Phyre^2

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Description	RVBD0634A_(-)_731116_731367
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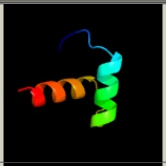
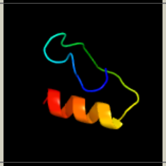
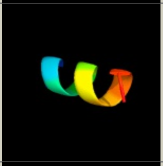
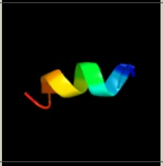
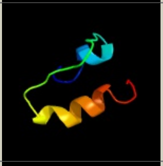
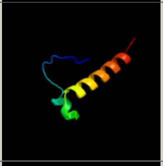
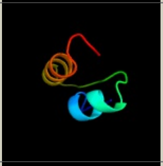
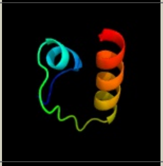
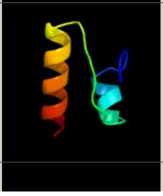
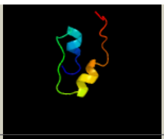
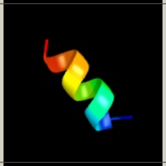
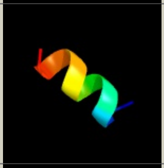
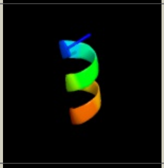
Unique Job ID	2f9c5d572d2998ad

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c6a7vU_	Alignment		97.7	46	**PDB header:**toxin/antitoxin **Chain:** U: **PDB Molecule:**antitoxin vapb11; **PDBTitle:** crystal structure of mycobacterium tuberculosis vapbc11 toxin-2 antitoxin complex
2	c2vdwA_	Alignment		63.1	29	**PDB header:**transferase **Chain:** A: **PDB Molecule:**vaccinia virus capping enzyme d1 subunit; **PDBTitle:** guanosine n7 methyl-transferase sub-complex (d1-d12) of the2 vaccinia virus mrna capping enzyme
3	c6q56C_	Alignment		30.6	29	**PDB header:**rna binding protein **Chain:** C: **PDB Molecule:**trna (adenine(22)-n(1))-methyltransferase; **PDBTitle:** crystal structure of the b. subtilis m1a22 trna methyltransferase trmk
4	c2mxdA_	Alignment		25.2	64	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**viral protein genome-linked; **PDBTitle:** solution structure of vpg of porcine sapovirus
5	c2m4hA_	Alignment		24.8	58	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**feline calicivirus vpg protein; **PDBTitle:** solution structure of the core domain (10-76) of the feline2 calicivirus vpg protein
6	c3fuxB_	Alignment		24.0	21	**PDB header:**transferase **Chain:** B: **PDB Molecule:**dimethyladenosine transferase; **PDBTitle:** t. thermophilus 16s rrna a1518 and a1519 methyltransferase (ksga) in2 complex with 5'-methylthioadenosine in space group p212121
7	d2hzaa1	Alignment		18.7	36	**Fold:**Ribbon-helix-helix **Superfamily:**Ribbon-helix-helix **Family:**CopG-like
8	d2f8la1	Alignment		18.3	26	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**N-6 DNA Methylase-like
9	c4ponB_	Alignment		17.0	17	**PDB header:**transferase **Chain:** B: **PDB Molecule:**putative rna methylase; **PDBTitle:** the crystal structure of a putative sam-dependent methyltransferase,2 ytqb, from bacillus subtilis
10	d1o54a_	Alignment		16.9	23	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**tRNA(1-methyladenosine) methyltransferase-like
11	c1dl5A_	Alignment		16.7	26	**PDB header:**transferase **Chain:** A: **PDB Molecule:**protein-l-isoaspartate o-methyltransferase; **PDBTitle:** protein-l-isoaspartate o-methyltransferase

12	c3g07C_	Alignment		15.6	22	**PDB header:**transferase **Chain:** C: **PDB Molecule:**7sk snrna methylphosphate capping enzyme; **PDBTitle:** methyltransferase domain of human bicoid-interacting protein 3 homolog2 (drosophila)
13	c5oy4Y_	Alignment		15.2	36	**PDB header:**transferase **Chain:** Y: **PDB Molecule:**proto-oncogene frat1; **PDBTitle:** gsk3beta complex with n-(6-(3,4-dihydroxyphenyl)-1h-pyrazolo[3,4-2 b]pyridin-3-yl)acetamide
14	c3zrkX_	Alignment		14.5	36	**PDB header:**transferase/peptide **Chain:** X: **PDB Molecule:**proto-oncogene frat1; **PDBTitle:** identification of 2-(4-pyridyl)thienopyridinones as gsk-3beta2 inhibitors
15	c3zrlX_	Alignment		14.3	36	**PDB header:**transferase/peptide **Chain:** X: **PDB Molecule:**proto-oncogene frat1; **PDBTitle:** identification of 2-(4-pyridyl)thienopyridinones as gsk-3beta2 inhibitors
16	c3zrmX_	Alignment		14.3	36	**PDB header:**transferase/peptide **Chain:** X: **PDB Molecule:**proto-oncogene frat1; **PDBTitle:** identification of 2-(4-pyridyl)thienopyridinones as gsk-2 3beta inhibitors
17	c1gngX_	Alignment		13.9	36	**PDB header:**transferase **Chain:** X: **PDB Molecule:**frattide; **PDBTitle:** glycogen synthase kinase-3 beta (gsk3) complex with frattide2 peptide
18	c3zrkY_	Alignment		13.4	36	**PDB header:**transferase/peptide **Chain:** Y: **PDB Molecule:**proto-oncogene frat1; **PDBTitle:** identification of 2-(4-pyridyl)thienopyridinones as gsk-3beta2 inhibitors
19	c3zrlY_	Alignment		13.3	36	**PDB header:**transferase/peptide **Chain:** Y: **PDB Molecule:**proto-oncogene frat1; **PDBTitle:** identification of 2-(4-pyridyl)thienopyridinones as gsk-3beta2 inhibitors
20	c3zrmY_	Alignment		13.3	36	**PDB header:**transferase/peptide **Chain:** Y: **PDB Molecule:**proto-oncogene frat1; **PDBTitle:** identification of 2-(4-pyridyl)thienopyridinones as gsk-2 3beta inhibitors
21	c1gngY_	Alignment	not modelled	13.2	36	**PDB header:**transferase **Chain:** Y: **PDB Molecule:**frattide; **PDBTitle:** glycogen synthase kinase-3 beta (gsk3) complex with frattide2 peptide
22	c4afjY_	Alignment	not modelled	13.2	36	**PDB header:**transferase/peptide **Chain:** Y: **PDB Molecule:**proto-oncogene frat1; **PDBTitle:** 5-aryl-4-carboxamide-1,3-oxazoles: potent and selective gsk-32 inhibitors
23	c4ckcD_	Alignment	not modelled	13.1	31	**PDB header:**transferase/hydrolase **Chain:** D: **PDB Molecule:**mrna-capping enzyme catalytic subunit; **PDBTitle:** vaccinia virus capping enzyme complexed with sah (monoclinic form)
24	c3ckkA_	Alignment	not modelled	13.1	29	**PDB header:**transferase **Chain:** A: **PDB Molecule:**trna (guanine-n(7)-)-methyltransferase; **PDBTitle:** crystal structure of human methyltransferase-like protein 1
25	c5oy4X_	Alignment	not modelled	13.0	36	**PDB header:**transferase **Chain:** X: **PDB Molecule:**proto-oncogene frat1; **PDBTitle:** gsk3beta complex with n-(6-(3,4-dihydroxyphenyl)-1h-pyrazolo[3,4-2 b]pyridin-3-yl)acetamide
26	c2fk8A_	Alignment	not modelled	12.5	12	**PDB header:**transferase **Chain:** A: **PDB Molecule:**methoxy mycolic acid synthase 4; **PDBTitle:** crystal structure of hma (mmaa4) from mycobacterium tuberculosis2 complexed with s-adenosylmethionine
27	c2kz3A_	Alignment	not modelled	12.4	34	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**putative uncharacterized protein rad51l3; **PDBTitle:** backbone 1h, 13c, and 15n chemical shift assignments for human rad51d2 from 1 to 83
28	c4afjX_	Alignment	not modelled	12.1	36	**PDB header:**transferase/peptide **Chain:** X: **PDB Molecule:**proto-oncogene frat1; **PDBTitle:** 5-aryl-4-carboxamide-1,3-oxazoles: potent and selective gsk-32 inhibitors
						Fold:S-adenosyl-L-methionine-dependent methyltransferases

29	d1qama_	Alignment	not modelled	11.4	21	**Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**rRNA adenine dimethylase-like
30	c1x37A_	Alignment	not modelled	11.4	37	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**atp-dependent protease la 1; **PDBTitle:** structure of bacillus subtilis lon protease ssd domain
31	c3bgvC_	Alignment	not modelled	10.2	35	**PDB header:**transferase **Chain:** C: **PDB Molecule:**mrna cap guanine-n7 methyltransferase; **PDBTitle:** crystal structure of mrna cap guanine-n7 methyltransferase2 in complex with sah
32	d1d2ha_	Alignment	not modelled	10.1	13	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**Glycine N-methyltransferase
33	c6ifsB_	Alignment	not modelled	9.8	23	**PDB header:**transferase **Chain:** B: **PDB Molecule:**ribosomal rna small subunit methyltransferase a; **PDBTitle:** ksga from bacillus subtilis 168
34	d2fcaa1	Alignment	not modelled	9.5	21	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**TrmB-like
35	d1knza_	Alignment	not modelled	9.3	35	**Fold:**NSP3 homodimer **Superfamily:**NSP3 homodimer **Family:**NSP3 homodimer
36	c2h1rA_	Alignment	not modelled	8.3	29	**PDB header:**transferase **Chain:** A: **PDB Molecule:**dimethyladenosine transferase, putative; **PDBTitle:** crystal structure of a dimethyladenosine transferase from2 plasmodium falciparum
37	d1m6ya2	Alignment	not modelled	8.1	22	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**MraW-like putative methyltransferases
38	c1xrxD_	Alignment	not modelled	7.7	67	**PDB header:**replication inhibitor **Chain:** D: **PDB Molecule:**seqa protein; **PDBTitle:** crystal structure of a dna-binding protein
39	d1xrxa1	Alignment	not modelled	7.7	67	**Fold:**Ribbon-helix-helix **Superfamily:**Ribbon-helix-helix **Family:**SeqA N-terminal domain-like
40	d2nn6h3	Alignment	not modelled	7.6	38	**Fold:**Eukaryotic type KH-domain (KH-domain type I) **Superfamily:**Eukaryotic type KH-domain (KH-domain type I) **Family:**Eukaryotic type KH-domain (KH-domain type I)
41	c1m6yA_	Alignment	not modelled	7.6	22	**PDB header:**transferase **Chain:** A: **PDB Molecule:**s-adenosyl-methyltransferase mraw; **PDBTitle:** crystal structure analysis of tm0872, a putative sam-dependent2 methyltransferase, complexed with sah
42	c3uzuA_	Alignment	not modelled	7.5	30	**PDB header:**transferase **Chain:** A: **PDB Molecule:**ribosomal rna small subunit methyltransferase a; **PDBTitle:** the structure of the ribosomal rna small subunit methyltransferase a2 from burkholderia pseudomallei
43	c3grrA_	Alignment	not modelled	7.5	23	**PDB header:**transferase **Chain:** A: **PDB Molecule:**dimethyladenosine transferase; **PDBTitle:** crystal structure of the complex between s-adenosyl homocysteine and2 methanocaldococcus jannaschi dim1.
44	c3fydA_	Alignment	not modelled	7.5	23	**PDB header:**transferase **Chain:** A: **PDB Molecule:**probable dimethyladenosine transferase; **PDBTitle:** crystal structure of dim1 from the thermophilic archeon,2 methanocaldococcus jannaschi
45	c2kxwB_	Alignment	not modelled	7.3	44	**PDB header:**calcium-binding protein/metal transport **Chain:** B: **PDB Molecule:**sodium channel protein type 2 subunit alpha; **PDBTitle:** structure of the c-domain fragment of apo calmodulin bound to the iq2 motif of nav1.2
46	c2m5eB_	Alignment	not modelled	7.3	44	**PDB header:**calcium-binding protein/metal transport **Chain:** B: **PDB Molecule:**sodium channel protein type 2 subunit alpha; **PDBTitle:** structure of the c-domain of calcium-saturated calmodulin bound to the2 iq motif of nav1.2
47	c4jxjA_	Alignment	not modelled	7.2	29	**PDB header:**transferase **Chain:** A: **PDB Molecule:**ribosomal rna small subunit methyltransferase a; **PDBTitle:** crystal structure of ribosomal rna small subunit methyltransferase a2 from rickettsia bellii determined by iodide sad phasing
48	c4aoyD_	Alignment	not modelled	7.2	28	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**isocitrate dehydrogenase [nadp]; **PDBTitle:** open ctidh. the complex structures of isocitrate dehydrogenase from2 clostridium thermocellum and desulfotalea psychrophila, support a new3 active site locking mechanism
49	c6butB_	Alignment	not modelled	6.9	45	**PDB header:**membrane protein **Chain:** B: **PDB Molecule:**sodium channel protein type 2 subunit alpha; **PDBTitle:** solution structure of full-length apo mammalian calmodulin bound to2 the iq motif of the human voltage-gated sodium channel nav1.2
50	d2ieaa3	Alignment	not modelled	6.9	19	**Fold:**TK C-terminal domain-like **Superfamily:**TK C-terminal domain-like **Family:**Transketolase C-terminal domain-like
51	c3mznA_	Alignment	not modelled	6.9	27	**PDB header:**lyase **Chain:** A: **PDB Molecule:**glucarate dehydratase; **PDBTitle:** crystal structure of probable glucarate dehydratase from2 chromohalobacter salexigens dsm 3043
52	c1q5vB_	Alignment	not modelled	6.8	36	**PDB header:**transcription **Chain:** B: **PDB Molecule:**nickel responsive regulator; **PDBTitle:** apo-nikr
53	d2ahme1	Alignment	not modelled	6.8	20	**Fold:**Coronavirus NSP8-like **Superfamily:**Coronavirus NSP8-like

						Family: Coronavirus NSP8-like
54	d2fk8a1	Alignment	not modelled	6.5	15	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**Mycolic acid cyclopropane synthase
55	c3vjzB_	Alignment	not modelled	6.5	21	**PDB header:**gene regulation **Chain:** B: **PDB Molecule:**putative uncharacterized protein; **PDBTitle:** crystal structure of the dna mimic protein dmp19
56	c2pbfA_	Alignment	not modelled	6.3	21	**PDB header:**transferase **Chain:** A: **PDB Molecule:**protein-l-isoaspartate o-methyltransferase beta-aspartate **PDBTitle:** crystal structure of a putative protein-l-isoaspartate o-2 methyltransferase beta-aspartate methyltransferase (pcmt) from3 plasmodium falciparum in complex with s-adenosyl-l-homocysteine
57	c1mjeB_	Alignment	not modelled	6.2	46	**PDB header:**gene regulation/antitumor protein/dna **Chain:** B: **PDB Molecule:**deleted in split hand/split foot protein 1; **PDBTitle:** structure of a brca2-dss1-ssdna complex
58	c2ahmG_	Alignment	not modelled	6.2	20	**PDB header:**viral protein, replication **Chain:** G: **PDB Molecule:**replicase polyprotein 1ab, heavy chain; **PDBTitle:** crystal structure of sars-cov super complex of non-structural2 proteins: the hexadecamer
59	c4gitA_	Alignment	not modelled	6.2	35	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**lon protease; **PDBTitle:** crystal structure of alpha sub-domain of lon protease from2 brevibacillus thermoruber
60	d1yzha1	Alignment	not modelled	6.2	15	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**TrmB-like
61	c4dckA_	Alignment	not modelled	6.2	36	**PDB header:**transport protein/signaling protein **Chain:** A: **PDB Molecule:**sodium channel protein type 5 subunit alpha; **PDBTitle:** crystal structure of the c-terminus of voltage-gated sodium channel in2 complex with fgf13 and cam
62	c4rwzA_	Alignment	not modelled	6.1	19	**PDB header:**transferase **Chain:** A: **PDB Molecule:**putative rrna methyltransferase; **PDBTitle:** crystal structure of the antibiotic-resistance methyltransferase kmr
63	c2p7iB_	Alignment	not modelled	6.1	13	**PDB header:**transferase **Chain:** B: **PDB Molecule:**hypothetical protein; **PDBTitle:** crystal structure of a sam dependent methyl-transferase type 12 family2 protein (eca1738) from pectobacterium atrosepticum scri1043 at 1.74 a3 resolution
64	c5gjqY_	Alignment	not modelled	6.1	54	**PDB header:**hydrolase **Chain:** Y: **PDB Molecule:**26s proteasome complex subunit dss1; **PDBTitle:** structure of the human 26s proteasome bound to usp14-ubal
65	d2ifta1	Alignment	not modelled	6.0	18	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**YhhF-like
66	c3g5tA_	Alignment	not modelled	5.9	12	**PDB header:**transferase **Chain:** A: **PDB Molecule:**trans-aconitate 3-methyltransferase; **PDBTitle:** crystal structure of trans-aconitate 3-methyltransferase from yeast
67	c3p2kA_	Alignment	not modelled	5.8	11	**PDB header:**transferase **Chain:** A: **PDB Molecule:**16s rrna methylase; **PDBTitle:** structure of an antibiotic related methyltransferase
68	c5do0A_	Alignment	not modelled	5.8	24	**PDB header:**transferase **Chain:** A: **PDB Molecule:**protein lysine methyltransferase 1; **PDBTitle:** the structure of pkmt1 from rickettsia prowazekii
69	c2w6hG_	Alignment	not modelled	5.7	37	**PDB header:**hydrolase **Chain:** G: **PDB Molecule:**atp synthase subunit gamma, mitochondrial; **PDBTitle:** low resolution structures of bovine mitochondrial f1-atpase during2 controlled dehydration: hydration state 4a.
70	c2ozvA_	Alignment	not modelled	5.7	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**hypothetical protein atu0636; **PDBTitle:** crystal structure of a predicted o-methyltransferase, protein atu6362 from agrobacterium tumefaciens.
71	c1yb2A_	Alignment	not modelled	5.7	21	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein ta0852; **PDBTitle:** structure of a putative methyltransferase from thermoplasma2 acidophilum.
72	d1yb2a1	Alignment	not modelled	5.7	21	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**tRNA(1-methyladenosine) methyltransferase-like
73	c3d2lC_	Alignment	not modelled	5.6	11	**PDB header:**transferase **Chain:** C: **PDB Molecule:**sam-dependent methyltransferase; **PDBTitle:** crystal structure of sam-dependent methyltransferase (zp_00538691.1)2 from exiguobacterium sp. 255-15 at 1.90 a resolution
74	c3sm3A_	Alignment	not modelled	5.6	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**sam-dependent methyltransferases; **PDBTitle:** crystal structure of sam-dependent methyltransferases q8puk2_metma2 from methanosarcina mazei. northeast structural genomics consortium3 target mar262.
75	c6djyD_	Alignment	not modelled	5.5	25	**PDB header:**virus **Chain:** D: **PDB Molecule:**turret protein; **PDBTitle:** fako virus
76	c6daeC_	Alignment	not modelled	5.5	40	**PDB header:**calcium binding protein/membrane protein **Chain:** C: **PDB Molecule:**voltage-dependent l-type calcium channel subunit alpha-1c; **PDBTitle:** 2.0 angstrom crystal structure of the d95v ca/cam:cav1.2 iq domain2 complex
77	d1qyra_	Alignment	not modelled	5.5	23	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases

						Family:rRNA adenine dimethylase-like
78	c2ns5A_	Alignment	not modelled	5.4	55	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**partitioning-defective 3 homolog; **PDBTitle:** the conserved n-terminal domain of par-3 adopts a novel pb1-2 like structure required for par-3 oligomerization and3 apical membrane localization
79	c2m4gA_	Alignment	not modelled	5.3	86	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**murine norovirus vpg protein; **PDBTitle:** solution structure of the core domain (11-85) of the murine norovirus2 vpg protein
80	c2bj3D_	Alignment	not modelled	5.3	19	**PDB header:**transcription **Chain:** D: **PDB Molecule:**nickel responsive regulator; **PDBTitle:** nikr-apo
81	c3gdhC_	Alignment	not modelled	5.2	29	**PDB header:**transferase **Chain:** C: **PDB Molecule:**trimethylguanosine synthase homolog; **PDBTitle:** methyltransferase domain of human trimethylguanosine synthase 1 (tgs1)2 bound to m7gtp and adenosyl-homocysteine (active form)
82	c3fmtF_	Alignment	not modelled	5.2	67	**PDB header:**replication inhibitor/dna **Chain:** F: **PDB Molecule:**protein seqa; **PDBTitle:** crystal structure of seqa bound to dna
83	c4fsxB_	Alignment	not modelled	5.1	19	**PDB header:**transferase **Chain:** B: **PDB Molecule:**dna (cytosine-5)-methyltransferase 1; **PDBTitle:** crystal structure of se-substituted zea mays zmet2 in complex with sah
84	c2be6F_	Alignment	not modelled	5.1	40	**PDB header:**membrane protein **Chain:** F: **PDB Molecule:**voltage-dependent l-type calcium channel alpha-1c subunit; **PDBTitle:** 2.0 a crystal structure of the cav1.2 iq domain-ca/cam complex