

PETER KILFEATHER

Oxford, UK | +44 (0) 7852 766 732 | info@oxfordomics.com | oxfordomics.com

Founder and lead computational biologist at [Oxford Omics Ltd](https://oxfordomics.com), delivering end-to-end **multi-omics**, **machine-learning**, and **structural-biology** solutions to **biotech** and **academic** teams. Expert in **single-cell**, **CRISPR**, and **spatial transcriptomics**; experienced in **nanobody/antibody design** and **custom ML** pipelines. Produce high-quality, reproducible analyses, **dashboards**, and **pipelines** tailored to complex scientific workflows.



CORE SKILLS

- **Multi-omics:** scRNA-seq, Perturb-seq, spatial, bulk, long-read, CITE-seq
- **Machine learning:** Supervised modelling, deep learning for gene essentiality, ML-driven feature selection
- **Protein & antibody engineering:** Nanobody/antibody modelling (BoltzGen/Boltz2), AlphaFold prediction, peptide docking
- **Genomics:** CRISPR screens, variant calling (somatic/germline), *de novo* assembly, methylation & splicing
- **Pipeline engineering:** Nextflow, nf-core, Snakemake, CAP/CLIA-compliant pipelines
- **Cloud & HPC:** AWS, Benchling Warehouse, Docker, CI/CD, scalable GPU workflows

PROFESSIONAL EXPERIENCE

[Oxford Omics Ltd](https://oxfordomics.com)

Director & Computational Biologist, 2020 – Present

Lead multi-omics, ML, and structural-biology consulting for biotech and academic partners, delivering scalable pipelines, predictive models, and actionable biological insights.

- Designed and delivered **multi-omics workflows** across scRNA-seq, CITE-seq, Perturb-seq, spatial transcriptomics, bulk RNA-seq, methylation, splicing, and long-read sequencing (ONT & PacBio).
- Built **machine-learning and deep-learning models** for gene essentiality, tumour classification, feature-based biological prediction.
- Developed **Nextflow/Snakemake/nf-core pipelines**, including CAP/CLIA-compliant workflows, variant calling (WGS/WES, somatic & germline), CRISPR screens (targeted & genome-wide).
- Performed **nanobody/antibody structural modelling** using BoltzGen/Boltz2, and peptide docking using AlphaFold for early-stage discovery.
- Engineered cloud-native genomics infrastructure using **AWS, Benchling Warehouse, Docker**, and **CI/CD**.
- Advised on **CLIA validation, CRISPR library design**, and integrated multi-omics strategies for biotech partners.
- Built **R Shiny dashboards**, and **REST/SQL/Spark** data layers for interactive client data exploration.
- Provide **mentoring, technical upskilling, and staff-augmentation support** for teams needing expanded bioinformatics capacity or senior scientific guidance.

University of Oxford

DPhil & Postdoctoral Scientist, 2017 – 2023

Computational biologist in the Wade-Martins Laboratory of Molecular Neurodegeneration, focusing on spatial transcriptomics and neurodegenerative disease.

- Published first-author work in [Cell Reports \(2024\)](https://doi.org/10.1016/j.cell.2024.01.010) using single-cell spatial transcriptomic and translatomic profiling.
- Performed **scRNA-seq, spatial transcriptomic, ribosome profiling**, and high-resolution (200 nm) imaging-integrated transcriptomic workflows.

EDUCATION

- **DPhil**, University of Oxford, UK
- **DVM**, University of Bristol, UK

LEADERSHIP

Former Men's Captain & President, Christ Church Boat Club; national and international regatta competitor.