## **Tentative Outline**

### **Special Thematic Issue for Current Gene Therapy**

# Title of thematic issue: The therapeutic targets revealed by integrative network analysis of noncoding RNAs

Guest Editors: Tao Huang

Aims & Scope: The biological functions of noncoding RNAs, such as circRNA, lncRNA and microRNA, have been widely studied. The ceRNA network has been considered as a major regulatory mechanism. But the construction of ceRNA network is tricking. There are many different approaches. Some are based on sequence while others are based on correlation. And there is prior knowledge that need to be incorporated, such as the negative regulation between miRNA and target mRNA. After the ceRNA network is constructed, we need to search the network structure to find the triplet or clique. The functional annotation of key noncoding RNA is still an issue. Most of their functions are predicted. Little targets are validated by experiments. How to ensemble the prediction results of different methods is challenging. In this special issue, we would like to address these problems of noncoding RNA researches using advanced bioinformatics approaches and reveal the therapeutic targets in complex diseases, such as cancers, cardiovascular and immune diseases. The topics include but are not limited to:

- (1) ceRNA network construction
- (2) Co-expression network analysis
- (3) Differential co-expression
- (4) Bayesian network analysis
- (5) Module identification
- (6) Triplet or clique search
- (7) Function prediction of noncoding RNAs
- (8) The clinical investigation of noncoding RNAs

**Key words:** noncoding RNA, ceRNA network, network construction, functional annotation, topological analysis, complex diseases, cancer, cardiovascular diseases, immune diseases

#### **Subtopics:**

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

1. Systematic identification of lncRNAs and circRNAs-associated ceRNA networks in human cartilage degradation of osteoarthritis

Qi Huang

hqhq007@hotmail.com

2. Emerging roles of circRNA related to the mechanical stress in human lumbar disc degeneration Yu Feng

Fengyu@shutcm.edu.cn

3. The therapeutic potential and role of miRNA, lncRNA, and circRNA in systemic lupus erythematosus Jianfeng Li

lijianfeng0524@126.com

4. Integrative analysis of long non-coding RNAs and messenger RNA expression profiles in ossification of the ligamentum flavum of the spine

Beibei Dai

daibeibei.0823@163.com

5. Screening and bioinformatics analysis of mRNA, long non-coding RNA and circular RNA expression profiles in

osteoarthritis patients

Xianghui Du

duxianghui88@aliyun.com

6. Transcriptomic analysis of high-throughput sequencing about circRNA, lncRNA and mRNA in postmenopausal osteoporosis

JianHui Li

113132677@qq.com

7. Revealing new landscape of chronic bronchitis through circular RNA-miRNA-mRNA axis

Yan Xie

xieyan005@163.com

8. Molecular functions and specific roles of circRNAs in preeclampsia

Pengxiang Zheng

guohongpei@sina.com

9. Identification of key circRNAs/lncRNAs/miRNAs/mRNAs and pathways in the cardiovascular system

Xuewen Kang

13919026469@163.com

10. Competitive endogenous RNA network: potential implication for patients with hypopharyngeal squamous cell carcinoma

Yanli Wang

drwyl@126.com

## Schedule:

→ Manuscript submission deadline: 02/20/2021

♦ Peer Review Due: 03/20/2021♦ Revision Due: 04/30/2021

♦ Announcement of acceptance by the Guest Editors: 05/20/2021

→ Final manuscripts due: 06/20/2021

## **Contacts:**

Guest Editor: Tao Huang

Affiliation: Shanghai Institute of Nutrition and Health, Shanghai Institutes for Biological Sciences,

Chinese Academy of Sciences, Shanghai, China

Email: tohuangtao@126.com