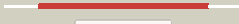
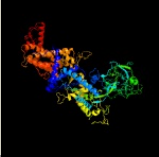


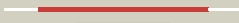














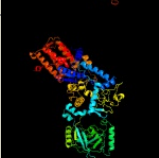


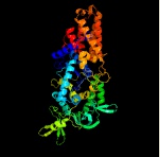
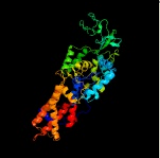
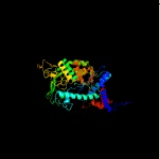
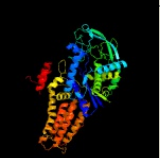


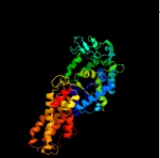




Phyre2

Email mdejesus@rockefeller.edu
 Description RVBD1536_(ileS)_1736525_1739650
 Date Fri Aug 2 13:30:12 BST 2019
 Unique Job ID 6c3faf1182eebb05

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1qu2A_	 Alignment		100.0	28	PDB header: ligase/rna Chain: A: PDB Molecule: isoleucyl-trna synthetase; PDBTitle: insights into editing from an ile-trna synthetase structure2 with trna(ile) and mupirocin
2	c1ileA_	 Alignment		100.0	44	PDB header: aminoacyl-trna synthetase Chain: A: PDB Molecule: isoleucyl-trna synthetase; PDBTitle: isoleucyl-trna synthetase
3	c1gaxB_	 Alignment		100.0	26	PDB header: ligase/rna Chain: B: PDB Molecule: valyl-trna synthetase; PDBTitle: crystal structure of thermus thermophilus valyl-trna2 synthetase complexed with trna(val) and valyl-adenylate3 analogue
4	c1wz2B_	 Alignment		100.0	20	PDB header: ligase/rna Chain: B: PDB Molecule: leucyl-trna synthetase; PDBTitle: the crystal structure of leucyl-trna synthetase and trna(leucine)2 complex
5	c2bytD_	 Alignment		100.0	22	PDB header: synthetase Chain: D: PDB Molecule: leucyl-trna synthetase; PDBTitle: thermus thermophilus leucyl-trna synthetase complexed with2 a trnaleu transcript in the post-editing conformation
6	c1wkbA_	 Alignment		100.0	20	PDB header: ligase Chain: A: PDB Molecule: leucyl-trna synthetase; PDBTitle: crystal structure of leucyl-trna synthetase from the2 archaeon pyrococcus horikoshii reveals a novel editing3 domain orientation
7	c4ariA_	 Alignment		100.0	22	PDB header: ligase/rna Chain: A: PDB Molecule: leucine--trna ligase; PDBTitle: ternary complex of e. coli leucyl-trna synthetase, trna(leu) and the2 benzoxaborole an2679 in the editing conformation
8	c6q8aA_	 Alignment		100.0	22	PDB header: ligase Chain: A: PDB Molecule: leucine--trna ligase; PDBTitle: neisseria gonorrhoeae leucyl-trna synthetase in complex with 5'-o-(n-2 (l-leucyl)-sulfamoyl)cytidine
9	c5ah5B_	 Alignment		100.0	18	PDB header: ligase/rna Chain: B: PDB Molecule: leucine--trna ligase; PDBTitle: crystal structure of the ternary complex of agrobacterium2 radiobacter k84 agn2 leuvs-trna-leuams
10	c1obhA_	 Alignment		100.0	23	PDB header: synthetase Chain: A: PDB Molecule: leucyl-trna synthetase; PDBTitle: leucyl-trna synthetase from thermus thermophilus complexed2 with a pre-transfer editing substrate analogue in both3 synthetic active site and editing site
11	c3ziuA_	 Alignment		100.0	24	PDB header: ligase Chain: A: PDB Molecule: leucyl-trna synthetase; PDBTitle: crystal structure of mycoplasma mobile leucyl-trna2 synthetase with leu-ams in the active site

12	c3ziuB	Alignment		100.0	22	PDB header: ligase Chain: B: PDB Molecule: leucyl-trna synthetase; PDBTitle: crystal structure of mycoplasma mobile leucyl-trna2 synthetase with leu-ams in the active site
13	c5gl7A	Alignment		100.0	18	PDB header: ligase Chain: A: PDB Molecule: methionine--trna ligase, cytoplasmic; PDBTitle: crystal structure of a truncated human cytosolic methionyl-trna2 synthetase
14	d1ffya3	Alignment		100.0	30	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Nucleotidylyl transferase Family: Class I aminoacyl-tRNA synthetases (RS), catalytic domain
15	c1rqgA	Alignment		100.0	19	PDB header: ligase Chain: A: PDB Molecule: methionyl-trna synthetase; PDBTitle: methionyl-trna synthetase from pyrococcus abyssi
16	d1h3na3	Alignment		100.0	28	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Nucleotidylyl transferase Family: Class I aminoacyl-tRNA synthetases (RS), catalytic domain
17	d1ilea3	Alignment		100.0	51	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Nucleotidylyl transferase Family: Class I aminoacyl-tRNA synthetases (RS), catalytic domain
18	c5urbB	Alignment		100.0	17	PDB header: ligase Chain: B: PDB Molecule: methionine--trna ligase; PDBTitle: crystal structure of methionyl-trna synthetase (metrs) from2 acinetobacter baumannii with bound l-methionine
19	c1pfuA	Alignment		100.0	21	PDB header: ligase Chain: A: PDB Molecule: methionyl-trna synthetase; PDBTitle: methionyl-trna synthetase from escherichia coli complexed2 with methionine phosphinate
20	c4qrdA	Alignment		100.0	29	PDB header: ligase/ligase inhibitor Chain: A: PDB Molecule: methionyl-trna synthetase; PDBTitle: 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	c3tunA	Alignment	not modelled	100.0	22	PDB header: ligase/ligase inhibitor Chain: A: PDB Molecule: methionyl-trna synthetase; PDBTitle: trypanosoma brucei methionyl-trna synthetase in complex with inhibitor2 chem 1356
22	c3kflA	Alignment	not modelled	100.0	26	PDB header: ligase Chain: A: PDB Molecule: methionyl-trna synthetase; PDBTitle: leishmania major methionyl-trna synthetase in complex with2 methionyladenylate and pyrophosphate
23	c1woyA	Alignment	not modelled	100.0	25	PDB header: ligase Chain: A: PDB Molecule: methionyl-trna synthetase; PDBTitle: crystal structure of methionyl trna synthetase y225f mutant2 from thermus thermophilus
24	d1ivsa4	Alignment	not modelled	100.0	31	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Nucleotidylyl transferase Family: Class I aminoacyl-tRNA synthetases (RS), catalytic domain
25	c4dlpA	Alignment	not modelled	100.0	26	PDB header: ligase Chain: A: PDB Molecule: aminoacyl-trna synthetase, class i:aminoacyl-trna PDBTitle: crystal structure of methionyl-trna synthetase metrs from brucella2 melitensis bound to selenomethionine
26	c5xgqB	Alignment	not modelled	100.0	21	PDB header: ligase Chain: B: PDB Molecule: methionine-trna ligase; PDBTitle: crystal structure of apo form (free-state) mycobacterium tuberculosis2 methionyl-trna synthetase
27	c2ct8A	Alignment	not modelled	100.0	27	PDB header: ligase/rna Chain: A: PDB Molecule: methionyl-trna synthetase; PDBTitle: crystal structure of aquifex aeolicus methionyl-trna2 synthetase complexed with trna(met) and methionyl-adenylate3 analogue
28	c2x1lC	Alignment	not modelled	100.0	29	PDB header: ligase Chain: C: PDB Molecule: methionyl-trna synthetase; PDBTitle: crystal structure of mycobacterium smegmatis methionyl-

						trna synthetase2 in complex with methionine and adenosine
29	c4dlpB_	Alignment	not modelled	100.0	22	PDB header: ligase Chain: B: PDB Molecule: aminoacyl-trna synthetase, class i:aminoacyl-trna PDBTitle: crystal structure of methionyl-trna synthetase metrs from brucella2 melitensis bound to selenomethionine
30	d1rqga2	Alignment	not modelled	100.0	24	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Nucleotidyl transferase Family: Class I aminoacyl-tRNA synthetases (RS), catalytic domain
31	d2d5ba2	Alignment	not modelled	100.0	32	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Nucleotidyl transferase Family: Class I aminoacyl-tRNA synthetases (RS), catalytic domain
32	d1pfva2	Alignment	not modelled	100.0	28	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Nucleotidyl transferase Family: Class I aminoacyl-tRNA synthetases (RS), catalytic domain
33	c5fodB_	Alignment	not modelled	100.0	20	PDB header: ligase Chain: B: PDB Molecule: leucyl-trna synthetase; PDBTitle: crystal structure of the p.falciiparum cytosolic leucyl-trna synthetase2 editing domain (space group p1) containing deletions of insertions 13 and 3
34	d1ludza_	Alignment	not modelled	100.0	41	Fold: ValRS/IleRS/LeuRS editing domain Superfamily: ValRS/IleRS/LeuRS editing domain Family: ValRS/IleRS/LeuRS editing domain
35	c1u0bB_	Alignment	not modelled	100.0	23	PDB header: ligase/rna Chain: B: PDB Molecule: cysteinyln trna; PDBTitle: crystal structure of cysteinyln-trna synthetase binary2 complex with trnacys
36	d1ffya2	Alignment	not modelled	100.0	34	Fold: ValRS/IleRS/LeuRS editing domain Superfamily: ValRS/IleRS/LeuRS editing domain Family: ValRS/IleRS/LeuRS editing domain
37	c4xkzA_	Alignment	not modelled	100.0	21	PDB header: ligase Chain: A: PDB Molecule: valine-trna ligase; PDBTitle: crystal structure of the c-terminal anticodon loop binding domain of a2 valyl-trna synthetase from pseudomonas aeruginosa
38	c5foga_	Alignment	not modelled	100.0	22	PDB header: lyase Chain: A: PDB Molecule: leucyl-trna synthetase; PDBTitle: crystal structure of hte cryptosporidium muris cytosolic2 leucyl-trna synthetase editing domain complex with a post-3 transfer editing analogue of norvaline (nv2aa)
39	c2wfdB_	Alignment	not modelled	100.0	20	PDB header: ligase Chain: B: PDB Molecule: leucyl-trna synthetase, cytoplasmic; PDBTitle: structure of the human cytosolic leucyl-trna synthetase2 editing domain
40	c3tqoA_	Alignment	not modelled	100.0	20	PDB header: ligase Chain: A: PDB Molecule: cysteinyln-trna synthetase; PDBTitle: structure of the cysteinyln-trna synthetase (cyss) from coxiella2 burnetii.
41	c5fofD_	Alignment	not modelled	100.0	19	PDB header: ligase Chain: D: PDB Molecule: leucyl-trna synthetase; PDBTitle: crystal structure of the p.knowlesi cytosolic leucyl-trna2 synthetase editing domain
42	d1ivsa2	Alignment	not modelled	100.0	19	Fold: Anticodon-binding domain of a subclass of class I aminoacyl-tRNA synthetases Superfamily: Anticodon-binding domain of a subclass of class I aminoacyl-tRNA synthetases Family: Anticodon-binding domain of a subclass of class I aminoacyl-tRNA synthetases
43	c2wfgA_	Alignment	not modelled	100.0	25	PDB header: ligase Chain: A: PDB Molecule: cytosolic leucyl-trna synthetase; PDBTitle: structure of the candida albicans cytosolic leucyl-trna2 synthetase editing domain bound to a benzoxaborole-amp3 adduct
44	d1h3na2	Alignment	not modelled	100.0	23	Fold: ValRS/IleRS/LeuRS editing domain Superfamily: ValRS/IleRS/LeuRS editing domain Family: ValRS/IleRS/LeuRS editing domain
45	c4k48A_	Alignment	not modelled	100.0	22	PDB header: ligase Chain: A: PDB Molecule: leucine--trna ligase; PDBTitle: structure of the streptococcus pneumoniae leucyl-trna synthetase2 editing domain
46	c3c8zB_	Alignment	not modelled	100.0	20	PDB header: ligase Chain: B: PDB Molecule: cysteinyln-trna synthetase; PDBTitle: the 1.6 a crystal structure of mshc: the rate limiting2 enzyme in the mycothiol biosynthetic pathway
47	c2ajhA_	Alignment	not modelled	100.0	22	PDB header: ligase Chain: A: PDB Molecule: leucyl-trna synthetase; PDBTitle: crystal structure of the editing domain of e. coli leucyl-trna2 synthetase complexes with methionine
48	c5agrA_	Alignment	not modelled	100.0	21	PDB header: ligase Chain: A: PDB Molecule: leucine--trna ligase; PDBTitle: 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
49	c3o0aB_	Alignment	not modelled	100.0	21	PDB header: ligase Chain: B: PDB Molecule: leucyl-trna synthetase subunit alpha; PDBTitle: crystal structure of the wild type cp1 hydrolytic domain from aquifex2 aeolicus leucyl-trna
50	d1wkaa1	Alignment	not modelled	100.0	35	Fold: ValRS/IleRS/LeuRS editing domain Superfamily: ValRS/IleRS/LeuRS editing domain Family: ValRS/IleRS/LeuRS editing domain
51	c3sp1B_	Alignment	not modelled	100.0	18	PDB header: ligase Chain: B: PDB Molecule: cysteinyln-trna synthetase; PDBTitle: crystal structure of cysteinyln-trna synthetase (cyss) from borrelia2 burgdorferi
52	d1qu3a1	Alignment	not modelled	100.0	22	Fold: Anticodon-binding domain of a subclass of class I aminoacyl-tRNA synthetases Superfamily: Anticodon-binding domain of a subclass of class I aminoacyl-tRNA synthetases Family: Anticodon-binding domain of a subclass of class I aminoacyl-tRNA synthetases

53	c3fnrA	Alignment	not modelled	100.0	19	PDB header: transferase Chain: A: PDB Molecule: arginyl-trna synthetase; PDBTitle: crystal structure of putative arginyl t-rna synthetase from2 campylobacter jejuni;
54	c3pz6F	Alignment	not modelled	100.0	23	PDB header: ligase Chain: F: PDB Molecule: leucyl-trna synthetase; PDBTitle: the crystal structure of gleans-cp1
55	d1ilea1	Alignment	not modelled	100.0	39	Fold: Anticodon-binding domain of a subclass of class I aminoacyl-tRNA synthetases Superfamily: Anticodon-binding domain of a subclass of class I aminoacyl-tRNA synthetases Family: Anticodon-binding domain of a subclass of class I aminoacyl-tRNA synthetases
56	d1ffya1	Alignment	not modelled	100.0	21	Fold: Anticodon-binding domain of a subclass of class I aminoacyl-tRNA synthetases Superfamily: Anticodon-binding domain of a subclass of class I aminoacyl-tRNA synthetases Family: Anticodon-binding domain of a subclass of class I aminoacyl-tRNA synthetases
57	d1li5a2	Alignment	not modelled	100.0	26	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Nucleotidyl transferase Family: Class I aminoacyl-tRNA synthetases (RS), catalytic domain
58	c6ao8A	Alignment	not modelled	100.0	17	PDB header: ligase Chain: A: PDB Molecule: arginine--trna ligase; PDBTitle: crystal structure of arginyl-trna synthetase from neisseria2 gonorrhoeae in complex with arginine
59	c1iq0A	Alignment	not modelled	100.0	19	PDB header: ligase Chain: A: PDB Molecule: arginyl-trna synthetase; PDBTitle: thermus thermophilus arginyl-trna synthetase
60	c4obyA	Alignment	not modelled	100.0	22	PDB header: ligase Chain: A: PDB Molecule: arginine--trna ligase; PDBTitle: crystal structure of e.coli arginyl-trna synthetase and ligand binding2 studies revealed key residues in arginine recognition
61	c5jldA	Alignment	not modelled	99.9	18	PDB header: ligase Chain: A: PDB Molecule: arginyl-trna synthetase, putative; PDBTitle: crystal structure of arginyl-trna synthetase from plasmodium2 falciparum (pfrrs)
62	d1h3na1	Alignment	not modelled	99.9	18	Fold: Anticodon-binding domain of a subclass of class I aminoacyl-tRNA synthetases Superfamily: Anticodon-binding domain of a subclass of class I aminoacyl-tRNA synthetases Family: Anticodon-binding domain of a subclass of class I aminoacyl-tRNA synthetases
63	c2zufA	Alignment	not modelled	99.9	19	PDB header: ligase/rna Chain: A: PDB Molecule: arginyl-trna synthetase; PDBTitle: crystal structure of pyrococcus horikoshii arginyl-trna2 synthetase complexed with trna(arg)
64	d1iq0a2	Alignment	not modelled	99.9	17	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Nucleotidyl transferase Family: Class I aminoacyl-tRNA synthetases (RS), catalytic domain
65	c4q2tB	Alignment	not modelled	99.9	17	PDB header: ligase Chain: B: PDB Molecule: arginine--trna ligase, cytoplasmic; PDBTitle: crystal structure of arginyl-trna synthetase complexed with l-arginine
66	d1irxa2	Alignment	not modelled	99.9	18	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Nucleotidyl transferase Family: Class I aminoacyl-tRNA synthetases (RS), catalytic domain
67	d1f7ua2	Alignment	not modelled	99.8	17	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Nucleotidyl transferase Family: Class I aminoacyl-tRNA synthetases (RS), catalytic domain
68	c4r3zB	Alignment	not modelled	99.8	17	PDB header: protein binding/ligase Chain: B: PDB Molecule: arginine--trna ligase, cytoplasmic; PDBTitle: crystal structure of human argrs-glnrs-aimp1 complex
69	d1rqga1	Alignment	not modelled	99.8	15	Fold: Anticodon-binding domain of a subclass of class I aminoacyl-tRNA synthetases Superfamily: Anticodon-binding domain of a subclass of class I aminoacyl-tRNA synthetases Family: Anticodon-binding domain of a subclass of class I aminoacyl-tRNA synthetases
70	c1f7uA	Alignment	not modelled	99.7	22	PDB header: ligase/rna Chain: A: PDB Molecule: arginyl-trna synthetase; PDBTitle: crystal structure of the arginyl-trna synthetase complexed with the2 trna(arg) and l-arg
71	c1g59A	Alignment	not modelled	99.6	18	PDB header: ligase/rna Chain: A: PDB Molecule: glutamyl-trna synthetase; PDBTitle: glutamyl-trna synthetase complexed with trna(glu).
72	d1pfva1	Alignment	not modelled	99.6	17	Fold: Anticodon-binding domain of a subclass of class I aminoacyl-tRNA synthetases Superfamily: Anticodon-binding domain of a subclass of class I aminoacyl-tRNA synthetases Family: Anticodon-binding domain of a subclass of class I aminoacyl-tRNA synthetases
73	c5h4vE	Alignment	not modelled	99.5	26	PDB header: ligase Chain: E: PDB Molecule: glutamate--trna ligase; PDBTitle: structure of glutamyl-trna synthetase (xoo1504) from xanthomonas2 oryzae pv. oryzae
74	c2ja2A	Alignment	not modelled	99.5	21	PDB header: ligase Chain: A: PDB Molecule: glutamyl-trna synthetase; PDBTitle: mycobacterium tuberculosis glutamyl-trna synthetase
75	d2d5ba1	Alignment	not modelled	99.5	15	Fold: Anticodon-binding domain of a subclass of class I aminoacyl-tRNA synthetases Superfamily: Anticodon-binding domain of a subclass of class I aminoacyl-tRNA synthetases Family: Anticodon-binding domain of a subclass of class I aminoacyl-tRNA synthetases
						PDB header: ligase Chain: A: PDB Molecule: glutamyl-trna synthetase 2;

76	c3afhA	Alignment	not modelled	99.4	19	PDBTitle: crystal structure of thermotoga maritima nondiscriminating glutamyl-tRNA synthetase in complex with a glutamyl-amp analog
77	c2cfoA	Alignment	not modelled	99.4	22	PDB header: ligase Chain: A: PDB Molecule: glutamyl-tRNA synthetase; PDBTitle: non-discriminating glutamyl-tRNA synthetase from <i>Thermosynechococcus elongatus</i> in complex with glu
78	c2o5rA	Alignment	not modelled	99.3	20	PDB header: ligase Chain: A: PDB Molecule: glutamyl-tRNA synthetase 1; PDBTitle: crystal structure of glutamyl-tRNA synthetase 1 (ec 6.1.1.17)2 (glutamate-tRNA ligase 1) (glurs 1) (tm1351) from <i>Thermotoga maritima</i> 3 at 2.5 Å resolution
79	c4griB	Alignment	not modelled	99.3	19	PDB header: ligase Chain: B: PDB Molecule: glutamate--tRNA ligase; PDBTitle: crystal structure of a glutamyl-tRNA synthetase glurs from <i>Borrelia burgdorferi</i> bound to glutamic acid and zinc
80	c5tgtA	Alignment	not modelled	99.2	24	PDB header: ligase Chain: A: PDB Molecule: glutamate--tRNA ligase; PDBTitle: crystal structure of glutamyl-tRNA synthetase glurs from <i>Pseudomonas aeruginosa</i>
81	c1irxA	Alignment	not modelled	98.5	20	PDB header: ligase Chain: A: PDB Molecule: lysyl-tRNA synthetase; PDBTitle: crystal structure of class I lysyl-tRNA synthetase
82	d1gtra2	Alignment	not modelled	98.4	21	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Nucleotidyl transferase Family: Class I aminoacyl-tRNA synthetases (RS), catalytic domain
83	c5zdoA	Alignment	not modelled	98.4	20	PDB header: ligase Chain: A: PDB Molecule: glutamine-tRNA ligase; PDBTitle: crystal structure analysis of ttqrs in co-crystallised with atp
84	c4r3zC	Alignment	not modelled	98.3	20	PDB header: protein binding/ligase Chain: C: PDB Molecule: glutamine--tRNA ligase; PDBTitle: crystal structure of human argRS-glnRS-aimp1 complex
85	c1exdA	Alignment	not modelled	98.3	23	PDB header: ligase/rna Chain: A: PDB Molecule: glutamyl-tRNA synthetase; PDBTitle: crystal structure of a tight-binding glutamine tRNA bound to glutamine aminoacyl tRNA synthetase
86	c2hz7A	Alignment	not modelled	98.3	26	PDB header: ligase Chain: A: PDB Molecule: glutamyl-tRNA synthetase; PDBTitle: crystal structure of the glutamyl-tRNA synthetase from <i>Deinococcus radiodurans</i>
87	c3aiiA	Alignment	not modelled	98.3	26	PDB header: ligase Chain: A: PDB Molecule: glutamyl-tRNA synthetase; PDBTitle: archaeal non-discriminating glutamyl-tRNA synthetase from <i>Methanothermobacter thermoautotrophicus</i>
88	d1nzza	Alignment	not modelled	98.3	25	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Nucleotidyl transferase Family: Class I aminoacyl-tRNA synthetases (RS), catalytic domain
89	c4ye6A	Alignment	not modelled	98.3	19	PDB header: ligase Chain: A: PDB Molecule: glutamine--tRNA ligase; PDBTitle: the crystal structure of the intact human glnRS
90	c5bnzA	Alignment	not modelled	98.2	19	PDB header: ligase Chain: A: PDB Molecule: glutamine--tRNA ligase; PDBTitle: crystal structure of glutamine-tRNA ligase /glutamyl-tRNA synthetase2 (glnRS) from <i>Pseudomonas aeruginosa</i>
91	c6b1pA	Alignment	not modelled	98.2	23	PDB header: ligase Chain: A: PDB Molecule: glutamate--tRNA ligase 1; PDBTitle: crystal structure of glutamate-tRNA synthetase from <i>Helicobacter pylori</i>
92	c4h3sA	Alignment	not modelled	98.2	21	PDB header: ligase Chain: A: PDB Molecule: glutamine-tRNA ligase; PDBTitle: the structure of glutamyl-tRNA synthetase from <i>Saccharomyces cerevisiae</i>
93	c4p2bA	Alignment	not modelled	98.1	22	PDB header: ligase Chain: A: PDB Molecule: glutamine aminoacyl-tRNA synthetase; PDBTitle: crystal structure of the apo form of the glutamyl-tRNA synthetase2 catalytic domain from <i>Toxoplasma gondii</i> .
94	d1j09a2	Alignment	not modelled	98.0	25	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Nucleotidyl transferase Family: Class I aminoacyl-tRNA synthetases (RS), catalytic domain
95	c4g6zA	Alignment	not modelled	98.0	28	PDB header: ligase Chain: A: PDB Molecule: glutamate-tRNA ligase; PDBTitle: crystal structure of a glutamyl-tRNA synthetase glurs from <i>Burkholderia thailandensis</i> bound to L-glutamate
96	c3al0C	Alignment	not modelled	97.8	25	PDB header: ligase/rna Chain: C: PDB Molecule: glutamyl-tRNA(gln) amidotransferase subunit c, linker, PDBTitle: crystal structure of the glutamine transamidosome from <i>Thermotoga maritima</i> in the glutamylation state.
97	c1h3eA	Alignment	not modelled	97.7	27	PDB header: ligase Chain: A: PDB Molecule: tyrosyl-tRNA synthetase; PDBTitle: tyrosyl-tRNA synthetase from <i>Thermus thermophilus</i> complexed with wild-2 type tRNA ^{tyr} (gua) and with atp and tyrosinol
98	c6b1zA	Alignment	not modelled	97.6	17	PDB header: ligase Chain: A: PDB Molecule: glutamate--tRNA ligase; PDBTitle: crystal structure of glutamate-tRNA synthetase from <i>Elizabethkingia anophelis</i>
99	c2janD	Alignment	not modelled	97.6	14	PDB header: ligase Chain: D: PDB Molecule: tyrosyl-tRNA synthetase; PDBTitle: tyrosyl-tRNA synthetase from <i>Mycobacterium tuberculosis</i> in 2 unliganded state
100	c6otjA	Alignment	not modelled	97.5	12	PDB header: ligase Chain: A: PDB Molecule: tyrosine--tRNA ligase; PDBTitle: crystal structure of tyrosyl-tRNA synthetase from <i>Neisseria gonorrhoeae</i> with bound L-tyr
101	c1jiiA	Alignment	not modelled	97.5	17	PDB header: ligase Chain: A: PDB Molecule: tyrosyl-tRNA synthetase; PDBTitle: crystal structure of <i>S. aureus</i> tyrrs in complex with sb-219383

102	c2cybA_	Alignment	not modelled	97.5	33	PDB header: ligase Chain: A: PDB Molecule: tyrosyl-trna synthetase; PDBTitle: crystal structure of tyrosyl-trna synthetase complexed with2 l-tyrosine from archaeoglobus fulgidus
103	d1jila_	Alignment	not modelled	97.5	18	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Nucleotidylyl transferase Family: Class I aminoacyl-tRNA synthetases (RS), catalytic domain
104	d1h3fa1	Alignment	not modelled	97.4	29	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Nucleotidylyl transferase Family: Class I aminoacyl-tRNA synthetases (RS), catalytic domain
105	c6mtkA_	Alignment	not modelled	97.4	21	PDB header: ligase Chain: A: PDB Molecule: tryptophanyl-trna synthetase; PDBTitle: crystal structure of tryptophanyl-trna synthetase from elizabethkingia2 anophelis nuhp1
106	c1x8xA_	Alignment	not modelled	97.3	16	PDB header: ligase Chain: A: PDB Molecule: tyrosyl-trna synthetase; PDBTitle: tyrosyl t-rna synthetase from e.coli complexed with tyrosine
107	c2g36A_	Alignment	not modelled	97.1	10	PDB header: ligase Chain: A: PDB Molecule: tryptophanyl-trna synthetase; PDBTitle: 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
108	c2rkjM_	Alignment	not modelled	96.9	10	PDB header: ligase/rna Chain: M: PDB Molecule: tyrosyl-trna synthetase; PDBTitle: cocrystal structure of a tyrosyl-trna synthetase splicing factor with2 a group i intron rna
109	d2ts1a_	Alignment	not modelled	96.8	18	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Nucleotidylyl transferase Family: Class I aminoacyl-tRNA synthetases (RS), catalytic domain
110	c2ts1A_	Alignment	not modelled	96.8	18	PDB header: ligase (synthetase) Chain: A: PDB Molecule: tyrosyl-trna synthetase; PDBTitle: structure of tyrosyl-t/rna synthetase refined at 2.3 angstroms2 resolution. interaction of the enzyme with the tyrosyl adenylate3 intermediate
111	c6n0wA_	Alignment	not modelled	96.7	12	PDB header: ligase Chain: A: PDB Molecule: tyrosine--trna ligase; PDBTitle: crystal structure of a tyrosine--trna ligase from elizabethkingia2 anophelis
112	c3vgjB_	Alignment	not modelled	96.5	15	PDB header: ligase Chain: B: PDB Molecule: tyrosyl-trna synthetase, putative; PDBTitle: crystal of plasmodium falciparum tyrosyl-trna synthetase (pftyrrs)in2 complex with adenylate analog
113	c5tevA_	Alignment	not modelled	96.5	22	PDB header: ligase Chain: A: PDB Molecule: tryptophan--trna ligase; PDBTitle: crystal structure of a tryptophanyl-trna synthetase from neisseria2 gonorrhoeae, apo
114	c2cyaA_	Alignment	not modelled	96.4	23	PDB header: ligase Chain: A: PDB Molecule: tyrosyl-trna synthetase; PDBTitle: crystal structure of tyrosyl-trna synthetase from aeropyrum pernix
115	c3hzzD_	Alignment	not modelled	96.4	9	PDB header: ligase Chain: D: PDB Molecule: tryptophanyl-trna synthetase; PDBTitle: tryptophanyl-trna synthetase homolog from entamoeba histolytica
116	c6byqA_	Alignment	not modelled	96.4	31	PDB header: ligase Chain: A: PDB Molecule: tyrosine--trna ligase; PDBTitle: crystal structure of tyrosine-trna ligase from helicobacter pylori g27
117	c3a05A_	Alignment	not modelled	96.3	18	PDB header: ligase Chain: A: PDB Molecule: tryptophanyl-trna synthetase; PDBTitle: crystal structure of tryptophanyl-trna synthetase from2 hyperthermophilic archaeon, aeropyrum pernix k1 complex3 with tryptophan
118	c5ekdA_	Alignment	not modelled	96.3	12	PDB header: ligase/antibiotic Chain: A: PDB Molecule: tryptophan--trna ligase, mitochondrial; PDBTitle: human mitochondrial tryptophanyl-trna synthetase bound by indolmycin2 and mn*atp.
119	d1n3la_	Alignment	not modelled	96.2	12	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Nucleotidylyl transferase Family: Class I aminoacyl-tRNA synthetases (RS), catalytic domain
120	c3tzeA_	Alignment	not modelled	96.2	20	PDB header: ligase Chain: A: PDB Molecule: tryptophanyl-trna synthetase; PDBTitle: crystal structure of a tryptophanyl-trna synthetase from2 encephalitozoon cuniculi bound to tryptophan