Supplementary Material

Origin of the mobile di-hydro-pteroate synthase gene determining sulfonamide resistance in clinical isolates

Miquel Sánchez-Osuna[1], Pilar Cortés[1], Jordi Barbé[1*], Ivan Erill[2*]

*** Correspondence:** Corresponding Authors: jordi.barbe@uab.cat; erill@umbc.edu

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Leptospira santarosai          VLLNEGITQE-QLIFDPGMGFFLSPDFQVSFEVLRKI
Leptospira interrogans         ILLNAGIAQE-QLIFDPGMGFFLSSDFQVSFEVLKKI
Leptospira alstonii            EMLESGISQE-QLIFDPGMGFFLSPDFQISFEVLRKI
Leptospira biflexa             DLTAMGISES-SIFFDPGMGFFLSDDPMVSFRVLQDL
Sul2 Ecoli 2                   ALTGAGIKRN-RLVLDPGMGFFLGAAPETSLSVLARF
Sul2 Apleuropneumoniae         ALTGAGIKRN-RLVLDPGMGFFLGAAPETSLSVLARF
Sul2 Ecoli 1                   ALTGAGIKRN-RLVLDPGMGFFLGAAPETSLSVLARF
Parvibaculum  lavamentivorans  ALEQAGIARA-RVILDPGMGFFVGPRPETSFSILARL
Candidatus Phaeomarinobacter   GLAASGIARE-RLVLDPGMGFFLGTDPEVSLEVLRHV
Sul1 Cglutamicum               ALRRSGVAAD-RLILDPGMGFFLSPAPETSLHVLSNL
Sul1 Ecloacae                  ALRRSGVAAD-RLILDPGLGFFLSPAPETSLHVLSNL
Sul3 Ecoli                     ALVEAGVKRE-RIILDPGMGFFLGSNPETSILVLKRF
Sul3 SCholeraesuis             ALVEAGVKRE-RIILDPGMGFFLGSNPETSILVLKRF
Chlamydia trachomatis          QFAQVGLDTSWQVVFDPGIGF--GKTPVQSMLLMDGV
Chlamydia muridarum            TFAQIGLDTSWQVVFDPGIGF--GKTPVQSMQLMEGV
Chlamydophila caviae           AFVALGLRQD-QIIFDPGIGF--GTTQIQALNVLHKM
Chlamydia psittaci             AFVALGLSKD-QIIFDPGIGF--GTTPIQALNVLHRM
Chlamydia felis                AFTALGLNLD-QIIFDPGIGF--GTSPIQALHVLHRM
Chlamydia avium                FCDHLGLDCS-QIIFDPGIGF--GTTSIQAMYILQKM
Chlamydia gallinacea           FCDRLGLDCS-QIIFDPGIGF--GTTSIQAMRILREM
Chlamydophila pneumoniae       MFSDVGLNAN-QVIFDPGIGF--GKGAAQSLATLYEI
Parachlamydia acanthamoebae    ELKKNGVKEE-RIILDPGIGF--GKTVDDNLQIIQNL
Waddlia chondrophila           ALQKAGIKEN-NIIIDPGIGF--GKTVEDNYQILHNL
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Supplementary Data 3 – Detail of the multiple sequence alignment region containing the two-amino acid signature motif including Sul sequences and FolP sequences from members of the *Rhodobiaceae*, the *Leptospiraceae* and the Chlamydiae.