
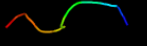
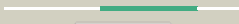


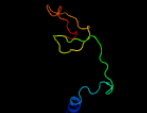





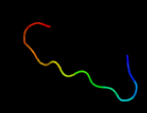
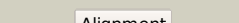


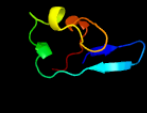



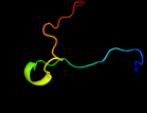


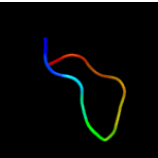
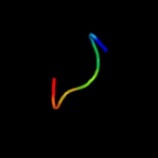
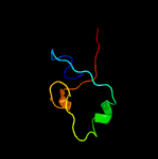
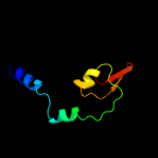
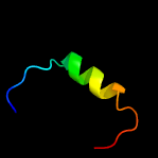



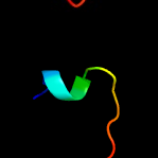


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2295 (-) _2566782_2567420
Date	Mon Aug 5 13:25:43 BST 2019
Unique Job ID	73c140df282d448c

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1bh7A_	 Alignment		61.6	45	PDB header: membrane protein Chain: A; PDB Molecule: band 3; PDBTitle: a low energy structure for the final cytoplasmic loop of band 3, nmr, minimized average structure
2	c4kjeA_	 Alignment		40.3	15	PDB header: oxidoreductase Chain: A; PDB Molecule: glutaredoxin; PDBTitle: atomic resolution structure of pfgrx1
3	c6iqwA_	 Alignment		38.3	21	PDB header: rna binding protein/rna Chain: A; PDB Molecule: csml; PDBTitle: cryo-em structure of csm effector complex
4	c3fzaA_	 Alignment		35.6	16	PDB header: oxidoreductase Chain: A; PDB Molecule: glutaredoxin; PDBTitle: crystal structure of poplar glutaredoxin s12 in complex with2 glutathione and beta-mercaptoethanol
5	c4i2uA_	 Alignment		35.1	18	PDB header: oxidoreductase Chain: A; PDB Molecule: glutaredoxin; PDBTitle: crystal structure of the reduced glutaredoxin from chlorella2 sorokiniana t-89 in complex with glutathione
6	c2v5iA_	 Alignment		32.2	64	PDB header: viral protein Chain: A; PDB Molecule: salmonella typhimurium db7155 bacteriophage det7 tailspike; PDBTitle: structure of the receptor-binding protein of bacteriophage det7: a2 podoviral tailspike in a myovirus
7	c1x31D_	 Alignment		30.0	17	PDB header: oxidoreductase Chain: D; PDB Molecule: sarcosine oxidase delta subunit; PDBTitle: crystal structure of heterotetrameric sarcosine oxidase from2 corynebacterium sp. u-96
8	d1nnqa2	 Alignment		26.8	35	Fold: Rubredoxin-like Superfamily: Rubredoxin-like Family: Rubredoxin
9	c4iloA_	 Alignment		25.5	31	PDB header: unknown function Chain: A; PDB Molecule: ct398; PDBTitle: 2.12a resolution structure of ct398 from chlamydia trachomatis
10	c1x4jA_	 Alignment		24.1	26	PDB header: structural genomics, unknown function Chain: A; PDB Molecule: ring finger protein 38; PDBTitle: solution structure of ring finger in ring finger protein 38
11	c2in3A_	 Alignment		23.9	43	PDB header: isomerase Chain: A; PDB Molecule: hypothetical protein; PDBTitle: crystal structure of a putative protein disulfide isomerase from2 nitrosomonas europaea

12	d2ct1a1	Alignment		23.3	27	Fold: beta-beta-alpha zinc fingers Superfamily: beta-beta-alpha zinc fingers Family: Classic zinc finger, C2H2
13	c3kzqE_	Alignment		21.9	43	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
14	d1lkoa2	Alignment		21.4	23	Fold: Rubredoxin-like Superfamily: Rubredoxin-like Family: Rubredoxin
15	c6ifnA_	Alignment		21.3	13	PDB header: rna binding protein Chain: A: PDB Molecule: type iii-a crispr-associated protein csm1; PDBTitle: crystal structure of type iii-a crispr csm complex
16	c3mhyC_	Alignment		20.7	17	PDB header: protein transport Chain: C: PDB Molecule: vacuolar protein sorting-associated protein 4; PDBTitle: crystal structure of vps4 and vta1
17	d2fc7a1	Alignment		20.3	17	Fold: RING/U-box Superfamily: RING/U-box Family: ZZ domain
18	c6ghbB_	Alignment		20.2	43	PDB header: protein binding Chain: B: PDB Molecule: supf0413 protein gk0824; PDBTitle: crystal structure of spx in complex with yjbh (oxidized)
19	c3vlfB_	Alignment		20.1	31	PDB header: chaperone/protein binding Chain: B: PDB Molecule: 26s protease regulatory subunit 7 homolog; PDBTitle: crystal structure of yeast proteasome interacting protein
20	c2dzoD_	Alignment		19.9	15	PDB header: protein binding Chain: D: PDB Molecule: 26s protease regulatory subunit 6b homolog; PDBTitle: crystal structure analysis of yeast nas6p complexed with2 the proteasome subunit, rpt3
21	c6ghcA_	Alignment	not modelled	19.8	22	PDB header: hydrolase Chain: A: PDB Molecule: 5-methylcytosine-specific restriction enzyme a; PDBTitle: modification dependent ecomcra restriction endonuclease
22	d1ivma_	Alignment	not modelled	19.5	25	Fold: Lysozyme-like Superfamily: Lysozyme-like Family: C-type lysozyme
23	c4qf3A_	Alignment	not modelled	19.4	24	PDB header: transcription Chain: A: PDB Molecule: bromodomain adjacent to zinc finger domain protein 2b; PDBTitle: crystal structure of human baz2b phd zinc finger in the free form
24	d2ct7a1	Alignment	not modelled	19.3	26	Fold: RING/U-box Superfamily: RING/U-box Family: IBR domain
25	d1qqya_	Alignment	not modelled	18.9	25	Fold: Lysozyme-like Superfamily: Lysozyme-like Family: C-type lysozyme
26	c2dvwB_	Alignment	not modelled	18.8	23	PDB header: cell cycle/protein-binding Chain: B: PDB Molecule: 26s protease regulatory subunit 6b; PDBTitle: structure of the oncoprotein gankyrin in complex with s62 atpase of the 26s proteasome PDB header: oxidoreductase Chain: A: PDB Molecule: dithiol glutaredoxin 1; PDBTitle: solution structure of the dithiol glutaredoxin 2-c-grx1 from the2 pathogen trypanosoma brucei brucei
27	c2mygA_	Alignment	not modelled	18.3	15	PDB header: hydrolase Chain: A: PDB Molecule: endo-beta-1,4-glucanase (celulase b); PDBTitle: the native structure of the family 46 carbohydrate-
28	c4uznA_	Alignment	not modelled	18.2	28	

						binding2 module (cbm46) of endo-beta-1,4-glucanase b (cel5b) from3 bacillus halodurans
29	c2mvwA_	Alignment	not modelled	17.9	23	PDB header: metal binding protein Chain: A: PDB Molecule: protein pml; PDBTitle: solution structure of the trim19 b-box1 (b1) of human promyelocytic2 leukemia (pml)
30	d2nwdx1	Alignment	not modelled	17.4	22	Fold: Lysozyme-like Superfamily: Lysozyme-like Family: C-type lysozyme
31	c5gtxA_	Alignment	not modelled	17.4	14	PDB header: oxidoreductase Chain: A: PDB Molecule: buckwheat glutaredoxin; PDBTitle: crystal structure of mutated buckwheat glutaredoxin
32	c3qmxA_	Alignment	not modelled	17.2	19	PDB header: electron transport Chain: A: PDB Molecule: glutaredoxin a; PDBTitle: x-ray crystal structure of synechocystis sp. pcc 6803 glutaredoxin a
33	d1juga_	Alignment	not modelled	17.1	26	Fold: Lysozyme-like Superfamily: Lysozyme-like Family: C-type lysozyme
34	c2m13A_	Alignment	not modelled	17.0	22	PDB header: metal binding protein Chain: A: PDB Molecule: cytoplasmic polyadenylation element-binding protein 1; PDBTitle: the zz domain of cytoplasmic polyadenylation element binding protein 12 (cpeb1)
35	c2e6rA_	Alignment	not modelled	17.0	24	PDB header: dna binding protein Chain: A: PDB Molecule: jumonji/arid domain-containing protein 1d; PDBTitle: solution structure of the phd domain in smcy protein
36	c5hfiA_	Alignment	not modelled	16.7	14	PDB header: oxidoreductase Chain: A: PDB Molecule: uncharacterized protein, cytosolic disulfide reductase PDBTitle: cytosolic disulfide reductase dsbm from pseudomonas aeruginosa with2 gsh
37	d1gd6a_	Alignment	not modelled	16.5	24	Fold: Lysozyme-like Superfamily: Lysozyme-like Family: C-type lysozyme
38	d1lsga1	Alignment	not modelled	16.3	19	Fold: Lysozyme-like Superfamily: Lysozyme-like Family: C-type lysozyme
39	d2eqla_	Alignment	not modelled	16.2	22	Fold: Lysozyme-like Superfamily: Lysozyme-like Family: C-type lysozyme
40	d2ctda2	Alignment	not modelled	16.0	44	Fold: beta-beta-alpha zinc fingers Superfamily: beta-beta-alpha zinc fingers Family: Classic zinc finger, C2H2
41	d1dx8a_	Alignment	not modelled	16.0	31	Fold: Rubredoxin-like Superfamily: Rubredoxin-like Family: Rubredoxin
42	d1dfxa2	Alignment	not modelled	15.6	27	Fold: Rubredoxin-like Superfamily: Rubredoxin-like Family: Desulforedoxin
43	c3gl5A_	Alignment	not modelled	15.5	57	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: putative dsba oxidoreductase sco1869; PDBTitle: crystal structure of probable dsba oxidoreductase sco1869 from2 streptomyces coelicolor
44	d2gzoa1	Alignment	not modelled	15.2	27	Fold: VC0467-like Superfamily: VC0467-like Family: VC0467-like
45	d1fkqa_	Alignment	not modelled	15.2	24	Fold: Lysozyme-like Superfamily: Lysozyme-like Family: C-type lysozyme
46	c2lvhA_	Alignment	not modelled	15.2	50	PDB header: metal binding protein Chain: A: PDB Molecule: putative zinc finger protein orf59a; PDBTitle: solution structure of the zinc finger afv1p06 protein from the2 hyperthermophilic archaeal virus afv1
47	c5x1hS_	Alignment	not modelled	15.0	16	PDB header: protein transport Chain: S: PDB Molecule: icmj (dotn); PDBTitle: structure of legionella pneumophila dotn
48	c6j6qF_	Alignment	not modelled	14.5	40	PDB header: splicing Chain: F: PDB Molecule: splicing factor yju2; PDBTitle: cryo-em structure of the yeast b*-b2 complex at an average resolution2 of 3.7 angstrom
49	c2goiC_	Alignment	not modelled	14.3	26	PDB header: cell adhesion, sugar binding protein Chain: C: PDB Molecule: sperm lysozyme-like protein 1; PDBTitle: crystal structure of mouse sperm c-type lysozyme-like protein 1
50	c5lj3D_	Alignment	not modelled	14.3	40	PDB header: splicing Chain: D: PDB Molecule: protein cwc16; PDBTitle: structure of the core of the yeast spliceosome immediately after2 branching
51	d1yuza2	Alignment	not modelled	14.1	27	Fold: Rubredoxin-like Superfamily: Rubredoxin-like Family: Rubredoxin
52	c2yt5A_	Alignment	not modelled	13.8	20	PDB header: transcription Chain: A: PDB Molecule: metal-response element-binding transcription PDBTitle: solution structure of the phd domain of metal-response2 element-binding transcription factor 2
53	c3riqA_	Alignment	not modelled	13.8	25	PDB header: viral protein Chain: A: PDB Molecule: tailspike protein; PDBTitle: siphovirus 9na tailspike receptor binding domain
54	c1rimA_	Alignment	not modelled	13.8	40	PDB header: de novo protein Chain: A: PDB Molecule: e6apc2 peptide;

						PDBTitle: e6-binding zinc finger (e6apc2)
55	c3uiwB_	Alignment	not modelled	13.5	18	PDB header: oxidoreductase Chain: B: PDB Molecule: glutaredoxin 2; PDBTitle: zebrafish grx2 (apo)
56	c5jpxA_	Alignment	not modelled	13.4	20	PDB header: metal binding protein Chain: A: PDB Molecule: e3 ubiquitin-protein ligase trim21; PDBTitle: solution structure of the trim21 b-box2 (b2)
57	d1ghla_	Alignment	not modelled	13.2	23	Fold: Lysozyme-like Superfamily: Lysozyme-like Family: C-type lysozyme
58	c5xzsA_	Alignment	not modelled	13.0	15	PDB header: transcription Chain: A: PDB Molecule: histone acetyltransferase p300; PDBTitle: cryo-em structure of p300
59	d1f6sa_	Alignment	not modelled	13.0	22	Fold: Lysozyme-like Superfamily: Lysozyme-like Family: C-type lysozyme
60	c1rikA_	Alignment	not modelled	12.8	40	PDB header: de novo protein Chain: A: PDB Molecule: e6apc1 peptide; PDBTitle: e6-binding zinc finger (e6apc1)
61	c2e5rA_	Alignment	not modelled	12.8	22	PDB header: dna binding protein Chain: A: PDB Molecule: dystrobrevin alpha; PDBTitle: solution structure of the zz domain of dystrobrevin alpha2 (dystrobrevin-alpha)
62	d1h7va_	Alignment	not modelled	12.7	31	Fold: Rubredoxin-like Superfamily: Rubredoxin-like Family: Rubredoxin
63	d1ibia2	Alignment	not modelled	12.6	63	Fold: Glucocorticoid receptor-like (DNA-binding domain) Superfamily: Glucocorticoid receptor-like (DNA-binding domain) Family: LIM domain
64	c2z2fA_	Alignment	not modelled	12.5	26	PDB header: hydrolase Chain: A: PDB Molecule: lysozyme c-2; PDBTitle: x-ray crystal structure of bovine stomach lysozyme
65	c2v3bB_	Alignment	not modelled	12.5	22	PDB header: oxidoreductase Chain: B: PDB Molecule: rubredoxin 2; PDBTitle: crystal structure of the electron transfer complex rubredoxin -2 rubredoxin reductase from pseudomonas aeruginosa.
66	d1rb9a_	Alignment	not modelled	12.4	31	Fold: Rubredoxin-like Superfamily: Rubredoxin-like Family: Rubredoxin
67	c3gmfA_	Alignment	not modelled	12.1	43	PDB header: oxidoreductase Chain: A: PDB Molecule: protein-disulfide isomerase; PDBTitle: crystal structure of protein-disulfide isomerase from novosphingobium2 aromaticivorans
68	d1iiza_	Alignment	not modelled	12.1	26	Fold: Lysozyme-like Superfamily: Lysozyme-like Family: C-type lysozyme
69	d1wena_	Alignment	not modelled	12.0	12	Fold: FYVE/PHD zinc finger Superfamily: FYVE/PHD zinc finger Family: PHD domain
70	c2lzeA_	Alignment	not modelled	11.7	14	PDB header: de novo protein Chain: A: PDB Molecule: a primordial catalytic fold generated by in vitro PDBTitle: ligase 10c
71	c2klxA_	Alignment	not modelled	11.7	18	PDB header: oxidoreductase Chain: A: PDB Molecule: glutaredoxin; PDBTitle: solution structure of glutaredoxin from bartonella henselae str.2 houston
72	d2rdva_	Alignment	not modelled	11.7	31	Fold: Rubredoxin-like Superfamily: Rubredoxin-like Family: Rubredoxin
73	c5wakB_	Alignment	not modelled	11.6	50	PDB header: transcription Chain: B: PDB Molecule: polycomb protein suz12; PDBTitle: crystal structure of a suz12-rbbp4 binary complex
74	c2jm1A_	Alignment	not modelled	11.5	28	PDB header: metal binding protein Chain: A: PDB Molecule: transcriptional regulator atrx; PDBTitle: structures and chemical shift assignments for the add domain of the2 atrx protein
75	d1iu5a_	Alignment	not modelled	11.5	35	Fold: Rubredoxin-like Superfamily: Rubredoxin-like Family: Rubredoxin
76	c2imeA_	Alignment	not modelled	11.5	14	PDB header: transferase Chain: A: PDB Molecule: 2-hydroxychromene-2-carboxylate isomerase; PDBTitle: 2-hydroxychromene-2-carboxylate isomerase: a kappa class glutathione-2 s-transferase from pseudomonas putida
77	c1yzxB_	Alignment	not modelled	10.9	14	PDB header: transferase Chain: B: PDB Molecule: glutathione s-transferase kappa 1; PDBTitle: crystal structure of human kappa class glutathione transferase
78	c1yuzB_	Alignment	not modelled	10.7	37	PDB header: oxidoreductase Chain: B: PDB Molecule: nigerythrin; PDBTitle: partially reduced state of nigerythrin
79	d6rxna_	Alignment	not modelled	10.6	24	Fold: Rubredoxin-like Superfamily: Rubredoxin-like Family: Rubredoxin
80	c3gn5B_	Alignment	not modelled	10.5	30	PDB header: dna binding protein Chain: B: PDB Molecule: hth-type transcriptional regulator mqsa (ygit/b3021); PDBTitle: structure of the e. coli protein mqsa (ygit/b3021)
						PDB header: oxidoreductase Chain: A: PDB Molecule: frne protein;

81	c5cohA	Alignment	not modelled	10.4	57	PDBTitle: crystal structure of a novel disulfide oxidoreductase from deinococcus2 radiodurans crystallized in presence of beta-mercaptoethanol
82	c6c24A	Alignment	not modelled	10.3	50	PDB header: gene regulation Chain: A: PDB Molecule: polycomb protein suz12; PDBTitle: cryo-em structure of prc2 bound to cofactors aebp2 and jarid2 in the2 extended active state
83	c2k5cA	Alignment	not modelled	10.2	18	PDB header: metal binding protein Chain: A: PDB Molecule: uncharacterized protein pf0385; PDBTitle: nmr structure for pf0385
84	d1x68a1	Alignment	not modelled	10.2	23	Fold: Glucocorticoid receptor-like (DNA-binding domain) Superfamily: Glucocorticoid receptor-like (DNA-binding domain) Family: LIM domain
85	c2hr5B	Alignment	not modelled	10.2	11	PDB header: metal binding protein Chain: B: PDB Molecule: rubrerythrin; PDBTitle: pf1283- rubrerythrin from pyrococcus furiosus iron bound form
86	c3mjhD	Alignment	not modelled	10.1	33	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
87	d1hhla	Alignment	not modelled	10.1	19	Fold: Lysozyme-like Superfamily: Lysozyme-like Family: C-type lysozyme
88	c2m4yA	Alignment	not modelled	10.0	28	PDB header: electron transport Chain: A: PDB Molecule: rubredoxin; PDBTitle: rubredoxin type protein from mycobacterium ulcerans
89	c2fe8B	Alignment	not modelled	9.9	21	PDB header: hydrolase Chain: B: PDB Molecule: replicase polyprotein 1ab; PDBTitle: sars coronavirus papain-like protease: structure of a viral2 deubiquitinating enzyme
90	d1r4wa	Alignment	not modelled	9.8	14	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: DsbA-like
91	d1vzia2	Alignment	not modelled	9.5	27	Fold: Rubredoxin-like Superfamily: Rubredoxin-like Family: Desulfiredoxin
92	c2mnyA	Alignment	not modelled	9.4	21	PDB header: oxidoreductase Chain: A: PDB Molecule: lysine-specific demethylase 5b; PDBTitle: nmr structure of kdm5b phd1 finger
93	c1freA	Alignment	not modelled	9.4	15	PDB header: zinc-binding protein Chain: A: PDB Molecule: nuclear factor xnf7; PDBTitle: xnf7 bbox, developmental protein, ph 7.5, 30 c, with zinc,2 nmr, 1 structure
94	c3fz5C	Alignment	not modelled	9.4	0	PDB header: isomerase Chain: C: PDB Molecule: possible 2-hydroxychromene-2-carboxylate isomerase; PDBTitle: crystal structure of possible 2-hydroxychromene-2-carboxylate2 isomerase from rhodobacter sphaeroides
95	c3c7mB	Alignment	not modelled	9.4	43	PDB header: oxidoreductase Chain: B: PDB Molecule: thiol:disulfide interchange protein dsba-like; PDBTitle: crystal structure of reduced dsbl
96	c3gn3B	Alignment	not modelled	9.3	43	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.
97	c3alrA	Alignment	not modelled	9.1	43	PDB header: metal binding protein Chain: A: PDB Molecule: nanos protein; PDBTitle: crystal structure of nanos
98	c2wwaj	Alignment	not modelled	9.0	18	PDB header: ribosome Chain: J: PDB Molecule: 60s ribosomal protein l19; PDBTitle: cryo-em structure of idle yeast ssh1 complex bound to the yeast 80s2 ribosome
99	c2aklA	Alignment	not modelled	9.0	28	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: phna-like protein pa0128; PDBTitle: solution structure for phn-a like protein pa0128 from2 pseudomonas aeruginosa