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Biophysical Society 2026 Annual Meeting Summary

The Biophysical Society 2026 Annual Meeting was a conference packed with knowledge from all areas of molecular biology research. The main question I was trying to answer at this conference was how $Ca_V1.2$ subunits affect channel inactivation; however, this conference was a bit smaller than the one from last year, so there were no sessions dedicated to specifically ion channel research. Due to this, I had to keep my eye out during any poster sessions for anyone who was doing research in this area.

On the first day of the conference, I was introduced by one of my lab's PhD students to the Don Bers' Lab at UC Davis. This group became our lab's favorite group to hang out with at the conference, and it provided me with great networking opportunities with researchers in California. Several of these individuals I still talk to today.

Outside of networking, the following is a list of my top five highlights from the conference.

1. I talked to a guy at my poster who gave me two papers that will be useful for the CaV1.2 paper. The first is "The α2δ-1 subunit remodels CaV1.2 voltage sensors and allows Ca2+ influx at physiological membrane potentials" (2016 JGP), which shows the CaV1.2 channel is functional without the delta subunit. The second paper is "Regulation of voltage-sensing structures of CaV1.2 calcium channel by the auxiliary β3-subunit" (JGP 2026), which shows the CaV1.2 channel is functional without the beta subunit. The second paper will be less useful since we must model the beta subunit to satisfy the reviewer, but it will be a nice article to validate the data in our paper from only the alpha subunit.
2. I talked to a PhD student at the University of Illinois Chicago who used AutoDock to dock 200,000 small molecules. She said she would give me the scripts she used to do so if I email her. Being able to dock many small molecules would be great for studying small molecule interactions with cytosolic regions.
3. Studying the Effects of Perturbations on Disordered Protein Ensembles Using Simulations – Sarah Rauscher – She does similar MD research to us, taking the AlphaFold models of proteins and simulating them in MD to gain insight into their intrinsically disordered regions. While she does not work on cardiac proteins, she may be an interesting reviewer for our MD work.
4. Recovering Equilibrium Statistics from Vitrified Cryo-EM Samples – Louis G. Smith – He does computational research on flash freezing stage of CryoEM. Specifically, he looks at inaccuracies of protein structure caused by this freezing process. His work may be nice to cite in our modeling papers to discuss the limitations of CryoEM.
5. Interference from Fret Measurements on the Orientation of the CaV1.1 II-III Loop Relative to RyR1 – Danielle M. Heebner – She discussed a CryoEM structure of the complex between RyR1 and CaV1.1. This structure could be a useful guide in case we want to do a large box simulation of CaV1.2 with RyR2 (it may be too big, but it will be interesting to see the complex throughout time). She pointed to

a reference that suggested only the beta-1 subunit, stac3, and junctophilin are needed for the complex to be functional.

Overall, the conference was tremendously beneficial to me. I met about twenty scientists through the wide array of networking opportunities available. Additionally, I was able to find tons of new concepts to use in my research, most of which I would never have known to look for on my own. What I learned from this conference is going to push my research much further than it would have gone otherwise, and the connections I made will help me accelerate my research career in the upcoming years.