

Phyre2

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Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1tfua_	Alignment		100.0	100	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Nucleotidyl transferase Family: Adenylyltransferase
2	d1vlha_	Alignment		100.0	50	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Nucleotidyl transferase Family: Adenylyltransferase
3	c3x1mC_	Alignment		100.0	40	PDB header: transferase Chain: C: PDB Molecule: phosphopantetheine adenylyltransferase; PDBTitle: crystal structure of phosphopantetheine adenylyltransferase/ppat from2 pseudomonas aeruginosa with coa
4	d1o6ba_	Alignment		100.0	43	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Nucleotidyl transferase Family: Adenylyltransferase
5	c3ikzA_	Alignment		100.0	42	PDB header: transferase Chain: A: PDB Molecule: phosphopantetheine adenylyltransferase; PDBTitle: crystal structure of phosphopantetheine adenylyltransferase from2 burkholderia pseudomallei
6	d1od6a_	Alignment		100.0	50	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Nucleotidyl transferase Family: Adenylyltransferase
7	c5h16D_	Alignment		100.0	41	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.
8	d1qjca_	Alignment		100.0	44	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Nucleotidyl transferase Family: Adenylyltransferase
9	c3f3mA_	Alignment		100.0	45	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
10	c3nv7A_	Alignment		100.0	34	PDB header: transferase Chain: A: PDB Molecule: phosphopantetheine adenylyltransferase; PDBTitle: crystal structure of h.pylori phosphopantetheine adenylyltransferase2 mutant i4v/n76y
11	c3nd5D_	Alignment		100.0	39	PDB header: transferase Chain: D: PDB Molecule: phosphopantetheine adenylyltransferase; PDBTitle: crystal structure of phosphopantetheine adenylyltransferase (ppat)2 from enterococcus faecalis

12	c4f3rC_	Alignment		100.0	39	PDB header: transferase Chain: C: PDB Molecule: phosphopantetheine adenylyltransferase; PDBTitle: structure of phosphopantetheine adenylyltransferase (cbu_0288) from2 coxiella burnetii
13	d1nuua_	Alignment		100.0	21	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Nucleotidylyl transferase Family: Adenylyltransferase
14	d1kr2a_	Alignment		100.0	18	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Nucleotidylyl transferase Family: Adenylyltransferase
15	c1yunB_	Alignment		100.0	24	PDB header: transferase Chain: B: PDB Molecule: probable nicotinate-nucleotide PDBTitle: crystal structure of nicotinic acid mononucleotide2 adenylyltransferase from pseudomonas aeruginosa
16	c4wsoA_	Alignment		100.0	16	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
17	d1k4ma_	Alignment		100.0	19	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Nucleotidylyl transferase Family: Adenylyltransferase
18	d1kama_	Alignment		100.0	16	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Nucleotidylyl transferase Family: Adenylyltransferase
19	c2h29A_	Alignment		100.0	16	PDB header: transferase Chain: A: PDB Molecule: probable nicotinate-nucleotide PDBTitle: crystal structure of nicotinic acid mononucleotide2 adenylyltransferase from staphylococcus aureus: product3 bound form 1
20	c4rpiA_	Alignment		100.0	17	PDB header: transferase Chain: A: PDB Molecule: nicotinate-nucleotide adenylyltransferase; PDBTitle: crystal structure of nicotinate mononucleotide adenylyltransferase2 from mycobacterium tuberculosis
21	d1ej2a_	Alignment	not modelled	100.0	15	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Nucleotidylyl transferase Family: Adenylyltransferase
22	c3e27B_	Alignment	not modelled	100.0	18	PDB header: transferase Chain: B: PDB Molecule: nicotinate (nicotinamide) nucleotide adenylyltransferase; PDBTitle: nicotinic acid mononucleotide (namn) adenylyltransferase from bacillus2 anthracis: product complex
23	c2qjoB_	Alignment	not modelled	100.0	19	PDB header: transferase, hydrolase Chain: B: PDB Molecule: bifunctional nmn adenylyltransferase/nudix hydrolase; PDBTitle: crystal structure of a bifunctional nmn adenylyltransferase/adp ribose2 pyrophosphatase (nadm) complexed with adprp and nad from3 synechocystis sp.
24	d1f9aa_	Alignment	not modelled	100.0	19	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Nucleotidylyl transferase Family: Adenylyltransferase
25	c5lltB_	Alignment	not modelled	100.0	16	PDB header: transferase Chain: B: PDB Molecule: nicotinate-nucleotide adenylyltransferase; PDBTitle: plasmodium falciparum nicotinic acid mononucleotide2 adenylyltransferase complexed with naad
26	c3h05A_	Alignment	not modelled	100.0	17	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
27	c6gyeB_	Alignment	not modelled	100.0	13	PDB header: transport protein Chain: B: PDB Molecule: nicotinamide-nucleotide adenylyltransferase nadr family / PDBTitle: crystal structure of nadr protein in complex with nr
						PDB header: hydrolase, transferase Chain: A: PDB Molecule: nicotinamide-nucleotide

28	c2r5wA	Alignment	not modelled	99.9	15	adenylyltransferase; PDBTitle: crystal structure of a bifunctional nmn2 adenylyltransferase/adp ribose pyrophosphatase from3 francisella tularensis
29	d1coza	Alignment	not modelled	99.9	18	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Nucleotidylyl transferase Family: Cytidylyltransferase
30	d1lw7a1	Alignment	not modelled	99.9	16	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Nucleotidylyl transferase Family: Adenylyltransferase
31	c2b7ID	Alignment	not modelled	99.9	23	PDB header: transferase Chain: D: PDB Molecule: glycerol-3-phosphate cytidylyltransferase; PDBTitle: crystal structure of ctp:glycerol-3-phosphate2 cytidylyltransferase from staphylococcus aureus
32	c1lw7A	Alignment	not modelled	99.8	15	PDB header: transferase Chain: A: PDB Molecule: transcriptional regulator nadr; PDBTitle: nadr protein from haemophilus influenzae
33	d1mrza2	Alignment	not modelled	99.8	20	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Nucleotidylyl transferase Family: Adenylyltransferase
34	c4zcsE	Alignment	not modelled	99.7	15	PDB header: transferase Chain: E: PDB Molecule: choline-phosphate cytidylyltransferase; PDBTitle: crystal structure of the c-terminal catalytic domain of plasmodium2 falciparum ctp:phosphocholine cytidylyltransferase in complex with3 cdp-choline
35	c5xf2B	Alignment	not modelled	99.7	16	PDB header: transferase Chain: B: PDB Molecule: putative cytidylyltransferase; PDBTitle: crystal structure of semet-hldc from burkholderia pseudomallei
36	c3glvB	Alignment	not modelled	99.7	22	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
37	c3elbA	Alignment	not modelled	99.6	17	PDB header: transferase Chain: A: PDB Molecule: ethanolamine-phosphate cytidylyltransferase; PDBTitle: human ctp: phosphoethanolamine cytidylyltransferase in complex with2 cmp
38	c3op1A	Alignment	not modelled	99.6	19	PDB header: transferase Chain: A: PDB Molecule: macrolide-efflux protein; PDBTitle: crystal structure of macrolide-efflux protein sp_1110 from2 streptococcus pneumoniae
39	c2x0kB	Alignment	not modelled	99.6	19	PDB header: transferase Chain: B: PDB Molecule: riboflavin biosynthesis protein ribf; PDBTitle: crystal structure of modular fad synthetase from2 corynebacterium ammoniagenes
40	c3gmiA	Alignment	not modelled	99.5	14	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
41	c1t6zB	Alignment	not modelled	99.5	22	PDB header: transferase Chain: B: PDB Molecule: riboflavin kinase/fmn adenylyltransferase; PDBTitle: crystal structure of riboflavin bound tm379
42	c3hl4B	Alignment	not modelled	99.4	15	PDB header: transferase Chain: B: PDB Molecule: choline-phosphate cytidylyltransferase a; PDBTitle: crystal structure of a mammalian ctp:phosphocholine2 cytidylyltransferase with cdp-choline
43	c5x3dA	Alignment	not modelled	99.3	14	PDB header: transferase Chain: A: PDB Molecule: phosphoenolpyruvate phosphomutase; PDBTitle: crystal structure of hep-cmp-bound form of cytidylyltransferase2 (cytase) domain of fom1 from streptomyces wedmorensis
44	c4mvcA	Alignment	not modelled	99.2	14	PDB header: transferase Chain: A: PDB Molecule: choline-phosphate cytidylyltransferase a; PDBTitle: crystal structure of a mammalian cytidylyltransferase
45	c3do8B	Alignment	not modelled	99.2	13	PDB header: transferase Chain: B: PDB Molecule: phosphopantetheine adenylyltransferase; PDBTitle: the crystal structure of the protein with unknown function from2 archaeoglobus fulgidus
46	c5y0tD	Alignment	not modelled	99.1	18	PDB header: ligase Chain: D: PDB Molecule: thermotoga maritima tmcal; PDBTitle: crystal structure of thermotoga maritima tmcal bound with alpha-thio2 atp(form ii)
47	c5y0nB	Alignment	not modelled	99.1	14	PDB header: ligase Chain: B: PDB Molecule: upf0348 protein b4417_3650; PDBTitle: crystal structure of bacillus subtilis tmcal bound with atp (semet2 derivative)
48	d1v47a2	Alignment	not modelled	99.0	16	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Nucleotidylyl transferase Family: ATP sulfurylase catalytic domain
49	d1x6va2	Alignment	not modelled	99.0	16	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Nucleotidylyl transferase Family: ATP sulfurylase catalytic domain
50	c1r6xA	Alignment	not modelled	99.0	18	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
51	d1g8fa2	Alignment	not modelled	99.0	18	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Nucleotidylyl transferase Family: ATP sulfurylase catalytic domain
52	c1xnjB	Alignment	not modelled	98.9	14	PDB header: transferase Chain: B: PDB Molecule: bifunctional 3'-phosphoadenosine 5'-phosphosulfate PDBTitle: aps complex of human paps synthetase 1 PDB header: transferase

53	c1xjqA_	Alignment	not modelled	98.9	14	Chain: A: PDB Molecule: bifunctional 3'-phosphoadenosine 5'-phosphosulfate PDBTitle: adp complex of human paps synthetase 1
54	c3cr8C_	Alignment	not modelled	98.9	14	PDB header: transferase Chain: C: PDB Molecule: sulfate adenylyltransferase, adenylylsulfate kinase; PDBTitle: hexameric aps kinase from thiobacillus denitrificans
55	c2qjfB_	Alignment	not modelled	98.9	14	PDB header: transferase Chain: B: PDB Molecule: bifunctional 3'-phosphoadenosine 5'- PDBTitle: crystal structure of atp-sulfurylase domain of human paps2 synthetase 1
56	c1g8gB_	Alignment	not modelled	98.9	19	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	98.9	20	PDB header: transferase Chain: B: PDB Molecule: sulfate adenylyltransferase; PDBTitle: crystal structure of p. chrysogenum atp sulfurylase in the t-state
58	d1jhda2	Alignment	not modelled	98.9	20	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Nucleotidylyl transferase Family: ATP sulfurylase catalytic domain
59	d1m8pa2	Alignment	not modelled	98.8	19	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Nucleotidylyl transferase Family: ATP sulfurylase catalytic domain
60	c1jhdA_	Alignment	not modelled	98.8	17	PDB header: transferase Chain: A: PDB Molecule: sulfate adenylyltransferase; PDBTitle: crystal structure of bacterial atp sulfurylase from the2 riftia pachyptila symbiont
61	c1v47B_	Alignment	not modelled	98.7	15	PDB header: transferase Chain: B: PDB Molecule: atp sulfurylase; PDBTitle: crystal structure of atp sulfurylase from thermus2 thermophilus hb8 in complex with aps
62	c2gksB_	Alignment	not modelled	98.5	15	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
63	c3guzB_	Alignment	not modelled	98.2	23	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
64	d1v8fa_	Alignment	not modelled	97.3	31	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Nucleotidylyl transferase Family: Pantothenate synthetase (Pantoate-beta-alanine ligase, PanC)
65	c4mafH_	Alignment	not modelled	97.1	17	PDB header: transferase Chain: H: PDB Molecule: atp sulfurylase; PDBTitle: soybean atp sulfurylase
66	c2ejcA_	Alignment	not modelled	97.0	29	PDB header: ligase Chain: A: PDB Molecule: pantoate--beta-alanine ligase; PDBTitle: crystal structure of pantoate--beta-alanine ligase (panc)2 from thermotoga maritima
67	d1ihoA_	Alignment	not modelled	97.0	33	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Nucleotidylyl transferase Family: Pantothenate synthetase (Pantoate-beta-alanine ligase, PanC)
68	c3uk2B_	Alignment	not modelled	97.0	26	PDB header: ligase Chain: B: PDB Molecule: pantothenate synthetase; PDBTitle: the structure of pantothenate synthetase from burkholderia2 thailandensis
69	c3ag5A_	Alignment	not modelled	96.9	22	PDB header: ligase Chain: A: PDB Molecule: pantothenate synthetase; PDBTitle: crystal structure of pantothenate synthetase from staphylococcus2 aureus
70	c3n8hA_	Alignment	not modelled	96.9	31	PDB header: ligase Chain: A: PDB Molecule: pantothenate synthetase; PDBTitle: crystal structure of pantoate-beta-alanine ligase from francisella2 tularensis
71	c3innB_	Alignment	not modelled	96.5	37	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
72	c5kwvA_	Alignment	not modelled	96.3	29	PDB header: ligase Chain: A: PDB Molecule: pantothenate synthetase; PDBTitle: crystal structure of a pantoate-beta-alanine ligase from neisseria2 gonorrhoeae with bound amppnp
73	c3mxtA_	Alignment	not modelled	96.2	32	PDB header: ligase Chain: A: PDB Molecule: pantothenate synthetase; PDBTitle: crystal structure of pantoate-beta-alanine ligase from campylobacter2 jejuni
74	d2a84a1	Alignment	not modelled	96.0	37	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Nucleotidylyl transferase Family: Pantothenate synthetase (Pantoate-beta-alanine ligase, PanC)
75	c4hwgA_	Alignment	not modelled	51.7	11	PDB header: isomerase Chain: A: PDB Molecule: udp-n-acetylglucosamine 2-epimerase; PDBTitle: structure of udp-n-acetylglucosamine 2-epimerase from rickettsia2 bellii
76	c2ct8A_	Alignment	not modelled	46.3	20	PDB header: ligase/rna Chain: A: PDB Molecule: methionyl-trna synthetase; PDBTitle: crystal structure of aquifex aeolicus methionyl-trna2 synthetase complexed with trna(met) and methionyl-adenylate3 analogue
77	d1rqga2	Alignment	not modelled	41.0	21	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Nucleotidylyl transferase Family: Class I aminoacyl-tRNA synthetases (RS), catalytic domain
78	d2d5ba2	Alignment	not modelled	37.0	21	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Nucleotidylyl transferase Family: Class I aminoacyl-tRNA synthetases (RS), catalytic domain

79	c3tqoA_	Alignment	not modelled	36.7	20	PDB header: ligase Chain: A: PDB Molecule: cysteinyI-trna synthetase; PDBTitle: structure of the cysteinyI-trna synthetase (cyss) from coxiella2 burnetii.
80	c3ziuA_	Alignment	not modelled	33.8	20	PDB header: ligase Chain: A: PDB Molecule: leucyl-trna synthetase; PDBTitle: crystal structure of mycoplasma mobile leucyl-trna2 synthetase with leu-ams in the active site
81	c3ziuB_	Alignment	not modelled	33.8	20	PDB header: ligase Chain: B: PDB Molecule: leucyl-trna synthetase; PDBTitle: crystal structure of mycoplasma mobile leucyl-trna2 synthetase with leu-ams in the active site
82	c3focB_	Alignment	not modelled	26.5	22	PDB header: ligase Chain: B: PDB Molecule: tryptophanyl-trna synthetase; PDBTitle: tryptophanyl-trna synthetase from giardia lamblia
83	c5urbB_	Alignment	not modelled	23.9	18	PDB header: ligase Chain: B: PDB Molecule: methionine--trna ligase; PDBTitle: crystal structure of methionyl-trna synthetase (metrs) from2 acinetobacter baumannii with bound l-methionine
84	c4wv4A_	Alignment	not modelled	22.6	21	PDB header: transcription Chain: A: PDB Molecule: transcription initiation factor tfiid subunit 10; PDBTitle: heterodimer of taf8/taf10
85	c3c8zB_	Alignment	not modelled	21.9	23	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
86	c3tunA_	Alignment	not modelled	21.5	20	PDB header: ligase/ligase inhibitor Chain: A: PDB Molecule: methionyl-trna synthetase; PDBTitle: trypanosoma brucei methionyl-trna synthetase in complex with inhibitor2 chem 1356
87	c1r6tA_	Alignment	not modelled	21.5	16	PDB header: ligase Chain: A: PDB Molecule: tryptophanyl-trna synthetase; PDBTitle: crystal structure of human tryptophanyl-trna synthetase
88	d1li5a2	Alignment	not modelled	20.3	13	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Nucleotidylyl transferase Family: Class I aminoacyl-tRNA synthetases (RS), catalytic domain
89	c2x1IC_	Alignment	not modelled	19.9	17	PDB header: ligase Chain: C: PDB Molecule: methionyl-trna synthetase; PDBTitle: crystal structure of mycobacterium smegmatis methionyl-trna synthetase2 in complex with methionine and adenosine
90	d1iq0a2	Alignment	not modelled	19.7	28	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Nucleotidylyl transferase Family: Class I aminoacyl-tRNA synthetases (RS), catalytic domain
91	c4dIpA_	Alignment	not modelled	17.5	13	PDB header: ligase Chain: A: PDB Molecule: aminoacyl-trna synthetase, class i:aminoacyl-trna PDBTitle: crystal structure of methionyl-trna synthetase metrs from brucella2 melitensis bound to selenomethionine
92	d2bisa1	Alignment	not modelled	16.7	30	Fold: UDP-Glycosyltransferase/glycogen phosphorylase Superfamily: UDP-Glycosyltransferase/glycogen phosphorylase Family: Glycosyl transferases group 1
93	c3beoA_	Alignment	not modelled	15.9	5	PDB header: isomerase Chain: A: PDB Molecule: udp-n-acetylglucosamine 2-epimerase; PDBTitle: a structural basis for the allosteric regulation of non-2 hydrolyzing udp-glcnaC 2-epimerases
94	d1jw2a_	Alignment	not modelled	15.4	14	Fold: Open three-helical up-and-down bundle Superfamily: Hemolysin expression modulating protein HHA Family: Hemolysin expression modulating protein HHA
95	c3kfiA_	Alignment	not modelled	15.3	23	PDB header: ligase Chain: A: PDB Molecule: methionyl-trna synthetase; PDBTitle: leishmania major methionyl-trna synthetase in complex with2 methionyladenylate and pyrophosphate
96	c1pfuA_	Alignment	not modelled	14.9	20	PDB header: ligase Chain: A: PDB Molecule: methionyl-trna synthetase; PDBTitle: methionyl-trna synthetase from escherichia coli complexed2 with methionine phosphinate
97	c5xgqB_	Alignment	not modelled	14.9	16	PDB header: ligase Chain: B: PDB Molecule: methionine-trna ligase; PDBTitle: crystal structure of apo form (free-state) mycobacterium tuberculosis2 methionyl-trna synthetase
98	c1iq0A_	Alignment	not modelled	13.8	20	PDB header: ligase Chain: A: PDB Molecule: arginyl-trna synthetase; PDBTitle: thermus thermophilus arginyl-trna synthetase
99	c1woyA_	Alignment	not modelled	13.5	13	PDB header: ligase Chain: A: PDB Molecule: methionyl-trna synthetase; PDBTitle: crystal structure of methionyl trna synthetase y225f mutant2 from thermus thermophilus