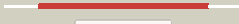



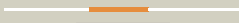
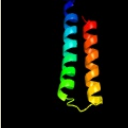





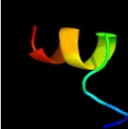



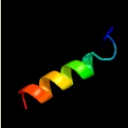

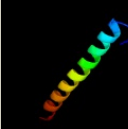



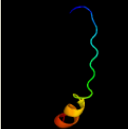
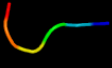

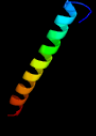



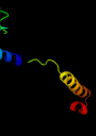




Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2968c_(-)_3323081_3323713
Date	Thu Aug 8 16:20:13 BST 2019
Unique Job ID	f935398aef9cfa1c

Detailed template
information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3kp9A_	 Alignment		100.0	23	PDB header: blood coagulation,oxidoreductase Chain: A: PDB Molecule: vkorc1/thioredoxin domain protein; PDBTitle: structure of a bacterial homolog of vitamin k epoxide reductase
2	c2k74A_	 Alignment		93.4	24	PDB header: membrane protein, oxidoreductase Chain: A: PDB Molecule: disulfide bond formation protein b; PDBTitle: solution nmr structure of dsbb-ubiquinone complex
3	c5ir6A_	 Alignment		82.9	13	PDB header: oxidoreductase Chain: A: PDB Molecule: bd-type quinol oxidase subunit i; PDBTitle: the structure of bd oxidase from geobacillus thermodenitrificans
4	c3e9jC_	 Alignment		70.6	13	PDB header: oxidoreductase Chain: C: PDB Molecule: thio/disulfide oxidoreductase dsbb; PDBTitle: structure of the charge-transfer intermediate of the2 transmembrane redox catalyst dsbb
5	d2hi7b1	 Alignment		64.4	16	Fold: Bromodomain-like Superfamily: DsbB-like Family: DsbB-like
6	c5y7iB_	 Alignment		30.3	38	PDB header: transport protein Chain: B: PDB Molecule: chloride intracellular channel protein 2; PDBTitle: structure of tilapia fish clic2
7	c2voyG_	 Alignment		20.7	20	PDB header: hydrolase Chain: G: PDB Molecule: sarcoplasmic/endoplasmic reticulum calcium atpase 1; PDBTitle: cryoem model of copa, the copper transporting atpase from2 archaeoglobus fulgidus
8	c2n1pA_	 Alignment		17.8	28	PDB header: viral protein Chain: A: PDB Molecule: non-structural protein 5b, ns5b; PDBTitle: structure of the c-terminal membrane domain of hcv ns5b protein
9	d1v54j_	 Alignment		17.0	6	Fold: Single transmembrane helix Superfamily: Mitochondrial cytochrome c oxidase subunit VIIa Family: Mitochondrial cytochrome c oxidase subunit VIIa
10	d2dlka1	 Alignment		14.9	31	Fold: beta-beta-alpha zinc fingers Superfamily: beta-beta-alpha zinc fingers Family: Classic zinc finger, C2H2
11	c6f46A_	 Alignment		14.3	32	PDB header: apoptosis Chain: A: PDB Molecule: bcl-2-like protein 1; PDBTitle: structure of the transmembrane helix of bclxl in phospholipid2 nanodiscs

12	d1wjpa2	Alignment		14.1	83	Fold: beta-beta-alpha zinc fingers Superfamily: beta-beta-alpha zinc fingers Family: Classic zinc finger, C2H2
13	c5hfiA	Alignment		11.1	60	PDB header: oxidoreductase Chain: A: PDB Molecule: uncharacterized protein, cytosolic disulfide reductase PDBTitle: cytosolic disulfide reductase dsbm from pseudomonas aeruginosa with2 gsh
14	c2y69W	Alignment		10.9	6	PDB header: electron transport Chain: W: PDB Molecule: cytochrome c oxidase polypeptide 7a1; PDBTitle: bovine heart cytochrome c oxidase re-refined with molecular oxygen
15	c5z62J	Alignment		10.7	6	PDB header: electron transport Chain: J: PDB Molecule: cytochrome c oxidase subunit 7a2, mitochondrial; PDBTitle: structure of human cytochrome c oxidase
16	c6ithA	Alignment		10.1	22	PDB header: membrane protein Chain: A: PDB Molecule: syndecan-2; PDBTitle: structure of the transmembrane domain of syndecan 2 in micelles
17	c2k9hA	Alignment		9.3	100	PDB header: metal binding protein Chain: A: PDB Molecule: glycoprotein; PDBTitle: the hantavirus glycoprotein g1 tail contains a dual cchc-2 type classical zinc fingers
18	c6hwhX	Alignment		9.1	9	PDB header: electron transport Chain: X: PDB Molecule: cytochrome c oxidase polypeptide 4; PDBTitle: structure of a functional obligate respiratory supercomplex from2 mycobacterium smegmatis
19	c3kzqE	Alignment		8.9	40	PDB header: structural genomics, unknown function Chain: E: PDB Molecule: putative uncharacterized protein vp2116; PDBTitle: the crystal structure of the protein with unknown function from vibrio2 parahaemolyticus rimd 2210633
20	c2in3A	Alignment		8.8	40	PDB header: isomerase Chain: A: PDB Molecule: hypothetical protein; PDBTitle: crystal structure of a putative protein disulfide isomerase from2 nitrosomonas europaea
21	c3jcuw	Alignment	not modelled	8.7	57	PDB header: membrane protein Chain: W: PDB Molecule: photosystem ii reaction center w protein, chloroplastic; PDBTitle: cryo-em structure of spinach psii-lhcii supercomplex at 3.2 angstrom2 resolution
22	d2o4da1	Alignment	not modelled	8.7	44	Fold: AhpD-like Superfamily: AhpD-like Family: Atu0492-like
23	c4npbA	Alignment	not modelled	8.4	75	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
24	c3nznA	Alignment	not modelled	8.2	50	PDB header: oxidoreductase Chain: A: PDB Molecule: glutaredoxin; PDBTitle: the crystal structure of the glutaredoxin from methanosarcina mazei2 go1
25	d1abaa	Alignment	not modelled	8.1	50	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: Thioltransferase
26	c6ghbB	Alignment	not modelled	7.6	80	PDB header: protein binding Chain: B: PDB Molecule: upf0413 protein gk0824; PDBTitle: crystal structure of spx in complex with yjbh (oxidized)
27	d1kqpa	Alignment	not modelled	7.3	17	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Adenine nucleotide alpha hydrolases-like Family: N-type ATP pyrophosphatases
28	c1t3bA	Alignment	not modelled	7.3	75	PDB header: isomerase Chain: A: PDB Molecule: thiol:disulfide interchange protein dsbc; PDBTitle: x-ray structure of dsbc from haemophilus influenzae
						PDB header: transferase

29	c3bbyA	Alignment	not modelled	7.3	23	Chain: A: PDB Molecule: uncharacterized gst-like protein yfrc; PDBTitle: crystal structure of glutathione s-transferase (np_416804.1) from2 escherichia coli k12 at 1.85 a resolution
30	c1jzdA	Alignment	not modelled	7.3	50	PDB header: oxidoreductase Chain: A: PDB Molecule: thiol:disulfide interchange protein dsbc; PDBTitle: dsbc-dsbdalpha complex
31	c2l7xA	Alignment	not modelled	7.3	80	PDB header: viral protein Chain: A: PDB Molecule: envelope glycoprotein; PDBTitle: crimean congo hemorrhagic fever gn zinc finger
32	c5cbfA	Alignment	not modelled	7.2	15	PDB header: transport protein Chain: A: PDB Molecule: ion transport 2 domain protein; PDBTitle: structural and functional characterization of a calcium-activated2 cation channel from tsukamurella paurometabola
33	d1twfj	Alignment	not modelled	7.1	38	Fold: DNA/RNA-binding 3-helical bundle Superfamily: RNA polymerase subunit RPB10 Family: RNA polymerase subunit RPB10
34	c2elpA	Alignment	not modelled	7.1	100	PDB header: transcription Chain: A: PDB Molecule: zinc finger protein 406; PDBTitle: solution structure of the 13th c2h2 zinc finger of human2 zinc finger protein 406
35	c2kb1A	Alignment	not modelled	6.9	16	PDB header: membrane protein Chain: A: PDB Molecule: wsk3; PDBTitle: nmr studies of a channel protein without membrane:2 structure and dynamics of water-solubilized kcsc
36	c2jz8A	Alignment	not modelled	6.8	57	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein bh09830; PDBTitle: solution nmr structure of bh09830 from bartonella henselae2 modeled with one zn+2 bound. northeast structural genomics3 consortium target bnr55
37	c3lgcA	Alignment	not modelled	6.8	100	PDB header: unknown function Chain: A: PDB Molecule: glutaredoxin 1; PDBTitle: crystal structure of glutaredoxin 1 from francisella tularensis
38	c3mjhD	Alignment	not modelled	6.6	63	PDB header: protein transport Chain: D: PDB Molecule: early endosome antigen 1; PDBTitle: crystal structure of human rab5a in complex with the c2h2 zinc finger2 of eea1
39	c3gv1A	Alignment	not modelled	6.5	75	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: disulfide interchange protein; PDBTitle: crystal structure of disulfide interchange protein from neisseria2 gonorrhoeae
40	c4q16C	Alignment	not modelled	6.5	13	PDB header: ligase Chain: C: PDB Molecule: nh(3)-dependent nad(+) synthetase; PDBTitle: structure of nad+ synthetase from deinococcus radiodurans
41	c4ml1D	Alignment	not modelled	6.4	50	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)
42	c2pbzC	Alignment	not modelled	6.2	15	PDB header: ligase Chain: C: PDB Molecule: hypothetical protein; PDBTitle: crystal structure of an imp biosynthesis protein purp from2 thermococcus kodakaraensis
43	c2lorA	Alignment	not modelled	6.2	24	PDB header: membrane protein Chain: A: PDB Molecule: transmembrane protein 141; PDBTitle: backbone structure of human membrane protein tmem141
44	c1v57A	Alignment	not modelled	6.0	100	PDB header: isomerase Chain: A: PDB Molecule: thiol:disulfide interchange protein dsbg; PDBTitle: crystal structure of the disulfide bond isomerase dsbg
45	d1t3ba1	Alignment	not modelled	5.9	75	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: DsbC/DsbG C-terminal domain-like
46	c4pwoA	Alignment	not modelled	5.9	75	PDB header: structural genomics Chain: A: PDB Molecule: dsba; PDBTitle: crystal structure of dsba from the gram positive bacterium2 corynebacterium diphtheriae
47	c2jadA	Alignment	not modelled	5.9	43	PDB header: electron transport Chain: A: PDB Molecule: yellow fluorescent protein glutaredoxin fusion protein; PDBTitle: yellow fluorescent protein - glutaredoxin fusion protein
48	d1v58a1	Alignment	not modelled	5.8	100	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: DsbC/DsbG C-terminal domain-like
49	c4tr1A	Alignment	not modelled	5.8	75	PDB header: oxidoreductase Chain: A: PDB Molecule: glutaredoxin 3; PDBTitle: crystal structure of gsh-bound cgrx2/c15s
50	c3gn3B	Alignment	not modelled	5.7	50	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: putative protein-disulfide isomerase; PDBTitle: crystal structure of a putative protein-disulfide isomerase from2 pseudomonas syringae to 2.5a resolution.
51	c4qiWV	Alignment	not modelled	5.7	23	PDB header: transcription Chain: V: PDB Molecule: dna-directed rna polymerase subunit n; PDBTitle: crystal structure of euryarchaeal rna polymerase from thermococcus2 kodakarensis
52	d1k18a	Alignment	not modelled	5.6	75	Fold: Zinc finger domain of DNA polymerase-alpha Superfamily: Zinc finger domain of DNA polymerase-alpha Family: Zinc finger domain of DNA polymerase-alpha
53	c3qmxA	Alignment	not modelled	5.4	75	PDB header: electron transport Chain: A: PDB Molecule: glutaredoxin a; PDBTitle: x-ray crystal structure of synechocystis sp. pcc 6803 glutaredoxin a
54	c3gmfA	Alignment	not modelled	5.4	60	PDB header: oxidoreductase Chain: A: PDB Molecule: protein-disulfide isomerase; PDBTitle: crystal structure of protein-disulfide isomerase from novosphingobium2 aromaticivorans
						Fold: Thioredoxin fold

55	d1rk4a2	Alignment	not modelled	5.3	30	Superfamily: Thioredoxin-like Family: Glutathione S-transferase (GST), N-terminal domain
56	d1eeja1	Alignment	not modelled	5.2	75	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: DsbC/DsbG C-terminal domain-like
57	d1eysh2	Alignment	not modelled	5.0	24	Fold: Single transmembrane helix Superfamily: Photosystem II reaction centre subunit H, transmembrane region Family: Photosystem II reaction centre subunit H, transmembrane region