




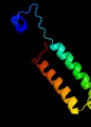



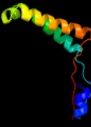



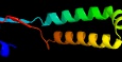



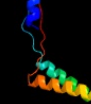




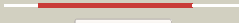
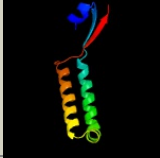
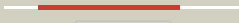
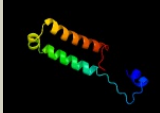



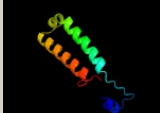



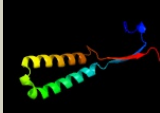
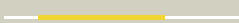
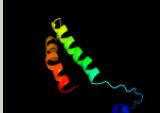




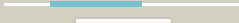
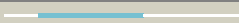
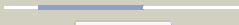
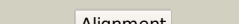


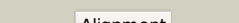



Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0521 (-) _612601_612906
Date	Fri Jul 26 01:50:07 BST 2019
Unique Job ID	0272d234f1b2969e

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d2o57a1	 Alignment		98.8	30	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: Mycolic acid cyclopropane synthase
2	c5gm2E_	 Alignment		97.3	21	PDB header: transferase Chain: E: PDB Molecule: o-methyltransferase; PDBTitle: crystal structure of methyltransferase tled complexed with sah and2 teleocidin a1
3	c5wp5A_	 Alignment		97.0	19	PDB header: transferase Chain: A: PDB Molecule: phosphomethylethanolamine n-methyltransferase 2; PDBTitle: arabidopsis thaliana phosphoethanolamine n-methyltransferase 22 (atpmt2) in complex with sah
4	c4iv0B_	 Alignment		96.9	11	PDB header: transferase Chain: B: PDB Molecule: phosphoethanolamine n-methyltransferase, putative; PDBTitle: crystal structure of n-methyl transferase from plasmodium vivax2 complexed with s-adenosyl methionine and phosphate
5	c2fk8A_	 Alignment		96.8	14	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
6	d1tpya_	 Alignment		96.2	17	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: Mycolic acid cyclopropane synthase
7	d1kpga_	 Alignment		95.5	21	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: Mycolic acid cyclopropane synthase
8	c3busB_	 Alignment		95.4	18	PDB header: transferase Chain: B: PDB Molecule: methyltransferase; PDBTitle: crystal structure of rebm
9	d2fk8a1	 Alignment		95.3	14	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: Mycolic acid cyclopropane synthase
10	d1llea_	 Alignment		94.8	21	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: Mycolic acid cyclopropane synthase
11	c4krhB_	 Alignment		93.5	18	PDB header: transferase Chain: B: PDB Molecule: phosphoethanolamine n-methyltransferase 2; PDBTitle: semet haemonchus contortus phosphoethanolamine n-methyltransferase 22 in complex with s-adenosyl-l-methionine

12	d1kpia_	 Alignment		93.1	16	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: Mycolic acid cyclopropane synthase
13	c4ineB_	 Alignment		93.0	14	PDB header: transferase Chain: B: PDB Molecule: protein pmt-2; PDBTitle: crystal structure of n-methyl transferase (pmt-2) from caenorhabditis2 elegant complexed with s-adenosyl homocysteine and3 phosphoethanolamine
14	c5z9oA_	 Alignment		92.7	18	PDB header: transferase Chain: A: PDB Molecule: cyclopropane-fatty-acyl-phospholipid synthase; PDBTitle: the crystal structure of cyclopropane-fatty-acyl-phospholipid synthase2 from lactobacillus acidophilus
15	c3ujcA_	 Alignment		92.3	14	PDB header: transferase Chain: A: PDB Molecule: phosphoethanolamine n-methyltransferase; PDBTitle: phosphoethanolamine methyltransferase mutant (h132a) from plasmodium2 falciparum in complex with phosphocholine
16	c4pneA_	 Alignment		89.4	24	PDB header: biosynthetic protein Chain: A: PDB Molecule: methyltransferase-like protein; PDBTitle: crystal structure of the [4+2]-cyclase spnf
17	c6bqcA_	 Alignment		78.5	14	PDB header: transferase Chain: A: PDB Molecule: cyclopropane-fatty-acyl-phospholipid synthase; PDBTitle: cyclopropane fatty acid synthase from e. coli
18	d1nkva_	 Alignment		75.7	19	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: Hypothetical Protein Yjhp
19	d1q08a_	 Alignment		43.4	21	Fold: Putative DNA-binding domain Superfamily: Putative DNA-binding domain Family: DNA-binding N-terminal domain of transcription activators
20	c2rq5A_	 Alignment		34.5	17	PDB header: transcription Chain: A: PDB Molecule: protein jumonji; PDBTitle: solution structure of the at-rich interaction domain (arid)2 of jumonji/jarid2
21	c6nuwG_	 Alignment	not modelled	33.0	13	PDB header: cell cycle Chain: G: PDB Molecule: inner kinetochore subunit nkp1; PDBTitle: yeast ctf19 complex
22	c1ye9E_	 Alignment	not modelled	32.1	17	PDB header: oxidoreductase Chain: E: PDB Molecule: catalase hpii; PDBTitle: crystal structure of proteolytically truncated catalase2 hpii from e. coli
23	c2jrza_	 Alignment	not modelled	29.3	18	PDB header: oxidoreductase Chain: A: PDB Molecule: histone demethylase jarid1c; PDBTitle: solution structure of the bright/arid domain from the human2 jarid1c protein.
24	c4p47A_	 Alignment	not modelled	28.3	15	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 ochrobactrum anthropi (oant_4429), target efi-510151, c-terminus bound3 in ligand binding pocket
25	c4qoqC_	 Alignment	not modelled	28.3	15	PDB header: oxidoreductase Chain: C: PDB Molecule: catalase; PDBTitle: structure of bacillus pumilus catalase with guaiacol bound
26	d1e93a_	 Alignment	not modelled	24.1	17	Fold: Heme-dependent catalase-like Superfamily: Heme-dependent catalase-like Family: Heme-dependent catalases
27	d1ig8a1	 Alignment	not modelled	22.9	13	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: Hexokinase
28	d1yoza1	 Alignment	not modelled	20.7	31	Fold: AF0941-like Superfamily: AF0941-like Family: AF0941-like

29	c1f4jC_	Alignment	not modelled	20.0	10	PDB header: oxidoreductase Chain: C: PDB Molecule: catalase; PDBTitle: structure of tetragonal crystals of human erythrocyte catalase
30	c4cabA_	Alignment	not modelled	19.4	23	PDB header: oxidoreductase Chain: A: PDB Molecule: catalase; PDBTitle: the refined structure of catalase dr1998 from deinococcus radiodurans2 at 2.6 a resolution
31	d1m7sa_	Alignment	not modelled	19.0	17	Fold: Heme-dependent catalase-like Superfamily: Heme-dependent catalase-like Family: Heme-dependent catalases
32	c3e4cB_	Alignment	not modelled	17.5	29	PDB header: hydrolase Chain: B: PDB Molecule: caspase-1; PDBTitle: procaspase-1 zymogen domain crystal strucutre
33	c3h11A_	Alignment	not modelled	17.0	30	PDB header: apoptosis Chain: A: PDB Molecule: casp8 and fadd-like apoptosis regulator; PDBTitle: zymogen caspase-8:c-flipl protease domain complex
34	d2io8a1	Alignment	not modelled	16.3	35	Fold: PreATP-grasp domain Superfamily: PreATP-grasp domain Family: Glutathionylspermidine synthase substrate-binding domain-like
35	d1dgfa_	Alignment	not modelled	16.2	10	Fold: Heme-dependent catalase-like Superfamily: Heme-dependent catalase-like Family: Heme-dependent catalases
36	c2xq1M_	Alignment	not modelled	15.7	24	PDB header: oxidoreductase Chain: M: PDB Molecule: peroxisomal catalase; PDBTitle: crystal structure of peroxisomal catalase from the yeast hansenula2 polymorpha
37	d2j78a1	Alignment	not modelled	15.7	26	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Family 1 of glycosyl hydrolase
38	d1uwsa_	Alignment	not modelled	15.4	29	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Family 1 of glycosyl hydrolase
39	c6g21B_	Alignment	not modelled	15.3	15	PDB header: hydrolase Chain: B: PDB Molecule: probable feruloyl esterase b-2; PDBTitle: crystal structure of an esterase from aspergillus oryzae
40	d1fp1d1	Alignment	not modelled	15.1	18	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Plant O-methyltransferase, N-terminal domain
41	c6c4rA_	Alignment	not modelled	14.7	24	PDB header: oxidoreductase Chain: A: PDB Molecule: staphylopine dehydrogenase; PDBTitle: staphylopine dehydrogenase (saodh) - apo
42	c1ig8A_	Alignment	not modelled	14.4	13	PDB header: transferase Chain: A: PDB Molecule: hexokinase pii; PDBTitle: crystal structure of yeast hexokinase pii with the correct2 amino acid sequence
43	c2wsiA_	Alignment	not modelled	14.4	15	PDB header: transferase Chain: A: PDB Molecule: fad synthetase; PDBTitle: crystal structure of yeast fad synthetase (fad1) in complex2 with fad
44	c4wwrB_	Alignment	not modelled	14.4	21	PDB header: transport protein Chain: B: PDB Molecule: ubiquitin-like protein 4a; PDBTitle: crystal structure of bag6-ubl4a dimerization domain
45	c1cp3B_	Alignment	not modelled	14.2	38	PDB header: hydrolase/hydrolase inhibitor Chain: B: PDB Molecule: apopain; PDBTitle: crystal structure of the complex of apopain with the tetrapeptide2 inhibitor ace-dvad-fmc
46	c2fp3A_	Alignment	not modelled	14.1	14	PDB header: hydrolysis/apoptosis Chain: A: PDB Molecule: caspase nc; PDBTitle: crystal structure of the drosophila initiator caspase dronc
47	d1gwea_	Alignment	not modelled	14.0	17	Fold: Heme-dependent catalase-like Superfamily: Heme-dependent catalase-like Family: Heme-dependent catalases
48	d1c20a_	Alignment	not modelled	14.0	15	Fold: DNA/RNA-binding 3-helical bundle Superfamily: ARID-like Family: ARID domain
49	c2yqeA_	Alignment	not modelled	13.6	28	PDB header: dna binding protein Chain: A: PDB Molecule: jumonji/arid domain-containing protein 1d; PDBTitle: solution structure of the arid domain of jarid1d protein
50	c4iyrB_	Alignment	not modelled	13.6	35	PDB header: hydrolase Chain: B: PDB Molecule: caspase-6; PDBTitle: crystal structure of full-length caspase-6 zymogen
51	c1kmcB_	Alignment	not modelled	13.4	24	PDB header: apoptosis/hydrolase Chain: B: PDB Molecule: caspase-7; PDBTitle: crystal structure of the caspase-7 / xiap-bir2 complex
52	c6fatA_	Alignment	not modelled	13.2	20	PDB header: hydrolase Chain: A: PDB Molecule: carboxylic ester hydrolase; PDBTitle: the crystal structure of a feruloyl esterase c from fusarium2 oxysporum.
53	d1q9ua_	Alignment	not modelled	13.1	29	Fold: TBP-like Superfamily: TT1751-like Family: TT1751-like
54	c4wwrD_	Alignment	not modelled	13.1	21	PDB header: transport protein Chain: D: PDB Molecule: ubiquitin-like protein 4a; PDBTitle: crystal structure of bag6-ubl4a dimerization domain
55	c1ysmA_	Alignment	not modelled	12.7	23	PDB header: metal binding protein Chain: A: PDB Molecule: calcyclin-binding protein; PDBTitle: nmr structure of n-terminal domain (residues 1-77) of siah-2 interacting protein.

56	d1ysma1	Alignment	not modelled	12.7	23	Fold: Long alpha-hairpin Superfamily: Calcyclin-binding protein-like Family: Siah interacting protein N terminal domain-like
57	d1si8a_	Alignment	not modelled	12.6	21	Fold: Heme-dependent catalase-like Superfamily: Heme-dependent catalase-like Family: Heme-dependent catalases
58	c1nmqB_	Alignment	not modelled	12.6	38	PDB header: apoptosis, hydrolase Chain: B: PDB Molecule: caspase-3; PDBTitle: extendend tethering: in situ assembly of inhibitors
59	d2d5ua1	Alignment	not modelled	12.5	16	Fold: PUG domain-like Superfamily: PUG domain-like Family: PUG domain
60	c4pakA_	Alignment	not modelled	12.5	22	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 verminephrobacter eiseniae ef01-2 (veis_3954, target efi-510324) a3 nephridial symbiont of the earthworm eisenia foetida, bound to (r)-4 pantoic acid
61	d1j3ma_	Alignment	not modelled	12.5	24	Fold: TBP-like Superfamily: TT1751-like Family: TT1751-like
62	d4blca_	Alignment	not modelled	12.2	13	Fold: Heme-dependent catalase-like Superfamily: Heme-dependent catalase-like Family: Heme-dependent catalases
63	d1m72a_	Alignment	not modelled	12.2	24	Fold: Caspase-like Superfamily: Caspase-like Family: Caspase catalytic domain
64	d1ig6a_	Alignment	not modelled	12.1	19	Fold: DNA/RNA-binding 3-helical bundle Superfamily: ARID-like Family: ARID domain
65	c5jftB_	Alignment	not modelled	12.1	19	PDB header: hydrolase/hydrolase inhibitor Chain: B: PDB Molecule: caspase 3, apoptosis-related cysteine protease a; PDBTitle: zebra fish caspase-3
66	c3wmtA_	Alignment	not modelled	12.0	18	PDB header: hydrolase Chain: A: PDB Molecule: probable feruloyl esterase b-1; PDBTitle: crystal structure of feruloyl esterase b from aspergillus oryzae
67	c4e1rA_	Alignment	not modelled	11.5	39	PDB header: dna binding protein Chain: A: PDB Molecule: protein lsr2; PDBTitle: crystal structure of the dimerization domain of lsr2 from2 mycobacterium tuberculosis in the p 31 2 1 space group
68	c4e1pA_	Alignment	not modelled	11.5	39	PDB header: dna binding protein Chain: A: PDB Molecule: protein lsr2; PDBTitle: crystal structure of the dimerization domain of lsr2 from2 mycobacterium tuberculosis in the p 1 21 1 space group
69	c3zey8_	Alignment	not modelled	11.4	46	PDB header: ribosome Chain: 8: PDB Molecule: ribosomal protein s29, putative; PDBTitle: high-resolution cryo-electron microscopy structure of the trypanosoma2 brucei ribosome
70	c3uoaB_	Alignment	not modelled	10.4	27	PDB header: hydrolase/hydrolase inhibitor Chain: B: PDB Molecule: mucosa-associated lymphoid tissue lymphoma translocation PDBTitle: crystal structure of the malt1 paracaspase (p21 form)
71	c2nn3D_	Alignment	not modelled	10.4	24	PDB header: hydrolase Chain: D: PDB Molecule: caspase-1; PDBTitle: structure of pro-sf-caspase-1
72	c4m9rB_	Alignment	not modelled	10.4	15	PDB header: hydrolase Chain: B: PDB Molecule: cell death protein 3; PDBTitle: crystal structure of ced-3
73	c5zigD_	Alignment	not modelled	10.3	26	PDB header: isomerase Chain: D: PDB Molecule: cellobiose 2-epimerase; PDBTitle: the structure of cellobiose 2-epimerase from spirochaeta thermophila2 dsm 6192
74	c4r27B_	Alignment	not modelled	10.3	26	PDB header: hydrolase Chain: B: PDB Molecule: glycoside hydrolase; PDBTitle: crystal structure of beta-glycosidase bgl167
75	d1czan1	Alignment	not modelled	10.1	12	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: Hexokinase
76	c1kmiZ_	Alignment	not modelled	10.1	24	PDB header: signaling protein Chain: Z: PDB Molecule: chemotaxis protein chez; PDBTitle: crystal structure of an e.coli chemotaxis protein, chez
77	c1cw5A_	Alignment	not modelled	10.0	19	PDB header: toxin Chain: A: PDB Molecule: type iia bacteriocin carnobacteriocin b2; PDBTitle: solution structure of carnobacteriocin b2
78	c3fxtB_	Alignment	not modelled	9.8	5	PDB header: gene regulation Chain: B: PDB Molecule: nucleoside diphosphate-linked moiety x motif 6; PDBTitle: crystal structure of the n-terminal domain of human nudt6
79	d1nw9b_	Alignment	not modelled	9.8	30	Fold: Caspase-like Superfamily: Caspase-like Family: Caspase catalytic domain
80	c3edqC_	Alignment	not modelled	9.7	38	PDB header: hydrolase/hydrolase inhibitor Chain: C: PDB Molecule: caspase-3; PDBTitle: crystal structure of caspase-3 with inhibitor ac-ldesd-cho
81	c2lm1A_	Alignment	not modelled	9.6	19	PDB header: dna binding protein Chain: A: PDB Molecule: lysine-specific demethylase lid; PDBTitle: solution nmr structure of lysine-specific demethylase lid from2 drosophila melanogaster, northeast structural genomics

				consortium3 target fr824d	
82	c2fipA_	Alignment	not modelled	9.6	24 PDB header: transcription Chain: A: PDB Molecule: late genes activator; PDBTitle: phage phi29 transcription regulator p4
83	d1f1ja_	Alignment	not modelled	9.5	24 Fold: Caspase-like Superfamily: Caspase-like Family: Caspase catalytic domain
84	c5vakA_	Alignment	not modelled	9.5	18 PDB header: signaling protein Chain: A: PDB Molecule: beta-klotho; PDBTitle: crystal structure of beta-klotho, domain 1
85	c2v7yA_	Alignment	not modelled	9.5	19 PDB header: chaperone Chain: A: PDB Molecule: chaperone protein dnak; PDBTitle: crystal structure of the molecular chaperone dnak from2 geobacillus kaustophilus hta426 in post-atp hydrolysis3 state
86	c3sipC_	Alignment	not modelled	9.4	24 PDB header: hydrolase/ligase/hydrolase Chain: C: PDB Molecule: caspase; PDBTitle: crystal structure of drice and diap1-bir1 complex
87	c2funB_	Alignment	not modelled	9.3	19 PDB header: apoptosis/hydrolase Chain: B: PDB Molecule: caspase-8; PDBTitle: alternative p35-caspase-8 complex
88	c6qgbA_	Alignment	not modelled	9.3	28 PDB header: hydrolase Chain: A: PDB Molecule: mono(2-hydroxyethyl) terephthalate hydrolase; PDBTitle: crystal structure of ideonella sakaiensis mhetase bound to benzoic2 acid
89	c2j2mD_	Alignment	not modelled	9.0	17 PDB header: oxidoreductase Chain: D: PDB Molecule: catalase; PDBTitle: crystal structure analysis of catalase from exiguobacterium2 oxidotolerans
90	d1bg3a1	Alignment	not modelled	8.9	12 Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: Hexokinase
91	c2wdpA_	Alignment	not modelled	8.9	33 PDB header: hydrolase Chain: A: PDB Molecule: caspase-6; PDBTitle: crystal structure of ligand free human caspase-6
92	cli51A_	Alignment	not modelled	8.9	24 PDB header: hydrolase/hydrolase inhibitor Chain: A: PDB Molecule: caspase-7 subunit p20; PDBTitle: crystal structure of caspase-7 complexed with xiap
93	c5u1dX_	Alignment	not modelled	8.8	28 PDB header: transport protein Chain: X: PDB Molecule: tap transporter inhibitor icp47; PDBTitle: cryo-em structure of the human tap atp-binding cassette transporter
94	d1x1ia1	Alignment	not modelled	8.6	12 Fold: alpha/alpha toroid Superfamily: Chondroitin AC/alginate lyase Family: Hyaluronate lyase-like catalytic, N-terminal domain
95	c2ql5A_	Alignment	not modelled	8.5	24 PDB header: hydrolase/hydrolase inhibitor Chain: A: PDB Molecule: caspase-7; PDBTitle: crystal structure of caspase-7 with inhibitor ac-dmqd-cho
96	c6axfG_	Alignment	not modelled	8.3	12 PDB header: protein binding Chain: G: PDB Molecule: ras guanyl-releasing protein 2; PDBTitle: structure of rasgrp2 in complex with rap1b
97	d1qwla_	Alignment	not modelled	8.2	17 Fold: Heme-dependent catalase-like Superfamily: Heme-dependent catalase-like Family: Heme-dependent catalases
98	c3p45l_	Alignment	not modelled	8.1	33 PDB header: hydrolase Chain: I: PDB Molecule: caspase-6; PDBTitle: crystal structure of apo-caspase-6 at physiological ph
99	c2jxjA_	Alignment	not modelled	7.9	22 PDB header: oxidoreductase Chain: A: PDB Molecule: histone demethylase jarid1a; PDBTitle: nmr structure of the arid domain from the histone h3k42 demethylase rbp2