

Prediction of new vaccine targets in the core genome of *Corynebacterium pseudotuberculosis* through omics approaches and reverse vaccinology

Carlos Leonardo Araújo, Jorianne Thyeska Castro Alves, Wylerson Nogueira, LINO CESAR DE SOUSA PEREIRA, anne cybelle pinto gomide, Rommel Thiago Jucá Ramos, Vasco A de C Azevedo, Artur Silva, adriana ribeiro carneiro folador

Universidade Federal do Pará

Abstract

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