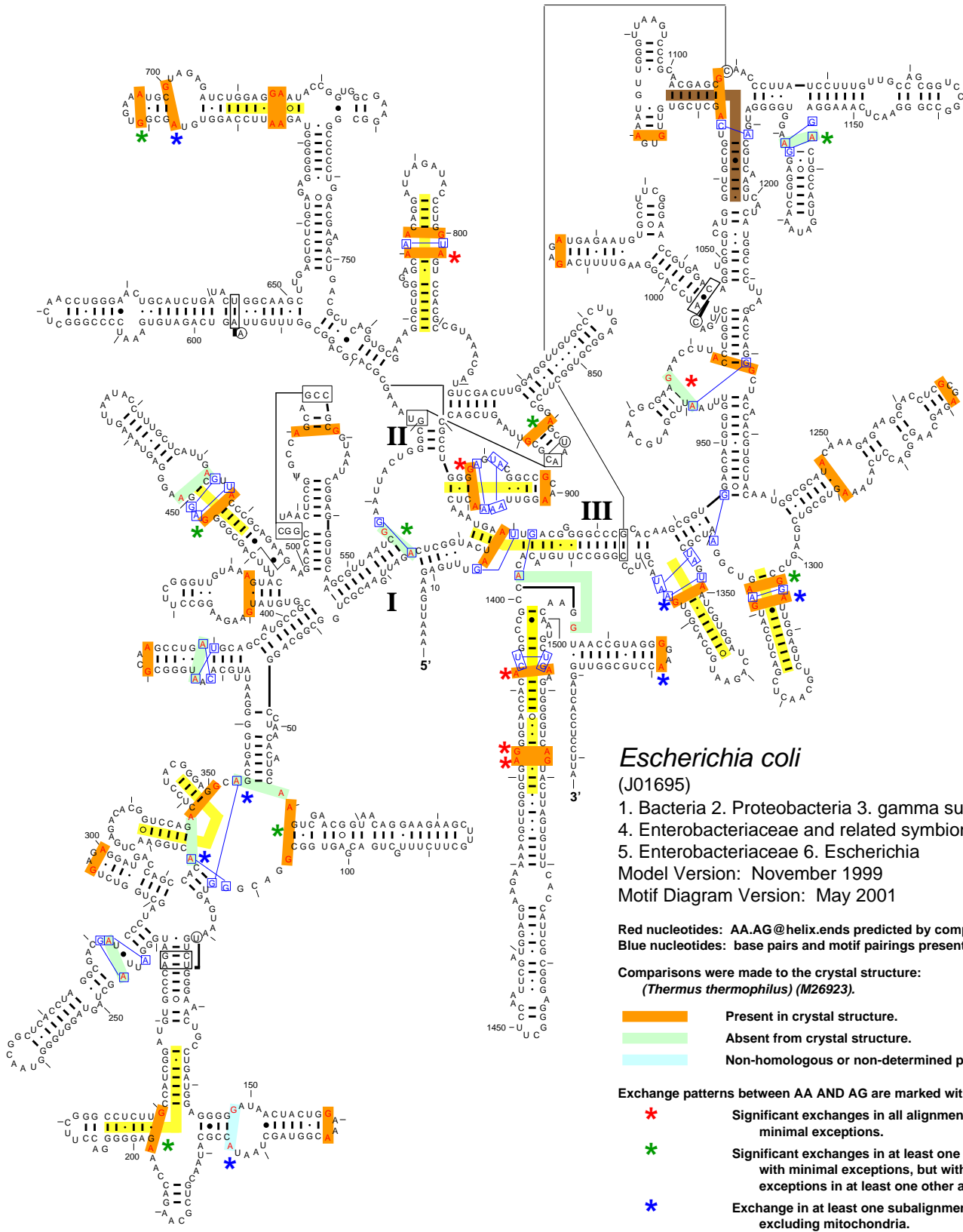


# AA.AG@helix.ends: small subunit ribosomal RNA Comparison of Predicted and Crystal Structures



## *Escherichia coli*

(J01695)

1. Bacteria 2. Proteobacteria 3. gamma subdivision
  4. Enterobacteriaceae and related symbionts
  5. Enterobacteriaceae 6. Escherichia
- Model Version: November 1999  
Motif Diagram Version: May 2001

Red nucleotides: AA.AG@helix.ends predicted by comparative analysis.  
Blue nucleotides: base pairs and motif pairings present in crystal structure.

Comparisons were made to the crystal structure:  
(*Thermus thermophilus*) (M26923).

- Present in crystal structure.
- Absent from crystal structure.
- Non-homologous or non-determined pairing.

Exchange patterns between AA AND AG are marked with \* .

- \* Significant exchanges in all alignments with minimal exceptions.
- \* Significant exchanges in at least one alignment with minimal exceptions, but with more exceptions in at least one other alignment.
- \* Exchange in at least one subalignment, excluding mitochondria.

(none) Invariant AA OR AG.

Coaxial stacking possibilities for crystal structure interactions adjacent to AA.AG@helix.ends:

- Potential interaction; not present.
- Coaxial stacking present in crystal structure.