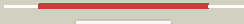



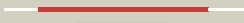





















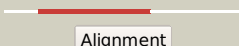

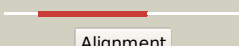

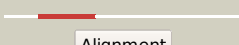

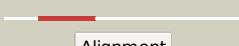

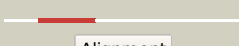


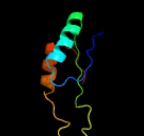

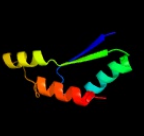
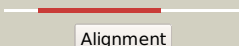


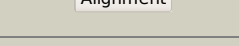

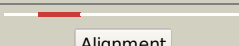
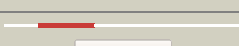



# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3602c_panC_4044460_4045389
Date	Fri Aug 9 18:20:28 BST 2019
Unique Job ID	812cd99a3998f5ca

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">d2a84a1</a>	 Alignment		100.0	100	<b>Fold:</b> Adenine nucleotide alpha hydrolase-like <b>Superfamily:</b> Nucleotidylyl transferase <b>Family:</b> Pantothenate synthetase (Pantoate-beta-alanine ligase, PanC)
2	<a href="#">c2ejcA</a>	 Alignment		100.0	41	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> pantoate--beta-alanine ligase; <b>PDBTitle:</b> crystal structure of pantoate--beta-alanine ligase (panc)2 from thermotoga maritima
3	<a href="#">d1ihoA</a>	 Alignment		100.0	45	<b>Fold:</b> Adenine nucleotide alpha hydrolase-like <b>Superfamily:</b> Nucleotidylyl transferase <b>Family:</b> Pantothenate synthetase (Pantoate-beta-alanine ligase, PanC)
4	<a href="#">c3mxtA</a>	 Alignment		100.0	36	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> pantothenate synthetase; <b>PDBTitle:</b> crystal structure of pantoate-beta-alanine ligase from campylobacter2 jejuni
5	<a href="#">c3ag5A</a>	 Alignment		100.0	40	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> pantothenate synthetase; <b>PDBTitle:</b> crystal structure of pantothenate synthetase from staphylococcus2 aureus
6	<a href="#">d1v8fa</a>	 Alignment		100.0	46	<b>Fold:</b> Adenine nucleotide alpha hydrolase-like <b>Superfamily:</b> Nucleotidylyl transferase <b>Family:</b> Pantothenate synthetase (Pantoate-beta-alanine ligase, PanC)
7	<a href="#">c3uk2B</a>	 Alignment		100.0	44	<b>PDB header:</b> ligase <b>Chain:</b> B: <b>PDB Molecule:</b> pantothenate synthetase; <b>PDBTitle:</b> the structure of pantothenate synthetase from burkholderia2 thailandensis
8	<a href="#">c3innB</a>	 Alignment		100.0	44	<b>PDB header:</b> ligase <b>Chain:</b> B: <b>PDB Molecule:</b> pantothenate synthetase; <b>PDBTitle:</b> crystal structure of pantoate-beta-alanine-ligase in complex2 with atp at low occupancy at 2.1 a resolution
9	<a href="#">c3n8hA</a>	 Alignment		100.0	37	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> pantothenate synthetase; <b>PDBTitle:</b> crystal structure of pantoate-beta-alanine ligase from francisella2 tularensis
10	<a href="#">c5kwvA</a>	 Alignment		100.0	47	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> pantothenate synthetase; <b>PDBTitle:</b> crystal structure of a pantoate-beta-alanine ligase from neisseria2 gonorrhoeae with bound amppnp
11	<a href="#">c3guzB</a>	 Alignment		100.0	48	<b>PDB header:</b> ligase <b>Chain:</b> B: <b>PDB Molecule:</b> pantothenate synthetase; <b>PDBTitle:</b> structural and substrate-binding studies of pantothenate2 synthenate (ps)provide insights into homotropic inhibition3 by pantoate in ps's

12	<a href="#">c2x0kB_</a>	 Alignment		97.9	14	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> riboflavin biosynthesis protein ribf; <b>PDBTitle:</b> crystal structure of modular fad synthetase from2 corynebacterium ammoniagenes
13	<a href="#">c5xf2B_</a>	 Alignment		97.4	19	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> putative cytidyltransferase; <b>PDBTitle:</b> crystal structure of semet-hldc from burkholderia pseudomallei
14	<a href="#">c3glvB_</a>	 Alignment		97.0	20	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> B: <b>PDB Molecule:</b> lipopolysaccharide core biosynthesis protein; <b>PDBTitle:</b> crystal structure of the lipopolysaccharide core biosynthesis protein2 from thermoplasma volcanium gss1
15	<a href="#">c3gmiA_</a>	 Alignment		96.8	16	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> upf0348 protein mj0951; <b>PDBTitle:</b> crystal structure of a protein of unknown function from2 methanocaldococcus jannaschii
16	<a href="#">c3elbA_</a>	 Alignment		96.4	16	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> ethanolamine-phosphate cytidyltransferase; <b>PDBTitle:</b> human ctp: phosphoethanolamine cytidyltransferase in complex with2 cmp
17	<a href="#">d1coza_</a>	 Alignment		96.3	21	<b>Fold:</b> Adenine nucleotide alpha hydrolase-like <b>Superfamily:</b> Nucleotidyl transferase <b>Family:</b> Cytidyltransferase
18	<a href="#">c4zcsE_</a>	 Alignment		96.1	16	<b>PDB header:</b> transferase <b>Chain:</b> E: <b>PDB Molecule:</b> choline-phosphate cytidyltransferase; <b>PDBTitle:</b> crystal structure of the c-terminal catalytic domain of plasmodium2 falciparum ctp:phosphocholine cytidyltransferase in complex with3 cdp-choline
19	<a href="#">c3op1A_</a>	 Alignment		96.1	25	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> macrolide-efflux protein; <b>PDBTitle:</b> crystal structure of macrolide-efflux protein sp_1110 from2 streptococcus pneumoniae
20	<a href="#">d1qjca_</a>	 Alignment		95.9	19	<b>Fold:</b> Adenine nucleotide alpha hydrolase-like <b>Superfamily:</b> Nucleotidyl transferase <b>Family:</b> Adenylyltransferase
21	<a href="#">c3ikzA_</a>	 Alignment	not modelled	95.9	15	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> phosphopantetheine adenylyltransferase; <b>PDBTitle:</b> crystal structure of phosphopantetheine adenylyltransferase from2 burkholderia pseudomallei
22	<a href="#">c3x1mC_</a>	 Alignment	not modelled	95.9	15	<b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> phosphopantetheine adenylyltransferase; <b>PDBTitle:</b> crystal structure of phosphopantetheine adenylyltransferase/ppat from2 pseudomonas aeruginosa with coa
23	<a href="#">c3nv7A_</a>	 Alignment	not modelled	95.9	10	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> phosphopantetheine adenylyltransferase; <b>PDBTitle:</b> crystal structure of h.pylori phosphopantetheine adenylyltransferase2 mutant i4v/n76y
24	<a href="#">c5h16D_</a>	 Alignment	not modelled	95.7	24	<b>PDB header:</b> transferase <b>Chain:</b> D: <b>PDB Molecule:</b> phosphopantetheine adenylyltransferase; <b>PDBTitle:</b> crystal structure of the complex of phosphopantetheine2 adenylyltransferase from acinetobacter baumannii with citrate at 2.33 a resolution.
25	<a href="#">d1vlha_</a>	 Alignment	not modelled	95.5	17	<b>Fold:</b> Adenine nucleotide alpha hydrolase-like <b>Superfamily:</b> Nucleotidyl transferase <b>Family:</b> Adenylyltransferase
26	<a href="#">c2b7ID_</a>	 Alignment	not modelled	95.5	21	<b>PDB header:</b> transferase <b>Chain:</b> D: <b>PDB Molecule:</b> glycerol-3-phosphate cytidyltransferase; <b>PDBTitle:</b> crystal structure of ctp:glycerol-3-phosphate2 cytidyltransferase from staphylococcus aureus
27	<a href="#">c6gyeB_</a>	 Alignment	not modelled	95.4	18	<b>PDB header:</b> transport protein <b>Chain:</b> B: <b>PDB Molecule:</b> nicotinamide-nucleotide adenylyltransferase nadr family / <b>PDBTitle:</b> crystal structure of nadr protein in complex with nr
28	<a href="#">c5y0nB_</a>	 Alignment	not modelled	95.2	24	<b>PDB header:</b> ligase <b>Chain:</b> B: <b>PDB Molecule:</b> upf0348 protein b4417_3650; <b>PDBTitle:</b> crystal structure of bacillus subtilis tmc1 bound with atp (semet2 derivative)

29	<a href="#">d1o6ba</a>	Alignment	not modelled	95.2	18	<b>Fold:</b> Adenine nucleotide alpha hydrolase-like <b>Superfamily:</b> Nucleotidylyl transferase <b>Family:</b> Adenylyltransferase
30	<a href="#">d1mrza2</a>	Alignment	not modelled	95.2	17	<b>Fold:</b> Adenine nucleotide alpha hydrolase-like <b>Superfamily:</b> Nucleotidylyl transferase <b>Family:</b> Adenylyltransferase
31	<a href="#">c5x3dA</a>	Alignment	not modelled	95.0	18	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> phosphoenolpyruvate phosphomutase; <b>PDBTitle:</b> crystal structure of hep-cmp-bound form of cytidylyltransferase2 (cytase) domain of fom1 from streptomyces wedmorensis
32	<a href="#">c3e27B</a>	Alignment	not modelled	95.0	16	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> nicotinate (nicotinamide) nucleotide adenylyltransferase; <b>PDBTitle:</b> nicotinic acid mononucleotide (namn) adenylyltransferase from bacillus2 anthracis: product complex
33	<a href="#">c5y0tD</a>	Alignment	not modelled	94.5	18	<b>PDB header:</b> ligase <b>Chain:</b> D: <b>PDB Molecule:</b> thermotoga maritima tmcal; <b>PDBTitle:</b> crystal structure of thermotoga maritima tmcal bound with alpha-thio2 atp(form ii)
34	<a href="#">c1t6zB</a>	Alignment	not modelled	94.3	18	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> riboflavin kinase/fmn adenylyltransferase; <b>PDBTitle:</b> crystal structure of riboflavin bound tm379
35	<a href="#">c4f3rC</a>	Alignment	not modelled	94.3	13	<b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> phosphopantetheine adenylyltransferase; <b>PDBTitle:</b> structure of phosphopantetheine adenylyltransferase (cbu_0288) from2 coxiella burnetii
36	<a href="#">c3hl4B</a>	Alignment	not modelled	94.0	18	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> choline-phosphate cytidylyltransferase a; <b>PDBTitle:</b> crystal structure of a mammalian ctp:phosphocholine2 cytidylyltransferase with cdp-choline
37	<a href="#">d1tfua</a>	Alignment	not modelled	93.9	20	<b>Fold:</b> Adenine nucleotide alpha hydrolase-like <b>Superfamily:</b> Nucleotidylyl transferase <b>Family:</b> Adenylyltransferase
38	<a href="#">c3f3mA</a>	Alignment	not modelled	93.8	9	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> phosphopantetheine adenylyltransferase; <b>PDBTitle:</b> six crystal structures of two phosphopantetheine adenylyltransferases2 reveal an alternative ligand binding mode and an associated3 structural change
39	<a href="#">d1f9aa</a>	Alignment	not modelled	93.7	13	<b>Fold:</b> Adenine nucleotide alpha hydrolase-like <b>Superfamily:</b> Nucleotidylyl transferase <b>Family:</b> Adenylyltransferase
40	<a href="#">c2r5wA</a>	Alignment	not modelled	92.8	15	<b>PDB header:</b> hydrolase, transferase <b>Chain:</b> A: <b>PDB Molecule:</b> nicotinamide-nucleotide adenylyltransferase; <b>PDBTitle:</b> crystal structure of a bifunctional nmn2 adenylyltransferase/adp ribose pyrophosphatase from3 francisella tularensis
41	<a href="#">c2h29A</a>	Alignment	not modelled	92.8	7	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> probable nicotinate-nucleotide <b>PDBTitle:</b> crystal structure of nicotinic acid mononucleotide2 adenylyltransferase from staphylococcus aureus: product3 bound form 1
42	<a href="#">c1lw7A</a>	Alignment	not modelled	92.5	11	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulator nadr; <b>PDBTitle:</b> nadr protein from haemophilus influenzae
43	<a href="#">d1lw7a1</a>	Alignment	not modelled	92.4	15	<b>Fold:</b> Adenine nucleotide alpha hydrolase-like <b>Superfamily:</b> Nucleotidylyl transferase <b>Family:</b> Adenylyltransferase
44	<a href="#">c3nd5D</a>	Alignment	not modelled	92.4	20	<b>PDB header:</b> transferase <b>Chain:</b> D: <b>PDB Molecule:</b> phosphopantetheine adenylyltransferase; <b>PDBTitle:</b> crystal structure of phosphopantetheine adenylyltransferase (ppat)2 from enterococcus faecalis
45	<a href="#">d1od6a</a>	Alignment	not modelled	92.0	31	<b>Fold:</b> Adenine nucleotide alpha hydrolase-like <b>Superfamily:</b> Nucleotidylyl transferase <b>Family:</b> Adenylyltransferase
46	<a href="#">d1jhda2</a>	Alignment	not modelled	91.9	18	<b>Fold:</b> Adenine nucleotide alpha hydrolase-like <b>Superfamily:</b> Nucleotidylyl transferase <b>Family:</b> ATP sulfurylase catalytic domain
47	<a href="#">c1v47B</a>	Alignment	not modelled	91.9	24	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> atp sulfurylase; <b>PDBTitle:</b> crystal structure of atp sulfurylase from thermus2 thermophilus hb8 in complex with aps
48	<a href="#">c5lltB</a>	Alignment	not modelled	91.7	2	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> nicotinate-nucleotide adenylyltransferase; <b>PDBTitle:</b> plasmodium falciparum nicotinic acid mononucleotide2 adenylyltransferase complexed with naad
49	<a href="#">c1yunB</a>	Alignment	not modelled	91.6	20	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> probable nicotinate-nucleotide <b>PDBTitle:</b> crystal structure of nicotinic acid mononucleotide2 adenylyltransferase from pseudomonas aeruginosa
50	<a href="#">c4rpiA</a>	Alignment	not modelled	91.4	26	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> nicotinate-nucleotide adenylyltransferase; <b>PDBTitle:</b> crystal structure of nicotinate mononucleotide adenylyltransferase2 from mycobacterium tuberculosis
51	<a href="#">c3cr8C</a>	Alignment	not modelled	90.9	12	<b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> sulfate adenylyltransferase, adenylylsulfate kinase; <b>PDBTitle:</b> hexameric aps kinase from thiobacillus denitrificans
52	<a href="#">d1ej2a</a>	Alignment	not modelled	90.7	20	<b>Fold:</b> Adenine nucleotide alpha hydrolase-like <b>Superfamily:</b> Nucleotidylyl transferase <b>Family:</b> Adenylyltransferase
53	<a href="#">c2qjoB</a>	Alignment	not modelled	90.3	19	<b>PDB header:</b> transferase, hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> bifunctional nmn adenylyltransferase/nudix hydrolase; <b>PDBTitle:</b> crystal structure of a bifunctional nmn

						adenylyltransferase/adp ribose2 pyrophosphatase (nadm) complexed with adprp and nad from3 synechocystis sp.
54	<a href="#">c1m8pB_</a>	Alignment	not modelled	89.7	19	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> sulfate adenylyltransferase; <b>PDBTitle:</b> crystal structure of p. chrysogenum atp sulfurylase in the t-state
55	<a href="#">c4wsoA_</a>	Alignment	not modelled	89.7	31	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> probable nicotinate-nucleotide adenylyltransferase; <b>PDBTitle:</b> x-ray crystal structure of a nicotinate nucleotide adenylyltransferase2 from burkholderia thailandensis bound to nad
56	<a href="#">c2gksB_</a>	Alignment	not modelled	89.6	27	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> bifunctional sat/aps kinase; <b>PDBTitle:</b> crystal structure of the bi-functional atp sulfurylase-aps kinase from2 aquifex aeolicus, a chemolithotrophic thermophile
57	<a href="#">d1g8fa2</a>	Alignment	not modelled	89.3	19	<b>Fold:</b> Adenine nucleotide alpha hydrolase-like <b>Superfamily:</b> Nucleotidyl transferase <b>Family:</b> ATP sulfurylase catalytic domain
58	<a href="#">d1v47a2</a>	Alignment	not modelled	89.3	21	<b>Fold:</b> Adenine nucleotide alpha hydrolase-like <b>Superfamily:</b> Nucleotidyl transferase <b>Family:</b> ATP sulfurylase catalytic domain
59	<a href="#">c1r6xA_</a>	Alignment	not modelled	88.8	20	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> atp:sulfate adenylyltransferase; <b>PDBTitle:</b> the crystal structure of a truncated form of yeast atp2 sulfurylase, lacking the c-terminal aps kinase-like domain,3 in complex with sulfate
60	<a href="#">c3h05A_</a>	Alignment	not modelled	88.5	8	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein vpa0413; <b>PDBTitle:</b> the crystal structure of a putative nicotinate-nucleotide2 adenylyltransferase from vibrio parahaemolyticus
61	<a href="#">d1m8pa2</a>	Alignment	not modelled	88.4	21	<b>Fold:</b> Adenine nucleotide alpha hydrolase-like <b>Superfamily:</b> Nucleotidyl transferase <b>Family:</b> ATP sulfurylase catalytic domain
62	<a href="#">c2cycB_</a>	Alignment	not modelled	87.7	11	<b>PDB header:</b> ligase <b>Chain:</b> B: <b>PDB Molecule:</b> tyrosyl-trna synthetase; <b>PDBTitle:</b> crystal structure of tyrosyl-trna synthetase complexed with l-tyrosine2 from pyrococcus horikoshii
63	<a href="#">c1jhdA_</a>	Alignment	not modelled	87.3	17	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> sulfate adenylyltransferase; <b>PDBTitle:</b> crystal structure of bacterial atp sulfurylase from the2 riftia pachyptila symbiont
64	<a href="#">c2cybA_</a>	Alignment	not modelled	86.8	15	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> tyrosyl-trna synthetase; <b>PDBTitle:</b> crystal structure of tyrosyl-trna synthetase complexed with2 l-tyrosine from archaeoglobus fulgidus
65	<a href="#">d1kama_</a>	Alignment	not modelled	86.7	18	<b>Fold:</b> Adenine nucleotide alpha hydrolase-like <b>Superfamily:</b> Nucleotidyl transferase <b>Family:</b> Adenylyltransferase
66	<a href="#">c4mvcA_</a>	Alignment	not modelled	85.8	29	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> choline-phosphate cytidyl transferase a; <b>PDBTitle:</b> crystal structure of a mammalian cytidyl transferase
67	<a href="#">c1g8gB_</a>	Alignment	not modelled	83.6	21	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> sulfate adenylyltransferase; <b>PDBTitle:</b> atp sulfurylase from s. cerevisiae: the binary product complex with2 aps
68	<a href="#">d1kr2a_</a>	Alignment	not modelled	83.3	17	<b>Fold:</b> Adenine nucleotide alpha hydrolase-like <b>Superfamily:</b> Nucleotidyl transferase <b>Family:</b> Adenylyltransferase
69	<a href="#">c3vgjB_</a>	Alignment	not modelled	83.2	12	<b>PDB header:</b> ligase <b>Chain:</b> B: <b>PDB Molecule:</b> tyrosyl-trna synthetase, putative; <b>PDBTitle:</b> crystal of plasmodium falciparum tyrosyl-trna synthetase (pftyrrs)in2 complex with adenylate analog
70	<a href="#">d1nuua_</a>	Alignment	not modelled	82.7	15	<b>Fold:</b> Adenine nucleotide alpha hydrolase-like <b>Superfamily:</b> Nucleotidyl transferase <b>Family:</b> Adenylyltransferase
71	<a href="#">c2j5bA_</a>	Alignment	not modelled	82.7	12	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> tyrosyl-trna synthetase; <b>PDBTitle:</b> structure of the tyrosyl trna synthetase from acanthamoeba polyphaga2 mimivirus complexed with tyrosinol
72	<a href="#">c3focB_</a>	Alignment	not modelled	82.6	17	<b>PDB header:</b> ligase <b>Chain:</b> B: <b>PDB Molecule:</b> tryptophanyl-trna synthetase; <b>PDBTitle:</b> tryptophanyl-trna synthetase from giardia lamblia
73	<a href="#">c3do8B_</a>	Alignment	not modelled	79.2	32	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> phosphopantetheine adenylyltransferase; <b>PDBTitle:</b> the crystal structure of the protein with unknown function from2 archaeoglobus fulgidus
74	<a href="#">d1x6va2</a>	Alignment	not modelled	78.8	10	<b>Fold:</b> Adenine nucleotide alpha hydrolase-like <b>Superfamily:</b> Nucleotidyl transferase <b>Family:</b> ATP sulfurylase catalytic domain
75	<a href="#">d1i6la_</a>	Alignment	not modelled	74.6	16	<b>Fold:</b> Adenine nucleotide alpha hydrolase-like <b>Superfamily:</b> Nucleotidyl transferase <b>Family:</b> Class I aminoacyl-tRNA synthetases (RS), catalytic domain
76	<a href="#">d1k4ma_</a>	Alignment	not modelled	73.9	23	<b>Fold:</b> Adenine nucleotide alpha hydrolase-like <b>Superfamily:</b> Nucleotidyl transferase <b>Family:</b> Adenylyltransferase
77	<a href="#">c1xjqA_</a>	Alignment	not modelled	69.4	10	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> bifunctional 3'-phosphoadenosine 5'-phosphosulfate <b>PDBTitle:</b> adp complex of human paps synthetase 1
78	<a href="#">c1xnjB_</a>	Alignment	not modelled	65.1	13	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> bifunctional 3'-phosphoadenosine 5'-phosphosulfate <b>PDBTitle:</b> aps complex of human paps synthetase 1
79	<a href="#">c3ivpB_</a>	Alignment	not modelled	63.6	15	<b>PDB header:</b> ligase <b>Chain:</b> B: <b>PDB Molecule:</b> tryptophanyl-trna synthetase;

79	<a href="#">c3jx6B</a>	Alignment	not modelled	63.8	13	<b>PDBTitle:</b> crystal structure of pyrococcus horikoshii tryptophanyl-trna2 synthetase in complex with trpamp
80	<a href="#">c3ctzA</a>	Alignment	not modelled	62.6	10	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> xaa-pro aminopeptidase 1; <b>PDBTitle:</b> structure of human cytosolic x-prolyl aminopeptidase
81	<a href="#">c1h3eA</a>	Alignment	not modelled	61.7	17	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> tyrosyl-trna synthetase; <b>PDBTitle:</b> tyrosyl-trna synthetase from thermus thermophilus complexed with wild-2 type trnatyr(gua) and with atp and tyrosinol
82	<a href="#">c6byqA</a>	Alignment	not modelled	60.7	20	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> tyrosine--trna ligase; <b>PDBTitle:</b> crystal structure of tyrosine-trna ligase from helicobacter pylori g27
83	<a href="#">c2yv4A</a>	Alignment	not modelled	59.5	15	<b>PDB header:</b> rna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical protein ph0435; <b>PDBTitle:</b> crystal structure of c-terminal sua5 domain from pyrococcus horikoshii2 hypothetical sua5 protein ph0435
84	<a href="#">c3igsB</a>	Alignment	not modelled	59.4	21	<b>PDB header:</b> isomerase <b>Chain:</b> B: <b>PDB Molecule:</b> n-acetylmannosamine-6-phosphate 2-epimerase 2; <b>PDBTitle:</b> structure of the salmonella enterica n-acetylmannosamine-6-phosphate2 2-epimerase
85	<a href="#">c3prhB</a>	Alignment	not modelled	58.3	13	<b>PDB header:</b> ligase <b>Chain:</b> B: <b>PDB Molecule:</b> tryptophanyl-trna synthetase; <b>PDBTitle:</b> tryptophanyl-trna synthetase val144pro mutant from b. subtilis
86	<a href="#">c2cyaA</a>	Alignment	not modelled	58.2	14	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> tyrosyl-trna synthetase; <b>PDBTitle:</b> crystal structure of tyrosyl-trna synthetase from aeropyrum pernix
87	<a href="#">c6otjA</a>	Alignment	not modelled	55.2	20	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> tyrosine--trna ligase; <b>PDBTitle:</b> crystal structure of tyrosyl-trna synthetase from neisseria2 gonorrhoeae with bound l-tyr
88	<a href="#">c2yy5C</a>	Alignment	not modelled	50.5	14	<b>PDB header:</b> ligase <b>Chain:</b> C: <b>PDB Molecule:</b> tryptophanyl-trna synthetase; <b>PDBTitle:</b> crystal structure of tryptophanyl-trna synthetase from mycoplasma2 pneumoniae
89	<a href="#">d1zh8a1</a>	Alignment	not modelled	50.1	12	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
90	<a href="#">c2g36A</a>	Alignment	not modelled	49.5	22	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> tryptophanyl-trna synthetase; <b>PDBTitle:</b> crystal structure of tryptophanyl-trna synthetase (ec 6.1.1.2)2 (tryptophan-trna ligase)(trprs) (tm0492) from thermotoga maritima at3 2.50 a resolution
91	<a href="#">c2qjfB</a>	Alignment	not modelled	49.0	15	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> bifunctional 3'-phosphoadenosine 5'- <b>PDBTitle:</b> crystal structure of atp-sulfurylase domain of human paps2 synthetase 1
92	<a href="#">c1q11A</a>	Alignment	not modelled	47.9	12	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> tyrosyl-trna synthetase; <b>PDBTitle:</b> crystal structure of an active fragment of human tyrosyl-trna2 synthetase with tyrosinol
93	<a href="#">c2xsbA</a>	Alignment	not modelled	47.4	21	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> hyaluronoglucosaminidase; <b>PDBTitle:</b> ogoga pugnac complex
94	<a href="#">d1xjca</a>	Alignment	not modelled	46.9	26	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> Nitrogenase iron protein-like
95	<a href="#">d2f48a1</a>	Alignment	not modelled	46.6	23	<b>Fold:</b> Phosphofructokinase <b>Superfamily:</b> Phosphofructokinase <b>Family:</b> Phosphofructokinase
96	<a href="#">c4s2tP</a>	Alignment	not modelled	45.5	13	<b>PDB header:</b> hydrolase/hydrolase inhibitor <b>Chain:</b> P: <b>PDB Molecule:</b> protein app-1; <b>PDBTitle:</b> crystal structure of x-prolyl aminopeptidase from caenorhabditis2 elegans: a cytosolic enzyme with a di-nuclear active site
97	<a href="#">c2ip1A</a>	Alignment	not modelled	42.8	11	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> tryptophanyl-trna synthetase; <b>PDBTitle:</b> crystal structure analysis of s. cerevisiae tryptophanyl trna2 synthetase
98	<a href="#">c2higA</a>	Alignment	not modelled	42.7	17	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> 6-phospho-1-fructokinase; <b>PDBTitle:</b> crystal structure of phosphofructokinase apoenzyme from trypanosoma2 brucei.
99	<a href="#">c3n9iA</a>	Alignment	not modelled	42.7	20	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> tryptophanyl-trna synthetase; <b>PDBTitle:</b> crystal structure of tryptophanyl-trna synthetase from yersinia pestis2 co92
100	<a href="#">c4pt2B</a>	Alignment	not modelled	40.9	30	<b>PDB header:</b> virus like particle <b>Chain:</b> B: <b>PDB Molecule:</b> encapsulin protein; <b>PDBTitle:</b> myxococcus xanthus encapsulin protein (enca)
101	<a href="#">c5b19A</a>	Alignment	not modelled	40.9	17	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> aspartate racemase; <b>PDBTitle:</b> picophilus torridus aspartate racemase
102	<a href="#">c6bqzA</a>	Alignment	not modelled	39.5	22	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> tyrosine--trna ligase; <b>PDBTitle:</b> crystal structure of tyrosine-trna synthetase from acetobacter2 baumannii with bound l-tyrosine
103	<a href="#">c4oudB</a>	Alignment	not modelled	39.5	23	<b>PDB header:</b> ligase <b>Chain:</b> B: <b>PDB Molecule:</b> tyrosyl-trna synthetase; <b>PDBTitle:</b> engineered tyrosyl-trna synthetase with the nonstandard amino acid l-2 4,4-biphenylalanine
104	<a href="#">c3p0jD</a>	Alignment	not modelled	39.5	14	<b>PDB header:</b> ligase <b>Chain:</b> D: <b>PDB Molecule:</b> tyrosyl-trna synthetase; <b>PDBTitle:</b> leishmania major tyrosyl-trna synthetase in complex with tyrosinol,2 triclinic crystal form 1



105	<a href="#">d1fpza_</a>	Alignment	not modelled	39.5	21	<b>Fold:</b> (Phosphotyrosine protein) phosphatases II <b>Superfamily:</b> (Phosphotyrosine protein) phosphatases II <b>Family:</b> Dual specificity phosphatase-like
106	<a href="#">c4oh7B_</a>	Alignment	not modelled	39.1	17	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> ornithine carbamoyltransferase; <b>PDBTitle:</b> crystal structure of ornithine carbamoyltransferase from brucella2 melitensis
107	<a href="#">c1zxaA_</a>	Alignment	not modelled	38.3	21	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> 6-phosphofructokinase; <b>PDBTitle:</b> the crystal structure of phosphofructokinase from lactobacillus2 delbrueckii
108	<a href="#">c2jmlA_</a>	Alignment	not modelled	38.0	12	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> dna binding domain/transcriptional regulator; <b>PDBTitle:</b> solution structure of the n-terminal domain of cara repressor
109	<a href="#">c2janD_</a>	Alignment	not modelled	37.7	17	<b>PDB header:</b> ligase <b>Chain:</b> D: <b>PDB Molecule:</b> tyrosyl-trna synthetase; <b>PDBTitle:</b> tyrosyl-trna synthetase from mycobacterium tuberculosis in2 unliganded state
110	<a href="#">d1vi9a_</a>	Alignment	not modelled	37.1	14	<b>Fold:</b> Ribokinase-like <b>Superfamily:</b> Ribokinase-like <b>Family:</b> PfkB-like kinase
111	<a href="#">c3wg9D_</a>	Alignment	not modelled	36.8	14	<b>PDB header:</b> transcription <b>Chain:</b> D: <b>PDB Molecule:</b> redox-sensing transcriptional repressor rex; <b>PDBTitle:</b> crystal structure of rsp, a rex-family repressor
112	<a href="#">c4ew6A_</a>	Alignment	not modelled	36.6	8	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> d-galactose-1-dehydrogenase protein; <b>PDBTitle:</b> crystal structure of d-galactose-1-dehydrogenase protein from2 rhizobium etli
113	<a href="#">c4oudA_</a>	Alignment	not modelled	36.4	23	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> tyrosyl-trna synthetase; <b>PDBTitle:</b> engineered tyrosyl-trna synthetase with the nonstandard amino acid l-2 4,4-biphenylalanine
114	<a href="#">d1jlua_</a>	Alignment	not modelled	36.1	14	<b>Fold:</b> Adenine nucleotide alpha hydrolase-like <b>Superfamily:</b> Nucleotidyl transferase <b>Family:</b> Class I aminoacyl-tRNA synthetases (RS), catalytic domain
115	<a href="#">c5ijxA_</a>	Alignment	not modelled	35.7	13	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> tyrosine--trna ligase, mitochondrial; <b>PDBTitle:</b> crystal structure of a c-terminally truncated coccidioides posadasii2 mitochondrial tyrosyl-trna synthetase
116	<a href="#">c2pqmA_</a>	Alignment	not modelled	35.6	12	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> cysteine synthase; <b>PDBTitle:</b> crystal structure of cysteine synthase (oass) from entamoeba2 histolytica at 1.86 a resolution
117	<a href="#">c6mtkA_</a>	Alignment	not modelled	35.5	21	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> tryptophanyl-trna synthetase; <b>PDBTitle:</b> crystal structure of tryptophanyl-trna synthetase from elizabethkingia2 anophelis nuhp1
118	<a href="#">c4s1aB_</a>	Alignment	not modelled	34.9	9	<b>PDB header:</b> unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> crystal structure of a hypothetical protein cthe_0052 from2 ruminiclostridium thermocellum atcc 27405
119	<a href="#">d1ekxa2</a>	Alignment	not modelled	34.5	15	<b>Fold:</b> ATC-like <b>Superfamily:</b> Aspartate/ornithine carbamoyltransferase <b>Family:</b> Aspartate/ornithine carbamoyltransferase
120	<a href="#">d1emsa2</a>	Alignment	not modelled	34.4	17	<b>Fold:</b> Carbon-nitrogen hydrolase <b>Superfamily:</b> Carbon-nitrogen hydrolase <b>Family:</b> Nitrilase