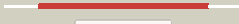



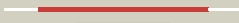

















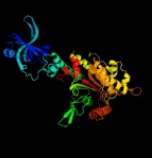





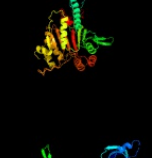




# Phyre2

|               |                                  |
|---------------|----------------------------------|
| Email         | mdejesus@rockefeller.edu         |
| Description   | RVBD2572c_(aspS)_2896023_2897813 |
| Date          | Wed Aug 7 12:50:21 BST 2019      |
| Unique Job ID | 51c41cf747024209                 |

Detailed template information

| #  | Template                | Alignment Coverage  | 3D Model  | Confidence | % i.d. | Template Information   |
|----|-------------------------|---|---|------------|--------|--|
| 1  | <a href="#">c1eqrC_</a> |  Alignment   |    | 100.0      | 47     | <b>PDB header:</b> ligase<br><b>Chain:</b> C; <b>PDB Molecule:</b> aspartyl-trna synthetase;<br><b>PDBTitle:</b> crystal structure of free aspartyl-trna synthetase from2 escherichia coli   |
| 2  | <a href="#">c4wj4A_</a> |  Alignment   |    | 100.0      | 49     | <b>PDB header:</b> ligase/rna<br><b>Chain:</b> A; <b>PDB Molecule:</b> aspartate--trna(asp/asn) ligase;<br><b>PDBTitle:</b> crystal structure of non-discriminating aspartyl-trna synthetase from2 pseudomonas aeruginosa complexed with trna(asn) and aspartic acid |
| 3  | <a href="#">c4ah6B_</a> |  Alignment   |    | 100.0      | 39     | <b>PDB header:</b> ligase<br><b>Chain:</b> B; <b>PDB Molecule:</b> aspartate--trna ligase, mitochondrial;<br><b>PDBTitle:</b> human mitochondrial aspartyl-trna synthetase   |
| 4  | <a href="#">c1efwA_</a> |  Alignment   |   | 100.0      | 51     | <b>PDB header:</b> ligase/rna<br><b>Chain:</b> A; <b>PDB Molecule:</b> aspartyl-trna synthetase;<br><b>PDBTitle:</b> crystal structure of aspartyl-trna synthetase from thermus2 thermophilus complexed to trnaasp from escherichia coli                             |
| 5  | <a href="#">c4o2dB_</a> |  Alignment |  | 100.0      | 81     | <b>PDB header:</b> ligase<br><b>Chain:</b> B; <b>PDB Molecule:</b> aspartate--trna ligase;<br><b>PDBTitle:</b> crystal structure of aspartyl-trna synthetase from mycobacterium2 smegmatis with bound aspartic acid  |
| 6  | <a href="#">c4up8A_</a> |  Alignment |  | 100.0      | 27     | <b>PDB header:</b> ligase<br><b>Chain:</b> A; <b>PDB Molecule:</b> lysine--trna ligase;<br><b>PDBTitle:</b> crystal structure of entamoeba histolytica lysyl-trna synthetase apo2 form   |
| 7  | <a href="#">c4upaA_</a> |  Alignment |  | 100.0      | 25     | <b>PDB header:</b> ligase<br><b>Chain:</b> A; <b>PDB Molecule:</b> lysine--trna ligase;<br><b>PDBTitle:</b> crystal structure of entamoeba histolytica lysyl-trna synthetase in2 complex with amppnp   |
| 8  | <a href="#">c4ex5A_</a> |  Alignment |  | 100.0      | 25     | <b>PDB header:</b> transferase<br><b>Chain:</b> A; <b>PDB Molecule:</b> lysine--trna ligase;<br><b>PDBTitle:</b> crystal structure of lysyl-trna synthetase lysrs from burkholderia2 thailandensis bound to lysine   |
| 9  | <a href="#">c6ns0A_</a> |  Alignment |  | 100.0      | 23     | <b>PDB header:</b> ligase<br><b>Chain:</b> A; <b>PDB Molecule:</b> lysine--trna ligase;<br><b>PDBTitle:</b> crystal structure of lysyl-trna synthetase from chlamydia trachomatis2 complexed with l-lysine and cladosporin   |
| 10 | <a href="#">c1b8aB_</a> |  Alignment |  | 100.0      | 31     | <b>PDB header:</b> ligase<br><b>Chain:</b> B; <b>PDB Molecule:</b> protein (aspartyl-trna synthetase);<br><b>PDBTitle:</b> aspartyl-trna synthetase  |
| 11 | <a href="#">c1wydB_</a> |  Alignment |  | 100.0      | 32     | <b>PDB header:</b> ligase<br><b>Chain:</b> B; <b>PDB Molecule:</b> hypothetical aspartyl-trna synthetase;<br><b>PDBTitle:</b> crystal structure of aspartyl-trna synthetase from sulfobolus tokodaii   |

|    |                         |           |   |       |    |   |
|----|-------------------------|-----------|---|-------|----|---|
| 12 | <a href="#">c1e22A_</a> | Alignment |     | 100.0 | 27 | <b>PDB header:</b> ligase<br><b>Chain:</b> A: <b>PDB Molecule:</b> lysyl-trna synthetase;<br><b>PDBTitle:</b> lysyl-trna synthetase (lysu) hexagonal form complexed with2 lysine and the non-hydrolysable atp analogue amp-pcp  |
| 13 | <a href="#">c5elnC_</a> | Alignment |    | 100.0 | 25 | <b>PDB header:</b> ligase<br><b>Chain:</b> C: <b>PDB Molecule:</b> lysine--trna ligase;<br><b>PDBTitle:</b> crystal structure of lysyl-trna synthetase from cryptosporidium parvum2 complexed with l-lysine   |
| 14 | <a href="#">c3bjub_</a> | Alignment |    | 100.0 | 24 | <b>PDB header:</b> ligase<br><b>Chain:</b> B: <b>PDB Molecule:</b> lysyl-trna synthetase;<br><b>PDBTitle:</b> crystal structure of tetrameric form of human lysyl-trna synthetase   |
| 15 | <a href="#">c6od8A_</a> | Alignment |    | 100.0 | 24 | <b>PDB header:</b> ligase<br><b>Chain:</b> A: <b>PDB Molecule:</b> putative aspartyl-trna synthetase;<br><b>PDBTitle:</b> crystal structure of a putative aspartyl-trna synthetase from2 leishmania major friedlin  |
| 16 | <a href="#">c3e9hb_</a> | Alignment |    | 100.0 | 25 | <b>PDB header:</b> ligase<br><b>Chain:</b> B: <b>PDB Molecule:</b> lysyl-trna synthetase;<br><b>PDBTitle:</b> lysyl-trna synthetase from bacillus stearothermophilus2 complexed with l-lysylsulfamoyl adenosine   |
| 17 | <a href="#">c1asyA_</a> | Alignment |   | 100.0 | 27 | <b>PDB header:</b> complex (aminoacyl-trna synthase/trna)<br><b>Chain:</b> A: <b>PDB Molecule:</b> aspartyl-trna synthetase;<br><b>PDBTitle:</b> class ii aminoacyl transfer rna synthetases: crystal2 structure of yeast aspartyl-trna synthetase complexed with3 trna asp |
| 18 | <a href="#">c5vl1D_</a> | Alignment |  | 100.0 | 26 | <b>PDB header:</b> ligase<br><b>Chain:</b> D: <b>PDB Molecule:</b> lysine--trna ligase;<br><b>PDBTitle:</b> crystal structure of lysyl-trna synthetase from mycobacterium ulcerans2 complexed with l-lysine   |
| 19 | <a href="#">c5hggD_</a> | Alignment |  | 100.0 | 25 | <b>PDB header:</b> ligase/ligase inhibitor<br><b>Chain:</b> D: <b>PDB Molecule:</b> lysine--trna ligase;<br><b>PDBTitle:</b> loa loa lysyl-trna synthetase in complex with cladosporin.   |
| 20 | <a href="#">c4h02B_</a> | Alignment |  | 100.0 | 22 | <b>PDB header:</b> ligase<br><b>Chain:</b> B: <b>PDB Molecule:</b> lysyl-trna synthetase;<br><b>PDBTitle:</b> crystal structure of p. falciparum lysyl-trna synthetase  |
| 21 | <a href="#">c2xgtB_</a> | Alignment | not modelled  | 100.0 | 27 | <b>PDB header:</b> ligase<br><b>Chain:</b> B: <b>PDB Molecule:</b> asparaginyl-trna synthetase, cytoplasmic;<br><b>PDBTitle:</b> asparaginyl-trna synthetase from brugia malayi complexed2 with the sulphamoyl analogue of asparaginyl-adenylate                            |
| 22 | <a href="#">c1x55A_</a> | Alignment | not modelled  | 100.0 | 29 | <b>PDB header:</b> ligase<br><b>Chain:</b> A: <b>PDB Molecule:</b> asparaginyl-trna synthetase;<br><b>PDBTitle:</b> crystal structure of asparaginyl-trna synthetase from pyrococcus2 horikoshii complexed with asparaginyl-adenylate analogue                              |
| 23 | <a href="#">c3i7fA_</a> | Alignment | not modelled  | 100.0 | 25 | <b>PDB header:</b> ligase<br><b>Chain:</b> A: <b>PDB Molecule:</b> aspartyl-trna synthetase;<br><b>PDBTitle:</b> aspartyl trna synthetase from entamoeba histolytica  |
| 24 | <a href="#">c3m4gA_</a> | Alignment | not modelled  | 100.0 | 29 | <b>PDB header:</b> ligase<br><b>Chain:</b> A: <b>PDB Molecule:</b> asparaginyl-trna synthetase, putative;<br><b>PDBTitle:</b> entamoeba histolytica asparaginyl-trna synthetase (asrns)   |
| 25 | <a href="#">c5zg8A_</a> | Alignment | not modelled  | 100.0 | 28 | <b>PDB header:</b> ligase<br><b>Chain:</b> A: <b>PDB Molecule:</b> asparagine--trna ligase;<br><b>PDBTitle:</b> crystal structure of ttnrs  |
| 26 | <a href="#">c5xixD_</a> | Alignment | not modelled  | 100.0 | 24 | <b>PDB header:</b> ligase<br><b>Chain:</b> D: <b>PDB Molecule:</b> asparagine--trna ligase, cytoplasmic;<br><b>PDBTitle:</b> the canonical domain of human asparaginyl-trna synthetase  |
| 27 | <a href="#">c6pqhA_</a> | Alignment | not modelled  | 100.0 | 24 | <b>PDB header:</b> ligase<br><b>Chain:</b> A: <b>PDB Molecule:</b> asparagine--trna ligase;<br><b>PDBTitle:</b> crystal structure of asparagine-trna ligase from elizabethkingia sp.2 ccug 26117  |
| 28 | <a href="#">c4j15A_</a> | Alignment | not modelled  | 100.0 | 29 | <b>PDB header:</b> ligase<br><b>Chain:</b> A: <b>PDB Molecule:</b> aspartate--trna ligase, cytoplasmic;<br><b>PDBTitle:</b> crystal structure of human cytosolic aspartyl-trna synthetase, a2 component of multi-trna synthetase complex                                    |

|    |                         |           |              |       |    |  |
|----|-------------------------|-----------|--------------|-------|----|--|
| 29 | <a href="#">d1c0aa3</a> | Alignment | not modelled | 100.0 | 51 | <b>Fold:</b> Class II aaRS and biotin synthetases<br><b>Superfamily:</b> Class II aaRS and biotin synthetases<br><b>Family:</b> Class II aminoacyl-tRNA synthetase (aaRS)-like, catalytic domain   |
| 30 | <a href="#">c1n9wA</a>  | Alignment | not modelled | 100.0 | 36 | <b>PDB header:</b> biosynthetic protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> aspartyl-trna synthetase 2;<br><b>PDBTitle:</b> crystal structure of the non-discriminating and archaeal-2 type aspartyl-trna synthetase from thermus thermophilus            |
| 31 | <a href="#">d1l0wa3</a> | Alignment | not modelled | 100.0 | 59 | <b>Fold:</b> Class II aaRS and biotin synthetases<br><b>Superfamily:</b> Class II aaRS and biotin synthetases<br><b>Family:</b> Class II aminoacyl-tRNA synthetase (aaRS)-like, catalytic domain   |
| 32 | <a href="#">d1eova2</a> | Alignment | not modelled | 100.0 | 29 | <b>Fold:</b> Class II aaRS and biotin synthetases<br><b>Superfamily:</b> Class II aaRS and biotin synthetases<br><b>Family:</b> Class II aminoacyl-tRNA synthetase (aaRS)-like, catalytic domain   |
| 33 | <a href="#">d1b8aa2</a> | Alignment | not modelled | 100.0 | 31 | <b>Fold:</b> Class II aaRS and biotin synthetases<br><b>Superfamily:</b> Class II aaRS and biotin synthetases<br><b>Family:</b> Class II aminoacyl-tRNA synthetase (aaRS)-like, catalytic domain   |
| 34 | <a href="#">d1n9wa2</a> | Alignment | not modelled | 100.0 | 36 | <b>Fold:</b> Class II aaRS and biotin synthetases<br><b>Superfamily:</b> Class II aaRS and biotin synthetases<br><b>Family:</b> Class II aminoacyl-tRNA synthetase (aaRS)-like, catalytic domain   |
| 35 | <a href="#">c4lnsA</a>  | Alignment | not modelled | 100.0 | 17 | <b>PDB header:</b> ligase<br><b>Chain:</b> A: <b>PDB Molecule:</b> asparagine synthetase a;<br><b>PDBTitle:</b> crystal structure of asparagine synthetase a (asna) from trypanosoma2 brucei   |
| 36 | <a href="#">d1nnha</a>  | Alignment | not modelled | 100.0 | 25 | <b>Fold:</b> Class II aaRS and biotin synthetases<br><b>Superfamily:</b> Class II aaRS and biotin synthetases<br><b>Family:</b> Class II aminoacyl-tRNA synthetase (aaRS)-like, catalytic domain   |
| 37 | <a href="#">d1e1oa2</a> | Alignment | not modelled | 100.0 | 26 | <b>Fold:</b> Class II aaRS and biotin synthetases<br><b>Superfamily:</b> Class II aaRS and biotin synthetases<br><b>Family:</b> Class II aminoacyl-tRNA synthetase (aaRS)-like, catalytic domain   |
| 38 | <a href="#">d1bbua2</a> | Alignment | not modelled | 100.0 | 25 | <b>Fold:</b> Class II aaRS and biotin synthetases<br><b>Superfamily:</b> Class II aaRS and biotin synthetases<br><b>Family:</b> Class II aminoacyl-tRNA synthetase (aaRS)-like, catalytic domain   |
| 39 | <a href="#">c3g1zB</a>  | Alignment | not modelled | 100.0 | 22 | <b>PDB header:</b> ligase<br><b>Chain:</b> B: <b>PDB Molecule:</b> putative lysyl-trna synthetase;<br><b>PDBTitle:</b> structure of idp01693/yjea, a potential t-rna synthetase from2 salmonella typhimurium   |
| 40 | <a href="#">c2znjB</a>  | Alignment | not modelled | 100.0 | 27 | <b>PDB header:</b> ligase<br><b>Chain:</b> B: <b>PDB Molecule:</b> putative uncharacterized protein;<br><b>PDBTitle:</b> crystal structure of pyrrolysyl-trna synthetase from2 desulfitobacterium hafniense  |
| 41 | <a href="#">c2zimA</a>  | Alignment | not modelled | 100.0 | 24 | <b>PDB header:</b> ligase<br><b>Chain:</b> A: <b>PDB Molecule:</b> pyrrolysyl-trna synthetase;<br><b>PDBTitle:</b> pyrrolysyl-trna synthetase bound to adenylated pyrrolysine and2 pyrophosphate   |
| 42 | <a href="#">d1c0aa1</a> | Alignment | not modelled | 100.0 | 51 | <b>Fold:</b> OB-fold<br><b>Superfamily:</b> Nucleic acid-binding proteins<br><b>Family:</b> Anticodon-binding domain   |
| 43 | <a href="#">d1kmma2</a> | Alignment | not modelled | 100.0 | 22 | <b>Fold:</b> Class II aaRS and biotin synthetases<br><b>Superfamily:</b> Class II aaRS and biotin synthetases<br><b>Family:</b> Class II aminoacyl-tRNA synthetase (aaRS)-like, catalytic domain   |
| 44 | <a href="#">c1z7nB</a>  | Alignment | not modelled | 100.0 | 14 | <b>PDB header:</b> transferase<br><b>Chain:</b> B: <b>PDB Molecule:</b> atp phosphoribosyltransferase regulatory subunit;<br><b>PDBTitle:</b> atp phosphoribosyl transferase (hiszg atp-ptase) from2 lactococcus lactis with bound prpp substrate              |
| 45 | <a href="#">c6ezdD</a>  | Alignment | not modelled | 100.0 | 28 | <b>PDB header:</b> ligase<br><b>Chain:</b> D: <b>PDB Molecule:</b> pyrrolysyl-trna synthetase;<br><b>PDBTitle:</b> pyrrolysyl-trna synthetase from candidatus methanomethylophilus alvus2 (mmapylrs)   |
| 46 | <a href="#">d1h4vb2</a> | Alignment | not modelled | 100.0 | 20 | <b>Fold:</b> Class II aaRS and biotin synthetases<br><b>Superfamily:</b> Class II aaRS and biotin synthetases<br><b>Family:</b> Class II aminoacyl-tRNA synthetase (aaRS)-like, catalytic domain   |
| 47 | <a href="#">c5groA</a>  | Alignment | not modelled | 100.0 | 40 | <b>PDB header:</b> ligase<br><b>Chain:</b> A: <b>PDB Molecule:</b> aspartate--trna(asp/asn) ligase;<br><b>PDBTitle:</b> crystal structure of the n-terminal anticodon-binding domain of non-2 discriminating aspartyl-trna synthetase from helicobacter pylori |
| 48 | <a href="#">d1l0wa1</a> | Alignment | not modelled | 100.0 | 48 | <b>Fold:</b> OB-fold<br><b>Superfamily:</b> Nucleic acid-binding proteins<br><b>Family:</b> Anticodon-binding domain   |
| 49 | <a href="#">c4gn5A</a>  | Alignment | not modelled | 100.0 | 26 | <b>PDB header:</b> de novo protein/hydrolase<br><b>Chain:</b> A: <b>PDB Molecule:</b> obody am3l15;<br><b>PDBTitle:</b> obody am3l15 bound to hen egg-white lysozyme   |
| 50 | <a href="#">c2rhqA</a>  | Alignment | not modelled | 100.0 | 20 | <b>PDB header:</b> ligase<br><b>Chain:</b> A: <b>PDB Molecule:</b> phenylalanyl-trna synthetase alpha chain;<br><b>PDBTitle:</b> phers from staphylococcus haemolyticus- rational protein engineering2 and inhibitor studies                                   |
| 51 | <a href="#">d1qe0a2</a> | Alignment | not modelled | 100.0 | 13 | <b>Fold:</b> Class II aaRS and biotin synthetases<br><b>Superfamily:</b> Class II aaRS and biotin synthetases<br><b>Family:</b> Class II aminoacyl-tRNA synthetase (aaRS)-like, catalytic domain   |
| 52 | <a href="#">d1b8aa1</a> | Alignment | not modelled | 99.9  | 33 | <b>Fold:</b> OB-fold<br><b>Superfamily:</b> Nucleic acid-binding proteins<br><b>Family:</b> Anticodon-binding domain   |
| 53 | <a href="#">d1wu7a2</a> | Alignment | not modelled | 99.9  | 19 | <b>Fold:</b> Class II aaRS and biotin synthetases<br><b>Superfamily:</b> Class II aaRS and biotin synthetases<br><b>Family:</b> Class II aminoacyl-tRNA synthetase (aaRS)-like, catalytic domain   |
| 54 | <a href="#">c3racA</a>  | Alignment | not modelled | 99.9  | 19 | <b>PDB header:</b> ligase<br><b>Chain:</b> A: <b>PDB Molecule:</b> histidine-trna ligase;  |

|    |                         |           |              |      |    |  |
|----|-------------------------|-----------|--------------|------|----|--|
| 54 | <a href="#">c1a6A</a>   | Alignment | not modelled | 99.9 | 19 | <b>PDBTitle:</b> crystal structure of histidine--trna ligase subunit from <i>Alicyclobacillus acidocaldarius</i> subsp. <i>acidocaldarius</i> DSM 446.   |
| 55 | <a href="#">d1e1oa1</a> | Alignment | not modelled | 99.9 | 27 | <b>Fold:</b> OB-fold<br><b>Superfamily:</b> Nucleic acid-binding proteins<br><b>Family:</b> Anticodon-binding domain   |
| 56 | <a href="#">d1bbua1</a> | Alignment | not modelled | 99.9 | 31 | <b>Fold:</b> OB-fold<br><b>Superfamily:</b> Nucleic acid-binding proteins<br><b>Family:</b> Anticodon-binding domain   |
| 57 | <a href="#">d1ijca</a>  | Alignment | not modelled | 99.9 | 28 | <b>Fold:</b> Class II aaRS and biotin synthetases<br><b>Superfamily:</b> Class II aaRS and biotin synthetases<br><b>Family:</b> Class II aminoacyl-tRNA synthetase (aaRS)-like, catalytic domain   |
| 58 | <a href="#">c1b70A</a>  | Alignment | not modelled | 99.9 | 28 | <b>PDB header:</b> ligase<br><b>Chain:</b> A: <b>PDB Molecule:</b> phenylalanyl-trna synthetase;<br><b>PDBTitle:</b> phenylalanyl trna synthetase complexed with phenylalanine   |
| 59 | <a href="#">c1eiya</a>  | Alignment | not modelled | 99.9 | 28 | <b>PDB header:</b> ligase/rna<br><b>Chain:</b> A: <b>PDB Molecule:</b> phenylalanyl-trna synthetase;<br><b>PDBTitle:</b> the crystal structure of phenylalanyl-trna synthetase from <i>Thermus2 thermophilus</i> complexed with cognate trna <sup>phe</sup>                            |
| 60 | <a href="#">d1eova1</a> | Alignment | not modelled | 99.9 | 22 | <b>Fold:</b> OB-fold<br><b>Superfamily:</b> Nucleic acid-binding proteins<br><b>Family:</b> Anticodon-binding domain   |
| 61 | <a href="#">d1krta</a>  | Alignment | not modelled | 99.9 | 28 | <b>Fold:</b> OB-fold<br><b>Superfamily:</b> Nucleic acid-binding proteins<br><b>Family:</b> Anticodon-binding domain   |
| 62 | <a href="#">d1n9wa1</a> | Alignment | not modelled | 99.9 | 37 | <b>Fold:</b> OB-fold<br><b>Superfamily:</b> Nucleic acid-binding proteins<br><b>Family:</b> Anticodon-binding domain   |
| 63 | <a href="#">c4p74D</a>  | Alignment | not modelled | 99.9 | 30 | <b>PDB header:</b> ligase/ligase inhibitor<br><b>Chain:</b> D: <b>PDB Molecule:</b> phenylalanine--trna ligase alpha subunit;<br><b>PDBTitle:</b> phers in complex with compound 3a  |
| 64 | <a href="#">c3pcoC</a>  | Alignment | not modelled | 99.8 | 24 | <b>PDB header:</b> ligase<br><b>Chain:</b> C: <b>PDB Molecule:</b> phenylalanyl-trna synthetase, alpha subunit;<br><b>PDBTitle:</b> crystal structure of <i>E. coli</i> phenylalanine-trna synthetase complexed2 with phenylalanine and amp  |
| 65 | <a href="#">c4glaD</a>  | Alignment | not modelled | 99.8 | 26 | <b>PDB header:</b> hydrolase/de novo protein<br><b>Chain:</b> D: <b>PDB Molecule:</b> obody n18;<br><b>PDBTitle:</b> obody n18 bound to hen egg-white lysozyme   |
| 66 | <a href="#">c3l4gl</a>  | Alignment | not modelled | 99.7 | 32 | <b>PDB header:</b> ligase<br><b>Chain:</b> I: <b>PDB Molecule:</b> phenylalanyl-trna synthetase alpha chain;<br><b>PDBTitle:</b> crystal structure of homo sapiens cytoplasmic phenylalanyl-trna2 synthetase   |
| 67 | <a href="#">c3l4gC</a>  | Alignment | not modelled | 99.7 | 30 | <b>PDB header:</b> ligase<br><b>Chain:</b> C: <b>PDB Molecule:</b> phenylalanyl-trna synthetase alpha chain;<br><b>PDBTitle:</b> crystal structure of homo sapiens cytoplasmic phenylalanyl-trna2 synthetase   |
| 68 | <a href="#">c2odrD</a>  | Alignment | not modelled | 99.7 | 23 | <b>PDB header:</b> ligase<br><b>Chain:</b> D: <b>PDB Molecule:</b> phosphoseryl-trna synthetase;<br><b>PDBTitle:</b> methanococcus maripaludis phosphoseryl-trna synthetase  |
| 69 | <a href="#">c2odrC</a>  | Alignment | not modelled | 99.7 | 23 | <b>PDB header:</b> ligase<br><b>Chain:</b> C: <b>PDB Molecule:</b> phosphoseryl-trna synthetase;<br><b>PDBTitle:</b> methanococcus maripaludis phosphoseryl-trna synthetase  |
| 70 | <a href="#">c2du4B</a>  | Alignment | not modelled | 99.6 | 25 | <b>PDB header:</b> ligase/rna<br><b>Chain:</b> B: <b>PDB Molecule:</b> o-phosphoseryl-trna synthetase;<br><b>PDBTitle:</b> crystal structure of <i>Archaeoglobus fulgidus</i> o-phosphoseryl-2 trna synthetase complexed with trnacys  |
| 71 | <a href="#">c2odrB</a>  | Alignment | not modelled | 99.6 | 22 | <b>PDB header:</b> ligase<br><b>Chain:</b> B: <b>PDB Molecule:</b> phosphoseryl-trna synthetase;<br><b>PDBTitle:</b> methanococcus maripaludis phosphoseryl-trna synthetase  |
| 72 | <a href="#">c2odrA</a>  | Alignment | not modelled | 99.6 | 24 | <b>PDB header:</b> ligase<br><b>Chain:</b> A: <b>PDB Molecule:</b> phosphoseryl-trna synthetase;<br><b>PDBTitle:</b> methanococcus maripaludis phosphoseryl-trna synthetase  |
| 73 | <a href="#">c2du3A</a>  | Alignment | not modelled | 99.6 | 24 | <b>PDB header:</b> ligase/rna<br><b>Chain:</b> A: <b>PDB Molecule:</b> o-phosphoseryl-trna synthetase;<br><b>PDBTitle:</b> crystal structure of <i>Archaeoglobus fulgidus</i> o-phosphoseryl-2 trna synthetase complexed with trnacys and o-phosphoserine                              |
| 74 | <a href="#">c2du7C</a>  | Alignment | not modelled | 99.6 | 23 | <b>PDB header:</b> ligase<br><b>Chain:</b> C: <b>PDB Molecule:</b> o-phosphoseryl-trna synthetase;<br><b>PDBTitle:</b> crystal structure of methanococcus jannaschii o-phosphoseryl-trna2 synthetase   |
| 75 | <a href="#">c3od1A</a>  | Alignment | not modelled | 99.5 | 17 | <b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> atp phosphoribosyltransferase regulatory subunit;<br><b>PDBTitle:</b> the crystal structure of an atp phosphoribosyltransferase regulatory2 subunit/histidyl-trna synthetase from <i>Bacillus halodurans</i> C |
| 76 | <a href="#">c1adyA</a>  | Alignment | not modelled | 99.5 | 20 | <b>PDB header:</b> trna synthetase<br><b>Chain:</b> A: <b>PDB Molecule:</b> histidyl-trna synthetase;<br><b>PDBTitle:</b> histidyl-trna synthetase in complex with histidyl-adenylate  |
| 77 | <a href="#">d1z7ma1</a> | Alignment | not modelled | 99.5 | 18 | <b>Fold:</b> Class II aaRS and biotin synthetases<br><b>Superfamily:</b> Class II aaRS and biotin synthetases<br><b>Family:</b> Class II aminoacyl-tRNA synthetase (aaRS)-like, catalytic domain   |
| 78 | <a href="#">d1c0aa2</a> | Alignment | not modelled | 99.4 | 36 | <b>Fold:</b> DcoH-like<br><b>Superfamily:</b> GAD domain-like<br><b>Family:</b> GAD domain   |
| 79 | <a href="#">c3cmqA</a>  | Alignment | not modelled | 99.3 | 23 | <b>PDB header:</b> ligase<br><b>Chain:</b> A: <b>PDB Molecule:</b> phenylalanyl-trna synthetase, mitochondrial;<br><b>PDBTitle:</b> crystal structure of human mitochondrial phenylalanine   |

|     |                         |           |              |      |    |  |
|-----|-------------------------|-----------|--------------|------|----|--|
|     |                         |           |              |      |    | trna synthetase  |
| 80  | <a href="#">c6girA_</a> | Alignment | not modelled | 99.3 | 18 | <b>PDB header:</b> cytosolic protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> serine--trna ligase, cytoplasmic;<br><b>PDBTitle:</b> arabidopsis thaliana cytosolic seryl-trna synthetase   |
| 81  | <a href="#">c6mn8A_</a> | Alignment | not modelled | 99.3 | 12 | <b>PDB header:</b> ligase<br><b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein;<br><b>PDBTitle:</b> crystal structure of prolyl-trna synthetase from onchocerca volvulus2 with bound halofuginone and nucleotide       |
| 82  | <a href="#">c1nyqA_</a> | Alignment | not modelled | 99.2 | 17 | <b>PDB header:</b> ligase<br><b>Chain:</b> A: <b>PDB Molecule:</b> threonyl-trna synthetase 1;<br><b>PDBTitle:</b> structure of staphylococcus aureus threonyl-trna synthetase2 complexed with an analogue of threonyl adenylate   |
| 83  | <a href="#">d1nyra4</a> | Alignment | not modelled | 99.2 | 17 | <b>Fold:</b> Class II aaRS and biotin synthetases<br><b>Superfamily:</b> Class II aaRS and biotin synthetases<br><b>Family:</b> Class II aminoacyl-tRNA synthetase (aaRS)-like, catalytic domain                                   |
| 84  | <a href="#">c1wu7A_</a> | Alignment | not modelled | 99.2 | 16 | <b>PDB header:</b> ligase<br><b>Chain:</b> A: <b>PDB Molecule:</b> histidyl-trna synthetase;<br><b>PDBTitle:</b> crystal structure of histidyl-trna synthetase from2 thermoplasma acidophilum                                      |
| 85  | <a href="#">c2i4IC_</a> | Alignment | not modelled | 99.2 | 17 | <b>PDB header:</b> ligase<br><b>Chain:</b> C: <b>PDB Molecule:</b> proline-trna ligase;<br><b>PDBTitle:</b> rhodopseudomonas palustris prolyl-trna synthetase  |
| 86  | <a href="#">c5zy9D_</a> | Alignment | not modelled | 99.2 | 21 | <b>PDB header:</b> ligase<br><b>Chain:</b> D: <b>PDB Molecule:</b> threonyl-trna synthase;<br><b>PDBTitle:</b> structural basis for a trna synthetase  |
| 87  | <a href="#">d1l0wa2</a> | Alignment | not modelled | 99.2 | 42 | <b>Fold:</b> DCoH-like<br><b>Superfamily:</b> GAD domain-like<br><b>Family:</b> GAD domain   |
| 88  | <a href="#">c2el9B_</a> | Alignment | not modelled | 99.1 | 20 | <b>PDB header:</b> ligase<br><b>Chain:</b> B: <b>PDB Molecule:</b> histidyl-trna synthetase;<br><b>PDBTitle:</b> crystal structure of e.coli histidyl-trna synthetase2 complexed with a histidyl-adenylate analogue                |
| 89  | <a href="#">c3a32A_</a> | Alignment | not modelled | 99.1 | 18 | <b>PDB header:</b> ligase<br><b>Chain:</b> A: <b>PDB Molecule:</b> probable threonyl-trna synthetase 1;<br><b>PDBTitle:</b> crystal structure of putative threonyl-trna synthetase thrs-1 from2 aeropyrum pernix                   |
| 90  | <a href="#">c5m8hB_</a> | Alignment | not modelled | 99.1 | 11 | <b>PDB header:</b> transferase<br><b>Chain:</b> B: <b>PDB Molecule:</b> atp phosphoribosyltransferase regulatory subunit;<br><b>PDBTitle:</b> atp phosphoribosyltransferase (hiszg atpprt) from psychrobacter2 arcticus            |
| 91  | <a href="#">c3ugtD_</a> | Alignment | not modelled | 99.1 | 16 | <b>PDB header:</b> ligase<br><b>Chain:</b> D: <b>PDB Molecule:</b> threonyl-trna synthetase, mitochondrial;<br><b>PDBTitle:</b> crystal structure of the yeast mitochondrial threonyl-trna synthetase2 - orthorhombic crystal form |
| 92  | <a href="#">d1qf6a4</a> | Alignment | not modelled | 99.1 | 16 | <b>Fold:</b> Class II aaRS and biotin synthetases<br><b>Superfamily:</b> Class II aaRS and biotin synthetases<br><b>Family:</b> Class II aminoacyl-tRNA synthetase (aaRS)-like, catalytic domain                                   |
| 93  | <a href="#">d1hc7a2</a> | Alignment | not modelled | 99.1 | 9  | <b>Fold:</b> Class II aaRS and biotin synthetases<br><b>Superfamily:</b> Class II aaRS and biotin synthetases<br><b>Family:</b> Class II aminoacyl-tRNA synthetase (aaRS)-like, catalytic domain                                   |
| 94  | <a href="#">c5ucmB_</a> | Alignment | not modelled | 99.1 | 15 | <b>PDB header:</b> ligase<br><b>Chain:</b> B: <b>PDB Molecule:</b> proline--trna ligase;<br><b>PDBTitle:</b> crystal structure of prolyl-trna synthetase from pseudomonas2 aeruginosa  |
| 95  | <a href="#">c5e3iA_</a> | Alignment | not modelled | 99.1 | 18 | <b>PDB header:</b> ligase<br><b>Chain:</b> A: <b>PDB Molecule:</b> histidine--trna ligase;<br><b>PDBTitle:</b> crystal structure of a histidyl-trna synthetase from acetobacter2 baumannii with bound l-histidine and atp          |
| 96  | <a href="#">c1fyfB_</a> | Alignment | not modelled | 99.1 | 15 | <b>PDB header:</b> ligase<br><b>Chain:</b> B: <b>PDB Molecule:</b> threonyl-trna synthetase;<br><b>PDBTitle:</b> crystal structure of a truncated form of threonyl-trna2 synthetase complexed with a seryl adenylate analog        |
| 97  | <a href="#">c4e51B_</a> | Alignment | not modelled | 99.1 | 19 | <b>PDB header:</b> ligase<br><b>Chain:</b> B: <b>PDB Molecule:</b> histidine--trna ligase;<br><b>PDBTitle:</b> crystal structure of a histidyl-trna synthetase hisrs from2 burkholderia thailandensis bound to histidine           |
| 98  | <a href="#">c3hriF_</a> | Alignment | not modelled | 99.1 | 16 | <b>PDB header:</b> ligase<br><b>Chain:</b> F: <b>PDB Molecule:</b> histidyl-trna synthetase;<br><b>PDBTitle:</b> histidyl-trna synthetase (apo) from trypanosoma brucei  |
| 99  | <a href="#">c5znjA_</a> | Alignment | not modelled | 99.0 | 19 | <b>PDB header:</b> ligase<br><b>Chain:</b> A: <b>PDB Molecule:</b> proline--trna ligase;<br><b>PDBTitle:</b> crystal structure of a bacterial prors with ligands   |
| 100 | <a href="#">c4hwtA_</a> | Alignment | not modelled | 99.0 | 17 | <b>PDB header:</b> ligase/ligase inhibitor<br><b>Chain:</b> A: <b>PDB Molecule:</b> threonine--trna ligase, cytoplasmic;<br><b>PDBTitle:</b> crystal structure of human threonyl-trna synthetase bound to a novel2 inhibitor       |
| 101 | <a href="#">c2j3mA_</a> | Alignment | not modelled | 99.0 | 17 | <b>PDB header:</b> ligase<br><b>Chain:</b> A: <b>PDB Molecule:</b> prolyl-trna synthetase;<br><b>PDBTitle:</b> prolyl-trna synthetase from enterococcus faecalis complexed2 with atp, manganese and prolinol                       |
| 102 | <a href="#">c5xiiC_</a> | Alignment | not modelled | 99.0 | 10 | <b>PDB header:</b> ligase<br><b>Chain:</b> C: <b>PDB Molecule:</b> prolyl-trna synthetase (prors);<br><b>PDBTitle:</b> crystal structure of toxoplasma gondii prolyl-trna synthetase (tgprsr)2 in complex with inhibitor 6         |
| 103 | <a href="#">c6nhiA_</a> | Alignment | not modelled | 99.0 | 17 | <b>PDB header:</b> ligase<br><b>Chain:</b> A: <b>PDB Molecule:</b> histidine--trna ligase;<br><b>PDBTitle:</b> crystal structure of histidine--trna ligase from elizabethkingia sp.2 ccug 26117                                    |
| 104 | <a href="#">c1h4tD_</a> | Alignment | not modelled | 99.0 | 10 | <b>PDB header:</b> aminoacyl-trna synthetase<br><b>Chain:</b> D: <b>PDB Molecule:</b> prolyl-trna synthetase;<br><b>PDBTitle:</b> prolyl-trna synthetase from thermus thermophilus complexed2 with l-proline                       |
| 105 | <a href="#">c1qf6A_</a> | Alignment | not modelled | 99.0 | 16 | <b>PDB header:</b> ligase/rna<br><b>Chain:</b> A: <b>PDB Molecule:</b> threonyl-trna synthetase;<br><b>PDBTitle:</b> structure of e. coli threonyl-trna synthetase complexed   |

|     |                         |           |              |      |    |   |
|-----|-------------------------|-----------|--------------|------|----|---|
|     |                         |           |              |      |    | with its2 cognate trna  |
| 106 | <a href="#">c3lssA_</a> | Alignment | not modelled | 99.0 | 13 | <b>PDB header:</b> ligase<br><b>Chain:</b> A: <b>PDB Molecule:</b> seryl-trna synthetase;<br><b>PDBTitle:</b> trypanosoma brucei seryl-trna synthetase in complex with atp  |
| 107 | <a href="#">c6oteA_</a> | Alignment | not modelled | 99.0 | 21 | <b>PDB header:</b> ligase<br><b>Chain:</b> A: <b>PDB Molecule:</b> seryl-trna synthetase, cytoplasmic;<br><b>PDBTitle:</b> crystal structure of seryl-trna synthetase (serrs) from2 cryptosporidium parvum complexed with l-serylsulfamoyl adenosine  |
| 108 | <a href="#">d1nj8a3</a> | Alignment | not modelled | 99.0 | 16 | <b>Fold:</b> Class II aaRS and biotin synthetases<br><b>Superfamily:</b> Class II aaRS and biotin synthetases<br><b>Family:</b> Class II aminoacyl-tRNA synthetase (aaRS)-like, catalytic domain  |
| 109 | <a href="#">c3ialB_</a> | Alignment | not modelled | 98.9 | 12 | <b>PDB header:</b> ligase<br><b>Chain:</b> B: <b>PDB Molecule:</b> prolyl-trna synthetase;<br><b>PDBTitle:</b> giardia lamblia prolyl-trna synthetase in complex with prolyl-2 adenylate  |
| 110 | <a href="#">c6nabB_</a> | Alignment | not modelled | 98.9 | 14 | <b>PDB header:</b> ligase<br><b>Chain:</b> B: <b>PDB Molecule:</b> prolyl-trna synthetase;<br><b>PDBTitle:</b> crystal structure of prolyl-trna synthetase from naegleria fowleri in2 complex with proline and adenosine monophosphate (amp)          |
| 111 | <a href="#">c1ggmB_</a> | Alignment | not modelled | 98.9 | 21 | <b>PDB header:</b> ligase<br><b>Chain:</b> B: <b>PDB Molecule:</b> glycine--trna ligase;<br><b>PDBTitle:</b> glycyL-trna synthetase from thermus thermophilus complexed with2 glycyL-adenylate  |
| 112 | <a href="#">c1nj8C_</a> | Alignment | not modelled | 98.9 | 16 | <b>PDB header:</b> ligase<br><b>Chain:</b> C: <b>PDB Molecule:</b> proline-trna synthetase;<br><b>PDBTitle:</b> crystal structure of prolyl-trna synthetase from2 methanocaldococcus janaschii  |
| 113 | <a href="#">c3netB_</a> | Alignment | not modelled | 98.9 | 24 | <b>PDB header:</b> ligase<br><b>Chain:</b> B: <b>PDB Molecule:</b> histidyl-trna synthetase;<br><b>PDBTitle:</b> crystal structure of histidyl-trna synthetase from nostoc sp. pcc 7120   |
| 114 | <a href="#">c4twaA_</a> | Alignment | not modelled | 98.9 | 12 | <b>PDB header:</b> ligase<br><b>Chain:</b> A: <b>PDB Molecule:</b> proline--trna ligase;<br><b>PDBTitle:</b> crystal structure of prolyl-trna synthetase (prs) from plasmodium2 falciparum  |
| 115 | <a href="#">c4hvcB_</a> | Alignment | not modelled | 98.9 | 12 | <b>PDB header:</b> ligase/ligase inhibitor<br><b>Chain:</b> B: <b>PDB Molecule:</b> bifunctional glutamate/proline--trna ligase;<br><b>PDBTitle:</b> crystal structure of human prolyl-trna synthetase in complex with2 halofuginone and atp analogue |
| 116 | <a href="#">d12asa_</a> | Alignment | not modelled | 98.9 | 24 | <b>Fold:</b> Class II aaRS and biotin synthetases<br><b>Superfamily:</b> Class II aaRS and biotin synthetases<br><b>Family:</b> Class II aminoacyl-tRNA synthetase (aaRS)-like, catalytic domain  |
| 117 | <a href="#">c5f9yB_</a> | Alignment | not modelled | 98.8 | 11 | <b>PDB header:</b> ligase<br><b>Chain:</b> B: <b>PDB Molecule:</b> aminoacyl-trna synthetase;<br><b>PDBTitle:</b> crystal structure of prolyl-trna synthetase from cryptosporidium2 parvum complexed with l-proline and amp                           |
| 118 | <a href="#">d1nj1a3</a> | Alignment | not modelled | 98.8 | 16 | <b>Fold:</b> Class II aaRS and biotin synthetases<br><b>Superfamily:</b> Class II aaRS and biotin synthetases<br><b>Family:</b> Class II aminoacyl-tRNA synthetase (aaRS)-like, catalytic domain  |
| 119 | <a href="#">c1atiA_</a> | Alignment | not modelled | 98.8 | 21 | <b>PDB header:</b> protein biosynthesis<br><b>Chain:</b> A: <b>PDB Molecule:</b> glycyl-trna synthetase;<br><b>PDBTitle:</b> crystal structure of glycyL-trna synthetase from thermus thermophilus  |
| 120 | <a href="#">c4g85A_</a> | Alignment | not modelled | 98.8 | 23 | <b>PDB header:</b> ligase<br><b>Chain:</b> A: <b>PDB Molecule:</b> histidine-trna ligase, cytoplasmic;<br><b>PDBTitle:</b> crystal structure of human hisrs   |