

Resource Summary Report

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[GSE17755](#)

RRID:SCR_003650

Type: Tool

Proper Citation

GSE17755 (RRID:SCR_003650)

Resource Information

URL: <http://ranchobiosciences.com/gse17755/>

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Description: Curated data set from a study that contains a gene expression profile of peripheral blood cells (PBMCs) isolated from patients (248 in total) with rheumatoid arthritis (RA)/ systemic lupus erythematosus (SLE)/ polyarticular type juvenile idiopathic arthritis (polyJIA)/ Systemic onset juvenile idiopathic arthritis (sJIA) vs healthy children (HC) and healthy individual (HI).

Abbreviations: GSE17755

Resource Type: data set, data or information resource

Keywords: gene expression profile, gene expression, juvenile, child, inflammation

Related Condition: Inflammatory disease, Rheumatoid arthritis, Systemic lupus erythematosus, Polyarticular type juvenile idiopathic arthritis, Systemic onset juvenile idiopathic arthritis

Availability: Free, Public

Resource Name: GSE17755

Resource ID: SCR_003650

Alternate IDs: nlx_157802

Record Creation Time: 20220129T080220+0000

Record Last Update: 20260805T044057+0000

Ratings and Alerts

No rating or validation information has been found for GSE17755.

No alerts have been found for GSE17755.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 16 mentions in open access literature.

Listed below are recent publications. The full list is available at [RRID](#) .

Sun Y, et al. (2025) Identifying Diagnostic Biomarkers for Electroacupuncture Treatment of Rheumatoid Arthritis Using Bioinformatic Analysis and Machine Learning Algorithms. *Journal of pain research*, 18, 3403.

Gao C, et al. (2025) Regulation of reactive oxygen species and the role of mitochondrial apoptotic-related genes in rheumatoid arthritis. *Scientific reports*, 15(1), 2165.

Zhang S, et al. (2025) Identification of hub immune-related genes and construction of predictive models for systemic lupus erythematosus by bioinformatics combined with machine learning. *Frontiers in medicine*, 12, 1557307.

Sheng L, et al. (2025) Identification of biomarkers related to neutrophil extracellular traps and potential therapeutic drugs for rheumatoid arthritis using computational analysis. *European journal of medical research*, 30(1), 965.

In Il, et al. (2024) Construction and validation of a diagnostic model for rheumatoid arthritis based on mitochondrial autophagy-related genes. *Heliyon*, 10(3), e24818.

Li X, et al. (2024) Revealing the impact of autophagy-related genes in rheumatoid arthritis: Insights from bioinformatics. *Heliyon*, 10(9), e29849.

Rajalingam A, et al. (2024) Identification of common genetic factors and immune-related pathways associating more than two autoimmune disorders: implications on risk, diagnosis, and treatment. *Genomics & informatics*, 22(1), 10.

Wang M, et al. (2023) Genome-wide identification of RNA modification-related single nucleotide polymorphisms associated with rheumatoid arthritis. *BMC genomics*, 24(1), 153.

Liu J, et al. (2021) A 9 mRNAs-based diagnostic signature for rheumatoid arthritis by integrating bioinformatic analysis and machine-learning. *Journal of orthopaedic surgery and research*, 16(1), 44.

Yu R, et al. (2021) Identification of Diagnostic Signatures and Immune Cell Infiltration Characteristics in Rheumatoid Arthritis by Integrating Bioinformatic Analysis and Machine-Learning Strategies. *Frontiers in immunology*, 12, 724934.

Liu Z, et al. (2019) A novel gene and pathway-level subtyping analysis scheme to understand biological mechanisms in complex disease: a case study in rheumatoid arthritis. *Genomics*, 111(3), 375.

Cervantes-Gracia K, et al. (2018) Integrative analysis of Multiple Sclerosis using a systems biology approach. *Scientific reports*, 8(1), 5633.

Mo XB, et al. (2018) Genome-Wide Identification of N6-Methyladenosine (m6A) SNPs Associated With Rheumatoid Arthritis. *Frontiers in genetics*, 9, 299.

Sampson DL, et al. (2017) A Four-Biomarker Blood Signature Discriminates Systemic Inflammation Due to Viral Infection Versus Other Etiologies. *Scientific reports*, 7(1), 2914.

Hao R, et al. (2017) Identification of dysregulated genes in rheumatoid arthritis based on bioinformatics analysis. *PeerJ*, 5, e3078.

Zhu H, et al. (2016) Gene-Based Genome-Wide Association Analysis in European and Asian Populations Identified Novel Genes for Rheumatoid Arthritis. *PloS one*, 11(11), e0167212.