


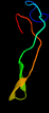
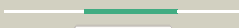








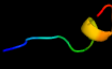










Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0049 (-)_52831_53244
Date	Tue Jul 23 14:50:08 BST 2019
Unique Job ID	9bc92ec2c528031c

Detailed template
information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d2a2pa1	 Alignment		68.1	46	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: Selenoprotein W-related
2	c3gn5B_	 Alignment		53.0	16	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)
3	d2fiya1	 Alignment		47.1	23	Fold: FdhE-like Superfamily: FdhE-like Family: FdhE-like
4	d1lv3a_	 Alignment		46.1	31	Fold: Glucocorticoid receptor-like (DNA-binding domain) Superfamily: Glucocorticoid receptor-like (DNA-binding domain) Family: Hypothetical zinc finger protein YacG
5	c2vjfB_	 Alignment		38.8	47	PDB header: ligase Chain: B: PDB Molecule: mdm4 protein; PDBTitle: crystal structure of the mdm2-mdmx ring domain heterodimer
6	c2f9iD_	 Alignment		38.7	30	PDB header: transferase Chain: D: PDB Molecule: acetyl-coenzyme a carboxylase carboxyl transferase subunit PDBTitle: crystal structure of the carboxyltransferase subunit of acc from2 staphylococcus aureus
7	d2a4ha1	 Alignment		34.7	42	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: Selenoprotein W-related
8	c4rvqA_	 Alignment		31.3	20	PDB header: transferase Chain: A: PDB Molecule: d-mycarose 3-c-methyltransferase; PDBTitle: crystal structure of mtmc in complex with sam and tdp
9	c5aj3p_	 Alignment		30.4	46	PDB header: ribosome Chain: P: PDB Molecule: mitoribosomal protein bs16m, mrps16; PDBTitle: structure of the small subunit of the mammalian mitoribosome
10	c6k2kA_	 Alignment		29.2	37	PDB header: structural protein Chain: A: PDB Molecule: mitochondrial ubiquitin ligase activator of nfkb 1; PDBTitle: solution structure of mul1-ring domain
11	c4ru1A_	 Alignment		27.6	14	PDB header: isomerase/dna Chain: A: PDB Molecule: dna topoisomerase 1; PDBTitle: crystal structure of full-length e.coli topoisomerase i in complex2 with ssdna

12	c1yuzB_	Alignment		26.9	20	PDB header: oxidoreductase Chain: B: PDB Molecule: nigerythrin; PDBTitle: partially reduced state of nigerythrin
13	d6rxna_	Alignment		26.9	31	Fold: Rubredoxin-like Superfamily: Rubredoxin-like Family: Rubredoxin
14	d2f9yb1	Alignment		26.3	42	Fold: ClpP/crotonase Superfamily: ClpP/crotonase Family: Biotin dependent carboxylase carboxyltransferase domain
15	c2f9yB_	Alignment		26.3	42	PDB header: ligase Chain: B: PDB Molecule: acetyl-coenzyme a carboxylase carboxyl transferase subunit PDBTitle: the crystal structure of the carboxyltransferase subunit of acc from2 escherichia coli
16	c2kn9A_	Alignment		26.1	25	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
17	d1qcva_	Alignment		25.9	25	Fold: Rubredoxin-like Superfamily: Rubredoxin-like Family: Rubredoxin
18	d1dx8a_	Alignment		25.8	31	Fold: Rubredoxin-like Superfamily: Rubredoxin-like Family: Rubredoxin
19	d1s24a_	Alignment		25.3	31	Fold: Rubredoxin-like Superfamily: Rubredoxin-like Family: Rubredoxin
20	c1s24A_	Alignment		25.3	31	PDB header: electron transport Chain: A: PDB Molecule: rubredoxin 2; PDBTitle: rubredoxin domain ii from pseudomonas oleovorans
21	c4u3eA_	Alignment	not modelled	25.2	20	PDB header: oxidoreductase Chain: A: PDB Molecule: ribonucleoside triphosphate reductase; PDBTitle: anaerobic ribonucleotide reductase
22	c5ntbB_	Alignment	not modelled	24.9	24	PDB header: protease inhibitor Chain: B: PDB Molecule: papain inhibitor; PDBTitle: streptomyces papain inhibitor (spi)
23	d1h7va_	Alignment	not modelled	24.9	31	Fold: Rubredoxin-like Superfamily: Rubredoxin-like Family: Rubredoxin
24	c2obkE_	Alignment	not modelled	24.7	25	PDB header: structural genomics, unknown function Chain: E: PDB Molecule: selt/selw/selh selenoprotein domain; PDBTitle: x-ray structure of the putative se binding protein from pseudomonas2 fluorescens. northeast structural genomics consortium target plr6.
25	d1iu5a_	Alignment	not modelled	24.7	38	Fold: Rubredoxin-like Superfamily: Rubredoxin-like Family: Rubredoxin
26	d1pfta_	Alignment	not modelled	24.3	29	Fold: Rubredoxin-like Superfamily: Zinc beta-ribbon Family: Transcriptional factor domain
27	d1jj2y_	Alignment	not modelled	24.2	25	Fold: Rubredoxin-like Superfamily: Zn-binding ribosomal proteins Family: Ribosomal protein L37ae
28	d1lroa_	Alignment	not modelled	24.0	31	Fold: Rubredoxin-like Superfamily: Rubredoxin-like Family: Rubredoxin
						PDB header: ribosome

29	c3j21i_	Alignment	not modelled	24.0	19	Chain: I: PDB Molecule: 50s ribosomal protein l13p; PDBTitle: promiscuous behavior of proteins in archaeal ribosomes revealed by 2 cryo-em: implications for evolution of eukaryotic ribosomes (50s3 ribosomal proteins)
30	c2v3bB_	Alignment	not modelled	24.0	25	PDB header: oxidoreductase Chain: B: PDB Molecule: rubredoxin 2; PDBTitle: crystal structure of the electron transfer complex2 rubredoxin - rubredoxin reductase from pseudomonas3 aeruginosa.
31	c2hr5B_	Alignment	not modelled	23.9	21	PDB header: metal binding protein Chain: B: PDB Molecule: rubrerythrin; PDBTitle: pf1283- rubrerythrin from pyrococcus furiosus iron bound form
32	c2zkrz_	Alignment	not modelled	23.8	19	PDB header: ribosomal protein/rna Chain: Z: PDB Molecule: e site t-rna; PDBTitle: structure of a mammalian ribosomal 60s subunit within an 80s complex2 obtained by docking homology models of the rna and proteins into an 3 8.7 a cryo-em map
33	c1yshD_	Alignment	not modelled	23.7	25	PDB header: structural protein/rna Chain: D: PDB Molecule: ribosomal protein l37a; PDBTitle: localization and dynamic behavior of ribosomal protein l30e
34	d2dsxa1	Alignment	not modelled	23.6	31	Fold: Rubredoxin-like Superfamily: Rubredoxin-like Family: Rubredoxin
35	d1vqoz1	Alignment	not modelled	23.4	19	Fold: Rubredoxin-like Superfamily: Zn-binding ribosomal proteins Family: Ribosomal protein L37ae
36	c6g5iy_	Alignment	not modelled	23.3	32	PDB header: ribosome Chain: Y: PDB Molecule: 40s ribosomal protein s24; PDBTitle: cryo-em structure of a late human pre-40s ribosomal subunit - state r
37	c3j39g_	Alignment	not modelled	23.1	38	PDB header: ribosome Chain: G: PDB Molecule: 60s ribosomal protein l7a; PDBTitle: structure of the d. melanogaster 60s ribosomal proteins
38	d1brfa_	Alignment	not modelled	23.1	38	Fold: Rubredoxin-like Superfamily: Rubredoxin-like Family: Rubredoxin
39	d2rdva_	Alignment	not modelled	23.1	38	Fold: Rubredoxin-like Superfamily: Rubredoxin-like Family: Rubredoxin
40	c1nuiA_	Alignment	not modelled	23.0	22	PDB header: replication Chain: A: PDB Molecule: dna primase/helicase; PDBTitle: crystal structure of the primase fragment of bacteriophage t7 primase-2 helicase protein
41	c3izrm_	Alignment	not modelled	23.0	25	PDB header: ribosome Chain: M: PDB Molecule: 60s ribosomal protein l23 (l14p); PDBTitle: localization of the large subunit ribosomal proteins into a 5.5 a2 cryo-em map of triticum aestivum translating 80s ribosome
42	c1s1i9_	Alignment	not modelled	22.8	25	PDB header: ribosome Chain: 9: PDB Molecule: 60s ribosomal protein l43; PDBTitle: structure of the ribosomal 80s-eef2-sordarin complex from yeast2 obtained by docking atomic models for rna and protein components into 3 a 11.7 a cryo-em map. this file, 1s1i, contains 60s subunit. the 40s4 ribosomal subunit is in file 1s1h.
43	c4g6vB_	Alignment	not modelled	22.6	38	PDB header: toxin Chain: B: PDB Molecule: cdii; PDBTitle: cdia-ct/cdii toxin and immunity complex from burkholderia pseudomallei
44	c3dexA_	Alignment	not modelled	22.6	33	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: sav_2001; PDBTitle: crystal structure of sav_2001 protein from streptomyces2 avermitilis, northeast structural genomics consortium3 target svr107.
45	c3j39p_	Alignment	not modelled	22.3	25	PDB header: ribosome Chain: P: PDB Molecule: 60s ribosomal protein l17; PDBTitle: structure of the d. melanogaster 60s ribosomal proteins
46	c5zi6E_	Alignment	not modelled	22.3	21	PDB header: ligase Chain: E: PDB Molecule: rna-binding e3 ubiquitin-protein ligase mex3c; PDBTitle: the ring domain structure of mex-3c
47	d4rxna_	Alignment	not modelled	22.2	31	Fold: Rubredoxin-like Superfamily: Rubredoxin-like Family: Rubredoxin
48	c2hdpB_	Alignment	not modelled	22.1	21	PDB header: ligase Chain: B: PDB Molecule: ubiquitin-protein ligase e3 mdm2; PDBTitle: solution structure of hdm2 ring finger domain
49	d1l1ta3	Alignment	not modelled	22.1	18	Fold: Glucocorticoid receptor-like (DNA-binding domain) Superfamily: Glucocorticoid receptor-like (DNA-binding domain) Family: C-terminal, Zn-finger domain of MutM-like DNA repair proteins
50	c2ojjB_	Alignment	not modelled	21.9	30	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: hypothetical protein; PDBTitle: crystal structure of q7waf1_borpa from bordetella parapertussis.2 northeast structural genomics target bpr68.
51	c2ms3A_	Alignment	not modelled	21.8	25	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
52	d1nw2a_	Alignment	not modelled	21.8	24	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: Thioltransferase
53	c3j3bg_	Alignment	not modelled	21.7	33	PDB header: ribosome Chain: G: PDB Molecule: 60s ribosomal protein l7a; PDBTitle: structure of the human 60s ribosomal proteins
						PDB header: ribosome

54	c2qa4Z_	Alignment	not modelled	21.7	19	Chain: Z; PDB Molecule: 50s ribosomal protein l37ae; PDBTitle: a more complete structure of the the l7/l12 stalk of the2 haloarcula marismortui 50s large ribosomal subunit
55	d1ffkw_	Alignment	not modelled	21.6	25	Fold: Rubredoxin-like Superfamily: Zn-binding ribosomal proteins Family: Ribosomal protein L37ae
56	c3eb6A_	Alignment	not modelled	21.6	40	PDB header: apoptosis, ligase Chain: A; PDB Molecule: baculoviral iap repeat-containing protein 3; PDBTitle: structure of the ciap2 ring domain bound to ubch5b
57	c4mo1B_	Alignment	not modelled	21.4	15	PDB header: transcription regulator Chain: B; PDB Molecule: antitermination protein q; PDBTitle: crystal structure of antitermination protein q from bacteriophage2 lambda. northeast structural genomics consortium target or18a.
58	c2p0gB_	Alignment	not modelled	20.9	36	PDB header: structural genomics, unknown function Chain: B; PDB Molecule: selenoprotein w-related protein; PDBTitle: crystal structure of selenoprotein w-related protein from vibrio2 cholerae. northeast structural genomics target vcr75
59	d2fa8a1	Alignment	not modelled	20.9	27	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: Selenoprotein W-related
60	d1tdza3	Alignment	not modelled	20.9	18	Fold: Glucocorticoid receptor-like (DNA-binding domain) Superfamily: Glucocorticoid receptor-like (DNA-binding domain) Family: C-terminal, Zn-finger domain of MutM-like DNA repair proteins
61	c3lzcj_	Alignment	not modelled	20.8	25	PDB header: ribosome Chain: I; PDB Molecule: 60s ribosomal protein rp10 (I10e); PDBTitle: localization of the large subunit ribosomal proteins into a 6.1 a2 cryo-em map of saccharomyces cerevisiae translating 80s ribosome
62	c2z1dA_	Alignment	not modelled	20.7	22	PDB header: metal binding protein Chain: A; PDB Molecule: hydrogenase expression/formation protein hypd; PDBTitle: crystal structure of [nife] hydrogenase maturation protein, hypd from2 thermococcus kodakaraensis
63	c3a44D_	Alignment	not modelled	20.6	22	PDB header: metal binding protein Chain: D; PDB Molecule: hydrogenase nickel incorporation protein hypa; PDBTitle: crystal structure of hypa in the dimeric form
64	c3jyw9_	Alignment	not modelled	20.2	25	PDB header: ribosome Chain: 9; PDB Molecule: 60s ribosomal protein l43; PDBTitle: structure of the 60s proteins for eukaryotic ribosome based on cryo-em2 map of thermomyces lanuginosus ribosome at 8.9a resolution
65	c4b6ap_	Alignment	not modelled	20.1	25	PDB header: ribosome Chain: P; PDB Molecule: 60s ribosomal protein l17-a; PDBTitle: cryo-em structure of the 60s ribosomal subunit in complex2 with arx1 and rei1
66	c3hi2C_	Alignment	not modelled	19.8	20	PDB header: dna binding protein/toxin Chain: C; PDB Molecule: hth-type transcriptional regulator mqa2 (ygit); PDBTitle: structure of the n-terminal domain of the e. coli antitoxin mqa2 (ygit/b3021) in complex with the e. coli toxin mqsr (ygiu/b3022)
67	c3d30A_	Alignment	not modelled	19.7	15	PDB header: peptidoglycan-binding protein Chain: A; PDB Molecule: expansin like protein; PDBTitle: structure of an expansin like protein from bacillus subtilis at 1.9a2 resolution
68	c2ma6A_	Alignment	not modelled	19.7	19	PDB header: ligase Chain: A; PDB Molecule: e3 ubiquitin-protein ligase rnf123; PDBTitle: solution nmr structure of the ring finger domain from the kip12 ubiquitination-promoting e3 complex protein 1 (kpc1/rnf123) from homo3 sapiens, northeast structural genomics consortium (nesg) target4 hr8700a
69	c2kw0A_	Alignment	not modelled	19.6	20	PDB header: oxidoreductase Chain: A; PDB Molecule: ccmh protein; PDBTitle: solution structure of n-terminal domain of ccmh from escherichia.coli
70	d2drpa2	Alignment	not modelled	19.5	63	Fold: beta-beta-alpha zinc fingers Superfamily: beta-beta-alpha zinc fingers Family: Classic zinc finger, C2H2
71	d1rb9a_	Alignment	not modelled	19.5	31	Fold: Rubredoxin-like Superfamily: Rubredoxin-like Family: Rubredoxin
72	c2ecgA_	Alignment	not modelled	19.4	33	PDB header: apoptosis Chain: A; PDB Molecule: baculoviral iap repeat-containing protein 4; PDBTitle: solution structure of the ring domain of the baculoviral2 iap repeat-containing protein 4 from homo sapiens
73	c5o5jR_	Alignment	not modelled	19.3	13	PDB header: ribosome Chain: R; PDB Molecule: 30s ribosomal protein s18 2; PDBTitle: structure of the 30s small ribosomal subunit from mycobacterium2 smegmatis
74	d1wwra1	Alignment	not modelled	18.9	11	Fold: Cytidine deaminase-like Superfamily: Cytidine deaminase-like Family: Deoxycytidylate deaminase-like
75	d1hk8a_	Alignment	not modelled	18.6	13	Fold: PFL-like glycol radical enzymes Superfamily: PFL-like glycol radical enzymes Family: Class III anaerobic ribonucleotide reductase NRDD subunit
76	c1hk8A_	Alignment	not modelled	18.6	13	PDB header: oxidoreductase Chain: A; PDB Molecule: anaerobic ribonucleotide-triphosphate reductase; PDBTitle: structural basis for allosteric substrate specificity regulation in2 class iii ribonucleotide reductases: nrdd in complex with dgtp
77	d1k82a3	Alignment	not modelled	18.6	12	Fold: Glucocorticoid receptor-like (DNA-binding domain) Superfamily: Glucocorticoid receptor-like (DNA-binding domain) Family: C-terminal, Zn-finger domain of MutM-like DNA repair

						proteins
78	c2ec1A	Alignment	not modelled	18.1	27	PDB header: metal binding protein Chain: A: PDB Molecule: ring-box protein 2; PDBTitle: solution structure of the ring domain of the human ring-box2 protein 2
79	d1r2za3	Alignment	not modelled	18.0	18	Fold: Glucocorticoid receptor-like (DNA-binding domain) Superfamily: Glucocorticoid receptor-like (DNA-binding domain) Family: C-terminal, Zn-finger domain of MutM-like DNA repair proteins
80	c2hl7A	Alignment	not modelled	17.9	30	PDB header: oxidoreductase Chain: A: PDB Molecule: cytochrome c-type biogenesis protein ccmh; PDBTitle: crystal structure of the periplasmic domain of ccmh from pseudomonas2 aeruginosa
81	c5aaqA	Alignment	not modelled	17.7	38	PDB header: calcium-binding protein Chain: A: PDB Molecule: calcium-binding and coiled-coil domain-containing protein PDBTitle: tbk1 recruitment to cytosol-invading salmonella induces2 anti-bacterial autophagy
82	c4esjA	Alignment	not modelled	17.5	36	PDB header: hydrolase/dna Chain: A: PDB Molecule: type-2 restriction enzyme dpni; PDBTitle: restriction endonuclease dpni in complex with target dna
83	d1k3xa3	Alignment	not modelled	17.5	12	Fold: Glucocorticoid receptor-like (DNA-binding domain) Superfamily: Glucocorticoid receptor-like (DNA-binding domain) Family: C-terminal, Zn-finger domain of MutM-like DNA repair proteins
84	d1kkoA2	Alignment	not modelled	17.2	24	Fold: Rubredoxin-like Superfamily: Rubredoxin-like Family: Rubredoxin
85	c3cc4Z	Alignment	not modelled	17.2	19	PDB header: ribosome Chain: Z: PDB Molecule: 50s ribosomal protein l37ae; PDBTitle: co-crystal structure of anisomycin bound to the 50s ribosomal subunit
86	c3lpeF	Alignment	not modelled	16.8	47	PDB header: transferase Chain: F: PDB Molecule: dna-directed rna polymerase subunit e"; PDBTitle: crystal structure of spt4/5ngn heterodimer complex from methanococcus2 jannaschii
87	d1oxna	Alignment	not modelled	16.7	20	Fold: Inhibitor of apoptosis (IAP) repeat Superfamily: Inhibitor of apoptosis (IAP) repeat Family: Inhibitor of apoptosis (IAP) repeat
88	c3zf7o	Alignment	not modelled	16.7	19	PDB header: ribosome Chain: O: PDB Molecule: 60s ribosomal protein l13a, putative; PDBTitle: high-resolution cryo-electron microscopy structure of the trypanosoma2 brucei ribosome
89	c4a17Y	Alignment	not modelled	16.5	25	PDB header: ribosome Chain: Y: PDB Molecule: rpl37a; PDBTitle: t.thermophila 60s ribosomal subunit in complex with2 initiation factor 6. this file contains 5s rrna,3 5.8s rrna and proteins of molecule 2.
90	c4xlqA	Alignment	not modelled	16.4	25	PDB header: hydrolase Chain: A: PDB Molecule: structure-specific endonuclease subunit slx1; PDBTitle: c. glabrata slx1 in complex with slx4ccd.
91	d1jd5a	Alignment	not modelled	16.3	18	Fold: Inhibitor of apoptosis (IAP) repeat Superfamily: Inhibitor of apoptosis (IAP) repeat Family: Inhibitor of apoptosis (IAP) repeat
92	d1yuza2	Alignment	not modelled	16.2	27	Fold: Rubredoxin-like Superfamily: Rubredoxin-like Family: Rubredoxin
93	c6ff4t	Alignment	not modelled	16.2	20	PDB header: splicing Chain: T: PDB Molecule: PDBTitle: human bact spliceosome core structure
94	d1iyma	Alignment	not modelled	16.2	38	Fold: RING/U-box Superfamily: RING/U-box Family: RING finger domain, C3HC4
95	d1xb0b	Alignment	not modelled	16.1	24	Fold: Inhibitor of apoptosis (IAP) repeat Superfamily: Inhibitor of apoptosis (IAP) repeat Family: Inhibitor of apoptosis (IAP) repeat
96	d2jz6a1	Alignment	not modelled	16.0	23	Fold: L28p-like Superfamily: L28p-like Family: Ribosomal protein L28
97	c2naxA	Alignment	not modelled	16.0	33	PDB header: metal binding protein Chain: A: PDB Molecule: protein pcf11; PDBTitle: structure of cchc zinc finger domain of pcf11
98	d2cona1	Alignment	not modelled	16.0	26	Fold: Rubredoxin-like Superfamily: NOB1 zinc finger-like Family: NOB1 zinc finger-like
99	c1z6uA	Alignment	not modelled	15.7	40	PDB header: ligase Chain: A: PDB Molecule: np95-like ring finger protein isoform b; PDBTitle: np95-like ring finger protein isoform b [homo sapiens]