

# JACK GISBY

✉ [j.gisby20@imperial.ac.uk](mailto:j.gisby20@imperial.ac.uk) ☎ (+44)7748 559964  
🐙 [github.com/jackgisby](https://github.com/jackgisby) 🆔 [orcid.org/0000-0003-0511-8123](https://orcid.org/0000-0003-0511-8123)

## EDUCATION

---

### Imperial College London

PhD Candidate

*August 2020 – July 2023*

- Thesis: Using Multi-Omics to Understand COVID-19, supervised by Dr James Peters.

### University of Birmingham

Biochemistry with Professional Placement (MSci) - First Class

*September 2016 – June 2020*

- Dissertation: A Prior Knowledge-Based Computational Workflow for *de novo* Structural Elucidation of Small Molecules in Mass Spectrometry Metabolomics, supervised by Dr Ralf Weber.

## RESEARCH EXPERIENCE

---

### PhD Research

Immunology and Inflammation, Imperial College London

*August 2020 – July 2023*

- Integrated proteomic, transcriptomic and genetic data to investigate the pathology of COVID-19.
- Applied longitudinal modelling, network analyses and supervised learning to high-dimensional datasets.
- Developed a Mendelian randomisation pipeline to find genetic variants that lead to severe COVID-19.
- Disseminated research findings through peer-reviewed publications and conference presentations.

### MSc Research

School of Biosciences, University of Birmingham

*October 2019 – June 2020*

- Developed a [Python package for improved annotation of LC-MS metabolomics spectra](#) 🐙.
- Created a deep learning-based anomaly detection model that classifies molecular structures.
- Adhered to software engineering best practices, including version control and automated testing.

### Research volunteer

School of Biosciences, University of Birmingham

*July 2019 – June 2020*

- Developed an R/Bioconductor package for [annotating rare transposons in genome sequences](#) 🐙.
- Mined sequence data to uncover the impact of DNA transposons on the evolution of host genes.

### Industrial placement

The Binding Site, Birmingham

*Aug 2018 – Jul 2019*

- Took responsibility for the timely delivery of assay development projects and statistical reports.
- Communicated with, and delivered presentations to, a wide variety of interdisciplinary staff.

## TEACHING EXPERIENCE

---

### Lecturing

Molecular Epidemiology MSc Module, Imperial College London

*September 2021 – December 2022*

- Developed and delivered lectures for RNA sequencing in the context of investigating genetic variation.
- Set homework and reading, in addition to final exam questions and marking schemes.

## Graduate Teaching Assistant

May 2022 – August 2022

Research Computing, Imperial College London

- Developed a [parallelised pipeline for RNA-seq data](#)  using Docker and Nextflow.
- Created teaching materials demonstrating best practices for building data pipelines.

## Mentoring

July 2021 – August 2022

Immunology and Inflammation, Imperial College London

- Co-supervised an undergraduate research project utilising proteomics to investigate Lupus.

## SKILLS

---

<b>Languages</b>	Proficient in Python, R, Bash, SQL, exposure to C++, Julia
<b>Tools</b>	Git/GitHub, Docker, Conda, Nextflow, Airflow, L <sup>A</sup> T <sub>E</sub> X
<b>Compute</b>	High performance computing clusters, Google Cloud Platform
<b>Data</b>	Transcriptomics (bulk and single cell RNA-seq), proteomics (Olink/SomaLogic assays), genomics (sequences and variants), metabolomics (LC-MS), clinical data
<b>Statistics</b>	Linear and mixed models, joint models, Mendelian randomisation & fine mapping, supervised learning (caret, scikit-learn, pytorch), network analysis (WGCNA)
<b>Software</b>	Package development (R, Python), containerisation (Docker, Singularity), continuous integration (unittest, testthat), version control (Git, GitHub)

## SELECTED PUBLICATIONS

---

- **Jack S. Gisby<sup>†</sup>**, Norzawani B. Buang<sup>†</sup>, Artemis Papadaki, Candice L. Clarke, Talat H. Malik, Nicholas Medjeral-Thomas, Damiola Pinheiro, Paige M. Mortimer, Shanice Lewis, Eleanor Sandhu, Stephen P. McAdoo, Maria F. Prendecki, Michelle Willicombe, Matthew C. Pickering, Marina Botto, David C. Thomas<sup>†</sup>, James E. Peters<sup>†</sup>. **Multi-omics identify LRR15 as a COVID-19 severity predictor and persistent pro-thrombotic signals in convalescence.** *medRxiv* 2022. [10.1101/2022.04.29.22274267](#)
- **Gisby JS**, Catoni M. **The widespread nature of Pack-TYPE transposons reveals their importance for plant genome evolution.** *PLOS Genetics* 2022. [10.1371/journal.pgen.1010078](#)
- Klaric L<sup>†</sup>, **Gisby JS<sup>†</sup>**, Papadaki A<sup>†</sup>, Muckian MD, Macdonald-Dunlop E, Zhao JH, Tokolyi A, Persyn E, Pairo-Castineira E, Morris AP, Kalnapekakis A, Richmond A, Landini A, Hedman K, Prins B, Zanetti D, Wheeler E, Kooperberg C, Yao C, Petrie JR, Fu J, Folkersen L, Walker M, Magnusson M, Eriksson N, Mattsson-Carlgren N, Timmers PRHJ, Hwang SJ, Enroth S, Gustafsson S, Vosa U, Chen Y, Siegbahn A, Reiner A, Johansson , Thorand B, Gigante B, Hayward C, Herder C, Gieger C, Langenberg C, Levy D, Zhernakova DV, Smith JG, Campbell H, Sundstrom J, Danesh J, Michalsson K, Suhre K, Lind L, Wallentin L, Padyukov L, Landn M, Wareham NJ, Gteson A, Hansson O, Eriksson P, Strawbridge RJ, Assimes TL, Esko T, Gyllenstein U, Baillie JK, Paul DS, Joshi PK, Butterworth AS, Mlarstig A, Pirastu N, Wilson JF<sup>†</sup>, Peters JE<sup>†</sup>. **Mendelian randomisation identifies alternative splicing of the FAS death receptor as a mediator of severe COVID-19.** *medRxiv* 2021. [2021.04.01.21254789](#)
- **Jack S. Gisby<sup>†</sup>**, Candice L Clarke<sup>†</sup>, Nicholas Medjeral-Thomas<sup>†</sup>, Talat H Malik, Artemis Papadaki, Paige M Mortimer, Norzawani B Buang, Shanice Lewis, Marie Pereira, Frederic Toulza, Ester Fagnano, Marie-Anne Mawhin, Emma E Dutton, Lunnathaya Tapeng, Arianne C Richard, Paul DW Kirk, Jacques Behmoaras, Eleanor Sandhu, Stephen P McAdoo, Maria F Prendecki, Matthew C Pickering, Marina Botto, Michelle Willicombe<sup>†</sup>, David C Thomas<sup>†</sup>, James E Peters<sup>†</sup>. **Longitudinal proteomic profiling of dialysis patients with COVID-19 reveals markers of severity and predictors of death.** *eLife* 2021. [10:e64827](#)

<sup>†</sup>Equal contributions

## CONFERENCES AND PRESENTATIONS

---

- **Rising Scientist Day 2022 (Poster)** - Multi-omics identify LRR15 as a COVID-19 severity predictor and persistent pro-thrombotic signals in convalescence
- **Biomarkers of the Future 2021 (Presentation)** - Longitudinal proteomic profiling of dialysis patients with COVID-19 reveals markers of severity and predictors of death
- **HUPO Reconnect 2021 (Poster)** - Longitudinal proteomic profiling of dialysis patients with COVID-19 reveals markers of severity and predictors of death
- **UK-CIC Immunology 2021 (Poster)** - Longitudinal proteomic profiling of dialysis patients with COVID-19 reveals markers of severity and predictors of death
- **Longitudinal Studies 2021, Wellcome Genome Campus (Presentation)** - Longitudinal proteomic profiling of dialysis patients with COVID-19 reveals markers of severity and predictors of death

## ADDITIONAL COURSES

---

- "From large datasets to biological insight" by Wellcome Connecting Science & EMBL-EBI
- "FAIR in (Biological) Practice" by University of Edinburgh (Ed-DaSH)
- "Data Science workflows with Nextflow" by University of Edinburgh (Ed-DaSH)
- "Introduction to Assessment and Feedback" by Imperial College London Graduate School
- "Introduction to Teaching and Learning" by Imperial College London Graduate School
- "Profiling and optimisation in Python" by Imperial College London Research Computing
- "Deep Learning in the Life Sciences" by MITx
- "Software Development with C++" by University of Birmingham Research Computing

## REFERENCES

---

Dr James Peters (PhD Supervisor)  
Clinical Reader in Rheumatology  
Faculty of Medicine  
Imperial College London  
Hammersmith  
W12 0NN  
j.peters@imperial.ac.uk

Dr Marco Catoni (Undergraduate Project)  
Lecturer in Plant Biology  
School of Biosciences  
University of Birmingham  
Edgbaston  
B15 2TT  
m.catoni@bham.ac.uk