

Advanced Biochemistry: Discussion on Gene Regulation and Transcription Factors

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Network motifs. Gene regulation networks include recurring patterns called network motifs, which have predictable and useful dynamics to allow for cell signaling and development. Each network motif has a biological function.

Discussion groups will focus on different network motifs, and each member of the group will independently search the literature for a natural system that includes their network motif. The natural systems that you find can include other types of regulation as well, and don't need to be limited to protein dynamics (e.g. RNAs, PTMs, and other macromolecular interactions are cool too).

Group 1: negative autoregulation

Group 2: coherent type-1 feed forward loop

Group 3: incoherent type-1 feed forward loop

Group 4: single input module

Group 5: double-negative feedback loop

Group 6: cascade

1. Sketch a picture of the gene circuit in the study you found. Transcription factors and regulated genes can be represented as nodes, arrows (\rightarrow) can represent activation, and flat ended arrows (\dashv) can represent repression or inhibition.

2. What are some features of the network motif that your group investigated that set it apart from simple regulation? Why are those features advantageous for the natural system you picked from the literature? You might consider the response time, the steady-state values of the output gene(s), the nature of the signal, the timing and length of the response to the signal, robustness to errors or mutations, or other factors.

Transcription factors. Find an experimentally solved structure or AlphaFold prediction of a structure for one of the transcription factors in your system. (AlphaFold predictions for proteins from several organisms can be found in the AlphaFold Protein Structure Database at <https://alphafold.ebi.ac.uk/>.) If there's no experimentally solved structure in the PDB for your transcription factor, you can also BLAST the sequence against the PDB to look for homologs in their DNA-bound/ligand-bound/apo states.

3. Based on the structure or structural model for your transcription factor, hypothesize what interactions and structural features allow the protein to regulate DNA-binding in response to the signal. How would you test your hypothesis?