

REGINA H REYNOLDS

Molecular biologist turned bioinformatician, with experience translating large-scale omics data into actionable insights for drug discovery. I've led cross-functional analyses across transcriptomics, genomics, and functional screens, collaborating closely across teams to build reproducible pipelines that support impactful R&D decisions. I'm driven by a commitment to scientific rigour, integrity, and transparency — and by a broader desire to make a meaningful contribution to the world through thoughtful, data-driven science.

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

CONTACT

✉ rhreynolds@hotmail.co.uk
🐙 [GitHub](#)
in [LinkedIn](#)
📖 [ResearchGate](#)



WORK EXPERIENCE

Present
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2022

Lead Bioinformatician

CoSyne Therapeutics

📍 London, UK

- Provide scientific and strategic leadership as co-lead of a 5-person computational biology team, setting research priorities in collaboration with team members, experimental and AI teams, and senior leadership.
- Drive company-wide 'omics initiatives spanning whole-genome sequencing, transcriptomics and CRISPRi screens to support target discovery in glioblastoma multiforme.
- Establish scalable, robust, and reproducible computational workflows through adoption of tools such as Nextflow and Seqera Cloud for workflow orchestration, Docker for containerisation, R targets for reproducible exploratory data analysis, and Cruft templates for project scaffolding.
- Contribute to shaping company culture through active involvement in recruitment and development of CoSyne's personal development framework.

2022
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2021

Research Fellow

University College London

📍 London, UK

- Lead analyst involved in processing and analysing transcriptomic data generated with the aim of identifying molecular signatures of Parkinson's disease progression. Work performed using R, Nextflow and Docker.
- Co-lead of Code and Pipeline Alignment Working Group in the Aligning Sciences Across Parkinson's' initiative. This group aimed to maximise the value of data generated from finite post-mortem brain tissues through code alignment, which would enable eventual meta-analysis.
- Published 1 co-first author research article.

2016
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2016

Research Assistant

University of Copenhagen

📍 Copenhagen, Denmark

- Led project exploring the interactions between miR-34a, Sirt1 and p53 in a Huntington's disease mouse model, which culminated in a first author publication².

PROGRAMMING LANGUAGES

R

Git/GitHub

Nextflow

Bash

docker

Python

Made with the R packages *datadrivencv* and *pagedown*.

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

Last updated on 2025-06-15.

EDUCATION

2021
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2016

• **PhD, Bioinformatics**

University College London

📍 London, UK

- Thesis: Exploring the importance of cell-type-specific gene expression regulation and splicing in Parkinson's disease³.
- Integrated GWAS summary statistics with bulk/single-cell transcriptomic, eQTL, and chromatin accessibility data to identify cell-type-specific regulatory mechanisms in Parkinson's disease. Methods used included partitioned heritability, COLOC, and MAGMA.
- Applied transcriptomic methods, including cell-type deconvolution, differential splicing analysis, and RNA-binding protein motif analysis, to investigate splicing alterations and their relevance to Lewy body diseases.
- Published 3 first/co-first author research articles and 1 first author review. Successfully secured £10,000 from Signe og Peter Gregersens Mindefond to undertake transcriptional profiling of Parkinson's disease brain tissue.

2016
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2014

• **MSc, Molecular Biomedicine**

University of Copenhagen

📍 Copenhagen, Denmark

- Thesis: Changes in the miR-34a-SIRT1 axis in Huntington's disease
- Grade: A (92.5%)

2013
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2010

• **BSc, Molecular Biomedicine**

University of Copenhagen

📍 Copenhagen, Denmark

- Thesis: Pro-apoptotic factors in Huntington's disease: a study in the R6/2 transgenic mouse model
- Grade: A (96.7%)

TEACHING EXPERIENCE

2025
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2021

• **Subsidiary PhD Supervisor**

University College London

📍 London, UK

- Secondary supervisor to Dr. Aaron Wagen. Provided support around transcriptomic analyses, bioinformatics workflows and statistical genetics.

2022
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2019

• **R fundamentals with Clinician Coders⁴**

University College London

📍 London, UK

- Developed materials⁵ and led workshops teaching basic R and tidy data principles to clinical academics.

2019
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2017

• **Omics Techniques**

King's College London

📍 London, UK

- Lectured graduate level students on the principles of genome-wide association studies and led a workshop on how/why to use the Genotype-Tissue Expression portal.



VOLUNTARY WORK

Present
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2018

Peer Reviewer

📍 London, UK

- Reviewer⁶ for several scientific journals.

2022
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2017

Mentor

[Social Mobility Foundation](#)

📍 London, UK

- Mentored 4 A-level students looking to work in the field of biomedical research.



KEY PUBLICATIONS

2023

Local genetic correlations exist among neurodegenerative and neuropsychiatric diseases⁷

NPJ Parkinson's disease

- Reynolds, RH, Wagen, AZ, Lona-Durazo, F, Scholz, SW, Shoai, M, Hardy, J, Gagliano Taliun, SA, Ryten, M
- Role: Co-first author, lead analyst and corresponding author.
- Analysis⁸ of local genetic correlations between neurodegenerative and neuropsychiatric disorders, with the aim of identifying genomic regions and genes that may drive pleiotropy.

A full list of publications is available online at <https://rhreynolds.github.io/cv>

2021

Cross-platform transcriptional profiling identifies common and distinct molecular pathologies in Lewy body disorders⁹

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 analysis¹⁰ of cell-type-specific changes in the Lewy body diseases.

2019

Informing disease modelling with brain-relevant functional genomic annotations¹¹

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 heritability¹²

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.

CONFERENCES

- 2022 • **AD/PD, Alzheimer's & Parkinson's Diseases Conference**
📍 Hybrid event
- Talk: Identifying genetic correlations among neurodegenerative and neuropsychiatric diseases
- 2021 • **Genomics of Brain Disorders**
📍 Virtual event
- Talk: Dysregulation of splicing in human brain from individuals with Lewy body disease informs disease mechanisms
- 2019 • **International Parkinson's Disease Genomics Consortium**
📍 London, UK
- Talk: Pairing bulk and single-nuclear RNA-seq to identify dementia-related pathways in PD
- 2019 • **AD/PD, Alzheimer's & Parkinson's Diseases Conference**
📍 Lisbon, Portugal
- Talk: Mapping Parkinson's disease heritability to specific brain cell types
 - Received mention in a blog post on Alzforum¹³.
- 2018 • **International Parkinson's Disease Genomics Consortium**
📍 Reykjavik, Iceland
- Talk: Moving beyond neurons: exploring the importance of cell type-specific gene expression in Parkinson's disease

LINKS

- 1: <https://parkinsonsroadmap.org/research-network/pd-functional-genomics/>
- 2: <https://pubmed.ncbi.nlm.nih.gov/29289683/>
- 3: <https://discovery.ucl.ac.uk/id/eprint/10119171/>
- 4: <https://www.ucl.ac.uk/school-life-medical-sciences/about-slms/office-vice-provost-health/academic-careers-office/career-schemes/clinician-coders>
- 5: <https://github.com/ClinicianCoders/ClinicianCoders>
- 6: <https://publons.com/researcher/3017104/regina-hertfelder-reynolds/peer-review/>
- 7: <https://pubmed.ncbi.nlm.nih.gov/37117178/>
- 8: <https://rhreynolds.github.io/neurodegen-psych-local-corr/>
- 9: <https://pubmed.ncbi.nlm.nih.gov/34309761/>
- 10: <https://rhreynolds.github.io/LBD-seq-bulk-analyses/>
- 11: <https://pubmed.ncbi.nlm.nih.gov/31603214/>
- 12: <https://pubmed.ncbi.nlm.nih.gov/31016231/>
- 13: <https://www.alzforum.org/news/conference-coverage/expression-expression-expression-time-get-board-eqtls>