

Table 2. Simulated growth rates and proton fluxes through ATPases for *Escherichia coli* MG1655 and *Synechocystis* sp. PCC6803 with and without PPRs, simulated by flux balance analysis of genome-scale metabolic reconstructions

Model simulation	Growth rate (/h)	Proton flux ATPase (mmol/g DW/h)	Simulation conditions	Refs
<i>E. coli</i> wild type	0.98	223	Standard aerobic growth	[54]
<i>E. coli</i> with PPRs ^a	1.0	228	Glucose substrate (10 mmol/g DW/h)	
<i>Synechocystis</i> wild type	0.052	50.2	Autotrophic growth	[58]
<i>Synechocystis</i> with PPRs ^b	0.057	55.2	Light-limited (30 mmol photons/g DW/h) Standard CO ₂ uptake (3.7 mmol/g DW/h)	

^aEstimated PPR proton flux of 10 mmol protons/g DW/h (Table 1) is added to the genome-scale metabolic reconstruction from cytoplasm to periplasm.

^bEstimated PPR proton flux of 10 mmol protons/g DW/h (Table 1) is added the genome-scale metabolic reconstruction from cytoplasm to thylakoid. DW, dry weight.