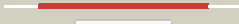



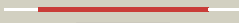




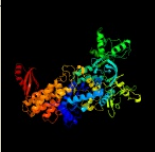













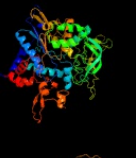
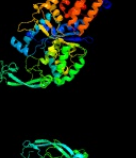



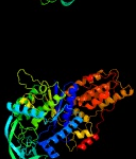

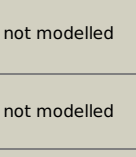


# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0041_(leuS)_43562_46471
Date	Tue Jul 23 14:50:07 BST 2019
Unique Job ID	e5e855f70169a7dc

Detailed template information

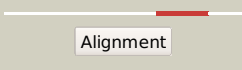
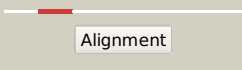
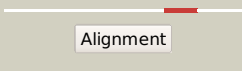
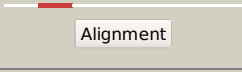
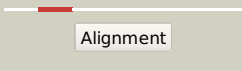
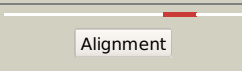
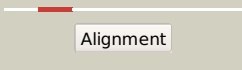
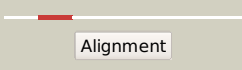
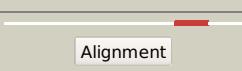
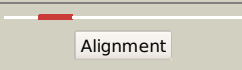
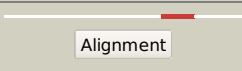
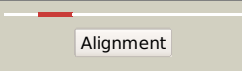
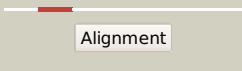
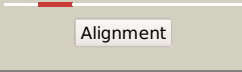
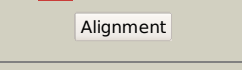
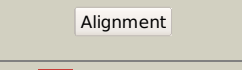
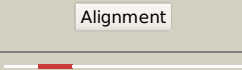
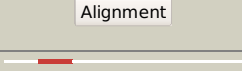
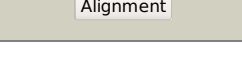
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1	<a href="#">c2bytD_</a>	 Alignment		100.0	43	<b>PDB header:</b> synthetase <b>Chain:</b> D: <b>PDB Molecule:</b> leucyl-trna synthetase; <b>PDBTitle:</b> thermus thermophilus leucyl-trna synthetase complexed with2 a trnaleu transcript in the post-editing conformation
2	<a href="#">c4ariA_</a>	 Alignment		100.0	40	<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
3	<a href="#">c6q8aA_</a>	 Alignment		100.0	37	<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
4	<a href="#">c1qu2A_</a>	 Alignment		100.0	20	<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
5	<a href="#">c5ah5B_</a>	 Alignment		100.0	31	<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-s-trna-leuams
6	<a href="#">c1obhA_</a>	 Alignment		100.0	42	<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
7	<a href="#">c1wz2B_</a>	 Alignment		100.0	18	<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
8	<a href="#">c1gaxB_</a>	 Alignment		100.0	23	<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
9	<a href="#">c1ileA_</a>	 Alignment		100.0	20	<b>PDB header:</b> aminoacyl-trna synthetase <b>Chain:</b> A: <b>PDB Molecule:</b> isoleucyl-trna synthetase; <b>PDBTitle:</b> isoleucyl-trna synthetase
10	<a href="#">c1wkbA_</a>	 Alignment		100.0	19	<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
11	<a href="#">c3ziuA_</a>	 Alignment		100.0	45	<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

12	<a href="#">c3ziuB</a>	Alignment		100.0	47	<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
13	<a href="#">d1h3na3</a>	Alignment		100.0	43	<b>Fold:</b> Adenine nucleotide alpha hydrolase-like <b>Superfamily:</b> Nucleotidylyl transferase <b>Family:</b> Class I aminoacyl-tRNA synthetases (RS), catalytic domain
14	<a href="#">c5gl7A</a>	Alignment		100.0	22	<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
15	<a href="#">c1rqgA</a>	Alignment		100.0	23	<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
16	<a href="#">d1ffya3</a>	Alignment		100.0	25	<b>Fold:</b> Adenine nucleotide alpha hydrolase-like <b>Superfamily:</b> Nucleotidylyl transferase <b>Family:</b> Class I aminoacyl-tRNA synthetases (RS), catalytic domain
17	<a href="#">c1pfuA</a>	Alignment		100.0	24	<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	22	<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="#">c5urbB</a>	Alignment		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 methionyl-trna synthetase (metrs) from2 acinetobacter baumannii with bound l-methionine
20	<a href="#">c4qrdA</a>	Alignment		100.0	25	<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
21	<a href="#">c3kfiA</a>	Alignment	not modelled	100.0	22	<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
22	<a href="#">d1ilea3</a>	Alignment	not modelled	100.0	24	<b>Fold:</b> Adenine nucleotide alpha hydrolase-like <b>Superfamily:</b> Nucleotidylyl transferase <b>Family:</b> Class I aminoacyl-tRNA synthetases (RS), catalytic domain
23	<a href="#">c1woyA</a>	Alignment	not modelled	100.0	22	<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
24	<a href="#">c4dlpA</a>	Alignment	not modelled	100.0	27	<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
25	<a href="#">d1ivsa4</a>	Alignment	not modelled	100.0	28	<b>Fold:</b> Adenine nucleotide alpha hydrolase-like <b>Superfamily:</b> Nucleotidylyl transferase <b>Family:</b> Class I aminoacyl-tRNA synthetases (RS), catalytic domain
26	<a href="#">c5xgqB</a>	Alignment	not modelled	100.0	24	<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
27	<a href="#">c2ct8A</a>	Alignment	not modelled	100.0	25	<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
28	<a href="#">c4dlpB</a>	Alignment	not modelled	100.0	28	<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
29	<a href="#">c2x1IC</a>	Alignment	not modelled	100.0	26	<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
30	<a href="#">d1rqga2</a>	Alignment	not modelled	100.0	26	<b>Fold:</b> Adenine nucleotide alpha hydrolase-like <b>Superfamily:</b> Nucleotidyl transferase <b>Family:</b> Class I aminoacyl-tRNA synthetases (RS), catalytic domain
31	<a href="#">d2d5ba2</a>	Alignment	not modelled	100.0	25	<b>Fold:</b> Adenine nucleotide alpha hydrolase-like <b>Superfamily:</b> Nucleotidyl transferase <b>Family:</b> Class I aminoacyl-tRNA synthetases (RS), catalytic domain
32	<a href="#">d1pfva2</a>	Alignment	not modelled	100.0	24	<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="#">c5fodB</a>	Alignment	not modelled	100.0	20	<b>PDB header:</b> ligase <b>Chain:</b> B: <b>PDB Molecule:</b> leucyl-trna synthetase; <b>PDBTitle:</b> crystal structure of the p.falciarium cytosolic leucyl-trna synthetase2 editing domain (space group p1) containing deletions of insertions 13 and 3
34	<a href="#">c5agrA</a>	Alignment	not modelled	100.0	98	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> leucine--trna ligase; <b>PDBTitle:</b> crystal structure of the leurs editing domain of mycobacterium2 tuberculosis in complex with the adduct (s)-3-(aminomethyl)-7-3 ethoxybenzo[c][1,2]oxaborol-1(3h)-ol-amp
35	<a href="#">d1h3na2</a>	Alignment	not modelled	100.0	52	<b>Fold:</b> ValRS/IleRS/LeuRS editing domain <b>Superfamily:</b> ValRS/IleRS/LeuRS editing domain <b>Family:</b> ValRS/IleRS/LeuRS editing domain
36	<a href="#">c3o0aB</a>	Alignment	not modelled	100.0	44	<b>PDB header:</b> ligase <b>Chain:</b> B: <b>PDB Molecule:</b> leucyl-trna synthetase subunit alpha; <b>PDBTitle:</b> crystal structure of the wild type cp1 hydrolytic domain from aquifex2 aeolicus leucyl-trna
37	<a href="#">c4k48A</a>	Alignment	not modelled	100.0	52	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> leucine--trna ligase; <b>PDBTitle:</b> structure of the streptococcus pneumoniae leucyl-trna synthetase2 editing domain
38	<a href="#">c2ajhA</a>	Alignment	not modelled	100.0	40	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> leucyl-trna synthetase; <b>PDBTitle:</b> crystal structure of the editing domain of e. coli leucyl-trna2 synthetase complexes with methionine
39	<a href="#">d1ludza</a>	Alignment	not modelled	100.0	22	<b>Fold:</b> ValRS/IleRS/LeuRS editing domain <b>Superfamily:</b> ValRS/IleRS/LeuRS editing domain <b>Family:</b> ValRS/IleRS/LeuRS editing domain
40	<a href="#">c2wfdB</a>	Alignment	not modelled	100.0	17	<b>PDB header:</b> ligase <b>Chain:</b> B: <b>PDB Molecule:</b> leucyl-trna synthetase, cytoplasmic; <b>PDBTitle:</b> structure of the human cytosolic leucyl-trna synthetase2 editing domain
41	<a href="#">c5fofD</a>	Alignment	not modelled	100.0	11	<b>PDB header:</b> ligase <b>Chain:</b> D: <b>PDB Molecule:</b> leucyl-trna synthetase; <b>PDBTitle:</b> crystal structure of the p.knowlesi cytosolic leucyl-trna2 synthetase editing domain
42	<a href="#">c5fogA</a>	Alignment	not modelled	100.0	17	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> leucyl-trna synthetase; <b>PDBTitle:</b> crystal structure of hte cryptosporidium muris cytosolic2 leucyl-trna synthetase editing domain complex with a post-3 transfer editing analogue of norvaline (nv2aa)
43	<a href="#">d1wkaa1</a>	Alignment	not modelled	100.0	30	<b>Fold:</b> ValRS/IleRS/LeuRS editing domain <b>Superfamily:</b> ValRS/IleRS/LeuRS editing domain <b>Family:</b> ValRS/IleRS/LeuRS editing domain
44	<a href="#">c1u0bB</a>	Alignment	not modelled	100.0	19	<b>PDB header:</b> ligase/rna <b>Chain:</b> B: <b>PDB Molecule:</b> cysteinyln trna; <b>PDBTitle:</b> crystal structure of cysteinyln-trna synthetase binary2 complex with trnacys
45	<a href="#">d1ffya2</a>	Alignment	not modelled	100.0	18	<b>Fold:</b> ValRS/IleRS/LeuRS editing domain <b>Superfamily:</b> ValRS/IleRS/LeuRS editing domain <b>Family:</b> ValRS/IleRS/LeuRS editing domain
46	<a href="#">c3pz6F</a>	Alignment	not modelled	100.0	19	<b>PDB header:</b> ligase <b>Chain:</b> F: <b>PDB Molecule:</b> leucyl-trna synthetase; <b>PDBTitle:</b> the crystal structure of glleurs-cp1
47	<a href="#">c2wfgA</a>	Alignment	not modelled	100.0	19	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> cytosolic leucyl-trna synthetase; <b>PDBTitle:</b> structure of the candida albicans cytosolic leucyl-trna2 synthetase editing domain bound to a benzoxaborole-amp3 adduct
48	<a href="#">c3tqoA</a>	Alignment	not modelled	100.0	22	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> cysteinyln-trna synthetase; <b>PDBTitle:</b> structure of the cysteinyln-trna synthetase (cyss) from coxiella2 burnetii.
49	<a href="#">c3c8zB</a>	Alignment	not modelled	100.0	25	<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
50	<a href="#">c3sp1B</a>	Alignment	not modelled	100.0	16	<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
51	<a href="#">d1l15a2</a>	Alignment	not modelled	100.0	25	<b>Fold:</b> Adenine nucleotide alpha hydrolase-like <b>Superfamily:</b> Nucleotidyl transferase <b>Family:</b> Class I aminoacyl-tRNA synthetases (RS), catalytic domain
52	<a href="#">c3fnrA</a>	Alignment	not modelled	100.0	20	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> arginyln-trna synthetase; <b>PDBTitle:</b> crystal structure of putative arginyln t-rna synthetase from2 campylobacter jejuni;
53	<a href="#">c1iq0A</a>	Alignment	not modelled	100.0	17	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> arginyln-trna synthetase; <b>PDBTitle:</b> thermus thermophilus arginyln-trna synthetase
						<b>PDB header:</b> ligase

54	<a href="#">c4xkzA</a>	Alignment	not modelled	99.9	20	<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
55	<a href="#">c6ao8A</a>	Alignment	not modelled	99.9	18	<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
56	<a href="#">d1ivsa2</a>	Alignment	not modelled	99.9	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
57	<a href="#">c4obyA</a>	Alignment	not modelled	99.9	19	<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
58	<a href="#">d1h3na1</a>	Alignment	not modelled	99.9	39	<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
59	<a href="#">d1ilea1</a>	Alignment	not modelled	99.9	22	<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
60	<a href="#">c5jldA</a>	Alignment	not modelled	99.9	12	<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)
61	<a href="#">d1qu3a1</a>	Alignment	not modelled	99.9	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
62	<a href="#">d1ffya1</a>	Alignment	not modelled	99.9	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
63	<a href="#">d1iq0a2</a>	Alignment	not modelled	99.9	18	<b>Fold:</b> Adenine nucleotide alpha hydrolase-like <b>Superfamily:</b> Nucleotidyl transferase <b>Family:</b> Class I aminoacyl-tRNA synthetases (RS), catalytic domain
64	<a href="#">c2zufA</a>	Alignment	not modelled	99.8	20	<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)
65	<a href="#">d1rqga1</a>	Alignment	not modelled	99.7	15	<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
66	<a href="#">c1f7uA</a>	Alignment	not modelled	99.5	19	<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
67	<a href="#">c4r3zB</a>	Alignment	not modelled	99.5	23	<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
68	<a href="#">c4q2tB</a>	Alignment	not modelled	99.4	14	<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
69	<a href="#">d1lrxA2</a>	Alignment	not modelled	99.4	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
70	<a href="#">d2d5ba1</a>	Alignment	not modelled	99.4	15	<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
71	<a href="#">d1pfva1</a>	Alignment	not modelled	99.4	11	<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
72	<a href="#">d1f7ua2</a>	Alignment	not modelled	99.3	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
73	<a href="#">c1g59A</a>	Alignment	not modelled	99.3	23	<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).
74	<a href="#">c1lrxA</a>	Alignment	not modelled	98.2	23	<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
75	<a href="#">c4griB</a>	Alignment	not modelled	98.1	13	<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
						<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> glutamyl-trna synthetase 1;

76	<a href="#">c2o5rA_</a>	Alignment	not modelled	98.0	9	<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 <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
77	<a href="#">c3afhA_</a>	Alignment	not modelled	98.0	8	<b>Fold:</b> Adenine nucleotide alpha hydrolase-like <b>Superfamily:</b> Nucleotidyl transferase <b>Family:</b> Class I aminoacyl-tRNA synthetases (RS), catalytic domain
78	<a href="#">d1qtra2</a>	Alignment	not modelled	97.9	34	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> glutamyl-trna synthetase; <b>PDBTitle:</b> mycobacterium tuberculosis glutamyl-trna synthetase
79	<a href="#">c2ja2A_</a>	Alignment	not modelled	97.9	11	<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
80	<a href="#">c5h4vE_</a>	Alignment	not modelled	97.9	11	<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
81	<a href="#">c2cfoA_</a>	Alignment	not modelled	97.8	27	<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
82	<a href="#">c3aiaA_</a>	Alignment	not modelled	97.7	28	<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
83	<a href="#">c5tgtA_</a>	Alignment	not modelled	97.7	12	<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
84	<a href="#">c6b1pA_</a>	Alignment	not modelled	97.6	23	<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
85	<a href="#">c4r3zC_</a>	Alignment	not modelled	97.6	22	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> glutaminyl-trna synthetase; <b>PDBTitle:</b> crystal structure of the glutaminyl-trna synthetase from deinococcus2 radiodurans
86	<a href="#">c2hz7A_</a>	Alignment	not modelled	97.5	24	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> glutamine-trna ligase; <b>PDBTitle:</b> the structure of glutaminyl-trna synthetase from saccharomyces2 cerevisiae
87	<a href="#">c4h3sA_</a>	Alignment	not modelled	97.5	28	<b>PDB header:</b> ligase/rna <b>Chain:</b> A: <b>PDB Molecule:</b> glutaminyl-trna synthetase; <b>PDBTitle:</b> crystal structure of a tight-binding glutamine trna bound2 to glutamine aminoacyl trna synthetase
88	<a href="#">c1exdA_</a>	Alignment	not modelled	97.5	24	<b>Fold:</b> Adenine nucleotide alpha hydrolase-like <b>Superfamily:</b> Nucleotidyl transferase <b>Family:</b> Class I aminoacyl-tRNA synthetases (RS), catalytic domain
89	<a href="#">d1nzza_</a>	Alignment	not modelled	97.5	26	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> glutamine-trna ligase; <b>PDBTitle:</b> crystal structure analysis of ttqrs in co-crystallised with atp
90	<a href="#">c5zdoA_</a>	Alignment	not modelled	97.4	29	<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
91	<a href="#">c6b1zA_</a>	Alignment	not modelled	97.4	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.
92	<a href="#">c3al0C_</a>	Alignment	not modelled	97.4	30	<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 /glutaminyl-trna synthetase2 (glnrs) from pseudomonas aeruginosa
93	<a href="#">c5bnzA_</a>	Alignment	not modelled	97.3	22	<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
94	<a href="#">c4ye6A_</a>	Alignment	not modelled	97.3	21	<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 glutaminyl-trna synthetase2 catalytic domain from toxoplasma gondii.
95	<a href="#">c4p2bA_</a>	Alignment	not modelled	97.3	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
96	<a href="#">d1j09a2</a>	Alignment	not modelled	97.0	23	<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
97	<a href="#">c4q6zA_</a>	Alignment	not modelled	96.9	23	<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
98	<a href="#">c6mtkA_</a>	Alignment	not modelled	96.5	11	<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
99	<a href="#">c1h3eA_</a>	Alignment	not modelled	96.5	21	<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
100	<a href="#">c6otjA_</a>	Alignment	not modelled	96.3	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
101	<a href="#">c2cybA_</a>	Alignment	not modelled	96.0	13	

102	<a href="#">c5ekdA</a>	 Alignment	not modelled	95.9	11	<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.
103	<a href="#">c3hv0A</a>	 Alignment	not modelled	95.6	17	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> tryptophanyl-trna synthetase; <b>PDBTitle:</b> tryptophanyl-trna synthetase from cryptosporidium parvum
104	<a href="#">c2janD</a>	 Alignment	not modelled	95.4	21	<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
105	<a href="#">d2ts1a</a>	 Alignment	not modelled	95.3	24	<b>Fold:</b> Adenine nucleotide alpha hydrolase-like <b>Superfamily:</b> Nucleotidyl transferase <b>Family:</b> Class I aminoacyl-tRNA synthetases (RS), catalytic domain
106	<a href="#">c2ts1A</a>	 Alignment	not modelled	95.3	24	<b>PDB header:</b> ligase (synthetase) <b>Chain:</b> A: <b>PDB Molecule:</b> tyrosyl-trna synthetase; <b>PDBTitle:</b> structure of tyrosyl-t/rna synthetase refined at 2.3 angstroms2 resolution. interaction of the enzyme with the tyrosyl adenylate3 intermediate
107	<a href="#">d1h3fa1</a>	 Alignment	not modelled	95.2	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
108	<a href="#">c3vgjB</a>	 Alignment	not modelled	94.9	15	<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
109	<a href="#">c3a05A</a>	 Alignment	not modelled	94.9	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 from2 hyperthermophilic archaeon, aeropyrum pernix k1 complex3 with tryptophan
110	<a href="#">d1i6la</a>	 Alignment	not modelled	94.8	7	<b>Fold:</b> Adenine nucleotide alpha hydrolase-like <b>Superfamily:</b> Nucleotidyl transferase <b>Family:</b> Class I aminoacyl-tRNA synthetases (RS), catalytic domain
111	<a href="#">c2j5bA</a>	 Alignment	not modelled	94.8	15	<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
112	<a href="#">c1x8xA</a>	 Alignment	not modelled	94.6	19	<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
113	<a href="#">c2quiB</a>	 Alignment	not modelled	94.5	16	<b>PDB header:</b> ligase <b>Chain:</b> B: <b>PDB Molecule:</b> tryptophanyl-trna synthetase; <b>PDBTitle:</b> crystal structures of human tryptophanyl-trna synthetase in2 complex with tryptophanamide and atp
114	<a href="#">d1j1ua</a>	 Alignment	not modelled	94.2	18	<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="#">c3n9iA</a>	 Alignment	not modelled	94.1	14	<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
116	<a href="#">c3focB</a>	 Alignment	not modelled	94.1	14	<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
117	<a href="#">c2pidB</a>	 Alignment	not modelled	94.0	26	<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="#">d1jila</a>	 Alignment	not modelled	94.0	17	<b>Fold:</b> Adenine nucleotide alpha hydrolase-like <b>Superfamily:</b> Nucleotidyl transferase <b>Family:</b> Class I aminoacyl-tRNA synthetases (RS), catalytic domain
119	<a href="#">c1jiiA</a>	 Alignment	not modelled	94.0	16	<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
120	<a href="#">d1r6ta2</a>	 Alignment	not modelled	93.8	17	<b>Fold:</b> Adenine nucleotide alpha hydrolase-like <b>Superfamily:</b> Nucleotidyl transferase <b>Family:</b> Class I aminoacyl-tRNA synthetases (RS), catalytic domain