Hierarchy and feedback in the evolution of the Escherichia coli transcription network.

Lagomarsino MC, Jona P, Bassetti B, Isambert H

Proc Natl Acad Sci U S A 2007 Mar 27 **104**(13):5516-20 [abstract on PubMed] [citations on Google Scholar] [related articles] [full text] [order article]

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Evaluated 8 Jun 2007
Relevant Sections

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Regine Hengge Free University of Berlin, Germany MICROBIOLOGY Hypothesis New Finding	**Why is the organisation of real-life transcriptional networks so different from that of random networks? These authors answer this question by investigating the evolutionary development of the Escherichia coli transcription network.** This network has a strikingly "flat" hierarchy; transcription factors (TF) of the same homology class strongly tend to populate the same hierarchical layer; direct autoregulation is abundant, but indirect feedbacks nearly absent; and genes acquired by horizontal gene transfer seem to accumulate in the lowest level of target genes. Based on these properties, the authors identify the major evolutionary driving forces as ancient gene duplications, suppression of cross-regulation of duplicated autoregulated TFs, and horizontal gene transfer affecting network periphery during more recent evolutionary stages.