

REGINA H REYNOLDS

★ KEY PUBLICATIONS

2021

- **Cross-platform transcriptional profiling identifies common and distinct molecular pathologies in Lewy body disorders¹**

Acta Neuropathologica

- Feleke, R, **Reynolds, RH**, Smith, A, Tilley, B, Gagliano Taliun, SA, Hardy, J, Matthews, PM, Gentleman, S, Owen , D, Johnson, MR, Srivastava, P, Ryten, M
- **Role:** Co-first author and analyst.
- Transcriptomic analysis² of cell-type-specific changes in the Lewy body diseases.

2020

- **Dystonia genes functionally converge in specific neurons and share neurobiology with psychiatric disorders³**

Brain

- Mencacci, NE, **Reynolds, RH**, Garcia Ruiz, S, Vandrovčova, J, Forabosco, P, Sánchez-Ferrer, A, Volpati, V, UK Brain Expression Consortium, International Parkinson's Disease Genomics Consortium, Weale, ME, Bhatia, KP, Webber, C, Hardy, J, Botía, JA, Ryten, M
- **Role:** Co-first author and analyst.
- Integrative omics analysis of monogenic dystonias, with the aim of improving our understanding of the pathways driving this clinically heterogeneous group of movement disorders.

2019

- **Informing disease modelling with brain-relevant functional genomic annotations⁴**

Brain

- **Reynolds, RH**, Hardy, J, Ryten, M, Gagliano Taliun, SA
- **Role:** First author.
- Review of conceptual advances in the generation of brain-relevant functional genomic annotations and among tools that allow integration of these annotations with genome-wide association summary statistics.

2019

- **Moving beyond neurons: the Role of cell type-specific gene regulation in Parkinson's disease heritability⁵**

NPJ Parkinson's disease

- **Reynolds, RH**, Botía, JA, Nalls, MA, International Parkinson's Disease Genomic Consortium (IPDGC), System Genomics of Parkinson's Disease (SGPD), Hardy, J, Gagliano Taliun, SA, Ryten, M
- **Role:** First author and lead analyst.
- Analysis of Parkinson's disease common variation, with the aim of identifying cell types and pathways of importance to disease risk.

2018

- **Perturbations in the p53/miR-34a/SIRT1 pathway in the R6/2 Huntington's disease model⁶**

Molecular and Cellular Neuroscience

- **Reynolds, RH**, Petersen, MH, Willert, CW, Heinrich, M, Nymann, N, Dall, M, Treebak, JT, Björkqvist, M, Silahtaroglu, A, Hasholt, L and Nørremølle, A
- **Role:** First author, lead experimentalist and analyst.

View this publications list online with links at <https://rhreynolds.github.io/cv>

CONTACT

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/in LinkedIn

/e ResearchGate

The long-form version of my CV is available [here](#).

Made with the R packages [datadrivencv](#) and [pagedown](#).

The source code is available [GitHub](#).

Last updated on 2022-05-18.

PUBLICATIONS

- 2021 • **A genetic link between risk for Alzheimer's disease and severe COVID-19 outcomes via the OAS1 gene⁷**
Brain
• Magusali, N, Graham, AC, Piers, TM, Panichnantakul, P, Yaman, U, Shoai, M, **Reynolds, RH** et al.
• **Role:** Adviser. Reviewed and critiqued statistical analyses and manuscript.
- 2021 • **Mitochondrial-nuclear cross-talk in the human brain is modulated by cell type and perturbed in neurodegenerative disease⁸**
Communications Biology
• Fairbrother-Browne, A, Ali, A, **Reynolds, RH** et al.
• **Role:** Adviser. Advised on tools available for cell-type specificity and heritability analyses.
- 2021 • **A systems-level analysis highlights microglial activation as a modifying factor in common epilepsies⁹**
Neuropathology and Applied Neurobiology
• Altmann, A, Ryten, M, Di Nunzio, M, Ravizza, T, Tolomeo, D, **Reynolds, RH** et al.
• **Role:** Analyst. Collated gene lists designed to capture microglial states.
- 2021 • **An integrated genomic approach to dissect the genetic landscape regulating the cell-to-cell transfer of α -synuclein¹⁰**
Cell Reports
• Kara, E, Crimi, A, Wiedmer, A, Emmenegger, M, Manzoni, C, Bandres-Ciga, S, D'Sa, K, **Reynolds, RH** et al.
• **Role:** Analyst. Performed expression-weighted cell-type enrichment analyses.
- 2021 • **Heritability enrichment implicates microglia in Parkinson's disease pathogenesis¹¹**
Annals of Neurology
• Andersen, MS, Bandres-Ciga, S, **Reynolds, RH** et al.
• **Role:** Adviser. Reviewed and critiqued statistical analyses and manuscript.
- 2021 • **Human-lineage-specific genomic elements: relevance to neurodegenerative disease and APOE transcript usage¹²**
Nature Communications
• Chen, Z, Zhang, D, **Reynolds, RH** et al.
• **Role:** Analyst. Performed partitioned SNP-heritability analyses.
- 2021 • **Identification of Candidate Parkinson Disease Genes by Integrating Genome-Wide Association Study, Expression, and Epigenetic Data Sets¹³**
JAMA Neurology
• Kia, DA, Zhang, D, Guelfi, S, Manzoni, C, Hubbard, L, **Reynolds, RH** et al.
• **Role:** Analyst. Involved in cell-type annotation of prioritised genes.

2021

- **Modelling multifunctionality of genes with secondary gene co-expression networks in human brain provides novel disease insights¹⁴**
Bioinformatics
 - Sánchez, JA, Gil-Martínez, AL, Cisterna, A, García-Ruiz, S, Gómez-Pascual, A, **Reynolds, RH** et al.
 - **Role:** Adviser. Reviewed and critiqued statistical analyses and manuscript.

2021

- **Genome sequencing analysis identifies new loci associated with Lewy body dementia and provides insights into the complex genetic architecture¹⁵**
Nature Genetics
 - Chia, R, Sabir, MS, Bandres-Ciga, S, Saez-Atienzar, S, **Reynolds, RH** et al.
 - **Role:** Analyst. Performed colocalisation analyses and gene expression analyses.

2021

- **CoExp Web, a web tool for the exploitation of co-expression networks¹⁶**
Frontiers in Genetics
 - García-Ruiz, S, Gil-Martínez, AL, Cisterna, A, Jurado, F, **Reynolds, RH** et al.
 - **Role:** Analyst. Involved in cell-type annotation of gene co-expression networks.

2021

- **Genetic determinants of survival in progressive supranuclear palsy: a genome-wide association study¹⁷**
Lancet Neurology
 - Jabbari, E, Koga, S, Valentino, R, **Reynolds, RH** et al.
 - **Role:** Analyst. Performed colocalisation analyses.

2021

- **Genome-wide association studies of cognitive and motor progression in Parkinson's disease¹⁸**
Movement Disorders
 - Tan, MMX, Lawton, MA, Jabbari, E, **Reynolds, RH** et al.
 - **Role:** Adviser. Reviewed and critiqued statistical analyses and manuscript.

2021

- **Genetic analysis of amyotrophic lateral sclerosis identifies contributing pathways and cell types¹⁹**
Science Advances
 - Saez-Atienzar, S, Bandres-Ciga, S, Langston, RG, Kim, JJ, Choi, SW, **Reynolds, RH** et al.
 - **Role:** Adviser. Reviewed and critiqued statistical analyses and manuscript.

2020

- **Differences in network controllability and regional gene expression underlie hallucinations in Parkinson's disease²⁰**
Brain
 - Zarkali, A, McColgan, P, Ryten, M, **Reynolds, RH** et al.
 - **Role:** Adviser. Reviewed and critiqued statistical analyses and manuscript.

- 2020
- Dementia risk in Parkinson's disease is associated with interhemispheric connectivity loss and determined by regional gene expression²¹
NeuroImage: Clinical
 - Zarkali, A, McColgan, P, Ryten, M, **Reynolds, RH** et al.
 - **Role:** Adviser. Reviewed and critiqued statistical analyses and manuscript.
- 2020
- Analysis of brain atrophy and local gene expression in genetic frontotemporal dementia²²
Brain Communications
 - Altmann, A, Cash, DM, Bocchetta, M, Heller, C, **Reynolds, RH** et al.
 - **Role:** Analyst. Performed expression-weighted cell-type enrichment analyses.
- 2020
- Incomplete annotation of disease-associated genes is limiting our understanding of Mendelian and complex neurogenetic disorders²³
Science Advances
 - Zhang, D, Guelfi, S, Ruiz, SG, Costa, B, **Reynolds, RH** et al.
 - **Role:** Analyst. Performed expression-weighted cell-type enrichment analyses.
- 2020
- Regulatory sites for known and novel splicing in human basal ganglia are enriched for disease-relevant information²⁴
Nature Communications
 - Guelfi, S*, D'Sa, K*, Botía, JA*, Vandrovčová, J, **Reynolds, RH** et al.
 - **Role:** Experimentalist and analyst. Performed PCR validation of transcription and partitioned SNP-heritability analyses.
- 2019
- Genetic variability in response to amyloid beta deposition influences Alzheimer's risk²⁵
Brain Communications
 - Salih, DA, Bayram, S, Guelfi, S, **Reynolds, RH** et al.
 - **Role:** Analyst. Performed colocalisation analyses.
- 2019
- Mitochondria function associated genes contribute to Parkinson's Disease risk and later age at onset²⁶
NPJ Parkinson's disease
 - Billingsley, KJ, Barbosa, IA, Bandrés-Ciga S, Quinn, JP, Bubb, VJ, Deshpande, C, Botía, JA, **Reynolds, RH** et al.
 - **Role:** Analyst. Performed expression-weighted cell-type enrichment analyses.
- 2018
- Variation at the TRIM11 locus modifies Progressive Supranuclear Palsy phenotype²⁷
Annals of Neurology
 - Jabbari, E, John, W, Tan, MMX, Maryam, S, Pittman, A, Ferrari, R, Mok, KY, Zhang, D, **Reynolds, RH** et al.
 - **Role:** Analyst. Performed gene-based association testing and analysis of gene expression data.



PRE-PRINTS

- 2022 • **ggtranscript: an R package for the visualization and interpretation of transcript isoforms using ggplot2²⁸**
bioRxiv
• Gustavsson, EK, Zhang, D, **Reynolds, RH**, Ruiz, SG, Ryten, MR
• **Role:** Adviser. Performed beta testing and critiqued manuscript.
- 2021 • **Genome-wide association study of REM sleep behaviour disorder identifies novel loci with distinct polygenic and brain expression effects²⁹**
medRxiv
• Krohn, L, Heilbron, K, Blauwendraat, C, **Reynolds, RH**, et al.
• **Role:** Analyst. Performed colocalisation analyses and gene expression analyses.
- 2021 • **Detection of pathogenic splicing events from RNA-sequencing data using dasper³⁰**
bioRxiv
• Zhang, D, **Reynolds, RH**, et al.
• **Role:** Adviser. Helped guide and troubleshoot feature selection for outlier detection of splicing events.
- 2019 • **ERASE: Extended Randomization for assessment of annotation enrichment in ASE datasets³¹**
bioRxiv
• D'Sa, K, Reynolds RH et al.
• **Role:** Analyst. Performed partitioned SNP-heritability analyses.
- 2018 • **G2P: Using machine learning to understand and predict genes causing rare neurological disorders³²**
bioRxiv
• Botía, JA, Guelfi, S, Zhang, D, D'Sa, K, **Reynolds, RH** et al.
• **Role:** Adviser. Helped interpret the output of machine-learning-based models to distinguish disease genes from non-disease genes.