Tentative Outline

Special Thematic Issue for Combinatorial Chemistry & High Throughput Screening

Application of dCas9-based Capture of the Regions of Interest in the Genome by Pooled sgRNA Libraries

Guest Editors: Dr. Yujing Li

Aims & Scope:

The system consisting of clusters of regularly interspaced short palindromic repeats (CRISPR) and a bacterial DNA-cut enzyme Cas9 (CRISPR-Cas9), has been recognized as the most powerful tool for genome engineering. Emerging evidences have confirmed the advantages of the CRISPR-Cas9, such as programmability, simplicity, reproducibility and high efficiency, over other conventional tools in terms of genome reorganization and editing. As a result, this tool has enabled and facilitated the genome manipulation at both genomic and epigenomic levels. Initially, the CRISPR-Cas9 system was applied for genome editing mainly in genetic knock out or knock-in of the coding genes. Then more important functions of this system attracted significant attention to both genomic and epigenomic screens via Cas9 or a catalytically inactive Cas9 also called dead Cas9 or dCas9. More specifically, in the past several years, the CRISPR-Cas9 has been comprehensively applied to 1) genetic knock out screens; 2) high throughput screening with Cas9 or dCas9-based effectors with pools of gRNAs; 3) regulatory elements on the non-coding sequence screening based on the nuclease mutagenesis; 3) CRISPR-based interference screens; and 4) CRISPR-based activation screens. Although all the high throughput screening strategies still face some technical challenges and need further improvements, significant achievements have been made in manipulation of the genome and epigenome as well as in the identification of the novel regulatory elements /factors. Theoretically, the significant achievements already made are inspiring scientists in the related research field to advance the study on the genetic and epigenetic regulation mechanisms for wide spectrum of life processes. Medically, this system could be finally applied to correct the aberrant genes caustically responsible for the human diseases. Thus, it is of importance to publish a special issue in CCHTS to address the achievements in CRISPR-Cas9 based high-throughput genetic screening made in recent years.

Keywords: CRISPR-Cas9, genome editing, high throughput screening, transcription repression, transcription activation, gRNA pooled library, programmable deaminase, non-coding RNA, knock out, loss of function, epigenome.

Subtopics:

The subtopics to be covered within this issue are listed below:

We invite the scientists in the field of genetics, epigenetics, genomics, epigenomics involved in CRISPR-Cas9 based high throughput screening to contribute their research or review articles to the special issue. The range of the special issue will refer but not limit to the following:

Potential topics in this Issue

1. New improvements on CRISPR-Cas9 methodologies for high throughput screening
2. Application of dCas9-based capture of the regions of interest in the genome for sequencing by pooled sgRNA libraries.
3. Application of CRISPR-Cas9 in functional genomics study to induce repression or activation transcriptionally.
4. Application of nuclease mutagenesis based screens to identify the putative regulatory elements.

Schedule:

- ✧ Manuscript submission deadline: March 31, 2020
- ✧ Peer Review Due: May 31, 2020
- ✧ Revision Due: July 31, 2020

- ✧ Announcement of acceptance by the Guest Editors: August 30, 2020
- ✧ Final manuscripts due: September 30, 2020

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