

Genome-scale metabolic network analysis and drug targeting of multi-drug resistant pathogen *Acinetobacter baumannii* AYE

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Acinetobacter baumannii has emerged as a new clinical threat to human health, particularly to the ill patients in hospital environment. For systematic study of this organism, we reconstructed its genome-scale metabolic network based on genome annotation data, metabolic databases and literatures. The metabolite essentiality approach was then undertaken to predict essential metabolites that are critical to the cell growth. The EMFilter, a framework that filters initially predicted essential metabolites to find the most effective ones as drug targets, was also developed. [This work was supported by the Korean Systems Biology Research Project (M10309020000-03B5002-00000) of the Ministry of Education, Science and Technology (MEST). Further supports by the World Class University Program from the MEST, LG Chem Chair Professorship, IBM SUR program, and Microsoft are appreciated.]