

EPIFACTORS: A COMPREHENSIVE DATABASE OF HUMAN EPIGENETIC
FACTORS AND COMPLEXES

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Epigenetics refers to stable and long-term alterations of cellular traits that are not caused by changes in the DNA sequence per se. Rather, covalent modifications of DNA and histones affect gene expression and genome stability via proteins that recognize and act upon such modifications. Many enzymes that catalyze epigenetic modifications or are critical for enzymatic complexes have been discovered, encouraging investigators to study their role in diverse normal and pathological processes. Rapidly growing knowledge in the area has resulted in the need for a resource that compiles, organizes and presents curated information to the researchers in an easily accessible and user friendly form. Here we present EpiFactors, a manually curated database providing information about epigenetic regulators, their complexes, targets and products. EpiFactors contains information on 815 proteins, including 95 histones and protamines. For all genes we include expressions values across a collection of 573 human primary cell samples (200 cell types from up to 3 donors), covering most mammalian cell steady states, 250 different cancer cell lines (representing 154 distinct cancer subtypes) and 152 human post-mortem tissues, obtained by FANTOM5 consortium using

CAGE (Cap Analysis of Gene Expression) technique. EpiFactors also contains information on 69 protein complexes that are involved in epigenetic regulation. The resource is practical for a wide range of users, including biologists, pharmacologists and clinicians.

Web-site: <http://epifactors.autosome.ru>