

# Structural studies of the UxuR and ExuR proteins, regulators of hexuronate metabolism in gammaproteobacteria.

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An alternative branch of sugar metabolism that allows bacteria to survive under stress is the Ashwell pathway involving catabolism of D-hexuronic acids. This metabolic pathway is essential for the formation of colonies and motility of *E. coli*. The final product of hexuronic acid metabolism of hexuronic acids is pyruvate that eventually results from the transfer of the Ashwell cycle passing into the Entner-Doudoroff pathway.

Processes of hexuronate utilization are controlled by the two paralogous – transcription factors, UxuR and ExuR. ExuR has likely emerged by duplication of an ancestral *uxuR* gene. Both proteins belong to the GntR family transcription factors, whose members share high structural similarity. To date, 3D structures of only few GntR-family proteins have been solved. Based on amino acid sequences, closest relatives of UxuR and ExuR with known structure are FadR from *Escherichia coli* and GntR from *Bacillus cereus*. However, the amino acid identity of these proteins does not exceed 25%.

To understand how UxuR and ExuR interact with their DNA targets for cooperative regulation of hexouronate metabolism, one needs a reliable structure of at least one of these regulators. In order to study their structure, ExuR and UxuR have been isolated and purified, and first crystals have been just obtained.

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