




FEB 07, 2024

## Differential gene expression analysis

 In 1 collection

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### ABSTRACT

Differential gene expression analysis from Kilfeather, Khoo et al., 2024

#### DOI:

[dx.doi.org/10.17504/protocols.io.5jyl8p7k9g2w/v1](https://dx.doi.org/10.17504/protocols.io.5jyl8p7k9g2w/v1)

**Protocol Citation:** Peter Kilfeather 2024. Differential gene expression analysis. **protocols.io** <https://dx.doi.org/10.17504/protocols.io.5jyl8p7k9g2w/v1>

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**Protocol status:** Working  
We use this protocol and it's working

**Created:** Feb 07, 2024

Last Modified: Feb 07, 2024

PROTOCOL integer ID: 94804

**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 Differential gene expression analysis in TRAP samples (including calculation of gene enrichment and depletion, relative to tissue homogenate RNA) was performed using DESeq2 (v1.36.0, RRID:SCR\_015687) in R (v4.2.1, RRID:SCR\_001905) with Bioconductor (v3.15, RRID:SCR\_006442). Adaptive shrinkage of log fold change estimates was performed using ashR. The following settings were changed from defaults: minReplicatesForReplace = Inf, cooksCutoff = Inf, filterFun = iHW, lfcThreshold =  $\log_2(1.05)$ . Genes were classed as significantly differentially expressed with an FDR-adjust  $P$  value  $< 0.01$ . Protein-protein interactions were obtained using STRINGdb (version 11) with a minimum confidence threshold of 0.4.