

Supplemental Fig. 1A. Sequence alignment of the RtxA toxin of *Kingella kingae* strain 269-492 (ABK58601) with its closest counterparts from *Moraxella bovis* (ABR28460), *Moraxella bovoculi* (ABA39414) and *Moraxella ovis* (ABA39419).

An asterisk indicates a residue identical in all the proteins. High and low consensus sequences are in red and blue, respectively.

The sequences were aligned by using the multiple sequence alignment with hierarchical clustering: <http://multalin.toulouse.inra.fr/multalin/> (Corpet, Nucleic Acids Res. 1988 25;16(22):10881-90).

