OpenFold Member PUXANO Secures Prestigious GPU Resources for Protein Design Innovation

PUXANO, a leading platform-based biotech company, has been awarded valuable GPU computation resources on the Karolina cluster. This significant recognition comes from the EuroHPC Joint Undertaking (JU) and the Partnership for Advanced Computing in Europe (PRACE), highlighting PUXANO's cutting-edge approach to protein design.

The GPU resources allocated to PUXANO will play a crucial role in the advancement of a new version of the Genie diffusion model (Genie 3.0) that is being developed by Yeqing Lin and Minji Lee from the Mohammed AlQuraishi Lab at Columbia University. This novel model will be 10x larger than the previous Genie model releases and will introduce new capabilities for protein design that were previously unattainable. Furthermore, the PUXANO platform for high-throughput experimental validation of protein designs will be used to validate the proteins designed for different tasks.

Once completed, this innovative model could be seamlessly integrated into the OpenFold suite, significantly enhancing its already robust collection of open source de novo protein prediction models. This integration represents a pivotal step forward, reinforcing OpenFold's commitment to pushing the boundaries of de novo protein prediction and protein design.

About PUXANO

PUXANO (www.puxano.com) is a platform-based biotechnology company specializing in protein design and structure-based protein research (cryoEM) for membrane proteins and protein complexes.

Useful Links:

- Mohammed AlQuraishi Lab: https://www.aqlab.io/
- OpenFold initiative: https://openfold.io/
- EuroHPC Joint Undertaking (JU): https://eurohpc-ju.europa.eu/
- Partnership for Advanced Computing in Europe (PRACE): https://prace-ri.eu/

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