

The quantitative metabolome data and protein profiling of the *Escherichia coli*
when a single amino acid is supplied in media

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Complex media containing free amino acids originating from peptone or yeast extract are often used to improve the productivity in recombinant protein production processes. This occurs because L-amino acids for *E.coli* work as either 'energy amino acids' which are catabolised to provide energy, or 'protein amino acids' which are incorporated into protein. To predict results of recombinant protein production processes *E.coli*, supplying amino acids with in silico experiment, it is required to obtain a lot of metabolic data about the *E.coli* metabolome when the amino acid is supplied. A lot of basic data are needed because the metabolism of *E.coli* changes in media containing amino acid. To obtain the data about amino acid metabolism of *E.coli*, we carried out batch fermentation of *E.coli* W3110 having a selected single amino acid in medium. 10 amino acids—His, Ser, Trp, Phe, Tyr, Ala, Val, Leu, Asp, Glu— were respectively supplied. We analyzed organic acids and amino acids excreted to medium quantitatively. And after hydrolyzing total proteins of the cell, we measured total amino acid of proteins constructing the cell in respective experiments.