

Feb 07, 2024

Gene set enrichment analysis

 In 1 collection

DOI

dx.doi.org/10.17504/protocols.io.kxygx3d2wg8j/v1

Peter Kilfeather¹

¹University of Oxford



Peter Kilfeather

Create & collaborate more with a free account

Edit and publish protocols, collaborate in communities, share insights through comments, and track progress with run records.

Create free account

OPEN  ACCESS



DOI: <https://dx.doi.org/10.17504/protocols.io.kxygx3d2wg8j/v1>

Protocol Citation: Peter Kilfeather 2024. Gene set enrichment analysis. **protocols.io**

<https://dx.doi.org/10.17504/protocols.io.kxygx3d2wg8j/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: February 07, 2024

Last Modified: February 07, 2024

Protocol Integer ID: 94808

Keywords: enrichment analysis gene, enrichment analysis, enrichment analysis from kilfeather, enrichment, gene

Funders Acknowledgements:

Aligning Science Across Parkinson's

Grant ID: ASAP-020370

Monument Trust Discovery Award from Parkinson's UK

Grant ID: J-1403

Abstract

Gene set enrichment analysis from Kilfeather, Khoo et al., 2024

Troubleshooting



Protocol

- 1 No statistical methods were used to predetermine sample sizes, but our sample sizes for TRAP analyses surpass those reported in previous publications^{23,28,87} and our sample sizes for Stereo-seq samples are comparable with or exceed those of similar spatial transcriptomic datasets¹¹. All statistical analyses were performed with R (v4.2.1) and Python (v3.9). All *P* values were modified to an FDR of 1, 5 or 10 % as described in the text with the Benjamini & Hochberg method.