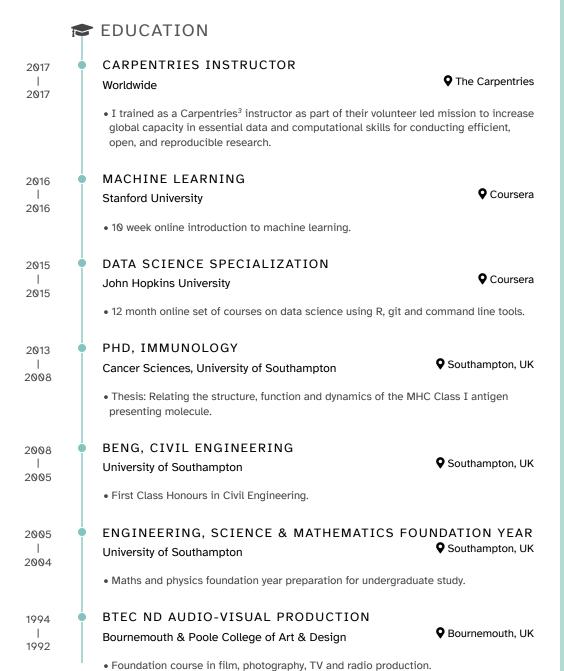
# **Alistair Bailey**

I am a researcher at the Centre for Proteomic Research and Cancer Sciences Unit at the University of Southampton. My research interests are in antigen processing and presentation by class I MHC molecules, data science and proteomics. My role is primarily as an informatician. The project I currently work on aims to improve immunotherapy treatment for cancer patients.  $^{\rm I}$  I also contribute to research into the role of MHC molecules in skin sensitization to chemical allergens, and contagious cancer in the Tasmanian Devil. I am also a Data and Software Carpentry instructor.





View this CV online with links at ab604.uk/cv/cv.html

#### CONTACT

- ab604@soton.ac.uk
- **y** alistair604
- github.com/ab604
- **𝚱** ab604.uk

## SKILLS

R	
Python	
Bash	
SQL	
Markdown	
Git	
Latex	

Made with the R package pagedown.

The source code is available on github.com/ab604/abailey-cv.

The font is Atkinson Hyperlegible

Last updated on 2021-11-23.

## RESEARCH EXPERIENCE

Current 2018

#### RESEARCH FELLOW

Centre for Proteomic Research/Cancer Sciences, University of Southampton Southampton, UK

• Cancer Research UK Accelerator: this project aims to identify potential treatment targets for hard to treat cancers such as lung cancer using peptidomics methods.

In my role, I process, analyse and manage data from various 'omics technologies, primarily whole exome sequencing, RNAseq and proteomics. Proteomics data I receive as Thermo raw data and process with Peaks Studio<sup>4</sup>, and post-process in R and RStudio. Whole exome and transcriptomics data I receive as fastq files and I use a mixture of command line tools using bash scripts and R and RStudio. I tend to follow the Broad Institute Best Practices for genomic data analysis<sup>5</sup> and Cornell Bioinformatics Core<sup>6</sup> for transcriptomic data processing. Scripts and processed data are managed using git and Gitlab version control. Raw data is backed up remotely and deposited along with processed outputs public repositories such as EBI PRIDE and the European Phenome-Genome Archive following FAIR protocols. My primary computer is a Linux Ubuntu machine, but I also use Windows.

- We have also developed our method to identify treatment targets for infectious diseases such as influenza.
- In 2020 I also worked to develop a COVID19 test using proteomics methods.

2018 2015

#### RESEARCH FELLOW

Centre for Proteomic Research/Cancer Sciences, University of Southampton Southampton, UK

• Developed peptidomics methodology at the UoS for research into the role of MHC molecules in skin sensitisation to chemical allergy.

2015 2013

#### RESEARCH FELLOW

Cancer Sciences, University of Southampton

Southampton, UK

• MRC Centenary Fellow



#### INDUSTRY EXPERIENCE

2012 2012

#### INTERNSHIP

Globecast

Microsoft Research

• Cambridge, UK

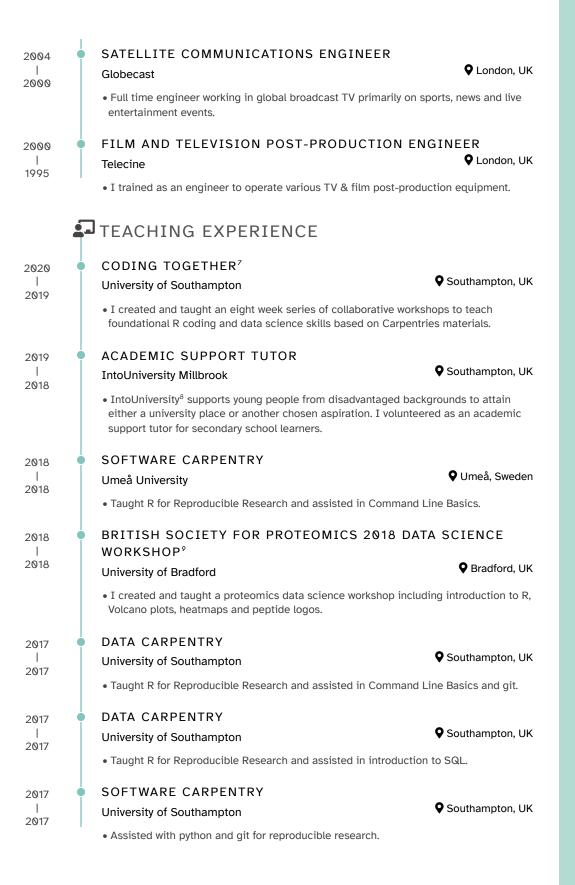
• Helped develop computational model of MHC I peptide selection.

2012 2004

#### FREELANCE SATELLITE COMMUNICATIONS ENGINEER Q London, UK

• I continued to work as an engineer in broadcast TV from 2004 and 2012 on major events such as the Olympics and Football World Cup.

I have worked in a variety of roles ranging from engineering to research scientist. I like collaborative environments where I can learn from my peers.



I am passionate about teaching foundational coding and data science skills to researchers and developing evidence-based best practices. I am especially interested in helping novices and making coding more accessible to all.

### PUBLICATIONS

2021 2021 THE DIFFERENTIATION STATE OF THE SCHWANN CELL PROGENITOR DRIVES PHENOTYPIC VARIATION BETWEEN TWO CONTAGIOUS CANCERS<sup>10</sup>

#### **PLOS Pathogens**

• Rachel S. Owen, Sri H. Ramarathinam, Alistair Bailey, Annalisa Gastaldello, Kathryn Hussey, Paul J. Skipp, Anthony W. Purcell, Hannah V. Siddle

2021 2021 CHARACTERIZATION OF THE CLASS I MHC PEPTIDOME RESULTING FROM DNCB EXPOSURE OF HACAT CELLS<sup>11</sup>

#### **Toxicological Sciences**

· Alistair Bailey, Ben Nicholas, Rachel Darley, Erika Parkinson, Ying Teo, Maja Aleksic, Gavin Maxwell, Tim Elliott, Michael Ardern-Jones, Paul Skipp.

2021 2021 IMMUNOPEPTIDOMIC ANALYSIS OF INFLUENZA A VIRUS INFECTED HUMAN TISSUES IDENTIFIES INTERNAL PROTEINS AS A RICH SOURCE OF HLA LIGANDS<sup>12</sup>

Ben Nicholas, Alistair Bailey, Karl J. Staples, Tom Wilkinson, Tim Elliott, Paul Skipp.

2021 2021 THE IMMUNOPEPTIDOMES OF TWO TRANSMISSIBLE CANCERS AND THEIR HOST HAVE A COMMON, DOMINANT PEPTIDE MOTIF<sup>13</sup>

#### Immunology

• Annalisa Gastaldello, Sri H. Ramarathinam, Alistair Bailey, Rachel Owen, Steven Turner, N. Kontouli, Tim Elliott, Paul Skipp, Anthony W. Purcell, Hannah V. Siddle.

2019 2019 DYNAMICALLY DRIVEN ALLOSTERY IN MHC PROTEINS: PEPTIDE-DEPENDENT TUNING OF CLASS I MHC GLOBAL FLEXIBILITY14

#### Frontiers in Immunology

• Cory M. Ayres, Esam T. Abualrous, Alistair Bailey, Christian Abraham, Lance M. Hellman, Steven A. Corcelli, Frank Noé, Tim Elliott, Brian M. Baker.

2017 2017 DIRECT EVIDENCE FOR CONFORMATIONAL DYNAMICS IN MAJOR HISTOCOMPATIBILITY COMPLEX CLASS I MOLECULES<sup>15</sup>

#### JBC.

• Andy van Hateren, Malcolm Anderson, Alistair Bailey, Jörn M. Werner, Paul Skipp, Tim Elliott.

2017 | 2017 RECENT ADVANCES IN MAJOR HISTOCOMPATIBILITY COMPLEX CLASS I ANTIGEN PRESENTATION: PLASTIC MHC MOLECULES AND TAPBPR MEDIATED QUALITY CONTROL<sup>16</sup>

F1000 Research

• Andy van Hateren, Alistair Bailey, Tim Elliott.

2014 | 2014 TWO POLYMORPHISMS FACILITATE DIFFERENCES IN PLASTICITY BETWEEN TWO CHICKEN MAJOR HISTOCOMPATIBILITY COMPLEX CLASS I PROTEINS<sup>17</sup>

PLoS One

• Alistair Bailey, Andy van Hateren, Tim Elliott, Jörn M. Werner.

2013 | 2013 A MECHANISTIC BASIS FOR THE CO-EVOLUTION OF CHICKEN TAPASIN AND MAJOR HISTOCOMPATIBILITY COMPLEX CLASS I PROTEINS<sup>18</sup>

JBC

 Andy van Hateren, Rachel Carter, Alistair Bailey, Nasia Kontouli, Anthony P. Williams, Jim Kaufman, Tim Elliott.

2010 | 2010 THE CELL BIOLOGY OF MAJOR HISTOCOMPATIBILITY COMPLEX CLASS I ASSEMBLY: TOWARDS A MOLECULAR UNDERSTANDING<sup>19</sup>

Tissue Antigens

• A. Van Hateren, E. James, A. Bailey, A. Phillips, N. Dalchau, T. Elliott



- 1• https://www.cancerresearchuk.org/funding-for-researchers/accelerator-award/portfolio-funded -projects-outputs
- 2. https://carpentries.org/
- 3. https://carpentries.org/
- 4. https://www.bioinfor.com/peaks-studio/
- 5. https://gatk.broadinstitute.org/hc/en-us
- 6. https://abc.med.cornell.edu/
- 7. https://ab604.github.io/docs/coding-together-2019/
- 8. https://intouniversity.org/
- 9. https://ab604.github.io/docs/bspr\_workshop\_2018/index.html
- $\textbf{10.} \ \textbf{https://journals.plos.org/plospathogens/article?} id = \textbf{10.1371/journal.ppat.1010033}$
- 11. https://doi.org/10.1093/toxsci/kfaa184
- 12. https://doi.org/10.1101/2021.08.17.456620
- 13. https://doi.org/10.1111/imm.13307
- 14. https://doi.org/10.3389/fimmu.2019.00966
- 15. https://doi.org/10.1074/jbc.M117.809624
- 16. https://doi.org/10.12688/f1000research.10474.1
- 17. https://doi.org/10.1371/journal.pone.0089657
- 18. https://doi.org/10.1074/jbc.M113.474031

19. https://doi.org/10.1111/j.1399-0039.2010.01550.x