Ribosomes are the universal cellular machines that translate the genetic code into proteins in all organisms. The ribosome’s active site for peptide bond formation (called the peptidyl transferase center) resides within a universal highly conserved region of the contemporary ribosome and is composed solely of RNA components. Structural analysis supported by comprehensive mutagenesis experiments and quantum mechanical calculations, led to the identification within the concurrent ribosome an internal architectural element that seems to be the remnant of the ancient version of this machine, which was capable of non-coded peptide bond formation and the production of short oligopeptides. Comprised of 180 nucleotides this architectural element confines a void that provides stereochemistry appropriate for peptide bond formation, for substrate-mediated catalysis, and for the succession of this reaction, hence enables the polymerase activity of the ribosome. The universality of this region implies its existence irrespective of environmental conditions, indicates that it may represent the proto-ribosome and supports the suggestion that it evolved by gene duplication or gene fusion, which later underwent mutational optimization towards the accommodation of two similar, albeit not identical, substrates. A substantial increase in its catalytic rate and the eventual progress towards programmed decoding could be obtained by the inclusion of peripheral elements, as observed independently, elsewhere, by categorizing the nature of internal interactions within the contemporary ribosome. Experimental results and conceptual issues will be presented.