PI profile

## Jenny Taylor

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|  | **Associate Professor Jenny Taylor**  **Titles**: Associate Professor, Co-Theme Lead, Oxford Biomedical Research Centre Genomic Medicine Theme, Group Leader / PI, Fellow and Member of Congregation  **Location**: Wellcome Centre for Human Genetics  **Department**: Nuffield Department of Medicine  **Group**: Taylor Group  **Webpage**: [Jenny Taylor — Wellcome Centre for Human Genetics (ox.ac.uk)](https://www.well.ox.ac.uk/people/jenny-taylor) [Contacts for Genomic Medicine - NIHR Oxford Biomedical Research Centre](https://oxfordbrc.nihr.ac.uk/research-themes-overview/genomic-medicine/contacts/)  **Email**: jenny.taylor@well.ox.ac.uk  **PA**: Donna: brcpa@well.ox.ac.uk |

### GMS themes:

[Please retain any that describe your research, deleting others:]

* Genomic and –omic technologies
* Functional genomics
* Genome biology (genomes and genetic variation)
* Genomics of disease
* Genomic analysis (bioinformatics and statistical genetics)
* From genes to clinic (target discovery, structural biology, medicinal chemistry)
* Application of genomics in the clinic (diagnostics and therapeutics)

### Research Overview

Jenny was a co-investigator on the WGS500 project, which was a forerunner to the UK’s 100,000 Genomes Project and also led a team to establish the clinical framework and infrastructure for WGS within the Oxford hospital setting. She continues to participate in the Genomics England programme through its Clinical Interpretation Partnerships.

This group is part of the NIHR Oxford Biomedical Research Centre’s Genomic Medicine Theme, a translational research programme. As a clinical genome sequencing programme, strongly connected with clinical diagnostic genomics labs, our results also have the potential to inform molecular diagnoses and treatment selection for patients. We are also involved in analysing data from the Genomics England 100,000 genomes programme, which would present an ideal opportunity for GMS students to analyse a wealth of WGS data.

Our group focuses on application of whole genome sequencing for understanding the pathogenesis of a broad spectrum of rare diseases, with the aim of identifying novel disease genes. We also apply whole genome sequencing mutation profiling for cancer patients. Genetic analysis involves a suite of custom and commercial bioinformatics and protein informatics software packages to filter the likely pathogenic variants and assess the impact of the mutations. Potential novel disease genes may then be followed up using a range of functional studies including CRISPR gene editing and molecular/cellular biology approaches, often in collaboration with other groups. Currently, putative novel genes in neurological, developmental and immunological conditions are the focus of our research.

Project areas: whole genome sequencing, bioinformatics, rare diseases, genetic and functional studies

### Specific project proposals:

* Exploring novel disease genes in
* Exploring pathogenicity of non-coding and structural variants for Rare Diseases using 100,000 Genomes Project dataset

Please contact me directly for further information.

*These pages were reviewed/updated:* ***2nd August 2021***

**Previous**

‘Genome sequencing data analysis (for bioinformaticians or lab scientists), including identification of copy number & single nucleotide and intronic / non coding variants’, ‘Biological annotation and interpretation of putative variants emerging from genome sequencing’ and ‘Functional studies to identify pathogenicity of novel disease genes, including CRISPR based gene editing‘.

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Insert any additional project description(s) on subsequent pages if applicable. Please use the same template and use separate pages for each project.