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Systematic Bioinformatics Studies for the Development of the Targeted Therapeutics (Targeting Diverse RNA Level Mechanisms and Gene Fusions)

Dr. Kim is an Assistant Professor in Bioinformatics at the School of Biomedical Informatics of The University of Texas Health Science Center at Houston. Dr. Kim's research expertise lies in computational biology for precision medicine based on accurate cellular mechanisms with bioinformatics and genomic data science approaches. She was awarded the Outstanding Investigator Award in 2020 by NIGMS with a study aiming to infer the origin and functional aspects of new genes using bioinformatics and deep learning approaches. In this awarded project, she and her lab members are studying the origin of new genes and downstream effects, and genomic features through multiple Bioinformatics tools and deep learning methods. Recently, they predicted the 3D structures of new proteins, which were translated from new genes (fusion genes), performed the virtual screening of the potentially interacting small molecules, functional annotation of fusion proteins, and build a protein version FusionGDB (FusionPDB). Her group will report multiple integrative studies of fusion proteins per important gene groups such as kinase, transcription factor, and transmembrane proteins to provide new knowledge for the therapeutic target candidates in human fusion genes. In this talk, she will present her previous and ongoing studies on developing therapeutic targets in RNA-level mechanisms and gene fusions.