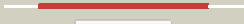











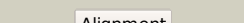













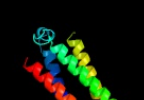






Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0036c_(-)_39056_39829
Date	Tue Jul 23 14:50:06 BST 2019
Unique Job ID	0eb3a431f8494b7b

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2nsfA_	 Alignment		100.0	15	PDB header: isomerase Chain: A: PDB Molecule: hypothetical protein cgl3021; PDBTitle: crystal structure of the mycothiol-dependent maleylpyruvate isomerase
2	d2nsfa1	 Alignment		100.0	13	Fold: DinB/YfiT-like putative metalloenzymes Superfamily: DinB/YfiT-like putative metalloenzymes Family: Maleylpyruvate isomerase-like
3	c5civA_	 Alignment		99.4	13	PDB header: unknown function Chain: A: PDB Molecule: sibling bacteriocin; PDBTitle: sibling lethal factor precursor - dfsb
4	c5cogB_	 Alignment		99.4	9	PDB header: unknown function Chain: B: PDB Molecule: irc4; PDBTitle: crystal structure of yeast irc4
5	c4n6cB_	 Alignment		99.4	6	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of the b1rzq2 protein from streptococcus pneumoniae.2 northeast structural genomics consortium (nesg) target spr36.
6	d1rxqa_	 Alignment		99.1	13	Fold: DinB/YfiT-like putative metalloenzymes Superfamily: DinB/YfiT-like putative metalloenzymes Family: YfiT-like putative metal-dependent hydrolases
7	c5cofA_	 Alignment		99.0	7	PDB header: unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of uncharacterised protein q1r1x2 from escherichia2 coli uti89
8	c6anrA_	 Alignment		99.0	9	PDB header: hydrolase Chain: A: PDB Molecule: colibactin self-protection protein clbs; PDBTitle: crystal structure of a self resistance protein clbs from colibactin2 biosynthetic gene cluster
9	c2rd9C_	 Alignment		98.9	10	PDB header: hydrolase Chain: C: PDB Molecule: bh0186 protein; PDBTitle: crystal structure of a putative yfiT-like metal-dependent hydrolase2 (bh0186) from bacillus halodurans c-125 at 2.30 a resolution
10	c6iz2A_	 Alignment		98.9	19	PDB header: unknown function Chain: A: PDB Molecule: dinb/yfiT family protein; PDBTitle: crystal structure of dinb/yfiT protein dr0053 from d. radiodurans r1
11	c5cqvb_	 Alignment		98.9	9	PDB header: unknown function Chain: B: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of uncharacterized protein q8dww2 from streptococcus2 agalactiae

12	c3cexB	Alignment		98.8	8	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of the conserved protein of locus ef_3021 from2 enterococcus faecalis
13	d2ou6a1	Alignment		98.7	14	Fold: DinB/YfiT-like putative metalloenzymes Superfamily: DinB/YfiT-like putative metalloenzymes Family: DinB-like
14	c3dkaA	Alignment		98.6	10	PDB header: unknown function Chain: A: PDB Molecule: dinb-like protein; PDBTitle: crystal structure of a dinb-like protein (yjoa, bsu12410) from2 bacillus subtilis at 2.30 a resolution
15	c3di5A	Alignment		98.5	14	PDB header: metal binding protein Chain: A: PDB Molecule: dinb-like protein; PDBTitle: crystal structure of a dinb-like protein (bce_4655) from bacillus2 cereus atcc 10987 at 2.01 a resolution
16	c2yqyB	Alignment		98.5	22	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: hypothetical protein ttha0303; PDBTitle: crystal structure of tt2238, a four-helix bundle protein
17	c2qe9B	Alignment		98.5	11	PDB header: hydrolase Chain: B: PDB Molecule: uncharacterized protein yiza; PDBTitle: crystal structure of a putative metal-dependent hydrolase (yiza,2 bsu10800) from bacillus subtilis at 1.90 a resolution
18	d2p1aa1	Alignment		98.4	11	Fold: DinB/YfiT-like putative metalloenzymes Superfamily: DinB/YfiT-like putative metalloenzymes Family: DinB-like
19	c3e4xB	Alignment		98.4	10	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: apc36150; PDBTitle: crystal structure of putative metal-dependent hydrolases2 apc36150
20	d2hkva1	Alignment		98.0	19	Fold: DinB/YfiT-like putative metalloenzymes Superfamily: DinB/YfiT-like putative metalloenzymes Family: DinB-like
21	c4nssA	Alignment	not modelled	94.8	20	PDB header: unknown function Chain: A: PDB Molecule: mycobacterial protein; PDBTitle: a structural and functional investigation of a novel protein from2 mycobacterium smegmatis implicated in mycobacterial macrophage3 survivability
22	d2nsfa2	Alignment	not modelled	93.4	17	Fold: SCP-like Superfamily: SCP-like Family: Micthiol-dependent maleylpyruvate isomerase C-terminal domain-like
23	c5wk0A	Alignment	not modelled	90.7	12	PDB header: unknown function Chain: A: PDB Molecule: damage-inducible protein dinb; PDBTitle: crystal structure of the bacillithiol transferase bsta from2 staphylococcus aureus.
24	c2qn1A	Alignment	not modelled	89.9	13	PDB header: signaling protein Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of a putative dna damage-inducible protein2 (chu_0679) from cytophaga hutchinsonii atcc 33406 at 1.50 a3 resolution
25	d1pz4a	Alignment	not modelled	83.8	10	Fold: SCP-like Superfamily: SCP-like Family: Sterol carrier protein, SCP
26	d1c44a	Alignment	not modelled	74.3	19	Fold: SCP-like Superfamily: SCP-like Family: Sterol carrier protein, SCP
27	c4ueiA	Alignment	not modelled	47.9	18	PDB header: transferase Chain: A: PDB Molecule: sterol carrier protein 2/3-oxoacyl-coa thiolase; PDBTitle: solution structure of the sterol carrier protein domain 22 of helicoverpa armigera
28	c2i00D	Alignment	not modelled	43.3	16	PDB header: transferase Chain: D: PDB Molecule: acetyltransferase, gnat family;

28	c2v0b	Alignment	not modelled	43.3	10	PDBTitle: crystal structure of acetyltransferase (gnat family) from enterococcus2 faecalis
29	c6h6pA	Alignment	not modelled	42.5	16	PDB header: lipid binding protein Chain: A: PDB Molecule: ubiquinone biosynthesis protein ubij; PDBTitle: ubij-scp2 ubiquinone synthesis protein
30	d1lktA	Alignment	not modelled	40.4	20	Fold: SCP-like Superfamily: SCP-like Family: Sterol carrier protein, SCP
31	c3bn8A	Alignment	not modelled	39.7	14	PDB header: transport protein Chain: A: PDB Molecule: putative sterol carrier protein 2; PDBTitle: crystal structure of a putative sterol carrier protein type 2 (af1534)2 from archaeoglobus fulgidus dsm 4304 at 2.11 a resolution
32	d2cfua1	Alignment	not modelled	39.5	17	Fold: SCP-like Superfamily: SCP-like Family: Alkylsulfatase C-terminal domain-like
33	c4jgxB	Alignment	not modelled	36.4	26	PDB header: lipid binding protein Chain: B: PDB Molecule: fatty acid-binding protein; PDBTitle: the structure of sterol carrier protein 2 from the yeast yarrowia2 lipolytica
34	c3bkrA	Alignment	not modelled	35.0	23	PDB header: lipid binding protein Chain: A: PDB Molecule: sterol carrier protein-2 like-3; PDBTitle: crystal structure of sterol carrier protein-2 like-3 (scp2-2 l3) from aedes aegypti
35	d1v8ca2	Alignment	not modelled	32.4	30	Fold: TBP-like Superfamily: MoaD-related protein, C-terminal domain Family: MoaD-related protein, C-terminal domain
36	c2jobA	Alignment	not modelled	24.7	80	PDB header: lipid binding protein Chain: A: PDB Molecule: antilipopolsaccharide factor; PDBTitle: solution structure of an antilipopolsaccharide factor from2 shrimp and its possible lipid a binding site
37	c4x8bA	Alignment	not modelled	23.9	11	PDB header: oxidoreductase Chain: A: PDB Molecule: sulfoxide synthase egtb; PDBTitle: ergothioneine-biosynthetic sulfoxide synthase egtb, apo form
38	c6qkja	Alignment	not modelled	18.0	12	PDB header: oxidoreductase Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: egtb from chloracidobacterium thermophilum, a type ii sulfoxide2 synthase in complex with n,n,n-trimethyl-histidine
39	c3bdqB	Alignment	not modelled	15.7	10	PDB header: lipid transport Chain: B: PDB Molecule: sterol carrier protein 2-like 2; PDBTitle: room temperture crystal structure of sterol carrier protein-2 2 like-2
40	d1liea	Alignment	not modelled	12.2	38	Fold: Class II MHC-associated invariant chain ectoplasmic trimerization domain Superfamily: Class II MHC-associated invariant chain ectoplasmic trimerization domain Family: Class II MHC-associated invariant chain ectoplasmic trimerization domain
41	c3a0aE	Alignment	not modelled	11.8	71	PDB header: structural protein Chain: E: PDB Molecule: collagen-like peptide; PDBTitle: structure of (ppg)4-opg-(ppg)4, monoclinic, twinned crystal
42	c3a0aB	Alignment	not modelled	11.8	71	PDB header: structural protein Chain: B: PDB Molecule: collagen-like peptide; PDBTitle: structure of (ppg)4-opg-(ppg)4, monoclinic, twinned crystal
43	c3a0aF	Alignment	not modelled	11.3	71	PDB header: structural protein Chain: F: PDB Molecule: collagen-like peptide; PDBTitle: structure of (ppg)4-opg-(ppg)4, monoclinic, twinned crystal
44	c3a0aD	Alignment	not modelled	11.3	71	PDB header: structural protein Chain: D: PDB Molecule: collagen-like peptide; PDBTitle: structure of (ppg)4-opg-(ppg)4, monoclinic, twinned crystal
45	c3a0aA	Alignment	not modelled	10.5	71	PDB header: structural protein Chain: A: PDB Molecule: collagen-like peptide; PDBTitle: structure of (ppg)4-opg-(ppg)4, monoclinic, twinned crystal
46	c2dkzA	Alignment	not modelled	10.2	26	PDB header: signaling protein Chain: A: PDB Molecule: hypothetical protein loc64762; PDBTitle: solution structure of the sam_pnt-domain of the2 hypothetical protein loc64762
47	c3a0aC	Alignment	not modelled	9.3	71	PDB header: structural protein Chain: C: PDB Molecule: collagen-like peptide; PDBTitle: structure of (ppg)4-opg-(ppg)4, monoclinic, twinned crystal
48	c6m8nA	Alignment	not modelled	9.1	24	PDB header: hydrolase Chain: A: PDB Molecule: p5afcna; PDBTitle: endo-fucoidan hydrolase p5afcna from glycoside hydrolase family 107
49	c2d3fA	Alignment	not modelled	7.4	71	PDB header: structural protein Chain: A: PDB Molecule: collagen model peptides (pro-pro-gly)4-pro-hyp- PDBTitle: crystal structures of collagen model peptides (pro-pro-gly)2 4-pro-hyp-gly-(pro-pro-gly)4
50	c2d3fC	Alignment	not modelled	7.4	71	PDB header: structural protein Chain: C: PDB Molecule: collagen model peptides (pro-pro-gly)4-pro-hyp- PDBTitle: crystal structures of collagen model peptides (pro-pro-gly)2 4-pro-hyp-gly-(pro-pro-gly)4
51	c2d3fB	Alignment	not modelled	7.4	71	PDB header: structural protein Chain: B: PDB Molecule: collagen model peptides (pro-pro-gly)4-pro-hyp- PDBTitle: crystal structures of collagen model peptides (pro-pro-gly)2 4-pro-hyp-gly-(pro-pro-gly)4
52	c1x1kE	Alignment	not modelled	7.4	71	PDB header: structural protein Chain: E: PDB Molecule: host-guest peptide (pro-pro-gly)4-(pro-allohyp- PDBTitle: host-guest peptide (pro-pro-gly)4-(pro-allohyp-gly)-(pro-2

						pro-gly)4
53	c1x1kA_	Alignment	not modelled	6.8	71	PDB header: structural protein Chain: A: PDB Molecule: host-guest peptide (pro-pro-gly)4-(pro-allohyp- PDBTitle: host-guest peptide (pro-pro-gly)4-(pro-allohyp-gly)-(pro-2 pro-gly)4
54	c1x1kD_	Alignment	not modelled	6.8	71	PDB header: structural protein Chain: D: PDB Molecule: host-guest peptide (pro-pro-gly)4-(pro-allohyp- PDBTitle: host-guest peptide (pro-pro-gly)4-(pro-allohyp-gly)-(pro-2 pro-gly)4
55	c2d3fD_	Alignment	not modelled	6.8	71	PDB header: structural protein Chain: D: PDB Molecule: collagen model peptides (pro-pro-gly)4- pro-hyp- PDBTitle: crystal structures of collagen model peptides (pro-pro- gly)2 4-pro-hyp-gly-(pro-pro-gly)4
56	c2d3fE_	Alignment	not modelled	6.8	71	PDB header: structural protein Chain: E: PDB Molecule: collagen model peptides (pro-pro-gly)4- pro-hyp- PDBTitle: crystal structures of collagen model peptides (pro-pro- gly)2 4-pro-hyp-gly-(pro-pro-gly)4
57	c1x1kB_	Alignment	not modelled	6.8	71	PDB header: structural protein Chain: B: PDB Molecule: host-guest peptide (pro-pro-gly)4-(pro-allohyp- PDBTitle: host-guest peptide (pro-pro-gly)4-(pro-allohyp-gly)-(pro-2 pro-gly)4
58	c2d3fF_	Alignment	not modelled	6.8	71	PDB header: structural protein Chain: F: PDB Molecule: collagen model peptides (pro-pro-gly)4- pro-hyp- PDBTitle: crystal structures of collagen model peptides (pro-pro- gly)2 4-pro-hyp-gly-(pro-pro-gly)4
59	c1x1kC_	Alignment	not modelled	6.8	71	PDB header: structural protein Chain: C: PDB Molecule: host-guest peptide (pro-pro-gly)4-(pro-allohyp- PDBTitle: host-guest peptide (pro-pro-gly)4-(pro-allohyp-gly)-(pro-2 pro-gly)4
60	c3abnC_	Alignment	not modelled	6.5	71	PDB header: structural protein Chain: C: PDB Molecule: collagen-like peptide; PDBTitle: crystal structure of (pro-pro-gly)4-hyp-asp-gly-(pro-pro- gly)4 at 1.022 a
61	c4idiA_	Alignment	not modelled	6.4	5	PDB header: protein binding Chain: A: PDB Molecule: oryza sativa rum1-related; PDBTitle: crystal structure of rum1-related protein from plasmodium yoelii,2 py06420
62	c3abnB_	Alignment	not modelled	6.0	71	PDB header: structural protein Chain: B: PDB Molecule: collagen-like peptide; PDBTitle: crystal structure of (pro-pro-gly)4-hyp-asp-gly-(pro-pro- gly)4 at 1.022 a
63	c1x1kF_	Alignment	not modelled	6.0	71	PDB header: structural protein Chain: F: PDB Molecule: host-guest peptide (pro-pro-gly)4-(pro-allohyp- PDBTitle: host-guest peptide (pro-pro-gly)4-(pro-allohyp-gly)-(pro-2 pro-gly)4
64	d1tc3c_	Alignment	not modelled	5.8	4	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Recombinase DNA-binding domain