



FEB 07, 2024

🌐 GWAS prioritization analysis

📁 In 1 collection

Peter Kilfeather¹

¹University of Oxford

PK



Peter Kilfeather

OPEN  ACCESS



ABSTRACT

GWAS prioritization analysis from Kilfeather, Khoo et al., 2024

DOI:

dx.doi.org/10.17504/protocols.io.q26g7pe61gwz/v1

Protocol Citation:

Peter Kilfeather 2024. GWAS prioritization analysis.

protocols.io

<https://dx.doi.org/10.17504/protocols.io.q26g7pe61gwz/v1>

License: This is an open access protocol distributed under the terms of the [Creative Commons Attribution License](#), which permits unrestricted use, distribution, and reproduction in any medium, provided the original author and source are credited

Protocol status:

Working
We use this protocol and it's working

Created: Feb 07, 2024

Last Modified: Feb 07, 2024

PROTOCOL integer ID: 94807

Funders Acknowledgement:

Aligning Science Across

Parkinson's

Grant ID: ASAP-020370

Monument Trust Discovery Award

from Parkinson's UK

Grant ID: J-1403

Protocol

- 1 A list of 303 genes (sourced from Nalls et al., 2019 supplementary materials), containing SNPs at an $r^2 > 0.5$ and located within ± 1 Mb of 107 common risk variants for sporadic PD was used for prioritization analysis. To convert between human and mouse gene symbols, homologene (v1.4.68.19.3.27, RRID:SCR_002924) and biomaRt (v2.52.0, RRID:SCR_019214) were used. TRAP enrichment (measured as the product of the \log_2 fold-change and FDR-adjusted P value) and specificity indices for DAT-TRAP samples were used for gene prioritization, per lead SNP.