

## Event metadata

|                           |  |
|---------------------------|--|
| <b>Event title</b>        | ProteinDJ: A modular and open-source framework for protein design workflows  |
| <b>Event type</b>         | Webinar  |
| <b>Date of event</b>      | 7 October 2025   |
| <b>Time of event</b>      | 12pm AEDT  |
| <b>Topic description</b>  | <p>This webinar is part of the series “Leveraging deep learning to design custom protein-binding proteins”.</p> <p>Deep learning methods are speeding up the process of designing proteins with desirable biophysical properties. This fast moving field leverages computational workflows that integrate deep learning models like RFdiffusion, ProteinMPNN, Bindcraft with protein structural prediction methods (AlphaFold, Chai-1, Boltz-2) and traditional structural biology methods to improve protein design success rates.</p> <p>This webinar series features case studies from leaders in the field and is designed to inspire and help you recognise potential applications of this new approach to the design of protein-binding-proteins. Join us to hear how software such as Bindcraft is being applied to different research questions and gain hints and tips on using them in your own work.</p> <p>This series is brought to you by the <a href="#">Community for Structural Biology Computing in Australia</a>.</p> |
| <b>Speakers</b>           | Dr Josh Hardy, WEHI  |
| <b>Format description</b> | Webinar presentation followed by a brief question and answer session   |
| <b>Identifier(s)/URL</b>  | <a href="https://www.biocommons.org.au/events/protein-binder-series">https://www.biocommons.org.au/events/protein-binder-series</a>  |
| <b>Licence</b>            | Materials are shared under a Creative Commons Attribution 4.0 International agreement unless   |

|                               |   |
|-------------------------------|---|
|                               | otherwise stated on the materials   |
| <b>Keywords</b>               | Bioinformatics <a href="http://edamontology.org/topic_0091">http://edamontology.org/topic_0091</a><br>Structural biology <a href="http://edamontology.org/topic_1317">http://edamontology.org/topic_1317</a><br>Protein interactions <a href="http://edamontology.org/topic_0128">http://edamontology.org/topic_0128</a><br>AI<br>Deep learning |
| <b>Contact</b>                | training@biocommons.org.au  |
| <b>Audience</b>               | These webinars are intended for structural biologists but are suitable for anyone who is curious about <i>de novo</i> protein design.   |
| <b>Prerequisites</b>          | None  |
| <b>Technical requirements</b> | None  |
| <b>Learning outcomes</b>      | By the end of this webinar you should be able to: <ul style="list-style-type: none"> <li>Describe a use case of deep learning in the design of custom protein-binding-proteins</li> </ul>   |
| <b>Training materials</b>     | Materials shared in this Zenodo record:<br><br>Hardy_slides_2025 (PDF): Slides presented during the webinar<br><br>Materials shared elsewhere:<br><br>A recording of this webinar is available on the Australian BioCommons YouTube channel:<br><a href="https://youtu.be/xwvF62HxaF0">https://youtu.be/xwvF62HxaF0</a>                         |
| <b>Related materials</b>      | ProteinDJ is openly available on GitHub:<br><a href="https://github.com/PapenfussLab/proteindj">https://github.com/PapenfussLab/proteindj</a><br><br>ProteinDJ is described in the preprint:<br><a href="https://www.biorxiv.org/content/10.1101/2025.09.24.678028v1">https://www.biorxiv.org/content/10.1101/2025.09.24.678028v1</a>           |