

Scientific Meeting Report:

SMBE Australasian Protein Structural Phylogenetics Meeting 2026 (APSPM 2026)

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APSPM 2026 is one edition of the regional meeting program of The Society for Molecular Biology & Evolution (SMBE), and was held in The University of Queensland, Brisbane, Australia from February 15 to 18 (**Fig. 1**). A main objective of APSPM 2026 was to address ongoing challenges in linking protein function and evolution by leveraging recent advances in protein structure prediction. This objective aligns firmly with my doctoral research, and attending the meeting proved fruitful. I had informative discussions with experts, learned the current state and direction of the field, and expanded my network.

The available spots for in-person attendance were limited to 50 and thus highly competitive. So I was immensely grateful to be given the opportunity to attend the meeting in-person, and deliver an oral presentation on my doctoral research. I am quite honored to have been awarded an intercontinental travel grant by APSPM 2026 organizers, and a grant by the Department of Genetics (National Institute of Genetics), SOKENDAI. These grants enabled my attendance.



Fig. 1. Attending APSPM 2026. *Left*) Meeting logo. A printed, encapsulated version of the logo was given to attendees. This logo nicely highlights central themes of the meeting and the scenery in Brisbane. *Middle*) Meeting location. The meeting was held at a top university in Australia. A student very kindly took a photo of me at the entrance. *Right*) Main room for oral presentations during a break.

All the talks were fascinating and educational. I was particularly attentive to research methods, since this is critical for results interpretation, and can be a start point of innovations. Efforts to understand evolutionary relationships among protein sequences have led to developing strategies that incorporate structural data determined experimentally or predicted using state-of-the-art programs such as AlphaFold. One strategy focuses on well-defined structures and summarizes the physical geometry of residues (i.e., amino acids) in 3D space as characters analogous to amino acid symbols. This strategy is implemented in the popular software suite called “foldseek”, and is useful to search for homology among highly dissimilar sequences. A separate strategy focuses on structural flexibility (i.e., less well-defined, presumably dynamic structures) by leveraging various information such as atom bonding or “protein language models”. The oral presentations helped deepen my understanding of these strategies and learn how various instantiations of these strategies are employed for various purposes including ancestral sequence reconstruction and divergence estimation. The workshops, which included tutorials by foldseek developers, helped me develop hands-on experience applying the strategies. These experiences led me to recognize the latest advances and ongoing challenges in the field.

Since the meeting had a limited size and focused theme, I could engage in many in-depth discussions with leading researchers or simply listen and learn from discussions. These discussions partly covered my doctoral research attempting to address the relevance of high structural flexibility

in protein function, and were valuable. They led me to consider how to improve my ongoing work. I also expanded my network, potentially opening doors for collaboration and research opportunities. My oral presentation appeared to be well-received; I got many interesting comments that gave me ideas, and was honored with a best oral presentation jointly awarded by the Australian Centre for Ecogenomics and the APSPM 2026 organizers.



Fig. 2. Oral presentation. *Left*) Start of my oral presentation. An attendee very kindly took a photo of me during my oral presentation. *Right*) Cap that I received as part of the award for a best student oral presentation. This is an apt memorabilia of my visit to Brisbane and APSPM 2026 attendance.

The closing session of the meeting was inspiring because we discussed the utility of incorporating protein structural information in phylogenetics studies, considered main limitations, and how to address such limitations. I saw, in real-time, how the field is developing and setting priorities.

Overall, I think APSPM 2026 was superb. The scope might appear niche at face value, but the talks had far-reaching implications not only in evolution, but also in areas such as predicting protein function, developing therapeutics. Critically, I learned a lot from the terrific oral presentations, workshops and discussions. In the midst of this, I had the chance to walk in and around Brisbane and behold spectacular scenery (**Fig. 3**).

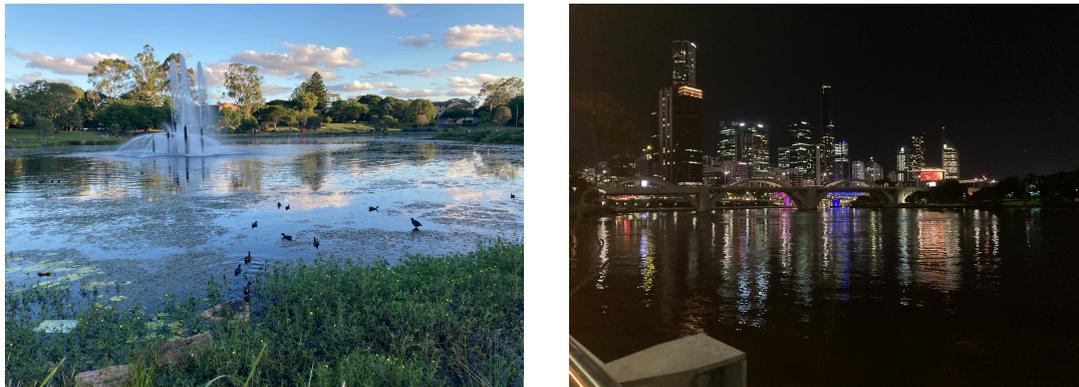


Fig. 3. Pleasant scenery in Brisbane. *Left*) A lake in the St. Lucia Campus of the University of Queensland. *Right*) City skyline and bridge as viewed from a ferry moving along Brisbane river.

External links (Last accessed on March 2, 2026)

Official meeting webpage: <https://biosig.lab.uq.edu.au/strphy26/strphy26>

Social media page that covered the meeting: <https://bsky.app/profile/strphy.bsky.social>