**COMPUTER ANALYSIS OF BASE PAIRING FREE-ENERGY BETWEEN SHINE-DALGARNO SEQUENCE AND 16S RRNA SEQUENCE IN VARIOUS PROCARYOTES.**

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It is well accepted that the 3' end of 16S rRNA is directly involved in the procaryotic translation initiation by pairing with the Shine-Dalgarno (SD) sequence, which is located in the ribosome-binding site of mRNA. We comprehensively calculated free-energy values of the base pairing between the 3' end of 16S rRNA and the 5' UTR of mRNA, in order to detect the mRNA binding sequence in 16S rRNA for various procaryotes.

The average free-energy values are sharply dropped a few bps upstream of the start codon in *E. coli*, which is consistent with the model that the 3' end of 16S rRNA interacts with the SD sequence.  
*H. influenzae* shows quite a similar pattern, indicating that the organism has basically the same translation initiation mechanism. Other species, such as *Mycoplasma pneumoniae*,*Helicobacter pylori*, and *Synecholystis*PCC6803, also show free-energy drops, although the drops are less evident and the shape of the drops is significantly different from that of *E.coli* and *H. influenzae*.

No free-energy drops can be seen in the genomes of *Aquifex aeolicus* and the three archibacteria (*Archaeoglobus fulgibus*, *Methanobacterium thermoautotrophicum*, and *Methanococcus jannaschii*), suggesting that 16S rRNA of those procaryotes does not base pair with a specific region of mRNA.