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 resume online with links at https://rhreynolds.github.io/cv

WORK EXPERIENCE

Present | 2022

Lead Computational Biologist

CoSyne Therapeutics — London, UK

- Provide scientific and strategic leadership as lead of a 5-person computational biology team, translating high-level objectives into clear milestones and actionable plans, managing tight deadlines and resources, and setting research priorities in collaboration with team members, experimental, engineering, 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 line management; growing the computational biology team from 2 to 5 people; active involvement in recruitment across multiple teams; and contributing to the development of CoSyne's personal development framework.

2025 | 2022

Honorary Senior Research Fellow

University College London — London, UK

- Acted as secondary supervisor to a PhD student and served on the thesis committee for another. Additionally contributed to analyses and provided input on papers across multiple research projects.

2022 | 2021

Research Fellow

University College London — London, UK

- Lead analyst involved in processing and analysing transcriptomic data to identify molecular signatures of Parkinson's disease progression. Worked within a large, multi-PI team and coordinated with researchers to align analytical approaches. Work performed using R, Nextflow, and Docker.
- Co-lead of Code and Pipeline Alignment Working Group in the Aligning Sciences Across Parkinson's[7] initiative, facilitating the standardisation of data processing pipelines and coding practices across 10 international research teams, resulting in actionable recommendations to enhance data harmonisation and enable meta-analysis of post-mortem brain tissue datasets.
- Published 1 co-first author research article.

CONTACT

- rhreynolds@hotmail.co.uk
- GitHub
- LinkedIn
- ResearchGate

LANGUAGES

- R
- Bash
- Python

TOOLS

- Git/GitHub/GitLab
- Nextflow
- docker

The long-form version of my CV, with a list of conferences attended, teaching experience and voluntary work is available here.

The source code is available GitHub.

Last updated on 2025-06-22.

2016 | 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, serving as lead experimentalist and analyst; work culminated in a first author publication[2].
- In addition to these roles, facilitated collaboration with another research group and coordinated experiments with lab technicians, students, and researchers to support project goals.

EDUCATION

2021 | 2016

PhD, Bioinformatics

University College London — London, UK

- Thesis: Exploring the importance of cell-type-specific gene expression regulation and splicing in Parkinson's disease[3].
- 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 | 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 | 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%)

KEY PUBLICATIONS

2023

Local genetic correlations exist among neurodegenerative and neuropsychiatric diseases[4]

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.
- Analysis[5] 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 disorders[6]

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 analysis[7] of cell-type-specific changes in the Lewy body diseases.

2019

Informing disease modelling with brain-relevant functional genomic annotations[8]

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 heritability[9]

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.

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://pubmed.ncbi.nlm.nih.gov/37117178/
5: https://rhreynolds.github.io/neurodegen-psych-local-corr/
6: https://pubmed.ncbi.nlm.nih.gov/34309761/
7: https://rhreynolds.github.io/LBD-seq-bulk-analyses/
8: https://pubmed.ncbi.nlm.nih.gov/31603214/
9: https://pubmed.ncbi.nlm.nih.gov/31016231/