

Resource Summary Report

Generated by [RRID](#) on Aug 5, 2026

[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.