

## Special Issue

# CRISPR/Cas Systems and Genome Editing—3rd Edition

### Message from the Guest Editor

The harnessing of CRISPR/Cas (Clustered Regularly Interspaced Short Palindromic Repeats/CRISPR-associated genes) systems for the detection, chemical modification, and sequence editing of nucleic acids has dramatically changed many fields of fundamental science, biotechnology, and biomedicine.

Natural CRISPR/Cas systems are well suited to disrupting coding and non-coding sequences in the genome, are much less effective at distinguishing and editing sequences with single-nucleotide differences, and are prone to recognizing similar sequences in the genome. Therefore, further exploration of the CRISPR/Cas field continues both to find new genome and epigenome editors, and to engineer known editors to overcome their shortcomings to make their applications more efficient, predictable, and safe. The aim of this Special Issue is to gather knowledge on the current state of the rapidly growing field of CRISPR/Cas systems and other genome editing tools in fundamental science, biotechnology, and biomedicine.

### Guest Editor

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The International Journal of Molecular Sciences (*IJMS*, ISSN 1422-0067) is an open access journal, which was established in 2000. The journal aims to provide a forum for scholarly research on a range of topics, including biochemistry, molecular and cell biology, molecular biophysics, molecular medicine, and all aspects of molecular research in chemistry. *IJMS* publishes both original research and review articles, and regularly publishes special issues to highlight advances at the cutting edge of research. We invite you to read recent articles published in *IJMS* and consider publishing your next paper with us.

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