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Integration of biomass functions of genome-scale metabolic models with experimental data reveals universally essential cofactors in prokaryotes

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Knowledge of the core biochemical composition of the cell is critical for genome-scale metabolic modelling. In order to identify the universal core organic cofactors for prokaryotes, we performed a detailed analysis of biomass objective functions (BOFs) of 71 manually curated genome-scale prokaryotic models. These were then compared and integrated with the ModelSEED framework for biomass composition, experimental data on gene essentiality, curated enzyme-cofactor association data and a comprehensive survey of the literature. Surprisingly, no cofactor was present in all the BOFs analysed, including the important redox cofactor nicotinamide adenine dinucleotide (NAD) or its derivatives. Our results indicate not only the redox cofactors but also others such as coenzyme A, flavins and thiamin as universally essential for prokaryotes and therefore as important to include in the BOFs of future genome-scale models of prokaryotic organisms.