genes

an Open Access Journal by MDPI

IMPACT FACTOR 3.5

Indexed in: PubMed

CITESCORE 5.1

Genomic Aberrations in Hematologic Malignancies

Guest Editors:

Dr. Zhenya Tang
Departments of Hematopathology, The University of Texas MD Anderson Cancer Center, 1515 Holcombe Blvd., Houston, TX 77030, USA

Dr. Zejuan Li
Weill Cornell Medical College, Houston Methodist Hospital, Houston, TX 77030, USA

Deadline for manuscript submissions:
closed (15 April 2024)

Message from the Guest Editors

Recurrent chromosomal abnormalities are very common in a variety of hematological malignancies, such as translocations and/or inversions related to the formation of fusion genes such as t(9;22)(q34.1;q11.2) and related BCR::ABL1; t(8;21)(q22;q22.1) and related RUNX1::RUNX1T1; inv(16)(p13.1q22)/(16;16)(p13.1;q22) and related CBFB::MYH11; t(15;17)(q24;q21) and related PML::RARA; t(12;21)(p13.2;q22.1) and related ETV6::RUNX1; and a wide spectrum of 11q23 abnormalities/KMT2A(MLL) gene rearrangement and related fusion genes in both myeloid and lymphoid neoplasms. They are widely applied as biomarkers for the diagnosis of specific entities and/or sub-entities of hematological malignancies, targeted therapies, and prognostic predictions in the field of hemato-oncology. Attributed to the widespread application of advanced next-generation sequencing (NGS)-based technologies and genome-wide comprehensive studies, tremendous novel fusion genes as well as chromosomal abnormalities have been identified in hematological malignancies in the past several decades. They all play important roles in the era of precision medicine.

GCAT TACG GCAT genes

IMPACT FACTOR 3.5 | Indexed in: PubMed | CITESCORE 5.1

an Open Access Journal by MDPI

Editor-in-Chief

Prof. Dr. Selvarangan Ponnazhagan
Department of Pathology, The University of Alabama at Birmingham, 1825 University Blvd, SHEL 814, Birmingham, AL 35294-2182, USA

Message from the Editor-in-Chief

Genes are central to our understanding of biology, and modern advances such as genomics and genome editing have maintained genetics as a vibrant, diverse and fastmoving 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?

Author Benefits

Open Access: free for readers, with article processing charges (APC) paid by authors or their institutions.
High Visibility: indexed within Scopus, SCIE (Web of Science), PubMed, MEDLINE, PMC, Embase, PubAg, and other databases.
Journal Rank: JCR - Q2 (*Genetics & Heredity*) / CiteScore - Q2 (*Genetics*)

Contact Us

Genes Editorial Office
MDPI, St. Alban-Anlage 66
4052 Basel, Switzerland

Tel: +41 61 683 77 34
www.mdpi.com

mdpi.com/journal/genes
genes@mdpi.com
𝕏@Genes_MDPI