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## *In silico* profiling of single nucleotide polymorphisms in EZH2 gene and their involvement in cancer progression

Richa Vasan, Manjari Trivedi, Sulekha Nair, Divanshu Gupta, Lekshmi Mohan and Trupti N V Patel VIT University, India

Enhancer of Zeste Homolog 2 or EZH2 is an enzyme that plays an active role in transcriptional repression of several genes over successive cell generations, especially during embryonic cell development and cellular differentiation. The catalytic subunit of human polycomb repressive complex 2, EZH2 acts by tri-methylating lysine 27 of histone 3 protein on DNA. EZH2 is also known to act as the scaffolding protein for the action of DNA methyltransferases, which further helps in chromatin condensation and gene silencing. EZH2 is over-expressed and is a major biomarker for cancers of prostate, breast, brain and other cancer progressions, including those of the bladder, gastric, liver and blood (leukemia). The most important contribution is that this overexpression leads to silencing of the major tumor-suppressor genes through increased levels of histone methylation in the promoter regions of these genes. In the present study we aim to retrieve the known mutations in EZH2 (single nucleotide polymorphisms-SNPs) from the COSMIC database and look at the severity of each mutation on the functionality of the enzyme using multiple in silico approaches including Molecular Dynamics Simulation.

## **Biography**

Richa Vasan is in her 5th year of MSc Integrated Biotechnology at VIT Vellore-632014, Tamil Nadu. She has worked on various research projects during the past 3 years and is working on the foresaid project since last 6 months.

tnpatel@vit.ac.in