Special Issue

Advances of Brain Transcriptomics

Message from the Guest Editors

Advancements in RNA-Seq technology have underlined its power for elucidating the brain gene networks responsible for various stressful factors, as well as pathologies like Alzheimer and Parkinson, and other neurological diseases including schizophrenia and depressive disorders. Single cell RNA-seq allows for ascertaining various neurons and glia cell identities by elucidating the specific marker genes within them. Multiple databases like ASCOT and Genome (for elucidating the tissue/cell specific AS profiles for each gene) are arising, underlining the research of brain transcriptome structural and expression variability as a top priority. Additionally, there is a genetic based vs. acquired trait paradigm, which would be represented by both genetic studies based on animal model strains/breeds (e.g., tame foxes, aggressive strains of rats, etc.), and those that acquired the trait within single generation upon administering certain stress-related protocols. In this Issue, we hope to address the spectra of physiological studies, including, but not limited to, animal models of social stress response and various brain disease related data/models using the abovementioned approaches.

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Genes is central to our understanding of biology, and modern advances such as genomics and genome editing have maintained genetics as a vibrant, diverse and fast-moving field. There is a need for good quality, open access journals in this area, and the *Genes* team aims to provide expert manuscript handling, serious peer review, and rapid publication across the whole discipline of genetics. Starting in 2010, the journal is now well established and recognised. Why not consider *Genes* for your next genetics paper?

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