

Deuterium induces a distinctive proteome in *Escherichia coli*

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Figure legends

Figure S1. Complete set of significantly regulated Gene ontology (GO) classes for proteomes obtained from *E. coli* cells exponentially grown in protonated M9 minimal (M9H3e) vs. protonated full (LBe) medium. The analysis is reduced to (GO classes, for which $\geq 75\%$ of the contained proteins (total number N_{tot}) were observed with such low variation that they could be classified as either strongly (at least two-fold) up-regulated (number N_{up}), strongly (at least two-fold) down-regulated (number N_{down}), or as not strongly regulated (less than two-fold, number $N_{\text{not-regulated}}$). An entire GO class is considered as strongly up- (red) or downregulated (blue) when $\geq 50\%$ of its significantly detected proteins ($N_{\text{up}} + N_{\text{not-regulated}} + N_{\text{down}}$) are at least two-fold up- or downregulated, respectively. Several clusters (magenta) also showed significant combined up- and down-regulation [$(N_{\text{up}} + N_{\text{down}})/(N_{\text{up}} + N_{\text{not-regulated}} + N_{\text{down}}) \geq 50\%$] of their detected proteins, albeit they were not significantly regulated in one direction (up or down). The values in the last line of each GO class indicate from left to right: the number of significantly up-regulated N_{up} , significantly not-regulated $N_{\text{not-regulated}}$, significantly down-regulated N_{down} , not significantly detected $N_{\text{not-significant}}$, as well as the total number of proteins in the class N_{tot} .

Figure S2. Complete set of regulated Gene ontology (GO) classes for proteomes obtained from *E. coli* cells exponentially grown in deuterated M9 minimal (M9D3e) vs. protonated M9 minimal (M9H3e) medium. The analysis, color coding and annotation are identical to the comparison of protonated M9 minimal (M9H3e) vs. protonated full (LBe) medium shown in Figure S2.



