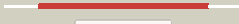



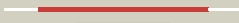




















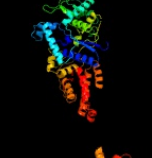
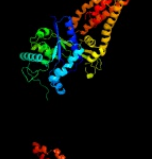

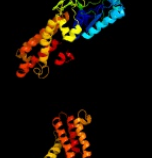

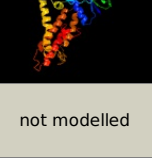


# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1292_(argS)_1446385_1448037
Date	Wed Jul 31 22:05:38 BST 2019
Unique Job ID	f590372f5fc3aa6c

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c4r3zB_</a>	 Alignment		100.0	24	<b>PDB header:</b> protein binding/ligase <b>Chain:</b> B: <b>PDB Molecule:</b> arginine--trna ligase, cytoplasmic; <b>PDBTitle:</b> crystal structure of human argrs-glnrs-aimp1 complex
2	<a href="#">c1f7uA_</a>	 Alignment		100.0	28	<b>PDB header:</b> ligase/rna <b>Chain:</b> A: <b>PDB Molecule:</b> arginyl-trna synthetase; <b>PDBTitle:</b> crystal structure of the arginyl-trna synthetase complexed with the2 trna(arg) and l-arg
3	<a href="#">c2zufA_</a>	 Alignment		100.0	28	<b>PDB header:</b> ligase/rna <b>Chain:</b> A: <b>PDB Molecule:</b> arginyl-trna synthetase; <b>PDBTitle:</b> crystal structure of pyrococcus horikoshii arginyl-trna2 synthetase complexed with trna(arg)
4	<a href="#">c5jldA_</a>	 Alignment		100.0	16	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> arginyl-trna synthetase, putative; <b>PDBTitle:</b> crystal structure of arginyl-trna synthetase from plasmodium2 falciparum (pfrrs)
5	<a href="#">c6ao8A_</a>	 Alignment		100.0	27	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> arginine--trna ligase; <b>PDBTitle:</b> crystal structure of arginyl-trna_synthetase from neisseria2 gonorrhoeae in complex with arginine
6	<a href="#">c4obyA_</a>	 Alignment		100.0	26	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> arginine--trna ligase; <b>PDBTitle:</b> crystal structure of e.coli arginyl-trna synthetase and ligand binding2 studies revealed key residues in arginine recognition
7	<a href="#">c4q2tB_</a>	 Alignment		100.0	23	<b>PDB header:</b> ligase <b>Chain:</b> B: <b>PDB Molecule:</b> arginine--trna ligase, cytoplasmic; <b>PDBTitle:</b> crystal structure of arginyl-trna synthetase complexed with l-arginine
8	<a href="#">c1iq0A_</a>	 Alignment		100.0	26	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> arginyl-trna synthetase; <b>PDBTitle:</b> thermus thermophilus arginyl-trna synthetase
9	<a href="#">c3fnrA_</a>	 Alignment		100.0	33	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> arginyl-trna synthetase; <b>PDBTitle:</b> crystal structure of putative arginyl t-rna synthetase from2 campylobacter jejuni;
10	<a href="#">d1f7ua2</a>	 Alignment		100.0	23	<b>Fold:</b> Adenine nucleotide alpha hydrolase-like <b>Superfamily:</b> Nucleotidylyl transferase <b>Family:</b> Class I aminoacyl-tRNA synthetases (RS), catalytic domain
11	<a href="#">d1iq0a2</a>	 Alignment		100.0	21	<b>Fold:</b> Adenine nucleotide alpha hydrolase-like <b>Superfamily:</b> Nucleotidylyl transferase <b>Family:</b> Class I aminoacyl-tRNA synthetases (RS), catalytic domain

12	<a href="#">c2x1C_</a>	Alignment		100.0	19	<b>PDB header:</b> ligase <b>Chain:</b> C: <b>PDB Molecule:</b> methionyl-trna synthetase; <b>PDBTitle:</b> crystal structure of mycobacterium smegmatis methionyl-trna synthetase2 in complex with methionine and adenosine
13	<a href="#">c2ct8A_</a>	Alignment		100.0	17	<b>PDB header:</b> ligase/rna <b>Chain:</b> A: <b>PDB Molecule:</b> methionyl-trna synthetase; <b>PDBTitle:</b> crystal structure of aquifex aeolicus methionyl-trna2 synthetase complexed with trna(met) and methionyl-adenylate3 analogue
14	<a href="#">c4qrdA_</a>	Alignment		100.0	20	<b>PDB header:</b> ligase/ligase inhibitor <b>Chain:</b> A: <b>PDB Molecule:</b> methionyl-trna synthetase; <b>PDBTitle:</b> structure of methionyl-trna synthetase in complex with n-(1h-2 benzimidazol-2-ylmethyl)-n'-(2,4-dichlorophenyl)-6-(morpholin-4-yl)-3,1,3,5-triazine-2,4-diamine
15	<a href="#">c3tqoA_</a>	Alignment		100.0	16	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> cysteinyl-trna synthetase; <b>PDBTitle:</b> structure of the cysteinyl-trna synthetase (cyss) from coxiella2 burnetii.
16	<a href="#">c1woyA_</a>	Alignment		100.0	20	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> methionyl-trna synthetase; <b>PDBTitle:</b> crystal structure of methionyl trna synthetase y225f mutant2 from thermus thermophilus
17	<a href="#">c1pfuA_</a>	Alignment		100.0	19	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> methionyl-trna synthetase; <b>PDBTitle:</b> methionyl-trna synthetase from escherichia coli complexed2 with methionine phosphinate
18	<a href="#">c3tunA_</a>	Alignment		100.0	18	<b>PDB header:</b> ligase/ligase inhibitor <b>Chain:</b> A: <b>PDB Molecule:</b> methionyl-trna synthetase; <b>PDBTitle:</b> trypanosoma brucei methionyl-trna synthetase in complex with inhibitor2 chem 1356
19	<a href="#">c3kflA_</a>	Alignment		100.0	19	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> methionyl-trna synthetase; <b>PDBTitle:</b> leishmania major methionyl-trna synthetase in complex with2 methionyladenylate and pyrophosphate
20	<a href="#">c5urbB_</a>	Alignment		100.0	20	<b>PDB header:</b> ligase <b>Chain:</b> B: <b>PDB Molecule:</b> methionine--trna ligase; <b>PDBTitle:</b> crystal structure of methionyl-trna synthetase (metrs) from2 acinetobacter baumannii with bound l-methionine
21	<a href="#">c1rqgA_</a>	Alignment	not modelled	100.0	18	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> methionyl-trna synthetase; <b>PDBTitle:</b> methionyl-trna synthetase from pyrococcus abyssi
22	<a href="#">c1u0bB_</a>	Alignment	not modelled	100.0	21	<b>PDB header:</b> ligase/rna <b>Chain:</b> B: <b>PDB Molecule:</b> cysteinyl trna; <b>PDBTitle:</b> crystal structure of cysteinyl-trna synthetase binary2 complex with trnacys
23	<a href="#">c4dlpB_</a>	Alignment	not modelled	100.0	19	<b>PDB header:</b> ligase <b>Chain:</b> B: <b>PDB Molecule:</b> aminoacyl-trna synthetase, class i:aminoacyl-trna <b>PDBTitle:</b> crystal structure of methionyl-trna synthetase metrs from brucella2 melitensis bound to selenomethionine
24	<a href="#">d1ll5a2</a>	Alignment	not modelled	100.0	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
25	<a href="#">c4dlpA_</a>	Alignment	not modelled	100.0	18	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> aminoacyl-trna synthetase, class i:aminoacyl-trna <b>PDBTitle:</b> crystal structure of methionyl-trna synthetase metrs from brucella2 melitensis bound to selenomethionine
26	<a href="#">c5gl7A_</a>	Alignment	not modelled	100.0	14	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> methionine--trna ligase, cytoplasmic; <b>PDBTitle:</b> crystal structure of a truncated human cytosolic methionyl-trna2 synthetase
27	<a href="#">d1pfva2</a>	Alignment	not modelled	100.0	20	<b>Fold:</b> Adenine nucleotide alpha hydrolase-like <b>Superfamily:</b> Nucleotidyl transferase <b>Family:</b> Class I aminoacyl-tRNA synthetases (RS), catalytic domain
28	<a href="#">d1ivsa4</a>	Alignment	not modelled	100.0	22	<b>Fold:</b> Adenine nucleotide alpha hydrolase-like <b>Superfamily:</b> Nucleotidyl transferase <b>Family:</b> Class I aminoacyl-tRNA synthetases (RS), catalytic domain

29	<a href="#">d2d5ba2</a>	Alignment	not modelled	100.0	22	<b>Fold:</b> Adenine nucleotide alpha hydrolase-like <b>Superfamily:</b> Nucleotidyl transferase <b>Family:</b> Class I aminoacyl-tRNA synthetases (RS), catalytic domain
30	<a href="#">c5xgqB</a>	Alignment	not modelled	100.0	18	<b>PDB header:</b> ligase <b>Chain:</b> B: <b>PDB Molecule:</b> methionine-trna ligase; <b>PDBTitle:</b> crystal structure of apo form (free-state) mycobacterium tuberculosis2 methionyl-trna synthetase
31	<a href="#">c3sp1B</a>	Alignment	not modelled	100.0	19	<b>PDB header:</b> ligase <b>Chain:</b> B: <b>PDB Molecule:</b> cysteinyln-trna synthetase; <b>PDBTitle:</b> crystal structure of cysteinyln-trna synthetase (cyss) from borrelia2 burgdorferi
32	<a href="#">d1irxa2</a>	Alignment	not modelled	100.0	15	<b>Fold:</b> Adenine nucleotide alpha hydrolase-like <b>Superfamily:</b> Nucleotidyl transferase <b>Family:</b> Class I aminoacyl-tRNA synthetases (RS), catalytic domain
33	<a href="#">d1rqga2</a>	Alignment	not modelled	100.0	21	<b>Fold:</b> Adenine nucleotide alpha hydrolase-like <b>Superfamily:</b> Nucleotidyl transferase <b>Family:</b> Class I aminoacyl-tRNA synthetases (RS), catalytic domain
34	<a href="#">d1ffya3</a>	Alignment	not modelled	100.0	21	<b>Fold:</b> Adenine nucleotide alpha hydrolase-like <b>Superfamily:</b> Nucleotidyl transferase <b>Family:</b> Class I aminoacyl-tRNA synthetases (RS), catalytic domain
35	<a href="#">c1gaxB</a>	Alignment	not modelled	100.0	22	<b>PDB header:</b> ligase/rna <b>Chain:</b> B: <b>PDB Molecule:</b> valyl-trna synthetase; <b>PDBTitle:</b> crystal structure of thermus thermophilus valyl-trna2 synthetase complexed with trna(val) and valyl-adenylate3 analogue
36	<a href="#">c3ziua</a>	Alignment	not modelled	100.0	16	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> leucyl-trna synthetase; <b>PDBTitle:</b> crystal structure of mycoplasma mobile leucyl-trna2 synthetase with leu-ams in the active site
37	<a href="#">c1qu2A</a>	Alignment	not modelled	100.0	23	<b>PDB header:</b> ligase/rna <b>Chain:</b> A: <b>PDB Molecule:</b> isoleucyl-trna synthetase; <b>PDBTitle:</b> insights into editing from an ile-trna synthetase structure2 with trna(ile) and mupirocin
38	<a href="#">c3ziub</a>	Alignment	not modelled	100.0	13	<b>PDB header:</b> ligase <b>Chain:</b> B: <b>PDB Molecule:</b> leucyl-trna synthetase; <b>PDBTitle:</b> crystal structure of mycoplasma mobile leucyl-trna2 synthetase with leu-ams in the active site
39	<a href="#">c3c8zB</a>	Alignment	not modelled	100.0	20	<b>PDB header:</b> ligase <b>Chain:</b> B: <b>PDB Molecule:</b> cysteinyln-trna synthetase; <b>PDBTitle:</b> the 1.6 a crystal structure of mshc: the rate limiting2 enzyme in the mycothiol biosynthetic pathway
40	<a href="#">c5ah5B</a>	Alignment	not modelled	100.0	22	<b>PDB header:</b> ligase/rna <b>Chain:</b> B: <b>PDB Molecule:</b> leucine--trna ligase; <b>PDBTitle:</b> crystal structure of the ternary complex of agrobacterium2 radiobacter k84 agnb2 leu-trna-leuams
41	<a href="#">c1ileA</a>	Alignment	not modelled	100.0	17	<b>PDB header:</b> aminoacyl-trna synthetase <b>Chain:</b> A: <b>PDB Molecule:</b> isoleucyl-trna synthetase; <b>PDBTitle:</b> isoleucyl-trna synthetase
42	<a href="#">c1wz2B</a>	Alignment	not modelled	100.0	20	<b>PDB header:</b> ligase/rna <b>Chain:</b> B: <b>PDB Molecule:</b> leucyl-trna synthetase; <b>PDBTitle:</b> the crystal structure of leucyl-trna synthetase and trna(leucine)2 complex
43	<a href="#">d1iq0a1</a>	Alignment	not modelled	100.0	33	<b>Fold:</b> Anticodon-binding domain of a subclass of class I aminoacyl-tRNA synthetases <b>Superfamily:</b> Anticodon-binding domain of a subclass of class I aminoacyl-tRNA synthetases <b>Family:</b> Anticodon-binding domain of a subclass of class I aminoacyl-tRNA synthetases
44	<a href="#">d1ilea3</a>	Alignment	not modelled	100.0	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
45	<a href="#">c1wkbA</a>	Alignment	not modelled	100.0	20	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> leucyl-trna synthetase; <b>PDBTitle:</b> crystal structure of leucyl-trna synthetase from the2 archaeon pyrococcus horikoshii reveals a novel editing3 domain orientation
46	<a href="#">c1obhA</a>	Alignment	not modelled	100.0	24	<b>PDB header:</b> synthetase <b>Chain:</b> A: <b>PDB Molecule:</b> leucyl-trna synthetase; <b>PDBTitle:</b> leucyl-trna synthetase from thermus thermophilus complexed2 with a pre-transfer editing substrate analogue in both3 synthetic active site and editing site
47	<a href="#">c4ariA</a>	Alignment	not modelled	100.0	21	<b>PDB header:</b> ligase/rna <b>Chain:</b> A: <b>PDB Molecule:</b> leucine--trna ligase; <b>PDBTitle:</b> ternary complex of e. coli leucyl-trna synthetase, trna(leu) and the2 benzoxaborole an2679 in the editing conformation
48	<a href="#">d1f7ua1</a>	Alignment	not modelled	100.0	40	<b>Fold:</b> Anticodon-binding domain of a subclass of class I aminoacyl-tRNA synthetases <b>Superfamily:</b> Anticodon-binding domain of a subclass of class I aminoacyl-tRNA synthetases <b>Family:</b> Anticodon-binding domain of a subclass of class I aminoacyl-tRNA synthetases
49	<a href="#">c2bytD</a>	Alignment	not modelled	100.0	22	<b>PDB header:</b> synthetase <b>Chain:</b> D: <b>PDB Molecule:</b> leucyl-trna synthetase; <b>PDBTitle:</b> thermus thermophilus leucyl-trna synthetase complexed with2 a trnaleu transcript in the post-editing conformation
50	<a href="#">d1h3na3</a>	Alignment	not modelled	100.0	22	<b>Fold:</b> Adenine nucleotide alpha hydrolase-like <b>Superfamily:</b> Nucleotidyl transferase <b>Family:</b> Class I aminoacyl-tRNA synthetases (RS), catalytic domain
51	<a href="#">c6q8aA</a>	Alignment	not modelled	99.9	25	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> leucine--trna ligase; <b>PDBTitle:</b> neisseria gonorrhoeae leucyl-trna synthetase in complex with 5'-o-(n-2 (l-leucyl)-sulfamoyl)cytidine
52	<a href="#">c1irxA</a>	Alignment	not modelled	99.9	16	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> lysyl-trna synthetase; <b>PDBTitle:</b> crystal structure of class i lysyl-trna synthetase
53	<a href="#">c1g59A</a>	Alignment	not modelled	99.9	21	<b>PDB header:</b> ligase/rna <b>Chain:</b> A: <b>PDB Molecule:</b> glutamyl-trna synthetase; <b>PDBTitle:</b> glutamyl-trna synthetase complexed with trna(glu).

54	<a href="#">c6b1pA</a>	Alignment	not modelled	99.9	16	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> glutamate--trna ligase 1; <b>PDBTitle:</b> crystal structure of glutamate-trna synthetase from helicobacter2 pylori
55	<a href="#">c5h4vE</a>	Alignment	not modelled	99.9	18	<b>PDB header:</b> ligase <b>Chain:</b> E: <b>PDB Molecule:</b> glutamate--trna ligase; <b>PDBTitle:</b> structure of glutamyl-trna synthetase (xoo1504) from xanthomonas2 oryzae pv. oryzae
56	<a href="#">c5tgtA</a>	Alignment	not modelled	99.9	17	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> glutamate--trna ligase; <b>PDBTitle:</b> crystal structure of glytamyl-trna synthetase glurs from pseudomonas2 aeruginosa
57	<a href="#">c2cfoA</a>	Alignment	not modelled	99.9	17	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> glutamyl-trna synthetase; <b>PDBTitle:</b> non-discriminating glutamyl-trna synthetase from2 thermosynechococcus elongatus in complex with glu
58	<a href="#">c3gdzA</a>	Alignment	not modelled	99.9	31	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> arginyl-trna synthetase; <b>PDBTitle:</b> crystal structure of arginyl-trna synthetase from klebsiella2 pneumoniae subsp. pneumoniae
59	<a href="#">c3afhA</a>	Alignment	not modelled	99.9	18	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> glutamyl-trna synthetase 2; <b>PDBTitle:</b> crystal structure of thermotoga maritima nondiscriminating glutamyl-2 trna synthetase in complex with a glutamyl-amp analog
60	<a href="#">c2ja2A</a>	Alignment	not modelled	99.9	17	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> glutamyl-trna synthetase; <b>PDBTitle:</b> mycobacterium tuberculosis glutamyl-trna synthetase
61	<a href="#">c2o5rA</a>	Alignment	not modelled	99.8	18	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> glutamyl-trna synthetase 1; <b>PDBTitle:</b> crystal structure of glutamyl-trna synthetase 1 (ec 6.1.1.17)2 (glutamate-trna ligase 1) (glurs 1) (tm1351) from thermotoga maritima3 at 2.5 a resolution
62	<a href="#">c4griB</a>	Alignment	not modelled	99.8	16	<b>PDB header:</b> ligase <b>Chain:</b> B: <b>PDB Molecule:</b> glutamate--trna ligase; <b>PDBTitle:</b> crystal structure of a glutamyl-trna synthetase glurs from borrelia2 burgdorferi bound to glutamic acid and zinc
63	<a href="#">c6b1zA</a>	Alignment	not modelled	99.8	20	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> glutamate--trna ligase; <b>PDBTitle:</b> crystal structure of glutamate-trna synthetase from elizabethkingia2 anophelis
64	<a href="#">d1qtra2</a>	Alignment	not modelled	99.8	13	<b>Fold:</b> Adenine nucleotide alpha hydrolase-like <b>Superfamily:</b> Nucleotidyl transferase <b>Family:</b> Class I aminoacyl-tRNA synthetases (RS), catalytic domain
65	<a href="#">c3al0C</a>	Alignment	not modelled	99.8	20	<b>PDB header:</b> ligase/rna <b>Chain:</b> C: <b>PDB Molecule:</b> glutamyl-trna(gln) amidotransferase subunit c,linker, <b>PDBTitle:</b> crystal structure of the glutamine transamidosome from thermotoga2 maritima in the glutamylation state.
66	<a href="#">c4g6zA</a>	Alignment	not modelled	99.8	21	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> glutamate-trna ligase; <b>PDBTitle:</b> crystal structure of a glutamyl-trna synthetase glurs from2 burkholderia thailandensis bound to l-glutamate
67	<a href="#">d1iq0a3</a>	Alignment	not modelled	99.7	31	<b>Fold:</b> RRF/tRNA synthetase additional domain-like <b>Superfamily:</b> Arginyl-tRNA synthetase (ArgRS), N-terminal 'additional' domain <b>Family:</b> Arginyl-tRNA synthetase (ArgRS), N-terminal 'additional' domain
68	<a href="#">d1j09a2</a>	Alignment	not modelled	99.7	20	<b>Fold:</b> Adenine nucleotide alpha hydrolase-like <b>Superfamily:</b> Nucleotidyl transferase <b>Family:</b> Class I aminoacyl-tRNA synthetases (RS), catalytic domain
69	<a href="#">d1f7ua3</a>	Alignment	not modelled	99.7	27	<b>Fold:</b> RRF/tRNA synthetase additional domain-like <b>Superfamily:</b> Arginyl-tRNA synthetase (ArgRS), N-terminal 'additional' domain <b>Family:</b> Arginyl-tRNA synthetase (ArgRS), N-terminal 'additional' domain
70	<a href="#">c1exdA</a>	Alignment	not modelled	99.6	15	<b>PDB header:</b> ligase/rna <b>Chain:</b> A: <b>PDB Molecule:</b> glutamyl-trna synthetase; <b>PDBTitle:</b> crystal structure of a tight-binding glutamine trna bound2 to glutamine aminoacyl trna synthetase
71	<a href="#">c2hz7A</a>	Alignment	not modelled	99.6	19	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> glutamyl-trna synthetase; <b>PDBTitle:</b> crystal structure of the glutamyl-trna synthetase from deinococcus2 radiodurans
72	<a href="#">c5bnzA</a>	Alignment	not modelled	99.5	14	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> glutamine--trna ligase; <b>PDBTitle:</b> crystal structure of glutamine-trna ligase /glutamyl-trna synthetase2 (glnrs) from pseudomonas aeruginosa
73	<a href="#">c4p2bA</a>	Alignment	not modelled	99.5	16	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> glutamine aminoacyl-trna synthetase; <b>PDBTitle:</b> crystal structure of the apo form of the glutamyl-trna synthetase2 catalytic domain from toxoplasma gondii.
74	<a href="#">d1nzja</a>	Alignment	not modelled	99.5	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
75	<a href="#">c4r3zC</a>	Alignment	not modelled	99.4	21	<b>PDB header:</b> protein binding/ligase <b>Chain:</b> C: <b>PDB Molecule:</b> glutamine--trna ligase; <b>PDBTitle:</b> crystal structure of human argrs-glnrs-aimp1 complex
76	<a href="#">c4h3sA</a>	Alignment	not modelled	99.4	16	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> glutamine-trna ligase; <b>PDBTitle:</b> the structure of glutamyl-trna synthetase from saccharomyces2 cerevisiae
77	<a href="#">c5zdoA</a>	Alignment	not modelled	99.3	19	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> glutamine-trna ligase; <b>PDBTitle:</b> crystal structure analysis of ttgrs in co-crystallised with atp
78	<a href="#">c3aiiA</a>	Alignment	not modelled	99.2	15	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> glutamyl-trna synthetase; <b>PDBTitle:</b> archaeal non-discriminating glutamyl-trna synthetase

						from2 methanothermobacter thermautotrophicus
79	<a href="#">c4ye6A</a>	Alignment	not modelled	99.1	15	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> glutamine--trna ligase; <b>PDBTitle:</b> the crystal structure of the intact human glnrs
80	<a href="#">d1rqga1</a>	Alignment	not modelled	98.2	10	<b>Fold:</b> Anticodon-binding domain of a subclass of class I aminoacyl-tRNA synthetases <b>Superfamily:</b> Anticodon-binding domain of a subclass of class I aminoacyl-tRNA synthetases <b>Family:</b> Anticodon-binding domain of a subclass of class I aminoacyl-tRNA synthetases
81	<a href="#">c2cybA</a>	Alignment	not modelled	98.0	18	<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
82	<a href="#">c1h3eA</a>	Alignment	not modelled	97.9	16	<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
83	<a href="#">c6mtkA</a>	Alignment	not modelled	97.9	15	<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
84	<a href="#">c1x8xA</a>	Alignment	not modelled	97.8	14	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> tyrosyl-trna synthetase; <b>PDBTitle:</b> tyrosyl t-rna synthetase from e.coli complexed with tyrosine
85	<a href="#">c2g36A</a>	Alignment	not modelled	97.7	17	<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
86	<a href="#">c6otjA</a>	Alignment	not modelled	97.7	13	<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
87	<a href="#">d1jila</a>	Alignment	not modelled	97.6	13	<b>Fold:</b> Adenine nucleotide alpha hydrolase-like <b>Superfamily:</b> Nucleotidyl transferase <b>Family:</b> Class I aminoacyl-tRNA synthetases (RS), catalytic domain
88	<a href="#">c1jiiA</a>	Alignment	not modelled	97.6	13	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> tyrosyl-trna synthetase; <b>PDBTitle:</b> crystal structure of s. aureus tyrrs in complex with sb-219383
89	<a href="#">c2el7A</a>	Alignment	not modelled	97.6	16	<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 thermus2 thermophilus
90	<a href="#">c5tevA</a>	Alignment	not modelled	97.6	18	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> tryptophan--trna ligase; <b>PDBTitle:</b> crystal structure of a tryptophanyl-trna synthetase from neisseria2 gonorrhoeae, apo
91	<a href="#">d1h3fa1</a>	Alignment	not modelled	97.6	19	<b>Fold:</b> Adenine nucleotide alpha hydrolase-like <b>Superfamily:</b> Nucleotidyl transferase <b>Family:</b> Class I aminoacyl-tRNA synthetases (RS), catalytic domain
92	<a href="#">d1pfva1</a>	Alignment	not modelled	97.6	17	<b>Fold:</b> Anticodon-binding domain of a subclass of class I aminoacyl-tRNA synthetases <b>Superfamily:</b> Anticodon-binding domain of a subclass of class I aminoacyl-tRNA synthetases <b>Family:</b> Anticodon-binding domain of a subclass of class I aminoacyl-tRNA synthetases
93	<a href="#">d2d5ba1</a>	Alignment	not modelled	97.6	14	<b>Fold:</b> Anticodon-binding domain of a subclass of class I aminoacyl-tRNA synthetases <b>Superfamily:</b> Anticodon-binding domain of a subclass of class I aminoacyl-tRNA synthetases <b>Family:</b> Anticodon-binding domain of a subclass of class I aminoacyl-tRNA synthetases
94	<a href="#">c3vgjB</a>	Alignment	not modelled	97.6	19	<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
95	<a href="#">c2ts1A</a>	Alignment	not modelled	97.5	14	<b>PDB header:</b> ligase (synthetase) <b>Chain:</b> A: <b>PDB Molecule:</b> tyrosyl-trna synthetase; <b>PDBTitle:</b> structure of tyrosyl-trna synthetase refined at 2.3 angstroms2 resolution. interaction of the enzyme with the tyrosyl adenylate3 intermediate
96	<a href="#">d2ts1a</a>	Alignment	not modelled	97.5	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
97	<a href="#">c3tzeA</a>	Alignment	not modelled	97.5	17	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> tryptophanyl-trna synthetase; <b>PDBTitle:</b> crystal structure of a tryptophanyl-trna synthetase from2 encephalitozoon cuniculi bound to tryptophan
98	<a href="#">c3jxeB</a>	Alignment	not modelled	97.4	20	<b>PDB header:</b> ligase <b>Chain:</b> B: <b>PDB Molecule:</b> tryptophanyl-trna synthetase; <b>PDBTitle:</b> crystal structure of pyrococcus horikoshii tryptophanyl-trna2 synthetase in complex with trpamp
99	<a href="#">c6byqA</a>	Alignment	not modelled	97.4	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
100	<a href="#">c2j5bA</a>	Alignment	not modelled	97.4	18	<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
101	<a href="#">c2cyaA</a>	Alignment	not modelled	97.4	19	<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
102	<a href="#">c3focB</a>	Alignment	not modelled	97.1	15	<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

103	<a href="#">c2rkjM_</a>	Alignment	not modelled	97.1	18	<b>PDB header:</b> ligase/rna <b>Chain:</b> M: <b>PDB Molecule:</b> tyrosyl-trna synthetase; <b>PDBTitle:</b> cocrystal structure of a tyrosyl-trna synthetase splicing factor with2 a group i intron rna
104	<a href="#">c3a05A_</a>	Alignment	not modelled	97.0	18	<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 from2 hyperthermophilic archaeon, aeropyrum pernix k1 complex3 with tryptophan
105	<a href="#">c2cycB_</a>	Alignment	not modelled	97.0	15	<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
106	<a href="#">c3p0jD_</a>	Alignment	not modelled	96.7	20	<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
107	<a href="#">c3prhB_</a>	Alignment	not modelled	96.6	15	<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
108	<a href="#">c3h3rD_</a>	Alignment	not modelled	96.5	10	<b>PDB header:</b> ligase <b>Chain:</b> D: <b>PDB Molecule:</b> tryptophanyl-trna synthetase; <b>PDBTitle:</b> tryptophanyl-trna synthetase homolog from entamoeba histolytica
109	<a href="#">c4xkzA_</a>	Alignment	not modelled	96.2	8	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> valine-trna ligase; <b>PDBTitle:</b> crystal structure of the c-terminal anticodon loop binding domain of a2 valyl-trna synthetase from pseudomonas aeruginosa
110	<a href="#">d1qu3a1</a>	Alignment	not modelled	95.0	13	<b>Fold:</b> Anticodon-binding domain of a subclass of class I aminoacyl-tRNA synthetases <b>Superfamily:</b> Anticodon-binding domain of a subclass of class I aminoacyl-tRNA synthetases <b>Family:</b> Anticodon-binding domain of a subclass of class I aminoacyl-tRNA synthetases
111	<a href="#">d1ilea1</a>	Alignment	not modelled	93.8	16	<b>Fold:</b> Anticodon-binding domain of a subclass of class I aminoacyl-tRNA synthetases <b>Superfamily:</b> Anticodon-binding domain of a subclass of class I aminoacyl-tRNA synthetases <b>Family:</b> Anticodon-binding domain of a subclass of class I aminoacyl-tRNA synthetases
112	<a href="#">d1ffya1</a>	Alignment	not modelled	93.7	13	<b>Fold:</b> Anticodon-binding domain of a subclass of class I aminoacyl-tRNA synthetases <b>Superfamily:</b> Anticodon-binding domain of a subclass of class I aminoacyl-tRNA synthetases <b>Family:</b> Anticodon-binding domain of a subclass of class I aminoacyl-tRNA synthetases
113	<a href="#">d1n3la_</a>	Alignment	not modelled	92.9	23	<b>Fold:</b> Adenine nucleotide alpha hydrolase-like <b>Superfamily:</b> Nucleotidyl transferase <b>Family:</b> Class I aminoacyl-tRNA synthetases (RS), catalytic domain
114	<a href="#">c5ihxB_</a>	Alignment	not modelled	92.6	18	<b>PDB header:</b> ligase <b>Chain:</b> B: <b>PDB Molecule:</b> tyrosine--trna ligase, mitochondrial; <b>PDBTitle:</b> crystal structure of a c-terminally truncated aspergillus nidulans2 mitochondrial tyrosyl-trna synthetase
115	<a href="#">c2janD_</a>	Alignment	not modelled	92.6	27	<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
116	<a href="#">c5ekdA_</a>	Alignment	not modelled	92.1	26	<b>PDB header:</b> ligase/antibiotic <b>Chain:</b> A: <b>PDB Molecule:</b> tryptophan--trna ligase, mitochondrial; <b>PDBTitle:</b> human mitochondrial tryptophanyl-trna synthetase bound by indolmycin2 and mn*atp.
117	<a href="#">c2pidB_</a>	Alignment	not modelled	92.1	21	<b>PDB header:</b> ligase <b>Chain:</b> B: <b>PDB Molecule:</b> tyrosyl-trna synthetase; <b>PDBTitle:</b> crystal structure of human mitochondrial tyrosyl-trna synthetase in2 complex with an adenylate analog
118	<a href="#">c1q11A_</a>	Alignment	not modelled	92.0	21	<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
119	<a href="#">d1jlua_</a>	Alignment	not modelled	91.8	23	<b>Fold:</b> Adenine nucleotide alpha hydrolase-like <b>Superfamily:</b> Nucleotidyl transferase <b>Family:</b> Class I aminoacyl-tRNA synthetases (RS), catalytic domain
120	<a href="#">c2dlcX_</a>	Alignment	not modelled	91.8	26	<b>PDB header:</b> ligase/trna <b>Chain:</b> X: <b>PDB Molecule:</b> tyrosyl-trna synthetase, cytoplasmic; <b>PDBTitle:</b> crystal structure of the ternary complex of yeast tyrosyl-trna2 synthetase