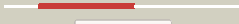



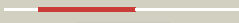








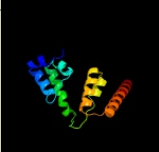







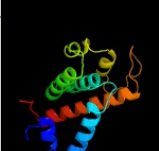
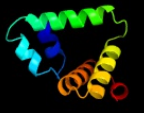










Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2159c_(-)_2420639_2421673
Date	Mon Aug 5 13:25:28 BST 2019
Unique Job ID	a78aeaaf2bfc3b03

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d2prra1	 Alignment		100.0	16	Fold: AhpD-like Superfamily: AhpD-like Family: Atu0492-like
2	d2oyoa1	 Alignment		100.0	18	Fold: AhpD-like Superfamily: AhpD-like Family: Atu0492-like
3	d2pfxa1	 Alignment		100.0	14	Fold: AhpD-like Superfamily: AhpD-like Family: Atu0492-like
4	c3c1lB_	 Alignment		100.0	17	PDB header: oxidoreductase Chain: B: PDB Molecule: putative antioxidant defense protein mlr4105; PDBTitle: crystal structure of an antioxidant defense protein (mlr4105) from2 mesorhizobium loti maff303099 at 2.00 a resolution
5	c6ohiA_	 Alignment		100.0	14	PDB header: biosynthetic protein Chain: A: PDB Molecule: debrominase bmp8; PDBTitle: crystal structure of the debrominase bmp8 (apo)
6	c3lvyB_	 Alignment		100.0	16	PDB header: lyase Chain: B: PDB Molecule: carboxymuconolactone decarboxylase family; PDBTitle: crystal structure of carboxymuconolactone decarboxylase2 family protein smu.961 from streptococcus mutans
7	d2ouwa1	 Alignment		99.9	20	Fold: AhpD-like Superfamily: AhpD-like Family: TTHA0727-like
8	d2gmya1	 Alignment		99.9	10	Fold: AhpD-like Superfamily: AhpD-like Family: Atu0492-like
9	d2o4da1	 Alignment		99.9	17	Fold: AhpD-like Superfamily: AhpD-like Family: Atu0492-like
10	c2qeua_	 Alignment		99.6	20	PDB header: lyase Chain: A: PDB Molecule: putative carboxymuconolactone decarboxylase; PDBTitle: crystal structure of putative carboxymuconolactone decarboxylase2 (yp_555818.1) from burkholderia xenovorans lb400 at 1.65 a resolution
11	c5dj4D_	 Alignment		99.6	14	PDB header: signaling protein Chain: D: PDB Molecule: sestrin-2; PDBTitle: leucine-bound sestrin2 from homo sapiens

12	d2cwqa1	Alignment		99.4	18	Fold: AhpD-like Superfamily: AhpD-like Family: TTHA0727-like
13	c5dipB	Alignment		99.4	23	PDB header: oxidoreductase Chain: B: PDB Molecule: alkyl hydroperoxide reductase ahpd; PDBTitle: crystal structure of lpg0406 in reduced form from legionella2 pneumophila
14	c1p8cD	Alignment		99.3	18	PDB header: structural genomics, unknown function Chain: D: PDB Molecule: conserved hypothetical protein; PDBTitle: crystal structure of tm1620 (apc4843) from thermotoga2 maritima
15	d1vkea	Alignment		99.3	22	Fold: AhpD-like Superfamily: AhpD-like Family: CMD-like
16	c5gzxD	Alignment		99.2	20	PDB header: hydrolase Chain: D: PDB Molecule: (r)-2-haloacid dehalogenase; PDBTitle: the complex structure of d-2-haloacid dehalogenase mutant with d-2-cpa
17	c3beyC	Alignment		99.2	18	PDB header: structural genomics, unknown function Chain: C: PDB Molecule: conserved protein o27018; PDBTitle: crystal structure of the protein o27018 from methanobacterium2 thermoautotrophicum. northeast structural genomics consortium target3 tt217
18	d2q0ta1	Alignment		99.1	14	Fold: AhpD-like Superfamily: AhpD-like Family: AhpD
19	c3d7iB	Alignment		99.1	9	PDB header: lyase Chain: B: PDB Molecule: carboxymuconolactone decarboxylase family protein; PDBTitle: crystal structure of carboxymuconolactone decarboxylase family protein2 possibly involved in oxygen detoxification (1591455) from3 methanococcus jannaschii at 1.75 a resolution
20	d1vkeb	Alignment		98.9	18	Fold: AhpD-like Superfamily: AhpD-like Family: CMD-like
21	d1knca	Alignment	not modelled	98.8	25	Fold: AhpD-like Superfamily: AhpD-like Family: AhpD
22	c3bjxB	Alignment	not modelled	98.2	18	PDB header: hydrolase Chain: B: PDB Molecule: halocarboxylic acid dehalogenase dehi; PDBTitle: structure of a group i haloacid dehalogenase from2 pseudomonas putida strain pp3
23	c4n2xF	Alignment	not modelled	98.0	23	PDB header: hydrolase Chain: F: PDB Molecule: dl-2-haloacid dehalogenase; PDBTitle: crystal structure of dl-2-haloacid dehalogenase
24	c4g9qA	Alignment	not modelled	97.9	11	PDB header: lyase Chain: A: PDB Molecule: 4-carboxymuconolactone decarboxylase; PDBTitle: crystal structure of a 4-carboxymuconolactone decarboxylase
25	d2af7a1	Alignment	not modelled	97.3	15	Fold: AhpD-like Superfamily: AhpD-like Family: CMD-like
26	c6igzK	Alignment	not modelled	42.8	32	PDB header: plant protein Chain: K: PDB Molecule: psak; PDBTitle: structure of psi-lhci
27	d1abaa	Alignment	not modelled	36.0	28	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: Thioltransferase
28	c1t3bA	Alignment	not modelled	32.3	33	PDB header: isomerase Chain: A: PDB Molecule: thiol:disulfide interchange protein dsbc; PDBTitle: x-ray structure of dsbc from haemophilus influenzae
29	c1v57A	Alignment	not modelled	31.5	25	PDB header: isomerase Chain: A: PDB Molecule: thiol:disulfide interchange protein dsbg;

						PDBTitle: crystal structure of the disulfide bond isomerase dsbg
30	d1t3ba1	Alignment	not modelled	29.8	33	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: DsbC/DsbG C-terminal domain-like
31	c4npbA	Alignment	not modelled	29.8	33	PDB header: isomerase Chain: A: PDB Molecule: protein disulfide isomerase ii; PDBTitle: the crystal structure of thiol:disulfide interchange protein dsbc from2 yersinia pestis co92
32	c4ml1D	Alignment	not modelled	29.2	25	PDB header: isomerase Chain: D: PDB Molecule: dsbp; PDBTitle: disulfide isomerase (dsbp) from multidrug resistance inca/c2 transferable plasmid in oxidized state (p212121 space group)
33	d1qpza1	Alignment	not modelled	27.5	19	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: GalR/LacI-like bacterial regulator
34	c3dvwA	Alignment	not modelled	27.2	25	PDB header: oxidoreductase Chain: A: PDB Molecule: thiol:disulfide interchange protein dsba; PDBTitle: crystal structure of reduced dsba1 from neisseria2 meningitidis
35	c1jzdA	Alignment	not modelled	26.8	22	PDB header: oxidoreductase Chain: A: PDB Molecule: thiol:disulfide interchange protein dsbc; PDBTitle: dsbc-dsbdalpha complex
36	c3gv1A	Alignment	not modelled	26.7	25	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: disulfide interchange protein; PDBTitle: crystal structure of disulfide interchange protein from neisseria2 gonorrhoeae
37	c3hd5A	Alignment	not modelled	24.3	21	PDB header: oxidoreductase Chain: A: PDB Molecule: thiol:disulfide interchange protein dsba; PDBTitle: crystal structure of a thiol:disulfide interchange protein2 dsba from bordetella parapertussis
38	c4jr6A	Alignment	not modelled	23.5	19	PDB header: oxidoreductase Chain: A: PDB Molecule: possible conserved membrane or secreted protein; PDBTitle: crystal structure of dsba from mycobacterium tuberculosis (reduced)
39	c4p3yB	Alignment	not modelled	23.1	29	PDB header: translation/oxidoreductase Chain: B: PDB Molecule: thiol:disulfide interchange protein; PDBTitle: crystal structure of acinetobacter baumannii dsba in complex with ef-2 tu
40	d1eeja1	Alignment	not modelled	23.0	33	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: DsbC/DsbG C-terminal domain-like
41	d1beda	Alignment	not modelled	23.0	25	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: DsbA-like
42	c3bcia	Alignment	not modelled	22.2	19	PDB header: oxidoreductase Chain: A: PDB Molecule: disulfide bond protein a; PDBTitle: crystal structure of staphylococcus aureus dsba
43	c3l9vE	Alignment	not modelled	21.8	33	PDB header: oxidoreductase Chain: E: PDB Molecule: putative thiol-disulfide isomerase or thioredoxin; PDBTitle: crystal structure of salmonella enterica serovar typhimurium srga
44	d1efaa1	Alignment	not modelled	21.8	18	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: GalR/LacI-like bacterial regulator
45	c5h1nB	Alignment	not modelled	21.5	21	PDB header: unknown function Chain: B: PDB Molecule: upf0253 protein yaep; PDBTitle: crystal structure of sf173 from shigella flexneri
46	c3ic4A	Alignment	not modelled	21.1	12	PDB header: oxidoreductase Chain: A: PDB Molecule: glutaredoxin (grx-1); PDBTitle: the crystal structure of the glutaredoxin(grx-1) from archaeoglobus2 fulgidus
47	c3h93A	Alignment	not modelled	20.7	33	PDB header: transcription regulator Chain: A: PDB Molecule: thiol:disulfide interchange protein dsba; PDBTitle: crystal structure of pseudomonas aeruginosa dsba
48	c6eezC	Alignment	not modelled	19.9	14	PDB header: isomerase Chain: C: PDB Molecule: dsba-like disulfide oxidoreductase; PDBTitle: crystal structure of the thiol-disulfide exchange protein alpha-dsba22 from wolbachia pipientis
49	c4xvwK	Alignment	not modelled	19.7	25	PDB header: isomerase Chain: K: PDB Molecule: dsba-like protein; PDBTitle: crystal structure of proteus mirabilis scsc in a compact conformation
50	c3f4tA	Alignment	not modelled	19.3	19	PDB header: oxidoreductase Chain: A: PDB Molecule: putative uncharacterized protein; PDBTitle: crystal structure of wolbachia pipientis alpha-dsba1 c97a/c146a
51	c3c7mB	Alignment	not modelled	19.0	19	PDB header: oxidoreductase Chain: B: PDB Molecule: thiol:disulfide interchange protein dsba-like; PDBTitle: crystal structure of reduced dsbl
52	d1v58a1	Alignment	not modelled	18.9	25	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: DsbC/DsbG C-terminal domain-like
53	c6ijjK	Alignment	not modelled	18.7	27	PDB header: membrane protein Chain: K: PDB Molecule: psak; PDBTitle: photosystem i of chlamydomonas reinhardtii
54	c4pwoA	Alignment	not modelled	18.7	19	PDB header: structural genomics Chain: A: PDB Molecule: dsba; PDBTitle: crystal structure of dsba from the gram positive bacterium2 corynebacterium diphtheriae
55	c2remB	Alignment	not modelled	18.6	25	PDB header: oxidoreductase Chain: B: PDB Molecule: disulfide oxidoreductase; PDBTitle: crystal structure of oxidoreductase dsba from xylella

						fastidiosa
56	d1fvka_	Alignment	not modelled	18.4	33	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: DsbA-like
57	c5kbcA_	Alignment	not modelled	18.3	13	PDB header: oxidoreductase Chain: A: PDB Molecule: dsba; PDBTitle: crystal structure of chlamydia trachomatis dsba
58	c6dxnC_	Alignment	not modelled	18.3	20	PDB header: oxidoreductase Chain: C: PDB Molecule: thiol:disulfide interchange protein; PDBTitle: 1.95 angstrom resolution crystal structure of dsba disulfide2 interchange protein from klebsiella pneumoniae.
59	c4p6iB_	Alignment	not modelled	18.1	10	PDB header: hydrolase Chain: B: PDB Molecule: crispr-associated endoribonuclease cas2; PDBTitle: crystal structure of the cas1-cas2 complex from escherichia coli
60	c3gmfA_	Alignment	not modelled	17.8	20	PDB header: oxidoreductase Chain: A: PDB Molecule: protein-disulfide isomerase; PDBTitle: crystal structure of protein-disulfide isomerase from novosphingobium2 aromaticivorans
61	c3mcnA_	Alignment	not modelled	17.5	9	PDB header: transferase Chain: A: PDB Molecule: 2-amino-4-hydroxy-6-hydroxymethyl-dihydropteridine PDBTitle: crystal structure of the 6-hydroxymethyl-7,8-dihydropterin2 pyrophosphokinase dihydropteroate synthase bifunctional enzyme from3 francisella tularensis
62	d2bjca1	Alignment	not modelled	17.5	18	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: GalR/LacI-like bacterial regulator
63	c4k2dA_	Alignment	not modelled	17.4	29	PDB header: oxidoreductase Chain: A: PDB Molecule: thiol:disulfide interchange protein; PDBTitle: crystal structure of burkholderia pseudomallei dsba
64	c4n30A_	Alignment	not modelled	17.2	25	PDB header: oxidoreductase Chain: A: PDB Molecule: protein disulfide isomerase; PDBTitle: crystal structure of pseudomonas aeruginosa dsba2
65	c4fybA_	Alignment	not modelled	17.1	13	PDB header: oxidoreductase Chain: A: PDB Molecule: thiol:disulfide interchange protein (dsbc); PDBTitle: structural and functional characterizations of a thioredoxin-fold2 protein from helicobacter pylori
66	c3lgcA_	Alignment	not modelled	16.8	26	PDB header: unknown function Chain: A: PDB Molecule: glutaredoxin 1; PDBTitle: crystal structure of glutaredoxin 1 from francisella tularensis
67	d2hsga1	Alignment	not modelled	16.8	14	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: GalR/LacI-like bacterial regulator
68	c2e7pC_	Alignment	not modelled	16.8	22	PDB header: electron transport Chain: C: PDB Molecule: glutaredoxin; PDBTitle: crystal structure of the holo form of glutaredoxin c1 from populus2 tremula x tremuloides
69	c4z7xA_	Alignment	not modelled	16.7	13	PDB header: oxidoreductase Chain: A: PDB Molecule: mdba; PDBTitle: mdba protein, a thiol-disulfide oxidoreductase from actinomyces oris.
70	c4tr1A_	Alignment	not modelled	16.1	26	PDB header: oxidoreductase Chain: A: PDB Molecule: glutaredoxin 3; PDBTitle: crystal structure of gsh-bound cgrx2/c15s
71	c3feuA_	Alignment	not modelled	15.9	22	PDB header: oxidoreductase Chain: A: PDB Molecule: putative lipoprotein; PDBTitle: crystal structure of dsba-like thioredoxin domain vf_a0457 from vibrio2 fischeri
72	d1z6ma1	Alignment	not modelled	15.8	29	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: DsbA-like
73	c4r33A_	Alignment	not modelled	15.4	33	PDB header: lyase Chain: A: PDB Molecule: nosl; PDBTitle: x-ray structure of the tryptophan lyase nosl with tryptophan and s-2 adenosyl-l-homocysteine bound
74	c3ghaA_	Alignment	not modelled	15.2	19	PDB header: oxidoreductase Chain: A: PDB Molecule: disulfide bond formation protein d; PDBTitle: crystal structure of etda-treated bdbd (reduced)
75	c4jrrC_	Alignment	not modelled	15.2	33	PDB header: oxidoreductase Chain: C: PDB Molecule: thiol:disulfide interchange protein dsba; PDBTitle: crystal structure of disulfide bond oxidoreductase dsba1 from2 legionella pneumophila
76	c4od7A_	Alignment	not modelled	15.1	22	PDB header: oxidoreductase/peptide Chain: A: PDB Molecule: thiol:disulfide interchange protein; PDBTitle: complex structure of proteus mirabilis dsba (c30s) with a non-2 covalently bound peptide pwatcds
77	c1nm3B_	Alignment	not modelled	14.9	33	PDB header: electron transport Chain: B: PDB Molecule: protein hi0572; PDBTitle: crystal structure of heamophilus influenza hybrid-prx5
78	c3dprD_	Alignment	not modelled	14.8	100	PDB header: virus Chain: D: PDB Molecule: protein vp4; PDBTitle: human rhinovirus 2 bound to a concatamer of the vldl receptor module2 v3
79	c1fpn4_	Alignment	not modelled	14.8	100	PDB header: virus Chain: 4: PDB Molecule: coat protein vp4; PDBTitle: human rhinovirus serotype 2 (hrv2)
80	c1v9u4_	Alignment	not modelled	14.8	100	PDB header: virus/receptor Chain: 4: PDB Molecule: coat protein vp4; PDBTitle: human rhinovirus 2 bound to a fragment of its cellular2 receptor protein
81	c4gxzB_	Alignment	not modelled	14.7	25	PDB header: isomerase Chain: B: PDB Molecule: suppression of copper sensitivity protein; PDBTitle: crystal structure of a periplasmic thioredoxin-like protein

						from2 salmonella enterica serovar typhimurium
82	d1m9ia1	Alignment	not modelled	14.6	13	Fold: Annexin Superfamily: Annexin Family: Annexin
83	c1avcA	Alignment	not modelled	13.8	13	PDB header: calcium/phospholipid-binding protein Chain: A; PDB Molecule: annexin vi; PDBTitle: bovine annexin vi (calcium-bound)
84	c3gykC	Alignment	not modelled	13.5	29	PDB header: oxidoreductase Chain: C; PDB Molecule: 27kda outer membrane protein; PDBTitle: the crystal structure of a thioredoxin-like oxidoreductase from2 silicibacter pomeroyi dss-3
85	c2lqoA	Alignment	not modelled	13.3	21	PDB header: oxidoreductase Chain: A; PDB Molecule: putative glutaredoxin rv3198.1/mt3292; PDBTitle: mrx1 reduced
86	d1fova	Alignment	not modelled	13.1	33	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: Thioltransferase
87	d1xgsa1	Alignment	not modelled	12.7	32	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Methionine aminopeptidase, insert domain
88	c2yruA	Alignment	not modelled	12.5	17	PDB header: apoptosis Chain: A; PDB Molecule: steroid receptor rna activator 1; PDBTitle: solution structure of mouse steroid receptor rna activator2 1 (sra1) protein
89	c2jbcC	Alignment	not modelled	12.4	22	PDB header: electron transport Chain: C; PDB Molecule: photosynthetic reaction center cytochrome c subunit; PDBTitle: photosynthetic reaction center from blastochloris viridis
90	d1b6aa1	Alignment	not modelled	12.4	9	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Methionine aminopeptidase, insert domain
91	c2m80A	Alignment	not modelled	12.2	28	PDB header: oxidoreductase Chain: A; PDB Molecule: glutaredoxin-8; PDBTitle: solution structure of yeast dithiol glutaredoxin grx8
92	c3hkpP	Alignment	not modelled	12.1	80	PDB header: transferase Chain: P; PDB Molecule: dna-directed rna polymerase subunit p; PDBTitle: the x-ray crystal structure of rna polymerase from archaea
93	c2znmA	Alignment	not modelled	12.0	17	PDB header: oxidoreductase Chain: A; PDB Molecule: thiol:disulfide interchange protein dsba; PDBTitle: oxidoreductase nmdb3 from neisseria meningitidis
94	c1a6bB	Alignment	not modelled	11.9	33	PDB header: viral protein/dna Chain: B; PDB Molecule: zinc finger protein ncp10; PDBTitle: nmr structure of the complex between the zinc finger2 protein ncp10 of moloney murine leukemia virus and a3 sequence of the psi-packaging domain of hiv-1, 204 structures
95	d1luxda	Alignment	not modelled	11.9	19	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: GalR/LacI-like bacterial regulator
96	c3zjA	Alignment	not modelled	11.8	31	PDB header: oxidoreductase Chain: A; PDB Molecule: thioredoxin; PDBTitle: crystal structure of the thioredoxin-like protein bc3987
97	c3nznA	Alignment	not modelled	11.8	20	PDB header: oxidoreductase Chain: A; PDB Molecule: glutaredoxin; PDBTitle: the crystal structure of the glutaredoxin from methanosarcina mazei2 go1
98	c3s63B	Alignment	not modelled	11.7	26	PDB header: lipid binding protein Chain: B; PDB Molecule: saposin-like protein; PDBTitle: saposin-like protein na-slp-1
99	c4qiWP	Alignment	not modelled	11.4	50	PDB header: transcription Chain: P; PDB Molecule: dna-directed rna polymerase subunit p; PDBTitle: crystal structure of euryarchaeal rna polymerase from thermococcus2 kodakarensis