

## Carbon signatures in amino acids during deep-sea anoxic methanotrophy

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Microorganisms play a central role in both methane production and consumption in the global carbon cycle. Oceanic methane from global deep-sea sediment is largely consumed through microbially mediated sulfate-coupled oxidation, resulting in  $^{13}\text{C}$ -depleted cell biomass of anaerobic methanotrophic archaea (ANME). The general ecological importance of subseafloor ANME has been well recognized in the last two decades. However, the crucial biochemical pathways for the overall anaerobic oxidation of methane (AOM) still remain enigmatic. In the present study, methanotrophic pathways were analyzed to trace  $^{13}\text{C}$ -depleted amino acid biosynthesis in two clades of ANME (ANME-1 and ANME-2) from the Black Sea. Compound-specific analysis of ANME-dominated microbial mats showed a significant  $^{13}\text{C}$ -depletion trend in association with increasing carbon numbers in protein-derived amino acid families within the pyruvate family in the order of alanine, valine, isoleucine and leucine down to -114‰. This result indicates a stepwise elongation of  $^{13}\text{C}$ -depleted carbon during amino acid biosynthesis. The overall results suggest that intracellular protein amino acids and the most  $^{13}\text{C}$ -depleted signature of leucine, which has a specific branched-chain structure, are potentially propagated as isoprenoid precursor molecules into archaeal biosynthesis, resulting in the extremely  $^{13}\text{C}$ - and  $^{14}\text{C}$ -depleted nature of ANME cells in the deep microbial oasis.

### References:

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### Supplementary Information:

<https://www.nature.com/articles/s41598-018-31004-5#article-info>

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