

- Tambets R., Kolde A., Kolberg P., Love M.I., and Alasoo K., 2024, Extensive co-regulation of neighboring genes complicates the use of eQTLs in target gene prioritization, *Human Genetics and Genomics Advances*, 5(4): 100187.  
<https://doi.org/10.1016/j.xhgg.2024.100348>
- Votava J.A., and Parks B.W., 2021, Cross-species data integration to prioritize causal genes in lipid metabolism, *Current Opinion in Lipidology*, 32(2): 141-146.  
<https://doi.org/10.1097/MOL.0000000000000742>
- Wainberg M., Sinnott-Armstrong N., Mancuso N., Barbeira A.N., Knowles D.A., Golan D., Ermel R., Ruusalepp A., Quertermous T., Hao K., Björkegren J.L.M., Im H.K., Pasaniuc B., Rivas M.A., and Kundaje A., 2019, Opportunities and challenges for transcriptome-wide association studies, *Nature Genetics*, 51(4): 592-599.  
<https://doi.org/10.1038/s41588-019-0385-z>
- Wallace C., 2021, A more accurate method for colocalisation analysis allowing for multiple causal variants, *PLoS Genetics*, 17(9): e1009440.  
<https://doi.org/10.1371/journal.pgen.1009440>
- Xie Y., Shan N., Zhao H., and Hou L., 2021, Transcriptome-wide association studies: general framework and methods, *Quantitative Biology*, 9(2): 141-150.  
<https://doi.org/10.15302/J-QB-020-0228>
- Zhang J., and Zhao H., 2023, eQTL studies: from bulk tissues to single cells, *Journal of Genetics and Genomics*, 50(12): 925-933.  
<https://doi.org/10.1016/j.jgg.2023.05.003>
- Zhang Y., Wang M., Li Z., Yang X., Li K., Xie A., Dong F., Wang S., Yan J., and Liu J., 2024, An overview of detecting gene-trait associations by integrating GWAS summary statistics and eQTLs, *Science China Life Sciences*, 67(6): 1133-1154.  
<https://doi.org/10.1007/s11427-023-2522-8>
- Zhao S., Crouse W., Qian S., Luo K., Stephens M., and He X., 2022, Adjusting for genetic confounders in transcriptome-wide association studies leads to reliable detection of causal genes, *bioRxiv*, 2022(9): 1-46.  
<https://doi.org/10.1101/2022.09.27.509700>
- Zheng Z., Huang D., Wang J., Zhao K., Zhou Y., Guo Z., Zhai S., Xu H., Cui H., Yao H., Wang Z., Yi X., Zhang S., Sham P.C., and Li M.J., 2020, QTLbase: an integrative resource for quantitative trait loci across multiple human molecular phenotypes, *Nucleic Acids Research*, 48(D1): D983-D991.  
<https://doi.org/10.1093/nar/gkz888>
- Zhu H., and Zhou X., 2020, Transcriptome-wide association studies: a view from Mendelian randomization, *Quantitative Biology*, 2020: 1-15.
- Zuber V., Grinberg N.F., Gill D., Manipur I., Slob E.A., Patel A., Wallace C., and Burgess S., 2022, Combining evidence from Mendelian randomization and colocalization: review and comparison of approaches, *The American Journal of Human Genetics*, 109(5): 767-782.  
<https://doi.org/10.1016/j.ajhg.2022.04.001>

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