



## **Prediction of Key Transcription Factors-Genes Regulatory Network of Ankylosing Spondylitis Based on Transcription Factor Prognosis System**

**Hai-feng Song<sup>1\*</sup>, Jun-wei Gao<sup>1</sup>, Shu-gang Li<sup>2</sup>, Ying-peng Xia<sup>1</sup>, Qing-feng Shen<sup>1</sup>, Shi-bo Ma<sup>1</sup> and Yang Liu<sup>1</sup>**

*<sup>1</sup>Department of Spine Surgery, Tianjin Union Medicine Center, Tianjin, 300121, P.R. China*

*<sup>2</sup>Department of Orthopedic Surgery, Peking Union Medical College Hospital, Chinese Academy of Medical Science, Beijing 100730, P.R. China*

**KEYWORDS** Ankylosing Spondylitis. Different Expressed Genes. Intervertebral Joints. Transcription Factors. Patient and Public Involvements Network

**ABSTRACT** Ankylosing spondylitis (AS), characterized by inflammation in dorsal and intervertebral joints, is a rheumatic disease that leading to varying degrees of structural and functional impairment. Current therapeutic methods have some disadvantages, so clarifying the underlying mechanism and developing new treatment for AS are urgent. The aim of this article is to identify the key transcription factors (TFs) of AS and find new ways for AS treatment. First, the researchers used transcription factor prognosis system, which included enrichment analysis, directly impact value and indirect impact value to find the key TFs targeted different expressed genes. Then the patient and public involvements network was used to integrate the results of the above three methods for analysis. Finally, the researchers obtained the optimal TFs. In summary, this study's analysis based on bioinformatics methods discovered optimal 30 key TFs related to AS. This study may provide important potential therapeutic targets for AS.