

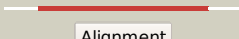

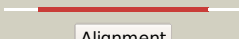



















Phyre2

Email mdejesus@rockefeller.edu
 Description RVBD2421c_(nadD)_2718183_2718818
 Date Wed Aug 7 12:50:04 BST 2019
 Unique Job ID 165c57d0189fdf4f

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1yunB_	 Alignment		100.0	32	PDB header: transferase Chain: B: PDB Molecule: probable nicotinate-nucleotide PDBTitle: crystal structure of nicotinic acid mononucleotide2 adenylyltransferase from pseudomonas aeruginosa
2	d1k4ma_	 Alignment		100.0	31	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Nucleotidylyl transferase Family: Adenylyltransferase
3	c4wsoA_	 Alignment		100.0	39	PDB header: transferase Chain: A: PDB Molecule: probable nicotinate-nucleotide adenylyltransferase; PDBTitle: x-ray crystal structure of a nicotinate nucleotide adenylyltransferase2 from burkholderia thailandensis bound to nad
4	d1kr2a_	 Alignment		100.0	24	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Nucleotidylyl transferase Family: Adenylyltransferase
5	c4rpiA_	 Alignment		100.0	99	PDB header: transferase Chain: A: PDB Molecule: nicotinate-nucleotide adenylyltransferase; PDBTitle: crystal structure of nicotinate mononucleotide adenylyltransferase2 from mycobacterium tuberculosis
6	d1nuua_	 Alignment		100.0	23	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Nucleotidylyl transferase Family: Adenylyltransferase
7	d1kama_	 Alignment		100.0	40	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Nucleotidylyl transferase Family: Adenylyltransferase
8	c3e27B_	 Alignment		100.0	39	PDB header: transferase Chain: B: PDB Molecule: nicotinate (nicotinamide) nucleotide adenylyltransferase; PDBTitle: nicotinic acid mononucleotide (namn) adenylyltransferase from bacillus2 anthracis: product complex
9	c2h29A_	 Alignment		100.0	34	PDB header: transferase Chain: A: PDB Molecule: probable nicotinate-nucleotide adenylyltransferase from staphylococcus aureus: product3 bound form 1
10	c5lttB_	 Alignment		100.0	23	PDB header: transferase Chain: B: PDB Molecule: nicotinate-nucleotide adenylyltransferase; PDBTitle: plasmodium falciparum nicotinic acid mononucleotide2 adenylyltransferase complexed with naad
11	d1od6a_	 Alignment		100.0	21	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Nucleotidylyl transferase Family: Adenylyltransferase

12	d1tfua_	Alignment		100.0	19	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Nucleotidylyl transferase Family: Adenylyltransferase
13	d1vlha_	Alignment		100.0	21	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Nucleotidylyl transferase Family: Adenylyltransferase
14	d1o6ba_	Alignment		100.0	17	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Nucleotidylyl transferase Family: Adenylyltransferase
15	c5h16D_	Alignment		100.0	20	PDB header: transferase Chain: D: PDB Molecule: phosphopantetheine adenylyltransferase; PDBTitle: crystal structure of the complex of phosphopantetheine2 adenylyltransferase from acinetobacter baumannii with citrate at 2.33 a resolution.
16	c3ikzA_	Alignment		100.0	20	PDB header: transferase Chain: A: PDB Molecule: phosphopantetheine adenylyltransferase; PDBTitle: crystal structure of phosphopantetheine adenylyltransferase from2 burkholderia pseudomallei
17	c3x1mC_	Alignment		100.0	22	PDB header: transferase Chain: C: PDB Molecule: phosphopantetheine adenylyltransferase; PDBTitle: crystal structure of phosphopantetheine adenylyltransferase/ppat from2 pseudomonas aeruginosa with coa
18	c3f3mA_	Alignment		100.0	20	PDB header: transferase Chain: A: PDB Molecule: phosphopantetheine adenylyltransferase; PDBTitle: six crystal structures of two phosphopantetheine adenylyltransferases2 reveal an alternative ligand binding mode and an associated3 structural change
19	c3nd5D_	Alignment		100.0	20	PDB header: transferase Chain: D: PDB Molecule: phosphopantetheine adenylyltransferase; PDBTitle: crystal structure of phosphopantetheine adenylyltransferase (ppat)2 from enterococcus faecalis
20	d1qjca_	Alignment		100.0	21	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Nucleotidylyl transferase Family: Adenylyltransferase
21	c4f3rC_	Alignment	not modelled	100.0	18	PDB header: transferase Chain: C: PDB Molecule: phosphopantetheine adenylyltransferase; PDBTitle: structure of phosphopantetheine adenylyltransferase (cbu_0288) from2 coxiella burnetii
22	c3nv7A_	Alignment	not modelled	100.0	17	PDB header: transferase Chain: A: PDB Molecule: phosphopantetheine adenylyltransferase; PDBTitle: crystal structure of h.pylori phosphopantetheine adenylyltransferase2 mutant i4v/n76y
23	d1f9aa_	Alignment	not modelled	100.0	19	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Nucleotidylyl transferase Family: Adenylyltransferase
24	d1ej2a_	Alignment	not modelled	100.0	19	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Nucleotidylyl transferase Family: Adenylyltransferase
25	c3h05A_	Alignment	not modelled	100.0	20	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein vpa0413; PDBTitle: the crystal structure of a putative nicotinate-nucleotide2 adenylyltransferase from vibrio parahaemolyticus
26	c2qjoB_	Alignment	not modelled	100.0	16	PDB header: transferase, hydrolase Chain: B: PDB Molecule: bifunctional nmh adenylyltransferase/nudix hydrolase; PDBTitle: crystal structure of a bifunctional nmh adenylyltransferase/adp ribose2 pyrophosphatase (nadm) complexed with adprp and nad from3 synechocystis sp.
27	c6gyeB_	Alignment	not modelled	100.0	21	PDB header: transport protein Chain: B: PDB Molecule: nicotinamide-nucleotide adenylyltransferase nadr family / PDBTitle: crystal structure of nadr protein in complex with nr
28	c2r5wA_	Alignment	not modelled	100.0	14	PDB header: hydrolase, transferase Chain: A: PDB Molecule: nicotinamide-nucleotide adenylyltransferase;

28	c1j9wA	Alignment	not modelled	99.9	14	PDBTitle: crystal structure of a bifunctional nmn2 adenylyltransferase/adenylyltransferase from <i>Francisella tularensis</i>
29	c1lw7A	Alignment	not modelled	99.8	20	PDB header: transferase Chain: A: PDB Molecule: transcriptional regulator nadr; PDBTitle: nadr protein from <i>Haemophilus influenzae</i>
30	d1lw7a1	Alignment	not modelled	99.8	19	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Nucleotidyl transferase Family: Adenylyltransferase
31	d1mrza2	Alignment	not modelled	99.8	17	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Nucleotidyl transferase Family: Adenylyltransferase
32	c2b7ID	Alignment	not modelled	99.7	19	PDB header: transferase Chain: D: PDB Molecule: glycerol-3-phosphate cytidyltransferase; PDBTitle: crystal structure of ctp:glycerol-3-phosphate2 cytidyltransferase from <i>Staphylococcus aureus</i>
33	d1coza	Alignment	not modelled	99.6	22	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Nucleotidyl transferase Family: Cytidyltransferase
34	c5y0tD	Alignment	not modelled	99.5	16	PDB header: ligase Chain: D: PDB Molecule: thermotoga maritima tmcal; PDBTitle: crystal structure of thermotoga maritima tmcal bound with alpha-thio2 atp(form ii)
35	c4zcsE	Alignment	not modelled	99.5	20	PDB header: transferase Chain: E: PDB Molecule: choline-phosphate cytidyltransferase; PDBTitle: crystal structure of the c-terminal catalytic domain of plasmodium2 falciparum ctp:phosphocholine cytidyltransferase in complex with3 cdp-choline
36	c5y0nB	Alignment	not modelled	99.5	18	PDB header: ligase Chain: B: PDB Molecule: upf0348 protein b4417_3650; PDBTitle: crystal structure of bacillus subtilis tmcal bound with atp (semet2 derivative)
37	c3gmiA	Alignment	not modelled	99.5	16	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: upf0348 protein mj0951; PDBTitle: crystal structure of a protein of unknown function from2 methanocaldococcus jannaschii
38	c5xf2B	Alignment	not modelled	99.3	17	PDB header: transferase Chain: B: PDB Molecule: putative cytidyltransferase; PDBTitle: crystal structure of semet-hldc from burkholderia pseudomallei
39	c3do8B	Alignment	not modelled	99.3	26	PDB header: transferase Chain: B: PDB Molecule: phosphopantetheine adenylyltransferase; PDBTitle: the crystal structure of the protein with unknown function from2 archaeoglobus fulgidus
40	c3glvB	Alignment	not modelled	99.1	24	PDB header: biosynthetic protein Chain: B: PDB Molecule: lipopolysaccharide core biosynthesis protein; PDBTitle: crystal structure of the lipopolysaccharide core biosynthesis protein2 from thermoplasma volcanium gss1
41	c1t6zB	Alignment	not modelled	99.1	19	PDB header: transferase Chain: B: PDB Molecule: riboflavin kinase/fmn adenylyltransferase; PDBTitle: crystal structure of riboflavin bound tm379
42	c3op1A	Alignment	not modelled	99.1	18	PDB header: transferase Chain: A: PDB Molecule: macrolide-efflux protein; PDBTitle: crystal structure of macrolide-efflux protein sp_1110 from2 streptococcus pneumoniae
43	c3elbA	Alignment	not modelled	99.0	22	PDB header: transferase Chain: A: PDB Molecule: ethanolamine-phosphate cytidyltransferase; PDBTitle: human ctp: phosphoethanolamine cytidyltransferase in complex with2 cmp
44	c2x0kB	Alignment	not modelled	98.9	17	PDB header: transferase Chain: B: PDB Molecule: riboflavin biosynthesis protein ribf; PDBTitle: crystal structure of modular fad synthetase from2 corynebacterium ammoniagenes
45	c3hl4B	Alignment	not modelled	98.9	25	PDB header: transferase Chain: B: PDB Molecule: choline-phosphate cytidyltransferase a; PDBTitle: crystal structure of a mammalian ctp:phosphocholine2 cytidyltransferase with cdp-choline
46	d1jhda2	Alignment	not modelled	98.8	18	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Nucleotidyl transferase Family: ATP sulfurylase catalytic domain
47	c1jhdA	Alignment	not modelled	98.7	15	PDB header: transferase Chain: A: PDB Molecule: sulfate adenylyltransferase; PDBTitle: crystal structure of bacterial atp sulfurylase from the2 riftia pachyptila symbiont
48	d1x6va2	Alignment	not modelled	98.6	13	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Nucleotidyl transferase Family: ATP sulfurylase catalytic domain
49	c2qjfB	Alignment	not modelled	98.6	13	PDB header: transferase Chain: B: PDB Molecule: bifunctional 3'-phosphoadenosine 5'- PDBTitle: crystal structure of atp-sulfurylase domain of human paps2 synthetase 1
50	c5x3dA	Alignment	not modelled	98.5	25	PDB header: transferase Chain: A: PDB Molecule: phosphoenolpyruvate phosphomutase; PDBTitle: crystal structure of hep-cmp-bound form of cytidyltransferase2 (cytase) domain of fom1 from streptomyces wedmorensis
51	d1g8fa2	Alignment	not modelled	98.4	17	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Nucleotidyl transferase Family: ATP sulfurylase catalytic domain
52	d1v47a2	Alignment	not modelled	98.4	17	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Nucleotidyl transferase Family: ATP sulfurylase catalytic domain
53	c1r6xA	Alignment	not modelled	98.4	15	PDB header: transferase Chain: A: PDB Molecule: atp:sulfate adenylyltransferase; PDBTitle: the crystal structure of a truncated form of yeast atp2

						sulfurylase, lacking the c-terminal aps kinase-like domain,3 in complex with sulfate
54	c3cr8C_	Alignment	not modelled	98.3	15	PDB header: transferase Chain: C: PDB Molecule: sulfate adenylyltransferase, adenylylsulfate kinase; PDBTitle: hexameric aps kinase from thiobacillus denitrificans
55	c4mvcA_	Alignment	not modelled	98.3	19	PDB header: transferase Chain: A: PDB Molecule: choline-phosphate cytidylyltransferase a; PDBTitle: crystal structure of a mammalian cytidylyltransferase
56	c1g8gB_	Alignment	not modelled	98.3	13	PDB header: transferase Chain: B: PDB Molecule: sulfate adenylyltransferase; PDBTitle: atp sulfurylase from s. cerevisiae: the binary product complex with2 aps
57	c1m8pB_	Alignment	not modelled	98.3	13	PDB header: transferase Chain: B: PDB Molecule: sulfate adenylyltransferase; PDBTitle: crystal structure of p. chrysogenum atp sulfurylase in the t-state
58	c1xjqA_	Alignment	not modelled	98.2	14	PDB header: transferase Chain: A: PDB Molecule: bifunctional 3'-phosphoadenosine 5'-phosphosulfate PDBTitle: adp complex of human paps synthetase 1
59	d1m8pa2	Alignment	not modelled	98.1	14	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Nucleotidylyl transferase Family: ATP sulfurylase catalytic domain
60	c1xnjB_	Alignment	not modelled	98.1	13	PDB header: transferase Chain: B: PDB Molecule: bifunctional 3'-phosphoadenosine 5'-phosphosulfate PDBTitle: aps complex of human paps synthetase 1
61	c2gksB_	Alignment	not modelled	97.9	13	PDB header: transferase Chain: B: PDB Molecule: bifunctional sat/aps kinase; PDBTitle: crystal structure of the bi-functional atp sulfurylase-aps kinase from2 aquifex aeolicus, a chemolithotrophic thermophile
62	c1v47B_	Alignment	not modelled	97.8	17	PDB header: transferase Chain: B: PDB Molecule: atp sulfurylase; PDBTitle: crystal structure of atp sulfurylase from thermus2 thermophilus hb8 in complex with aps
63	c4mafH_	Alignment	not modelled	96.3	14	PDB header: transferase Chain: H: PDB Molecule: atp sulfurylase; PDBTitle: soybean atp sulfurylase
64	c3guzB_	Alignment	not modelled	96.2	18	PDB header: ligase Chain: B: PDB Molecule: pantothenate synthetase; PDBTitle: structural and substrate-binding studies of pantothenate2 synthenate (ps)provide insights into homotropic inhibition3 by pantoate in ps's
65	c3ag5A_	Alignment	not modelled	92.0	20	PDB header: ligase Chain: A: PDB Molecule: pantothenate synthetase; PDBTitle: crystal structure of pantothenate synthetase from staphylococcus2 aureus
66	d1v8fa_	Alignment	not modelled	91.8	22	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Nucleotidylyl transferase Family: Pantothenate synthetase (Pantoate-beta-alanine ligase, PanC)
67	c2ejcA_	Alignment	not modelled	91.1	22	PDB header: ligase Chain: A: PDB Molecule: pantoate--beta-alanine ligase; PDBTitle: crystal structure of pantoate--beta-alanine ligase (panc)2 from thermotoga maritima
68	d1ihoa_	Alignment	not modelled	91.0	20	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Nucleotidylyl transferase Family: Pantothenate synthetase (Pantoate-beta-alanine ligase, PanC)
69	c3n8hA_	Alignment	not modelled	90.2	16	PDB header: ligase Chain: A: PDB Molecule: pantothenate synthetase; PDBTitle: crystal structure of pantoate-beta-alanine ligase from francisella2 tularensis
70	c3innB_	Alignment	not modelled	88.7	21	PDB header: ligase Chain: B: PDB Molecule: pantothenate synthetase; PDBTitle: crystal structure of pantoate-beta-alanine-ligase in complex2 with atp at low occupancy at 2.1 a resolution
71	c5kwvA_	Alignment	not modelled	88.5	21	PDB header: ligase Chain: A: PDB Molecule: pantothenate synthetase; PDBTitle: crystal structure of a pantoate-beta-alanine ligase from neisseria2 gonorrhoeae with bound amppnp
72	c3uk2B_	Alignment	not modelled	88.3	18	PDB header: ligase Chain: B: PDB Molecule: pantothenate synthetase; PDBTitle: the structure of pantothenate synthetase from burkholderia2 thailandensis
73	d2a84a1	Alignment	not modelled	85.4	28	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Nucleotidylyl transferase Family: Pantothenate synthetase (Pantoate-beta-alanine ligase, PanC)
74	c3mxtA_	Alignment	not modelled	79.0	20	PDB header: ligase Chain: A: PDB Molecule: pantothenate synthetase; PDBTitle: crystal structure of pantoate-beta-alanine ligase from campylobacter2 jejuni
75	c4wv4A_	Alignment	not modelled	43.3	23	PDB header: transcription Chain: A: PDB Molecule: transcription initiation factor tfiif subunit 10; PDBTitle: heterodimer of taf8/taf10
76	c3ktmB_	Alignment	not modelled	34.0	13	PDB header: cell adhesion, signaling protein Chain: B: PDB Molecule: amyloid beta a4 protein; PDBTitle: structure of the heparin-induced e1-dimer of the amyloid precursor2 protein (app)
77	c2w48D_	Alignment	not modelled	32.8	13	PDB header: transcription Chain: D: PDB Molecule: sorbitol operon regulator; PDBTitle: crystal structure of the full-length sorbitol operon2 regulator sorc from klebsiella pneumoniae
78	c3hv0A_	Alignment	not modelled	32.6	16	PDB header: ligase Chain: A: PDB Molecule: tryptophanyl-trna synthetase; PDBTitle: tryptophanyl-trna synthetase from cryptosporidium parvum

79	d1mwpA	Alignment	not modelled	31.1	13	Fold: SRCR-like Superfamily: A heparin-binding domain Family: A heparin-binding domain
80	c3sp1B	Alignment	not modelled	27.9	7	PDB header: ligase Chain: B: PDB Molecule: cysteinyI-trna synthetase; PDBTitle: crystal structure of cysteinyI-trna synthetase (cyss) from borrelia2 burgdorferi
81	c4j75B	Alignment	not modelled	22.8	19	PDB header: ligase Chain: B: PDB Molecule: tryptophanyl-trna synthetase; PDBTitle: crystal structure of a parasite trna synthetase, product-bound
82	c3c8zB	Alignment	not modelled	21.1	11	PDB header: ligase Chain: B: PDB Molecule: cysteinyI-trna synthetase; PDBTitle: the 1.6 a crystal structure of mshc: the rate limiting2 enzyme in the mycothiol biosynthetic pathway
83	c1u0bB	Alignment	not modelled	20.8	19	PDB header: ligase/rna Chain: B: PDB Molecule: cysteinyI trna; PDBTitle: crystal structure of cysteinyI-trna synthetase binary2 complex with trnacys
84	c1r6tA	Alignment	not modelled	19.7	15	PDB header: ligase Chain: A: PDB Molecule: tryptophanyl-trna synthetase; PDBTitle: crystal structure of human tryptophanyl-trna synthetase
85	d1iq0a2	Alignment	not modelled	18.9	21	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Nucleotidylyl transferase Family: Class I aminoacyl-tRNA synthetases (RS), catalytic domain
86	c5ykrB	Alignment	not modelled	16.8	24	PDB header: transferase Chain: B: PDB Molecule: probable aminotransferase; PDBTitle: crystal structure of a glutamate-1-semialdehyde-aminomutase from2 pseudomonas aeruginosa pao1
87	c3focB	Alignment	not modelled	16.5	17	PDB header: ligase Chain: B: PDB Molecule: tryptophanyl-trna synthetase; PDBTitle: tryptophanyl-trna synthetase from giardia lamblia
88	d1v32a	Alignment	not modelled	16.2	22	Fold: SWIB/MDM2 domain Superfamily: SWIB/MDM2 domain Family: SWIB/MDM2 domain
89	c6byqA	Alignment	not modelled	16.1	19	PDB header: ligase Chain: A: PDB Molecule: tyrosine--trna ligase; PDBTitle: crystal structure of tyrosine-trna ligase from helicobacter pylori g27
90	d1v31a	Alignment	not modelled	15.8	16	Fold: SWIB/MDM2 domain Superfamily: SWIB/MDM2 domain Family: SWIB/MDM2 domain
91	c4zm3C	Alignment	not modelled	14.1	27	PDB header: transferase Chain: C: PDB Molecule: aminotransferase; PDBTitle: crystal structure of plp-dependent 3-aminobenzoate synthase pctv wild-2 type
92	c3tqoA	Alignment	not modelled	14.1	13	PDB header: ligase Chain: A: PDB Molecule: cysteinyI-trna synthetase; PDBTitle: structure of the cysteinyI-trna synthetase (cyss) from coxiella2 burnetii.
93	d1uyra1	Alignment	not modelled	13.8	15	Fold: ClpP/crotonase Superfamily: ClpP/crotonase Family: Biotin dependent carboxylase carboxyltransferase domain
94	c3jxeB	Alignment	not modelled	13.5	10	PDB header: ligase Chain: B: PDB Molecule: tryptophanyl-trna synthetase; PDBTitle: crystal structure of pyrococcus horikoshii tryptophanyl-trna2 synthetase in complex with trpamp
95	d2izva1	Alignment	not modelled	13.4	16	Fold: SOCS box-like Superfamily: SOCS box-like Family: SOCS box-like
96	c3a05A	Alignment	not modelled	13.2	15	PDB header: ligase Chain: A: PDB Molecule: tryptophanyl-trna synthetase; PDBTitle: crystal structure of tryptophanyl-trna synthetase from2 hyperthermophilic archaeon, aeropyrum pernix k1 complex3 with tryptophan
97	c5ixiA	Alignment	not modelled	13.1	7	PDB header: cytokine Chain: A: PDB Molecule: tyrosine-protein kinase jak1; PDBTitle: structure of human jak1 ferm/sh2 in complex with ifn1r1/il10ra chimera
98	d1uhra	Alignment	not modelled	12.1	23	Fold: SWIB/MDM2 domain Superfamily: SWIB/MDM2 domain Family: SWIB/MDM2 domain
99	c3fnrA	Alignment	not modelled	12.0	21	PDB header: transferase Chain: A: PDB Molecule: arginyl-trna synthetase; PDBTitle: crystal structure of putative arginyl t-rna synthetase from2 campylobacter jejuni;