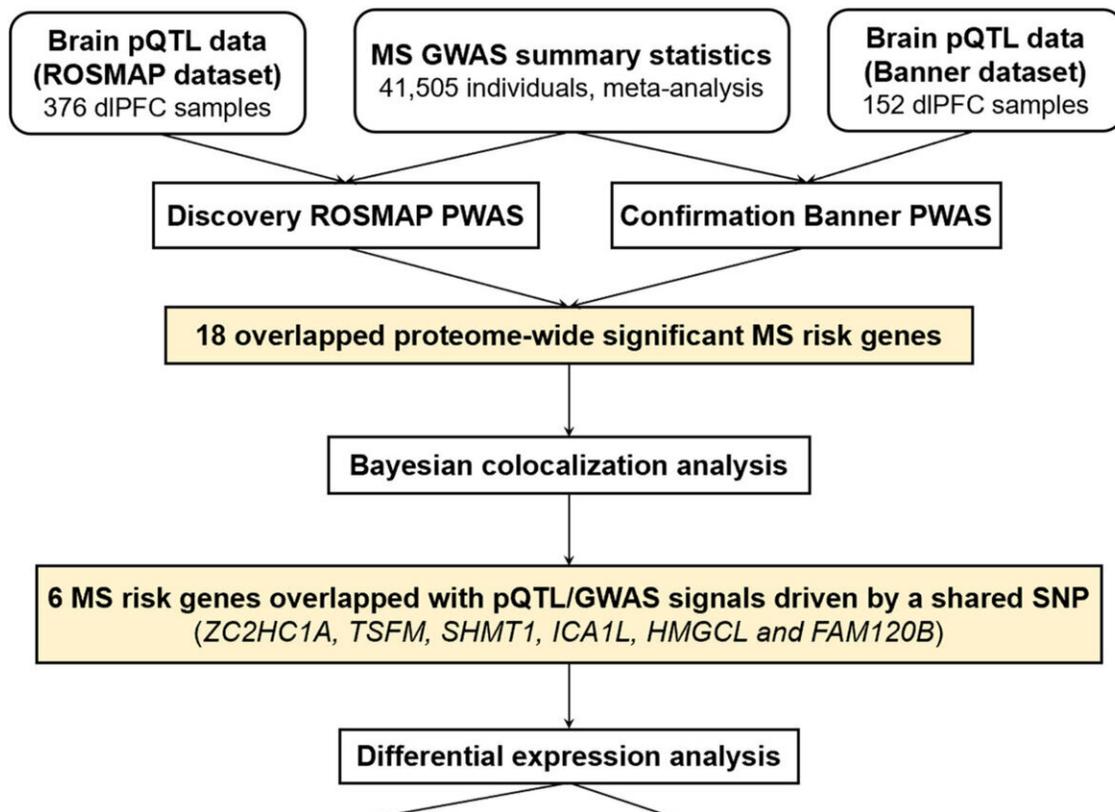


Scientists uncover new genes linked to multiple sclerosis

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The integrated analysis approach used in present study to systematically link protein biomarkers to MS. Firstly, a two-stage PWAS analysis was performed using independent pQTL data (ROSMAP and Banner datasets) and summary statistics from a large-scale MS GWAS. Subsequently, we conducted Bayesian colocalization to identify risk genes with pQTL/GWAS signals driven by shared SNPs. Finally, differential expression analysis was carried out to explore the risk gene dysregulation in MS white matter and cortical gray matter with different histological manifestation (WM/GM lesions and NAWM/NAGM) as compared

to healthy controls. pQTL, protein quantitative trait locus; ROSMAP, Religious Orders Study and Rush Memory and Aging Project; MS, multiple sclerosis; GWAS, genome-wide association study; PWAS, proteome-wide association study; SNP, single nucleotide polymorphism; WM, white matter; GM, gray matter; NAWM, normal appearing white matter; NAGM, normal appearing gray matter. Credit: *Annals of Clinical and Translational Neurology* (2022). DOI: 10.1002/acn3.51699

New research published in the *Annals of Clinical and Translational Neurology* has identified three genes and their expressed proteins that may be involved in the pathogenesis of multiple sclerosis.

By comparing information on the genes and proteins expressed in the brains of thousands of individuals with and without multiple sclerosis, investigators discovered different expression levels of the *SHMT1*, *FAM120B*, and *ICAIL* genes (and their proteins) in brain tissues of patients versus controls.

Studying the functions of these [genes](#) may uncover new information on the mechanisms involved in the development and progression of multiple sclerosis. "Our findings shed new light on the pathogenesis of MS and prioritized promising targets for future therapy research," the authors wrote.

More information: Brain proteome-wide association study linking-genes in multiple sclerosis pathogenesis, *Annals of Clinical and Translational Neurology* (2022). [DOI: 10.1002/acn3.51699](https://doi.org/10.1002/acn3.51699)

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