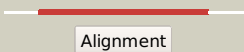

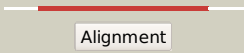



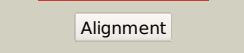



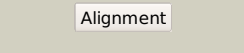

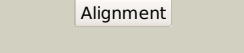
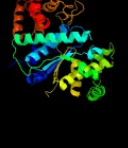


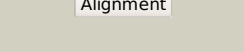

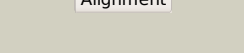
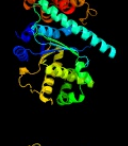
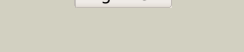












# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1689_(tyrS)_1913609_1914883
Date	Fri Aug 2 13:30:28 BST 2019
Unique Job ID	8a52ddca2634ae6d

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c2janD_</a>	 Alignment		100.0	100	<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
2	<a href="#">c6otjA_</a>	 Alignment		100.0	46	<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
3	<a href="#">c4oudA_</a>	 Alignment		100.0	44	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> tyrosyl-trna synthetase; <b>PDBTitle:</b> engineered tyrosyl-trna synthetase with the nonstandard amino acid l-2 4,4-biphenylalanine
4	<a href="#">c1h3eA_</a>	 Alignment		100.0	26	<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
5	<a href="#">c4oudB_</a>	 Alignment		100.0	46	<b>PDB header:</b> ligase <b>Chain:</b> B: <b>PDB Molecule:</b> tyrosyl-trna synthetase; <b>PDBTitle:</b> engineered tyrosyl-trna synthetase with the nonstandard amino acid l-2 4,4-biphenylalanine
6	<a href="#">c6n0wA_</a>	 Alignment		100.0	45	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> tyrosine--trna ligase; <b>PDBTitle:</b> crystal structure of a tyrosine--trna ligase from elizabethkingia2 anophelis
7	<a href="#">c2rkjM_</a>	 Alignment		100.0	35	<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
8	<a href="#">c5ijxA_</a>	 Alignment		100.0	35	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> tyrosine--trna ligase, mitochondrial; <b>PDBTitle:</b> crystal structure of a c-terminally truncated coccidioides posadasii2 mitochondrial tyrosyl-trna synthetase
9	<a href="#">c2pidB_</a>	 Alignment		100.0	40	<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
10	<a href="#">c5ihxB_</a>	 Alignment		100.0	35	<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
11	<a href="#">d1jila_</a>	 Alignment		100.0	49	<b>Fold:</b> Adenine nucleotide alpha hydrolase-like <b>Superfamily:</b> Nucleotidyl transferase <b>Family:</b> Class I aminoacyl-tRNA synthetases (RS), catalytic domain

12	<a href="#">c1x8xA</a>	Alignment		100.0	53	<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
13	<a href="#">c1jiiA</a>	Alignment		100.0	49	<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
14	<a href="#">d2ts1a</a>	Alignment		100.0	55	<b>Fold:</b> Adenine nucleotide alpha hydrolase-like <b>Superfamily:</b> Nucleotidylyl transferase <b>Family:</b> Class I aminoacyl-tRNA synthetases (RS), catalytic domain
15	<a href="#">c2ts1A</a>	Alignment		100.0	55	<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
16	<a href="#">d1h3fa1</a>	Alignment		100.0	29	<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="#">c6byqA</a>	Alignment		100.0	28	<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
18	<a href="#">c2cybA</a>	Alignment		100.0	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 complexed with 2 l-tyrosine from archaeoglobus fulgidus
19	<a href="#">c3tzeA</a>	Alignment		100.0	15	<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 from 2 encephalitozoon cuniculi bound to tryptophan
20	<a href="#">c2quiB</a>	Alignment		100.0	17	<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 in 2 complex with tryptophanamide and atp
21	<a href="#">c1r6tA</a>	Alignment	not modelled	100.0	18	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> tryptophanyl-tRNA synthetase; <b>PDBTitle:</b> crystal structure of human tryptophanyl-tRNA synthetase
22	<a href="#">c2cyaA</a>	Alignment	not modelled	100.0	16	<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
23	<a href="#">c3jxeB</a>	Alignment	not modelled	100.0	16	<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
24	<a href="#">c3focB</a>	Alignment	not modelled	100.0	17	<b>PDB header:</b> ligase <b>Chain:</b> B: <b>PDB Molecule:</b> tryptophanyl-tRNA synthetase; <b>PDBTitle:</b> tryptophanyl-tRNA synthetase from giardia lamblia
25	<a href="#">c3kt3D</a>	Alignment	not modelled	100.0	15	<b>PDB header:</b> ligase <b>Chain:</b> D: <b>PDB Molecule:</b> tryptophanyl-tRNA synthetase, cytoplasmic; <b>PDBTitle:</b> crystal structure of s. cerevisiae tryptophanyl-tRNA synthetase in 2 complex with trpamp
26	<a href="#">c4j75B</a>	Alignment	not modelled	100.0	17	<b>PDB header:</b> ligase <b>Chain:</b> B: <b>PDB Molecule:</b> tryptophanyl-tRNA synthetase; <b>PDBTitle:</b> crystal structure of a parasite tRNA synthetase, product-bound
27	<a href="#">c3hztD</a>	Alignment	not modelled	100.0	11	<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
28	<a href="#">d1r6ta2</a>	Alignment	not modelled	100.0	17	<b>Fold:</b> Adenine nucleotide alpha hydrolase-like <b>Superfamily:</b> Nucleotidylyl transferase <b>Family:</b> Class I aminoacyl-tRNA synthetases (RS), catalytic domain
						<b>PDB header:</b> ligase

29	<a href="#">c3vgjB_</a>	Alignment	not modelled	100.0	15	<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
30	<a href="#">c2cycB_</a>	Alignment	not modelled	100.0	18	<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
31	<a href="#">c6bqzA_</a>	Alignment	not modelled	100.0	32	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> tyrosine--trna ligase; <b>PDBTitle:</b> crystal structure of tyrosine-trna synthetase from acinetobacter2 baumannii with bound l-tyrosine
32	<a href="#">c3a05A_</a>	Alignment	not modelled	100.0	16	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> tryptophanyl-trna synthetase; <b>PDBTitle:</b> crystal structure of tyrosyl-trna synthetase from2 hyperthermophilic archaeon, aeropyrum pernix k1 complex3 with tryptophan
33	<a href="#">c3i05B_</a>	Alignment	not modelled	100.0	14	<b>PDB header:</b> ligase <b>Chain:</b> B: <b>PDB Molecule:</b> tryptophanyl-trna synthetase; <b>PDBTitle:</b> tryptophanyl-trna synthetase from trypanosoma brucei
34	<a href="#">c1r6uB_</a>	Alignment	not modelled	100.0	15	<b>PDB header:</b> ligase <b>Chain:</b> B: <b>PDB Molecule:</b> tryptophanyl-trna synthetase; <b>PDBTitle:</b> crystal structure of an active fragment of human tryptophanyl-trna2 synthetase with cytokine activity
35	<a href="#">c2el7A_</a>	Alignment	not modelled	100.0	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 thermus2 thermophilus
36	<a href="#">c3hv0A_</a>	Alignment	not modelled	100.0	16	<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
37	<a href="#">c3p0jD_</a>	Alignment	not modelled	100.0	18	<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
38	<a href="#">d1jlua_</a>	Alignment	not modelled	100.0	18	<b>Fold:</b> Adenine nucleotide alpha hydrolase-like <b>Superfamily:</b> Nucleotidylyl transferase <b>Family:</b> Class I aminoacyl-tRNA synthetases (RS), catalytic domain
39	<a href="#">c1q11A_</a>	Alignment	not modelled	100.0	14	<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
40	<a href="#">d1n3la_</a>	Alignment	not modelled	100.0	14	<b>Fold:</b> Adenine nucleotide alpha hydrolase-like <b>Superfamily:</b> Nucleotidylyl transferase <b>Family:</b> Class I aminoacyl-tRNA synthetases (RS), catalytic domain
41	<a href="#">c2ip1A_</a>	Alignment	not modelled	100.0	14	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> tryptophanyl-trna synthetase; <b>PDBTitle:</b> crystal structure analysis of s. cerevisiae tryptophanyl trna2 synthetase
42	<a href="#">c2dlcX_</a>	Alignment	not modelled	100.0	14	<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
43	<a href="#">c2j5bA_</a>	Alignment	not modelled	100.0	17	<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
44	<a href="#">c1vi8C_</a>	Alignment	not modelled	100.0	18	<b>Chain:</b> C: <b>PDB Molecule:</b> tryptophanyl-trna synthetase; <b>PDBTitle:</b> crystal structure of tryptophanyl trna synthetase ii from deinococcus2 radiodurans in complex with l-trp
45	<a href="#">c5ekdA_</a>	Alignment	not modelled	100.0	14	<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.
46	<a href="#">c3n9iA_</a>	Alignment	not modelled	100.0	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 yersinia pestis2 co92
47	<a href="#">d1i6la_</a>	Alignment	not modelled	100.0	14	<b>Fold:</b> Adenine nucleotide alpha hydrolase-like <b>Superfamily:</b> Nucleotidylyl transferase <b>Family:</b> Class I aminoacyl-tRNA synthetases (RS), catalytic domain
48	<a href="#">c5tevA_</a>	Alignment	not modelled	100.0	15	<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
49	<a href="#">c3m5wB_</a>	Alignment	not modelled	100.0	13	<b>PDB header:</b> ligase <b>Chain:</b> B: <b>PDB Molecule:</b> tryptophanyl-trna synthetase; <b>PDBTitle:</b> crystal structure of tryptophanyl-trna synthetase from campylobacter2 jejuni
50	<a href="#">c6ncrB_</a>	Alignment	not modelled	100.0	14	<b>PDB header:</b> ligase <b>Chain:</b> B: <b>PDB Molecule:</b> tryptophan--trna ligase; <b>PDBTitle:</b> crystal structure of tryptophan-trna ligase from chlamydia trachomatis2 with bound l-tryptophan
51	<a href="#">c3sz3A_</a>	Alignment	not modelled	100.0	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 vibrio cholerae2 with an endogenous tryptophan
52	<a href="#">c6mtkA_</a>	Alignment	not modelled	100.0	13	<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
53	<a href="#">c2g36A_</a>	Alignment	not modelled	100.0	20	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> tryptophanyl-trna synthetase; <b>PDBTitle:</b> crystal structure of tryptophanyl-trna synthetase (ec 6.1.1.2)2 (tryptophan-trna ligase)(trprs) (tm0492) from thermotoga maritima at3 2.50 a resolution
54	<a href="#">c3prhB_</a>	Alignment	not modelled	100.0	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
55	<a href="#">c2yy5C_</a>	Alignment	not modelled	100.0	13	<b>PDB header:</b> ligase <b>Chain:</b> C: <b>PDB Molecule:</b> tryptophanyl-trna synthetase; <b>PDBTitle:</b> crystal structure of tryptophanyl-trna synthetase from mycoplasma2 pneumoniae
56	<a href="#">d1jh3a_</a>	Alignment	not modelled	99.9	32	<b>Fold:</b> Alpha-L RNA-binding motif <b>Superfamily:</b> Alpha-L RNA-binding motif <b>Family:</b> Tyrosyl-tRNA synthetase (TyrRS), C-terminal domain
57	<a href="#">d1h3fa2</a>	Alignment	not modelled	99.6	24	<b>Fold:</b> Alpha-L RNA-binding motif <b>Superfamily:</b> Alpha-L RNA-binding motif <b>Family:</b> Tyrosyl-tRNA synthetase (TyrRS), C-terminal domain
58	<a href="#">c2ktiA_</a>	Alignment	not modelled	98.9	23	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> tyrosyl-trna synthetase; <b>PDBTitle:</b> structure of c-terminal domain from mttyrss of a. nidulans
59	<a href="#">d1ivs4</a>	Alignment	not modelled	98.8	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
60	<a href="#">c2x1lC_</a>	Alignment	not modelled	98.7	18	<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
61	<a href="#">d1li5a2</a>	Alignment	not modelled	98.5	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
62	<a href="#">c2ct8A_</a>	Alignment	not modelled	98.4	16	<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
63	<a href="#">c2cfoA_</a>	Alignment	not modelled	98.4	20	<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
64	<a href="#">c3tqoA_</a>	Alignment	not modelled	98.3	14	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> cysteiny-trna synthetase; <b>PDBTitle:</b> structure of the cysteiny-trna synthetase (cyss) from coxiella2 burnetii.
65	<a href="#">c1u0bB_</a>	Alignment	not modelled	98.3	15	<b>PDB header:</b> ligase/rna <b>Chain:</b> B: <b>PDB Molecule:</b> cysteiny trna; <b>PDBTitle:</b> crystal structure of cysteiny-trna synthetase binary2 complex with trnacys
66	<a href="#">c6b1pA_</a>	Alignment	not modelled	98.3	19	<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
67	<a href="#">d1gtra2</a>	Alignment	not modelled	98.1	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
68	<a href="#">c3c8zB_</a>	Alignment	not modelled	98.1	19	<b>PDB header:</b> ligase <b>Chain:</b> B: <b>PDB Molecule:</b> cysteiny-trna synthetase; <b>PDBTitle:</b> the 1.6 a crystal structure of mshc: the rate limiting2 enzyme in the mycothiol biosynthetic pathway
69	<a href="#">c3sp1B_</a>	Alignment	not modelled	98.0	15	<b>PDB header:</b> ligase <b>Chain:</b> B: <b>PDB Molecule:</b> cysteiny-trna synthetase; <b>PDBTitle:</b> crystal structure of cysteiny-trna synthetase (cyss) from borrelia2 burgdorferi
70	<a href="#">d1ffya3</a>	Alignment	not modelled	97.9	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
71	<a href="#">c1qu2A_</a>	Alignment	not modelled	97.9	22	<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
72	<a href="#">c1lrxA_</a>	Alignment	not modelled	97.9	14	<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
73	<a href="#">d1f7ua2</a>	Alignment	not modelled	97.8	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
74	<a href="#">c1ileA_</a>	Alignment	not modelled	97.7	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
75	<a href="#">d1ilea3</a>	Alignment	not modelled	97.7	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
76	<a href="#">d1c06a_</a>	Alignment	not modelled	97.6	15	<b>Fold:</b> Alpha-L RNA-binding motif <b>Superfamily:</b> Alpha-L RNA-binding motif <b>Family:</b> Ribosomal protein S4
77	<a href="#">c2cqjA_</a>	Alignment	not modelled	97.6	21	<b>PDB header:</b> rna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> u3 small nucleolar ribonucleoprotein protein <b>PDBTitle:</b> solution structure of the s4 domain of u3 small nucleolar2 ribonucleoprotein protein imp3 homolog
78	<a href="#">c3fnrA_</a>	Alignment	not modelled	97.6	15	<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;
79	<a href="#">c1gaxB_</a>	Alignment	not modelled	97.6	20	<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
80	<a href="#">c4r3zB_</a>	Alignment	not modelled	97.5	15	<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

81	<a href="#">c5ah5B</a>	Alignment	not modelled	97.5	18	<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-rna-leuams
82	<a href="#">d1p9ka</a>	Alignment	not modelled	97.5	22	<b>Fold:</b> Alpha-L RNA-binding motif <b>Superfamily:</b> Alpha-L RNA-binding motif <b>Family:</b> Ybcj-like
83	<a href="#">c6nd4Z</a>	Alignment	not modelled	97.5	13	<b>PDB header:</b> ribosome <b>Chain:</b> Z: <b>PDB Molecule:</b> imp3; <b>PDBTitle:</b> conformational switches control early maturation of the eukaryotic2 small ribosomal subunit
84	<a href="#">c1woyA</a>	Alignment	not modelled	97.4	19	<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
85	<a href="#">c5jpbq</a>	Alignment	not modelled	97.4	19	<b>PDB header:</b> ribosome <b>Chain:</b> B: <b>PDB Molecule:</b> wd40 domain proteins; <b>PDBTitle:</b> cryo-em structure of the 90s pre-ribosome
86	<a href="#">c3kflA</a>	Alignment	not modelled	97.4	15	<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
87	<a href="#">d1dm9a</a>	Alignment	not modelled	97.4	23	<b>Fold:</b> Alpha-L RNA-binding motif <b>Superfamily:</b> Alpha-L RNA-binding motif <b>Family:</b> Heat shock protein 15 kD
88	<a href="#">c1dm9A</a>	Alignment	not modelled	97.4	23	<b>PDB header:</b> structural genomics <b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical 15.5 kd protein in mrca-pcka intergenic <b>PDBTitle:</b> heat shock protein 15 kd
89	<a href="#">c3afhA</a>	Alignment	not modelled	97.4	14	<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
90	<a href="#">c5o5jD</a>	Alignment	not modelled	97.3	21	<b>PDB header:</b> ribosome <b>Chain:</b> D: <b>PDB Molecule:</b> 30s ribosomal protein s4; <b>PDBTitle:</b> structure of the 30s small ribosomal subunit from mycobacterium2 smegmatis
91	<a href="#">d2d5ba2</a>	Alignment	not modelled	97.3	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
92	<a href="#">d2uubd1</a>	Alignment	not modelled	97.3	23	<b>Fold:</b> Alpha-L RNA-binding motif <b>Superfamily:</b> Alpha-L RNA-binding motif <b>Family:</b> Ribosomal protein S4
93	<a href="#">c4griB</a>	Alignment	not modelled	97.3	15	<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
94	<a href="#">c4qrdA</a>	Alignment	not modelled	97.3	12	<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
95	<a href="#">c3tunA</a>	Alignment	not modelled	97.3	15	<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
96	<a href="#">c3j20D</a>	Alignment	not modelled	97.3	18	<b>PDB header:</b> ribosome <b>Chain:</b> D: <b>PDB Molecule:</b> 30s ribosomal protein s4p; <b>PDBTitle:</b> promiscuous behavior of proteins in archaeal ribosomes revealed by2 cryo-em: implications for evolution of eukaryotic ribosomes (30s3 ribosomal subunit)
97	<a href="#">c1wkbA</a>	Alignment	not modelled	97.2	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
98	<a href="#">c4g6zA</a>	Alignment	not modelled	97.2	15	<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
99	<a href="#">c5h4vE</a>	Alignment	not modelled	97.1	19	<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
100	<a href="#">c5xyil</a>	Alignment	not modelled	97.1	18	<b>PDB header:</b> ribosome <b>Chain:</b> J: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> small subunit of trichomonas vaginalis ribosome
101	<a href="#">c1g59A</a>	Alignment	not modelled	97.1	20	<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).
102	<a href="#">c5tgtA</a>	Alignment	not modelled	97.1	15	<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
103	<a href="#">c3zey6</a>	Alignment	not modelled	97.1	20	<b>PDB header:</b> ribosome <b>Chain:</b> 6: <b>PDB Molecule:</b> 40s ribosomal protein s9, putative; <b>PDBTitle:</b> high-resolution cryo-electron microscopy structure of the trypanosoma2 brucei ribosome
104	<a href="#">d1j09a2</a>	Alignment	not modelled	97.1	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
105	<a href="#">c2xzmD</a>	Alignment	not modelled	97.1	18	<b>PDB header:</b> ribosome <b>Chain:</b> D: <b>PDB Molecule:</b> ribosomal protein s4 containing protein; <b>PDBTitle:</b> crystal structure of the eukaryotic 40s ribosomal2 subunit in complex with initiation factor 1. this file3 contains the 40s subunit and initiation factor for4 molecule 1

106	<a href="#">d2gy9d1</a>	Alignment	not modelled	97.1	17	<b>Fold:</b> Alpha-L RNA-binding motif <b>Superfamily:</b> Alpha-L RNA-binding motif <b>Family:</b> Ribosomal protein S4
107	<a href="#">c6ao8A</a>	Alignment	not modelled	97.1	17	<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
108	<a href="#">c3bbnD</a>	Alignment	not modelled	97.1	21	<b>PDB header:</b> ribosome <b>Chain:</b> D: <b>PDB Molecule:</b> ribosomal protein s4; <b>PDBTitle:</b> homology model for the spinach chloroplast 30s subunit fitted to 9.4a2 cryo-em map of the 70s chlororibosome.
109	<a href="#">c1s1hD</a>	Alignment	not modelled	97.0	19	<b>PDB header:</b> ribosome <b>Chain:</b> D: <b>PDB Molecule:</b> 40s ribosomal protein s9-a; <b>PDBTitle:</b> structure of the ribosomal 80s-eef2-sordarin complex from yeast2 obtained by docking atomic models for rna and protein components into3 a 11.7 a cryo-em map. this file, 1s1h, contains 40s subunit. the 60s4 ribosomal subunit is in file 1s1i.
110	<a href="#">c3ziuA</a>	Alignment	not modelled	97.0	21	<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
111	<a href="#">c4ye6A</a>	Alignment	not modelled	97.0	13	<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
112	<a href="#">c5wxmA</a>	Alignment	not modelled	97.0	13	<b>PDB header:</b> ribosomal protein <b>Chain:</b> A: <b>PDB Molecule:</b> u3 small nucleolar ribonucleoprotein protein imp3; <b>PDBTitle:</b> crystal structure of the imp3 and mpp10 complex
113	<a href="#">c3ziuB</a>	Alignment	not modelled	97.0	23	<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
114	<a href="#">c1exdA</a>	Alignment	not modelled	96.9	17	<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
115	<a href="#">c4r3zC</a>	Alignment	not modelled	96.9	13	<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
116	<a href="#">c1wz2B</a>	Alignment	not modelled	96.9	17	<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
117	<a href="#">c1pfuA</a>	Alignment	not modelled	96.9	16	<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
118	<a href="#">c5zdoA</a>	Alignment	not modelled	96.9	17	<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
119	<a href="#">c4h3sA</a>	Alignment	not modelled	96.8	17	<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
120	<a href="#">c5urbB</a>	Alignment	not modelled	96.8	17	<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