R.H. Amanda Ng

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PROFESSIONAL SUMMARY

PhD-trained Bioinformatics Scientist with expertise in spatial omics, bioimage analysis, and scientific software development. Experienced in building scalable end-to-end analytical pipelines for Cell Painting and spatial transcriptomics platforms (COMET, CosMx, Visium, Stereo-CITE-Seq), spanning HPC workflows, data infrastructure, and full-stack applications. Proven ability to translate biological and technical requirements into reproducible, production-ready computational solutions.

EXPERIENCE

ImmunoQs | Bioinformatics Scientist **Singapore, Singapore**
(Startup focused on Spatial Omics Data Hosting and Processing) Nov 2024 – Nov 2025

- Architected a modular, automated analysis pipeline (R/Shell) for ImmunoQs-MGI partnership, enabling scalable hosting and standardized processing for MGI's Stereo-CITE-Seq product.
- Developed generalized tools (Python/R) for bioimage data management—including CZI to OME-TIFF conversion—and standardized QC reporting, resulting in weekly efficiency gains for the Data Analytics Team.
- Built an automated client-facing QC reporting platform using R and Bootstrap, streamlining delivery of analytical metrics and raw data outputs.
- Managed the CosMx spatial transcriptomics infrastructure for a multi-institutional longitudinal study (CUHK, IMCB/A*STAR)
- Refactored legacy codebases to ensure 100% analytical reproducibility while executing end-to-end workflows, including cell-type annotation and pathway enrichment.

Georg Winter Lab, Center for Molecular Medicine | Pre-Doctoral Research Fellow **Vienna, Austria**
(Research Laboratory focused on Chemical Biology, Cancer and Gene Control) Sep 2019 – Dec 2023

- Led the development of the "Isogenic Cell Painting assay", the first high-throughput imaging approach for discovering molecular glues.
- Deployed automated image segmentation (cellpose v2) and feature extraction (CellProfiler) pipelines on high-performance computing clusters.
- Engineered a custom feature selection strategy employing Kendall's tau-b correlation coefficients to identify subtle morphological signatures; grounded the statistical model in the mechanism-of-action of molecular glues ensuring high-fidelity hit discovery.
- Developed a network analysis approach to compare morphological signatures of hit compounds, enabling the prioritization of candidates with unique biological profiles.
- Led end-to-end data analysis workflows and high-dimensional data visualization for the discovery of novel molecular glues, resulting in a first-author publication in ACS Chemical Biology and presentations to global scientific cohorts.

EDUCATION

Medical University of Vienna **Vienna, Austria**
PhD working on Cell Morphology Analysis Oct 2019 – Sep 2024

- PhD Dissertation: Isogenic CPA: A morphological profiling approach for discovering molecular glues
- Symposium Organization: Organized and secured funding for the institute-wide Career Symposiums for PhD students in 2021 and 2022, and the Ubiquitin and Friends Symposium 2022.
- Organization Development & Compliance: Partnered with HR, faculty, PhD Representatives, and Postdoctoral Representatives to audit and enhance workplace infrastructure, directly resulting in the institute's accreditation with the European Commission's HR Excellence Research Award.

National University of Singapore **Singapore, Singapore**
BSc with Honors (Life Sciences) | NUS Second Upper Honors equivalent | CAP 4.48/5.00 Aug 2015 – Jun 2019

- Honors Dissertation: Identification and characterisation of par-1 suppressors in *Caenorhabditis elegans*
- Interdisciplinary Academic Programmes: University Scholar's Programme; Special Programme in Science.

PERSONAL PROJECTS

Tangential Almond | Link: tangentialalmond.cc Mar 2026 – Present

(Self-hosted Personal Blog on Coding Projects and AI)

- Self-hosted the blog using an old Android mobile device and served the blog using Cloudflare Tunnel.
- Created the blog using Hugo for static site generation and Tailwind CSS/daisyUI as the CSS framework.
- Writing posts on coding projects and learning journey in AI.

TeaDex | Link: github.com/TangentialAlmond/teadex Nov 2025 – Present

(Full Stack Tea Database Cataloguing Tea Origination, Production Methods and Types)

- Architected a full-stack Create, Read, Update, Delete (CRUD) application using the MERN stack to catalogue information on tea leaves and their processing workflow.
- Implemented secure file handling and storage using Multer and AWS S3 for visual documentation, and designed a systematic database schema in Mongoose for text documentation.
- Collated end user feedback from connections within the tea community.

PUBLICATIONS

Degradome analysis to identify direct protein substrates of small-molecule degraders. Jochem, M.; Schrempf A.; Wagner, L.-M.; Cisneros, J.A.; **Ng, A.**; Winter, G.E.; Krijgsvelf, J. Cell Chem Biol. 2025.

Large-scale chemoproteomics expedites drug discovery and predicts ligand behavior in cells. Offensperger, F.*; Tin, G.*; Duran-Frigola, M.* *et al.*; **Ng, A.** [collaboration between CeMM and Pfizer] Science. 2024. *equal contribution

Discovery of molecular glue degraders via isogenic morphological profiling. **Ng, A.***; Offensperger, F.*; Cisneros, J.A.*; Scholes, N.; Malik, M.; Villanti, L.; Rukavina, A.; Ferrada, E.; Hannich, J.T.; Koeren, A.; Kubicek, S.; Superti-Furga, G.; Winter, G.E. ACS Chem. Biol. 2023. *equal contribution
GitHub repository: https://github.com/GWinterLab/IsogenicCPA/tree/main

CONFERENCES & SEMINARS

Dana Faber Targeted Protein Degradation Series **Remote**
Invited speaker Feb 2024
Title: Isogenic CPA: A morphological profiling approach for discovering molecular glues

Keystone Conference 2022: Modern Phenotypic Drug Discovery **Denver, USA**
Poster presentation May 2022
Title: Identifying CRBN-dependent molecular glue degraders with novel targets via morphological profiling

SKILLS, ACTIVITIES, & INTERESTS

- **Languages:** English (Native), Mandarin (Intermediate), German (Beginner), Japanese (Beginner).
- **Web development:** MERN stack (MongoDB, Express.js, React, Node.js), Hugo, TailwindCSS/daisyUI, Bootstrap
- **Data Visualization & Analysis:** Python (Pandas/Polars, Seaborn/Matplotlib, Scikit-learn, Plotly, Networkx), R (tidyverse/ggplot2), Adobe Illustrator
- **DevOps & Tools:** Git, VS Code, Bash/Shell, Docker/Singularity
- **Interests:** Tea cultivation, processing and preparation; trained in Japanese tea cultivation and production at Kyoto Obubu Tea Farms, and co-founder and community manager of a growing tea community in Singapore "SG Tea Friends".