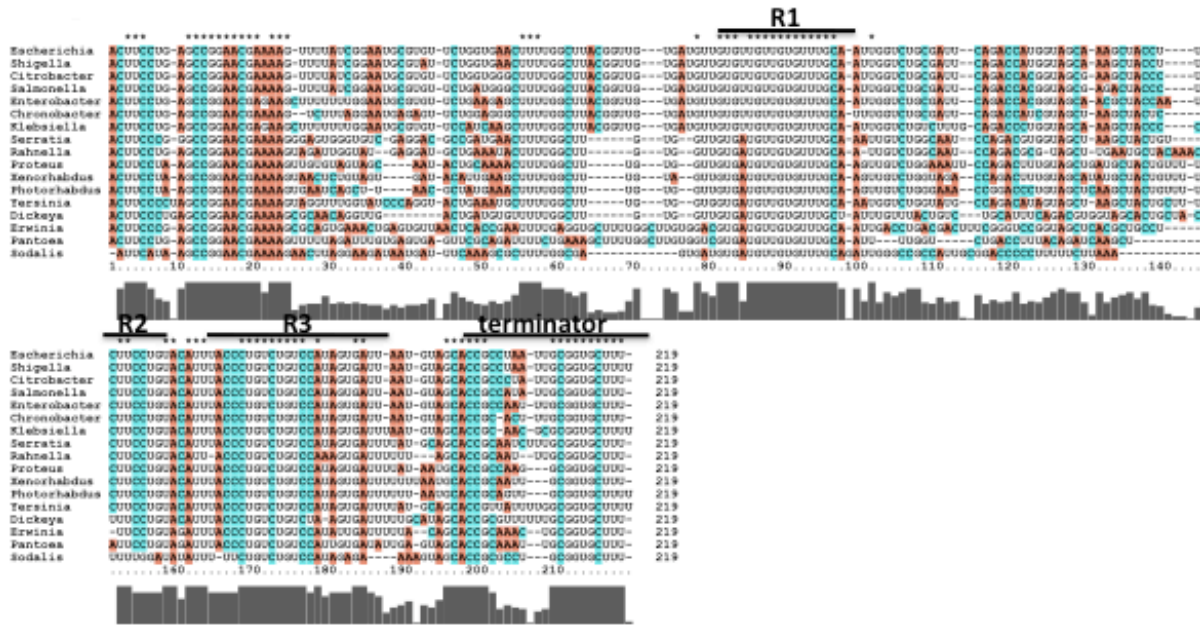


## S2A. Clustal alignment of *GcvB* in Enterobacteriaceae



## S2B. Complementarities between *gcvB* sRNAs and *phoP* mRNAs of several enterobacterial families.

The complementarities were found with the Mfold program using the default parameters and *GcvB* sequences in the R3 region and *phoP* sequences from -90 to +30 (+1 being the first nt of the translation initiation codon). In some cases, complementarities were lengthened by eye (in blue). The Shine-Dalgarno sequence and the initiation codon are in red. The maximum continuous complementarity length is given under each sequence.

*E. coli* K12 MG1655

*phoP* 5' UUUUAAUAAUUA-----AGACAGGGAGAAAUAAA AUGCGCGUACUGG3'  
*gcvB* 3' GUAAUAGUGAUACCUGUCUGUCCCAUUUAC5'

Maximum complementarity length : 8 nt

*Klebsiella pneumoniae* 342

*phoP* 5' UUA-----CU-AUCAACACAGGAAGGGAGAACAGUC AUGCGCGUACUCG3'  
*gcvB* 3' UAAUUUAGA-UACC--UGUCUGUCCCAUUUAC5'

Maximum complementarity length : 5 nt

*Photobacterium luminescens* TT01

*phoP* 5' AAUAACUGCC-UGCUGGAGAGGAAUUUUAUCC AUGCGGAUAUUGA3'  
*gcvB* 3' TUUUCGUGGCGUUGACGCCAC-GUAAUUUUUAGUGAUACCUGUCUGUCCCAUU5'

Maximum complementarity length : 11 nt

*Proteus mirabilis* HI4320

*phoP* 5' UGAUUUUUACUGAUGUAC--ACAAGGUGAAU AUGCGGAUCUAAA3'  
*gcvB* 3' UUUUAGUG-AUACCUGUCUGUCCCAUUUAC5'

Maximum complementarity length : 6 nt

*Serratia proteamaculans* 568

*phoP* 5' UGUUCACCCGCAGAUUUACAGGAGUCCGCCAUGCGAGUACUGG3'  
*gcvB* 3' UUUUAGU-GAUACCUGUCUGUCC-CAUUUAC5'

Maximum complementarity length : 5 nt

*Shigella flexneri*

*phoP* 5' UUA--CACUAUUUUAAUAAUUAAGACAGGGAGAAAUAAAAAUGCGCGUACUGG  
*gcvB* 3' GUAAUUAGUGAUA-----CCUGUCUGUCCCAUUUAC

Maximum complementarity length : 8 nt

*Xenorhabdus bovienii* SS-2004

*phoP* 5' GUAAACGUUACUGAUUAGUAUAAGGAAUCAUUAUGCGUAUACUCA  
*gcvB* 3' AAUUUUUUUAGUGAUACCUGUCUGUCCCAUU

Maximum complementarity length : 14 nt

*Rahnella sp.* Y9602

*phoP* 5' TUUUUCGCGCUGUCAGGAUAAGG-~~A~~AUCACCAUGCGAAUUUUAG  
*gcvB* 3' UUAGUGAAACCUGUCUGUCCCAUUACA5'

Maximum complementarity length : 5 nt