Draft genome sequence of a copper-resistant marine bacterium, Pantoea agglomerans strain LMAE-2, a bacterial strain with potential use in bioremediation

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Pantoea agglomerans LMAE-2 was isolated from seabed sediment moderately contaminated with Cu2+. Here, we report its draft genome sequence, which has a size of 4.98 Mb. The presence of cop genes related with copper homeostasis in its genome may explain the resistance and strengthen its potential for use as bioremediation agent. © 2016 Corsini et al.