




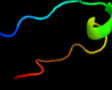



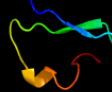














Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2708c (-)_3021558_3021806
Date	Wed Aug 7 12:50:36 BST 2019
Unique Job ID	14344109a0873e94

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3rmsA_	 Alignment		62.2	27	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of uncharacterized protein svir_20580 from <i>Saccharomonospora viridis</i>
2	d2gmga1	 Alignment		46.8	47	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: PF0610-like
3	d1s24a_	 Alignment		36.4	43	Fold: Rubredoxin-like Superfamily: Rubredoxin-like Family: Rubredoxin
4	c1s24A_	 Alignment		36.4	43	PDB header: electron transport Chain: A: PDB Molecule: rubredoxin 2; PDBTitle: rubredoxin domain ii from <i>Pseudomonas oleovorans</i>
5	d1dx8a_	 Alignment		33.5	34	Fold: Rubredoxin-like Superfamily: Rubredoxin-like Family: Rubredoxin
6	c5xvsA_	 Alignment		33.2	16	PDB header: hydrolase Chain: A: PDB Molecule: gdp/udp-n,n'-diacetyl bacillosamine 2-epimerase PDBTitle: crystal structure of udp-glcnaC 2-epimerase neuc complexed with udp
7	c2kdxA_	 Alignment		30.9	33	PDB header: metal-binding protein Chain: A: PDB Molecule: hydrogenase/urease nickel incorporation protein PDBTitle: solution structure of hypa protein
8	c3vthA_	 Alignment		28.5	38	PDB header: transferase Chain: A: PDB Molecule: hydrogenase maturation factor; PDBTitle: crystal structure of full-length hypf in the phosphate- and 2 nucleotide-bound form
9	c5mg5W_	 Alignment		26.0	47	PDB header: transferase Chain: W: PDB Molecule: 2,4-diacetylphloroglucinol biosynthesis protein; PDBTitle: a multi-component acyltransferase phlabc from <i>Pseudomonas protegens</i> 2 soaked with the monoacetylphloroglucinol (mapg)
10	d2dsxa1	 Alignment		25.8	43	Fold: Rubredoxin-like Superfamily: Rubredoxin-like Family: Rubredoxin
11	d2gnra1	 Alignment		25.4	47	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: SSO2064-like

12	c4g9iA_	Alignment		25.2	31	PDB header: transferase Chain: A: PDB Molecule: hydrogenase maturation protein hypf; PDBTitle: crystal structure of t.kodakarensis hypf
13	c2v3bB_	Alignment		23.8	52	PDB header: oxidoreductase Chain: B: PDB Molecule: rubredoxin 2; PDBTitle: crystal structure of the electron transfer complex rubredoxin -2 rubredoxin reductase from pseudomonas aeruginosa.
14	c2p58A_	Alignment		22.9	26	PDB header: transport protein/chaperone Chain: A: PDB Molecule: putative type iii secretion protein yscs; PDBTitle: structure of the yersinia pestis type iii secretion system needle2 protein yscf in complex with its chaperones ysce/yscg
15	d1qcva_	Alignment		22.1	33	Fold: Rubredoxin-like Superfamily: Rubredoxin-like Family: Rubredoxin
16	c6ok1B_	Alignment		21.8	40	PDB header: transport protein Chain: B: PDB Molecule: chsh2(duf35); PDBTitle: ltp2-chsh2(duf35) aldolase
17	c3gv1A_	Alignment		21.3	47	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: disulfide interchange protein; PDBTitle: crystal structure of disulfide interchange protein from neisseria2 gonorrhoeae
18	c2r37A_	Alignment		20.9	6	PDB header: oxidoreductase Chain: A: PDB Molecule: glutathione peroxidase 3; PDBTitle: crystal structure of human glutathione peroxidase 3 (selenocysteine to2 glycine mutant)
19	c5dldA_	Alignment		19.8	17	PDB header: isomerase Chain: A: PDB Molecule: udp-n-acetylglucosamine 2-epimerase; PDBTitle: crystal structure of a udp-n-acetylglucosamine 2-epimerase from2 burkholderia vietnamiensis complexed with udp-glcnaac and udp
20	c3pe3D_	Alignment		18.9	20	PDB header: transferase Chain: D: PDB Molecule: udp-n-acetylglucosamine--peptide n- PDBTitle: structure of human o-glcnaac transferase and its complex with a peptide2 substrate
21	d1h7va_	Alignment	not modelled	18.9	34	Fold: Rubredoxin-like Superfamily: Rubredoxin-like Family: Rubredoxin
22	c1v57A_	Alignment	not modelled	18.7	33	PDB header: isomerase Chain: A: PDB Molecule: thiol:disulfide interchange protein dsbg; PDBTitle: crystal structure of the disulfide bond isomerase dsbg
23	c6et9H_	Alignment	not modelled	18.5	60	PDB header: transferase Chain: H: PDB Molecule: pfam duf35; PDBTitle: structure of the acetoacetyl-coa-thiolase/hmg-coa-synthase complex2 from methanothermococcus thermolithotrophicus at 2.75 a
24	d4rxna_	Alignment	not modelled	18.5	48	Fold: Rubredoxin-like Superfamily: Rubredoxin-like Family: Rubredoxin
25	d1u5sb1	Alignment	not modelled	18.4	33	Fold: Glucocorticoid receptor-like (DNA-binding domain) Superfamily: Glucocorticoid receptor-like (DNA-binding domain) Family: LIM domain
26	c2ms3A_	Alignment	not modelled	18.3	38	PDB header: electron transport Chain: A: PDB Molecule: anaerobic nitric oxide reductase flavorubredoxin; PDBTitle: the nmr structure of the rubredoxin domain of the no reductase2 flavorubredoxin from escherichia coli
27	d1v87a_	Alignment	not modelled	17.3	38	Fold: RING/U-box Superfamily: RING/U-box Family: RING finger domain, C3HC4
28	c4nncA_	Alignment	not modelled	17.1	18	PDB header: lyase Chain: A: PDB Molecule: obca, oxalate biosynthetic component a; PDBTitle: ternary complex of obca with c4-coa adduct and oxalate

29	c4nesA	Alignment	not modelled	16.9	12	PDB header: isomerase Chain: A: PDB Molecule: udp-n-acetylglucosamine 2-epimerase; PDBTitle: crystal structure of methanocaldococcus jannaschii udp-glcnae 2-2 epimerase in complex with udp-glcnae and udp
30	c5n9mA	Alignment	not modelled	16.2	26	PDB header: transferase Chain: A: PDB Molecule: cobyrinic acid synthase; PDBTitle: crystal structure of gatd - a glutamine amidotransferase from <i>Staphylococcus aureus</i> involved in peptidoglycan amidation
31	c3zeyC	Alignment	not modelled	16.0	27	PDB header: ribosome Chain: C: PDB Molecule: 40s ribosomal protein sa, putative; PDBTitle: high-resolution cryo-electron microscopy structure of the <i>Trypanosoma brucei</i> ribosome
32	c4ml1D	Alignment	not modelled	15.9	27	PDB header: isomerase Chain: D: PDB Molecule: dsbp; PDBTitle: disulfide isomerase (dsbp) from multidrug resistance <i>inca/c2</i> transferable plasmid in oxidized state (p212121 space group)
33	d1n5ga	Alignment	not modelled	15.5	24	Fold: Zinc finger domain of DNA polymerase-alpha Superfamily: Zinc finger domain of DNA polymerase-alpha Family: Zinc finger domain of DNA polymerase-alpha
34	d1v58a1	Alignment	not modelled	15.0	33	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: DsbC/DsbG C-terminal domain-like
35	c3brnA	Alignment	not modelled	14.5	22	PDB header: ligand binding protein Chain: A: PDB Molecule: lipocalin; PDBTitle: crystal structure of am182 serotonin complex
36	c3hugL	Alignment	not modelled	13.9	31	PDB header: transcription/membrane protein Chain: J: PDB Molecule: probable conserved membrane protein; PDBTitle: crystal structure of <i>Mycobacterium tuberculosis</i> anti-sigma factor <i>rslA2</i> in complex with -35 promoter binding domain of <i>sigL</i>
37	c2f9yB	Alignment	not modelled	13.8	35	PDB header: ligase Chain: B: PDB Molecule: acetyl-coenzyme a carboxylase carboxyl transferase subunit PDBTitle: the crystal structure of the carboxyltransferase subunit of <i>acc</i> from <i>Escherichia coli</i>
38	d2f9yb1	Alignment	not modelled	13.8	35	Fold: ClpP/crotonase Superfamily: ClpP/crotonase Family: Biotin dependent carboxylase carboxyltransferase domain
39	c2vlvA	Alignment	not modelled	13.7	18	PDB header: oxidoreductase Chain: A: PDB Molecule: thioredoxin h isoform 2.; PDBTitle: crystal structure of barley thioredoxin h isoform 2 in partially 2 radiation-reduced state
40	c3tsuA	Alignment	not modelled	13.0	38	PDB header: transferase Chain: A: PDB Molecule: transcriptional regulatory protein; PDBTitle: crystal structure of <i>E. coli</i> hypf with amp-pnp and carbamoyl phosphate
41	d1ubdc2	Alignment	not modelled	13.0	50	Fold: beta-beta-alpha zinc fingers Superfamily: beta-beta-alpha zinc fingers Family: Classic zinc finger, C2H2
42	c2f9iD	Alignment	not modelled	12.8	20	PDB header: transferase Chain: D: PDB Molecule: acetyl-coenzyme a carboxylase carboxyl transferase subunit PDBTitle: crystal structure of the carboxyltransferase subunit of <i>acc</i> from <i>Staphylococcus aureus</i>
43	c4ex8A	Alignment	not modelled	12.5	44	PDB header: ligase Chain: A: PDB Molecule: alna; PDBTitle: crystal structure of the prealnumycin c-glycosynthase <i>alna</i>
44	c4gijC	Alignment	not modelled	12.4	25	PDB header: hydrolase Chain: C: PDB Molecule: pseudouridine-5'-phosphate glycosidase; PDBTitle: crystal structure of pseudouridine monophosphate glycosidase complexed 2 with sulfate
45	d1a8oa	Alignment	not modelled	12.3	54	Fold: Acyl carrier protein-like Superfamily: Retrovirus capsid dimerization domain-like Family: Retrovirus capsid protein C-terminal domain
46	c3iz6A	Alignment	not modelled	12.3	40	PDB header: ribosome Chain: A: PDB Molecule: 40s ribosomal protein sa (s2p); PDBTitle: localization of the small subunit ribosomal proteins into a 5.5 a2 cryo-em map of <i>Triticum aestivum</i> translating 80s ribosome
47	c2vsnB	Alignment	not modelled	12.2	25	PDB header: transferase Chain: B: PDB Molecule: xcogt; PDBTitle: structure and topological arrangement of an o-glcnae2 transferase homolog: insight into molecular control of 3 intracellular glycosylation
48	c1d4uA	Alignment	not modelled	12.1	29	PDB header: dna binding protein Chain: A: PDB Molecule: nucleotide excision repair protein xpa (xpa-mbd); PDBTitle: interactions of human nucleotide excision repair protein 2 xpa with rpa70 and dna: chemical shift mapping and 15n nmr3 relaxation studies
49	c1k98A	Alignment	not modelled	12.0	60	PDB header: transferase Chain: A: PDB Molecule: methionine synthase; PDBTitle: adomet complex of meth c-terminal fragment
50	c2q6vA	Alignment	not modelled	12.0	21	PDB header: transferase Chain: A: PDB Molecule: glucuronosyltransferase gumk; PDBTitle: crystal structure of gumk in complex with udp
51	c3izbA	Alignment	not modelled	11.9	33	PDB header: ribosome Chain: A: PDB Molecule: 40s ribosomal protein rps0 (s2p); PDBTitle: localization of the small subunit ribosomal proteins into a 6.1 a2 cryo-em map of <i>Saccharomyces cerevisiae</i> translating 80s ribosome
52	c6ro4G	Alignment	not modelled	11.8	25	PDB header: translocase Chain: G: PDB Molecule: dna repair protein complementing xp-a cells; PDBTitle: structure of the core <i>tfiih</i> -xpa-dna complex
53	d2f8aa1	Alignment	not modelled	11.8	21	Fold: Thioredoxin fold Superfamily: Thioredoxin-like

						Family:Glutathione peroxidase-like
54	c5xyiA_	Alignment	not modelled	11.8	33	PDB header: ribosome Chain: A: PDB Molecule: 40s ribosomal protein sa; PDBTitle: small subunit of trichomonas vaginalis ribosome
55	c3bchA_	Alignment	not modelled	11.7	27	PDB header: cell adhesion, ribosomal protein Chain: A: PDB Molecule: 40s ribosomal protein sa; PDBTitle: crystal structure of the human laminin receptor precursor
56	c2o2kA_	Alignment	not modelled	11.7	46	PDB header: transferase Chain: A: PDB Molecule: methionine synthase; PDBTitle: crystal structure of the activation domain of human2 methionine synthase isoform/mutant d963e/k1071n
57	c1jzdA_	Alignment	not modelled	11.5	7	PDB header: oxidoreductase Chain: A: PDB Molecule: thiol:disulfide interchange protein dsbc; PDBTitle: dsbc-dsbdalpha complex
58	c6fqbE_	Alignment	not modelled	11.3	35	PDB header: ligase Chain: E: PDB Molecule: cobyrinic acid synthase; PDBTitle: murt/gatd peptidoglycan amidotransferase complex from streptococcus2 pneumoniae r6
59	d1x3ha1	Alignment	not modelled	11.2	20	Fold: Glucocorticoid receptor-like (DNA-binding domain) Superfamily: Glucocorticoid receptor-like (DNA-binding domain) Family: LIM domain
60	c2xznB_	Alignment	not modelled	11.2	40	PDB header: ribosome Chain: B: PDB Molecule: rps0e; PDBTitle: crystal structure of the eukaryotic 40s ribosomal2 subunit in complex with initiation factor 1. this file3 contains the 40s subunit and initiation factor for4 molecule 2
61	c1s1hB_	Alignment	not modelled	11.1	33	PDB header: ribosome Chain: B: PDB Molecule: 40s ribosomal protein s0-a; PDBTitle: structure of the ribosomal 80s-eef2-sordarin complex from yeast2 obtained by docking atomic models for rna and protein components into3 a 11.7 a cryo-em map. this file, 1s1h, contains 40s subunit. the 60s4 ribosomal subunit is in file 1s1i.
62	d2rdva_	Alignment	not modelled	11.1	48	Fold: Rubredoxin-like Superfamily: Rubredoxin-like Family: Rubredoxin
63	c4gxzB_	Alignment	not modelled	10.7	40	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
64	c3f4tA_	Alignment	not modelled	10.4	15	PDB header: oxidoreductase Chain: A: PDB Molecule: putative uncharacterized protein; PDBTitle: crystal structure of wolbachia pipientis alpha-dsba1 c97a/c146a
65	d1vi6a_	Alignment	not modelled	10.2	47	Fold: Flavodoxin-like Superfamily: Ribosomal protein S2 Family: Ribosomal protein S2
66	c6g4wr_	Alignment	not modelled	10.1	33	PDB header: ribosome Chain: R: PDB Molecule: 40s ribosomal protein s17; PDBTitle: cryo-em structure of a late human pre-40s ribosomal subunit - state a
67	c4uj3B_	Alignment	not modelled	10.1	21	PDB header: transport protein Chain: B: PDB Molecule: rab-3a-interacting protein; PDBTitle: crystal structure of human rab11-rabin8-fip3
68	d1iroa_	Alignment	not modelled	10.0	33	Fold: Rubredoxin-like Superfamily: Rubredoxin-like Family: Rubredoxin
69	c2fqhA_	Alignment	not modelled	10.0	57	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein ta0938; PDBTitle: nmr structure of hypothetical protein ta0938 from2 termoplasma acidophilum
70	c5yt6B_	Alignment	not modelled	9.9	57	PDB header: protein binding Chain: B: PDB Molecule: tax1-binding protein 1; PDBTitle: crystal structure of tax1bp1 ubz2 in complex with mono-ubiquitin
71	c3emxB_	Alignment	not modelled	9.9	33	PDB header: oxidoreductase Chain: B: PDB Molecule: thioredoxin; PDBTitle: crystal structure of thioredoxin from aeropyrum pernix
72	c1t3bA_	Alignment	not modelled	9.8	27	PDB header: isomerase Chain: A: PDB Molecule: thiol:disulfide interchange protein dsbc; PDBTitle: x-ray structure of dsbc from haemophilus influenzae
73	c2kn9A_	Alignment	not modelled	9.8	33	PDB header: electron transport Chain: A: PDB Molecule: rubredoxin; PDBTitle: solution structure of zinc-substituted rubredoxin b (rv3250c) from2 mycobacterium tuberculosis. seattle structural genomics center for3 infectious disease target mytud.01635.a
74	c3bbnB_	Alignment	not modelled	9.7	20	PDB header: ribosome Chain: B: PDB Molecule: ribosomal protein s2; PDBTitle: homology model for the spinach chloroplast 30s subunit fitted to 9.4a2 cryo-em map of the 70s chlororibosome.
75	c5c00B_	Alignment	not modelled	9.4	20	PDB header: oxidoreductase Chain: B: PDB Molecule: mdba protein; PDBTitle: mdba protein, a thiol-disulfide oxidoreductase from corynebacterium2 diphtheriae
76	d1t3ba1	Alignment	not modelled	9.3	27	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: DsbC/DsbG C-terminal domain-like
77	d1brfa_	Alignment	not modelled	9.2	33	Fold: Rubredoxin-like Superfamily: Rubredoxin-like Family: Rubredoxin
78	d1mska_	Alignment	not modelled	9.2	46	Fold: Methionine synthase activation domain-like Superfamily: Methionine synthase activation domain-like Family: Methionine synthase SAM-binding domain
						PDB header: transferase

79	c5djsA_	Alignment	not modelled	9.2	30	Chain: A; PDB Molecule: tetratricopeptide tpr_2 repeat protein; PDBTitle: thermobaculum terrenum o-glcnac transferase mutant - k341m
80	c3gn3B_	Alignment	not modelled	9.1	27	PDB header: structural genomics, unknown function Chain: B; PDB Molecule: putative protein-disulfide isomerase; PDBTitle: crystal structure of a putative protein-disulfide isomerase from <i>Pseudomonas syringae</i> to 2.5 Å resolution.
81	c3hd5A_	Alignment	not modelled	8.9	27	PDB header: oxidoreductase Chain: A; PDB Molecule: thiol:disulfide interchange protein dsba; PDBTitle: crystal structure of a thiol:disulfide interchange protein2 dsba from <i>Bordetella parapertussis</i>
82	c3ghaA_	Alignment	not modelled	8.8	31	PDB header: oxidoreductase Chain: A; PDB Molecule: disulfide bond formation protein d; PDBTitle: crystal structure of etda-treated bdbd (reduced)
83	c3ot5D_	Alignment	not modelled	8.8	14	PDB header: isomerase Chain: D; PDB Molecule: udp-n-acetylglucosamine 2-epimerase; PDBTitle: 2.2 Å resolution crystal structure of putative udp-n-2 acetylglucosamine 2-epimerase from <i>Listeria monocytogenes</i>
84	d2epa1	Alignment	not modelled	8.8	83	Fold: beta-beta-alpha zinc fingers Superfamily: beta-beta-alpha zinc fingers Family: Classic zinc finger, C2H2
85	c4n30A_	Alignment	not modelled	8.7	40	PDB header: oxidoreductase Chain: A; PDB Molecule: protein disulfide isomerase; PDBTitle: crystal structure of <i>Pseudomonas aeruginosa</i> dsba2
86	c5zvlB_	Alignment	not modelled	8.7	20	PDB header: oxidoreductase Chain: B; PDB Molecule: glutaredoxin; PDBTitle: crystal structure of wheat glutarredoxin
87	d1hyua4	Alignment	not modelled	8.6	23	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: PDI-like
88	d1vd4a_	Alignment	not modelled	8.6	33	Fold: Rubredoxin-like Superfamily: Zinc beta-ribbon Family: Transcriptional factor domain
89	c5wuqD_	Alignment	not modelled	8.5	23	PDB header: metal binding protein Chain: D; PDB Molecule: anti-sigma-w factor rsiw; PDBTitle: crystal structure of sigw in complex with its anti-sigma rsiw, a zinc2 binding form
90	d1iu5a_	Alignment	not modelled	8.5	33	Fold: Rubredoxin-like Superfamily: Rubredoxin-like Family: Rubredoxin
91	d1mwpa_	Alignment	not modelled	8.5	34	Fold: SRCR-like Superfamily: A heparin-binding domain Family: A heparin-binding domain
92	c2k8vA_	Alignment	not modelled	8.5	22	PDB header: oxidoreductase Chain: A; PDB Molecule: thioredoxin domain-containing protein 12; PDBTitle: solution structure of oxidised erp18
93	c4bmjC_	Alignment	not modelled	8.4	30	PDB header: apoptosis Chain: C; PDB Molecule: tax1-binding protein 1; PDBTitle: structure of the ubz1and2 tandem of the ubiquitin-binding adaptor2 protein tax1bp1
94	c3j6vB_	Alignment	not modelled	8.4	20	PDB header: ribosome Chain: B; PDB Molecule: 28s ribosomal protein s2, mitochondrial; PDBTitle: cryo-em structure of the small subunit of the mammalian mitochondrial2 ribosome
95	c5cm2M_	Alignment	not modelled	8.3	33	PDB header: transferase Chain: M; PDB Molecule: trna methyltransferase activator subunit; PDBTitle: insights into molecular plasticity in protein complexes from trm9-2 trm112 trna modifying enzyme crystal structure
96	d1lv3a_	Alignment	not modelled	8.2	30	Fold: Glucocorticoid receptor-like (DNA-binding domain) Superfamily: Glucocorticoid receptor-like (DNA-binding domain) Family: Hypothetical zinc finger protein YacG
97	d1to6a_	Alignment	not modelled	8.2	39	Fold: Glycerate kinase I Superfamily: Glycerate kinase I Family: Glycerate kinase I
98	c4npbA_	Alignment	not modelled	8.2	20	PDB header: isomerase Chain: A; PDB Molecule: protein disulfide isomerase ii; PDBTitle: the crystal structure of thiol:disulfide interchange protein dsbc from <i>Yersinia pestis</i> co92
99	c3bu1A_	Alignment	not modelled	8.2	15	PDB header: ligand binding protein Chain: A; PDB Molecule: lipocalin; PDBTitle: crystal structure of monomine-histamine complex