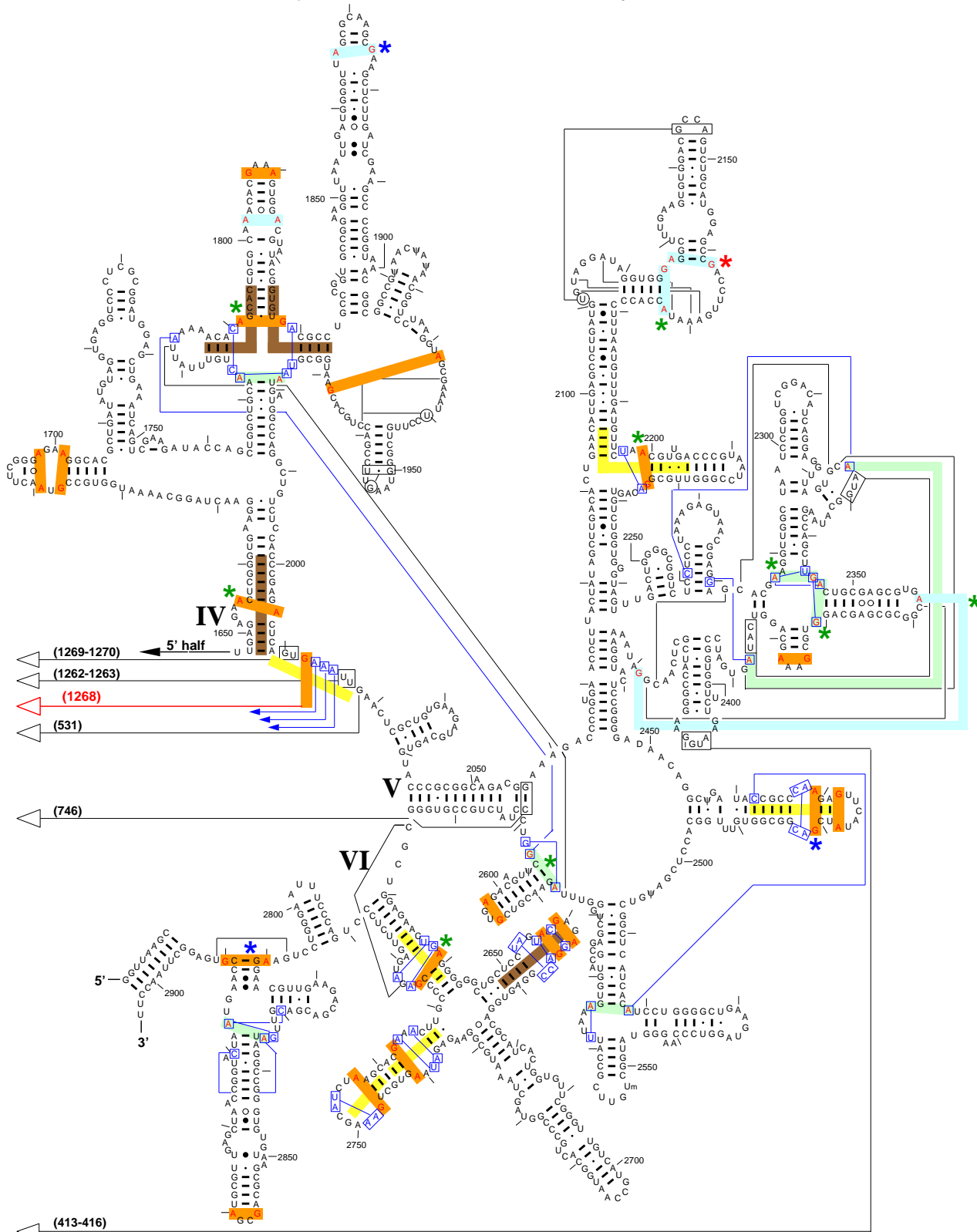


# AA.AG@helix.ends: large subunit ribosomal RNA - 3' half

## 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: (*Haloarcula marismortui*) (AF034620).

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

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

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

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.