

Systematic framework for the generation of gene–transcript–protein–reaction associations in human metabolism

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Alternative splicing of a gene generates multiple transcripts, which are translated to protein isoforms. Due to the important roles of alternative splicing, we present a systematic framework for the generation of gene–transcript–protein–reaction associations (GeTPRA) in human metabolism. The framework involves a generic human genome–scale metabolic model (GEM) that is biochemically consistent and transcript–level data compatible. We show that a generic human GEM can be used to generate GeTPRA, which can be deployed to further upgrade the human GEM. The framework will contribute to better understanding human metabolism and enable medical applications. [This work was supported by the Technology Development Program to Solve Climate Changes on Systems Metabolic Engineering for Biorefineries (NRF–2012M1A2A2026556 and NRF–2012M1A2A2026557) from the Ministry of Science and ICT through the National Research Foundation of Korea.]