>	 Alignment		100.0	16	<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
7	<a href="#">c3e4xB_</a>	 Alignment		100.0	18	<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
8	<a href="#">c3di5A_</a>	 Alignment		99.9	20	<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
9	<a href="#">d2hkva1</a>	 Alignment		99.9	13	<b>Fold:</b> DinB/YfiT-like putative metalloenzymes <b>Superfamily:</b> DinB/YfiT-like putative metalloenzymes <b>Family:</b> DinB-like
10	<a href="#">c5wk0A_</a>	 Alignment		99.9	14	<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.
11	<a href="#">c2qe9B_</a>	 Alignment		99.9	14	<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

12	<a href="#">c2rd9C_</a>	Alignment		99.9	11	<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
13	<a href="#">c2qn1A_</a>	Alignment		99.8	21	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> crystal structure of a putative dna damage-inducible protein2 (chu_0679) from cytophaga hutchinsonii atcc 33406 at 1.50 a3 resolution
14	<a href="#">c5cogB_</a>	Alignment		99.7	9	<b>PDB header:</b> unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> irc4; <b>PDBTitle:</b> crystal structure of yeast irc4
15	<a href="#">c6qkjA_</a>	Alignment		99.6	12	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> egtb from chloracidobacterium thermophilum, a type ii sulfoxide2 synthase in complex with n,n,n-trimethyl-histidine
16	<a href="#">c5civA_</a>	Alignment		99.5	12	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> sibling bacteriocin; <b>PDBTitle:</b> sibling lethal factor precursor - dfsb
17	<a href="#">c2yqyB_</a>	Alignment		99.4	16	<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
18	<a href="#">c4n6cB_</a>	Alignment		99.4	14	<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.
19	<a href="#">c6anrA_</a>	Alignment		99.4	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
20	<a href="#">c5cofA_</a>	Alignment		99.4	13	<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
21	<a href="#">c4x8bA_</a>	Alignment	not modelled	99.3	13	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> sulfoxide synthase egtb; <b>PDBTitle:</b> ergothioneine-biosynthetic sulfoxide synthase egtb, apo form
22	<a href="#">d2nsfa1</a>	Alignment	not modelled	99.2	12	<b>Fold:</b> DinB/YfiT-like putative metalloenzymes <b>Superfamily:</b> DinB/YfiT-like putative metalloenzymes <b>Family:</b> Maleylpyruvate isomerase-like
23	<a href="#">c5cqyB_</a>	Alignment	not modelled	99.1	11	<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
24	<a href="#">c2nsfA_</a>	Alignment	not modelled	98.8	13	<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
25	<a href="#">d2f22a1</a>	Alignment	not modelled	97.2	14	<b>Fold:</b> DinB/YfiT-like putative metalloenzymes <b>Superfamily:</b> DinB/YfiT-like putative metalloenzymes <b>Family:</b> DinB-like
26	<a href="#">c5da5R_</a>	Alignment	not modelled	54.3	24	<b>PDB header:</b> oxidoreductase <b>Chain:</b> R: <b>PDB Molecule:</b> rru_a0973; <b>PDBTitle:</b> crystal structure of rhodospirillum rubrum rru_a0973
27	<a href="#">d1zpya1</a>	Alignment	not modelled	44.8	20	<b>Fold:</b> Ferritin-like <b>Superfamily:</b> Ferritin-like <b>Family:</b> half-ferritin
28	<a href="#">c5n5fC_</a>	Alignment	not modelled	42.7	12	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> encapsulated ferritin; <b>PDBTitle:</b> crystal structure of haliangium ochraceum encapsulated ferritin
29	<a href="#">c6hk5A_</a>	Alignment	not modelled	40.9	21	<b>PDB header:</b> metal binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> cooj; <b>PDBTitle:</b> x-ray structure of a truncated mutant of the

30	<a href="#">c6hk5H_</a>	Alignment	not modelled	40.4	21	metallochaperone cooj2 with a high-affinity nickel-binding site <b>PDB header:</b> metal binding protein <b>Chain:</b> H: <b>PDB Molecule:</b> cooj; <b>PDBTitle:</b> x-ray structure of a truncated mutant of the metallochaperone cooj2 with a high-affinity nickel-binding site
31	<a href="#">c4ui9E_</a>	Alignment	not modelled	24.4	15	<b>PDB header:</b> cell cycle <b>Chain:</b> E: <b>PDB Molecule:</b> anaphase-promoting complex subunit 16; <b>PDBTitle:</b> atomic structure of the human anaphase-promoting complex
32	<a href="#">c3qthA_</a>	Alignment	not modelled	17.3	10	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> crystal structure of a dinb-like protein (cps_3021) from colwellia2 psychrerythraea 34h at 2.20 a resolution
33	<a href="#">d1o5ha_</a>	Alignment	not modelled	7.4	12	<b>Fold:</b> Methenyltetrahydrofolate cyclohydrolase-like <b>Superfamily:</b> Methenyltetrahydrofolate cyclohydrolase-like <b>Family:</b> Methenyltetrahydrofolate cyclohydrolase-like
34	<a href="#">d1ov9a_</a>	Alignment	not modelled	5.8	17	<b>Fold:</b> H-NS histone-like proteins <b>Superfamily:</b> H-NS histone-like proteins <b>Family:</b> H-NS histone-like proteins
35	<a href="#">c2l7kA_</a>	Alignment	not modelled	5.7	29	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> solution nmr structure of protein cd1104.2 from clostridium difficile,2 northeast structural genomics consortium target cfr130
36	<a href="#">c2fhoA_</a>	Alignment	not modelled	5.2	13	<b>PDB header:</b> rna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> spliceosomal protein sf3b155; <b>PDBTitle:</b> nmr solution structure of the human spliceosomal protein2 complex p14-sf3b155