EDITORIAL

Journal Current Genomics: News and Editorial Prospects

On behalf of the editorial board, thank you for your continuous support to Current Genomics. We are pleased to announce that Current Genomics maintains its position as a leading journal in the field of genome sciences and related fields with a JCI impact factor of 2.174 and 5-year impact factor of 3.090.

Current Genomics will keep welcoming manuscripts in the fields of genomics, systems biology, bioinformatics, machine learning, network inference, quantitative biology and synthetic biology for the study of evolution, development, maintenance and aging and of human diseases. Epigenetics, single cell studies and studies of extracellular vesicles as well as clinical genomics and precision medicine are topics of particular interest. The journal also covers plant genomics. The journal does not consider articles dealing with breeding and livestock.

Current Genomics publishes reviews, position papers, original papers and opinion letters.

Some of the top cited articles in the past 7 years:

- MicroRNA in aging: From discovery to biology [1].

- Mitochondria and organismal longevity [2].

- Molecular mechanisms involved in the aging of the T-cell immune response [3].

- Preimplantation genetic diagnosis for aneuploidy and translocations using array comparative genomic hybridization [4].

- Application of genomic tools in plant breeding [5].

- Olfactory receptor multigene family in vertebrates: from the viewpoint of evolutionary genomics [6].

- Computational prediction of protein-protein interaction networks: Algorithms and resources [7].

- Regulation of cellulase and hemicellulase gene expression in fungi [8].

- Integrated Analysis of Transcriptomic and Proteomic Data [9].

- KRAB-Zinc Finger Proteins: A Repressor Family Displaying Multiple Biological Functions [10].

- Compatible Solute Engineering in Plants for Abiotic Stress Tolerance - Role of Glycine Betaine [11].

- Studies on the pathophysiology and genetic basis of migraine [12].

- The mechanistic links between proteasome activity, aging and agerelated diseases [13].

- Impact of next generation sequencing techniques in food microbiology [14].

- Circular RNAs in eukaryotic cells [15].

- Reverse engineering of genome-wide gene regulatory networks from gene expression data [16].

- DNA secondary structure at chromosomal fragile sites in human disease [17].

- Clinical next generation sequencing for precision medicine in cancer [18].

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