

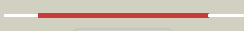








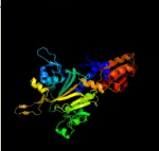

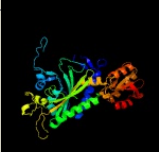








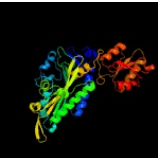

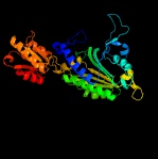
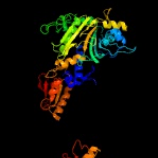

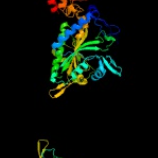
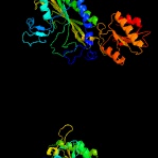
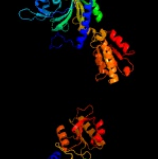



# Phyre2

Email mdejesus@rockefeller.edu  
 Description RVBD2845c\_(proS)\_3151212\_3152960  
 Date Wed Aug 7 12:50:51 BST 2019  
 Unique Job ID baa0c618df6f6407

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c5znjA_</a>	 Alignment		100.0	39	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> proline--trna ligase; <b>PDBTitle:</b> crystal structure of a bacterial prors with ligands
2	<a href="#">c5ucmB_</a>	 Alignment		100.0	42	<b>PDB header:</b> ligase <b>Chain:</b> B: <b>PDB Molecule:</b> proline--trna ligase; <b>PDBTitle:</b> crystal structure of prolyl-trna synthetase from pseudomonas2 aeruginosa
3	<a href="#">c2j3mA_</a>	 Alignment		100.0	41	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> prolyl-trna synthetase; <b>PDBTitle:</b> prolyl-trna synthetase from enterococcus faecalis complexed2 with atp, manganese and prolinol
4	<a href="#">c2i4IC_</a>	 Alignment		100.0	43	<b>PDB header:</b> ligase <b>Chain:</b> C: <b>PDB Molecule:</b> proline-trna ligase; <b>PDBTitle:</b> rhodopseudomonas palustris prolyl-trna synthetase
5	<a href="#">c4kqeA_</a>	 Alignment		100.0	17	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> glycine--trna ligase; <b>PDBTitle:</b> the mutant structure of the human glycyl-trna synthetase e71g
6	<a href="#">c4kr3A_</a>	 Alignment		100.0	20	<b>PDB header:</b> ligase/rna <b>Chain:</b> A: <b>PDB Molecule:</b> glycine--trna ligase; <b>PDBTitle:</b> glycyl-trna synthetase mutant e71g in complex with trna-gly
7	<a href="#">c1ggmB_</a>	 Alignment		100.0	23	<b>PDB header:</b> ligase <b>Chain:</b> B: <b>PDB Molecule:</b> glycine--trna ligase; <b>PDBTitle:</b> glycyl-trna synthetase from thermus thermophilus complexed with2 glycyl-adenylate
8	<a href="#">c3ialB_</a>	 Alignment		100.0	26	<b>PDB header:</b> ligase <b>Chain:</b> B: <b>PDB Molecule:</b> prolyl-trna synthetase; <b>PDBTitle:</b> giardia lamblia prolyl-trna synthetase in complex with prolyl-2 adenylate
9	<a href="#">c2pmfA_</a>	 Alignment		100.0	22	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> glycyl-trna synthetase; <b>PDBTitle:</b> the crystal structure of a human glycyl-trna synthetase mutant
10	<a href="#">c6nabB_</a>	 Alignment		100.0	22	<b>PDB header:</b> ligase <b>Chain:</b> B: <b>PDB Molecule:</b> prolyl-trna synthetase; <b>PDBTitle:</b> crystal structure of prolyl-trna synthetase from naegleria fowleri in2 complex with proline and adenosine monophosphphate (amp)
11	<a href="#">c1atiA_</a>	 Alignment		100.0	22	<b>PDB header:</b> protein biosynthesis <b>Chain:</b> A: <b>PDB Molecule:</b> glycyl-trna synthetase; <b>PDBTitle:</b> crystal structure of glycyl-trna synthetase from thermus thermophilus

12	<a href="#">c4twaA_</a>	Alignment		100.0	20	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> proline--trna ligase; <b>PDBTitle:</b> crystal structure of prolyl-trna synthetase (prs) from plasmodium2 falciparum
13	<a href="#">c4hvcB_</a>	Alignment		100.0	22	<b>PDB header:</b> ligase/ligase inhibitor <b>Chain:</b> B: <b>PDB Molecule:</b> bifunctional glutamate/proline--trna ligase; <b>PDBTitle:</b> crystal structure of human prolyl-trna synthetase in complex with2 halofuginone and atp analogue
14	<a href="#">c5xiiC_</a>	Alignment		100.0	23	<b>PDB header:</b> ligase <b>Chain:</b> C: <b>PDB Molecule:</b> prolyl-trna synthetase (prors); <b>PDBTitle:</b> crystal structure of toxoplasma gondii prolyl-trna synthetase (tgprs)2 in complex with inhibitor 6
15	<a href="#">c5z5eB_</a>	Alignment		100.0	19	<b>PDB header:</b> ligase <b>Chain:</b> B: <b>PDB Molecule:</b> neq417; <b>PDBTitle:</b> crystal structure of the glycyL-trna synthetase (glyrs) in2 nanoarchaeum equitans
16	<a href="#">c5f9yB_</a>	Alignment		100.0	23	<b>PDB header:</b> ligase <b>Chain:</b> B: <b>PDB Molecule:</b> aminoacyl-trna synthetase; <b>PDBTitle:</b> crystal structure of prolyl-trna synthetase from cryptosporidium2 parvum complexed with l-proline and amp
17	<a href="#">c1qf6A_</a>	Alignment		100.0	20	<b>PDB header:</b> ligase/rna <b>Chain:</b> A: <b>PDB Molecule:</b> threonyl-trna synthetase; <b>PDBTitle:</b> structure of e. coli threonyl-trna synthetase complexed with its2 cognate trna
18	<a href="#">c1nj8C_</a>	Alignment		100.0	25	<b>PDB header:</b> ligase <b>Chain:</b> C: <b>PDB Molecule:</b> proline-trna synthetase; <b>PDBTitle:</b> crystal structure of prolyl-trna synthetase from2 methanocaldococcus janaschii
19	<a href="#">c1nyqA_</a>	Alignment		100.0	27	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> threonyl-trna synthetase 1; <b>PDBTitle:</b> structure of staphylococcus aureus threonyl-trna synthetase2 complexed with an analogue of threonyl adenylate
20	<a href="#">c1h4tD_</a>	Alignment		100.0	23	<b>PDB header:</b> aminoacyl-trna synthetase <b>Chain:</b> D: <b>PDB Molecule:</b> prolyl-trna synthetase; <b>PDBTitle:</b> prolyl-trna synthetase from thermus thermophilus complexed2 with l-proline
21	<a href="#">c6mn8A_</a>	Alignment	not modelled	100.0	23	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> crystal structure of prolyl-trna synthetase from onchocerca volvulus2 with bound halofuginone and nucleotide
22	<a href="#">c5e6mA_</a>	Alignment	not modelled	100.0	19	<b>PDB header:</b> ligase/rna <b>Chain:</b> A: <b>PDB Molecule:</b> glycine--trna ligase; <b>PDBTitle:</b> crystal structure of human wild type glyrs bound with trnagly
23	<a href="#">c1nj2A_</a>	Alignment	not modelled	100.0	25	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> proline-trna synthetase; <b>PDBTitle:</b> crystal structure of prolyl-trna synthetase from methanothermobacter2 thermautotrophicus
24	<a href="#">c3a32A_</a>	Alignment	not modelled	100.0	17	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> probable threonyl-trna synthetase 1; <b>PDBTitle:</b> crystal structure of putative threonyl-trna synthetase thrrs-1 from2 aeropyrum pernix
25	<a href="#">c5zy9D_</a>	Alignment	not modelled	100.0	21	<b>PDB header:</b> ligase <b>Chain:</b> D: <b>PDB Molecule:</b> threonyl-trna synthase; <b>PDBTitle:</b> structural basis for a trna synthetase
26	<a href="#">c1fyfB_</a>	Alignment	not modelled	100.0	20	<b>PDB header:</b> ligase <b>Chain:</b> B: <b>PDB Molecule:</b> threonyl-trna synthetase; <b>PDBTitle:</b> crystal structure of a truncated form of threonyl-trna2 synthetase complexed with a seryl adenylate analog
27	<a href="#">c4hwtA_</a>	Alignment	not modelled	100.0	19	<b>PDB header:</b> ligase/ligase inhibitor <b>Chain:</b> A: <b>PDB Molecule:</b> threonine--trna ligase, cytoplasmic; <b>PDBTitle:</b> crystal structure of human threonyl-trna synthetase bound to a novel2 inhibitor
28	<a href="#">c3ikmC_</a>	Alignment	not modelled	100.0	20	<b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> dna polymerase subunit gamma-2; <b>PDBTitle:</b> crystal structure of human mitochondrial dna polymerase holoenzyme
						<b>PDB header:</b> ligase

29	<a href="#">c3ugtD</a>	Alignment	not modelled	100.0	20	<b>Chain:</b> D: <b>PDB Molecule:</b> threonyl-trna synthetase, mitochondrial; <b>PDBTitle:</b> crystal structure of the yeast mitochondrial threonyl-trna synthetase2 - orthorhombic crystal form
30	<a href="#">c1g5hA</a>	Alignment	not modelled	100.0	20	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> mitochondrial dna polymerase accessory subunit; <b>PDBTitle:</b> crystal structure of the accessory subunit of murine mitochondrial2 polymerase gamma
31	<a href="#">c5xiIA</a>	Alignment	not modelled	100.0	29	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> putative prolyl-trna synthetase; <b>PDBTitle:</b> crystal structure of leishmania major prolyl-trna synthetase (Imprs)
32	<a href="#">c1adyA</a>	Alignment	not modelled	100.0	19	<b>PDB header:</b> trna synthetase <b>Chain:</b> A: <b>PDB Molecule:</b> histidyl-trna synthetase; <b>PDBTitle:</b> histidyl-trna synthetase in complex with histidyl-adenylate
33	<a href="#">c2eI9B</a>	Alignment	not modelled	100.0	24	<b>PDB header:</b> ligase <b>Chain:</b> B: <b>PDB Molecule:</b> histidyl-trna synthetase; <b>PDBTitle:</b> crystal structure of e.coli histidyl-trna synthetase2 complexed with a histidyl-adenylate analogue
34	<a href="#">c3ikIA</a>	Alignment	not modelled	100.0	20	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> dna polymerase subunit gamma-2, mitochondrial; <b>PDBTitle:</b> crystal structure of pol gb delta-i4.
35	<a href="#">c6nhIA</a>	Alignment	not modelled	100.0	18	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> histidine--trna ligase; <b>PDBTitle:</b> crystal structure of histidine--trna ligase from elizabethkingia sp.2 ccug 26117
36	<a href="#">c1wu7A</a>	Alignment	not modelled	100.0	20	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> histidyl-trna synthetase; <b>PDBTitle:</b> crystal structure of histidyl-trna synthetase from2 thermoplasma acidophilum
37	<a href="#">c3netB</a>	Alignment	not modelled	100.0	19	<b>PDB header:</b> ligase <b>Chain:</b> B: <b>PDB Molecule:</b> histidyl-trna synthetase; <b>PDBTitle:</b> crystal structure of histidyl-trna synthetase from nostoc sp. pcc 7120
38	<a href="#">c4g84B</a>	Alignment	not modelled	100.0	18	<b>PDB header:</b> ligase <b>Chain:</b> B: <b>PDB Molecule:</b> histidine--trna ligase, cytoplasmic; <b>PDBTitle:</b> crystal structure of human hisrs
39	<a href="#">c5e3IA</a>	Alignment	not modelled	100.0	20	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> histidine--trna ligase; <b>PDBTitle:</b> crystal structure of a histidyl-trna synthetase from acinetobacter2 baumannii with bound l-histidine and atp
40	<a href="#">c3hriF</a>	Alignment	not modelled	100.0	19	<b>PDB header:</b> ligase <b>Chain:</b> F: <b>PDB Molecule:</b> histidyl-trna synthetase; <b>PDBTitle:</b> histidyl-trna synthetase (apo) from trypanosoma brucei
41	<a href="#">c1qe0B</a>	Alignment	not modelled	100.0	19	<b>PDB header:</b> ligase <b>Chain:</b> B: <b>PDB Molecule:</b> histidine--trna ligase; <b>PDBTitle:</b> crystal structure of apo s. aureus histidyl-trna synthetase
42	<a href="#">c4g85A</a>	Alignment	not modelled	100.0	20	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> histidine-trna ligase, cytoplasmic; <b>PDBTitle:</b> crystal structure of human hisrs
43	<a href="#">c4e51B</a>	Alignment	not modelled	100.0	22	<b>PDB header:</b> ligase <b>Chain:</b> B: <b>PDB Molecule:</b> histidine--trna ligase; <b>PDBTitle:</b> crystal structure of a histidyl-trna synthetase hisrs from2 burkholderia thailandensis bound to histidine
44	<a href="#">c4x5oB</a>	Alignment	not modelled	100.0	23	<b>PDB header:</b> ligase <b>Chain:</b> B: <b>PDB Molecule:</b> histidine--trna ligase, cytoplasmic; <b>PDBTitle:</b> human histidine trna synthetase
45	<a href="#">c3w3sA</a>	Alignment	not modelled	100.0	26	<b>PDB header:</b> ligase/rna <b>Chain:</b> A: <b>PDB Molecule:</b> type-2 serine--trna ligase; <b>PDBTitle:</b> crystal structure of a. aeolicus trnasec in complex with m. kandleri2 serrs
46	<a href="#">d1nj1a3</a>	Alignment	not modelled	100.0	24	<b>Fold:</b> Class II aaRS and biotin synthetases <b>Superfamily:</b> Class II aaRS and biotin synthetases <b>Family:</b> Class II aminoacyl-tRNA synthetase (aaRS)-like, catalytic domain
47	<a href="#">d1nj8a3</a>	Alignment	not modelled	100.0	27	<b>Fold:</b> Class II aaRS and biotin synthetases <b>Superfamily:</b> Class II aaRS and biotin synthetases <b>Family:</b> Class II aminoacyl-tRNA synthetase (aaRS)-like, catalytic domain
48	<a href="#">d1qf6a4</a>	Alignment	not modelled	100.0	20	<b>Fold:</b> Class II aaRS and biotin synthetases <b>Superfamily:</b> Class II aaRS and biotin synthetases <b>Family:</b> Class II aminoacyl-tRNA synthetase (aaRS)-like, catalytic domain
49	<a href="#">d1hc7a2</a>	Alignment	not modelled	100.0	28	<b>Fold:</b> Class II aaRS and biotin synthetases <b>Superfamily:</b> Class II aaRS and biotin synthetases <b>Family:</b> Class II aminoacyl-tRNA synthetase (aaRS)-like, catalytic domain
50	<a href="#">d1b76a2</a>	Alignment	not modelled	100.0	21	<b>Fold:</b> Class II aaRS and biotin synthetases <b>Superfamily:</b> Class II aaRS and biotin synthetases <b>Family:</b> Class II aminoacyl-tRNA synthetase (aaRS)-like, catalytic domain
51	<a href="#">d1atia2</a>	Alignment	not modelled	100.0	23	<b>Fold:</b> Class II aaRS and biotin synthetases <b>Superfamily:</b> Class II aaRS and biotin synthetases <b>Family:</b> Class II aminoacyl-tRNA synthetase (aaRS)-like, catalytic domain
52	<a href="#">c3od1A</a>	Alignment	not modelled	100.0	21	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> atp phosphoribosyltransferase regulatory subunit; <b>PDBTitle:</b> the crystal structure of an atp phosphoribosyltransferase regulatory2 subunit/histidyl-trna synthetase from bacillus halodurans c
53	<a href="#">d1nyra4</a>	Alignment	not modelled	100.0	21	<b>Fold:</b> Class II aaRS and biotin synthetases <b>Superfamily:</b> Class II aaRS and biotin synthetases <b>Family:</b> Class II aminoacyl-tRNA synthetase (aaRS)-like, catalytic domain
54	<a href="#">c5m8hB</a>	Alignment	not modelled	100.0	13	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> atp phosphoribosyltransferase regulatory subunit;

						<b>PDBTitle:</b> atp phosphoribosyltransferase (hiszg atpprt) from psychrobacter2 arcticus
55	<a href="#">c2cj9A</a>	Alignment	not modelled	100.0	25	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> seryl-trna synthetase; <b>PDBTitle:</b> crystal structure of methanosarcina barkeri seryl-trna synthetase2 complexed with an analog of seryladenylate
56	<a href="#">c3mf2B</a>	Alignment	not modelled	100.0	19	<b>PDB header:</b> ligase <b>Chain:</b> B: <b>PDB Molecule:</b> blI0957 protein; <b>PDBTitle:</b> crystal structure of class ii aaRS and biotin synthetases complexed with2 amp
57	<a href="#">d1seta2</a>	Alignment	not modelled	100.0	21	<b>Fold:</b> Class II aaRS and biotin synthetases <b>Superfamily:</b> Class II aaRS and biotin synthetases <b>Family:</b> Class II aminoacyl-tRNA synthetase (aaRS)-like, catalytic domain
58	<a href="#">c1wleB</a>	Alignment	not modelled	100.0	18	<b>PDB header:</b> ligase <b>Chain:</b> B: <b>PDB Molecule:</b> seryl-trna synthetase; <b>PDBTitle:</b> crystal structure of mammalian mitochondrial seryl-trna2 synthetase complexed with seryl-adenylate
59	<a href="#">c6bjcC</a>	Alignment	not modelled	100.0	25	<b>PDB header:</b> ligase <b>Chain:</b> C: <b>PDB Molecule:</b> serine-trna ligase; <b>PDBTitle:</b> crystal structure of cytoplasmic serine-trna ligase from naegleria2 fowleri in complex with amp
60	<a href="#">c1sryB</a>	Alignment	not modelled	100.0	21	<b>PDB header:</b> ligase(synthetase) <b>Chain:</b> B: <b>PDB Molecule:</b> seryl-trna synthetase; <b>PDBTitle:</b> refined crystal structure of the seryl-trna synthetase from2 thermus thermophilus at 2.5 angstroms resolution
61	<a href="#">c3lssA</a>	Alignment	not modelled	100.0	18	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> seryl-trna synthetase; <b>PDBTitle:</b> trypanosoma brucei seryl-trna synthetase in complex with atp
62	<a href="#">c3vbbB</a>	Alignment	not modelled	100.0	18	<b>PDB header:</b> ligase <b>Chain:</b> B: <b>PDB Molecule:</b> seryl-trna synthetase, cytoplasmic; <b>PDBTitle:</b> crystal structure of seryl-trna synthetase from human at 2.9 angstroms
63	<a href="#">c3qo8A</a>	Alignment	not modelled	100.0	17	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> seryl-trna synthetase, cytoplasmic; <b>PDBTitle:</b> crystal structure of seryl-trna synthetase from candida albicans
64	<a href="#">c6h9xA</a>	Alignment	not modelled	100.0	26	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> serine--trna ligase; <b>PDBTitle:</b> klebsiella pneumoniae seryl-trna synthetase in complex with the2 intermediate analog 5'-o-(n-(l-seryl)-sulfamoyl)adenosine
65	<a href="#">c2dq0A</a>	Alignment	not modelled	100.0	20	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> seryl-trna synthetase; <b>PDBTitle:</b> crystal structure of seryl-trna synthetase from pyrococcus2 horikoshii complexed with a seryl-adenylate analog
66	<a href="#">c6oteA</a>	Alignment	not modelled	100.0	22	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> seryl-trna synthetase, cytoplasmic; <b>PDBTitle:</b> crystal structure of seryl-trna synthetase (serrs) from2 cryptosporidium parvum complexed with l-serylsulfamoyl adenosine
67	<a href="#">c2dq3A</a>	Alignment	not modelled	100.0	24	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> seryl-trna synthetase; <b>PDBTitle:</b> crystal structure of aq_298
68	<a href="#">c6girA</a>	Alignment	not modelled	100.0	22	<b>PDB header:</b> cytosolic protein <b>Chain:</b> A: <b>PDB Molecule:</b> serine--trna ligase, cytoplasmic; <b>PDBTitle:</b> arabidopsis thaliana cytosolic seryl-trna synthetase
69	<a href="#">c3errB</a>	Alignment	not modelled	100.0	21	<b>PDB header:</b> ligase <b>Chain:</b> B: <b>PDB Molecule:</b> fusion protein of microtubule binding domain from mouse <b>PDBTitle:</b> microtubule binding domain from mouse cytoplasmic dynein as a fusion2 with seryl-trna synthetase
70	<a href="#">d1wu7a2</a>	Alignment	not modelled	100.0	21	<b>Fold:</b> Class II aaRS and biotin synthetases <b>Superfamily:</b> Class II aaRS and biotin synthetases <b>Family:</b> Class II aminoacyl-tRNA synthetase (aaRS)-like, catalytic domain
71	<a href="#">d1kmma2</a>	Alignment	not modelled	100.0	20	<b>Fold:</b> Class II aaRS and biotin synthetases <b>Superfamily:</b> Class II aaRS and biotin synthetases <b>Family:</b> Class II aminoacyl-tRNA synthetase (aaRS)-like, catalytic domain
72	<a href="#">d1g5ha2</a>	Alignment	not modelled	100.0	19	<b>Fold:</b> Class II aaRS and biotin synthetases <b>Superfamily:</b> Class II aaRS and biotin synthetases <b>Family:</b> Class II aminoacyl-tRNA synthetase (aaRS)-like, catalytic domain
73	<a href="#">d1z7ma1</a>	Alignment	not modelled	100.0	15	<b>Fold:</b> Class II aaRS and biotin synthetases <b>Superfamily:</b> Class II aaRS and biotin synthetases <b>Family:</b> Class II aminoacyl-tRNA synthetase (aaRS)-like, catalytic domain
74	<a href="#">d2g4ca2</a>	Alignment	not modelled	100.0	20	<b>Fold:</b> Class II aaRS and biotin synthetases <b>Superfamily:</b> Class II aaRS and biotin synthetases <b>Family:</b> Class II aminoacyl-tRNA synthetase (aaRS)-like, catalytic domain
75	<a href="#">c1z7nB</a>	Alignment	not modelled	100.0	13	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> atp phosphoribosyltransferase regulatory subunit; <b>PDBTitle:</b> atp phosphoribosyl transferase (hiszg atp-prtase) from2 lactococcus lactis with bound prpp substrate
76	<a href="#">c3racA</a>	Alignment	not modelled	100.0	16	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> histidine-trna ligase; <b>PDBTitle:</b> crystal structure of histidine--trna ligase subunit from2 alicyclobacillus acidocaldarius subsp. acidocaldarius dsm 446.
77	<a href="#">d1h4vb2</a>	Alignment	not modelled	100.0	19	<b>Fold:</b> Class II aaRS and biotin synthetases <b>Superfamily:</b> Class II aaRS and biotin synthetases <b>Family:</b> Class II aminoacyl-tRNA synthetase (aaRS)-like, catalytic domain
78	<a href="#">d1qe0a2</a>	Alignment	not modelled	100.0	18	<b>Fold:</b> Class II aaRS and biotin synthetases <b>Superfamily:</b> Class II aaRS and biotin synthetases <b>Family:</b> Class II aminoacyl-tRNA synthetase (aaRS)-like, catalytic domain
79	<a href="#">c3g1zB</a>	Alignment	not modelled	99.9	20	<b>PDB header:</b> ligase <b>Chain:</b> B: <b>PDB Molecule:</b> putative lysyl-trna synthetase; <b>PDBTitle:</b> structure of idp01693/yjea, a potential t-rna synthetase

						from2 salmonella typhimurium
80	<a href="#">d1nj1a1</a>	Alignment	not modelled	99.9	25	<b>Fold:</b> Anticodon-binding domain-like <b>Superfamily:</b> Class II aaRS ABD-related <b>Family:</b> Anticodon-binding domain of Class II aaRS
81	<a href="#">d1nj8a1</a>	Alignment	not modelled	99.9	27	<b>Fold:</b> Anticodon-binding domain-like <b>Superfamily:</b> Class II aaRS ABD-related <b>Family:</b> Anticodon-binding domain of Class II aaRS
82	<a href="#">d1bbua2</a>	Alignment	not modelled	99.9	17	<b>Fold:</b> Class II aaRS and biotin synthetases <b>Superfamily:</b> Class II aaRS and biotin synthetases <b>Family:</b> Class II aminoacyl-tRNA synthetase (aaRS)-like, catalytic domain
83	<a href="#">d1hc7a1</a>	Alignment	not modelled	99.9	35	<b>Fold:</b> Anticodon-binding domain-like <b>Superfamily:</b> Class II aaRS ABD-related <b>Family:</b> Anticodon-binding domain of Class II aaRS
84	<a href="#">d1usya_</a>	Alignment	not modelled	99.9	15	<b>Fold:</b> Class II aaRS and biotin synthetases <b>Superfamily:</b> Class II aaRS and biotin synthetases <b>Family:</b> Class II aminoacyl-tRNA synthetase (aaRS)-like, catalytic domain
85	<a href="#">d1e1oa2</a>	Alignment	not modelled	99.9	18	<b>Fold:</b> Class II aaRS and biotin synthetases <b>Superfamily:</b> Class II aaRS and biotin synthetases <b>Family:</b> Class II aminoacyl-tRNA synthetase (aaRS)-like, catalytic domain
86	<a href="#">d1qf6a1</a>	Alignment	not modelled	99.9	20	<b>Fold:</b> Anticodon-binding domain-like <b>Superfamily:</b> Class II aaRS ABD-related <b>Family:</b> Anticodon-binding domain of Class II aaRS
87	<a href="#">d1g5ha1</a>	Alignment	not modelled	99.9	17	<b>Fold:</b> Anticodon-binding domain-like <b>Superfamily:</b> Class II aaRS ABD-related <b>Family:</b> Anticodon-binding domain of Class II aaRS
88	<a href="#">d1nyra1</a>	Alignment	not modelled	99.9	25	<b>Fold:</b> Anticodon-binding domain-like <b>Superfamily:</b> Class II aaRS ABD-related <b>Family:</b> Anticodon-binding domain of Class II aaRS
89	<a href="#">d2g4ca1</a>	Alignment	not modelled	99.9	19	<b>Fold:</b> Anticodon-binding domain-like <b>Superfamily:</b> Class II aaRS ABD-related <b>Family:</b> Anticodon-binding domain of Class II aaRS
90	<a href="#">c6ezdD_</a>	Alignment	not modelled	99.9	14	<b>PDB header:</b> ligase <b>Chain:</b> D: <b>PDB Molecule:</b> pyrrolysyl-trna synthetase; <b>PDBTitle:</b> pyrrolysyl-trna synthetase from candidatus methanomethylophilus alvus2 (mmapylrs)
91	<a href="#">d1atia1</a>	Alignment	not modelled	99.9	22	<b>Fold:</b> Anticodon-binding domain-like <b>Superfamily:</b> Class II aaRS ABD-related <b>Family:</b> Anticodon-binding domain of Class II aaRS
92	<a href="#">c2zimA_</a>	Alignment	not modelled	99.9	18	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> pyrrolysyl-trna synthetase; <b>PDBTitle:</b> pyrrolysyl-trna synthetase bound to adenylated pyrrolysine and2 pyrophosphate
93	<a href="#">d1eova2</a>	Alignment	not modelled	99.8	19	<b>Fold:</b> Class II aaRS and biotin synthetases <b>Superfamily:</b> Class II aaRS and biotin synthetases <b>Family:</b> Class II aminoacyl-tRNA synthetase (aaRS)-like, catalytic domain
94	<a href="#">d1b8aa2</a>	Alignment	not modelled	99.8	20	<b>Fold:</b> Class II aaRS and biotin synthetases <b>Superfamily:</b> Class II aaRS and biotin synthetases <b>Family:</b> Class II aminoacyl-tRNA synthetase (aaRS)-like, catalytic domain
95	<a href="#">d1c0aa3</a>	Alignment	not modelled	99.8	24	<b>Fold:</b> Class II aaRS and biotin synthetases <b>Superfamily:</b> Class II aaRS and biotin synthetases <b>Family:</b> Class II aminoacyl-tRNA synthetase (aaRS)-like, catalytic domain
96	<a href="#">c2znjB_</a>	Alignment	not modelled	99.8	13	<b>PDB header:</b> ligase <b>Chain:</b> B: <b>PDB Molecule:</b> putative uncharacterized protein; <b>PDBTitle:</b> crystal structure of pyrrolysyl-trna synthetase from2 desulfotobacterium hafniense
97	<a href="#">d1l0wa3</a>	Alignment	not modelled	99.8	19	<b>Fold:</b> Class II aaRS and biotin synthetases <b>Superfamily:</b> Class II aaRS and biotin synthetases <b>Family:</b> Class II aminoacyl-tRNA synthetase (aaRS)-like, catalytic domain
98	<a href="#">d1kmma1</a>	Alignment	not modelled	99.8	29	<b>Fold:</b> Anticodon-binding domain-like <b>Superfamily:</b> Class II aaRS ABD-related <b>Family:</b> Anticodon-binding domain of Class II aaRS
99	<a href="#">d1wu7a1</a>	Alignment	not modelled	99.8	19	<b>Fold:</b> Anticodon-binding domain-like <b>Superfamily:</b> Class II aaRS ABD-related <b>Family:</b> Anticodon-binding domain of Class II aaRS
100	<a href="#">d1qe0a1</a>	Alignment	not modelled	99.8	20	<b>Fold:</b> Anticodon-binding domain-like <b>Superfamily:</b> Class II aaRS ABD-related <b>Family:</b> Anticodon-binding domain of Class II aaRS
101	<a href="#">d1h4vb1</a>	Alignment	not modelled	99.8	20	<b>Fold:</b> Anticodon-binding domain-like <b>Superfamily:</b> Class II aaRS ABD-related <b>Family:</b> Anticodon-binding domain of Class II aaRS
102	<a href="#">c2lw7A_</a>	Alignment	not modelled	99.7	19	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> histidine--trna ligase, cytoplasmic; <b>PDBTitle:</b> nmr solution structure of human hisrs splice variant
103	<a href="#">d1nnha_</a>	Alignment	not modelled	99.7	14	<b>Fold:</b> Class II aaRS and biotin synthetases <b>Superfamily:</b> Class II aaRS and biotin synthetases <b>Family:</b> Class II aminoacyl-tRNA synthetase (aaRS)-like, catalytic domain
104	<a href="#">c6pqhA_</a>	Alignment	not modelled	99.7	15	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> asparagine--trna ligase; <b>PDBTitle:</b> crystal structure of asparagine-trna ligase from elizabethkingia sp.2 ccug 26117
105	<a href="#">c3e9hB_</a>	Alignment	not modelled	99.6	16	<b>PDB header:</b> ligase <b>Chain:</b> B: <b>PDB Molecule:</b> lysyl-trna synthetase; <b>PDBTitle:</b> lysyl-trna synthetase from bacillus stearothermophilus2 complexed with l-lysylsulfamoyl adenosine
106	<a href="#">c1e22A_</a>	Alignment	not modelled	99.6	10	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> lysyl-trna synthetase;

106	<a href="#">c1g2zA_</a>	Alignment	not modelled	99.6	19	<b>PDBTitle:</b> lysyl-trna synthetase (lysu) hexagonal form complexed with2 lysine and the non-hydrolysable atp analogue amp-ppp <b>PDB header:</b> ligase
107	<a href="#">c1b70A_</a>	Alignment	not modelled	99.6	15	<b>Chain:</b> A: <b>PDB Molecule:</b> phenylalanyl-trna synthetase; <b>PDBTitle:</b> phenylalanyl trna synthetase complexed with phenylalanine
108	<a href="#">d1jjca_</a>	Alignment	not modelled	99.6	18	<b>Fold:</b> Class II aaRS and biotin synthetases <b>Superfamily:</b> Class II aaRS and biotin synthetases <b>Family:</b> Class II aminoacyl-tRNA synthetase (aaRS)-like, catalytic domain
109	<a href="#">c4up8A_</a>	Alignment	not modelled	99.6	14	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> lysine--trna ligase; <b>PDBTitle:</b> crystal structure of entamoeba histolytica lysyl-trna synthetase apo2 form
110	<a href="#">c5hgqD_</a>	Alignment	not modelled	99.5	16	<b>PDB header:</b> ligase/ligase inhibitor <b>Chain:</b> D: <b>PDB Molecule:</b> lysine--trna ligase; <b>PDBTitle:</b> loa loa lysyl-trna synthetase in complex with cladosporin.
111	<a href="#">c5elnC_</a>	Alignment	not modelled	99.5	14	<b>PDB header:</b> ligase <b>Chain:</b> C: <b>PDB Molecule:</b> lysine--trna ligase; <b>PDBTitle:</b> crystal structure of lysyl-trna synthetase from cryptosporidium parvum2 complexed with l-lysine
112	<a href="#">c3l4gl_</a>	Alignment	not modelled	99.5	14	<b>PDB header:</b> ligase <b>Chain:</b> I: <b>PDB Molecule:</b> phenylalanyl-trna synthetase alpha chain; <b>PDBTitle:</b> crystal structure of homo sapiens cytoplasmic phenylalanyl-trna2 synthetase
113	<a href="#">c4upaA_</a>	Alignment	not modelled	99.5	14	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> lysine--trna ligase; <b>PDBTitle:</b> crystal structure of entamoeba histolytica lysyl-trna synthetase in2 complex with amppnp
114	<a href="#">c3bjub_</a>	Alignment	not modelled	99.4	17	<b>PDB header:</b> ligase <b>Chain:</b> B: <b>PDB Molecule:</b> lysyl-trna synthetase; <b>PDBTitle:</b> crystal structure of tetrameric form of human lysyl-trna synthetase
115	<a href="#">c6ns0A_</a>	Alignment	not modelled	99.4	14	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> lysine--trna ligase; <b>PDBTitle:</b> crystal structure of lysyl-trna synthetase from chlamydia trachomatis2 complexed with l-lysine and cladosporin
116	<a href="#">c5vl1D_</a>	Alignment	not modelled	99.4	17	<b>PDB header:</b> ligase <b>Chain:</b> D: <b>PDB Molecule:</b> lysine--trna ligase; <b>PDBTitle:</b> crystal structure of lysyl-trna synthetase from mycobacterium ulcerans2 complexed with l-lysine
117	<a href="#">c4ex5A_</a>	Alignment	not modelled	99.4	20	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> lysine--trna ligase; <b>PDBTitle:</b> crystal structure of lysyl-trna synthetase lysrs from burkholderia2 thailandensis bound to lysine
118	<a href="#">c4h02B_</a>	Alignment	not modelled	99.4	15	<b>PDB header:</b> ligase <b>Chain:</b> B: <b>PDB Molecule:</b> lysyl-trna synthetase; <b>PDBTitle:</b> crystal structure of p. falciparum lysyl-trna synthetase
119	<a href="#">c1wydB_</a>	Alignment	not modelled	99.4	15	<b>PDB header:</b> ligase <b>Chain:</b> B: <b>PDB Molecule:</b> hypothetical aspartyl-trna synthetase; <b>PDBTitle:</b> crystal structure of aspartyl-trna synthetase from sulfolobus tokodaii
120	<a href="#">c4ah6B_</a>	Alignment	not modelled	99.4	19	<b>PDB header:</b> ligase <b>Chain:</b> B: <b>PDB Molecule:</b> aspartate--trna ligase, mitochondrial; <b>PDBTitle:</b> human mitochondrial aspartyl-trna synthetase