[1-41](#_ENREF_1)

1. Zafari, P. *et al.* Analysis of Helios gene expression and Foxp3 TSDR methylation in the newly diagnosed Rheumatoid Arthritis patients. *Immunol Invest* **47**, 632-642 (2018).

2. Fang, G. *et al.* Comprehensive analysis of gene expression and DNA methylation datasets identify valuable biomarkers for rheumatoid arthritis progression. *Oncotarget* **9**, 2977-2983 (2018).

3. Zhang, L. *et al.* Identification of pathogenic genes related to rheumatoid arthritis through integrated analysis of DNA methylation and gene expression profiling. *Gene* **634**, 62-67 (2017).

4. Sun, Z.H. *et al.* MeCP2 Regulates PTCH1 Expression Through DNA Methylation in Rheumatoid Arthritis. *Inflammation* **40**, 1497-1508 (2017).

5. Nair, N., Wilson, A.G. & Barton, A. DNA methylation as a marker of response in rheumatoid arthritis. *Pharmacogenomics* **18**, 1323-1332 (2017).

6. Meng, W. *et al.* DNA methylation mediates genotype and smoking interaction in the development of anti-citrullinated peptide antibody-positive rheumatoid arthritis. *Arthritis Res Ther* **19**, 71 (2017).

7. Lin, Y. & Luo, Z. Aberrant methylation patterns affect the molecular pathogenesis of rheumatoid arthritis. *Int Immunopharmacol* **46**, 141-145 (2017).

8. Horsburgh, S., Ciechomska, M. & O'Reilly, S. CpG-specific methylation at rheumatoid arthritis diagnosis as a marker of treatment response. *Epigenomics* **9**, 595-597 (2017).

9. Guo, S. *et al.* Genome-wide DNA methylation patterns in CD4+ T cells from Chinese Han patients with rheumatoid arthritis. *Mod Rheumatol* **27**, 441-447 (2017).

10. Glossop, J.R. *et al.* DNA methylation at diagnosis is associated with response to disease-modifying drugs in early rheumatoid arthritis. *Epigenomics* **9**, 419-428 (2017).

11. Plant, D. *et al.* Differential Methylation as a Biomarker of Response to Etanercept in Patients With Rheumatoid Arthritis. *Arthritis Rheumatol* **68**, 1353-60 (2016).

12. Maeshima, K. *et al.* Abnormal PTPN11 enhancer methylation promotes rheumatoid arthritis fibroblast-like synoviocyte aggressiveness and joint inflammation. *JCI Insight* **1**(2016).

13. Kojima, A. *et al.* Tumor necrosis factor-alpha gene promoter methylation in Japanese adults with chronic periodontitis and rheumatoid arthritis. *J Periodontal Res* **51**, 350-8 (2016).

14. Hammaker, D. *et al.* LBH Gene Transcription Regulation by the Interplay of an Enhancer Risk Allele and DNA Methylation in Rheumatoid Arthritis. *Arthritis Rheumatol* **68**, 2637-2645 (2016).

15. Gaur, N. *et al.* MicroRNAs interfere with DNA methylation in rheumatoid arthritis synovial fibroblasts. *RMD Open* **2**, e000299 (2016).

16. Fan, S. *et al.* Computationally expanding infinium HumanMethylation450 BeadChip array data to reveal distinct DNA methylation patterns of rheumatoid arthritis. *Bioinformatics* **32**, 1773-8 (2016).

17. Araki, Y. *et al.* Histone Methylation and STAT-3 Differentially Regulate Interleukin-6-Induced Matrix Metalloproteinase Gene Activation in Rheumatoid Arthritis Synovial Fibroblasts. *Arthritis Rheumatol* **68**, 1111-23 (2016).

18. Ai, R. *et al.* Joint-specific DNA methylation and transcriptome signatures in rheumatoid arthritis identify distinct pathogenic processes. *Nat Commun* **7**, 11849 (2016).

19. Liebling, M.R. Methylation of the CTLA-4 promoter and Treg cell dysfunction in rheumatoid arthritis: comment on the article by Cribbs et al. *Arthritis Rheumatol* **67**, 1406 (2015).

20. Glossop, J.R. *et al.* DNA methylation profiling of synovial fluid FLS in rheumatoid arthritis reveals changes common with tissue-derived FLS. *Epigenomics* **7**, 539-51 (2015).

21. de Andres, M.C. *et al.* Assessment of global DNA methylation in peripheral blood cell subpopulations of early rheumatoid arthritis before and after methotrexate. *Arthritis Res Ther* **17**, 233 (2015).

22. Cribbs, A., Feldmann, M. & Oppermann, U. Towards an understanding of the role of DNA methylation in rheumatoid arthritis: therapeutic and diagnostic implications. *Ther Adv Musculoskelet Dis* **7**, 206-19 (2015).

23. Yuan, F.L., Li, X., Xu, R.S., Jiang, D.L. & Zhou, X.G. DNA methylation: roles in rheumatoid arthritis. *Cell Biochem Biophys* **70**, 77-82 (2014).

24. van Steenbergen, H.W. *et al.* Differential methylation within the major histocompatibility complex region in rheumatoid arthritis: a replication study. *Rheumatology (Oxford)* **53**, 2317-8 (2014).

25. Kennedy, A. *et al.* A novel upstream enhancer of FOXP3, sensitive to methylation-induced silencing, exhibits dysregulated methylation in rheumatoid arthritis Treg cells. *Eur J Immunol* **44**, 2968-78 (2014).

26. Glossop, J.R. *et al.* Genome-wide DNA methylation profiling in rheumatoid arthritis identifies disease-associated methylation changes that are distinct to individual T- and B-lymphocyte populations. *Epigenetics* **9**, 1228-37 (2014).

27. Cribbs, A.P. *et al.* Treg cell function in rheumatoid arthritis is compromised by ctla-4 promoter methylation resulting in a failure to activate the indoleamine 2,3-dioxygenase pathway. *Arthritis Rheumatol* **66**, 2344-54 (2014).

28. Zhou, Q. *et al.* Research of the methylation status of miR-124a gene promoter among rheumatoid arthritis patients. *Clin Dev Immunol* **2013**, 524204 (2013).

29. Nakano, K., Boyle, D.L. & Firestein, G.S. Regulation of DNA methylation in rheumatoid arthritis synoviocytes. *J Immunol* **190**, 1297-303 (2013).

30. Miao, C.G. *et al.* New advances of microRNAs in the pathogenesis of rheumatoid arthritis, with a focus on the crosstalk between DNA methylation and the microRNA machinery. *Cell Signal* **25**, 1118-25 (2013).

31. Miao, C.G., Yang, Y.Y., He, X. & Li, J. New advances of DNA methylation and histone modifications in rheumatoid arthritis, with special emphasis on MeCP2. *Cell Signal* **25**, 875-82 (2013).

32. Liu, Y. *et al.* Epigenome-wide association data implicate DNA methylation as an intermediary of genetic risk in rheumatoid arthritis. *Nat Biotechnol* **31**, 142-7 (2013).

33. Guo, J. *et al.* [Peptidyl arginine deiminase 4 participates in the pathogenesis of rheumatoid arthritis by influencing histone methylation]. *Zhonghua Nei Ke Za Zhi* **52**, 928-31 (2013).

34. de la Rica, L. *et al.* Identification of novel markers in rheumatoid arthritis through integrated analysis of DNA methylation and microRNA expression. *J Autoimmun* **41**, 6-16 (2013).

35. Ishida, K. *et al.* Interleukin-6 gene promoter methylation in rheumatoid arthritis and chronic periodontitis. *J Periodontol* **83**, 917-25 (2012).

36. Liu, C.C. *et al.* Global DNA methylation, DNMT1, and MBD2 in patients with rheumatoid arthritis. *Immunol Lett* **135**, 96-9 (2011).

37. Karouzakis, E. *et al.* DNA methylation regulates the expression of CXCL12 in rheumatoid arthritis synovial fibroblasts. *Genes Immun* **12**, 643-52 (2011).

38. Nile, C.J., Read, R.C., Akil, M., Duff, G.W. & Wilson, A.G. Methylation status of a single CpG site in the IL6 promoter is related to IL6 messenger RNA levels and rheumatoid arthritis. *Arthritis Rheum* **58**, 2686-93 (2008).

39. Fu, L.H. *et al.* [Methylation status of the IL-10 gene promoter in the peripheral blood mononuclear cells of rheumatoid arthritis patients]. *Yi Chuan* **29**, 1357-61 (2007).

40. Hashimoto, H., Sohma, H., Nagao, M., Ishii, S. & Akino, T. Elevation of carboxyl methylation activity on GTP-binding protein gamma-subunit in synovial tissues from rheumatoid arthritis: how does elevation of the methylation relate to the signal transduction system of rheumatoid arthritis? *J Orthop Sci* **5**, 470-4 (2000).

41. Richardson, B. *et al.* Evidence for impaired T cell DNA methylation in systemic lupus erythematosus and rheumatoid arthritis. *Arthritis Rheum* **33**, 1665-73 (1990).