

Abstract Submitted  
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**Topological units of environmental signal processing in the transcriptional-regulatory network of *Escherichia coli***<sup>1</sup> GABOR BALAZSI, Northwestern University Medical School, ALBERT-LASZLO BARABASI, University of Notre Dame, ZOLTAN OLTVAI, Northwestern University Medical School — Recent evidence indicates that potential interactions within biochemical networks are differentially utilized according to the environmental conditions in which a cell exists. However, the topological units of this differential utilization have not been investigated. Here, we use the transcriptional regulatory network of *Escherichia coli* to identify such units, called origons, representing regulatory subnetworks which originate at a distinct class of sensor transcription factors. Using microarray data, we find that specific environmental signals affect mRNA expression levels significantly only within the origons responsible for their detection and processing. We also show that small regulatory interaction patterns, called subgraphs and motifs, occupy distinct positions in- and between origons, offering insights into their role in environmental information processing.

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Gabor Balazsi  
Northwestern University Medical School

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