

## Poster Presentation

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### *S9 is Essential to Ribosomal Function and LUCA is a Micrococcineae*

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A minimum universal fingerprint has been designed that captures and aligns over 10,116 bacterial, 939 eukaryotic, and 221 archaeal members of the family of ribosomal proteins that are labeled as S9 in most bacteria and archaea and S9 or S16 in eukaryota. All of the aligned S9/16 ribosomal proteins have five residues whose identities are 100% conserved and 58 residues whose identities are conserved at 70% or greater. Full length accurate alignment of all S9s was achieved by locating Gly(G), Ala(A), Arg(R) and Pro(P) residues that are highly conserved and by accurate location of sites of insertion and deletion. Gly residues in regions of the Ramachandran plot where other amino acids are rarely tolerated appear to be immutable. Crystal structures of bacterial, plant, fungal, and mammalian ribosomes support the conclusion that all S9/16 RibPros retain a common fold. All S9/16s end in a fully conserved Arg residue that extends deep into the ribosome forming hydrogen bonds to nucleotide residues of rRNA and the anticodon sequence of tRNAs. The significance of this remarkable conservation of amino acid identity, its interaction with tRNA and critical role in ribosome function has previously escaped detection. Hydrogen bonds link the terminal Arg of S9/16 with the tRNA in crystallographically determined structures in which the tRNA is in the polymerase (P) and exit(E) sites. Two ribosomal proteins of the large subunit (L28 and L35) form hydrogen bonds to nucleotides of the acceptor stem. A histidine of L35 that contacts the acceptor stem is conserved in 8000 L35s. Examination of the DNA encoding the S9s of all 730 species of actinobacteria reveals that the majority of them use only codons ending in G or C, have antisense open reading frames, rarely contain cysteine, and have GTG (Val) as their start code. Thus far examination of DNA encoding other ribosomal proteins of the small subunit (S2,S4,S7,S11,S19) finds a similar pattern only in S4s of Micrococcineae (a class of actinobacteria). These data indicate a critical role for S9/16 in ribosomal function throughout evolution and indicate that the last universal common ancestor is a Micrococcineae.

**Keywords:** Ribosome, GARP alignment, GTG Start code