

# Qisheng Pan

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## RESEARCH INTEREST

I studied missense variants in human genome using computational biophysical measurements and Artificial Intelligence. In particular, I investigated the structural consequences of missense mutations and developed machine learning model to better predict variant of unknown clinical significance.

## EDUCATION

<b>University of Queensland</b>	Brisbane, Australia
• Doctor of Philosophy (Computational Biology)	<i>Jun 2025 (expected)</i>
<b>University of Melbourne</b>	Melbourne, Australia
• Master of Science (Bioinformatics)	<i>2019-2021</i>
<b>South China Normal University</b>	Guangzhou, China
• Bachelor of Science (Biotechnology)	<i>2015-2019</i>

## PUBLICATIONS

1. **Pan Q**, Parra G, Myung Y et al. AlzDiscovery: A computational tool to identify Alzheimer's disease-causing missense mutations using protein structure information, Protein Sci 2024.
2. **Pan Q**, Portelli S, Nguyen TB et al. Characterization on the oncogenic effect of the missense mutations of p53 via machine learning, Brief Bioinform 2023;25.
3. Serghini A, Portelli S, Troadec G et al. Characterizing and predicting ccRCC-causing missense mutations in Von Hippel-Lindau disease, Hum Mol Genet 2023.
4. Jessen-Howard D, **Pan Q**, Ascher DB. Identifying the Molecular Drivers of Pathogenic Aldehyde Dehydrogenase Missense Mutations in Cancer and Non-Cancer Diseases, Int J Mol Sci 2023;24.
5. Zhou Y, **Pan Q**, Pires DEV et al. DDMut: predicting effects of mutations on protein stability using deep learning, Nucleic Acids Res 2023;51:W122-W128.
6. Boer JC, **Pan Q**, Holien JK et al. A bias of Asparagine to Lysine mutations in SARS-CoV-2 outside the receptor binding domain affects protein flexibility, Front Immunol 2022;13:954435.
7. **Pan Q**, Nguyen TB, Ascher DB et al. Systematic evaluation of computational tools to predict the effects of mutations on protein stability in the absence of experimental structures, Brief Bioinform 2022;23.
8. Han YY, Jin K, **Pan QS** et al. Microglial activation in the dorsal striatum participates in anxiety-like behavior in Cyld knockout mice, Brain Behav Immun 2020;89:326-338.

## TEACHING EXPERIENCES

<b>Tutor</b> , University of Queensland	<i>Feb 2025</i>
• <b>BINF6000: Bioinformatics Introduction</b>	
<b>Teaching Assistant</b> , University of Queensland	<i>Aug 2024</i>
• <b>BIOT7060: Frontiers in Medical Biotechnology</b>	
<b>Instructor</b> , University of Queensland	<i>Nov 2023</i>
• <b>Advanced Data Visualisation with ggplot2</b> : This workshop is the one that I designed, prepared, and delivered, focusing on practical skills on presenting data using R and ggplot2 package.	
<b>Teaching Assistant</b> , University of Queensland	<i>Sept 2022</i>
• <b>Computing4lifescience Series</b>	

## MENTORSHIP

**Research Supervisor** (UG: undergraduate, MS: master's)

Georgina Becerra Parra (UG, 2022, UQ), Dana Jessen-Howard (MS, 2023, UQ), Joshua Khoo (MS, 2024, UQ), Wuyang Ren (MS, 2025, UQ)

## HONOURS & AWARDS

• Conference support of SAAFE 2024 AMR Solutions Summit (\$1000)	<i>Sept 2024</i>
• Travel Awards of MM2023 conference (\$300)	<i>Dec 2023</i>
• SCMB Award for Outstanding Contribution to Research (Group Awards)	<i>Nov 2023</i>
• Student Prize in the CTCMS Seminar	<i>Mar 2023</i>
• Comprehensive Student Scholarship (\$500)	<i>Sept 2016</i>

## COLLABORATIONS

<b>Jeniffer Boer and Magdalena Plebanski, Royal Melbourne Institute of Technology, Australia</b>	<i>2022 - 2023</i>
• Investigating the variants of the Spike protein in Omicron SARS-CoV-2 virus	

## RESEARCH EXPERIENCES

<b>Characterising the pathogenic effect of missense mutations via machine learning</b>	<i>2022 - now</i>
• Leveraged different computational biophysical measurements to annotate missense variants.	
• Developed machine learning models to classify phenotypes of mutations.	
<b>Benchmarking computational biophysical measurements in the absence of experimental structures</b>	<i>2022 - now</i>
• Built high-throughput pipeline to generate protein homology models and AlphaFold models.	
• Used different metric to assess the predictive performance of various machine learning models.	

## PRESENTATIONS

1. Poster presentation in the Lorne Protein 2025 Conference (Australia)	<i>Nov 2024</i>
2. Poster presentation in the ABACBS 2024 Conference (Australia)	<i>Nov 2024</i>
3. Poster presentation in the SAAFE 2024 AMR Solutions Summit (Australia)	<i>Sept 2024</i>
4. Poster presentation in the Lorne Protein 2024 Conference (Australia)	<i>Feb 2024</i>
5. Oral and poster presentations in the MM2023 Conference (Australia)	<i>Dec 2023</i>
6. Poster presentation in the ABACBS 2023 Conference (Australia)	<i>Dec 2023</i>
7. Research Talk in the 22 <sup>nd</sup> International Conference on Bioinformatics (Australia)	<i>Nov 2023</i>
8. Lighting talk in the GenGen seminar (UQ)	<i>Apr 2023</i>
9. Oral presentations in the CTCMS seminar (UQ)	<i>Mar 2023</i>
10. Poster presentations in the Lorne Protein 2023 Conference (Australia)	<i>Feb 2023</i>
11. Poster presentation in the 18 <sup>th</sup> Annual Research Student Symposium (UQ)	<i>Nov 2022</i>
12. Oral presentations in the Joint Biomolecular and Medicinal Chemistry Theme Symposium (UQ)	<i>Apr 2022</i>

## TECHNICAL SKILLS

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Programming: Python, R, Linux Bash, JavaScript

Software: BLAST, MODELLER, PyMol, AutoDock Vina, GALAXY, etc.

Machine learning: Random Forest, Neural Network, Feature selection, etc.

## REFEREES

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David B. Ascher	Professor, University of Queensland	<a href="mailto:d.ascher@uq.edu.au">d.ascher@uq.edu.au</a>
Thanh-Binh Nguyen	Research Fellow, University of Queensland	<a href="mailto:thanhbinh.nguyen@uq.edu.au">thanhbinh.nguyen@uq.edu.au</a>
Stephanie Portelli	Research Fellow, University of Queensland	<a href="mailto:s.portelli@uq.edu.au">s.portelli@uq.edu.au</a>
Douglas E.V. Pires	Senior lecturer, University of Melbourne	<a href="mailto:douglas.pires@unimelb.edu.au">douglas.pires@unimelb.edu.au</a>
Cheng Long	Professor, South China Normal University	<a href="mailto:longcheng@m.scnu.edu.cn">longcheng@m.scnu.edu.cn</a>