



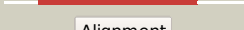

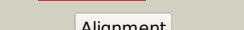







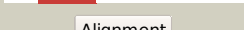

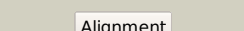

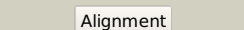




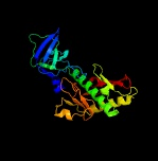









# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2555c_alaS_2873781_2876495
Date	Wed Aug 7 12:50:19 BST 2019
Unique Job ID	8db8c08487052773

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c3wqyB_</a>	 Alignment		100.0	28	<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
2	<a href="#">c2zzfA_</a>	 Alignment		100.0	32	<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
3	<a href="#">c2ztgA_</a>	 Alignment		100.0	29	<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
4	<a href="#">c1yfsB_</a>	 Alignment		100.0	48	<b>PDB header:</b> ligase <b>Chain:</b> B: <b>PDB Molecule:</b> alanyl-trna synthetase; <b>PDBTitle:</b> the crystal structure of alanyl-trna synthetase in complex2 with l-alanine
5	<a href="#">c3hxxA_</a>	 Alignment		100.0	47	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> alanyl-trna synthetase; <b>PDBTitle:</b> crystal structure of catalytic fragment of e. coli alars in complex2 with amppcp
6	<a href="#">c5knnG_</a>	 Alignment		100.0	43	<b>PDB header:</b> ligase <b>Chain:</b> G: <b>PDB Molecule:</b> alanine--trna ligase, cytoplasmic; <b>PDBTitle:</b> evolutionary gain of alanine mischarging to non-cognate trnas with a2 g4:u69 base pair
7	<a href="#">c4xeoB_</a>	 Alignment		100.0	44	<b>PDB header:</b> ligase <b>Chain:</b> B: <b>PDB Molecule:</b> alanine--trna ligase, cytoplasmic; <b>PDBTitle:</b> crystal structure of human alars catalytic domain with r329h mutation
8	<a href="#">d1riqa2</a>	 Alignment		100.0	55	<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
9	<a href="#">d1j5wa_</a>	 Alignment		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
10	<a href="#">c5f5wC_</a>	 Alignment		100.0	22	<b>PDB header:</b> ligase <b>Chain:</b> C: <b>PDB Molecule:</b> glycine--trna ligase alpha subunit; <b>PDBTitle:</b> crystal structure of the alpha subunit of glycyl trna synthetase2 (glyrs) from aquifex aeolicus in complex with an analog of glycyl3 adenylate (gly-sa)
11	<a href="#">c3rf1B_</a>	 Alignment		100.0	21	<b>PDB header:</b> ligase <b>Chain:</b> B: <b>PDB Molecule:</b> glycyl-trna synthetase alpha subunit; <b>PDBTitle:</b> the crystal structure of glycyl-trna synthetase subunit alpha from2 campylobacter jejuni subsp. jejuni nctc 11168

12	<a href="#">d1riqa1</a>	Alignment		100.0	38	<b>Fold:</b> Putative anticodon-binding domain of alanyl-tRNA synthetase (AlaRS) <b>Superfamily:</b> Putative anticodon-binding domain of alanyl-tRNA synthetase (AlaRS) <b>Family:</b> Putative anticodon-binding domain of alanyl-tRNA synthetase (AlaRS)
13	<a href="#">c3kewA</a>	Alignment		100.0	21	<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
14	<a href="#">c2e1bA</a>	Alignment		100.0	31	<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
15	<a href="#">d2e1ba2</a>	Alignment		100.0	30	<b>Fold:</b> RRF/tRNA synthetase additional domain-like <b>Superfamily:</b> ThrRS/AlaRS common domain <b>Family:</b> AlaX-like
16	<a href="#">d1v4pa</a>	Alignment		100.0	21	<b>Fold:</b> RRF/tRNA synthetase additional domain-like <b>Superfamily:</b> ThrRS/AlaRS common domain <b>Family:</b> AlaX-like
17	<a href="#">d1nyra3</a>	Alignment		99.9	19	<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
18	<a href="#">c2zvfG</a>	Alignment		99.9	21	<b>PDB header:</b> ligase <b>Chain:</b> G: <b>PDB Molecule:</b> alanyl-trna synthetase; <b>PDBTitle:</b> crystal structure of archaeoglobus fulgidus alanyl-trna2 synthetase c-terminal dimerization domain
19	<a href="#">c5t76A</a>	Alignment		99.9	22	<b>PDB header:</b> translation <b>Chain:</b> A: <b>PDB Molecule:</b> alanine--trna ligase, cytoplasmic; <b>PDBTitle:</b> a fragment of a human trna synthetase
20	<a href="#">d1tkea2</a>	Alignment		99.9	17	<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
21	<a href="#">c1nyqA</a>	Alignment	not modelled	99.9	16	<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
22	<a href="#">c1tkeA</a>	Alignment	not modelled	99.9	14	<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
23	<a href="#">c1qf6A</a>	Alignment	not modelled	99.9	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
24	<a href="#">c4v1ac</a>	Alignment	not modelled	99.8	14	<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
25	<a href="#">c3g98B</a>	Alignment	not modelled	99.7	22	<b>PDB header:</b> ligase <b>Chain:</b> B: <b>PDB Molecule:</b> alanyl-trna synthetase; <b>PDBTitle:</b> crystal structure of the c-ala domain from aquifex aeolicus2 alanyl-trna synthetase
26	<a href="#">d2e1ba1</a>	Alignment	not modelled	99.6	31	<b>Fold:</b> Reductase/isomerase/elongation factor common domain <b>Superfamily:</b> Translation proteins <b>Family:</b> AlaX-M N-terminal domain-like
27	<a href="#">c4ce4c</a>	Alignment	not modelled	99.4	11	<b>PDB header:</b> ribosome <b>Chain:</b> C: <b>PDB Molecule:</b> <b>PDBTitle:</b> 39s large subunit of the porcine mitochondrial ribosome
28	<a href="#">c5ghrA</a>	Alignment	not modelled	96.9	18	<b>PDB header:</b> dna binding protein/replication <b>Chain:</b> A: <b>PDB Molecule:</b> ssdna-specific exonuclease; <b>PDBTitle:</b> dna replication protein
						<b>PDB header:</b> ligase

29	<a href="#">c6ezdD</a>	Alignment	not modelled	93.1	19	<b>Chain:</b> D: <b>PDB Molecule:</b> pyrrolyl-trna synthetase; <b>PDBTitle:</b> pyrrolyl-trna synthetase from candidatus methanomethylophilus alvus2 (mmapylrs)
30	<a href="#">c5hgqD</a>	Alignment	not modelled	92.7	18	<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.
31	<a href="#">c4h02B</a>	Alignment	not modelled	92.1	19	<b>PDB header:</b> ligase <b>Chain:</b> B: <b>PDB Molecule:</b> lysyl-trna synthetase; <b>PDBTitle:</b> crystal structure of p. falciparum lysyl-trna synthetase
32	<a href="#">c2odrD</a>	Alignment	not modelled	89.6	19	<b>PDB header:</b> ligase <b>Chain:</b> D: <b>PDB Molecule:</b> phosphoseryl-trna synthetase; <b>PDBTitle:</b> methanococcus maripaludis phosphoseryl-trna synthetase
33	<a href="#">c2odrC</a>	Alignment	not modelled	87.7	18	<b>PDB header:</b> ligase <b>Chain:</b> C: <b>PDB Molecule:</b> phosphoseryl-trna synthetase; <b>PDBTitle:</b> methanococcus maripaludis phosphoseryl-trna synthetase
34	<a href="#">c1b70A</a>	Alignment	not modelled	86.8	22	<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
35	<a href="#">c2znjB</a>	Alignment	not modelled	84.7	16	<b>PDB header:</b> ligase <b>Chain:</b> B: <b>PDB Molecule:</b> putative uncharacterized protein; <b>PDBTitle:</b> crystal structure of pyrrolyl-trna synthetase from2 desulfitobacterium hafniense
36	<a href="#">d1kmma2</a>	Alignment	not modelled	84.5	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
37	<a href="#">d1jjca</a>	Alignment	not modelled	84.4	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
38	<a href="#">c1z7nB</a>	Alignment	not modelled	82.7	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 apt-ptase) from2 lactococcus lactis with bound prpp substrate
39	<a href="#">c3l4gC</a>	Alignment	not modelled	82.1	23	<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
40	<a href="#">d1h4vb2</a>	Alignment	not modelled	82.0	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
41	<a href="#">c2odrB</a>	Alignment	not modelled	81.1	20	<b>PDB header:</b> ligase <b>Chain:</b> B: <b>PDB Molecule:</b> phosphoseryl-trna synthetase; <b>PDBTitle:</b> methanococcus maripaludis phosphoseryl-trna synthetase
42	<a href="#">d1ir6a</a>	Alignment	not modelled	77.9	16	<b>Fold:</b> DHH phosphoesterases <b>Superfamily:</b> DHH phosphoesterases <b>Family:</b> Exonuclease RecJ
43	<a href="#">c1ir6A</a>	Alignment	not modelled	77.9	16	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> exonuclease recj; <b>PDBTitle:</b> crystal structure of exonuclease recj bound to manganese
44	<a href="#">d1qjta</a>	Alignment	not modelled	76.7	14	<b>Fold:</b> EF Hand-like <b>Superfamily:</b> EF-hand <b>Family:</b> Eps15 homology domain (EH domain)
45	<a href="#">c4lnsA</a>	Alignment	not modelled	76.2	17	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> asparagine synthetase a; <b>PDBTitle:</b> crystal structure of asparagine synthetase a (asna) from trypanosoma2 brucei
46	<a href="#">c3t5sA</a>	Alignment	not modelled	76.1	18	<b>PDB header:</b> immune system <b>Chain:</b> A: <b>PDB Molecule:</b> macrophage migration inhibitory factor; <b>PDBTitle:</b> structure of macrophage migration inhibitory factor from giardia2 lamblia
47	<a href="#">c1e22A</a>	Alignment	not modelled	75.4	23	<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
48	<a href="#">d1eova2</a>	Alignment	not modelled	74.9	27	<b>Fold:</b> Class II aaRS and biotin synthetases <b>Superfamily:</b> Class II aaRS and biotin synthetases <b>Family:</b> Class II aminoacyl-tRNA synthetase (aaRS)-like, catalytic domain
49	<a href="#">d1c0aa3</a>	Alignment	not modelled	74.7	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
50	<a href="#">c3l4gI</a>	Alignment	not modelled	73.6	25	<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
51	<a href="#">d1l0wa3</a>	Alignment	not modelled	73.4	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
52	<a href="#">c5xspB</a>	Alignment	not modelled	72.4	8	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> phosphodiesterase acting on cyclic dinucleotides; <b>PDBTitle:</b> the catalytic domain of gdpp with 5'-papa
53	<a href="#">c2xczA</a>	Alignment	not modelled	71.9	21	<b>PDB header:</b> immune system <b>Chain:</b> A: <b>PDB Molecule:</b> possible atls1-like light-inducible protein; <b>PDBTitle:</b> crystal structure of macrophage migration inhibitory factor homologue2 from prochlorococcus marinus
54	<a href="#">d1hfoa</a>	Alignment	not modelled	71.8	18	<b>Fold:</b> Tautomerase/MIF <b>Superfamily:</b> Tautomerase/MIF <b>Family:</b> MIF-related

55	<a href="#">c3g1zB</a>	Alignment	not modelled	71.3	11	<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
56	<a href="#">c5o1uB</a>	Alignment	not modelled	71.2	16	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> phosphodiesterase; <b>PDBTitle:</b> structure of wildtype t.maritima pde (tm1595) with amp and mn2+
57	<a href="#">c5t59D</a>	Alignment	not modelled	71.2	13	<b>PDB header:</b> cell cycle <b>Chain:</b> D: <b>PDB Molecule:</b> klla0f02343p; <b>PDBTitle:</b> structure of the mind complex shows a regulatory focus of yeast2 kinetochore assembly
58	<a href="#">d1dpta</a>	Alignment	not modelled	71.0	25	<b>Fold:</b> Tautomerase/MIF <b>Superfamily:</b> Tautomerase/MIF <b>Family:</b> MIF-related
59	<a href="#">d1zunb1</a>	Alignment	not modelled	70.6	17	<b>Fold:</b> Reductase/isomerase/elongation factor common domain <b>Superfamily:</b> Translation proteins <b>Family:</b> Elongation factors
60	<a href="#">c3b64A</a>	Alignment	not modelled	70.5	17	<b>PDB header:</b> cytokine <b>Chain:</b> A: <b>PDB Molecule:</b> macrophage migration inhibitory factor-like <b>PDBTitle:</b> macrophage migration inhibitory factor (mif) from2 /leishmania major
61	<a href="#">c5j21C</a>	Alignment	not modelled	70.4	20	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> bifunctional oligoribonuclease and pap phosphatase rnna; <b>PDBTitle:</b> structure of bacillus nanornase a (wt)
62	<a href="#">c3fwtA</a>	Alignment	not modelled	70.3	25	<b>PDB header:</b> cytokine <b>Chain:</b> A: <b>PDB Molecule:</b> macrophage migration inhibitory factor-like <b>PDBTitle:</b> crystal structure of leishmania major mif2
63	<a href="#">c1efwA</a>	Alignment	not modelled	70.0	13	<b>PDB header:</b> ligase/rna <b>Chain:</b> A: <b>PDB Molecule:</b> aspartyl-trna synthetase; <b>PDBTitle:</b> crystal structure of aspartyl-trna synthetase from thermus2 thermophilus complexed to trnaasp from escherichia coli
64	<a href="#">c2du7C</a>	Alignment	not modelled	69.7	23	<b>PDB header:</b> ligase <b>Chain:</b> C: <b>PDB Molecule:</b> o-phosphoseryl-trna synthetase; <b>PDBTitle:</b> crystal structure of methanococcus jannacsii o-phosphoseryl-trna2 synthetase
65	<a href="#">c3pcoC</a>	Alignment	not modelled	69.6	41	<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
66	<a href="#">c6pqhA</a>	Alignment	not modelled	69.3	20	<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
67	<a href="#">d1uiza</a>	Alignment	not modelled	68.9	21	<b>Fold:</b> Tautomerase/MIF <b>Superfamily:</b> Tautomerase/MIF <b>Family:</b> MIF-related
68	<a href="#">c2os5C</a>	Alignment	not modelled	68.3	11	<b>PDB header:</b> cytokine <b>Chain:</b> C: <b>PDB Molecule:</b> acemif; <b>PDBTitle:</b> macrophage migration inhibitory factor from ancylostoma ceylanicum
69	<a href="#">c5ejdK</a>	Alignment	not modelled	67.7	31	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> K: <b>PDB Molecule:</b> tqaa; <b>PDBTitle:</b> the crystal structure of holo t3ct
70	<a href="#">c2rhqA</a>	Alignment	not modelled	67.7	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
71	<a href="#">c1b8aB</a>	Alignment	not modelled	67.5	30	<b>PDB header:</b> ligase <b>Chain:</b> B: <b>PDB Molecule:</b> protein (aspartyl-trna synthetase); <b>PDBTitle:</b> aspartyl-trna synthetase
72	<a href="#">c3e9hB</a>	Alignment	not modelled	67.4	23	<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
73	<a href="#">d2gdga1</a>	Alignment	not modelled	66.2	29	<b>Fold:</b> Tautomerase/MIF <b>Superfamily:</b> Tautomerase/MIF <b>Family:</b> MIF-related
74	<a href="#">c2du4B</a>	Alignment	not modelled	66.1	21	<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
75	<a href="#">d1gd0a</a>	Alignment	not modelled	65.9	29	<b>Fold:</b> Tautomerase/MIF <b>Superfamily:</b> Tautomerase/MIF <b>Family:</b> MIF-related
76	<a href="#">c5zg8A</a>	Alignment	not modelled	65.8	21	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> asparagine--trna ligase; <b>PDBTitle:</b> crystal structure of ttnrs
77	<a href="#">c4ah6B</a>	Alignment	not modelled	65.7	7	<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
78	<a href="#">c4wj4A</a>	Alignment	not modelled	65.4	11	<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(asn) and aspartic acid
79	<a href="#">d1nnha</a>	Alignment	not modelled	65.3	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
80	<a href="#">c4o2dB</a>	Alignment	not modelled	64.8	21	<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
81	<a href="#">c3gacD_</a>	Alignment	not modelled	64.7	21	<b>PDB header:</b> cytokine <b>Chain:</b> D: <b>PDB Molecule:</b> macrophage migration inhibitory factor-like <b>PDBTitle:</b> structure of mif with hpp
82	<a href="#">c5xixD_</a>	Alignment	not modelled	64.3	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
83	<a href="#">d1n9wa2</a>	Alignment	not modelled	64.2	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
84	<a href="#">c1asyA_</a>	Alignment	not modelled	63.9	30	<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
85	<a href="#">c3bjuB_</a>	Alignment	not modelled	63.4	36	<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
86	<a href="#">d1b8aa2</a>	Alignment	not modelled	63.4	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
87	<a href="#">c6ns0A_</a>	Alignment	not modelled	63.4	18	<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
88	<a href="#">c1n9wA_</a>	Alignment	not modelled	63.0	21	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> A: <b>PDB Molecule:</b> aspartyl-trna synthetase 2; <b>PDBTitle:</b> crystal structure of the non-discriminating and archaeal-2 type aspartyl-trna synthetase from thermus thermophilus
89	<a href="#">c4x0oG_</a>	Alignment	not modelled	62.5	16	<b>PDB header:</b> transferase <b>Chain:</b> G: <b>PDB Molecule:</b> 3-oxoacyl-[acyl-carrier-protein] synthase 3 protein 2; <b>PDBTitle:</b> beta-ketoacyl-(acyl carrier protein) synthase iii-2 (fabh2) from2 vibrio cholerae soaked with acetyl-coa
90	<a href="#">c1wydB_</a>	Alignment	not modelled	62.5	27	<b>PDB header:</b> ligase <b>Chain:</b> B: <b>PDB Molecule:</b> hypothetical aspartyl-trna synthetase; <b>PDBTitle:</b> crystal structure of aspartyl-trna synthetase from sulfolobus tokodaii
91	<a href="#">c3i7fA_</a>	Alignment	not modelled	62.4	25	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> aspartyl-trna synthetase; <b>PDBTitle:</b> aspartyl trna synthetase from entamoeba histolytica
92	<a href="#">c2du3A_</a>	Alignment	not modelled	61.9	23	<b>PDB header:</b> ligase/rna <b>Chain:</b> A: <b>PDB Molecule:</b> o-phosphoserine-trna synthetase; <b>PDBTitle:</b> crystal structure of archaeoglobus fulgidus o-phosphoserine-trna synthetase complexed with trnacys and o-phosphoserine
93	<a href="#">c4upaA_</a>	Alignment	not modelled	61.9	36	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> lysine--trna ligase; <b>PDBTitle:</b> crystal structure of entamoeba histolytica lysyl-trna synthetase in2 complex with amppnp
94	<a href="#">c1qe0B_</a>	Alignment	not modelled	61.8	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
95	<a href="#">d1wu7a2</a>	Alignment	not modelled	61.8	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
96	<a href="#">c4dh4A_</a>	Alignment	not modelled	61.4	24	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> mif; <b>PDBTitle:</b> macrophage migration inhibitory factor toxoplasma gondii
97	<a href="#">d1fima_</a>	Alignment	not modelled	61.4	29	<b>Fold:</b> Tautomerase/MIF <b>Superfamily:</b> Tautomerase/MIF <b>Family:</b> MIF-related
98	<a href="#">c4j15A_</a>	Alignment	not modelled	61.3	29	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> aspartate--trna ligase, cytoplasmic; <b>PDBTitle:</b> crystal structure of human cytosolic aspartyl-trna synthetase, a2 component of multi-trna synthetase complex
99	<a href="#">c2zimA_</a>	Alignment	not modelled	61.3	20	<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
100	<a href="#">c1eqrC_</a>	Alignment	not modelled	61.2	14	<b>PDB header:</b> ligase <b>Chain:</b> C: <b>PDB Molecule:</b> aspartyl-trna synthetase; <b>PDBTitle:</b> crystal structure of free aspartyl-trna synthetase from2 escherichia coli
101	<a href="#">c5elnC_</a>	Alignment	not modelled	60.8	29	<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
102	<a href="#">d1qf6a4</a>	Alignment	not modelled	60.7	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="#">c2di4B_</a>	Alignment	not modelled	60.6	13	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> cell division protein ftsH homolog; <b>PDBTitle:</b> crystal structure of the ftsH protease domain
104	<a href="#">c2xgtB_</a>	Alignment	not modelled	60.5	21	<b>PDB header:</b> ligase <b>Chain:</b> B: <b>PDB Molecule:</b> asparaginyl-trna synthetase, cytoplasmic; <b>PDBTitle:</b> asparaginyl-trna synthetase from brugia malayi complexed2 with the sulphamoyl analogue of asparaginyl-adenylate
105	<a href="#">c6cuqB_</a>	Alignment	not modelled	60.2	21	<b>PDB header:</b> cytokine <b>Chain:</b> B: <b>PDB Molecule:</b> macrophage migration inhibitory factor-like protein; <b>PDBTitle:</b> crystal structure of macrophage migration inhibitory factor-like2 protein (ehmif) from entamoeba histolytica

106	<a href="#">d2di4a1</a>	Alignment	not modelled	60.1	13	<b>Fold:</b> FtsH protease domain-like <b>Superfamily:</b> FtsH protease domain-like <b>Family:</b> FtsH protease domain-like
107	<a href="#">d1bbua2</a>	Alignment	not modelled	59.3	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
108	<a href="#">c1eiyA_</a>	Alignment	not modelled	57.9	35	<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
109	<a href="#">c6od8A_</a>	Alignment	not modelled	57.7	25	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> putative aspartyl-trna synthetase; <b>PDBTitle:</b> crystal structure of a putative aspartyl-trna synthetase from2 leishmania major friedlin
110	<a href="#">c4up8A_</a>	Alignment	not modelled	57.5	36	<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
111	<a href="#">d1u6ea2</a>	Alignment	not modelled	57.5	15	<b>Fold:</b> Thiolase-like <b>Superfamily:</b> Thiolase-like <b>Family:</b> Chalcone synthase-like
112	<a href="#">c1x55A_</a>	Alignment	not modelled	57.4	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
113	<a href="#">c4p74D_</a>	Alignment	not modelled	57.3	41	<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
114	<a href="#">c4r3zA_</a>	Alignment	not modelled	57.1	19	<b>PDB header:</b> protein binding/ligase <b>Chain:</b> A: <b>PDB Molecule:</b> aminoacyl trna synthase complex-interacting multifunctional <b>PDBTitle:</b> crystal structure of human argrs-glnrs-aimp1 complex
115	<a href="#">c3zeyG_</a>	Alignment	not modelled	57.0	15	<b>PDB header:</b> ribosome <b>Chain:</b> G: <b>PDB Molecule:</b> 40s ribosomal protein s13, putative; <b>PDBTitle:</b> high-resolution cryo-electron microscopy structure of the trypanosoma2 brucei ribosome
116	<a href="#">c3devB_</a>	Alignment	not modelled	56.8	20	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> sh1221; <b>PDBTitle:</b> crystal structure of sh1221 protein from staphylococcus haemolyticus,2 northeast structural genomics consortium target shr87
117	<a href="#">c4ex5A_</a>	Alignment	not modelled	55.8	21	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> lysine--trna ligase; <b>PDBTitle:</b> crystal structure of lysyl-trna synthetase lysrs from burkholderia2 thailandensis bound to lysine
118	<a href="#">c3m4qA_</a>	Alignment	not modelled	54.7	25	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> asparaginyl-trna synthetase, putative; <b>PDBTitle:</b> entamoeba histolytica asparaginyl-trna synthetase (asnrns)
119	<a href="#">d1ub7a2</a>	Alignment	not modelled	52.5	26	<b>Fold:</b> Thiolase-like <b>Superfamily:</b> Thiolase-like <b>Family:</b> Chalcone synthase-like
120	<a href="#">d1z7ma1</a>	Alignment	not modelled	51.8	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