

Journal Information

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Classification History

Year	A+	A	B	C
2026		✓	✓	
2025		✓	✓	
2024		✓	✓	
2023		✓	✓	
2021/2022		✓	✓	
2020		✓	✓	
2019	✓	✓	✓	
2018		✓		

Classification: The table above shows all journal classifications recorded for each classification year in the Green Journals database. A journal may have more than one classification in the same year.

Recent Articles

Ethical challenges in patient-focused drug development for rare genetic diseases 2026-10-30 Authors: Meghan C. Halley, Matthew S. McCoy DOI: 10.1038/s41588-026-02824-3
A haplotype reference panel constructed from 490,319 UK Biobank genomes improves genotype imputation for global populations 2026-10-30 Authors: Lars Wienbrandt, Christoph Prieß, Marcus Schmöhl et al. DOI: 10.1038/s41588-026-02819-0
Population-scale single-nucleus multi-omic profiling of skeletal muscle reveals extensive context-specific genetic regulation 2026-10-28 Authors: Arushi Varshney, Nandini Manickam, Peter Orchard et al. DOI: 10.1038/s41588-026-02786-6
The Gujarat Tribal Genome Project (2kTGP) 2026-10-27 Authors: Nitin B. Shukla, Apurvasinh Puvar, Darshan Dharajiya et al. DOI: 10.1038/s41588-026-02820-7
fastGxE is a powerful method for uncovering genotype-environment interactions in biobanks 2026-10-26 DOI: 10.1038/s41588-026-02806-5

<p>Quantification method affects replicability of eQTL analysis, colocalization and TWAS</p> <p>2026-10-26</p> <p>Authors: S. Taylor Head, Sean T. Bresnahan, Yung-Han Chang et al.</p> <p>DOI: 10.1038/s41588-026-02827-0</p>
<p>Interferon-α directs hematopoietic stem cells toward competing fates</p> <p>2026-10-26</p> <p>Authors: Alba Rodriguez-Meira</p> <p>DOI: 10.1038/s41588-026-02797-3</p>
<p>Co-regulation confounds direction of genetic effects in transcriptome-wide association studies</p> <p>2026-10-22</p> <p>Authors: Tiffany Amariuta</p> <p>DOI: 10.1038/s41588-026-02793-7</p>
<p>Near-complete assembly of wild emmer wheat unveils centromere reorganization during polyploid evolution</p> <p>2026-10-22</p> <p>Authors: Congyang Yi, Qian Liu, Lisha Shen et al.</p> <p>DOI: 10.1038/s41588-026-02808-3</p>
<p>High false sign rates in transcriptome-wide association studies</p> <p>2026-10-22</p> <p>Authors: Peter A. Gerlach, Nikhil Milind, Jeffrey P. Spence et al.</p> <p>DOI: 10.1038/s41588-026-02796-4</p>