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Full Reference: **Nawaz U**, Aref A, Cheung M, Deng N, Gifford A, Jabson J, Koh J, Lau LMS, Livson O, Ludlow L, Mayoh C, McNamee N, Pathan M, Singh A, Zhou L, Hains PG, Robinson PJ, Reddel RR, Padhye B, Poulos RC. *Towards Proteome-Driven Precision Oncology: Large-Scale Standardized Cancer Proteomics and AI Modelling at ProCan.*

Conference/Meeting Name: 90th Cold Spring Harbor Symposium in Quantitative Biology: AI in Biology
Location: Cold Spring Harbor, New York, United States
Dates: 26 - 31 May 2026
Presentation Type: Poster



Photo from the opening night of the 90th CSHL symposium. Watching Jennifer Doudna's talk during the first session.

The Cold Spring Harbor Symposium on Quantitative Biology is one of the most historically significant meetings in the life sciences. Its name and origins connect directly to the emergence of a quantitative paradigm in biology, and past landmark Symposia have marked turning points such as recombinant DNA and the human genome. This year, the 90th Symposium was themed "AI in Biology." It was heavily oversubscribed, drawing over 450 participants on-site and around 200 online across academia, biotech and technology. The program ran as nine oral sessions, restricted to invited speakers, alongside the poster sessions, with intense days running from roughly 9 am to 10:30 pm.

A dominant theme was the rise of foundation models for human health, spanning cancer and neurodegenerative disorders, alongside "virtual patient" digital twins and the wider application of AI across basic biology. What made the meeting distinctive was its deliberate mixing of communities: leaders from AI and technology were placed directly alongside biologists, drug developers and clinicians, producing a rare and productive exchange between fields that seldom share a room.

The Symposium opened on the Tuesday evening with a striking introductory session. Jennifer Doudna spoke, followed by Pushmeet Kohli of Google DeepMind, who presented shortly after the launch of their AI Co-Scientist, a system that, given a research goal, generates and refines hypotheses through a tournament of competing agents. Alex Rives of Chan Zuckerberg Biohub and Hoifung Poon of Microsoft rounded out the opening. Eight further oral sessions followed over the week, with a breadth that spanned regulatory genomics, evolution, cells and tissues, clinical translation and precision oncology, two NeuroAI sessions, scientific agents and multimodal models, and proteins. The sessions that resonated most with me were Charlotte Bunne's work on virtual patients, Marinka Zitnik's on AI agents, and the broader use of multimodal foundation models.

I presented my poster on the second day. It covered my postdoctoral work at ProCan, where we use large-scale proteomic data to identify prognostic signatures in cancers, specifically my neuroblastoma

work, our computational pipelines, and my earlier OnCorr resource. The poster sessions were held in the evenings after the main sessions, which allowed for detailed discussion with researchers from very different fields, including colleagues from Noetik, where they are also using large-scale cancer proteogenomics data for precision oncology.

The knowledge gained from this meeting will directly benefit my research. Exposure to emerging resources including agentic workflows and new databases; and to frank discussions about the limitations of current data will inform how I design and validate proteomic signatures. My key take-home is that AI in biology is shifting from prediction toward causation, and that the biggest bottlenecks are no longer model architectures but data legibility, generating perturbation data at scale, and closing the human–AI collaboration loop.

A personal highlight was realising I was the only attendee from an Australian institute. Two other Australians were present, and, with some irony, both had previously been at the University of Adelaide's School of Biology, where I completed my honours.