

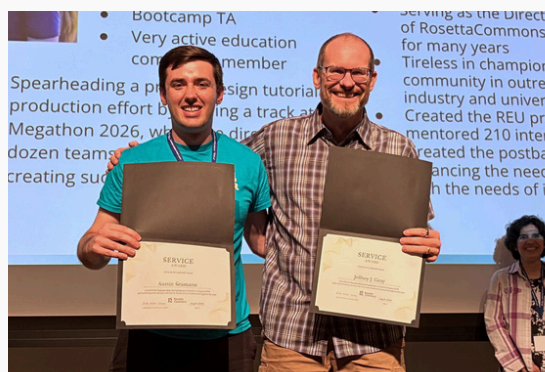
Welcome to our Monthly Newsletter

Catch-up with Jeff

Where in the world did Jeff visit? Keep reading to find out!



August means Summer RosettaCon in Seattle, Washington. This year we had our largest meeting ever, where we shared incredible scientific advances with the same contagious energy and optimism as always. We learned about combinations of Rosetta and AI, the largest protein language models to date, creative ways to probe dynamics with diffusion models and multi-state approaches, and how protein engineering can impact the global environment. Our Rosetta Commons REU interns gave flash talks and had high traffic at their posters. I was able to share our board's strategic work building capacity to support technical and community growth. And of course there was magic in our human interactions: the spontaneous mentoring, the ideas for collaborations, and the meals and activities together where we continued conversations (even a David-led walk through the bird sanctuary!). Thank you to all who joined and thus contributed to the magic.



On a personal note, I'm so humbled to receive the Service to Rosetta Award. This community has been a source of joy for me for so many years now, and it is an honor to be able to serve such a creative, supportive, impactful, and loving group of scientists. Again and again I've seen people bring ideas to strengthen our community, and we wrap around those ideas to support and make them reality, building layers upon layers of the special Rosetta Commons elements. A case in point is with the other Service Award winner, Austin Seamann, who spearheaded the production of protein design video tutorials during Megathon and was supported by dozens of volunteers (thank you and congrats Austin!). Thank you all for continuing to inspire me, and thank you for this meaningful recognition.



I'll leave you with a couple pictures from my post-RosettaCon activity: my first sea kayaking trip! We visited four islands over four days, shared fellowship over gourmet camp-cooked meals, and saw sea lions, sea stars, river otters, oyster catchers, and eagles. I hope you also have had the blessings of recharging with friends and family this summer.



Cheers,
Jeff

P.S. - Be on the lookout for Rosetta Commons mini-grant opportunities soon (including for biosecurity work).

Latest News

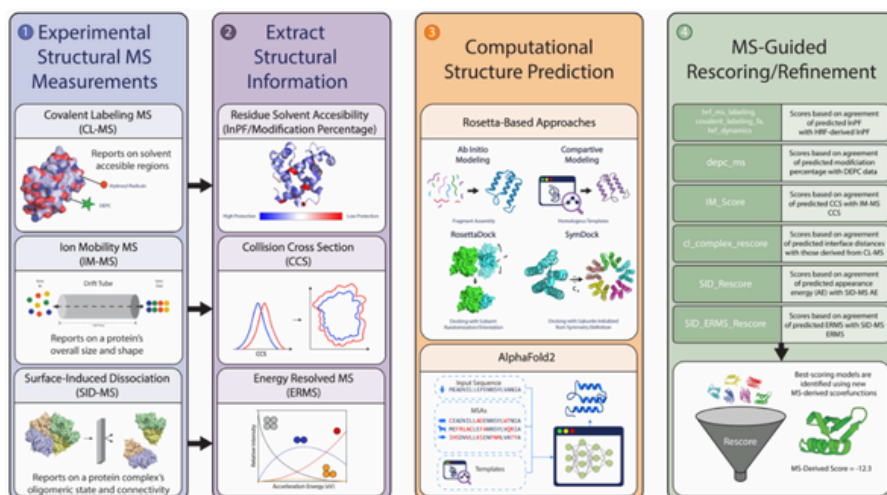
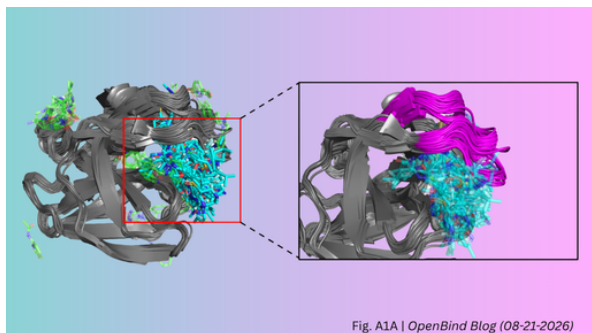


Fig. 1 | Drake et al. (2026)

Integrating Mass Spectrometry Restraints into Rosetta and AlphaFold Modeling Pipelines

Learn how combining structural mass spectrometry data with Rosetta and AlphaFold2 enhances computational protein structure prediction accuracy in this step-by-step tutorial guide.

[Find Out More](#)



New OpenBind-0 model and dataset benchmark co-folding tools in drug discovery

OpenBind has released OpenBind-0, a fully open-source co-folding model, alongside a dataset of 717 new ligand-bound structures to evaluate protein-ligand predictions in drug discovery.

[Find Out More](#)



RFdiffusion3 Simple Motif Scaffolding Tutorials Are Here

Follow these tutorials to learn the fundamentals of motif scaffolding, making RFD3 parameterization and setup simpler. These tutorials are part of our tutorial series from our Megathon event. More to come, so stay tuned!

[Watch the Tutorial](#)

Upcoming Events



Keystone Symposia - Winter RosettaCon 2027

Registration Opens Soon

Topic: Computational Design and Modeling of Biomolecules

Dates: March 29 - April 1, 2027

Location: La Fonda on the Plaza, Santa Fe, NM

[Learn More](#)



European RosettaCon 2026

Virtual Registration Open

Topic: Crossing Boundaries in Protein Design

Dates: October 28 - 30, 2026

Location: Universidade Nova de Lisboa, Lisbon, Portugal

[Register Today](#)

Member Spotlight

Kevin Drew, Ph.D.

*Assistant Professor
Drew Lab, University of Illinois Chicago*



About Kevin

Kevin earned a B.S. and M.S. in Computer Science from the University of Iowa and the University of Chicago, respectively. With that he planned to work on networking supercomputers together for astrophysics, until he came across protein folding and his interest in computational biology began. He originally joined Rich Bonneau's lab at NYU as a programmer, but then became a Ph.D. student helping to build that lab along the way as he researched protein folding (similar to AlphaFold today) and peptide mimics for target specific interactions in drugs. Kevin then stepped away from the Rosetta community to complete a postdoc at the University of Texas-Austin with Ed Marcotte looking at protein complexes. That led him to start his own lab in Chicago in January 2021, during the pandemic which made for a unique start-up process. His lab now has four graduate students that work on Rosetta-related projects as well as the stability of proteins and protein complexes to inform AI models. In his free time, he mainly hangs out with his family, but also enjoys reading a good science book, like those authored by Richard Dawkins.

Scientific Endeavors

Kevin's lab is currently trying to uncover the identities of protein assembly components, determine their 3D structure, and modulate their activity. To explore this, they are working on a wiring diagram of the molecules to determine what is actually physically touching. Then once the structure is identified, that informs the mechanism for how that structure functions. Check out a recent [paper](#) by his lab about direct contacts.

"Try to interact with as many people as possible. There is someone out there who probably has an answer to your immediate question, or if not, you'll help out the community by working on a new project with others."

"The people are brilliant, nice, and super willing to share their science with you, whether they are a PI or an undergrad."

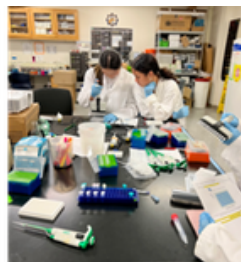
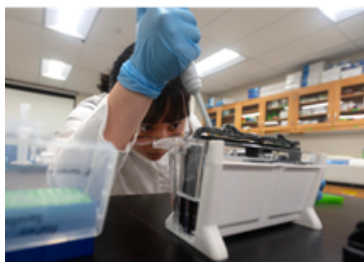
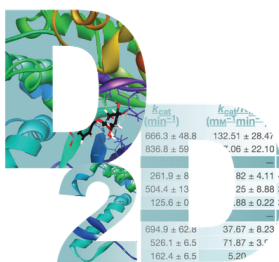
Rosetta Community

Kevin's main focus has always been on the people in the community followed closely by the science. Whereas the science keeps him coming back to engage with the community and tackle new challenges. He appreciates how similarities between challenges are used to help solve them collaboratively.

Email Kevin

Kevin's Lab

Announcements



Design2Data Protein Science CURE Recruiting Faculty Now

Design2Data (D2D) is a nationally networked Course-based Undergraduate Research Experience (CURE) program. In this program, your students will generate enzyme-function data through a shared design-build-test-learn workflow. Their work addresses a persistent bottleneck in AI-enabled protein science: the limited availability of structured, high-quality datasets. The workflow has been successfully integrated into courses across disciplines—including organic chemistry, genetics, biophysics, molecular biology, and biochemistry. We are welcoming new members for the 2026–2027 academic year and invite you to consider joining us. **Applications close September 12, 2026.**

[Learn More & Apply](#)

Rosetta Commons Jobs

Check out our jobs board for the latest postings.

[Jobs Board](#)

Join the conversation on our social channels.



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