



Erratum for Edwards et al., “Draft Genome Sequence of Uncultured Upland Soil Cluster *Gammaproteobacteria* Gives Molecular Insights into High-Affinity Methanotrophy”

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Page 2: Lines 11–14 should read as follows: “. . . Unlike the genomes of other gamma-proteobacterial methanotrophs, the USC γ draft genome contains nearly all essential genes for a complete serine biosynthesis pathway for formaldehyde assimilation. However, the enzymes unique to the typical RUMP pathway, hexulose-6-phosphate synthase and hexulose phosphate isomerase, were not detected. . . .”

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