

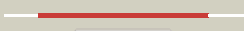




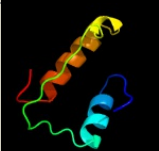







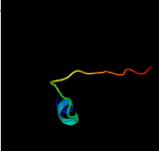



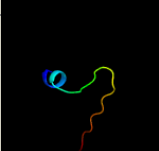

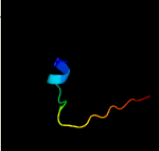
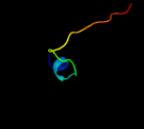
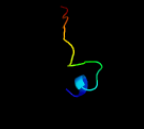

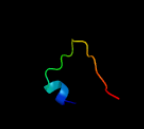
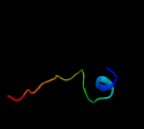
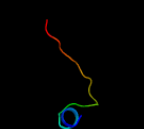
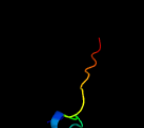




Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1888A (-) _2138451_2138624
Date	Fri Aug 2 13:30:50 BST 2019
Unique Job ID	c1eb0b7906589fbc

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d2uyoa1	 Alignment		99.7	63	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: ML2640-like
2	d1rjda_	 Alignment		99.4	20	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: Leucine carboxy methyltransferase Ppm1
3	c3ieiD_	 Alignment		99.2	24	PDB header: transferase Chain: D: PDB Molecule: leucine carboxyl methyltransferase 1; PDBTitle: crystal structure of human leucine carboxylmethyltransferase-1 in2 complex with s-adenosyl homocysteine
4	c3mntA_	 Alignment		99.2	21	PDB header: transferase Chain: A: PDB Molecule: leucine carboxyl methyltransferase 1; PDBTitle: crystal structure of human leucine carboxyl methyltransferase 1
5	c2zwaA_	 Alignment		97.9	27	PDB header: transferase Chain: A: PDB Molecule: leucine carboxyl methyltransferase 2; PDBTitle: crystal structure of trna wybutosine synthesizing enzyme2 tyw4
6	c2qe6B_	 Alignment		97.8	32	PDB header: transferase Chain: B: PDB Molecule: uncharacterized protein tfu_2867; PDBTitle: crystal structure of a putative methyltransferase (tfu_2867) from2 thermobifida fusca yx at 1.95 a resolution
7	c3giwA_	 Alignment		92.9	16	PDB header: unknown function Chain: A: PDB Molecule: protein of unknown function duf574; PDBTitle: crystal structure of a duf574 family protein (sav_2177) from2 streptomyces avermitilis ma-4680 at 1.45 a resolution
8	c6e7kB_	 Alignment		37.3	10	PDB header: hydrolase Chain: B: PDB Molecule: lipoprotein lipase; PDBTitle: structure of the lipoprotein lipase gpihbp1 complex that mediates2 plasma triglyceride hydrolysis
9	c1hplB_	 Alignment		33.6	14	PDB header: hydrolase(carboxylic esterase) Chain: B: PDB Molecule: lipase; PDBTitle: horse pancreatic lipase. the crystal structure at 2.3 angstroms2 resolution
10	d1rplA2	 Alignment		33.3	14	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Pancreatic lipase, N-terminal domain
11	c2pvsB_	 Alignment		31.4	14	PDB header: hydrolase Chain: B: PDB Molecule: pancreatic lipase-related protein 2; PDBTitle: structure of human pancreatic lipase related protein 22 mutant n336q

12	d1hpla2	Alignment		31.3	14	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Pancreatic lipase, N-terminal domain
13	d1etha2	Alignment		30.2	14	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Pancreatic lipase, N-terminal domain
14	d1af7a2	Alignment		29.5	17	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: Chemotaxis receptor methyltransferase CheR, C-terminal domain
15	c2pplA_	Alignment		28.9	14	PDB header: hydrolase Chain: A: PDB Molecule: pancreatic lipase-related protein 1; PDBTitle: human pancreatic lipase-related protein 1
16	c1gp1A_	Alignment		28.3	14	PDB header: serine esterase Chain: A: PDB Molecule: rp2 lipase; PDBTitle: rp2 lipase
17	d1gp1a2	Alignment		27.9	14	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Pancreatic lipase, N-terminal domain
18	d1bu8a2	Alignment		27.5	10	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Pancreatic lipase, N-terminal domain
19	d1co6a_	Alignment		27.4	22	Fold: Cytochrome c Superfamily: Cytochrome c Family: monodomain cytochrome c
20	d1lpbb2	Alignment		26.1	14	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Pancreatic lipase, N-terminal domain
21	c5xlxD_	Alignment	not modelled	25.0	17	PDB header: transferase Chain: D: PDB Molecule: chemotaxis protein methyltransferase 1; PDBTitle: crystal structure of the c-terminal domain of cher1 containing sah
22	c5vyeA_	Alignment	not modelled	23.7	14	PDB header: lyase Chain: A: PDB Molecule: l-threonine aldolase; PDBTitle: crystal structure of l-threonine aldolase from pseudomonas putida
23	c5ftwA_	Alignment	not modelled	23.2	7	PDB header: transferase Chain: A: PDB Molecule: chemotaxis protein methyltransferase; PDBTitle: crystal structure of glutamate o-methyltransferase in2 complex with s- adenosyl-l-homocysteine (sah) from3 bacillus subtilis
24	c5xlyA_	Alignment	not modelled	23.1	17	PDB header: transferase Chain: A: PDB Molecule: chemotaxis protein methyltransferase 1; PDBTitle: crystal structure of cher1 in complex with c-di-gmp-bound mapz
25	c1rp1A_	Alignment	not modelled	22.2	10	PDB header: hydrolase Chain: A: PDB Molecule: pancreatic lipase related protein 1; PDBTitle: dog pancreatic lipase related protein 1
26	c1af7A_	Alignment	not modelled	19.4	17	PDB header: methyltransferase Chain: A: PDB Molecule: chemotaxis receptor methyltransferase cher; PDBTitle: cher from salmonella typhimurium
27	c3ndhA_	Alignment	not modelled	18.2	29	PDB header: hydrolase/dna Chain: A: PDB Molecule: restriction endonuclease thai; PDBTitle: restriction endonuclease in complex with substrate dna
28	c2l9dA_	Alignment	not modelled	17.3	17	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: solution structure of the protein yp_546394.1, the first structural2 representative of the pfam family pf12112 PDB header: transferase/ligase

29	c5w87B_	Alignment	not modelled	16.6	17	Chain: B: PDB Molecule: probable e3 ubiquitin-protein ligase herc6; PDBTitle: crystal structure of the c-terminal lobe of the human herc6 hect2 domain
30	c4uy5A_	Alignment	not modelled	12.8	13	PDB header: transferase Chain: A: PDB Molecule: histidine-specific methyltransferase egtD; PDBTitle: crystal structure of histidine-specific methyltransferase egtD from <i>Mycobacterium smegmatis</i>
31	d2p3pa1	Alignment	not modelled	10.7	19	Fold: PG1388-like Superfamily: PG1388-like Family: PG1388-like
32	d1x9na1	Alignment	not modelled	10.3	19	Fold: ATP-dependent DNA ligase DNA-binding domain Superfamily: ATP-dependent DNA ligase DNA-binding domain Family: ATP-dependent DNA ligase DNA-binding domain
33	d3e46a1	Alignment	not modelled	10.0	50	Fold: RuvA C-terminal domain-like Superfamily: UBA-like Family: UBA domain
34	c3ggdA_	Alignment	not modelled	10.0	9	PDB header: transferase Chain: A: PDB Molecule: sam-dependent methyltransferase; PDBTitle: crystal structure of sam-dependent methyltransferase (yp_325210.1)2 from <i>Anabaena variabilis</i> atcc 29413 at 2.11 a resolution
35	c4rsxA_	Alignment	not modelled	9.9	23	PDB header: signaling protein Chain: A: PDB Molecule: type iii effector hopa1; PDBTitle: the structure of the effector protein from <i>Pseudomonas syringae</i> pv.2 tomato strain dc3000
36	d1m6ia3	Alignment	not modelled	9.7	53	Fold: CO dehydrogenase flavoprotein C-domain-like Superfamily: FAD/NAD-linked reductases, dimerisation (C-terminal) domain Family: FAD/NAD-linked reductases, dimerisation (C-terminal) domain
37	c5dpb_	Alignment	not modelled	9.6	20	PDB header: transferase Chain: B: PDB Molecule: protein lysine methyltransferase 2; PDBTitle: the structure of pkmt2 from <i>Rickettsia typhi</i> in complex with adohcy
38	c5lp8A_	Alignment	not modelled	9.5	18	PDB header: ligase Chain: A: PDB Molecule: e3 ubiquitin-protein ligase huwe1; PDBTitle: crystal structure of an asymmetric dimer of the ubiquitin ligase huwe1
39	d2hkja1	Alignment	not modelled	8.8	25	Fold: S13-like H2TH domain Superfamily: S13-like H2TH domain Family: Topoisomerase VI-B subunit middle domain
40	c1avyA_	Alignment	not modelled	8.5	38	PDB header: coiled coil Chain: A: PDB Molecule: fibrin; PDBTitle: fibrin deletion mutant m (bacteriophage t4)
41	c3g1nA_	Alignment	not modelled	8.1	18	PDB header: ligase Chain: A: PDB Molecule: e3 ubiquitin-protein ligase huwe1; PDBTitle: catalytic domain of the human e3 ubiquitin-protein ligase2 huwe1
42	c3cqbB_	Alignment	not modelled	7.6	21	PDB header: hydrolase Chain: B: PDB Molecule: probable protease htpX homolog; PDBTitle: crystal structure of heat shock protein htpX domain from <i>Vibrio parahaemolyticus</i> rimd 2210633
43	c1xdUA_	Alignment	not modelled	7.1	19	PDB header: transferase Chain: A: PDB Molecule: protein rdmb; PDBTitle: crystal structure of aclacinomycin-10-hydroxylase (rdmb) in complex2 with sinefungin (sfg)
44	d1kzyc2	Alignment	not modelled	7.0	21	Fold: BRCT domain Superfamily: BRCT domain Family: 53BP1
45	c3cggB_	Alignment	not modelled	7.0	23	PDB header: transferase Chain: B: PDB Molecule: sam-dependent methyltransferase; PDBTitle: crystal structure of tehB-like sam-dependent methyltransferase2 (np_600671.1) from <i>Corynebacterium glutamicum</i> atcc 13032 kitasato at3 2.00 a resolution
46	c3tl8K_	Alignment	not modelled	6.9	24	PDB header: transferase/ligase Chain: K: PDB Molecule: effector protein hopa2; PDBTitle: the avrptob-bak1 complex reveals two structurally similar2 kinaseinteracting domains in a single type iii effector
47	c5wujB_	Alignment	not modelled	6.9	25	PDB header: motor protein Chain: B: PDB Molecule: flagellar motor switch protein flig; PDBTitle: crystal structure of flif-flig complex from <i>H. pylori</i>
48	d2g7ja1	Alignment	not modelled	6.7	33	Fold: Secretion chaperone-like Superfamily: YgaC/TfoX-N like Family: YgaC-like
49	c6mroA_	Alignment	not modelled	6.6	10	PDB header: transferase Chain: A: PDB Molecule: methyl transferase from <i>Methanosarcina acetivorans</i> ; PDBTitle: crystal structure of methyl transferase from <i>Methanosarcina acetivorans</i> at 1.6 angstroms resolution, northeast structural3 genomics consortium (nesg) target mvr53.
50	c1fpqA_	Alignment	not modelled	6.3	13	PDB header: transferase Chain: A: PDB Molecule: isoliquritigenin 2'-O-methyltransferase; PDBTitle: crystal structure analysis of selenomethionine substituted chalcone O-2 methyltransferase
51	c3btzA_	Alignment	not modelled	6.3	19	PDB header: oxidoreductase/dna Chain: A: PDB Molecule: alpha-ketoglutarate-dependent dioxygenase alkB homolog 2; PDBTitle: crystal structure of human abh2 cross-linked to dsDNA
52	d1omha_	Alignment	not modelled	6.2	31	Fold: Origin of replication-binding domain, RBD-like Superfamily: Origin of replication-binding domain, RBD-like Family: Relaxase domain
53	c1dmIF_	Alignment	not modelled	6.2	50	PDB header: dna binding protein/transferase Chain: F: PDB Molecule: dna polymerase; PDBTitle: crystal structure of herpes simplex uL42 bound to the C-terminus of f2 hsv pol
54	c1dmIB_	Alignment	not modelled	6.2	50	PDB header: dna binding protein/transferase Chain: B: PDB Molecule: dna polymerase;

54	c1dmB_	Alignment	not modelled	6.2	50	PDBTitle: crystal structure of herpes simplex ul42 bound to the c-terminus of2 hsv pol
55	c1dmID_	Alignment	not modelled	6.2	50	PDB header: dna binding protein/transferase Chain: D: PDB Molecule: dna polymerase; PDBTitle: crystal structure of herpes simplex ul42 bound to the c-terminus of2 hsv pol
56	c1dmIH_	Alignment	not modelled	6.2	50	PDB header: dna binding protein/transferase Chain: H: PDB Molecule: dna polymerase; PDBTitle: crystal structure of herpes simplex ul42 bound to the c-terminus of2 hsv pol
57	d1k82a1	Alignment	not modelled	6.1	25	Fold: S13-like H2TH domain Superfamily: S13-like H2TH domain Family: Middle domain of MutM-like DNA repair proteins
58	c3a9fA_	Alignment	not modelled	6.0	13	PDB header: electron transport Chain: A: PDB Molecule: cytochrome c; PDBTitle: crystal structure of the c-terminal domain of cytochrome cz from2 chlorobium tepidum
59	c2k2pA_	Alignment	not modelled	5.9	20	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein atu1203; PDBTitle: solution nmr structure of protein atu1203 from agrobacterium2 tumefaciens. northeast structural genomics consortium (nesg) target3 att10, ontario center for structural proteomics target atc1183
60	c5do0A_	Alignment	not modelled	5.8	8	PDB header: transferase Chain: A: PDB Molecule: protein lysine methyltransferase 1; PDBTitle: the structure of pkmt1 from rickettsia prowazekii
61	c6j1xB_	Alignment	not modelled	5.8	23	PDB header: ligase Chain: B: PDB Molecule: nedd4-like e3 ubiquitin-protein ligase wwp1; PDBTitle: wwp1 close conformation
62	d1ufoa_	Alignment	not modelled	5.7	18	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Hypothetical protein TT1662
63	c2cosA_	Alignment	not modelled	5.7	31	PDB header: transferase Chain: A: PDB Molecule: serine/threonine protein kinase lats2; PDBTitle: solution structure of rsgi ruh-038, a uba domain from mouse2 lats2 (large tumor suppressor homolog 2)
64	c1jzdA_	Alignment	not modelled	5.6	31	PDB header: oxidoreductase Chain: A: PDB Molecule: thiol:disulfide interchange protein dsbc; PDBTitle: dsbc-dsbdalpha complex
65	c2lf6A_	Alignment	not modelled	5.5	29	PDB header: signaling protein Chain: A: PDB Molecule: effector protein hopab1; PDBTitle: solution nmr structure of hopabpph1448_220_320 from pseudomonas2 syringae pv. phaseolicola str. 1448a, midwest center for structural3 genomics target apc40132.4 and northeast structural genomics4 consortium target pst3a
66	c4htoA_	Alignment	not modelled	5.4	24	PDB header: ligase, dna binding protein Chain: A: PDB Molecule: dna ligase 4; PDBTitle: crystal structure of the dbd domain of human dna ligase iv apo form
67	c6cgaB_	Alignment	not modelled	5.2	25	PDB header: hydrolase Chain: B: PDB Molecule: polycomb protein asx; PDBTitle: structure of the pr-dub complex
68	c3i53A_	Alignment	not modelled	5.2	10	PDB header: transferase Chain: A: PDB Molecule: o-methyltransferase; PDBTitle: crystal structure of an o-methyltransferase (ncsb1) from2 neocarzinostatin biosynthesis in complex with s-adenosyl-l-3 homocysteine (sah)
69	c3g2qA_	Alignment	not modelled	5.2	15	PDB header: transferase Chain: A: PDB Molecule: pcza361.24; PDBTitle: crystal structure of the glycopeptide n-methyltransferase mtf2 complexed with sinefungin
70	c3u0vA_	Alignment	not modelled	5.2	15	PDB header: hydrolase Chain: A: PDB Molecule: lysophospholipase-like protein 1; PDBTitle: crystal structure analysis of human lyplal1
71	c3p0sA_	Alignment	not modelled	5.1	22	PDB header: virus Chain: A: PDB Molecule: capsid protein vp; PDBTitle: crystal structure of bombyx mori densovirus 1 capsid