It's been a remarkably full few months, so rather than a quick update we wanted to bring you the whole picture at once: new members, a first-of-its-kind summit, a major open dataset, a new academic fellowship, and a community challenge taking shape.

Thank you for building this with us.

MEMBERSHIP

Eleven new members join the consortium

OpenFold's network just grew by eleven organizations spanning therapeutic discovery, antibody design, GPCR biology, scientific software, molecular visualization, and AI-enabled R&D infrastructure. Please welcome:

WELCOMING

Absci • Adaptive Biotechnologies • Benchling • Chemical Computing Group • Daiichi Sankyo • Flagship Pioneering • Kiin Bio • Nanome • Nxera • Pledge Tx • Superluminal

Each member strengthens the shared effort to build high-performing, openly available AI models for biology and drug discovery, and to keep that infrastructure auditable, reproducible, and free to build on. It's a meaningful signal of the momentum behind open AI for the life sciences, and we're glad to have them.

— Read the full announcement →

BENCHMARKS

OpenBind's first blind benchmark, and an encouraging result for OpenFold3

OpenBind is a new UK-led open-science consortium, led by the Diamond Light Source, generating large-scale, high-quality protein–ligand structure and affinity data built specifically for AI. It runs CASP-style blind challenges in which the community predicts binding modes and is then scored against freshly generated experimental structures.

Its first public release centers on a public-health-relevant target, the Enterovirus A71 (EV-A71) 2A protease, pairing 925 crystallographic binding events across 699 compounds with affinity measurements for 601 of them, all released openly (CC0) as a training and stress-testing resource for the field.

The accompanying prospective assessment of co-folding methods carried a clear, two-sided message: there's real progress, and a long way still to go. Out of the box, even the strongest co-folding methods recovered the correct bound ligand pose only about half the time, and OpenFold3 outperformed AlphaFold3, a notable result for a fully open model. The standout, though, was what open data plus an open model made possible together: fine-tuning OpenFold3 on OpenBind's fragment-bound structures lifted its co-folding success from 36% to 76%, approaching the accuracy of re-docking. Co-folding tools are also beginning to outpace traditional physics-based docking on this set.

These are early numbers on a single target, so we won't over-generalize, but this is exactly the kind of open, rigorously blinded evaluation the field needs, and a clear vote of confidence in building on open models. We'll be following OpenBind's next rounds closely.

— Read OpenBind's first release →

COMMUNITY

First Annual CoFold Summit 2026 • Barcelona

Our inaugural CoFold Summit brought the co-folding community together in Barcelona this May for talks, panels, and a lot of hallway-track problem-solving on the future of open-source methods in structural biology and drug discovery. Organized by the OpenFold Consortium and hosted by OMSF, with thanks to our sponsors AMD, Apheris, and SandboxAQ.

Highlights from the inaugural CoFold Summit, Barcelona, May 2026.

Talks, the full agenda, and the photo gallery are all up on the website.

— Visit cofold.org →

OPEN DATA

A megascale open protein stability dataset

The Rocklin Lab at Northwestern University has released the MGnify Stability Dataset, a large-scale experimental resource containing folding-stability measurements for 1.8 million diverse protein domains, generated using cDNA display proteolysis. It's now freely available to the research community to accelerate better models for protein stability prediction. The work was supported in part by the OpenFold Consortium, which sponsors the Rocklin Lab as part of its broader mission to advance open biomolecular AI.

Datasets like this are central to OpenFold's roadmap: structure prediction alone isn't enough for the next generation of biomolecular AI. Models also need to learn biophysical properties like stability, folding, aggregation risk, and designability, which requires open, high-quality experimental data, including the negative data that's so often missing.

> *"This is exactly the kind of dataset the field needs to build better biomolecular AI."*
>
> WOODY SHERMAN · CHIEF INNOVATION OFFICER, PSITHERA · CHAIR, OPENFOLD EXECUTIVE COMMITTEE

— Read the full announcement →

FELLOWSHIP

New research fellowship at the UW Institute for Protein Design

OpenFold and the University of Washington's Institute for Protein Design (IPD), led by Nobel Laureate David Baker, have launched a new research fellowship to advance open-source AI for protein structure prediction and design. With funding from the consortium, fellows in the Baker Lab will focus on next-generation models for antibody–antigen design and structure prediction, an area that remains a real frontier for AI methods.

OpenFold engineers will help package, document, and maintain the resulting software so it can be widely used and sustained over time, and all models and code developed through the collaboration will be released under permissive licenses for researchers and companies worldwide.

— Read the full announcement →

EVENTS

OpenFold at Bio-IT World: a keynote panel on federated learning and drug discovery

Several OpenFold representatives joined industry leaders at the Bio-IT World Conference & Expo for a keynote panel titled "The Collaboration Breakthrough: How Federated Learning Is Rewriting the Rules of Drug Discovery." The session drew a packed audience and highlighted how shared foundation models, combined with federated learning and fine-tuning, can drive better decisions in drug discovery without requiring organizations to share proprietary data.

Woody Sherman presents during the federated-learning keynote panel at Bio-IT World.

The panel brought together Woody Sherman (PsiThera), Christina Taylor (Bayer), José-Tomás Prieto (Apheris), Arman Zaribafiyan (SandboxAQ), and Jonathan Gilbert (Lilly TuneLab) alongside Mohammed AlQuraishi (Columbia University), who framed the role of open foundation models as the shared starting point for collaborative AI in biomedicine. OpenFold's open-source ecosystem was featured as a prime example of community-driven software that lowers barriers,

enables transparent and auditable models, and creates impact beyond any single organization.

Key themes included the importance of community-driven development, with OpenFold cited as a model for how open infrastructure can accelerate innovation across the field. The panel also discussed priority areas for future community work, including explicit water molecules, antibody-antigen modeling, protein design, and improved access to experimental data.

— Read the full announcement →

Get involved

Membership in OpenFold is open to organizations across biotech, pharma, synthetic biology, software and technology, academia, and nonprofit research. If you'd like to learn more about joining or supporting the consortium, we'd love to hear from you.

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