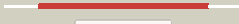



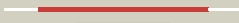

















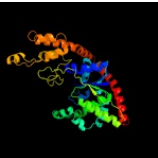



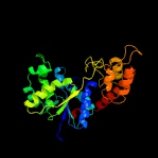
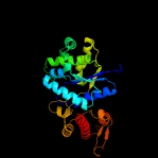
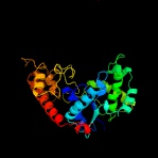
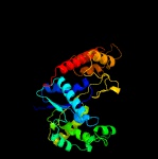
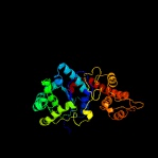


# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3336c_(trpS)_3722792_3723802
Date	Thu Aug 8 16:20:55 BST 2019
Unique Job ID	577ff6742a45c1fe

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c3n9iA_</a>	 Alignment		100.0	52	<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
2	<a href="#">d1i6la_</a>	 Alignment		100.0	51	<b>Fold:</b> Adenine nucleotide alpha hydrolase-like <b>Superfamily:</b> Nucleotidyl transferase <b>Family:</b> Class I aminoacyl-tRNA synthetases (RS), catalytic domain
3	<a href="#">c5ekdA_</a>	 Alignment		100.0	43	<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.
4	<a href="#">c3sz3A_</a>	 Alignment		100.0	49	<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
5	<a href="#">c3prhB_</a>	 Alignment		100.0	49	<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
6	<a href="#">c2yy5C_</a>	 Alignment		100.0	38	<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
7	<a href="#">c5tevA_</a>	 Alignment		100.0	33	<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
8	<a href="#">c1yi8C_</a>	 Alignment		100.0	31	<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 ii from deinococcus2 radiodurans in complex with l-trp
9	<a href="#">c3m5wB_</a>	 Alignment		100.0	33	<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
10	<a href="#">c6mtkA_</a>	 Alignment		100.0	35	<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
11	<a href="#">c2g36A_</a>	 Alignment		100.0	34	<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

12	<a href="#">c2el7A_</a>	Alignment		100.0	43	<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
13	<a href="#">c6ncrB_</a>	Alignment		100.0	32	<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
14	<a href="#">c2cycB_</a>	Alignment		100.0	21	<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
15	<a href="#">c3vgjB_</a>	Alignment		100.0	17	<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
16	<a href="#">c2quiB_</a>	Alignment		100.0	19	<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
17	<a href="#">c2cybA_</a>	Alignment		100.0	23	<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
18	<a href="#">c3kt3D_</a>	Alignment		100.0	24	<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 in2 complex with trpamp
19	<a href="#">c3tzeA_</a>	Alignment		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 a tryptophanyl-trna synthetase from2 encephalitozoon cuniculi bound to tryptophan
20	<a href="#">c3focB_</a>	Alignment		100.0	22	<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
21	<a href="#">c3jxeB_</a>	Alignment	not modelled	100.0	20	<b>PDB header:</b> ligase <b>Chain:</b> B: <b>PDB Molecule:</b> tryptophanyl-trna synthetase; <b>PDBTitle:</b> crystal structure of pyrococcus horikoshii tryptophanyl-trna2 synthetase in complex with trpamp
22	<a href="#">c4j75B_</a>	Alignment	not modelled	100.0	21	<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
23	<a href="#">d1r6ta2</a>	Alignment	not modelled	100.0	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
24	<a href="#">c3a05A_</a>	Alignment	not modelled	100.0	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 from2 hyperthermophilic archaeon, aeropyrum pernix k1 complex3 with tryptophan
25	<a href="#">c2cyaA_</a>	Alignment	not modelled	100.0	24	<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
26	<a href="#">c3h3rD_</a>	Alignment	not modelled	100.0	15	<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
27	<a href="#">c3p0jD_</a>	Alignment	not modelled	100.0	20	<b>PDB header:</b> ligase <b>Chain:</b> D: <b>PDB Molecule:</b> tyrosyl-trna synthetase; <b>PDBTitle:</b> leishmania major tyrosyl-trna synthetase in complex with tyrosinol,2 triclinic crystal form 1
28	<a href="#">c2j5bA_</a>	Alignment	not modelled	100.0	22	<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

29	<a href="#">c1r6tA</a>	Alignment	not modelled	100.0	19	<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
30	<a href="#">c2dlcX</a>	Alignment	not modelled	100.0	19	<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
31	<a href="#">c2ip1A</a>	Alignment	not modelled	100.0	22	<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
32	<a href="#">c1r6uB</a>	Alignment	not modelled	100.0	19	<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
33	<a href="#">c1q11A</a>	Alignment	not modelled	100.0	18	<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
34	<a href="#">d1n3la</a>	Alignment	not modelled	100.0	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
35	<a href="#">c3hv0A</a>	Alignment	not modelled	100.0	19	<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
36	<a href="#">d2ts1a</a>	Alignment	not modelled	100.0	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
37	<a href="#">c2ts1A</a>	Alignment	not modelled	100.0	19	<b>PDB header:</b> ligase (synthetase) <b>Chain:</b> A: <b>PDB Molecule:</b> tyrosyl-trna synthetase; <b>PDBTitle:</b> structure of tyrosyl-trna synthetase refined at 2.3 angstroms2 resolution. interaction of the enzyme with the tyrosyl adenylate3 intermediate
38	<a href="#">c6byqA</a>	Alignment	not modelled	100.0	20	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> tyrosine--trna ligase; <b>PDBTitle:</b> crystal structure of tyrosine-trna ligase from helicobacter pylori g27
39	<a href="#">c1jiiA</a>	Alignment	not modelled	100.0	18	<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
40	<a href="#">d1jila</a>	Alignment	not modelled	100.0	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
41	<a href="#">c1x8xA</a>	Alignment	not modelled	100.0	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
42	<a href="#">c2rkjM</a>	Alignment	not modelled	100.0	18	<b>PDB header:</b> ligase/rna <b>Chain:</b> M: <b>PDB Molecule:</b> tyrosyl-trna synthetase; <b>PDBTitle:</b> cocrystal structure of a tyrosyl-trna synthetase splicing factor with2 a group i intron rna
43	<a href="#">d1jlua</a>	Alignment	not modelled	100.0	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
44	<a href="#">c2janD</a>	Alignment	not modelled	100.0	17	<b>PDB header:</b> ligase <b>Chain:</b> D: <b>PDB Molecule:</b> tyrosyl-trna synthetase; <b>PDBTitle:</b> tyrosyl-trna synthetase from mycobacterium tuberculosis in2 unliganded state
45	<a href="#">c6otjA</a>	Alignment	not modelled	100.0	18	<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
46	<a href="#">c3i05B</a>	Alignment	not modelled	100.0	20	<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
47	<a href="#">c1h3eA</a>	Alignment	not modelled	100.0	22	<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
48	<a href="#">c5ihxB</a>	Alignment	not modelled	100.0	16	<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
49	<a href="#">d1h3fa1</a>	Alignment	not modelled	100.0	22	<b>Fold:</b> Adenine nucleotide alpha hydrolase-like <b>Superfamily:</b> Nucleotidyl transferase <b>Family:</b> Class I aminoacyl-tRNA synthetases (RS), catalytic domain
50	<a href="#">c2pidB</a>	Alignment	not modelled	100.0	20	<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
51	<a href="#">c6n0wA</a>	Alignment	not modelled	100.0	20	<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
52	<a href="#">c5ijxA</a>	Alignment	not modelled	100.0	15	<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
53	<a href="#">c4oudA</a>	Alignment	not modelled	100.0	18	<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
54	<a href="#">c4oudB</a>	Alignment	not modelled	100.0	19	<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

55	<a href="#">c6bqzA</a>	Alignment	not modelled	100.0	22	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> tyrosine--trna ligase; <b>PDBTitle:</b> crystal structure of tyrosine-trna synthetase from acinetobacter2 baumannii with bound l-tyrosine
56	<a href="#">c2x1lC</a>	Alignment	not modelled	98.7	22	<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
57	<a href="#">c2cfoA</a>	Alignment	not modelled	98.6	18	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> glutamyl-trna synthetase; <b>PDBTitle:</b> non-discriminating glutamyl-trna synthetase from2 thermosynechococcus elongatus in complex with glu
58	<a href="#">c6b1pA</a>	Alignment	not modelled	98.6	16	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> glutamate--trna ligase 1; <b>PDBTitle:</b> crystal structure of glutamate-trna synthetase from helicobacter2 pylori
59	<a href="#">c3tqoA</a>	Alignment	not modelled	98.5	16	<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.
60	<a href="#">c2ct8A</a>	Alignment	not modelled	98.5	22	<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
61	<a href="#">c1u0bB</a>	Alignment	not modelled	98.3	18	<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
62	<a href="#">c2o5rA</a>	Alignment	not modelled	98.3	18	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> glutamyl-trna synthetase 1; <b>PDBTitle:</b> crystal structure of glutamyl-trna synthetase 1 (ec 6.1.1.17)2 (glutamate-trna ligase 1) (glurs 1) (tm1351) from thermotoga maritima3 at 2.5 a resolution
63	<a href="#">c5h4vE</a>	Alignment	not modelled	98.3	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
64	<a href="#">d1rqga2</a>	Alignment	not modelled	98.2	12	<b>Fold:</b> Adenine nucleotide alpha hydrolase-like <b>Superfamily:</b> Nucleotidyl transferase <b>Family:</b> Class I aminoacyl-tRNA synthetases (RS), catalytic domain
65	<a href="#">d1ivsa4</a>	Alignment	not modelled	98.2	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
66	<a href="#">d1li5a2</a>	Alignment	not modelled	98.2	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
67	<a href="#">d1gtra2</a>	Alignment	not modelled	98.2	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="#">d1pfva2</a>	Alignment	not modelled	98.2	20	<b>Fold:</b> Adenine nucleotide alpha hydrolase-like <b>Superfamily:</b> Nucleotidyl transferase <b>Family:</b> Class I aminoacyl-tRNA synthetases (RS), catalytic domain
69	<a href="#">c3affhA</a>	Alignment	not modelled	98.1	21	<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
70	<a href="#">d2d5ba2</a>	Alignment	not modelled	98.1	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
71	<a href="#">c6b1zA</a>	Alignment	not modelled	98.1	18	<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
72	<a href="#">c3sp1B</a>	Alignment	not modelled	98.1	14	<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
73	<a href="#">c5tgtA</a>	Alignment	not modelled	98.1	22	<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
74	<a href="#">c1woyA</a>	Alignment	not modelled	98.0	17	<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
75	<a href="#">d1f7ua2</a>	Alignment	not modelled	98.0	15	<b>Fold:</b> Adenine nucleotide alpha hydrolase-like <b>Superfamily:</b> Nucleotidyl transferase <b>Family:</b> Class I aminoacyl-tRNA synthetases (RS), catalytic domain
76	<a href="#">c3al0C</a>	Alignment	not modelled	98.0	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.
77	<a href="#">c2ja2A</a>	Alignment	not modelled	97.9	22	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> glutamyl-trna synthetase; <b>PDBTitle:</b> mycobacterium tuberculosis glutamyl-trna synthetase
78	<a href="#">c3fnrA</a>	Alignment	not modelled	97.9	14	<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;
79	<a href="#">c4griB</a>	Alignment	not modelled	97.9	22	<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/rna

80	<a href="#">c1g59A_</a>	Alignment	not modelled	97.8	24	<b>Chain:</b> A: <b>PDB Molecule:</b> glutamyl-trna synthetase; <b>PDBTitle:</b> glutamyl-trna synthetase complexed with trna(glu).
81	<a href="#">c4g6zA_</a>	Alignment	not modelled	97.8	20	<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
82	<a href="#">d1nzza_</a>	Alignment	not modelled	97.6	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
83	<a href="#">d1lrx2</a>	Alignment	not modelled	97.6	16	<b>Fold:</b> Adenine nucleotide alpha hydrolase-like <b>Superfamily:</b> Nucleotidyl transferase <b>Family:</b> Class I aminoacyl-tRNA synthetases (RS), catalytic domain
84	<a href="#">d1j09a2</a>	Alignment	not modelled	97.5	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
85	<a href="#">c2hz7A_</a>	Alignment	not modelled	97.4	13	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> glutamyl-trna synthetase; <b>PDBTitle:</b> crystal structure of the glutamyl-trna synthetase from deinococcus2 radiodurans
86	<a href="#">c1exdA_</a>	Alignment	not modelled	97.4	16	<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
87	<a href="#">c5ah5B_</a>	Alignment	not modelled	97.3	14	<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 leurs-trna-leuams
88	<a href="#">c4r3zC_</a>	Alignment	not modelled	97.2	16	<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
89	<a href="#">c5bnzA_</a>	Alignment	not modelled	97.1	16	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> glutamine--trna ligase; <b>PDBTitle:</b> crystal structure of glutamine-trna ligase /glutamyl-trna synthetase2 (glnrs) from pseudomonas aeruginosa
90	<a href="#">c3aiiA_</a>	Alignment	not modelled	97.1	18	<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
91	<a href="#">c5zdoA_</a>	Alignment	not modelled	97.1	19	<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
92	<a href="#">c5gl7A_</a>	Alignment	not modelled	96.9	17	<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
93	<a href="#">c1qu2A_</a>	Alignment	not modelled	96.9	19	<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
94	<a href="#">c1rqqA_</a>	Alignment	not modelled	96.8	13	<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
95	<a href="#">c4qrdA_</a>	Alignment	not modelled	96.8	17	<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
96	<a href="#">c1f7uA_</a>	Alignment	not modelled	96.8	16	<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
97	<a href="#">c4h3sA_</a>	Alignment	not modelled	96.7	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
98	<a href="#">c4ye6A_</a>	Alignment	not modelled	96.7	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
99	<a href="#">c4p2bA_</a>	Alignment	not modelled	96.6	18	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> glutamine aminoacyl-trna synthetase; <b>PDBTitle:</b> crystal structure of the apo form of the glutamyl-trna synthetase2 catalytic domain from toxoplasma gondii.
100	<a href="#">c5xqgB_</a>	Alignment	not modelled	96.6	19	<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
101	<a href="#">c3tunA_</a>	Alignment	not modelled	96.5	11	<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
102	<a href="#">c1ileA_</a>	Alignment	not modelled	96.3	13	<b>PDB header:</b> aminoacyl-trna synthetase <b>Chain:</b> A: <b>PDB Molecule:</b> isoleucyl-trna synthetase; <b>PDBTitle:</b> isoleucyl-trna synthetase
103	<a href="#">c4dlpA_</a>	Alignment	not modelled	96.2	16	<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
104	<a href="#">c1lrxA_</a>	Alignment	not modelled	96.2	17	<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
105	<a href="#">c3kflA_</a>	Alignment	not modelled	96.1	10	<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 <b>Fold:</b> Adenine nucleotide alpha hydrolase-like

106	<a href="#">d1ffya3</a>	Alignment	not modelled	96.1	29	<b>Superfamily:</b> Nucleotidyl transferase <b>Family:</b> Class I aminoacyl-tRNA synthetases (RS), catalytic domain
107	<a href="#">c4dlpB</a>	Alignment	not modelled	95.9	14	<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
108	<a href="#">c1pfuA</a>	Alignment	not modelled	95.8	15	<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
109	<a href="#">c5urbB</a>	Alignment	not modelled	95.7	14	<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
110	<a href="#">c3ziuB</a>	Alignment	not modelled	95.6	13	<b>PDB header:</b> ligase <b>Chain:</b> B: <b>PDB Molecule:</b> leucyl-trna synthetase; <b>PDBTitle:</b> crystal structure of mycoplasma mobile leucyl-trna2 synthetase with leu-ams in the active site
111	<a href="#">d1ilea3</a>	Alignment	not modelled	95.4	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
112	<a href="#">c1gaxB</a>	Alignment	not modelled	95.3	13	<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
113	<a href="#">d1h3na3</a>	Alignment	not modelled	95.3	12	<b>Fold:</b> Adenine nucleotide alpha hydrolase-like <b>Superfamily:</b> Nucleotidyl transferase <b>Family:</b> Class I aminoacyl-tRNA synthetases (RS), catalytic domain
114	<a href="#">c3ziuA</a>	Alignment	not modelled	95.2	16	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> leucyl-trna synthetase; <b>PDBTitle:</b> crystal structure of mycoplasma mobile leucyl-trna2 synthetase with leu-ams in the active site
115	<a href="#">c3c8zB</a>	Alignment	not modelled	95.0	20	<b>PDB header:</b> ligase <b>Chain:</b> B: <b>PDB Molecule:</b> cysteinyln-trna synthetase; <b>PDBTitle:</b> the 1.6 a crystal structure of mshc: the rate limiting2 enzyme in the mycothiol biosynthetic pathway
116	<a href="#">c1wkbA</a>	Alignment	not modelled	95.0	14	<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
117	<a href="#">c4obyA</a>	Alignment	not modelled	94.6	25	<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
118	<a href="#">c6ao8A</a>	Alignment	not modelled	93.9	15	<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
119	<a href="#">c1wz2B</a>	Alignment	not modelled	93.4	25	<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
120	<a href="#">c1obhA</a>	Alignment	not modelled	93.2	14	<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