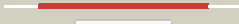



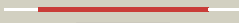


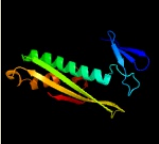



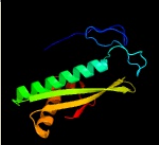









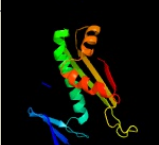


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2923c (-)_3238096_3238509
Date	Thu Aug 8 16:20:08 BST 2019
Unique Job ID	c5663927357062b0

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1ml8a_	 Alignment		99.9	19	Fold: OsmC-like Superfamily: OsmC-like Family: YhfA-like
2	c2egtA_	 Alignment		99.9	15	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein aq_1549; PDBTitle: crystal structure of hypothetical protein (aq1549) from aquifex2 aeolicus
3	d1vlaa_	 Alignment		99.9	18	Fold: OsmC-like Superfamily: OsmC-like Family: YhfA-like
4	d2onfa1	 Alignment		99.9	14	Fold: OsmC-like Superfamily: OsmC-like Family: Ohr/OsmC resistance proteins
5	c3eerA_	 Alignment		99.9	13	PDB header: oxidoreductase Chain: A: PDB Molecule: organic hydroperoxide resistance protein, putative; PDBTitle: high resolution structure of putative organic hydroperoxide resistance2 protein from vibrio cholerae o1 biovar eltor str. n16961
6	c6mjnC_	 Alignment		99.9	17	PDB header: oxidoreductase Chain: C: PDB Molecule: organic hydroperoxide resistance protein; PDBTitle: crystal structure of an organic hydroperoxide resistance protein osmc,2 predicted redox protein, regulator of sulfide bond formation from3 legionella pneumophila
7	d1qwia_	 Alignment		99.9	13	Fold: OsmC-like Superfamily: OsmC-like Family: Ohr/OsmC resistance proteins
8	c6d9nA_	 Alignment		99.9	18	PDB header: oxidoreductase Chain: A: PDB Molecule: organic hydroperoxide resistance protein; PDBTitle: crystal structure of an organic hydroperoxide resistance protein from2 elizabethkingia anophelis with crystallant-derived thiocyanate bound
9	d2pn2a1	 Alignment		99.9	17	Fold: OsmC-like Superfamily: OsmC-like Family: Ohr/OsmC resistance proteins
10	c2ql8A_	 Alignment		99.9	16	PDB header: oxidoreductase Chain: A: PDB Molecule: putative redox protein; PDBTitle: crystal structure of a putative redox protein (Isei_0423) from2 lactobacillus casei atcc 334 at 1.50 a resolution
11	d1lqla_	 Alignment		99.9	14	Fold: OsmC-like Superfamily: OsmC-like Family: Ohr/OsmC resistance proteins

12	c1lqE_	Alignment		99.9	14	PDB header: unknown function Chain: E: PDB Molecule: osmotical inducible protein c like family; PDBTitle: crystal structure of osmc like protein from mycoplasma2 pneumoniae
13	c4mh4B_	Alignment		99.9	15	PDB header: protein binding Chain: B: PDB Molecule: osmc-like protein; PDBTitle: crystal structure of osmc-like protein from burkholderia cenocepacia2 j2315
14	d1nyed_	Alignment		99.9	17	Fold: OsmC-like Superfamily: OsmC-like Family: Ohr/OsmC resistance proteins
15	d1uspa_	Alignment		99.8	19	Fold: OsmC-like Superfamily: OsmC-like Family: Ohr/OsmC resistance proteins
16	c2bjoA_	Alignment		99.8	17	PDB header: oxidoreductase Chain: A: PDB Molecule: organic hydroperoxide resistance protein ohrb; PDBTitle: crystal structure of the organic hydroperoxide resistance2 protein ohrb of bacillus subtilis
17	d1n2fa_	Alignment		99.8	18	Fold: OsmC-like Superfamily: OsmC-like Family: Ohr/OsmC resistance proteins
18	d1lukka_	Alignment		99.8	17	Fold: OsmC-like Superfamily: OsmC-like Family: Ohr/OsmC resistance proteins
19	d2opla1	Alignment		99.8	18	Fold: OsmC-like Superfamily: OsmC-like Family: Ohr/OsmC resistance proteins
20	c4nozA_	Alignment		99.8	20	PDB header: protein binding Chain: A: PDB Molecule: organic hydroperoxide resistance protein; PDBTitle: crystal structure of an organic hydroperoxide resistance protein from2 burkholderia cenocepacia
21	c3cjeA_	Alignment	not modelled	99.8	15	PDB header: oxidoreductase Chain: A: PDB Molecule: osmc-like protein; PDBTitle: crystal structure of an osmc-like hydroperoxide resistance protein2 (jann_2040) from jannaschia sp. ccs1 at 1.70 a resolution
22	d2d7va1	Alignment	not modelled	99.8	13	Fold: OsmC-like Superfamily: OsmC-like Family: Ohr/OsmC resistance proteins
23	c1zb8B_	Alignment	not modelled	99.8	16	PDB header: oxidoreductase Chain: B: PDB Molecule: organic hydroperoxide resistance protein; PDBTitle: crystal structure of xylella fastidiosa organic peroxide resistance2 protein
24	c2j0wA_	Alignment	not modelled	13.6	14	PDB header: transferase Chain: A: PDB Molecule: lysine-sensitive aspartokinase 3; PDBTitle: crystal structure of e. coli aspartokinase iii in complex2 with aspartate and adp (r-state)
25	d1eaqa_	Alignment	not modelled	11.8	38	Fold: Common fold of diphtheria toxin/transcription factors/cytochrome f Superfamily: p53-like transcription factors Family: RUNT domain
26	d2idla1	Alignment	not modelled	10.9	9	Fold: eIF1-like Superfamily: TM1457-like Family: TM1457-like
27	d1ljma_	Alignment	not modelled	10.6	38	Fold: Common fold of diphtheria toxin/transcription factors/cytochrome f Superfamily: p53-like transcription factors Family: RUNT domain
28	d1r5ta_	Alignment	not modelled	10.5	21	Fold: Cytidine deaminase-like Superfamily: Cytidine deaminase-like Family: Cytidine deaminase
						PDB header: isomerase

29	c3lnuA_	Alignment	not modelled	9.9	18	Chain: A: PDB Molecule: topoisomerase iv subunit b; PDBTitle: crystal structure of pare subunit
30	c4l0zA_	Alignment	not modelled	9.0	38	PDB header: transcription/dna Chain: A: PDB Molecule: runt-related transcription factor 1; PDBTitle: crystal structure of runx1 and ets1 bound to tcr alpha promoter2 (crystal form 2)
31	c3fxeA_	Alignment	not modelled	8.9	35	PDB header: unknown function Chain: A: PDB Molecule: protein icmq; PDBTitle: crystal structure of interacting domains of icmr and icmq (seleno-2 derivative)
32	d1zbsa2	Alignment	not modelled	8.8	40	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: BadF/BadG/BcrA/BcrD-like
33	c2lifA_	Alignment	not modelled	8.3	31	PDB header: viral protein, membrane protein Chain: A: PDB Molecule: core protein p21; PDBTitle: solution structure of kkgf
34	d1k0ma2	Alignment	not modelled	8.2	11	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: Glutathione S-transferase (GST), N-terminal domain
35	c2g0jA_	Alignment	not modelled	7.1	11	PDB header: unknown function Chain: A: PDB Molecule: hypothetical protein smu.848; PDBTitle: crystal structure of smu.848 from streptococcus mutans
36	c4u65F_	Alignment	not modelled	7.0	21	PDB header: transferase/hydrolase Chain: F: PDB Molecule: putative cystine protease; PDBTitle: structure of the periplasmic output domain of the legionella2 pneumophila lapd ortholog cdgs9 in complex with pseudomonas3 fluorescens lappg
37	c2yolA_	Alignment	not modelled	6.7	26	PDB header: hydrolase Chain: A: PDB Molecule: serine protease subunit ns2b, serine protease ns3; PDBTitle: west nile virus ns2b-ns3 protease in complex with 3,4-2 dichlorophenylacetyl-lys-lys-gcma
38	d1p42a1	Alignment	not modelled	6.6	20	Fold: Ribosomal protein S5 domain 2-like Superfamily: Ribosomal protein S5 domain 2-like Family: UDP-3-O-[3-hydroxymyristoyl] N-acetylglucosamine deacetylase LpxC
39	d1zxoal	Alignment	not modelled	6.5	30	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: BadF/BadG/BcrA/BcrD-like
40	d1prtd_	Alignment	not modelled	6.4	18	Fold: OB-fold Superfamily: Bacterial enterotoxins Family: Bacterial AB5 toxins, B-subunits
41	d2pc6a2	Alignment	not modelled	5.9	10	Fold: Ferredoxin-like Superfamily: ACT-like Family: IlvH-like
42	d2fgca2	Alignment	not modelled	5.9	14	Fold: Ferredoxin-like Superfamily: ACT-like Family: IlvH-like
43	c5wodA_	Alignment	not modelled	5.7	33	PDB header: de novo protein Chain: A: PDB Molecule: 38-mer peptide; PDBTitle: de novo design of covalently constrained meso-size protein scaffolds2 with unique tertiary structures
44	d2f1fa1	Alignment	not modelled	5.6	12	Fold: Ferredoxin-like Superfamily: ACT-like Family: IlvH-like
45	d2proc1	Alignment	not modelled	5.4	23	Fold: Alpha-lytic protease prodomain-like Superfamily: Alpha-lytic protease prodomain Family: Alpha-lytic protease prodomain