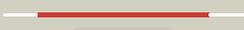
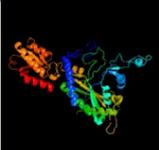
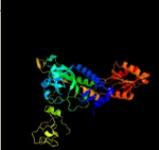


# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2614c_(thrS)_2941199_2943277
Date	Wed Aug 7 12:50:25 BST 2019
Unique Job ID	7427b1bfd007456d

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c1qf6A_</a>	 Alignment		100.0	40	<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
2	<a href="#">c1nyqA_</a>	 Alignment		100.0	42	<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
3	<a href="#">c3a32A_</a>	 Alignment		100.0	34	<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
4	<a href="#">c1fyfB_</a>	 Alignment		100.0	42	<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
5	<a href="#">c4hwtA_</a>	 Alignment		100.0	40	<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
6	<a href="#">c5zy9D_</a>	 Alignment		100.0	40	<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
7	<a href="#">c3ugtD_</a>	 Alignment		100.0	35	<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
8	<a href="#">c5ucmB_</a>	 Alignment		100.0	23	<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
9	<a href="#">c2i4IC_</a>	 Alignment		100.0	23	<b>PDB header:</b> ligase <b>Chain:</b> C: <b>PDB Molecule:</b> proline-trna ligase; <b>PDBTitle:</b> rhodopseudomonas palustris prolyl-trna synthetase
10	<a href="#">d1nyra4</a>	 Alignment		100.0	46	<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
11	<a href="#">c5znlA_</a>	 Alignment		100.0	21	<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

12	<a href="#">c1ggmB_</a>	Alignment		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
13	<a href="#">c4hvcB_</a>	Alignment		100.0	21	<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="#">c6nabB_</a>	Alignment		100.0	20	<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 monophosphate (amp)
15	<a href="#">c3w3sA_</a>	Alignment		100.0	18	<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="#">c6mn8A_</a>	Alignment		100.0	18	<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
17	<a href="#">c2j3mA_</a>	Alignment		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
18	<a href="#">c5xiiC_</a>	Alignment		100.0	19	<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
19	<a href="#">c3ialB_</a>	Alignment		100.0	23	<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
20	<a href="#">c1atiA_</a>	Alignment		100.0	18	<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
21	<a href="#">c4twaA_</a>	Alignment	not modelled	100.0	17	<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
22	<a href="#">c1nj8C_</a>	Alignment	not modelled	100.0	19	<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
23	<a href="#">c5f9yB_</a>	Alignment	not modelled	100.0	22	<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
24	<a href="#">d1qf6a4</a>	Alignment	not modelled	100.0	47	<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
25	<a href="#">c5e6mA_</a>	Alignment	not modelled	100.0	20	<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
26	<a href="#">c4kqeA_</a>	Alignment	not modelled	100.0	21	<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
27	<a href="#">c1h4tD_</a>	Alignment	not modelled	100.0	24	<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
28	<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

29	<a href="#">c4kr3A</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> glycyI-trna synthetase mutant e71g in complex with trna-gly
30	<a href="#">c1nj2A</a>	Alignment	not modelled	100.0	23	<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
31	<a href="#">c1g5hA</a>	Alignment	not modelled	100.0	16	<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
32	<a href="#">c2pmfA</a>	Alignment	not modelled	100.0	21	<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
33	<a href="#">c3iklA</a>	Alignment	not modelled	100.0	15	<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.
34	<a href="#">c3ikmC</a>	Alignment	not modelled	100.0	12	<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
35	<a href="#">c5xilA</a>	Alignment	not modelled	100.0	24	<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)
36	<a href="#">c2ei9B</a>	Alignment	not modelled	100.0	16	<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
37	<a href="#">c4v1ac</a>	Alignment	not modelled	100.0	17	<b>PDB header:</b> ribosome <b>Chain:</b> C: <b>PDB Molecule:</b> <b>PDBTitle:</b> structure of the large subunit of the mammalian mitoribosome, part 22 of 2
38	<a href="#">c4ce4c</a>	Alignment	not modelled	100.0	18	<b>PDB header:</b> ribosome <b>Chain:</b> C: <b>PDB Molecule:</b> <b>PDBTitle:</b> 39s large subunit of the porcine mitochondrial ribosome
39	<a href="#">c3netB</a>	Alignment	not modelled	100.0	16	<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
40	<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
41	<a href="#">c5e3lA</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 a histidyl-trna synthetase from acinetobacter2 baumannii with bound l-histidine and atp
42	<a href="#">c1qe0B</a>	Alignment	not modelled	100.0	17	<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
43	<a href="#">c3hriF</a>	Alignment	not modelled	100.0	18	<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
44	<a href="#">c2cj9A</a>	Alignment	not modelled	100.0	15	<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
45	<a href="#">c2dq0A</a>	Alignment	not modelled	100.0	17	<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
46	<a href="#">c1tkeA</a>	Alignment	not modelled	100.0	37	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> threonyl-trna synthetase; <b>PDBTitle:</b> crystal structure of the editing domain of threonyl-trna2 synthetase complexed with serine
47	<a href="#">c1wu7A</a>	Alignment	not modelled	100.0	18	<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
48	<a href="#">c6nhlA</a>	Alignment	not modelled	100.0	14	<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
49	<a href="#">c3qo8A</a>	Alignment	not modelled	100.0	16	<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
50	<a href="#">c4x5oB</a>	Alignment	not modelled	100.0	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
51	<a href="#">c4e51B</a>	Alignment	not modelled	100.0	17	<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
52	<a href="#">c1sryB</a>	Alignment	not modelled	100.0	17	<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
53	<a href="#">d1seta2</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
54	<a href="#">c2dq3A</a>	Alignment	not modelled	100.0	21	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> seryl-trna synthetase; <b>PDBTitle:</b> crystal structure of aq_298

55	<a href="#">c6oteA</a>	Alignment	not modelled	100.0	12	<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
56	<a href="#">c1wleB</a>	Alignment	not modelled	100.0	20	<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
57	<a href="#">c4g85A</a>	Alignment	not modelled	100.0	18	<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
58	<a href="#">c6bljC</a>	Alignment	not modelled	100.0	16	<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
59	<a href="#">c4g84B</a>	Alignment	not modelled	100.0	17	<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
60	<a href="#">c3vbbB</a>	Alignment	not modelled	100.0	16	<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
61	<a href="#">c3lssA</a>	Alignment	not modelled	100.0	17	<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="#">c6h9xA</a>	Alignment	not modelled	100.0	19	<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
63	<a href="#">d1nj8a3</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
64	<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
65	<a href="#">c6girA</a>	Alignment	not modelled	100.0	20	<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
66	<a href="#">d1hc7a2</a>	Alignment	not modelled	100.0	22	<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
67	<a href="#">d1nj1a3</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
68	<a href="#">c5m8hB</a>	Alignment	not modelled	100.0	15	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> atp phosphoribosyltransferase regulatory subunit; <b>PDBTitle:</b> atp phosphoribosyltransferase (hisz2 atpprt) from psychrobacter2 arcticus
69	<a href="#">d1nyra3</a>	Alignment	not modelled	100.0	43	<b>Fold:</b> RRF/tRNA synthetase additional domain-like <b>Superfamily:</b> ThrRS/AlaRS common domain <b>Family:</b> Threonyl-tRNA synthetase (ThrRS), second 'additional' domain
70	<a href="#">c3od1A</a>	Alignment	not modelled	100.0	14	<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
71	<a href="#">d1b76a2</a>	Alignment	not modelled	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
72	<a href="#">d1atia2</a>	Alignment	not modelled	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
73	<a href="#">d1tkea2</a>	Alignment	not modelled	100.0	41	<b>Fold:</b> RRF/tRNA synthetase additional domain-like <b>Superfamily:</b> ThrRS/AlaRS common domain <b>Family:</b> Threonyl-tRNA synthetase (ThrRS), second 'additional' domain
74	<a href="#">c3mf2B</a>	Alignment	not modelled	100.0	18	<b>PDB header:</b> ligase <b>Chain:</b> B: <b>PDB Molecule:</b> bll0957 protein; <b>PDBTitle:</b> crystal structure of class ii aaRS homologue (bll0957) complexed with2 amp
75	<a href="#">c6ezdD</a>	Alignment	not modelled	100.0	20	<b>PDB header:</b> ligase <b>Chain:</b> D: <b>PDB Molecule:</b> pyrrolyl-trna synthetase; <b>PDBTitle:</b> pyrrolyl-trna synthetase from candidatus methanomethylophilus alvus2 (mmapylrs)
76	<a href="#">d1g5ha2</a>	Alignment	not modelled	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
77	<a href="#">c3wqyB</a>	Alignment	not modelled	100.0	20	<b>PDB header:</b> ligase/rna <b>Chain:</b> B: <b>PDB Molecule:</b> alanine--trna ligase; <b>PDBTitle:</b> crystal structure of archaeoglobus fulgidus alanyl-trna synthetase in2 complex with wild-type trna(ala) having g3.u70
78	<a href="#">c2ztgA</a>	Alignment	not modelled	100.0	19	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> alanyl-trna synthetase; <b>PDBTitle:</b> crystal structure of archaeoglobus fulgidus alanyl-trna2 synthetase lacking the c-terminal dimerization domain in3 complex with ala-sa
79	<a href="#">d1wu7a2</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
80	<a href="#">c2zzfA_</a>	Alignment	not modelled	100.0	19 <b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> alanyl-trna synthetase; <b>PDBTitle:</b> crystal structure of alanyl-trna synthetase without oligomerization2 domain
81	<a href="#">d1kmma2</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
82	<a href="#">c2zimA_</a>	Alignment	not modelled	100.0	19 <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
83	<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
84	<a href="#">c2znjB_</a>	Alignment	not modelled	100.0	20 <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
85	<a href="#">d2g4ca2</a>	Alignment	not modelled	100.0	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
86	<a href="#">c1z7nB_</a>	Alignment	not modelled	100.0	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-ptase) from2 lactococcus lactis with bound prpp substrate
87	<a href="#">d1nyra1</a>	Alignment	not modelled	100.0	33 <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="#">c3racA_</a>	Alignment	not modelled	100.0	19 <b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> histidine-trna ligase; <b>PDBTitle:</b> crystal structre of histidine--trna ligase subunit from2 alicyclobacillus acidocaldarius subsp. acidocaldarius dsm 446.
89	<a href="#">d1qf6a1</a>	Alignment	not modelled	100.0	31 <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="#">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
91	<a href="#">c3kewA_</a>	Alignment	not modelled	100.0	18 <b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> dhha1 domain protein; <b>PDBTitle:</b> crystal structure of probable alanyl-trna-synthase from clostridium2 perfringens
92	<a href="#">d1v4pa_</a>	Alignment	not modelled	99.9	20 <b>Fold:</b> RRF/tRNA synthetase additional domain-like <b>Superfamily:</b> ThrRS/AlaRS common domain <b>Family:</b> AlaX-like
93	<a href="#">d1nj8a1</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
94	<a href="#">d1nj1a1</a>	Alignment	not modelled	99.9	24 <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
95	<a href="#">d1qe0a2</a>	Alignment	not modelled	99.9	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
96	<a href="#">d1hc7a1</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
97	<a href="#">d1g5ha1</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
98	<a href="#">c2e1bA_</a>	Alignment	not modelled	99.9	19 <b>PDB header:</b> ligase, hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> 216aa long hypothetical alanyl-trna synthetase; <b>PDBTitle:</b> crystal structure of the alax-m trans-editing enzyme from2 pyrococcus horikoshii
99	<a href="#">d1atia1</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
100	<a href="#">d2g4ca1</a>	Alignment	not modelled	99.9	15 <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="#">d1usya_</a>	Alignment	not modelled	99.9	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
102	<a href="#">c2lw7A_</a>	Alignment	not modelled	99.9	15 <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="#">d1wu7a1</a>	Alignment	not modelled	99.9	18 <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
104	<a href="#">d1kmma1</a>	Alignment	not modelled	99.9	16 <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
105	<a href="#">d1qe0a1</a>	Alignment	not modelled	99.8	12 <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

106	<a href="#">c3g1zB_</a>	Alignment	not modelled	99.8	16	<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
107	<a href="#">d1h4vb1</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
108	<a href="#">d1e1oa2</a>	Alignment	not modelled	99.8	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
109	<a href="#">d1bbua2</a>	Alignment	not modelled	99.8	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
110	<a href="#">d2e1ba2</a>	Alignment	not modelled	99.8	19	<b>Fold:</b> RRF/tRNA synthetase additional domain-like <b>Superfamily:</b> ThrRS/AlaRS common domain <b>Family:</b> AlaX-like
111	<a href="#">c1b70A_</a>	Alignment	not modelled	99.7	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
112	<a href="#">d1jica_</a>	Alignment	not modelled	99.7	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
113	<a href="#">d1nnha_</a>	Alignment	not modelled	99.6	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
114	<a href="#">c3l4gl_</a>	Alignment	not modelled	99.6	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
115	<a href="#">d1eova2</a>	Alignment	not modelled	99.6	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
116	<a href="#">d1b8aa2</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
117	<a href="#">d1c0aa3</a>	Alignment	not modelled	99.6	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
118	<a href="#">c1wwtA_</a>	Alignment	not modelled	99.6	18	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> threonyl-trna synthetase, cytoplasmic; <b>PDBTitle:</b> solution structure of the tgs domain from human threonyl-2 trna synthetase
119	<a href="#">d1l0wa3</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
120	<a href="#">c2odrB_</a>	Alignment	not modelled	99.5	16	<b>PDB header:</b> ligase <b>Chain:</b> B: <b>PDB Molecule:</b> phosphoseryl-trna synthetase; <b>PDBTitle:</b> methanococcus maripaludis phosphoseryl-trna synthetase