

Abstract Submitted  
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**Evolution and Biophysics of the *Escherichia coli lac* Operon** J. CHRISTIAN RAY, The University of Texas M. D. Anderson Cancer Center, OLEG IGOSHIN, Rice University, SELWYN QUAN, RUSSELL MONDS, Stanford University, TIM COOPER, The University of Houston, GÁBOR BALÁZSI, The University of Texas M. D. Anderson Cancer Center — To understand, predict, and control the evolution of living organisms, we consider biophysical effects and molecular network architectures. The lactose utilization system of *E. coli* is among the most well-studied molecular networks in biology, making it an ideal candidate for such studies. Simulations show how the genetic architecture of the wild-type operon attenuates large metabolic intermediate fluctuations that are predicted to occur in an equivalent system with the component genes on separate operons. Quantification of gene expression in the *lac* operon evolved in growth conditions containing constant lactose, alternating with glucose, or constant glucose, shows characteristic gene expression patterns depending on conditions. We are simulating these conditions to show context-dependent biophysical sources and costs of different *lac* operon architectures.

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