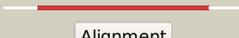
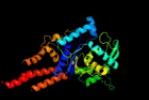


# Phyre2

|               |                                  |
|---------------|----------------------------------|
| Email         | mdejesus@rockefeller.edu         |
| Description   | RVBD2130c_(cysS)_2391223_2392467 |
| Date          | Mon Aug 5 13:25:25 BST 2019      |
| Unique Job ID | 87254a7df8bb8795                 |

Detailed template information

| #  | Template                | Alignment Coverage   | 3D Model  | Confidence | % i.d. | Template Information   |
|----|-------------------------|--|---|------------|--------|--|
| 1  | <a href="#">c3c8zB_</a> | <br>Alignment   |    | 100.0      | 76     | <b>PDB header:</b> ligase<br><b>Chain:</b> B: <b>PDB Molecule:</b> cysteinyI-trna synthetase;<br><b>PDBTitle:</b> the 1.6 a crystal structure of mshc: the rate limiting2 enzyme in the mycothiol biosynthetic pathway   |
| 2  | <a href="#">c1u0bB_</a> | <br>Alignment   |    | 100.0      | 37     | <b>PDB header:</b> ligase/rna<br><b>Chain:</b> B: <b>PDB Molecule:</b> cysteinyI trna;<br><b>PDBTitle:</b> crystal structure of cysteinyI-trna synthetase binary2 complex with trnacys   |
| 3  | <a href="#">c3sp1B_</a> | <br>Alignment   |    | 100.0      | 26     | <b>PDB header:</b> ligase<br><b>Chain:</b> B: <b>PDB Molecule:</b> cysteinyI-trna synthetase;<br><b>PDBTitle:</b> crystal structure of cysteinyI-trna synthetase (cyss) from borrelia2 burgdorferi   |
| 4  | <a href="#">c3tqoA_</a> | <br>Alignment   |    | 100.0      | 35     | <b>PDB header:</b> ligase<br><b>Chain:</b> A: <b>PDB Molecule:</b> cysteinyI-trna synthetase;<br><b>PDBTitle:</b> structure of the cysteinyI-trna synthetase (cyss) from coxiella2 burnetii.   |
| 5  | <a href="#">d1li5a2</a> | <br>Alignment |  | 100.0      | 43     | <b>Fold:</b> Adenine nucleotide alpha hydrolase-like<br><b>Superfamily:</b> Nucleotidyl transferase<br><b>Family:</b> Class I aminoacyI-trna synthetases (RS), catalytic domain  |
| 6  | <a href="#">c5gl7A_</a> | <br>Alignment |  | 100.0      | 14     | <b>PDB header:</b> ligase<br><b>Chain:</b> A: <b>PDB Molecule:</b> methionine--trna ligase, cytoplasmic;<br><b>PDBTitle:</b> crystal structure of a truncated human cytosolic methionyl-trna2 synthetase   |
| 7  | <a href="#">c1rqgA_</a> | <br>Alignment |  | 100.0      | 16     | <b>PDB header:</b> ligase<br><b>Chain:</b> A: <b>PDB Molecule:</b> methionyl-trna synthetase;<br><b>PDBTitle:</b> methionyl-trna synthetase from pyrococcus abyssii  |
| 8  | <a href="#">c2ct8A_</a> | <br>Alignment |  | 100.0      | 19     | <b>PDB header:</b> ligase/rna<br><b>Chain:</b> A: <b>PDB Molecule:</b> methionyl-trna synthetase;<br><b>PDBTitle:</b> crystal structure of aquifex aeolicus methionyl-trna2 synthetase complexed with trna(met) and methionyl-adenylate3 analogue  |
| 9  | <a href="#">c1woyA_</a> | <br>Alignment |  | 100.0      | 21     | <b>PDB header:</b> ligase<br><b>Chain:</b> A: <b>PDB Molecule:</b> methionyl-trna synthetase;<br><b>PDBTitle:</b> crystal structure of methionyl trna synthetase y225f mutant2 from thermus thermophilus   |
| 10 | <a href="#">c4qrdA_</a> | <br>Alignment |  | 100.0      | 18     | <b>PDB header:</b> ligase/ligase inhibitor<br><b>Chain:</b> A: <b>PDB Molecule:</b> methionyl-trna synthetase;<br><b>PDBTitle:</b> structure of methionyl-trna synthetase in complex with n-(1h-2 benzimidazol-2-ylmethyl)-n'-(2,4-dichlorophenyl)-6-(morpholin-4-yl)-3 1,3,5-triazine-2,4-diamine |
| 11 | <a href="#">c1pfuA_</a> | <br>Alignment |  | 100.0      | 18     | <b>PDB header:</b> ligase<br><b>Chain:</b> A: <b>PDB Molecule:</b> methionyl-trna synthetase;<br><b>PDBTitle:</b> methionyl-trna synthetase from escherichia coli complexed2 with methionine phosphinate   |

|    |                         |           |   |       |    |   |
|----|-------------------------|-----------|---|-------|----|---|
| 12 | <a href="#">c5urbB_</a> | Alignment |    | 100.0 | 18 | <b>PDB header:</b> ligase<br><b>Chain:</b> B: <b>PDB Molecule:</b> methionine--trna ligase;<br><b>PDBTitle:</b> crystal structure of methionyl-trna synthetase (metrs) from2 acinetobacter baumannii with bound l-methionine                      |
| 13 | <a href="#">c2x1lC_</a> | Alignment |    | 100.0 | 19 | <b>PDB header:</b> ligase<br><b>Chain:</b> C: <b>PDB Molecule:</b> methionyl-trna synthetase;<br><b>PDBTitle:</b> crystal structure of mycobacterium smegmatis methionyl-trna synthetase2 in complex with methionine and adenosine                |
| 14 | <a href="#">c3kflA_</a> | Alignment |    | 100.0 | 16 | <b>PDB header:</b> ligase<br><b>Chain:</b> A: <b>PDB Molecule:</b> methionyl-trna synthetase;<br><b>PDBTitle:</b> leishmania major methionyl-trna synthetase in complex with2 methionyladenylate and pyrophosphate                                |
| 15 | <a href="#">c3ziuB_</a> | Alignment |    | 100.0 | 15 | <b>PDB header:</b> ligase<br><b>Chain:</b> B: <b>PDB Molecule:</b> leucyl-trna synthetase;<br><b>PDBTitle:</b> crystal structure of mycoplasma mobile leucyl-trna2 synthetase with leu-ams in the active site                                     |
| 16 | <a href="#">c3tunA_</a> | Alignment |    | 100.0 | 18 | <b>PDB header:</b> ligase/ligase inhibitor<br><b>Chain:</b> A: <b>PDB Molecule:</b> methionyl-trna synthetase;<br><b>PDBTitle:</b> trypanosoma brucei methionyl-trna synthetase in complex with inhibitor2 chem 1356                              |
| 17 | <a href="#">c4dlpB_</a> | Alignment |   | 100.0 | 18 | <b>PDB header:</b> ligase<br><b>Chain:</b> B: <b>PDB Molecule:</b> aminoacyl-trna synthetase, class i:aminoacyl-trna<br><b>PDBTitle:</b> crystal structure of methionyl-trna synthetase metrs from brucella2 melitensis bound to selenomethionine |
| 18 | <a href="#">c3ziuA_</a> | Alignment |  | 100.0 | 16 | <b>PDB header:</b> ligase<br><b>Chain:</b> A: <b>PDB Molecule:</b> leucyl-trna synthetase;<br><b>PDBTitle:</b> crystal structure of mycoplasma mobile leucyl-trna2 synthetase with leu-ams in the active site                                     |
| 19 | <a href="#">c4dlpA_</a> | Alignment |  | 100.0 | 18 | <b>PDB header:</b> ligase<br><b>Chain:</b> A: <b>PDB Molecule:</b> aminoacyl-trna synthetase, class i:aminoacyl-trna<br><b>PDBTitle:</b> crystal structure of methionyl-trna synthetase metrs from brucella2 melitensis bound to selenomethionine |
| 20 | <a href="#">c1gaxB_</a> | Alignment |  | 100.0 | 22 | <b>PDB header:</b> ligase/rna<br><b>Chain:</b> B: <b>PDB Molecule:</b> valyl-trna synthetase;<br><b>PDBTitle:</b> crystal structure of thermus thermophilus valyl-trna2 synthetase complexed with trna(val) and valyl-adenylate3 analogue         |
| 21 | <a href="#">d1rqga2</a> | Alignment | not modelled  | 100.0 | 17 | <b>Fold:</b> Adenine nucleotide alpha hydrolase-like<br><b>Superfamily:</b> Nucleotidylyl transferase<br><b>Family:</b> Class I aminoacyl-tRNA synthetases (RS), catalytic domain   |
| 22 | <a href="#">d1ffya3</a> | Alignment | not modelled  | 100.0 | 17 | <b>Fold:</b> Adenine nucleotide alpha hydrolase-like<br><b>Superfamily:</b> Nucleotidylyl transferase<br><b>Family:</b> Class I aminoacyl-tRNA synthetases (RS), catalytic domain   |
| 23 | <a href="#">d1ivsa4</a> | Alignment | not modelled  | 100.0 | 18 | <b>Fold:</b> Adenine nucleotide alpha hydrolase-like<br><b>Superfamily:</b> Nucleotidylyl transferase<br><b>Family:</b> Class I aminoacyl-tRNA synthetases (RS), catalytic domain   |
| 24 | <a href="#">d1ilea3</a> | Alignment | not modelled  | 100.0 | 20 | <b>Fold:</b> Adenine nucleotide alpha hydrolase-like<br><b>Superfamily:</b> Nucleotidylyl transferase<br><b>Family:</b> Class I aminoacyl-tRNA synthetases (RS), catalytic domain   |
| 25 | <a href="#">c1qu2A_</a> | Alignment | not modelled  | 100.0 | 24 | <b>PDB header:</b> ligase/rna<br><b>Chain:</b> A: <b>PDB Molecule:</b> isoleucyl-trna synthetase;<br><b>PDBTitle:</b> insights into editing from an ile-trna synthetase structure2 with trna(ile) and mupirocin                                   |
| 26 | <a href="#">d2d5ba2</a> | Alignment | not modelled  | 100.0 | 22 | <b>Fold:</b> Adenine nucleotide alpha hydrolase-like<br><b>Superfamily:</b> Nucleotidylyl transferase<br><b>Family:</b> Class I aminoacyl-tRNA synthetases (RS), catalytic domain   |
| 27 | <a href="#">c3fnrA_</a> | Alignment | not modelled  | 100.0 | 17 | <b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> arginyl-trna synthetase;<br><b>PDBTitle:</b> crystal structure of putative arginyl t-rna synthetase from2 campylobacter jejuni;   |
| 28 | <a href="#">d1pfva2</a> | Alignment | not modelled  | 100.0 | 16 | <b>Fold:</b> Adenine nucleotide alpha hydrolase-like<br><b>Superfamily:</b> Nucleotidylyl transferase<br><b>Family:</b> Class I aminoacyl-tRNA synthetases (RS), catalytic domain   |
| 29 | <a href="#">c5ah5B_</a> | Alignment | not modelled  | 100.0 | 21 | <b>PDB header:</b> ligase/rna<br><b>Chain:</b> B: <b>PDB Molecule:</b> leucine--trna ligase;  |

|    |                         |           |              |       |    |   |
|----|-------------------------|-----------|--------------|-------|----|---|
| 29 | <a href="#">cJanB</a>   | Alignment | not modelled | 100.0 | 41 | <b>PDBTitle:</b> crystal structure of the ternary complex of agrobacterium2 radiobacter k84 agnb2 leuvs-trna-leuams<br><b>PDB header:</b> ligase/rna  |
| 30 | <a href="#">c1wz2B</a>  | Alignment | not modelled | 100.0 | 23 | <b>Chain:</b> B: <b>PDB Molecule:</b> leucyl-trna synthetase;<br><b>PDBTitle:</b> the crystal structure of leucyl-trna synthetase and trna(leucine)2 complex  |
| 31 | <a href="#">d1h3na3</a> | Alignment | not modelled | 100.0 | 21 | <b>Fold:</b> Adenine nucleotide alpha hydrolase-like<br><b>Superfamily:</b> Nucleotidyl transferase<br><b>Family:</b> Class I aminoacyl-tRNA synthetases (RS), catalytic domain   |
| 32 | <a href="#">c1wkbA</a>  | Alignment | not modelled | 100.0 | 19 | <b>PDB header:</b> ligase<br><b>Chain:</b> A: <b>PDB Molecule:</b> leucyl-trna synthetase;<br><b>PDBTitle:</b> crystal structure of leucyl-trna synthetase from the2 archaeon pyrococcus horikoshii reveals a novel editing3 domain orientation                               |
| 33 | <a href="#">c1ileA</a>  | Alignment | not modelled | 100.0 | 21 | <b>PDB header:</b> aminoacyl-trna synthetase<br><b>Chain:</b> A: <b>PDB Molecule:</b> isoleucyl-trna synthetase;<br><b>PDBTitle:</b> isoleucyl-trna synthetase  |
| 34 | <a href="#">c4ariA</a>  | Alignment | not modelled | 100.0 | 19 | <b>PDB header:</b> ligase/rna<br><b>Chain:</b> A: <b>PDB Molecule:</b> leucine--trna ligase;<br><b>PDBTitle:</b> ternary complex of e. coli leucyl-trna synthetase, trna(leu) and the2 benzoxaborole an2679 in the editing conformation                                       |
| 35 | <a href="#">c5xgqB</a>  | Alignment | not modelled | 100.0 | 21 | <b>PDB header:</b> ligase<br><b>Chain:</b> B: <b>PDB Molecule:</b> methionine-trna ligase;<br><b>PDBTitle:</b> crystal structure of apo form (free-state) mycobacterium tuberculosis2 methionyl-trna synthetase   |
| 36 | <a href="#">c6ao8A</a>  | Alignment | not modelled | 100.0 | 17 | <b>PDB header:</b> ligase<br><b>Chain:</b> A: <b>PDB Molecule:</b> arginine--trna ligase;<br><b>PDBTitle:</b> crystal structure of arginyl-trna synthetase from neisseria2 gonorrhoeae in complex with arginine   |
| 37 | <a href="#">d1irxa2</a> | Alignment | not modelled | 100.0 | 15 | <b>Fold:</b> Adenine nucleotide alpha hydrolase-like<br><b>Superfamily:</b> Nucleotidyl transferase<br><b>Family:</b> Class I aminoacyl-tRNA synthetases (RS), catalytic domain   |
| 38 | <a href="#">c2bytD</a>  | Alignment | not modelled | 100.0 | 27 | <b>PDB header:</b> synthetase<br><b>Chain:</b> D: <b>PDB Molecule:</b> leucyl-trna synthetase;<br><b>PDBTitle:</b> thermus thermophilus leucyl-trna synthetase complexed with2 a trnaleu transcript in the post-editing conformation  |
| 39 | <a href="#">c4obyA</a>  | Alignment | not modelled | 100.0 | 18 | <b>PDB header:</b> ligase<br><b>Chain:</b> A: <b>PDB Molecule:</b> arginine--trna ligase;<br><b>PDBTitle:</b> crystal structure of e.coli arginyl-trna synthetase and ligand binding2 studies revealed key residues in arginine recognition                                   |
| 40 | <a href="#">c1obhA</a>  | Alignment | not modelled | 100.0 | 24 | <b>PDB header:</b> synthetase<br><b>Chain:</b> A: <b>PDB Molecule:</b> leucyl-trna synthetase;<br><b>PDBTitle:</b> leucyl-trna synthetase from thermus thermophilus complexed2 with a pre-transfer editing substrate analogue in both3 synthetic active site and editing site |
| 41 | <a href="#">c6q8aA</a>  | Alignment | not modelled | 100.0 | 20 | <b>PDB header:</b> ligase<br><b>Chain:</b> A: <b>PDB Molecule:</b> leucine--trna ligase;<br><b>PDBTitle:</b> neisseria gonorrhoeae leucyl-trna synthetase in complex with 5'-o-(n-2 (l-leucyl)-sulfamoyl)cytidine   |
| 42 | <a href="#">c5jldA</a>  | Alignment | not modelled | 100.0 | 13 | <b>PDB header:</b> ligase<br><b>Chain:</b> A: <b>PDB Molecule:</b> arginyl-trna synthetase, putative;<br><b>PDBTitle:</b> crystal structure of arginyl-trna synthetase from plasmodium2 falciparum (pfrs)   |
| 43 | <a href="#">c1iq0A</a>  | Alignment | not modelled | 100.0 | 15 | <b>PDB header:</b> ligase<br><b>Chain:</b> A: <b>PDB Molecule:</b> arginyl-trna synthetase;<br><b>PDBTitle:</b> thermus thermophilus arginyl-trna synthetase  |
| 44 | <a href="#">c2zufA</a>  | Alignment | not modelled | 100.0 | 15 | <b>PDB header:</b> ligase/rna<br><b>Chain:</b> A: <b>PDB Molecule:</b> arginyl-trna synthetase;<br><b>PDBTitle:</b> crystal structure of pyrococcus horikoshii arginyl-trna2 synthetase complexed with trna(arg)  |
| 45 | <a href="#">d1f7ua2</a> | Alignment | not modelled | 100.0 | 16 | <b>Fold:</b> Adenine nucleotide alpha hydrolase-like<br><b>Superfamily:</b> Nucleotidyl transferase<br><b>Family:</b> Class I aminoacyl-tRNA synthetases (RS), catalytic domain   |
| 46 | <a href="#">d1qtra2</a> | Alignment | not modelled | 100.0 | 14 | <b>Fold:</b> Adenine nucleotide alpha hydrolase-like<br><b>Superfamily:</b> Nucleotidyl transferase<br><b>Family:</b> Class I aminoacyl-tRNA synthetases (RS), catalytic domain   |
| 47 | <a href="#">c4r3zB</a>  | Alignment | not modelled | 100.0 | 19 | <b>PDB header:</b> protein binding/ligase<br><b>Chain:</b> B: <b>PDB Molecule:</b> arginine--trna ligase, cytoplasmic;<br><b>PDBTitle:</b> crystal structure of human argrs-glnrs-aimp1 complex   |
| 48 | <a href="#">c1g59A</a>  | Alignment | not modelled | 100.0 | 16 | <b>PDB header:</b> ligase/rna<br><b>Chain:</b> A: <b>PDB Molecule:</b> glutamyl-trna synthetase;<br><b>PDBTitle:</b> glutamyl-trna synthetase complexed with trna(glu).   |
| 49 | <a href="#">c1f7uA</a>  | Alignment | not modelled | 100.0 | 17 | <b>PDB header:</b> ligase/rna<br><b>Chain:</b> A: <b>PDB Molecule:</b> arginyl-trna synthetase;<br><b>PDBTitle:</b> crystal structure of the arginyl-trna synthetase complexed with the2 trna(arg) and l-arg  |
| 50 | <a href="#">c3afhA</a>  | Alignment | not modelled | 100.0 | 16 | <b>PDB header:</b> ligase<br><b>Chain:</b> A: <b>PDB Molecule:</b> glutamyl-trna synthetase 2;<br><b>PDBTitle:</b> crystal structure of thermotoga maritima nondiscriminating glutamyl-2 trna synthetase in complex with a glutamyl-amp analog                                |
| 51 | <a href="#">c6b1pA</a>  | Alignment | not modelled | 100.0 | 20 | <b>PDB header:</b> ligase<br><b>Chain:</b> A: <b>PDB Molecule:</b> glutamate--trna ligase 1;<br><b>PDBTitle:</b> crystal structure of glutamate-trna synthetase from helicobacter2 pylori   |
| 52 | <a href="#">c2ja2A</a>  | Alignment | not modelled | 100.0 | 15 | <b>PDB header:</b> ligase<br><b>Chain:</b> A: <b>PDB Molecule:</b> glutamyl-trna synthetase;<br><b>PDBTitle:</b> mycobacterium tuberculosis glutamyl-trna synthetase  |
| 53 | <a href="#">d1iq0a2</a> | Alignment | not modelled | 100.0 | 14 | <b>Fold:</b> Adenine nucleotide alpha hydrolase-like<br><b>Superfamily:</b> Nucleotidyl transferase<br><b>Family:</b> Class I aminoacyl-tRNA synthetases (RS), catalytic domain   |
| 54 | <a href="#">c5h4vE</a>  | Alignment | not modelled | 100.0 | 19 | <b>PDB header:</b> ligase<br><b>Chain:</b> E: <b>PDB Molecule:</b> glutamate--trna ligase;<br><b>PDBTitle:</b> structure of glutamyl-trna synthetase (xoo1504) from xanthomonas2 oryzae pv. oryzae<br><b>PDB header:</b> ligase   |

|    |                         |           |              |       |    |  |
|----|-------------------------|-----------|--------------|-------|----|--|
| 55 | <a href="#">c4q2tB_</a> | Alignment | not modelled | 100.0 | 19 | <b>Chain:</b> B: <b>PDB Molecule:</b> arginine--trna ligase, cytoplasmic;<br><b>PDBTitle:</b> crystal structure of arginyl-trna synthetase complexed with l-arginine   |
| 56 | <a href="#">c2cfoA_</a> | Alignment | not modelled | 100.0 | 19 | <b>PDB header:</b> ligase<br><b>Chain:</b> A: <b>PDB Molecule:</b> glutamyl-trna synthetase;<br><b>PDBTitle:</b> non-discriminating glutamyl-trna synthetase from2 thermosynechococcus elongatus in complex with glu   |
| 57 | <a href="#">c4griB_</a> | Alignment | not modelled | 100.0 | 13 | <b>PDB header:</b> ligase<br><b>Chain:</b> B: <b>PDB Molecule:</b> glutamate--trna ligase;<br><b>PDBTitle:</b> crystal structure of a glutamyl-trna synthetase glurs from borrelia2 burgdorferi bound to glutamic acid and zinc  |
| 58 | <a href="#">c5tgtA_</a> | Alignment | not modelled | 100.0 | 13 | <b>PDB header:</b> ligase<br><b>Chain:</b> A: <b>PDB Molecule:</b> glutamate--trna ligase;<br><b>PDBTitle:</b> crystal structure of glytamyl-trna synthetase glurs from pseudomonas2 aeruginosa  |
| 59 | <a href="#">c1irxA_</a> | Alignment | not modelled | 100.0 | 14 | <b>PDB header:</b> ligase<br><b>Chain:</b> A: <b>PDB Molecule:</b> lysyl-trna synthetase;<br><b>PDBTitle:</b> crystal structure of class i lysyl-trna synthetase   |
| 60 | <a href="#">c2o5rA_</a> | Alignment | not modelled | 100.0 | 18 | <b>PDB header:</b> ligase<br><b>Chain:</b> A: <b>PDB Molecule:</b> glutamyl-trna synthetase 1;<br><b>PDBTitle:</b> crystal structure of glutamyl-trna synthetase 1 (ec 6.1.1.17)2 (glutamate-trna ligase 1) (glurs 1) (tm1351) from thermotoga maritima3 at 2.5 a resolution |
| 61 | <a href="#">c1exdA_</a> | Alignment | not modelled | 100.0 | 12 | <b>PDB header:</b> ligase/rna<br><b>Chain:</b> A: <b>PDB Molecule:</b> glutaminyl-trna synthetase;<br><b>PDBTitle:</b> crystal structure of a tight-binding glutamine trna bound2 to glutamine aminoacyl trna synthetase   |
| 62 | <a href="#">c2hz7A_</a> | Alignment | not modelled | 100.0 | 17 | <b>PDB header:</b> ligase<br><b>Chain:</b> A: <b>PDB Molecule:</b> glutaminyl-trna synthetase;<br><b>PDBTitle:</b> crystal structure of the glutaminyl-trna synthetase from deinococcus2 radiodurans   |
| 63 | <a href="#">c4p2bA_</a> | Alignment | not modelled | 100.0 | 16 | <b>PDB header:</b> ligase<br><b>Chain:</b> A: <b>PDB Molecule:</b> glutamine aminoacyl-trna synthetase;<br><b>PDBTitle:</b> crystal structure of the apo form of the glutaminyl-trna synthetase2 catalytic domain from toxoplasma gondii.                                    |
| 64 | <a href="#">c4g6zA_</a> | Alignment | not modelled | 100.0 | 18 | <b>PDB header:</b> ligase<br><b>Chain:</b> A: <b>PDB Molecule:</b> glutamate-trna ligase;<br><b>PDBTitle:</b> crystal structure of a glutamyl-trna synthetase glurs from2 burkholderia thailandensis bound to l-glutamate  |
| 65 | <a href="#">c3a10C_</a> | Alignment | not modelled | 100.0 | 18 | <b>PDB header:</b> ligase/rna<br><b>Chain:</b> C: <b>PDB Molecule:</b> glutamyl-trna(gln) amidotransferase subunit c,linker,<br><b>PDBTitle:</b> crystal structure of the glutamine transamidosome from thermotoga2 maritima in the glutamylation state.                     |
| 66 | <a href="#">c6b1zA_</a> | Alignment | not modelled | 100.0 | 17 | <b>PDB header:</b> ligase<br><b>Chain:</b> A: <b>PDB Molecule:</b> glutamate--trna ligase;<br><b>PDBTitle:</b> crystal structure of glutamate-trna synthetase from elizabethkingia2 anophelis  |
| 67 | <a href="#">c4r3zC_</a> | Alignment | not modelled | 99.9  | 14 | <b>PDB header:</b> protein binding/ligase<br><b>Chain:</b> C: <b>PDB Molecule:</b> glutamine--trna ligase;<br><b>PDBTitle:</b> crystal structure of human argrs-glnrs-aimp1 complex  |
| 68 | <a href="#">c5zdoA_</a> | Alignment | not modelled | 99.9  | 18 | <b>PDB header:</b> ligase<br><b>Chain:</b> A: <b>PDB Molecule:</b> glutamine-trna ligase;<br><b>PDBTitle:</b> crystal structure analysis of ttqrs in co-crystallised with atp  |
| 69 | <a href="#">c5bnzA_</a> | Alignment | not modelled | 99.9  | 12 | <b>PDB header:</b> ligase<br><b>Chain:</b> A: <b>PDB Molecule:</b> glutamine--trna ligase;<br><b>PDBTitle:</b> crystal structure of glutamine-trna ligase /glutaminyl-trna synthetase2 (glnrs) from pseudomonas aeruginosa   |
| 70 | <a href="#">c4h3sA_</a> | Alignment | not modelled | 99.9  | 16 | <b>PDB header:</b> ligase<br><b>Chain:</b> A: <b>PDB Molecule:</b> glutamine-trna ligase;<br><b>PDBTitle:</b> the structure of glutaminyl-trna synthetase from saccharomyces2 cerevisiae   |
| 71 | <a href="#">d1j09a2</a> | Alignment | not modelled | 99.9  | 17 | <b>Fold:</b> Adenine nucleotide alpha hydrolase-like<br><b>Superfamily:</b> Nucleotidyl transferase<br><b>Family:</b> Class I aminoacyl-tRNA synthetases (RS), catalytic domain  |
| 72 | <a href="#">c4ye6A_</a> | Alignment | not modelled | 99.9  | 13 | <b>PDB header:</b> ligase<br><b>Chain:</b> A: <b>PDB Molecule:</b> glutamine--trna ligase;<br><b>PDBTitle:</b> the crystal structure of the intact human glnrs   |
| 73 | <a href="#">c3aiiA_</a> | Alignment | not modelled | 99.9  | 18 | <b>PDB header:</b> ligase<br><b>Chain:</b> A: <b>PDB Molecule:</b> glutamyl-trna synthetase;<br><b>PDBTitle:</b> archaeal non-discriminating glutamyl-trna synthetase from2 methanothermobacter thermautotrophicus   |
| 74 | <a href="#">d1nzza_</a> | Alignment | not modelled | 99.8  | 14 | <b>Fold:</b> Adenine nucleotide alpha hydrolase-like<br><b>Superfamily:</b> Nucleotidyl transferase<br><b>Family:</b> Class I aminoacyl-tRNA synthetases (RS), catalytic domain  |
| 75 | <a href="#">c2cybA_</a> | Alignment | not modelled | 99.0  | 22 | <b>PDB header:</b> ligase<br><b>Chain:</b> A: <b>PDB Molecule:</b> tyrosyl-trna synthetase;<br><b>PDBTitle:</b> crystal structure of tyrosyl-trna synthetase complexed with2 l-tyrosine from archaeoglobus fulgidus  |
| 76 | <a href="#">c6mtkA_</a> | Alignment | not modelled | 99.0  | 14 | <b>PDB header:</b> ligase<br><b>Chain:</b> A: <b>PDB Molecule:</b> tryptophanyl-trna synthetase;<br><b>PDBTitle:</b> crystal structure of tryptophanyl-trna synthetase from elizabethkingia2 anophelis nuhp1   |
| 77 | <a href="#">c1h3eA_</a> | Alignment | not modelled | 98.9  | 21 | <b>PDB header:</b> ligase<br><b>Chain:</b> A: <b>PDB Molecule:</b> tyrosyl-trna synthetase;<br><b>PDBTitle:</b> tyrosyl-trna synthetase from thermus thermophilus complexed with wild-2 type trnatyr(gua) and with atp and tyrosinol   |
| 78 | <a href="#">c2el7A_</a> | Alignment | not modelled | 98.9  | 12 | <b>PDB header:</b> ligase<br><b>Chain:</b> A: <b>PDB Molecule:</b> tryptophanyl-trna synthetase;<br><b>PDBTitle:</b> crystal structure of tryptophanyl-trna synthetase from thermus2 thermophilus  |
| 79 | <a href="#">c6ncrB_</a> | Alignment | not modelled | 98.9  | 17 | <b>PDB header:</b> ligase<br><b>Chain:</b> B: <b>PDB Molecule:</b> tryptophan--trna ligase;<br><b>PDBTitle:</b> crystal structure of tryptophan-trna ligase from chlamydia trachomatis2 with bound l-tryptophan  |
| 80 | <a href="#">c5tevA_</a> | Alignment | not modelled | 98.8  | 14 | <b>PDB header:</b> ligase<br><b>Chain:</b> A: <b>PDB Molecule:</b> tryptophan--trna ligase;<br><b>PDBTitle:</b> crystal structure of a tryptophanyl-trna synthetase from   |

|     |                         |           |              |      |    |  |
|-----|-------------------------|-----------|--------------|------|----|--|
|     |                         |           |              |      |    | neisseria2 gonorrhoeae, apo  |
| 81  | <a href="#">c6otjA_</a> | Alignment | not modelled | 98.8 | 17 | <b>PDB header:</b> ligase<br><b>Chain:</b> A: <b>PDB Molecule:</b> tyrosine--trna ligase;<br><b>PDBTitle:</b> crystal structure of tyrosyl-trna synthetase from neisseria2 gonorrhoeae with bound l-tyr  |
| 82  | <a href="#">c2g36A_</a> | Alignment | not modelled | 98.7 | 18 | <b>PDB header:</b> ligase<br><b>Chain:</b> A: <b>PDB Molecule:</b> tryptophanyl-trna synthetase;<br><b>PDBTitle:</b> crystal structure of tryptophanyl-trna synthetase (ec 6.1.1.2)2 (tryptophan-trna ligase)(trprs) (tm0492) from thermotoga maritima at3 2.50 a resolution |
| 83  | <a href="#">c2cyaA_</a> | Alignment | not modelled | 98.7 | 19 | <b>PDB header:</b> ligase<br><b>Chain:</b> A: <b>PDB Molecule:</b> tyrosyl-trna synthetase;<br><b>PDBTitle:</b> crystal structure of tyrosyl-trna synthetase from aeropyrum pernix   |
| 84  | <a href="#">c2rkjM_</a> | Alignment | not modelled | 98.7 | 16 | <b>PDB header:</b> ligase/rna<br><b>Chain:</b> M: <b>PDB Molecule:</b> tyrosyl-trna synthetase;<br><b>PDBTitle:</b> cocrystal structure of a tyrosyl-trna synthetase splicing factor with2 a group i intron rna  |
| 85  | <a href="#">c3jxeB_</a> | Alignment | not modelled | 98.7 | 15 | <b>PDB header:</b> ligase<br><b>Chain:</b> B: <b>PDB Molecule:</b> tryptophanyl-trna synthetase;<br><b>PDBTitle:</b> crystal structure of pyrococcus horikoshii tryptophanyl-trna2 synthetase in complex with trpamp   |
| 86  | <a href="#">c2janD_</a> | Alignment | not modelled | 98.7 | 18 | <b>PDB header:</b> ligase<br><b>Chain:</b> D: <b>PDB Molecule:</b> tyrosyl-trna synthetase;<br><b>PDBTitle:</b> tyrosyl-trna synthetase from mycobacterium tuberculosis in2 unliganded state   |
| 87  | <a href="#">c3m5wB_</a> | Alignment | not modelled | 98.7 | 12 | <b>PDB header:</b> ligase<br><b>Chain:</b> B: <b>PDB Molecule:</b> tryptophanyl-trna synthetase;<br><b>PDBTitle:</b> crystal structure of tryptophanyl-trna synthetase from campylobacter2 jejuni  |
| 88  | <a href="#">c3a05A_</a> | Alignment | not modelled | 98.7 | 21 | <b>PDB header:</b> ligase<br><b>Chain:</b> A: <b>PDB Molecule:</b> tryptophanyl-trna synthetase;<br><b>PDBTitle:</b> crystal structure of tryptophanyl-trna synthetase from2 hyperthermophilic archaeon, aeropyrum pernix k1 complex3 with tryptophan                        |
| 89  | <a href="#">d1jila_</a> | Alignment | not modelled | 98.6 | 14 | <b>Fold:</b> Adenine nucleotide alpha hydrolase-like<br><b>Superfamily:</b> Nucleotidylyl transferase<br><b>Family:</b> Class I aminoacyl-tRNA synthetases (RS), catalytic domain  |
| 90  | <a href="#">d1h3fa1</a> | Alignment | not modelled | 98.6 | 19 | <b>Fold:</b> Adenine nucleotide alpha hydrolase-like<br><b>Superfamily:</b> Nucleotidylyl transferase<br><b>Family:</b> Class I aminoacyl-tRNA synthetases (RS), catalytic domain  |
| 91  | <a href="#">c3vgjB_</a> | Alignment | not modelled | 98.6 | 14 | <b>PDB header:</b> ligase<br><b>Chain:</b> B: <b>PDB Molecule:</b> tyrosyl-trna synthetase, putative;<br><b>PDBTitle:</b> crystal of plasmodium falciparum tyrosyl-trna synthetase (pftyrrs)in2 complex with adenylate analog  |
| 92  | <a href="#">c3prhB_</a> | Alignment | not modelled | 98.6 | 13 | <b>PDB header:</b> ligase<br><b>Chain:</b> B: <b>PDB Molecule:</b> tryptophanyl-trna synthetase;<br><b>PDBTitle:</b> tryptophanyl-trna synthetase val144pro mutant from b. subtilis  |
| 93  | <a href="#">c2j5bA_</a> | Alignment | not modelled | 98.6 | 26 | <b>PDB header:</b> ligase<br><b>Chain:</b> A: <b>PDB Molecule:</b> tyrosyl-trna synthetase;<br><b>PDBTitle:</b> structure of the tyrosyl trna synthetase from acanthamoeba polyphaga2 mimivirus complexed with tyrosynol   |
| 94  | <a href="#">c6n0wA_</a> | Alignment | not modelled | 98.5 | 16 | <b>PDB header:</b> ligase<br><b>Chain:</b> A: <b>PDB Molecule:</b> tyrosine--trna ligase;<br><b>PDBTitle:</b> crystal structure of a tyrosine--trna ligase from elizabethkingia2 anophelis   |
| 95  | <a href="#">c1yi8C_</a> | Alignment | not modelled | 98.5 | 17 | <b>PDB header:</b> ligase<br><b>Chain:</b> C: <b>PDB Molecule:</b> tryptophanyl-trna synthetase;<br><b>PDBTitle:</b> crystal structure of tryptophanyl trna synthetase ii from deinococcus2 radiodurans in complex with l-trp  |
| 96  | <a href="#">c3hztD_</a> | Alignment | not modelled | 98.5 | 15 | <b>PDB header:</b> ligase<br><b>Chain:</b> D: <b>PDB Molecule:</b> tryptophanyl-trna synthetase;<br><b>PDBTitle:</b> tryptophanyl-trna synthetase homolog from entamoeba histolytica   |
| 97  | <a href="#">c3tzeA_</a> | Alignment | not modelled | 98.5 | 20 | <b>PDB header:</b> ligase<br><b>Chain:</b> A: <b>PDB Molecule:</b> tryptophanyl-trna synthetase;<br><b>PDBTitle:</b> crystal structure of a tryptophanyl-trna synthetase from2 encephalitozoon cuniculi bound to tryptophan  |
| 98  | <a href="#">c1jiiA_</a> | Alignment | not modelled | 98.5 | 16 | <b>PDB header:</b> ligase<br><b>Chain:</b> A: <b>PDB Molecule:</b> tyrosyl-trna synthetase;<br><b>PDBTitle:</b> crystal structure of s. aureus tyrrs in complex with sb-219383   |
| 99  | <a href="#">c1x8xA_</a> | Alignment | not modelled | 98.4 | 15 | <b>PDB header:</b> ligase<br><b>Chain:</b> A: <b>PDB Molecule:</b> tyrosyl-trna synthetase;<br><b>PDBTitle:</b> tyrosyl t-rna synthetase from e.coli complexed with tyrosine   |
| 100 | <a href="#">c3focB_</a> | Alignment | not modelled | 98.4 | 17 | <b>PDB header:</b> ligase<br><b>Chain:</b> B: <b>PDB Molecule:</b> tryptophanyl-trna synthetase;<br><b>PDBTitle:</b> tryptophanyl-trna synthetase from giardia lamblia   |
| 101 | <a href="#">c4j75B_</a> | Alignment | not modelled | 98.4 | 16 | <b>PDB header:</b> ligase<br><b>Chain:</b> B: <b>PDB Molecule:</b> tryptophanyl-trna synthetase;<br><b>PDBTitle:</b> crystal structure of a parasite trna synthetase, product-bound  |
| 102 | <a href="#">c3kt3D_</a> | Alignment | not modelled | 98.4 | 17 | <b>PDB header:</b> ligase<br><b>Chain:</b> D: <b>PDB Molecule:</b> tryptophanyl-trna synthetase, cytoplasmic;<br><b>PDBTitle:</b> crystal structure of s. cerevisiae tryptophanyl-trna synthetase in2 complex with trpamp  |
| 103 | <a href="#">c5ekdA_</a> | Alignment | not modelled | 98.4 | 13 | <b>PDB header:</b> ligase/antibiotic<br><b>Chain:</b> A: <b>PDB Molecule:</b> tryptophan--trna ligase, mitochondrial;<br><b>PDBTitle:</b> human mitochondrial tryptophanyl-trna synthetase bound by indolmycin2 and mn*atp.  |
| 104 | <a href="#">d1i6la_</a> | Alignment | not modelled | 98.4 | 12 | <b>Fold:</b> Adenine nucleotide alpha hydrolase-like<br><b>Superfamily:</b> Nucleotidylyl transferase<br><b>Family:</b> Class I aminoacyl-tRNA synthetases (RS), catalytic domain  |
| 105 | <a href="#">d1li5a1</a> | Alignment | not modelled | 98.3 | 30 | <b>Fold:</b> Anticodon-binding domain of a subclass of class I aminoacyl-tRNA synthetases<br><b>Superfamily:</b> Anticodon-binding domain of a subclass of class I aminoacyl-tRNA synthetases<br><b>Family:</b> Anticodon-binding domain of a subclass of class I aminoacyl- |

|     |                         |           |              |      |    |  |
|-----|-------------------------|-----------|--------------|------|----|--|
|     |                         |           |              |      |    | tRNA synthetases   |
| 106 | <a href="#">c5ihxB_</a> | Alignment | not modelled | 98.2 | 13 | <b>PDB header:</b> ligase<br><b>Chain:</b> B: <b>PDB Molecule:</b> tyrosine--trna ligase, mitochondrial;<br><b>PDBTitle:</b> crystal structure of a c-terminally truncated aspergillus nidulans2 mitochondrial tyrosyl-trna synthetase   |
| 107 | <a href="#">c6byqA_</a> | Alignment | not modelled | 98.2 | 20 | <b>PDB header:</b> ligase<br><b>Chain:</b> A: <b>PDB Molecule:</b> tyrosine--trna ligase;<br><b>PDBTitle:</b> crystal structure of tyrosine-trna ligase from helicobacter pylori g27   |
| 108 | <a href="#">c2cycB_</a> | Alignment | not modelled | 98.1 | 16 | <b>PDB header:</b> ligase<br><b>Chain:</b> B: <b>PDB Molecule:</b> tyrosyl-trna synthetase;<br><b>PDBTitle:</b> crystal structure of tyrosyl-trna synthetase complexed with l-tyrosine2 from pyrococcus horikoshii   |
| 109 | <a href="#">c3n9iA_</a> | Alignment | not modelled | 98.1 | 14 | <b>PDB header:</b> ligase<br><b>Chain:</b> A: <b>PDB Molecule:</b> tryptophanyl-trna synthetase;<br><b>PDBTitle:</b> crystal structure of tryptophanyl-trna synthetase from yersinia pestis2 co92  |
| 110 | <a href="#">c2quiB_</a> | Alignment | not modelled | 98.1 | 16 | <b>PDB header:</b> ligase<br><b>Chain:</b> B: <b>PDB Molecule:</b> tryptophanyl-trna synthetase;<br><b>PDBTitle:</b> crystal structures of human tryptophanyl-trna synthetase in2 complex with tryptophanamide and atp   |
| 111 | <a href="#">c3p0jD_</a> | Alignment | not modelled | 98.1 | 17 | <b>PDB header:</b> ligase<br><b>Chain:</b> D: <b>PDB Molecule:</b> tyrosyl-trna synthetase;<br><b>PDBTitle:</b> leishmania major tyrosyl-trna synthetase in complex with tyrosinol,2 triclinic crystal form 1  |
| 112 | <a href="#">c2yy5C_</a> | Alignment | not modelled | 98.1 | 15 | <b>PDB header:</b> ligase<br><b>Chain:</b> C: <b>PDB Molecule:</b> tryptophanyl-trna synthetase;<br><b>PDBTitle:</b> crystal structure of tryptophanyl-trna synthetase from mycoplasma2 pneumoniae   |
| 113 | <a href="#">d2ts1a_</a> | Alignment | not modelled | 98.1 | 19 | <b>Fold:</b> Adenine nucleotide alpha hydrolase-like<br><b>Superfamily:</b> Nucleotidylyl transferase<br><b>Family:</b> Class I aminoacyl-tRNA synthetases (RS), catalytic domain  |
| 114 | <a href="#">c2ts1A_</a> | Alignment | not modelled | 98.1 | 19 | <b>PDB header:</b> ligase (synthetase)<br><b>Chain:</b> A: <b>PDB Molecule:</b> tyrosyl-trna synthetase;<br><b>PDBTitle:</b> structure of tyrosyl-trna synthetase refined at 2.3 angstroms2 resolution. interaction of the enzyme with the tyrosyl adenylate3 intermediate                   |
| 115 | <a href="#">d1u0bb1</a> | Alignment | not modelled | 98.0 | 25 | <b>Fold:</b> Anticodon-binding domain of a subclass of class I aminoacyl-tRNA synthetases<br><b>Superfamily:</b> Anticodon-binding domain of a subclass of class I aminoacyl-tRNA synthetases<br><b>Family:</b> Anticodon-binding domain of a subclass of class I aminoacyl-tRNA synthetases |
| 116 | <a href="#">c3hv0A_</a> | Alignment | not modelled | 97.4 | 23 | <b>PDB header:</b> ligase<br><b>Chain:</b> A: <b>PDB Molecule:</b> tryptophanyl-trna synthetase;<br><b>PDBTitle:</b> tryptophanyl-trna synthetase from cryptosporidium parvum  |
| 117 | <a href="#">d1j1ua_</a> | Alignment | not modelled | 97.4 | 15 | <b>Fold:</b> Adenine nucleotide alpha hydrolase-like<br><b>Superfamily:</b> Nucleotidylyl transferase<br><b>Family:</b> Class I aminoacyl-tRNA synthetases (RS), catalytic domain  |
| 118 | <a href="#">c2dlcX_</a> | Alignment | not modelled | 97.3 | 10 | <b>PDB header:</b> ligase/trna<br><b>Chain:</b> X: <b>PDB Molecule:</b> tyrosyl-trna synthetase, cytoplasmic;<br><b>PDBTitle:</b> crystal structure of the ternary complex of yeast tyrosyl-trna2 synthetase   |
| 119 | <a href="#">d1n3la_</a> | Alignment | not modelled | 96.9 | 11 | <b>Fold:</b> Adenine nucleotide alpha hydrolase-like<br><b>Superfamily:</b> Nucleotidylyl transferase<br><b>Family:</b> Class I aminoacyl-tRNA synthetases (RS), catalytic domain  |
| 120 | <a href="#">c3i05B_</a> | Alignment | not modelled | 96.9 | 20 | <b>PDB header:</b> ligase<br><b>Chain:</b> B: <b>PDB Molecule:</b> tryptophanyl-trna synthetase;<br><b>PDBTitle:</b> tryptophanyl-trna synthetase from trypanosoma brucei  |