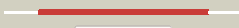












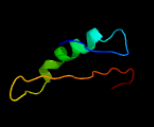

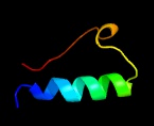

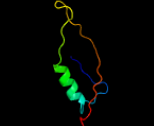

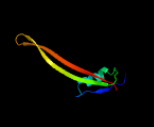


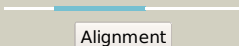

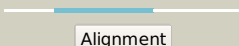

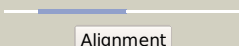

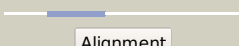
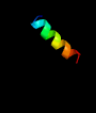
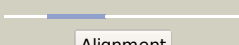

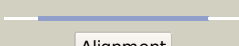
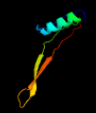
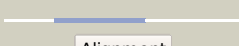

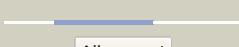

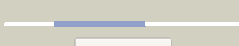
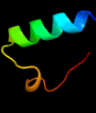
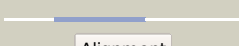

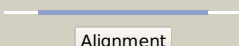
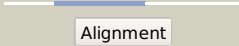

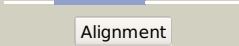
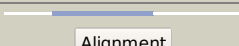



Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1498A (-)_1690140_1690352
Date	Fri Aug 2 13:30:08 BST 2019
Unique Job ID	08e1b7f4dfe91349

Detailed template
information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3oqtP_	 Alignment		100.0	100	PDB header: flavoprotein Chain: P: PDB Molecule: rv1498a protein; PDBTitle: crystal structure of rv1498a protein from mycobacterium tuberculosis
2	c6r1eC_	 Alignment		100.0	66	PDB header: flavoprotein Chain: C: PDB Molecule: dodecin; PDBTitle: structure of dodecin from streptomyces coelicolor
3	c2vxaL_	 Alignment		100.0	50	PDB header: flavoprotein Chain: L: PDB Molecule: dodecin; PDBTitle: h.halophila dodecin in complex with riboflavin
4	d2ux9a1	 Alignment		99.9	52	Fold: Dodecin subunit-like Superfamily: Dodecin-like Family: Dodecin-like
5	c3onrl_	 Alignment		99.9	23	PDB header: metal binding protein Chain: I: PDB Molecule: protein transport protein sece2; PDBTitle: crystal structure of the calcium chelating immunodominant antigen,2 calcium dodecin (rv0379),from mycobacterium tuberculosis with a novel3 calcium-binding site
6	d2cc6a1	 Alignment		99.3	23	Fold: Dodecin subunit-like Superfamily: Dodecin-like Family: Dodecin-like
7	c5lw8A_	 Alignment		65.9	13	PDB header: metal transport Chain: A: PDB Molecule: protein tonb; PDBTitle: nmr solution structure of helicobacter pylori tonb-ctd (residues 194-2 285)
8	d1ulqa2	 Alignment		46.4	23	Fold: Thiolase-like Superfamily: Thiolase-like Family: Thiolase-related
9	c6fipA_	 Alignment		41.3	20	PDB header: transport protein Chain: A: PDB Molecule: protein tonb; PDBTitle: solution nmr structure of pseudomonas aeruginosa tonb ctd
10	c2jxpA_	 Alignment		32.8	14	PDB header: lipoprotein Chain: A: PDB Molecule: putative lipoprotein b; PDBTitle: solution nmr structure of uncharacterized lipoprotein b2 from nitrosomonas europaea. northeast structural genomics3 target ner45a
11	c5csaA_	 Alignment		32.8	27	PDB header: ligase Chain: A: PDB Molecule: acetyl-coa carboxylase; PDBTitle: crystal structure of domains bt-bccp-ac1-ac5 of yeast acetyl-coa2 carboxylase

12	c4ubwB_	 Alignment		32.7	21	PDB header: transferase Chain: B: PDB Molecule: acetyl-coa acetyltransferase fada5; PDBTitle: apo structure of the 3-ketoacyl-coa thiolase fada5 from m.2 tuberculosis
13	d1m3ka2	 Alignment		30.8	27	Fold: Thiolase-like Superfamily: Thiolase-like Family: Thiolase-related
14	d1qd1a1	 Alignment		28.8	26	Fold: Ferredoxin-like Superfamily: Formiminotransferase domain of formiminotransferase-cyclodeaminase. Family: Formiminotransferase domain of formiminotransferase-cyclodeaminase.
15	d1fc3a_	 Alignment		28.2	28	Fold: DNA/RNA-binding 3-helical bundle Superfamily: C-terminal effector domain of the bipartite response regulators Family: Spo0A
16	d1lq1a_	 Alignment		26.9	28	Fold: DNA/RNA-binding 3-helical bundle Superfamily: C-terminal effector domain of the bipartite response regulators Family: Spo0A
17	c4q35B_	 Alignment		26.1	15	PDB header: membrane protein Chain: B: PDB Molecule: lps-assembly lipoprotein lpte; PDBTitle: structure of a membrane protein
18	c1ulqD_	 Alignment		25.9	25	PDB header: transferase Chain: D: PDB Molecule: putative acetyl-coa acetyltransferase; PDBTitle: crystal structure of tt0182 from thermus thermophilus hb8
19	d1wdkc2	 Alignment		25.0	30	Fold: Thiolase-like Superfamily: Thiolase-like Family: Thiolase-related
20	c1wl5A_	 Alignment		24.1	25	PDB header: transferase Chain: A: PDB Molecule: acetyl-coenzyme a acetyltransferase 2; PDBTitle: human cytosolic acetoacetyl-coa thiolase
21	c2ibyD_	 Alignment	not modelled	23.3	18	PDB header: transferase Chain: D: PDB Molecule: acetyl-coa acetyltransferase; PDBTitle: crystallographic and kinetic studies of human mitochondrial2 acetoacetyl-coa thiolase (t2): the importance of potassium and3 chloride for its structure and function
22	c3brtC_	 Alignment	not modelled	22.9	30	PDB header: transferase/transcription Chain: C: PDB Molecule: inhibitor of nuclear factor kappa-b kinase subunit beta, PDBTitle: nemo/ikkb association domain structure
23	c2k9kA_	 Alignment	not modelled	22.8	16	PDB header: metal transport Chain: A: PDB Molecule: tonb2; PDBTitle: molecular characterization of the tonb2 protein from vibrio2 anguillarum
24	c4c2jA_	 Alignment	not modelled	21.2	32	PDB header: transferase Chain: A: PDB Molecule: 3-ketoacyl-coa thiolase, mitochondrial; PDBTitle: crystal structure of human mitochondrial 3-ketoacyl-coa2 thiolase in complex with coa
25	c2m2kA_	 Alignment	not modelled	20.9	26	PDB header: transport protein Chain: A: PDB Molecule: hasb protein; PDBTitle: the structure of hasb ctd
26	c4e1lC_	 Alignment	not modelled	20.8	21	PDB header: transferase Chain: C: PDB Molecule: acetoacetyl-coa thiolase 2; PDBTitle: crystal structure of acetoacetyl-coa thiolase (thia2) from clostridium2 difficile
27	d1afwa2	 Alignment	not modelled	20.5	23	Fold: Thiolase-like Superfamily: Thiolase-like Family: Thiolase-related
28	c6bn2A_	 Alignment	not modelled	20.0	29	PDB header: transferase Chain: A: PDB Molecule: acetyl-coa acetyltransferase; PDBTitle: crystal structure of acetyl-coa acetyltransferase from elizabethkingia2 anophelis nuhp1

29	c3o6uB	Alignment	not modelled	19.8	17	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: uncharacterized protein cpe2226; PDBTitle: crystal structure of cpe2226 protein from clostridium perfringens.2 northeast structural genomics consortium target cpr195
30	d2dy1a3	Alignment	not modelled	19.5	28	Fold: Ribosomal protein S5 domain 2-like Superfamily: Ribosomal protein S5 domain 2-like Family: Translational machinery components
31	c2d9zA	Alignment	not modelled	19.2	21	PDB header: signaling protein Chain: A: PDB Molecule: protein kinase c, nu type; PDBTitle: solution structure of the ph domain of protein kinase c, nu2 type from human
32	d1tola2	Alignment	not modelled	18.0	11	Fold: ToIA/TonB C-terminal domain Superfamily: ToIA/TonB C-terminal domain Family: ToIA
33	c4eqvC	Alignment	not modelled	17.5	14	PDB header: transferase Chain: C: PDB Molecule: acetyl-coa acetyltransferase; PDBTitle: crystal structure of a monomeric scp2-thiolase like protein type 12 (stlp1) from mycobacterium smegmatis
34	c1tt9B	Alignment	not modelled	17.5	26	PDB header: transferase, lyase Chain: B: PDB Molecule: formimidoyltransferase-cyclodeaminase PDBTitle: structure of the bifunctional and golgi associated2 formiminotransferase cyclodeaminase octamer
35	c5oarC	Alignment	not modelled	17.3	33	PDB header: hydrolase Chain: C: PDB Molecule: beta-hexosaminidase; PDBTitle: crystal structure of native beta-n-acetylhexosaminidase isolated from2 aspergillus oryzae
36	d1dwna	Alignment	not modelled	17.1	26	Fold: RNA bacteriophage capsid protein Superfamily: RNA bacteriophage capsid protein Family: RNA bacteriophage capsid protein
37	c3ss6B	Alignment	not modelled	16.6	25	PDB header: transferase Chain: B: PDB Molecule: acetyl-coa acetyltransferase; PDBTitle: crystal structure of the bacillus anthracis acetyl-coa2 acetyltransferase
38	c3svkB	Alignment	not modelled	16.5	26	PDB header: transferase Chain: B: PDB Molecule: acetyl-coa acetyltransferase; PDBTitle: crystal structure of acetyl-coa acetyltransferase from mycobacterium2 avium
39	c2iikA	Alignment	not modelled	16.2	32	PDB header: transferase Chain: A: PDB Molecule: 3-ketoacyl-coa thiolase, peroxisomal; PDBTitle: crystal structure of human peroxisomal acetyl-coa acyl transferase 12 (acaal1)
40	c4g7xB	Alignment	not modelled	15.7	13	PDB header: protein binding/protein binding Chain: B: PDB Molecule: tola protein; PDBTitle: crystal structure of a complex between the ctxphi piii n-terminal2 domain and the vibrio cholerae tola c-terminal domain
41	c4nzsA	Alignment	not modelled	14.9	29	PDB header: transferase Chain: A: PDB Molecule: beta-ketothiolase bktb; PDBTitle: crystal structure of beta-ketothiolase bktb b from ralstonia eutropha2 h16
42	c5ab6E	Alignment	not modelled	14.8	11	PDB header: transport protein Chain: E: PDB Molecule: scp2-thiolase like protein; PDBTitle: crystal structure of trypanosoma brucei scp2-thiolase like2 protein (tbslp) in complex with acetoacetyl-coa.
43	c5vidL	Alignment	not modelled	14.6	30	PDB header: toxin Chain: I: PDB Molecule: bot.0671.2; PDBTitle: receptor binding domain of bont/b in complex with mini-protein binder2 bot.0671.2
44	c5vidG	Alignment	not modelled	14.6	30	PDB header: toxin Chain: G: PDB Molecule: bot.0671.2; PDBTitle: receptor binding domain of bont/b in complex with mini-protein binder2 bot.0671.2
45	d2bv3a3	Alignment	not modelled	14.5	36	Fold: Ribosomal protein S5 domain 2-like Superfamily: Ribosomal protein S5 domain 2-like Family: Translational machinery components
46	c4h62Q	Alignment	not modelled	14.1	24	PDB header: transcription Chain: Q: PDB Molecule: mediator of rna polymerase ii transcription subunit 17; PDBTitle: structure of the saccharomyces cerevisiae mediator subcomplex2 med17c/med11c/med22c
47	c1qd1A	Alignment	not modelled	13.7	26	PDB header: transferase Chain: A: PDB Molecule: formiminotransferase-cyclodeaminase; PDBTitle: the crystal structure of the formiminotransferase domain of2 formiminotransferase-cyclodeaminase.
48	d1kwia	Alignment	not modelled	13.4	12	Fold: Cystatin-like Superfamily: Cystatin/monellin Family: Cathelicidin motif
49	c4n45B	Alignment	not modelled	13.4	25	PDB header: transferase Chain: B: PDB Molecule: acetyl-coa acetyltransferase; PDBTitle: crystal structure of reduced form of thiolase from clostridium2 acetobutylicum
50	c3goaA	Alignment	not modelled	13.3	25	PDB header: transferase Chain: A: PDB Molecule: 3-ketoacyl-coa thiolase; PDBTitle: crystal structure of the salmonella typhimurium fada 3-ketoacyl-coa2 thiolase
51	d1ihra	Alignment	not modelled	13.3	14	Fold: ToIA/TonB C-terminal domain Superfamily: ToIA/TonB C-terminal domain Family: TonB
52	d1vkza1	Alignment	not modelled	13.0	24	Fold: Barrel-sandwich hybrid Superfamily: Rudiment single hybrid motif Family: BC C-terminal domain-like
53	c5ixmH	Alignment	not modelled	12.8	15	PDB header: transport protein Chain: H: PDB Molecule: lps-assembly lipoprotein lptc; PDBTitle: the lps transporter lptc from yersinia pestis, core complex
54	c3hz4A	Alignment	not modelled	12.5	29	PDB header: oxidoreductase Chain: A: PDB Molecule: thioredoxin; PDBTitle: crystal structure of thioredoxin from methanosarcina

					mazi
55	c1afwB_	Alignment	not modelled	12.0	25 PDB header: thiolase Chain: B: PDB Molecule: 3-ketoacetyl-coa thiolase; PDBTitle: the 1.8 angstrom crystal structure of the dimeric2 peroxisomal thiolase of saccharomyces cerevisiae
56	c2zkqe_	Alignment	not modelled	11.9	17 PDB header: ribosomal protein/rna Chain: E: PDB Molecule: rna expansion segment es6 part ii; PDBTitle: structure of a mammalian ribosomal 40s subunit within an 80s complex2 obtained by docking homology models of the rna and proteins into an3 8.7 a cryo-em map
57	d1nfpa_	Alignment	not modelled	11.9	38 Fold: TIM beta/alpha-barrel Superfamily: Bacterial luciferase-like Family: Non-fluorescent flavoprotein (LuxF, FP390)
58	d2c5c1	Alignment	not modelled	11.6	22 Fold: beta-Grasp (ubiquitin-like) Superfamily: Ubiquitin-like Family: Ras-binding domain, RBD
59	c6bjA_	Alignment	not modelled	11.4	11 PDB header: transferase Chain: A: PDB Molecule: acetyl-coa acetyltransferase a; PDBTitle: crystal structure of acat5 thiolase from ascaris suum in complex with2 coenzyme a
60	c3hk4B_	Alignment	not modelled	11.3	9 PDB header: lyase Chain: B: PDB Molecule: mlr7391 protein; PDBTitle: crystal structure of a putative snool-like polyketide cyclase2 [carbohydrate phosphatase] (mlr7391) from mesorhizobium loti at 1.963 a resolution
61	c4bl0B_	Alignment	not modelled	11.3	24 PDB header: cell cycle Chain: B: PDB Molecule: checkpoint serine/threonine-protein kinase bub1; PDBTitle: crystal structure of yeast bub3-bub1 bound to phospho-spc105
62	d1pkpa2	Alignment	not modelled	11.3	20 Fold: dsRBD-like Superfamily: dsRNA-binding domain-like Family: Ribosomal S5 protein, N-terminal domain
63	c6q2zB_	Alignment	not modelled	11.2	17 PDB header: unknown function Chain: B: PDB Molecule: upf0339 family protein; PDBTitle: nmr solution structure of the hvo_2922 protein from haloferax volcanii
64	c1gshA_	Alignment	not modelled	11.0	26 PDB header: glutathione biosynthesis ligase Chain: A: PDB Molecule: glutathione biosynthetic ligase; PDBTitle: structure of escherichia coli glutathione synthetase at ph 7.5
65	d2pjua1	Alignment	not modelled	11.0	22 Fold: Chelatase-like Superfamily: PrpR receptor domain-like Family: PrpR receptor domain-like
66	d2qale2	Alignment	not modelled	11.0	27 Fold: dsRBD-like Superfamily: dsRNA-binding domain-like Family: Ribosomal S5 protein, N-terminal domain
67	d2uube2	Alignment	not modelled	11.0	22 Fold: dsRBD-like Superfamily: dsRNA-binding domain-like Family: Ribosomal S5 protein, N-terminal domain
68	c6bjbB_	Alignment	not modelled	10.9	17 PDB header: transferase Chain: B: PDB Molecule: acetyl-coa acetyltransferase a; PDBTitle: crystal structure of acat2-c91s thiolase from ascaris suum in complex2 with propionyl-coa and nitrate
69	c2c7yB_	Alignment	not modelled	10.7	25 PDB header: transferase Chain: B: PDB Molecule: 3-ketoacyl-coa thiolase 2; PDBTitle: plant enzyme
70	c2ow8f_	Alignment	not modelled	10.6	27 PDB header: ribosome Chain: F: PDB Molecule: PDBTitle: crystal structure of a 70s ribosome-trna complex reveals functional2 interactions and rearrangements. this file, 2ow8, contains the 30s3 ribosome subunit, two trna, and mrna molecules. 50s ribosome subunit4 is in the file 1vsa.
71	c6aqpA_	Alignment	not modelled	10.5	29 PDB header: transferase Chain: A: PDB Molecule: acetyl-coa acetyltransferase; PDBTitle: aspergillus fumigatus cytosolic thiolase: acetylated enzyme in complex2 with coa and potassium ions
72	c4n6oB_	Alignment	not modelled	10.5	23 PDB header: hydrolase/hydrolase inhibitor Chain: B: PDB Molecule: cystatin-m; PDBTitle: crystal structure of reduced legumain in complex with cystatin e/m
73	c3brvC_	Alignment	not modelled	10.4	35 PDB header: transferase/transcription Chain: C: PDB Molecule: inhibitor of nuclear factor kappa-b kinase subunit beta; PDBTitle: nemo/ikkb association domain structure
74	d3eeqa1	Alignment	not modelled	10.2	11 Fold: CobE/GbiG C-terminal domain-like Superfamily: CobE/GbiG C-terminal domain-like Family: CobE/GbiG C-terminal domain-like
75	d1gsoa1	Alignment	not modelled	10.1	20 Fold: Barrel-sandwich hybrid Superfamily: Rudiment single hybrid motif Family: BC C-terminal domain-like
76	c1eg0B_	Alignment	not modelled	10.1	19 PDB header: ribosome PDB COMPND:
77	c2wuaA_	Alignment	not modelled	10.0	25 PDB header: transferase Chain: A: PDB Molecule: acetoacetyl coa thiolase; PDBTitle: structure of the peroxisomal 3-ketoacyl-coa thiolase from sunflower
78	c4eycA_	Alignment	not modelled	9.9	9 PDB header: unknown function Chain: A: PDB Molecule: cathelicidin antimicrobial peptide; PDBTitle: crystal structure of the cathelin-like domain of human cathelicidin2 ll-37 (hcd)
79	c2x9aB_	Alignment	not modelled	9.9	7 PDB header: viral protein Chain: B: PDB Molecule: membrane spanning protein, required for outer membrane PDBTitle: crystal structure of g3p from phage if1 in complex with

						its2 coreceptor, the c-terminal domain of tola
80	d1e5ma2	Alignment	not modelled	9.6	15	Fold: Thiolase-like Superfamily: Thiolase-like Family: Thiolase-related
81	c5xyiC	Alignment	not modelled	9.6	21	PDB header: ribosome Chain: C: PDB Molecule: uncharacterized protein; PDBTitle: small subunit of trichomonas vaginalis ribosome
82	c4wysB	Alignment	not modelled	9.6	25	PDB header: transferase Chain: B: PDB Molecule: acetyl-coa acetyltransferase; PDBTitle: crystal structure of thiolase from escherichia coli
83	d1tqyb2	Alignment	not modelled	9.4	26	Fold: Thiolase-like Superfamily: Thiolase-like Family: Thiolase-related
84	c3msoA	Alignment	not modelled	9.0	22	PDB header: isomerase Chain: A: PDB Molecule: steroid delta-isomerase; PDBTitle: crystal structure of a steroid delta-isomerase (np_250810.1) from2 pseudomonas aeruginosa at 2.57 a resolution
85	d1p9ya	Alignment	not modelled	8.9	18	Fold: Ribosome binding domain-like Superfamily: Trigger factor ribosome-binding domain Family: Trigger factor ribosome-binding domain
86	c3gkuB	Alignment	not modelled	8.8	20	PDB header: rna binding protein Chain: B: PDB Molecule: probable rna-binding protein; PDBTitle: crystal structure of a probable rna-binding protein from clostridium2 symbiosum atcc 14940
87	d1w26a2	Alignment	not modelled	8.7	21	Fold: Ribosome binding domain-like Superfamily: Trigger factor ribosome-binding domain Family: Trigger factor ribosome-binding domain
88	c2vu2D	Alignment	not modelled	8.6	29	PDB header: transferase Chain: D: PDB Molecule: acetyl-coa acetyltransferase; PDBTitle: biosynthetic thiolase from z. ramigera. complex with s-pantetheine-11-2 pivalate.
89	d1roaa	Alignment	not modelled	8.5	15	Fold: Cystatin-like Superfamily: Cystatin/monellin Family: Cystatins
90	c3by5A	Alignment	not modelled	8.4	19	PDB header: biosynthetic protein Chain: A: PDB Molecule: cobalamin biosynthesis protein; PDBTitle: crystal structure of cobalamin biosynthesis protein chig from2 agrobacterium tumefaciens str. c58
91	d3by5a1	Alignment	not modelled	8.4	19	Fold: CobE/GbiG C-terminal domain-like Superfamily: CobE/GbiG C-terminal domain-like Family: CobE/GbiG C-terminal domain-like
92	c3f40A	Alignment	not modelled	8.4	33	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized ntf2-like protein; PDBTitle: crystal structure of ntf2-like protein of unknown function2 (yp_677363.1) from cytophaga hutchinsonii atcc 33406 at 1.27 a3 resolution
93	c6et9D	Alignment	not modelled	8.3	18	PDB header: transferase Chain: D: PDB Molecule: acetyl-coa acetyltransferase thiolase; PDBTitle: structure of the acetoacetyl-coa-thiolase/hmg-coa-synthase complex2 from methanothermococcus thermolithotrophicus at 2.75 a
94	c3bbnE	Alignment	not modelled	8.3	23	PDB header: ribosome Chain: E: PDB Molecule: ribosomal protein s5; PDBTitle: homology model for the spinach chloroplast 30s subunit fitted to 9.4a2 cryo-em map of the 70s chlororibosome.
95	c2kxhB	Alignment	not modelled	8.3	30	PDB header: protein binding Chain: B: PDB Molecule: peptide of far upstream element-binding protein 1; PDBTitle: solution structure of the first two rrm domains of fir in the complex2 with fbp nbx peptide
96	d2coaa1	Alignment	not modelled	8.2	36	Fold: PH domain-like barrel Superfamily: PH domain-like Family: Pleckstrin-homology domain (PH domain)
97	d2w6ka1	Alignment	not modelled	8.2	21	Fold: CobE/GbiG C-terminal domain-like Superfamily: CobE/GbiG C-terminal domain-like Family: CobE/GbiG C-terminal domain-like
98	c4o9cC	Alignment	not modelled	8.1	32	PDB header: transferase Chain: C: PDB Molecule: acetyl-coa acetyltransferase; PDBTitle: crystal structure of beta-ketothiolase (phaa) from ralstonia eutropha2 h16
99	c2kzxA	Alignment	not modelled	8.0	17	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: solution nmr structure of a3dht5 from clostridium thermocellum,2 northeast structural genomics consortium target cmr116