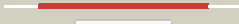



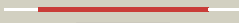








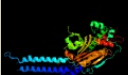










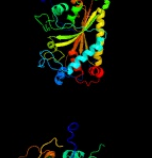
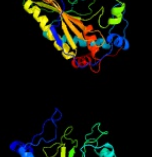
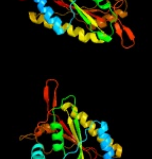



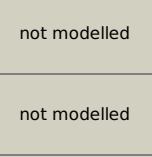


# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3834c_serS_4307833_4309092
Date	Fri Aug 9 18:20:54 BST 2019
Unique Job ID	0447e836831b8471

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c6h9xA_</a>	 Alignment		100.0	37	<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
2	<a href="#">c2dq0A_</a>	 Alignment		100.0	42	<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
3	<a href="#">c3lssA_</a>	 Alignment		100.0	36	<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
4	<a href="#">c1wleB_</a>	 Alignment		100.0	35	<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
5	<a href="#">c1sryB_</a>	 Alignment		100.0	41	<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
6	<a href="#">c2dq3A_</a>	 Alignment		100.0	42	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> seryl-trna synthetase; <b>PDBTitle:</b> crystal structure of aq_298
7	<a href="#">c6bljC_</a>	 Alignment		100.0	35	<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
8	<a href="#">c3vbbB_</a>	 Alignment		100.0	37	<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
9	<a href="#">c3qo8A_</a>	 Alignment		100.0	34	<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
10	<a href="#">c3errB_</a>	 Alignment		100.0	41	<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
11	<a href="#">c6girA_</a>	 Alignment		100.0	38	<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

12	<a href="#">c6oteA_</a>	Alignment		100.0	35	<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
13	<a href="#">d1seta2</a>	Alignment		100.0	45	<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
14	<a href="#">c2cj9A_</a>	Alignment		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 methanosarcina barkeri seryl-trna synthetase2 complexed with an analog of seryladenylate
15	<a href="#">c3w3sA_</a>	Alignment		100.0	20	<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
16	<a href="#">d1qf6a4</a>	Alignment		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
17	<a href="#">d1nyra4</a>	Alignment		100.0	16	<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
18	<a href="#">c1nyqA_</a>	Alignment		100.0	17	<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
19	<a href="#">d1nj8a3</a>	Alignment		100.0	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
20	<a href="#">c1qf6A_</a>	Alignment		100.0	17	<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
21	<a href="#">c3ialB_</a>	Alignment	not modelled	100.0	17	<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
22	<a href="#">d1nj1a3</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
23	<a href="#">d1hc7a2</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
24	<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 homologue (blI0957) complexed with2 amp
25	<a href="#">c6nabB_</a>	Alignment	not modelled	100.0	17	<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)
26	<a href="#">c4twaA_</a>	Alignment	not modelled	100.0	19	<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
27	<a href="#">d1b76a2</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
28	<a href="#">d1atia2</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
29	<a href="#">c5f9yB_</a>	Alignment	not modelled	100.0	17 <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
30	<a href="#">c5xiiC_</a>	Alignment	not modelled	100.0	18 <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
31	<a href="#">c1nj8C_</a>	Alignment	not modelled	100.0	17 <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
32	<a href="#">c4hvcB_</a>	Alignment	not modelled	100.0	17 <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
33	<a href="#">c1h4tD_</a>	Alignment	not modelled	100.0	21 <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
34	<a href="#">c5e6mA_</a>	Alignment	not modelled	100.0	16 <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
35	<a href="#">c1nj2A_</a>	Alignment	not modelled	100.0	18 <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 thermotrophicus
36	<a href="#">c5znjA_</a>	Alignment	not modelled	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 a bacterial prors with ligands
37	<a href="#">c6mn8A_</a>	Alignment	not modelled	100.0	16 <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
38	<a href="#">c5ucmB_</a>	Alignment	not modelled	100.0	17 <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
39	<a href="#">c2j3mA_</a>	Alignment	not modelled	100.0	21 <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
40	<a href="#">c5xilA_</a>	Alignment	not modelled	100.0	17 <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 (lmprs)
41	<a href="#">c1fyfB_</a>	Alignment	not modelled	100.0	18 <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
42	<a href="#">c2i4IC_</a>	Alignment	not modelled	100.0	17 <b>PDB header:</b> ligase <b>Chain:</b> C: <b>PDB Molecule:</b> proline-trna ligase; <b>PDBTitle:</b> rhodopseudomonas palustris prolyl-trna synthetase
43	<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
44	<a href="#">c1ggmB_</a>	Alignment	not modelled	100.0	17 <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
45	<a href="#">c5zy9D_</a>	Alignment	not modelled	100.0	19 <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
46	<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 thrs-1 from2 aeropyrum pernix
47	<a href="#">c1atiA_</a>	Alignment	not modelled	100.0	17 <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
48	<a href="#">c3ugtD_</a>	Alignment	not modelled	100.0	19 <b>PDB header:</b> ligase <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
49	<a href="#">c1g5hA_</a>	Alignment	not modelled	100.0	12 <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
50	<a href="#">c4kqeA_</a>	Alignment	not modelled	100.0	16 <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
51	<a href="#">c5z5eB_</a>	Alignment	not modelled	100.0	18 <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
52	<a href="#">c3ikIA_</a>	Alignment	not modelled	100.0	10 <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.
53	<a href="#">c2pmfA_</a>	Alignment	not modelled	100.0	16 <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
54	<a href="#">d1g5hA2</a>	Alignment	not modelled	100.0	14 <b>Fold:</b> Class II aaRS and biotin synthetases <b>Superfamily:</b> Class II aaRS and biotin synthetases

54	<a href="#">d1g3na2</a>	Alignment	not modelled	100.0	14	<b>Family:</b> Class II aminoacyl-tRNA synthetase (aaRS)-like, catalytic domain <b>PDB header:</b> transferase
55	<a href="#">c3ikmC</a>	Alignment	not modelled	100.0	12	<b>Chain:</b> C: <b>PDB Molecule:</b> dna polymerase subunit gamma-2; <b>PDBTitle:</b> crystal structure of human mitochondrial dna polymerase holoenzyme
56	<a href="#">c4kr3A</a>	Alignment	not modelled	100.0	15	<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
57	<a href="#">d2g4ca2</a>	Alignment	not modelled	100.0	12	<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="#">d1seta1</a>	Alignment	not modelled	99.9	30	<b>Fold:</b> Long alpha-hairpin <b>Superfamily:</b> tRNA-binding arm <b>Family:</b> Seryl-tRNA synthetase (SerRS)
59	<a href="#">c2e19B</a>	Alignment	not modelled	99.9	13	<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
60	<a href="#">c3hrif</a>	Alignment	not modelled	99.9	15	<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
61	<a href="#">c1qe0B</a>	Alignment	not modelled	99.9	11	<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
62	<a href="#">c5e3iA</a>	Alignment	not modelled	99.9	15	<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 acetobacter2 baumannii with bound l-histidine and atp
63	<a href="#">c1adyA</a>	Alignment	not modelled	99.8	15	<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
64	<a href="#">c1wu7A</a>	Alignment	not modelled	99.8	13	<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
65	<a href="#">c6ezdD</a>	Alignment	not modelled	99.8	13	<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)
66	<a href="#">c6nhia</a>	Alignment	not modelled	99.8	13	<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
67	<a href="#">c3netB</a>	Alignment	not modelled	99.8	21	<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
68	<a href="#">c4x5oB</a>	Alignment	not modelled	99.7	15	<b>PDB header:</b> ligase <b>Chain:</b> B: <b>PDB Molecule:</b> histidine--trna ligase, cytoplasmic; <b>PDBTitle:</b> human histidine trna synthetase
69	<a href="#">c5m8hB</a>	Alignment	not modelled	99.7	10	<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
70	<a href="#">c4e51B</a>	Alignment	not modelled	99.7	15	<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
71	<a href="#">c3od1A</a>	Alignment	not modelled	99.7	16	<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
72	<a href="#">c2zimA</a>	Alignment	not modelled	99.6	16	<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
73	<a href="#">c4g84B</a>	Alignment	not modelled	99.6	16	<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
74	<a href="#">c2znjB</a>	Alignment	not modelled	99.6	17	<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 desulfitobacterium hafniense
75	<a href="#">c4g85A</a>	Alignment	not modelled	99.6	16	<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
76	<a href="#">d1wu7a2</a>	Alignment	not modelled	99.5	13	<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
77	<a href="#">d1kmma2</a>	Alignment	not modelled	99.5	13	<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="#">c1z7nB</a>	Alignment	not modelled	99.3	17	<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
79	<a href="#">d1h4vb2</a>	Alignment	not modelled	99.3	16	<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
80	<a href="#">c2odrD_</a>	Alignment	not modelled	99.2	12	<b>PDB header:</b> ligase <b>Chain:</b> D: <b>PDB Molecule:</b> phosphoseryl-trna synthetase; <b>PDBTitle:</b> methanococcus maripaludis phosphoseryl-trna synthetase
81	<a href="#">c3racA_</a>	Alignment	not modelled	99.2	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.
82	<a href="#">c2odrC_</a>	Alignment	not modelled	99.2	13	<b>PDB header:</b> ligase <b>Chain:</b> C: <b>PDB Molecule:</b> phosphoseryl-trna synthetase; <b>PDBTitle:</b> methanococcus maripaludis phosphoseryl-trna synthetase
83	<a href="#">d1z7ma1</a>	Alignment	not modelled	99.2	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
84	<a href="#">c2odrA_</a>	Alignment	not modelled	99.1	11	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> phosphoseryl-trna synthetase; <b>PDBTitle:</b> methanococcus maripaludis phosphoseryl-trna synthetase
85	<a href="#">c2odrB_</a>	Alignment	not modelled	99.0	12	<b>PDB header:</b> ligase <b>Chain:</b> B: <b>PDB Molecule:</b> phosphoseryl-trna synthetase; <b>PDBTitle:</b> methanococcus maripaludis phosphoseryl-trna synthetase
86	<a href="#">c2du4B_</a>	Alignment	not modelled	99.0	12	<b>PDB header:</b> ligase/rna <b>Chain:</b> B: <b>PDB Molecule:</b> o-phosphoseryl-trna synthetase; <b>PDBTitle:</b> crystal structure of archaeoglobus fulgidus o-phosphoseryl-2 trna synthetase complexed with trnacys
87	<a href="#">c1b70A_</a>	Alignment	not modelled	99.0	17	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> phenylalanyl-trna synthetase; <b>PDBTitle:</b> phenylalanyl trna synthetase complexed with phenylalanine
88	<a href="#">d1jjca_</a>	Alignment	not modelled	99.0	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
89	<a href="#">c3l4gl_</a>	Alignment	not modelled	98.9	15	<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
90	<a href="#">c4p74D_</a>	Alignment	not modelled	98.9	13	<b>PDB header:</b> ligase/ligase inhibitor <b>Chain:</b> D: <b>PDB Molecule:</b> phenylalanine--trna ligase alpha subunit; <b>PDBTitle:</b> phers in complex with compound 3a
91	<a href="#">c3l4gC_</a>	Alignment	not modelled	98.9	12	<b>PDB header:</b> ligase <b>Chain:</b> C: <b>PDB Molecule:</b> phenylalanyl-trna synthetase alpha chain; <b>PDBTitle:</b> crystal structure of homo sapiens cytoplasmic phenylalanyl-trna2 synthetase
92	<a href="#">c2du7C_</a>	Alignment	not modelled	98.9	19	<b>PDB header:</b> ligase <b>Chain:</b> C: <b>PDB Molecule:</b> o-phosphoseryl-trna synthetase; <b>PDBTitle:</b> crystal structure of methanococcus jannacshii o-phosphoseryl-trna2 synthetase
93	<a href="#">c2du3A_</a>	Alignment	not modelled	98.8	16	<b>PDB header:</b> ligase/rna <b>Chain:</b> A: <b>PDB Molecule:</b> o-phosphoseryl-trna synthetase; <b>PDBTitle:</b> crystal structure of archaeoglobus fulgidus o-phosphoseryl-2 trna synthetase complexed with trnacys and o-phosphoserine
94	<a href="#">c1eiyA_</a>	Alignment	not modelled	98.8	18	<b>PDB header:</b> ligase/rna <b>Chain:</b> A: <b>PDB Molecule:</b> phenylalanyl-trna synthetase; <b>PDBTitle:</b> the crystal structure of phenylalanyl-trna synthetase from thermus2 thermophilus complexed with cognate trnaphe
95	<a href="#">d1qe0a2</a>	Alignment	not modelled	98.8	11	<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="#">d1e1oa2</a>	Alignment	not modelled	98.8	16	<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
97	<a href="#">c2rhgA_</a>	Alignment	not modelled	98.7	13	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> phenylalanyl-trna synthetase alpha chain; <b>PDBTitle:</b> phers from staphylococcus haemolyticus- rational protein engineering2 and inhibitor studies
98	<a href="#">d1l0wa3</a>	Alignment	not modelled	98.7	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
99	<a href="#">c3pcoC_</a>	Alignment	not modelled	98.7	14	<b>PDB header:</b> ligase <b>Chain:</b> C: <b>PDB Molecule:</b> phenylalanyl-trna synthetase, alpha subunit; <b>PDBTitle:</b> crystal structure of e. coli phenylalanine-trna synthetase complexed2 with phenylalanine and amp
100	<a href="#">d1c0aa3</a>	Alignment	not modelled	98.6	16	<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
101	<a href="#">d1nnha_</a>	Alignment	not modelled	98.6	16	<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
102	<a href="#">d1eova2</a>	Alignment	not modelled	98.6	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
103	<a href="#">c3g1zB_</a>	Alignment	not modelled	98.6	18	<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
104	<a href="#">c3e9hB_</a>	Alignment	not modelled	98.6	15	<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



105	<a href="#">d1bbua2</a>	Alignment	not modelled	98.6	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
106	<a href="#">d1b8aa2</a>	Alignment	not modelled	98.6	11	<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
107	<a href="#">c1e22A_</a>	Alignment	not modelled	98.5	19	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> lysyl-trna synthetase; <b>PDBTitle:</b> lysyl-trna synthetase (lysu) hexagonal form complexed with2 lysine and the non-hydrolysable atp analogue amp-pcp
108	<a href="#">c3bjuB_</a>	Alignment	not modelled	98.4	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
109	<a href="#">c5elnC_</a>	Alignment	not modelled	98.4	19	<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
110	<a href="#">c5vl1D_</a>	Alignment	not modelled	98.3	21	<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
111	<a href="#">c1asyA_</a>	Alignment	not modelled	98.3	15	<b>PDB header:</b> complex (aminoacyl-trna synthase/trna) <b>Chain:</b> A: <b>PDB Molecule:</b> aspartyl-trna synthetase; <b>PDBTitle:</b> class ii aminoacyl transfer rna synthetases: crystal2 structure of yeast aspartyl-trna synthetase complexed with3 trna asp
112	<a href="#">c5hggD_</a>	Alignment	not modelled	98.3	19	<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.
113	<a href="#">c6pqhA_</a>	Alignment	not modelled	98.3	17	<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
114	<a href="#">c4up8A_</a>	Alignment	not modelled	98.3	21	<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
115	<a href="#">c5xixD_</a>	Alignment	not modelled	98.3	18	<b>PDB header:</b> ligase <b>Chain:</b> D: <b>PDB Molecule:</b> asparagine--trna ligase, cytoplasmic; <b>PDBTitle:</b> the canonical domain of human asparaginyl-trna synthetase
116	<a href="#">c4o2dB_</a>	Alignment	not modelled	98.3	17	<b>PDB header:</b> ligase <b>Chain:</b> B: <b>PDB Molecule:</b> aspartate--trna ligase; <b>PDBTitle:</b> crystal structure of aspartyl-trna synthetase from mycobacterium2 smegmatis with bound aspartic acid
117	<a href="#">c1x55A_</a>	Alignment	not modelled	98.3	21	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> asparaginyl-trna synthetase; <b>PDBTitle:</b> crystal structure of asparaginyl-trna synthetase from pyrococcus2 horikoshii complexed with asparaginyl-adenylate analogue
118	<a href="#">c6ns0A_</a>	Alignment	not modelled	98.3	21	<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
119	<a href="#">c4ah6B_</a>	Alignment	not modelled	98.3	23	<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
120	<a href="#">c4wj4A_</a>	Alignment	not modelled	98.3	18	<b>PDB header:</b> ligase/rna <b>Chain:</b> A: <b>PDB Molecule:</b> aspartate--trna(asp/asn) ligase; <b>PDBTitle:</b> crystal structure of non-discriminating aspartyl-trna synthetase from2 pseudomonas aeruginosa complexed with trna(asp) and aspartic acid