Angus H. Bucknell

PhD Candidate · Molecular Plant-Microbe Interactions

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Summary

PhD candidate in molecular plant-microbe interactions at The Sainsbury Laboratory, using novel protein design and structural bioinformatics to decode effector function in the fungal blast pathogen Magnaporthe oryzae. Background in fungal transposon biology (Starships) and horizontal gene transfer. Active in public engagement and science communication.

Research Experience

PhD Candidate

Oct 2023 – present

The Sainsbury Laboratory, Norwich, UK · Supervisor: Prof. Nick Talbot

— Novel protein design in the Magnaporthe oryzae pathosystem

PhD Intern

Jun 2025 – Aug 2025

Sequence Analysis UK, Norwich, UK · Supervisor: Dr. Lisa Crossman

— 3-month placement outside primary field of research, as part of the doctoral training programme
— Analysed metagenome-assembled genomes as part of the WISH Fiji project

MSci Researcher

Sep 2022 – May 2023

School of Biosciences, University of Birmingham, UK · Supervisor: Dr. Megan McDonald

— Designed custom plasmids to screen for transposition events in Bipolaris sorokiniana
— Determined putative transposase expression via qPCR

VBC Summer School Student

Jul 2022 – Aug 2022

Gregor Mendel Institute, Vienna BioCenter, AT · Supervisor: Dr. Arturo Marí-Ordóñez

— Constructed retrotransposon phylogenies via Bash and R
— Assessed methylation landscape of Duckweeds via bisulfite PCR

Research Intern

Jul 2021 – Sep 2021

School of Biosciences, University of Birmingham, UK · Supervisor: Dr. Marco Catoni

— Determined consensus sequence of a transposon subgroup via MUSCLE
— Compared transposon frequencies within tree species using R

Education

PhD in Molecular Plant-Microbe Interactions

Oct 2023 – present

University of East Anglia, Norwich, UK

Thesis: Investigating Magnaporthe oryzae effectors through de novo protein binders
Funded through the NRPDTP (BBSRC grant BB/T008717/1)

MSci in Biosciences (1:1 with Honours)

2019 – 2023

University of Birmingham, UK

Publications & Preprints

* indicates co-authorship

1. Tagirdzhanova, G., Brown, N.E.*, **Bucknell, A.H.***, Cameron, E.S., Finn, R.D., Blaxter, M., McDonald, M.C., Gluck-Thaler, E., and Talbot, N.J. (2026). Tangerine: a new family of Starships from lichen-forming fungi. PNAS. doi: 10.1073/pnas.2534402123

2. Xi, Y., **Bucknell, A.H.**, Watson, J.L., Maqbool, A., Bennett, J.W., Goreshnik, I., Vafeados, D., Garcia Sanchez, M., Knight, G., Zdrzalek, R., Rodney, C.A., Saado, I., Stone, C.E., Turley, E.K., Yu, D.S., Gentle, A., Ryder, L.S., Yan, X., Were, V., Heddle, J.G., Baker, D., Emmrich, P.M.F., Talbot, N.J., Banfield, M.J., and Bentham, A.R. (2026). Computational design of de novo integrated domains enables rational control of pathogen effector recognition in plant NLR immune receptors. bioRxiv. doi: 10.64898/2026.07.10.737686

3. **Bucknell, A.H.***, Wilson, H.M.*, Gonçalves do Santos, K.C., Simpfendorfer, S., Milgate, A., Germain, H., Solomon, P.S., Bentham, A.R., and McDonald, M.C. (2025). Sanctuary: A Starship transposon facilitating the movement of the virulence factor ToxA in fungal wheat pathogens. mBio. doi: 10.1128/mbio.01371-25

4. Tagirdzhanova, G., Scharnagl, K., Sahu, N., Yan, X., **Bucknell, A.H.**, Bentham, A.R., Jégousse, C., Ament-Velàsquez, S.L., Brännström, I.O., Johannesson, H., MacLean, D., and Talbot, N.J. (2024). Complexity of the lichen symbiosis revealed by metagenome and transcriptome analysis of Xanthoria parietina. Current Biology, 35. doi:10.1016/j.cub.2024.12.041

5. **Bucknell, A.H.** and McDonald, M.C. (2023). That's no moon, it's a Starship: Giant transposons driving fungal horizontal gene transfer. Molecular Microbiology, 120, 555-563. doi:10.1111/mmi.15118

Conferences

Oral Presentations

- AI-driven protein design to understand effector function within the Magnaporthe oryzae rice pathosystem – 33rd Fungal Genetics Conference, Pacific Grove, US (2026)
- Engineering new-to-nature immune sensors for novel recognition of effectors in plant pathosystems – 20th IS-MPMI Congress, Cologne, DE (2025)
- Developing new-to-nature protein binders for the M. oryzae pathosystem – Advancing Plant Health Forum, Norwich, UK (2024)
- Using structural homology predictions to infer biological function of effector proteins during plant infections – NRPDTP Summer Conference, Norwich, UK (2024)
- In silico characterisation of Magnaporthe effector proteins – Magnafest, Pacific Grove, US (2024)

Poster Presentations

- AI-driven protein design to understand effector function within the Magnaporthe oryzae rice pathosystem – Mendel Early Career Symposium, Vienna, AT (2026). doi:10.5281/zenodo.20525051
- Structural bioinformatics to understand effector function within the Magnaporthe oryzae rice pathosystem – 33rd Fungal Genetics Conference, Pacific Grove, US (2026). doi:10.5281/zenodo.20525685
- Engineering new-to-nature immune sensors for novel recognition of Magnaporthe oryzae – 20th IS-MPMI Congress, Cologne, DE (2025). doi:10.5281/zenodo.15880523
- Finding function through form: predicting effector function in the blast fungus through structural biology – 32nd Fungal Genetics Conference, Pacific Grove, US (2024). doi:10.5281/zenodo.10793245

Committee Roles & Service

Departmental Service

- Member of the TSL MSc Selection Committee (2026)
- Member of the NRPDTP Summer Conference Organisation Committee (2026)
- Member of the TSL Awards Selection Committee (2025)
- Treasurer of the TSL Student Committee (2024-2025)

Peer Review

- Reviewer for Nature Communications

Science Communication

Public Engagement

- Volunteered at the TSL stall at the Norwich Science Festival (2024)
- Presented an accessible science talk at the JIC Year 10 Summer Camp (2024)
- Presented at Pint of Science on “Using shape to find function” in Norwich (2024)
- Presented at Pint of Science on “From one small step to a giant leap between fungi” in Birmingham (2023)

Stakeholder Engagement

- Presented to senior civil servants from the Environment Agency and the Department for Energy Security and Net Zero (2025)

Skills

LABORATORY
Molecular cloning & plasmid design, qPCR, bisulfite PCR, sequence alignment (MUSCLE), metagenomics

COMPUTATIONAL
Structural bioinformatics & protein structure prediction, de novo protein design, Python, Julia, R, Bash, phylogenetics