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Investigating functional relationships of five critical genes present in the familial non-synonymous loci with risk of having acute lymphoblastic leukemia

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A recent whole exome sequencing of Acute Lymphoblastic Leukemia (ALL) revealed that common variations in particular non-synonymous homozygous variants affects disease risk. The present work researches into the functional consequences of the polymorphisms in the following genes: B3GALTL (rs1041073), GEN1 (rs16981869), CA9 (rs2071676), CHIT1 (rs2297950), CHRNB1 (rs17856697), ERBB2 (rs1058808) and ZNF207 (rs3795244). The Polyphen scores were evaluated using the residue changes due to missense variations and protein identifiers generated GlobPlots to predict inherent protein disorders and ProtParam provided the 'instability indices'. Furthermore, metabolic pathways and protein networks were studied by Reactome Pathway Browser and String-db.

Biography

Erchin Serpedin has completed his specialization degree in Signal Processing and Transmission of Information from Ecole Superieure D'Electricite (SUPELEC), Paris, France, in 1992. He has received his MSc degree from the Georgia Institute of Technology, Atlanta, in 1992 and the PhD degree in Electrical Engineering from the University of Virginia, Charlottesville in 1999. He is currently a Professor in the Department of Electrical and Computer Engineering at Texas A&M University, College Station. He is the author of 2 research monographs, 1 textbook, 75 journal papers and 120 conference papers.

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