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Proteomic response of *Gordonia* sp. strain NB4-1Y provided with fluoroalkyl sulfonates for sulfur

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Per- and polyfluoroalkyl substances (PFAS) are a group of chemicals found in products including food packaging, cosmetics, water-repellent fabrics, non-stick cookware, and fire-fighting foams for hydrocarbon fires. Stable in part due to the strength of the carbon-fluorine bond, they bioaccumulate in both the environment and biological matrices, degrading over long periods of time into structurally smaller PFAS. Linked to liver toxicity and kidney cancer, effective methods to remove PFAS from soil, water and groundwater are not yet available. The soil bacterium, *Gordonia* sp. strain NB4-1Y, has been shown to utilize 6:2 fluorotelomer sulfonate (6:2 FTSA) and 6:2 fluorotelomer sulfonamide alkylbetaine (6:2 FTAB) as a sulfur source. Here, the proteomic response of NB4-1Y when given these PFAS as a sole added sulfur source is compared to NB4-1Y grown with magnesium sulfate or octanesulfonate. Optimization of protocols for cell lysis by bead beating followed by TRIzol protein extraction from NB4-1Y grown in rich medium has so far allowed for the resolution of over 1000 proteins by LC-MS/MS analysis. Next, proteomes of NB4-1Y grown with the following sulfur sources will be compared: 6:2 FTSA, 6:2 FTAB, 1-OCT, $MgSO_4$, 6:2 FTSA + $MgSO_4$, 6:2 FTAB + $MgSO_4$, and 1-OCT + $MgSO_4$. In combination with metabolome data, the goal is to identify specific enzymes responsible for the desulfonation and defluorination of 6:2 FTSA and 6:2 FTAB.