



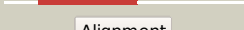

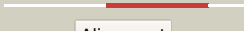

















Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2066_(cob)_2323183_2324709
Date	Mon Aug 5 13:25:18 BST 2019
Unique Job ID	875169cbbbb18639

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3nutC_	 Alignment		100.0	44	PDB header: transferase Chain: C: PDB Molecule: precorrin-3 methylase; PDBTitle: crystal structure of the methyltransferase cobj
2	c2zvba_	 Alignment		100.0	40	PDB header: transferase Chain: A: PDB Molecule: precorrin-3 c17-methyltransferase; PDBTitle: crystal structure of tt0207 from thermus thermophilus hb8
3	c2e0ka_	 Alignment		100.0	29	PDB header: transferase Chain: A: PDB Molecule: precorrin-2 c20-methyltransferase; PDBTitle: crystal structure of cbil, a methyltransferase involved in anaerobic2 vitamin b12 biosynthesis
4	c1pjtB_	 Alignment		100.0	22	PDB header: transferase/oxidoreductase/lyase Chain: B: PDB Molecule: siroheme synthase; PDBTitle: the structure of the ser128ala point-mutant variant of cysg, the2 multifunctional methyltransferase/dehydrogenase/ferrochelatae for3 siroheme synthesis
5	c2yboA_	 Alignment		100.0	22	PDB header: transferase Chain: A: PDB Molecule: methyltransferase; PDBTitle: the x-ray structure of the sam-dependent uroporphyrinogen2 iii methyltransferase nire from pseudomonas aeruginosa in3 complex with sah
6	c2qbaA_	 Alignment		100.0	33	PDB header: transferase Chain: A: PDB Molecule: precorrin-2 methyltransferase; PDBTitle: crystal structure of methanothermobacter thermautotrophicus cbil
7	d1s4da_	 Alignment		100.0	20	Fold: Tetrapyrrole methylase Superfamily: Tetrapyrrole methylase Family: Tetrapyrrole methylase
8	d1cbfa_	 Alignment		100.0	20	Fold: Tetrapyrrole methylase Superfamily: Tetrapyrrole methylase Family: Tetrapyrrole methylase
9	c1cbfA_	 Alignment		100.0	20	PDB header: methyltransferase Chain: A: PDB Molecule: cobalt-precorrin-4 transmethylase; PDBTitle: the x-ray structure of a cobalamin biosynthetic enzyme, cobalt2 precorrin-4 methyltransferase, cbif
10	d1pjqa2	 Alignment		100.0	23	Fold: Tetrapyrrole methylase Superfamily: Tetrapyrrole methylase Family: Tetrapyrrole methylase
11	c3kwpA_	 Alignment		100.0	16	PDB header: transferase Chain: A: PDB Molecule: predicted methyltransferase; PDBTitle: crystal structure of putative methyltransferase from lactobacillus2 brevis

12	c3ndcB_	Alignment		100.0	23	PDB header: transferase Chain: B: PDB Molecule: precorrin-4 c(11)-methyltransferase; PDBTitle: crystal structure of precorrin-4 c11-methyltransferase from2 rhodobacter capsulatus
13	c4e16A_	Alignment		100.0	17	PDB header: transferase Chain: A: PDB Molecule: precorrin-4 c(11)-methyltransferase; PDBTitle: precorrin-4 c(11)-methyltransferase from clostridium difficile
14	d1ve2a1	Alignment		100.0	26	Fold: Tetrapyrrole methylase Superfamily: Tetrapyrrole methylase Family: Tetrapyrrole methylase
15	d1va0a1	Alignment		100.0	26	Fold: Tetrapyrrole methylase Superfamily: Tetrapyrrole methylase Family: Tetrapyrrole methylase
16	c5hw4C_	Alignment		100.0	19	PDB header: transferase Chain: C: PDB Molecule: ribosomal rna small subunit methyltransferase i; PDBTitle: crystal structure of escherichia coli 16s rrna methyltransferase rsmi2 in complex with adomet
17	c3nd1B_	Alignment		100.0	22	PDB header: transferase Chain: B: PDB Molecule: precorrin-6a synthase/cobf protein; PDBTitle: crystal structure of precorrin-6a synthase from rhodobacter capsulatus
18	d1wyza1	Alignment		100.0	13	Fold: Tetrapyrrole methylase Superfamily: Tetrapyrrole methylase Family: Tetrapyrrole methylase
19	c2nnpA_	Alignment		100.0	18	PDB header: transferase Chain: A: PDB Molecule: putative cobalamin synthesis related protein; PDBTitle: crystal structure of putative cobalamin synthesis related protein2 (cobf) from corynebacterium diphtheriae
20	d2deka1	Alignment		100.0	18	Fold: Tetrapyrrole methylase Superfamily: Tetrapyrrole methylase Family: Tetrapyrrole methylase
21	c5n0sA_	Alignment	not modelled	100.0	16	PDB header: transferase Chain: A: PDB Molecule: peptide n-methyltransferase; PDBTitle: crystal structure of opha-deltac6 mutant y98a in complex with sam
22	d1vhva_	Alignment	not modelled	100.0	15	Fold: Tetrapyrrole methylase Superfamily: Tetrapyrrole methylase Family: Tetrapyrrole methylase
23	c3i4tA_	Alignment	not modelled	100.0	17	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: diphthine synthase; PDBTitle: crystal structure of putative diphthine synthase from entamoeba2 histolytica
24	d1wdea_	Alignment	not modelled	100.0	25	Fold: Tetrapyrrole methylase Superfamily: Tetrapyrrole methylase Family: Tetrapyrrole methylase
25	c2bb3B_	Alignment	not modelled	100.0	24	PDB header: transferase Chain: B: PDB Molecule: cobalamin biosynthesis precorrin-6y methylase (cbie); PDBTitle: crystal structure of cobalamin biosynthesis precorrin-6y methylase2 (cbie) from archaeoglobus fulgidus
26	d2bb3a1	Alignment	not modelled	100.0	25	Fold: Tetrapyrrole methylase Superfamily: Tetrapyrrole methylase Family: Tetrapyrrole methylase
27	c3hh1D_	Alignment	not modelled	99.9	21	PDB header: transferase Chain: D: PDB Molecule: tetrapyrrole methylase family protein; PDBTitle: the structure of a tetrapyrrole methylase family protein domain from2 chlorobium tepidum t1s
28	c3fq6A_	Alignment	not modelled	98.6	16	PDB header: transferase Chain: A: PDB Molecule: methyltransferase; PDBTitle: the crystal structure of a methyltransferase domain from bacteroides2 thetaiotaomicron vpi

29	c3vndD	Alignment	not modelled	93.6	16	PDB header: lyase Chain: D: PDB Molecule: tryptophan synthase alpha chain; PDBTitle: crystal structure of tryptophan synthase alpha-subunit from the2 psychrophile shewanella frigidimarina k14-2
30	c5ey5A	Alignment	not modelled	90.9	17	PDB header: lyase Chain: A: PDB Molecule: lbcats-a; PDBTitle: lbcats
31	c3navB	Alignment	not modelled	88.7	15	PDB header: lyase Chain: B: PDB Molecule: tryptophan synthase alpha chain; PDBTitle: crystal structure of an alpha subunit of tryptophan synthase from2 vibrio cholerae o1 biovar el tor str. n16961
32	c5kzmA	Alignment	not modelled	88.3	13	PDB header: lyase Chain: A: PDB Molecule: tryptophan synthase alpha chain; PDBTitle: crystal structure of tryptophan synthase alpha-beta chain complex from2 francisella tularensis
33	c2ekcA	Alignment	not modelled	79.4	12	PDB header: lyase Chain: A: PDB Molecule: tryptophan synthase alpha chain; PDBTitle: structural study of project id aq_1548 from aquifex aeolicus vf5
34	d1qopa	Alignment	not modelled	72.9	17	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Tryptophan biosynthesis enzymes
35	d1q7sa	Alignment	not modelled	72.0	28	Fold: Peptidyl-tRNA hydrolase II Superfamily: Peptidyl-tRNA hydrolase II Family: Peptidyl-tRNA hydrolase II
36	c2d3kA	Alignment	not modelled	70.2	24	PDB header: hydrolase Chain: A: PDB Molecule: peptidyl-trna hydrolase; PDBTitle: structural study on project id ph1539 from pyrococcus2 horikoshii ot3
37	d3erja1	Alignment	not modelled	63.5	21	Fold: Peptidyl-tRNA hydrolase II Superfamily: Peptidyl-tRNA hydrolase II Family: Peptidyl-tRNA hydrolase II
38	c4bucA	Alignment	not modelled	58.7	15	PDB header: ligase Chain: A: PDB Molecule: udp-n-acetylmuramoylalanine--d-glutamate ligase; PDBTitle: crystal structure of murd ligase from thermotoga maritima in apo form
39	c3zq4C	Alignment	not modelled	56.5	16	PDB header: hydrolase Chain: C: PDB Molecule: ribonuclease j 1; PDBTitle: unusual, dual endo- and exo-nuclease activity in the degradosome2 explained by crystal structure analysis of rnase j1
40	c3fpjA	Alignment	not modelled	56.1	13	PDB header: biosynthetic protein, transferase Chain: A: PDB Molecule: putative uncharacterized protein; PDBTitle: crystal structure of e81q mutant of mtas in complex with s-2 adenosylmethionine
41	c5k9xA	Alignment	not modelled	55.7	13	PDB header: lyase Chain: A: PDB Molecule: tryptophan synthase alpha chain; PDBTitle: crystal structure of tryptophan synthase alpha chain from legionella2 pneumophila subsp. pneumophila
42	c1xtyD	Alignment	not modelled	54.6	20	PDB header: hydrolase Chain: D: PDB Molecule: peptidyl-trna hydrolase; PDBTitle: crystal structure of sulfobolus solfataricus peptidyl-trna hydrolase
43	c6c4nB	Alignment	not modelled	53.3	18	PDB header: oxidoreductase Chain: B: PDB Molecule: pseudopaline dehydrogenase; PDBTitle: pseudopaline dehydrogenase (paodh) - nadp+ bound
44	c3b1fA	Alignment	not modelled	51.4	13	PDB header: oxidoreductase Chain: A: PDB Molecule: putative prephenate dehydrogenase; PDBTitle: crystal structure of prephenate dehydrogenase from streptococcus2 mutans
45	d2p1ra1	Alignment	not modelled	50.8	18	Fold: NAD kinase/diacylglycerol kinase-like Superfamily: NAD kinase/diacylglycerol kinase-like Family: Diacylglycerol kinase-like
46	c3k30B	Alignment	not modelled	46.9	14	PDB header: oxidoreductase Chain: B: PDB Molecule: histamine dehydrogenase; PDBTitle: histamine dehydrogenase from nocardioodes simplex
47	d2jfga2	Alignment	not modelled	46.1	15	Fold: MurD-like peptide ligases, peptide-binding domain Superfamily: MurD-like peptide ligases, peptide-binding domain Family: MurCDEF C-terminal domain
48	d1rlka	Alignment	not modelled	44.9	21	Fold: Peptidyl-tRNA hydrolase II Superfamily: Peptidyl-tRNA hydrolase II Family: Peptidyl-tRNA hydrolase II
49	c2a5hC	Alignment	not modelled	43.2	19	PDB header: isomerase Chain: C: PDB Molecule: l-lysine 2,3-aminomutase; PDBTitle: 2.1 angstrom x-ray crystal structure of lysine-2,3-aminomutase from2 clostridium subterminale sb4, with michaelis analog (l-alpha-lysine3 external aldimine form of pyridoxal-5'-phosphate).
50	c4txkA	Alignment	not modelled	40.3	20	PDB header: oxidoreductase Chain: A: PDB Molecule: protein-methionine sulfoxide oxidase mical1; PDBTitle: construct of mical-1 containing the monooxygenase and calponin2 homology domains
51	d2o8ra3	Alignment	not modelled	40.2	15	Fold: Phospholipase D/nuclease Superfamily: Phospholipase D/nuclease Family: Polyphosphate kinase C-terminal domain
52	c2zv3E	Alignment	not modelled	40.2	25	PDB header: hydrolase Chain: E: PDB Molecule: peptidyl-trna hydrolase; PDBTitle: crystal structure of project mj0051 from methanocaldococcus2 jannaschii dsm 2661
53	c5th5C	Alignment	not modelled	38.3	7	PDB header: lyase Chain: C: PDB Molecule: 7-carboxy-7-deazaguanine synthase; PDBTitle: crystal structure of quee from bacillus subtilis with 6-carboxypterin-2 5'-deoxyadenosyl ester bound
54	d2hzba1	Alignment	not modelled	37.6	14	Fold: CofD-like Superfamily: CofD-like

						Family:CofD-like
55	c5zbyA_	Alignment	not modelled	36.6	12	PDB header: hydrolase Chain: A: PDB Molecule: hydrogenase maturation protease hyci; PDBTitle: crystal structure of a [nife] hydrogenase maturation protease hyci2 from thermococcus kodakarensis kod1
56	c3mvaA_	Alignment	not modelled	35.9	15	PDB header: ligase Chain: A: PDB Molecule: udp-n-acetylmuramate:l-alanyl-gamma-d-glutamyl-medo- PDBTitle: crystal structure of a domain from a putative udp-n-acetylmuramate:l-2 alanyl-gamma-d-glutamyl-medo-diaminopimelate ligase from haemophilus3 ducreyi 35000hp
57	c2q7xA_	Alignment	not modelled	35.8	15	PDB header: transferase Chain: A: PDB Molecule: upf0052 protein sp_1565; PDBTitle: crystal structure of a putative phospho transferase (sp_1565) from2 streptococcus pneumoniae tigr4 at 2.00 a resolution
58	c5jg7A_	Alignment	not modelled	33.2	20	PDB header: metal transport Chain: A: PDB Molecule: fur regulated salmonella iron transporter; PDBTitle: crystal structure of putative periplasmic binding protein from2 salmonella typhimurium lt2
59	c3l7oB_	Alignment	not modelled	32.8	27	PDB header: isomerase Chain: B: PDB Molecule: ribose-5-phosphate isomerase a; PDBTitle: crystal structure of ribose-5-phosphate isomerase a from streptococcus2 mutans ua159
60	d1cfza_	Alignment	not modelled	32.7	17	Fold: Phosphorylase/hydrolase-like Superfamily: HybD-like Family: Hydrogenase maturing endopeptidase HybD
61	c2ppvA_	Alignment	not modelled	32.4	16	PDB header: transferase Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of a protein belonging to the upf0052 (se_0549) from2 staphylococcus epidermidis atcc 12228 at 2.00 a resolution
62	c1lkzB_	Alignment	not modelled	31.4	11	PDB header: isomerase Chain: B: PDB Molecule: ribose 5-phosphate isomerase a; PDBTitle: crystal structure of d-ribose-5-phosphate isomerase (rpiA) from2 escherichia coli.
63	c3rp7A_	Alignment	not modelled	31.1	16	PDB header: oxidoreductase Chain: A: PDB Molecule: flavoprotein monooxygenase; PDBTitle: crystal structure of klebsiella pneumoniae hpox complexed with fad and2 uric acid
64	c6c4rA_	Alignment	not modelled	30.3	18	PDB header: oxidoreductase Chain: A: PDB Molecule: staphylopine dehydrogenase; PDBTitle: staphylopine dehydrogenase (saodh) - apo
65	c4xwwA_	Alignment	not modelled	30.2	18	PDB header: rna binding protein/rna Chain: A: PDB Molecule: dr2417; PDBTitle: crystal structure of rnaase j complexed with rna
66	d2bona1	Alignment	not modelled	29.0	17	Fold: NAD kinase/diacylglycerol kinase-like Superfamily: NAD kinase/diacylglycerol kinase-like Family: Diacylglycerol kinase-like
67	c5v1tA_	Alignment	not modelled	28.8	12	PDB header: metal binding protein Chain: A: PDB Molecule: radical sam; PDBTitle: crystal structure of streptococcus suis suis bound to precursor2 peptide sua
68	c3lk7A_	Alignment	not modelled	28.5	13	PDB header: ligase Chain: A: PDB Molecule: udp-n-acetylmuramoylalanine--d-glutamate ligase; PDBTitle: the crystal structure of udp-n-acetylmuramoylalanine-d-glutamate2 (murd) ligase from streptococcus agalactiae to 1.5a
69	c4mjsO_	Alignment	not modelled	27.1	25	PDB header: transferase/protein binding Chain: Q: PDB Molecule: protein kinase c zeta type; PDBTitle: crystal structure of a pb1 complex
70	c1vqwB_	Alignment	not modelled	26.6	24	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: protein with similarity to flavin-containing PDBTitle: crystal structure of a protein with similarity to flavin-2 containing monooxygenases and to mammalian dimethylalanine3 monooxygenases
71	d2qv7a1	Alignment	not modelled	26.3	20	Fold: NAD kinase/diacylglycerol kinase-like Superfamily: NAD kinase/diacylglycerol kinase-like Family: Diacylglycerol kinase-like
72	c3en0A_	Alignment	not modelled	25.8	14	PDB header: hydrolase Chain: A: PDB Molecule: cyanophycinase; PDBTitle: the structure of cyanophycinase
73	c2r6r1_	Alignment	not modelled	25.4	13	PDB header: cell cycle Chain: 1: PDB Molecule: cell division protein ftsz; PDBTitle: aquifex aeolicus ftsz
74	c6c8vA_	Alignment	not modelled	25.1	8	PDB header: oxidoreductase Chain: A: PDB Molecule: coenzyme pqq synthesis protein e; PDBTitle: x-ray structure of pqqe from methylobacterium extorquens
75	d1ve5a1	Alignment	not modelled	25.0	13	Fold: Tryptophan synthase beta subunit-like PLP-dependent enzymes Superfamily: Tryptophan synthase beta subunit-like PLP-dependent enzymes Family: Tryptophan synthase beta subunit-like PLP-dependent enzymes
76	c3qfeB_	Alignment	not modelled	24.2	13	PDB header: lyase Chain: B: PDB Molecule: putative dihydrodipicolinate synthase family protein; PDBTitle: crystal structures of a putative dihydrodipicolinate synthase family2 protein from coccidioides immitis
77	c1w59B_	Alignment	not modelled	23.2	16	PDB header: cell division Chain: B: PDB Molecule: cell division protein ftsz homolog 1; PDBTitle: ftsz dimer, empty (m. jannaschii)
78	c4d9gA_	Alignment	not modelled	23.1	19	PDB header: lyase Chain: A: PDB Molecule: putative diaminopropionate ammonia-lyase; PDBTitle: crystal structure of selenomethionine incorporated holo2

						diaminopropionate ammonia lyase from escherichia coli
79	d1wu2a3	Alignment	not modelled	22.2	13	Fold: Molybdenum cofactor biosynthesis proteins Superfamily: Molybdenum cofactor biosynthesis proteins Family: MoeA central domain-like
80	c5u57B	Alignment	not modelled	21.5	20	PDB header: oxidoreductase Chain: B: PDB Molecule: (s)-2-hydroxypropylphosphonic acid epoxidase; PDBTitle: psf4 in complex with fe2+ and (s)-2-hpp
81	c3ktsA	Alignment	not modelled	21.2	11	PDB header: transcriptional regulator Chain: A: PDB Molecule: glycerol uptake operon antiterminator regulatory protein; PDBTitle: crystal structure of glycerol uptake operon antiterminator regulatory2 protein from listeria monocytogenes str. 4b f2365
82	c2bonB	Alignment	not modelled	21.1	22	PDB header: transferase Chain: B: PDB Molecule: lipid kinase; PDBTitle: structure of an escherichia coli lipid kinase (yegs)
83	d2vapa1	Alignment	not modelled	20.8	16	Fold: Tubulin nucleotide-binding domain-like Superfamily: Tubulin nucleotide-binding domain-like Family: Tubulin, GTPase domain
84	c2o8rA	Alignment	not modelled	20.7	15	PDB header: transferase Chain: A: PDB Molecule: polyphosphate kinase; PDBTitle: crystal structure of polyphosphate kinase from porphyromonas2 gingivalis
85	d1xdpa3	Alignment	not modelled	20.5	15	Fold: Phospholipase D/nuclease Superfamily: Phospholipase D/nuclease Family: Polyphosphate kinase C-terminal domain
86	c5t8xA	Alignment	not modelled	20.3	11	PDB header: oxidoreductase Chain: A: PDB Molecule: prephenate dehydrogenase 1; PDBTitle: prephenate dehydrogenase from soybean
87	c1xdoB	Alignment	not modelled	20.2	14	PDB header: transferase Chain: B: PDB Molecule: polyphosphate kinase; PDBTitle: crystal structure of escherichia coli polyphosphate kinase
88	c2e1mA	Alignment	not modelled	20.1	18	PDB header: oxidoreductase Chain: A: PDB Molecule: l-glutamate oxidase; PDBTitle: crystal structure of l-glutamate oxidase from streptomyces sp. x-119-6
89	d2bfdb2	Alignment	not modelled	19.7	28	Fold: TK C-terminal domain-like Superfamily: TK C-terminal domain-like Family: Branched-chain alpha-keto acid dehydrogenase beta-subunit, C-terminal-domain
90	d1pjqa1	Alignment	not modelled	19.7	17	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Siroheme synthase N-terminal domain-like
91	c3kwmC	Alignment	not modelled	19.3	15	PDB header: isomerase Chain: C: PDB Molecule: ribose-5-phosphate isomerase a; PDBTitle: crystal structure of ribose-5-isomerase a
92	c5dboA	Alignment	not modelled	19.2	9	PDB header: translation Chain: A: PDB Molecule: translation initiation factor eif2b-like protein; PDBTitle: crystal structure of the tetrameric eif2b-beta2-delta2 complex from c.2 thermophilum
93	d1ps9a3	Alignment	not modelled	18.7	18	Fold: Nucleotide-binding domain Superfamily: Nucleotide-binding domain Family: N-terminal domain of adrenodoxin reductase-like
94	c3vzdB	Alignment	not modelled	18.6	16	PDB header: transferase/inhibitor Chain: B: PDB Molecule: sphingosine kinase 1; PDBTitle: crystal structure of sphingosine kinase 1 with inhibitor and adp
95	c3h14A	Alignment	not modelled	18.6	20	PDB header: transferase Chain: A: PDB Molecule: aminotransferase, classes i and ii; PDBTitle: crystal structure of a putative aminotransferase from silicibacter2 pomeroyi
96	c2qv7A	Alignment	not modelled	18.5	15	PDB header: transferase Chain: A: PDB Molecule: diacylglycerol kinase dgkb; PDBTitle: crystal structure of diacylglycerol kinase dgkb in complex with adp2 and mg
97	d2ffea1	Alignment	not modelled	18.4	13	Fold: CofD-like Superfamily: CofD-like Family: CofD-like
98	d1kyqa1	Alignment	not modelled	18.4	11	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Siroheme synthase N-terminal domain-like
99	c1fncA	Alignment	not modelled	18.3	9	PDB header: oxidoreductase (nadp+(a),ferredoxin(a)) Chain: A: PDB Molecule: ferredoxin-nadp+ reductase; PDBTitle: refined crystal structure of spinach ferredoxin reductase2 at 1.7 angstroms resolution: oxidized, reduced, and 2'-3 phospho-5'-amp bound states