

ProteinGAN – deep learning framework for rapid generation of highly-functional synthetic enzyme libraries



Vilnius
University

Brief description of a technology

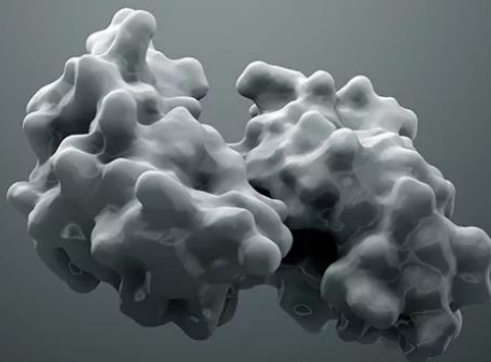
The immense size of protein sequence space and poor understanding of sequence-function relationships renders current protein library design methods highly inefficient. Deep learning based technology developed by Biomatter Designs – ProteinGAN – provides a way to generate highly diverse and functional synthetic enzyme libraries. Due to high amounts of mutations in each synthetic enzyme sequence (up to 50% currently shown) and their retained catalytic activity, the designed libraries can be subjected to exceptionally potent screening for improved activity, thermostability and other characteristics.

Fields of application

Protein engineering.

Technology readiness

Technology validated in lab.



Intellectual property

Patent applications: LT2018 542, LT2019 524, PCT/IB2019/058545.

Applicants: UAB „Biomatter Designs“ and Vilnius University.

Relevant publications

Repecka et al. (2019) Expanding functional protein sequence space using generative adversarial networks. *bioRxiv* 789719; doi: <https://doi.org/10.1101/789719>.

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