

## Literatuurlijst

Black, R. J., Cross, M., Haile, L. M., Culbreth, G. T., Steinmetz, J. D., Hagins, H., Kopec, J. A., Brooks, P. M., Woolf, A. D., Ong, K. L., Kopansky-Giles, D. R., Dreinhoefer, K. E., Betteridge, N., Aali, A., Abbasifard, M., Abbasi-Kangevari, M., Abdurehman, A. M., Abedi, A., Abidi, H., . . . March, L. M. (2023). Global, regional, and national burden of rheumatoid arthritis, 1990–2020, and projections to 2050: a systematic analysis of the Global Burden of Disease Study 2021. *The Lancet Rheumatology*, 5(10), e594–e610. [https://doi.org/10.1016/s2665-9913\(23\)00211-4](https://doi.org/10.1016/s2665-9913(23)00211-4)

Ding, Q., Xu, Q., Hong, Y., Zhou, H., He, X., Niu, C., Tian, Z., Li, H., Zeng, P., & Liu, J. (2024). Integrated analysis of single-cell RNA-seq, bulk RNA-seq, Mendelian randomization, and eQTL reveals T cell-related nomogram model and subtype classification in rheumatoid arthritis. *Frontiers in Immunology*, 15. <https://doi.org/10.3389/fimmu.2024.1399856>

Firestein, G. S. (2003). Evolving concepts of rheumatoid arthritis. *Nature*, 423(6937), 356–361. <https://doi.org/10.1038/nature01661>

Liao, Y., Smyth, G. K., & Shi, W. (2019). The R package Rsubread is easier, faster, cheaper and better for alignment and quantification of RNA sequencing reads. *Nucleic Acids Research*, 47(8), e47. <https://doi.org/10.1093/nar/gkz114>

Love, M. I., Huber, W., & Anders, S. (2014). Moderated estimation of fold change and dispersion for RNA-seq data with DESeq2. *Genome Biology*, 15(12). <https://doi.org/10.1186/s13059-014-0550-8>

Luo, W., & Brouwer, C. (2013). Pathview: an R/Bioconductor package for pathway-based data integration and visualization. *Bioinformatics*, 29(14), 1830–1831. <https://doi.org/10.1093/bioinformatics/btt285>

Morgan M, Pagès H, Obenchain V, Hayden N (2025). *Rsamtools: Binary alignment (BAM), FASTA, variant call (BCF), and tabix file import*. doi:10.18129/B9.bioc.Rsamtools, R package version 2.24.0, <https://bioconductor.org/packages/Rsamtools>.

Smolen, J. S., Aletaha, D., & McInnes, I. B. (2016). Rheumatoid arthritis. *The Lancet*, 388(10055), 2023–2038. [https://doi.org/10.1016/s0140-6736\(16\)30173-8](https://doi.org/10.1016/s0140-6736(16)30173-8)

Young MD, Wakefield MJ, Smyth GK, Oshlack A (2010). "Gene ontology analysis for RNA-seq: accounting for selection bias." *Genome Biology*, **11**, R14.