Systems metabolic engineering of *Escherichia coli* K-12 for the enhanced production of L-valine

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The L-valine production strain of E.coli was constructed by rational engineering based on in silico genome-scale metbolic network. The genes responsible for major competing pathways such as ilvA, panB, and leuA were knocked out to increase 2-ketoisovalerate availability which is the intermediate precursor of L-valine. Also another amplification target gene, the yga ZH encoding L-valine exporter was overexpressed. The cooverexpression of the lrp and ygaZH genes led to higher production of L-valine. Based on in silico simulation, aceF, mdh, and pfkA genes were identified as knockout target and finally the VAMF strain (Val △aceF△mdh△pfkA) overexpressing the ilvBN,ilvCDE,ygaZH,and lrp genes was constructed. [This work was supported by the Advanced Biomass R&D Center(ABC) of Global Frontier Project funded by the Ministry of Education, Science and Technology. Further supports by the World Class University Program(R32-2008-000-10142-0) of the MEST were appreciated.]