

- Patel A., Wang M., Ruan Y., Koyama S., Clarke S., Yang X., Tcheandjieu C., Agrawal S., Fahed A., Ellinor P., and Khera A., 2023, A multi-ancestry polygenic risk score improves risk prediction for coronary artery disease, *Nature Medicine*, 29(8): 1793-1803.
<https://doi.org/10.1038/s41591-023-02429-x>
- Ruan Y., Lin Y., Feng Y., Chen C., Lam M., Guo Z., He L., Sawa A., Martin A., Qin S., Huang H., and Ge T., 2021, Improving polygenic prediction in ancestrally diverse populations, *Nature Genetics*, 54(4): 573-580.
<https://doi.org/10.1038/s41588-022-01054-7>
- Sima C., Step K., Swart Y., Schurz H., Uren C., and Möller M., 2024, Methodologies underpinning polygenic risk score estimation: A comprehensive overview, *Human Genetics*, 143(11): 1265-1280.
<https://doi.org/10.1007/s00439-024-02710-0>
- Wand H., Lambert S., Tamburro C., Iacocca M., O'Sullivan J., Sillari C., Kullo I., Rowley R., Dron J., Dron J., Brockman D., Venner E., McCarthy M., Antoniou A., Easton D., Hegele R., Khera A., Chatterjee N., Kooperberg C., Edwards K., Vlessis K., Kinnear K., Danesh J., Parkinson H., Ramos E., Roberts M., Ormond K., Khoury M., Janssens A., Goddard K., Kraft P., MacArthur J., Inouye M., and Wojcik G., 2020, Improving reporting standards for polygenic scores in risk prediction studies, *Nature*, 591(7848): 211-219.
<https://doi.org/10.1038/s41586-021-03243-6>
- Wang X., Xu Y., Hu Z., and Xu C., 2018, Genomic selection methods for crop improvement, *The Crop Journal*, 6(4): 330-340.
<https://doi.org/10.1016/j.cj.2018.03.001>
- Wang Y., Namba S., Lopera E., Kerminen S., Tsuo K., Läll K., Kanai M., Zhou W., Wu K., Favé M., and Neale B., 2023, Global biobank analyses provide lessons for developing polygenic risk scores across diverse cohorts, *Cell Genomics*, 3(1): 100241.
<https://doi.org/10.1016/j.xgen.2022.100241>
- Weissbrod O., Kanai M., Shi H., Gazal S., Peyrot W., Khera A., Okada Y., Matsuda K., Yamanashi Y., Furukawa Y., and Price A., 2022, Leveraging fine-mapping and multi-population training data to improve cross-population polygenic risk scores, *Nature Genetics*, 54(4): 450-458.
<https://doi.org/10.1038/s41588-022-01036-9>
- Xiang R., Kelemen M., Xu Y., Harris L., Parkinson H., Inouye M., and Lambert S., 2024, Recent advances in polygenic scores: Translation, equitability, methods and FAIR tools, *Genome Medicine*, 16(1): 33.
<https://doi.org/10.1186/s13073-024-01304-9>
- Zhang H., Zhan J., Jin J., Zhang J., Lu W., Zhao R., Ahearn T., Yu Z., O'Connell J., Jiang Y., and Chatterjee N., 2023, A new method for multi-ancestry polygenic prediction improves performance across diverse populations, *Nature Genetics*, 55(10): 1757-1768.
<https://doi.org/10.1038/s41588-023-01501-z>

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