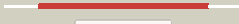



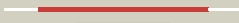




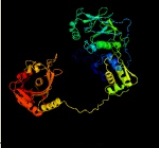























# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1650_(pheT)_1859765_1862260
Date	Fri Aug 2 13:30:24 BST 2019
Unique Job ID	d9f720afeabbf1d

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c4p71B_</a>	 Alignment		100.0	33	<b>PDB header:</b> ligase <b>Chain:</b> B: <b>PDB Molecule:</b> phenylalanine--trna ligase beta subunit; <b>PDBTitle:</b> apo phers from p. aeuriginosa
2	<a href="#">c3pcoD_</a>	 Alignment		100.0	32	<b>PDB header:</b> ligase <b>Chain:</b> D: <b>PDB Molecule:</b> phenylalanyl-trna synthetase, beta chain; <b>PDBTitle:</b> crystal structure of e. coli phenylalanine-trna synthetase complexed2 with phenylalanine and amp
3	<a href="#">c2rhsB_</a>	 Alignment		100.0	32	<b>PDB header:</b> ligase <b>Chain:</b> B: <b>PDB Molecule:</b> phenylalanyl-trna synthetase beta chain; <b>PDBTitle:</b> phers from staphylococcus haemolyticus- rational protein engineering2 and inhibitor studies
4	<a href="#">c2akwB_</a>	 Alignment		100.0	34	<b>PDB header:</b> ligase <b>Chain:</b> B: <b>PDB Molecule:</b> phenylalanyl-trna synthetase beta chain; <b>PDBTitle:</b> crystal structure of t.thermophilus phenylalanyl-trna synthetase2 complexed with p-cl-phenylalanine
5	<a href="#">c3l4gL_</a>	 Alignment		100.0	17	<b>PDB header:</b> ligase <b>Chain:</b> L: <b>PDB Molecule:</b> phenylalanyl-trna synthetase beta chain; <b>PDBTitle:</b> crystal structure of homo sapiens cytoplasmic phenylalanyl-trna2 synthetase
6	<a href="#">c2cxiA_</a>	 Alignment		100.0	16	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> phenylalanyl-trna synthetase beta chain; <b>PDBTitle:</b> crystal structure of an n-terminal fragment of the phenylalanyl-trna2 synthetase beta-subunit from pyrococcus horikoshii
7	<a href="#">d1jcb6</a>	 Alignment		100.0	41	<b>Fold:</b> PheT/TiIS domain <b>Superfamily:</b> PheT/TiIS domain <b>Family:</b> B3/B4 domain of PheRS, PheT
8	<a href="#">c3cmqA_</a>	 Alignment		100.0	15	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> phenylalanyl-trna synthetase, mitochondrial; <b>PDBTitle:</b> crystal structure of human mitochondrial phenylalanine trna synthetase
9	<a href="#">d1jcb5</a>	 Alignment		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
10	<a href="#">c3icaB_</a>	 Alignment		100.0	16	<b>PDB header:</b> ligase <b>Chain:</b> B: <b>PDB Molecule:</b> phenylalanyl-trna synthetase beta chain; <b>PDBTitle:</b> the crystal structure of the beta subunit of a phenylalanyl-trna2 synthetase from porphyromonas gingivalis w83
11	<a href="#">c3ig2B_</a>	 Alignment		100.0	18	<b>PDB header:</b> ligase <b>Chain:</b> B: <b>PDB Molecule:</b> phenylalanyl-trna synthetase beta chain; <b>PDBTitle:</b> the crystal structure of a putative phenylalanyl-trna synthetase2 (phers) beta chain domain from bacteroides fragilis to 2.1a

12	<a href="#">c2odrA_</a>	Alignment		100.0	15	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> phosphoseryl-trna synthetase; <b>PDBTitle:</b> methanococcus maripaludis phosphoseryl-trna synthetase
13	<a href="#">c2odrB_</a>	Alignment		100.0	15	<b>PDB header:</b> ligase <b>Chain:</b> B: <b>PDB Molecule:</b> phosphoseryl-trna synthetase; <b>PDBTitle:</b> methanococcus maripaludis phosphoseryl-trna synthetase
14	<a href="#">c3bu2B_</a>	Alignment		100.0	30	<b>PDB header:</b> rna binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> putative trna-binding protein; <b>PDBTitle:</b> crystal structure of a trna-binding protein from staphylococcus2 saprophyticus subsp. saprophyticus. northeast structural genomics3 consortium target syr77
15	<a href="#">c2odrC_</a>	Alignment		100.0	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
16	<a href="#">c2rhqA_</a>	Alignment		100.0	19	<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
17	<a href="#">d1jcb3</a>	Alignment		100.0	32	<b>Fold:</b> OB-fold <b>Superfamily:</b> Nucleic acid-binding proteins <b>Family:</b> Myf domain
18	<a href="#">c2odrD_</a>	Alignment		100.0	14	<b>PDB header:</b> ligase <b>Chain:</b> D: <b>PDB Molecule:</b> phosphoseryl-trna synthetase; <b>PDBTitle:</b> methanococcus maripaludis phosphoseryl-trna synthetase
19	<a href="#">d1jcb4</a>	Alignment		100.0	42	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> Anticodon-binding domain of PheRS <b>Family:</b> Anticodon-binding domain of PheRS
20	<a href="#">c4p74D_</a>	Alignment		99.9	18	<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
21	<a href="#">d1b7yb4</a>	Alignment	not modelled	99.9	40	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> Anticodon-binding domain of PheRS <b>Family:</b> Anticodon-binding domain of PheRS
22	<a href="#">c2e8gB_</a>	Alignment	not modelled	99.9	27	<b>PDB header:</b> rna binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> hypothetical protein ph0536; <b>PDBTitle:</b> the structure of protein from p. horikoshii at 1.7 angstrom2 resolution
23	<a href="#">c5zkqB_</a>	Alignment	not modelled	99.9	15	<b>PDB header:</b> ligase <b>Chain:</b> B: <b>PDB Molecule:</b> aminoacyl-trna synthetase-interacting multifunctional <b>PDBTitle:</b> crystal structure of c-terminal domain of plasmodium vivax p43
24	<a href="#">c2cwpA_</a>	Alignment	not modelled	99.9	23	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> metrs related protein; <b>PDBTitle:</b> crystal structure of metrs related protein from pyrococcus horikoshii
25	<a href="#">d1gd7a_</a>	Alignment	not modelled	99.9	19	<b>Fold:</b> OB-fold <b>Superfamily:</b> Nucleic acid-binding proteins <b>Family:</b> Myf domain
26	<a href="#">c5covA_</a>	Alignment	not modelled	99.8	22	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> naegleria gruberi rna ligase; <b>PDBTitle:</b> structure and mechanism of a eukaryal nick-sealing rna ligase k170m+mn
27	<a href="#">c5h34A_</a>	Alignment	not modelled	99.8	17	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> methionine-trna ligase; <b>PDBTitle:</b> crystal structure of the c-terminal domain of methionyl-trna2 synthetase (metrs-c) in nanoarchaeum equitans
28	<a href="#">d1pyba_</a>	Alignment	not modelled	99.8	23	<b>Fold:</b> OB-fold <b>Superfamily:</b> Nucleic acid-binding proteins <b>Family:</b> Myf domain

29	<a href="#">d1jcb2</a>	Alignment	not modelled	99.8	42	<b>Fold:</b> Putative DNA-binding domain <b>Superfamily:</b> Putative DNA-binding domain <b>Family:</b> Domains B1 and B5 of PheRS-beta, PheT
30	<a href="#">d1pxfa</a>	Alignment	not modelled	99.8	18	<b>Fold:</b> OB-fold <b>Superfamily:</b> Nucleic acid-binding proteins <b>Family:</b> Myf domain
31	<a href="#">d1jcb1</a>	Alignment	not modelled	99.8	41	<b>Fold:</b> Putative DNA-binding domain <b>Superfamily:</b> Putative DNA-binding domain <b>Family:</b> Domains B1 and B5 of PheRS-beta, PheT
32	<a href="#">d1mkha</a>	Alignment	not modelled	99.8	20	<b>Fold:</b> OB-fold <b>Superfamily:</b> Nucleic acid-binding proteins <b>Family:</b> Myf domain
33	<a href="#">c4r1jA</a>	Alignment	not modelled	99.8	15	<b>PDB header:</b> rna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> gu4 nucleic-binding protein 1; <b>PDBTitle:</b> crystal structure of arc1p-c
34	<a href="#">c5zdiB</a>	Alignment	not modelled	99.8	18	<b>PDB header:</b> chaperone <b>Chain:</b> B: <b>PDB Molecule:</b> protein secretion chaperonin csaa; <b>PDBTitle:</b> crystal structure of csaa chaperone protein from picrophilus torridus
35	<a href="#">c2q2iA</a>	Alignment	not modelled	99.8	14	<b>PDB header:</b> chaperone <b>Chain:</b> A: <b>PDB Molecule:</b> secretion chaperone; <b>PDBTitle:</b> crystal structure of the protein secretion chaperone csaa from2 agrobacterium tumefaciens.
36	<a href="#">c2nzoD</a>	Alignment	not modelled	99.8	12	<b>PDB header:</b> chaperone <b>Chain:</b> D: <b>PDB Molecule:</b> protein csaa; <b>PDBTitle:</b> crystal structure of a secretion chaperone csaa from bacillus subtilis2 in the space group p 32 2 1
37	<a href="#">d1fl0a</a>	Alignment	not modelled	99.7	19	<b>Fold:</b> OB-fold <b>Superfamily:</b> Nucleic acid-binding proteins <b>Family:</b> Myf domain
38	<a href="#">d1ntga</a>	Alignment	not modelled	99.7	22	<b>Fold:</b> OB-fold <b>Superfamily:</b> Nucleic acid-binding proteins <b>Family:</b> Myf domain
39	<a href="#">d1jca</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
40	<a href="#">c1b70A</a>	Alignment	not modelled	99.6	21	<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
41	<a href="#">c3l4gC</a>	Alignment	not modelled	99.5	18	<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
42	<a href="#">c3l4gI</a>	Alignment	not modelled	99.5	23	<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
43	<a href="#">c2du4B</a>	Alignment	not modelled	99.4	14	<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
44	<a href="#">c6ezdD</a>	Alignment	not modelled	99.4	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)
45	<a href="#">c2du3A</a>	Alignment	not modelled	99.4	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
46	<a href="#">c2du7C</a>	Alignment	not modelled	99.3	14	<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
47	<a href="#">c3pcoC</a>	Alignment	not modelled	99.3	15	<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
48	<a href="#">c2zimA</a>	Alignment	not modelled	99.3	14	<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
49	<a href="#">c1eyA</a>	Alignment	not modelled	99.3	20	<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
50	<a href="#">c2znjB</a>	Alignment	not modelled	99.1	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
51	<a href="#">c3hj7A</a>	Alignment	not modelled	97.7	22	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> trna(ile)-lysine synthase; <b>PDBTitle:</b> crystal structure of tils c-terminal domain
52	<a href="#">c3racA</a>	Alignment	not modelled	97.2	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 subunit from2 alicyclobacillus acidocaldarius subsp. acidocaldarius dsm 446.
53	<a href="#">c3od1A</a>	Alignment	not modelled	97.0	11	<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
54	<a href="#">d1kmma2</a>	Alignment	not modelled	96.7	19	<b>Fold:</b> Class II aaRS and biotin synthetases <b>Superfamily:</b> Class II aaRS and biotin synthetases

54	<a href="#">q1kmmqz</a>	Alignment	not modelled	96.7	19	<b>Family:</b> Class II aminoacyl-tRNA synthetase (aaRS)-like, catalytic domain <b>PDB header:</b> ligase
55	<a href="#">c2e19B</a>	Alignment	not modelled	96.5	17	<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
56	<a href="#">c2i41C</a>	Alignment	not modelled	96.5	15	<b>PDB header:</b> ligase <b>Chain:</b> C: <b>PDB Molecule:</b> proline-trna ligase; <b>PDBTitle:</b> rhodopseudomonas palustris prolyl-trna synthetase
57	<a href="#">c1z7nB</a>	Alignment	not modelled	96.4	12	<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
58	<a href="#">c3netB</a>	Alignment	not modelled	96.3	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
59	<a href="#">c3hrif</a>	Alignment	not modelled	96.3	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
60	<a href="#">c5m8hB</a>	Alignment	not modelled	96.3	15	<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
61	<a href="#">c3a2kB</a>	Alignment	not modelled	96.2	22	<b>PDB header:</b> ligase/rna <b>Chain:</b> B: <b>PDB Molecule:</b> trna(ile)-lysine synthase; <b>PDBTitle:</b> crystal structure of tils complexed with trna
62	<a href="#">c5zy9D</a>	Alignment	not modelled	96.2	13	<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
63	<a href="#">c1adyA</a>	Alignment	not modelled	96.2	17	<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	96.0	15	<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="#">c1nyqA</a>	Alignment	not modelled	95.9	8	<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
66	<a href="#">d1wu7a2</a>	Alignment	not modelled	95.9	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
67	<a href="#">c4hwtA</a>	Alignment	not modelled	95.7	14	<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
68	<a href="#">c5e3iA</a>	Alignment	not modelled	95.7	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 acetobacter2 baumannii with bound l-histidine and atp
69	<a href="#">c4e51B</a>	Alignment	not modelled	95.6	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
70	<a href="#">c3g1zB</a>	Alignment	not modelled	95.5	14	<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
71	<a href="#">d1h4vb2</a>	Alignment	not modelled	95.5	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
72	<a href="#">c6nh1A</a>	Alignment	not modelled	95.4	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
73	<a href="#">d1nyra4</a>	Alignment	not modelled	95.3	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
74	<a href="#">c2j3mA</a>	Alignment	not modelled	95.2	14	<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
75	<a href="#">d1z7ma1</a>	Alignment	not modelled	95.1	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
76	<a href="#">c5znjA</a>	Alignment	not modelled	95.1	12	<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
77	<a href="#">d1l0wa3</a>	Alignment	not modelled	95.0	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
78	<a href="#">c5ucmB</a>	Alignment	not modelled	94.9	12	<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
79	<a href="#">d1c0aa3</a>	Alignment	not modelled	94.6	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
						<b>PDB header:</b> ligase

80	<a href="#">c6oteA_</a>	Alignment	not modelled	94.4	10	<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 I-serylsulfamoyl adenosine
81	<a href="#">d1e1oa2</a>	Alignment	not modelled	93.8	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
82	<a href="#">c3a32A_</a>	Alignment	not modelled	93.8	14	<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
83	<a href="#">c4x5oB_</a>	Alignment	not modelled	93.7	16	<b>PDB header:</b> ligase <b>Chain:</b> B: <b>PDB Molecule:</b> histidine--trna ligase, cytoplasmic; <b>PDBTitle:</b> human histidine trna synthetase
84	<a href="#">d1qf6a4</a>	Alignment	not modelled	93.7	10	<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="#">c2dq3A_</a>	Alignment	not modelled	93.6	11	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> seryl-trna synthetase; <b>PDBTitle:</b> crystal structure of aq_298
86	<a href="#">d1nnha_</a>	Alignment	not modelled	93.4	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
87	<a href="#">c1qf6A_</a>	Alignment	not modelled	93.2	11	<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
88	<a href="#">d1b8aa2</a>	Alignment	not modelled	93.1	10	<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="#">d1bbua2</a>	Alignment	not modelled	93.1	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
90	<a href="#">c3ugtD_</a>	Alignment	not modelled	92.9	7	<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
91	<a href="#">d1seta2</a>	Alignment	not modelled	92.7	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
92	<a href="#">c1qe0B_</a>	Alignment	not modelled	92.2	16	<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
93	<a href="#">c4g84B_</a>	Alignment	not modelled	91.8	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
94	<a href="#">c2dq0A_</a>	Alignment	not modelled	91.8	11	<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
95	<a href="#">c1wleB_</a>	Alignment	not modelled	91.6	10	<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
96	<a href="#">d1nj8a3</a>	Alignment	not modelled	91.0	8	<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="#">c4kr3A_</a>	Alignment	not modelled	91.0	14	<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
98	<a href="#">c5z5eB_</a>	Alignment	not modelled	90.9	12	<b>PDB header:</b> ligase <b>Chain:</b> B: <b>PDB Molecule:</b> neq417; <b>PDBTitle:</b> crystal structure of the glycyI-trna synthetase (glyrs) in2 nanoarchaeum equitans
99	<a href="#">c4o2dB_</a>	Alignment	not modelled	90.8	19	<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
100	<a href="#">c3qo8A_</a>	Alignment	not modelled	90.8	10	<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
101	<a href="#">d1eova2</a>	Alignment	not modelled	90.6	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
102	<a href="#">c6bjjC_</a>	Alignment	not modelled	90.5	10	<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
103	<a href="#">c3lssA_</a>	Alignment	not modelled	90.2	13	<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
104	<a href="#">c3mf2B_</a>	Alignment	not modelled	89.8	13	<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
105	<a href="#">c3w3sA_</a>	Alignment	not modelled	89.5	14	<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
						<b>PDB header:</b> ligase/ligase inhibitor

106	<a href="#">c4hvcB_</a>	Alignment	not modelled	89.5	12	<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
107	<a href="#">c1sryB_</a>	Alignment	not modelled	89.4	14	<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
108	<a href="#">c3errB_</a>	Alignment	not modelled	88.9	14	<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
109	<a href="#">c1fyfB_</a>	Alignment	not modelled	87.9	9	<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
110	<a href="#">d1nj1a3</a>	Alignment	not modelled	87.4	10	<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
111	<a href="#">c6mn8A_</a>	Alignment	not modelled	87.3	13	<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
112	<a href="#">c4kqeA_</a>	Alignment	not modelled	86.6	18	<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
113	<a href="#">c5xiiC_</a>	Alignment	not modelled	86.5	11	<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
114	<a href="#">c4twaA_</a>	Alignment	not modelled	85.9	11	<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
115	<a href="#">c4g85A_</a>	Alignment	not modelled	84.1	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
116	<a href="#">c2cj9A_</a>	Alignment	not modelled	83.3	12	<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
117	<a href="#">c1ggmB_</a>	Alignment	not modelled	82.5	10	<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
118	<a href="#">c5f9yB_</a>	Alignment	not modelled	82.4	10	<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
119	<a href="#">c1nj2A_</a>	Alignment	not modelled	82.0	12	<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
120	<a href="#">c1nj8C_</a>	Alignment	not modelled	81.7	12	<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