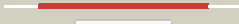
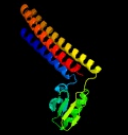


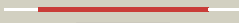
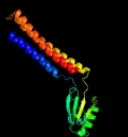



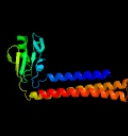

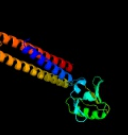



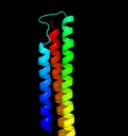





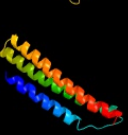
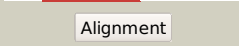





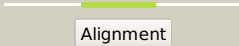

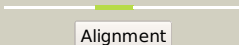
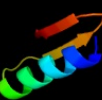
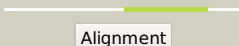

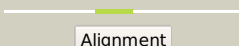
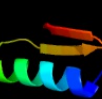
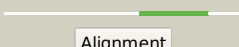

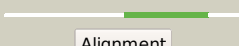
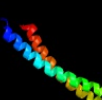
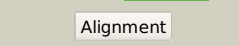
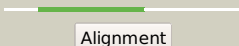
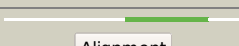

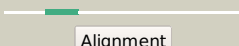
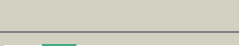



Phyre2

Email: mdejesus@rockefeller.edu
 Description: RVBD2882c_(frr)_3191654_3192211
 Date: Thu Aug 8 16:20:03 BST 2019
 Unique Job ID: 4d1a6d3ba00fc6c4

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1is1a_	 Alignment		100.0	44	Fold: RRF/tRNA synthetase additional domain-like Superfamily: Ribosome recycling factor, RRF Family: Ribosome recycling factor, RRF
2	c4gfqA_	 Alignment		100.0	50	PDB header: translation Chain: A: PDB Molecule: ribosome-recycling factor; PDBTitle: 2.65 angstrom resolution crystal structure of ribosome recycling2 factor (frr) from bacillus anthracis
3	d1ek8a_	 Alignment		100.0	40	Fold: RRF/tRNA synthetase additional domain-like Superfamily: Ribosome recycling factor, RRF Family: Ribosome recycling factor, RRF
4	d1wqga1	 Alignment		100.0	100	Fold: RRF/tRNA synthetase additional domain-like Superfamily: Ribosome recycling factor, RRF Family: Ribosome recycling factor, RRF
5	d1eh1a_	 Alignment		100.0	40	Fold: RRF/tRNA synthetase additional domain-like Superfamily: Ribosome recycling factor, RRF Family: Ribosome recycling factor, RRF
6	d1dd5a_	 Alignment		100.0	40	Fold: RRF/tRNA synthetase additional domain-like Superfamily: Ribosome recycling factor, RRF Family: Ribosome recycling factor, RRF
7	d1qe9a_	 Alignment		100.0	42	Fold: RRF/tRNA synthetase additional domain-like Superfamily: Ribosome recycling factor, RRF Family: Ribosome recycling factor, RRF
8	c3lf9A_	 Alignment		100.0	44	PDB header: immune system Chain: A: PDB Molecule: 4e10_d0_lis1a_001_c (t161); PDBTitle: crystal structure of hiv epitope-scaffold 4e10_d0_lis1a_001_c
9	c4l8iA_	 Alignment		100.0	16	PDB header: immune system Chain: A: PDB Molecule: rsv epitope scaffold ffl_005; PDBTitle: crystal structure of rsv epitope scaffold ffl_005
10	c1y698_	 Alignment		99.9	27	PDB header: ribosome Chain: 8: PDB Molecule: ribosome-recycling factor; PDB Fragment: unp residues 1-30 and 106-185; PDBTitle: rrf domain i in complex with the 50s ribosomal subunit from2 deinococcus radiodurans
11	c5mlc9_	 Alignment		99.9	34	PDB header: ribosome Chain: 9: PDB Molecule: ribosome-recycling factor, chloroplastic; PDBTitle: cryo-em structure of the spinach chloroplast ribosome reveals the2 location of plastid-specific ribosomal proteins and extensions

12	d1wiha_	 Alignment		99.9	25	Fold: RRF/tRNA synthetase additional domain-like Superfamily: Ribosome recycling factor, RRF Family: Ribosome recycling factor, RRF
13	c5wp3B_	 Alignment		97.8	38	PDB header: gene regulation Chain: B: PDB Molecule: eb22; PDBTitle: crystal structure of eed in complex with eb22
14	c4jlrS_	 Alignment		77.4	21	PDB header: immune system Chain: S: PDB Molecule: rsv_1isea designed scaffold; PDBTitle: crystal structure of a designed respiratory syncytial virus immunogen2 in complex with motavizumab
15	c2rrnA_	 Alignment		67.0	15	PDB header: protein transport Chain: A: PDB Molecule: probable secdf protein-export membrane protein; PDBTitle: solution structure of secdf periplasmic domain p4
16	d1in0a2	 Alignment		66.7	23	Fold: Ferredoxin-like Superfamily: YajQ-like Family: YajQ-like
17	c2c1nA_	 Alignment		65.5	14	PDB header: signaling protein Chain: A: PDB Molecule: 14-3-3 protein zeta/delta; PDBTitle: molecular basis for the recognition of phosphorylated and2 phosphoacetylated histone h3 by 14-3-3
18	c1in0B_	 Alignment		60.0	23	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: yajq protein; PDBTitle: yajq protein (hi1034)
19	c3tufA_	 Alignment		55.4	22	PDB header: signaling protein Chain: A: PDB Molecule: stage iii sporulation protein ah; PDBTitle: structure of the spoiiq-spoiiiah pore forming complex.
20	c2npmB_	 Alignment		54.5	19	PDB header: protein binding Chain: B: PDB Molecule: 14-3-3 domain containing protein; PDBTitle: crystal structure of cryptosporidium parvum 14-3-3 protein in complex2 with peptide
21	d1o9da_	 Alignment	not modelled	54.1	21	Fold: alpha-alpha superhelix Superfamily: 14-3-3 protein Family: 14-3-3 protein
22	c5b7wB_	 Alignment	not modelled	52.1	17	PDB header: unknown function Chain: B: PDB Molecule: upf0234 protein xc_3703; PDBTitle: crystal structure of the yajq-family protein xc_3703 from xanthomonas2 campestris pv.campestris
23	d2o8pa1	 Alignment	not modelled	51.5	16	Fold: alpha-alpha superhelix Superfamily: 14-3-3 protein Family: 14-3-3 protein
24	c3uz0A_	 Alignment	not modelled	51.0	22	PDB header: transport protein Chain: A: PDB Molecule: stage iii sporulation protein ah; PDBTitle: crystal structure of spoiiiah and spoiiq complex
25	d1iwga5	 Alignment	not modelled	49.4	19	Fold: Multidrug efflux transporter AcrB TolC docking domain; DN and DC subdomains Superfamily: Multidrug efflux transporter AcrB TolC docking domain; DN and DC subdomains Family: Multidrug efflux transporter AcrB TolC docking domain; DN and DC subdomains
26	c5ensA_	 Alignment	not modelled	49.1	18	PDB header: transport protein Chain: A: PDB Molecule: multidrug efflux pump subunit acrb,multidrug efflux pump PDBTitle: rhodamine bound structure of bacterial efflux pump.
27	d1iwga6	 Alignment	not modelled	47.0	16	Fold: Multidrug efflux transporter AcrB TolC docking domain; DN and DC subdomains Superfamily: Multidrug efflux transporter AcrB TolC docking domain; DN and DC subdomains Family: Multidrug efflux transporter AcrB TolC docking domain; DN and DC subdomains PDB header: de novo protein

28	c2k18A_	Alignment	not modelled	46.0	24	Chain: A; PDB Molecule: or15; PDBTitle: solution nmr structure of de novo designed ferredoxin-like fold2 protein, northeast structural genomics consortium target or15
29	c3m20A_	Alignment	not modelled	45.1	25	PDB header: isomerase Chain: A; PDB Molecule: 4-oxalocrotonate tautomerase, putative; PDBTitle: crystal structure of dmpi from archaeoglobus fulgidus determined to 2.37 angstroms resolution
30	c3ff5B_	Alignment	not modelled	43.2	19	PDB header: protein transport Chain: B; PDB Molecule: peroxisomal biogenesis factor 14; PDBTitle: crystal structure of the conserved n-terminal domain of the 2 peroxisomal matrix-protein-import receptor, pex14p
31	d2o02a1	Alignment	not modelled	40.8	15	Fold: alpha-alpha superhelix Superfamily: 14-3-3 protein Family: 14-3-3 protein
32	c3htkA_	Alignment	not modelled	39.7	23	PDB header: recombination/replication/ligase Chain: A; PDB Molecule: structural maintenance of chromosomes protein 5; PDBTitle: crystal structure of mms21 and smc5 complex
33	c5k1rB_	Alignment	not modelled	38.2	12	PDB header: lyase Chain: B; PDB Molecule: burkholderia pseudomallei sphingosine-1-phosphate lyase PDBTitle: structure of burkholderia pseudomallei k96243 sphingosine-1-phosphate2 lyase bpss2021
34	c1j1dF_	Alignment	not modelled	36.3	20	PDB header: contractile protein Chain: F; PDB Molecule: troponin i; PDBTitle: crystal structure of the 46kda domain of human cardiac2 troponin in the ca2+ saturated form
35	c6miwA_	Alignment	not modelled	36.1	18	PDB header: ligase Chain: A; PDB Molecule: e3 ubiquitin-protein ligase huwe1; PDBTitle: wwe domain of human huwe1
36	c3mafB_	Alignment	not modelled	33.0	9	PDB header: lyase Chain: B; PDB Molecule: sphingosine-1-phosphate lyase; PDBTitle: crystal structure of stsp1 (asymmetric form)
37	c4ovpB_	Alignment	not modelled	32.4	8	PDB header: solute-binding protein Chain: B; PDB Molecule: c4-dicarboxylate transport system substrate-binding PDBTitle: crystal structure of a trap periplasmic solute binding protein from 2 sulfitebacter sp. nas-14.1, target efi-510292, with bound alpha-d-3 manuronate
38	d1zh5a1	Alignment	not modelled	32.1	29	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: La domain
39	c5tw9D_	Alignment	not modelled	31.6	14	PDB header: lipid-binding protein Chain: D; PDB Molecule: iron uptake system component efeo; PDBTitle: 1.50 angstrom crystal structure of c-terminal fragment (residues 322-2 384) of iron uptake system component efeo from yersinia pestis.
40	d1vcsa1	Alignment	not modelled	29.7	25	Fold: STAT-like Superfamily: t-snare proteins Family: t-snare proteins
41	c3gasA_	Alignment	not modelled	28.4	6	PDB header: oxidoreductase Chain: A; PDB Molecule: heme oxygenase; PDBTitle: crystal structure of helicobacter pylori heme oxygenase hugz2 in complex with heme
42	c1j1eF_	Alignment	not modelled	27.9	21	PDB header: contractile protein Chain: F; PDB Molecule: troponin i; PDBTitle: crystal structure of the 52kda domain of human cardiac2 troponin in the ca2+ saturated form
43	d1zj8a1	Alignment	not modelled	27.4	17	Fold: Ferredoxin-like Superfamily: Nitrite/Sulfite reductase N-terminal domain-like Family: Duplicated SiR/NiR-like domains 1 and 3
44	c4o94B_	Alignment	not modelled	26.2	8	PDB header: transport protein Chain: B; PDB Molecule: trap dicarboxylate transporter dctp subunit; PDBTitle: crystal structure of a trap periplasmic solute binding protein from 2 rhodopseudomonas palustris haa2 (rpb_3329), target efi-510223, with 3 bound succinate
45	c4dl0J_	Alignment	not modelled	24.9	32	PDB header: hydrolase Chain: J; PDB Molecule: v-type proton atpase subunit e; PDBTitle: crystal structure of the heterotrimeric egchead peripheral stalk2 complex of the yeast vacuolar atpase
46	d1tz9a_	Alignment	not modelled	24.9	10	Fold: TIM beta/alpha-barrel Superfamily: Xylose isomerase-like Family: UxuA-like
47	c2k14A_	Alignment	not modelled	24.7	6	PDB header: unknown function Chain: A; PDB Molecule: yuaf protein; PDBTitle: solution structure of the soluble domain of the nfd2 protein yuaf from bacillus subtilis
48	d1lp1b_	Alignment	not modelled	24.6	30	Fold: immunoglobulin/albumin-binding domain-like Superfamily: Bacterial immunoglobulin/albumin-binding domains Family: Immunoglobulin-binding protein A modules
49	d1fc2c_	Alignment	not modelled	24.1	30	Fold: immunoglobulin/albumin-binding domain-like Superfamily: Bacterial immunoglobulin/albumin-binding domains Family: Immunoglobulin-binding protein A modules
50	c5j2lB_	Alignment	not modelled	23.6	30	PDB header: de novo protein Chain: B; PDB Molecule: protein design 2l4hc2_11; PDBTitle: de novo design of protein homo-oligomers with modular hydrogen bond2 network-mediated specificity
51	c3bdkB_	Alignment	not modelled	23.6	16	PDB header: lyase Chain: B; PDB Molecule: d-mannonate dehydratase; PDBTitle: crystal structure of streptococcus suis mannonate2 dehydratase complexed with substrate analogue
52	d2arza1	Alignment	not modelled	23.1	22	Fold: Split barrel-like Superfamily: FMN-binding split barrel Family: PNP-oxidase like PDB header: solute-binding protein

53	c4pfrA	Alignment	not modelled	22.5	10	Chain: A: PDB Molecule: trap dicarboxylate transporter, dctp subunit; PDBTitle: crystal structure of a trap periplasmic solute binding protein from2 rhodobacter sphaeroides (rsph17029_3541, target efi-510203), apo open3 partially disordered
54	d1deeg	Alignment	not modelled	22.4	15	Fold: immunoglobulin/albumin-binding domain-like Superfamily: Bacterial immunoglobulin/albumin-binding domains Family: Immunoglobulin-binding protein A modules
55	c4npyF	Alignment	not modelled	21.9	32	PDB header: protein binding Chain: Y: PDB Molecule: immunoglobulin g-binding protein a; PDBTitle: high-resolution structure of two tandem b domains of staphylococcal2 protein a connected by the conserved linker
56	c1kmiZ	Alignment	not modelled	21.4	18	PDB header: signaling protein Chain: Z: PDB Molecule: chemotaxis protein chez; PDBTitle: crystal structure of an e.coli chemotaxis protein, chez
57	d2jwda1	Alignment	not modelled	20.9	18	Fold: immunoglobulin/albumin-binding domain-like Superfamily: Bacterial immunoglobulin/albumin-binding domains Family: Immunoglobulin-binding protein A modules
58	c3onjA	Alignment	not modelled	20.3	21	PDB header: protein transport Chain: A: PDB Molecule: t-snare vti1; PDBTitle: crystal structure of yeast vti1p_habc domain
59	c1zdbA	Alignment	not modelled	19.8	32	PDB header: igg binding domain Chain: A: PDB Molecule: mini protein a domain, z38; PDBTitle: phage-selected mini protein a domain, z38, nmr, minimized2 mean structure
60	c2pfzA	Alignment	not modelled	18.4	8	PDB header: transport protein Chain: A: PDB Molecule: putative exported protein; PDBTitle: crystal structure of dctp6, a bordetella pertussis2 extracytoplasmic solute receptor binding pyroglutamic acid
61	c4eacC	Alignment	not modelled	18.4	10	PDB header: lyase Chain: C: PDB Molecule: mannonate dehydratase; PDBTitle: crystal structure of mannonate dehydratase from escherichia coli2 strain k12
62	c1j1eC	Alignment	not modelled	18.0	19	PDB header: contractile protein Chain: C: PDB Molecule: troponin i; PDBTitle: crystal structure of the 52kda domain of human cardiac2 troponin in the ca2+ saturated form
63	c3mc6C	Alignment	not modelled	17.9	12	PDB header: lyase Chain: C: PDB Molecule: sphingosine-1-phosphate lyase; PDBTitle: crystal structure of scdpl1
64	c2i9zB	Alignment	not modelled	17.6	29	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: putative septation protein spovg; PDBTitle: structural genomics, the crystal structure of full-length spovg from2 staphylococcus epidermidis atcc 12228
65	d2i9xa1	Alignment	not modelled	17.6	29	Fold: SpoVG-like Superfamily: SpoVG-like Family: SpoVG-like
66	c2b9bA	Alignment	not modelled	17.4	20	PDB header: viral protein Chain: A: PDB Molecule: fusion glycoprotein f0; PDBTitle: structure of the parainfluenza virus 5 f protein in its metastable,2 pre-fusion conformation
67	c4hhuA	Alignment	not modelled	17.2	23	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: or280; PDBTitle: crystal structure of engineered protein. northeast structural genomics2 consortium target or280.
68	d2dexx2	Alignment	not modelled	16.8	43	Fold: Cupredoxin-like Superfamily: Cupredoxins Family: Peptidylarginine deiminase Pad4, N-terminal domain
69	d2fqma1	Alignment	not modelled	16.7	26	Fold: Phosphoprotein oligomerization domain-like Superfamily: Phosphoprotein oligomerization domain-like Family: Phosphoprotein oligomerization domain-like
70	c2v8sv	Alignment	not modelled	15.2	24	PDB header: protein transport Chain: V: PDB Molecule: vesicle transport through interaction with PDBTitle: vti1b habc domain - epsinr enth domain complex
71	d2f23a1	Alignment	not modelled	15.0	15	Fold: Long alpha-hairpin Superfamily: GreA transcript cleavage protein, N-terminal domain Family: GreA transcript cleavage protein, N-terminal domain
72	c4ovsB	Alignment	not modelled	14.6	10	PDB header: solute-binding protein Chain: B: PDB Molecule: trap dicarboxylate transporter, dctp subunit; PDBTitle: crystal structure of a trap periplasmic solute binding protein from2 sulfurospirillum deleyianum dsm 6946 (sdel_0447), target efi-510309,3 with bound succinate
73	c2pfyA	Alignment	not modelled	14.5	11	PDB header: transport protein Chain: A: PDB Molecule: putative exported protein; PDBTitle: crystal structure of dctp7, a bordetella pertussis2 extracytoplasmic solute receptor binding pyroglutamic acid
74	c3b50A	Alignment	not modelled	14.5	6	PDB header: transport protein Chain: A: PDB Molecule: sialic acid-binding periplasmic protein siap; PDBTitle: structure of h. influenzae sialic acid binding protein2 bound to neu5ac.
75	c2etnA	Alignment	not modelled	14.0	17	PDB header: transcription Chain: A: PDB Molecule: anti-cleavage anti-grea transcription factor PDBTitle: crystal structure of thermus aquaticus gfh1
76	c3fkka	Alignment	not modelled	13.9	26	PDB header: lyase Chain: A: PDB Molecule: l-2-keto-3-deoxyarabonate dehydratase; PDBTitle: structure of l-2-keto-3-deoxyarabonate dehydratase
77	c4ovtA	Alignment	not modelled	13.3	14	PDB header: solute-binding protein Chain: A: PDB Molecule: trap dicarboxylate transporter, dctp subunit; PDBTitle: crystal structure of a trap periplasmic solute binding protein from2 ochrobacterium anthropi (oant_3902), target efi-510153, with bound l-3 fuconate PDB header: transport

78	c2vpnB_	Alignment	not modelled	13.2	11	Chain: B: PDB Molecule: periplasmic substrate binding protein; PDBTitle: high-resolution structure of the periplasmic ectoine-2 binding protein from teaabc trap-transporter of halomonas3 elongata
79	d1whra_	Alignment	not modelled	13.1	27	Fold: IF3-like Superfamily: R3H domain Family: R3H domain
80	c5ui3C_	Alignment	not modelled	13.1	14	PDB header: lyase Chain: C: PDB Molecule: dihydrodipicolinate synthase; PDBTitle: crystal structure of dhds from chlamydomonas reinhardtii
81	d2dula1	Alignment	not modelled	13.0	14	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: TRM1-like
82	c3f9tB_	Alignment	not modelled	12.8	14	PDB header: lyase Chain: B: PDB Molecule: l-tyrosine decarboxylase mfna; PDBTitle: crystal structure of l-tyrosine decarboxylase mfna (ec 4.1.1.25)2 (np_247014.1) from methanococcus jannaschii at 2.11 a resolution
83	c3gyyC_	Alignment	not modelled	12.8	10	PDB header: transport protein Chain: C: PDB Molecule: periplasmic substrate binding protein; PDBTitle: the ectoine binding protein of the teaabc trap transporter teaa in the2 apo-state
84	c3nqbB_	Alignment	not modelled	12.7	11	PDB header: hydrolase Chain: B: PDB Molecule: adenine deaminase 2; PDBTitle: crystal structure of adenine deaminase from agrobacterium tumefaciens2 (str. c 58)
85	d2qsba1	Alignment	not modelled	12.4	26	Fold: Bromodomain-like Superfamily: Ta0600-like Family: Ta0600-like
86	c3b4uB_	Alignment	not modelled	12.2	14	PDB header: lyase Chain: B: PDB Molecule: dihydrodipicolinate synthase; PDBTitle: crystal structure of dihydrodipicolinate synthase from agrobacterium2 tumefaciens str. c58
87	c2m5wA_	Alignment	not modelled	12.1	29	PDB header: rna binding protein Chain: A: PDB Molecule: lupus la protein; PDBTitle: nmr solution structure of the la motif (n-terminal domain, ntd) of2 dictyostelium discoideum la protein
88	d2i52a1	Alignment	not modelled	12.0	19	Fold: MK0786-like Superfamily: MK0786-like Family: MK0786-like
89	c2l5gB_	Alignment	not modelled	11.8	24	PDB header: transcription regulator Chain: B: PDB Molecule: putative uncharacterized protein ncor2; PDBTitle: co-ordinates and 1h, 13c and 15n chemical shift assignments for the2 complex of gps2 53-90 and smrt 167-207
90	c4nq8B_	Alignment	not modelled	11.7	14	PDB header: protein transport Chain: B: PDB Molecule: putative periplasmic substrate-binding transport protein; PDBTitle: crystal structure of a trap periplasmic solute binding protein from2 bordetella bronchiseptica (bb3421), target efi-510039, with density3 modeled as pantoate
91	c1x4rA_	Alignment	not modelled	11.6	10	PDB header: apoptosis Chain: A: PDB Molecule: parp14 protein; PDBTitle: solution structure of wwe domain in parp14 protein
92	d1lfup_	Alignment	not modelled	11.6	20	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Homeodomain
93	c4q6rB_	Alignment	not modelled	11.6	8	PDB header: lyase/lyase inhibitor Chain: B: PDB Molecule: sphingosine-1-phosphate lyase 1; PDBTitle: crystal structure of human sphingosine-1-phosphate lyase in complex2 with inhibitor 6-[(2r)-4-(4-benzyl-7-chlorophthalazin-1-yl)-2-3 methylpiperazin-1-yl]pyridine-3-carbonitrile
94	c4ng7A_	Alignment	not modelled	11.3	14	PDB header: transport protein Chain: A: PDB Molecule: trap periplasmic solute binding protein; PDBTitle: crystal structure of a trap periplasmic solute binding protein from2 citrobacter koseri (cko_04899), target efi-510094, apo, open3 structure
95	c4r86B_	Alignment	not modelled	11.3	19	PDB header: protein transport Chain: B: PDB Molecule: rnd family aminoglycoside/multidrug efflux pump; PDBTitle: crystal structure of aminoglycoside/multidrug efflux system acrd from2 salmonella typhimurium
96	d2ieca1	Alignment	not modelled	11.1	16	Fold: MK0786-like Superfamily: MK0786-like Family: MK0786-like
97	c3fxbB_	Alignment	not modelled	11.0	6	PDB header: transport protein Chain: B: PDB Molecule: trap dicarboxylate transporter, dctp subunit; PDBTitle: crystal structure of the ectoine-binding protein ueha
98	d1y13a_	Alignment	not modelled	10.8	21	Fold: T-fold Superfamily: Tetrahydrobiopterin biosynthesis enzymes-like Family: 6-pyruvoyl tetrahydropterin synthase
99	c3axtA_	Alignment	not modelled	10.8	13	PDB header: transferase Chain: A: PDB Molecule: probable n(2),n(2)-dimethylguanosine trna methyltransferase PDBTitle: complex structure of trna methyltransferase trm1 from aquifex aeolicus2 with s-adenosyl-l-methionine