

Helix Engineering: Combining the Power of 3DM with AI to Disrupt Protein Engineering





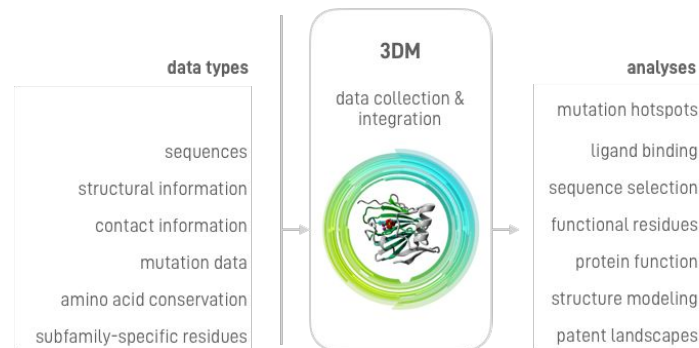
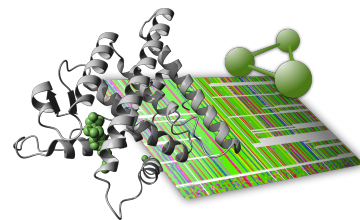
Bio-Product's mission is "Catalyzing Protein Research".

Bio-Product collaborates with

- 7 out of top 10 pharmaceutical companies
- biotech companies
- academic & research institutes

3DM

- a protein data and analysis platform
- better understand the role of amino acids
- design better experiments
- widely used in the protein engineering field

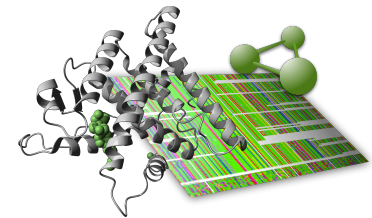
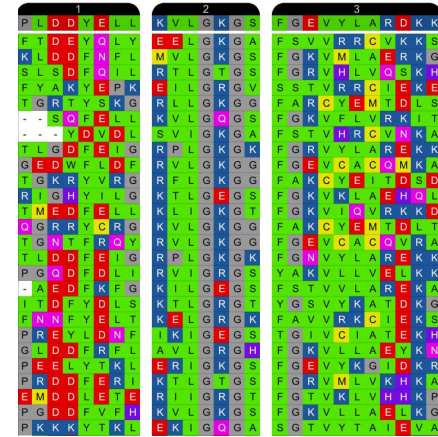


3DM collects many types of data for all sequences of complete superfamilies:

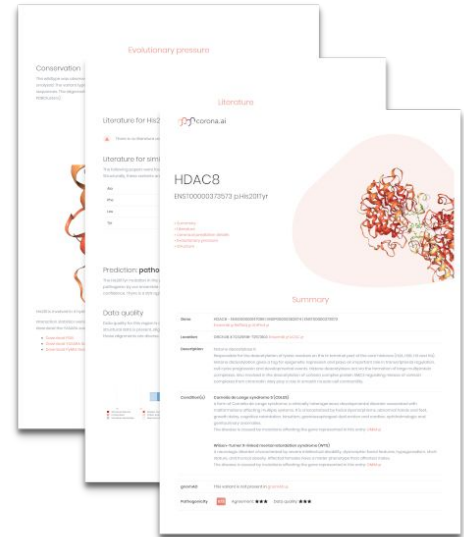
- Mutation data from literature, patents, mutation databases (we have biggest literature mutation collection in the world)
- Protein-protein and ligand contact data.
- Evolutionary alignment fingerprints (e.g. conservation, correlated mutations, aa distributions, etc)
- Disease information, chemical reaction data, SNP data

3DM contains many tools for the analysis of all this data:

- Tools for visualization of data in any protein structure
- Tools for easy analysis of the alignment.
- Cornet, for the analysis of correlated mutations
- All data and tools are connected in 3DM via the alignment.



- The next step? Combining this data with Machine Learning
- Built on 3DM features, using data from >33.000 3DM systems for **100% human variant coverage.**
- Helix Pathogenicity Predictor
 - Top of the line clinical predictions
 - High standards for performance assessment
 - Intuitive reports, web-interface, and APIs available
- Outperforms all other pathogenicity predictors in novel datasets for published cancer research and datasets with real novel clinical data (e.g. BRCA1, CHEK2, PALB2).
- **Predicts if a variant is pathogenic or not with 95% accuracy** on the complete human exome.
- Applicable to any organism (e.g. for strain engineering)



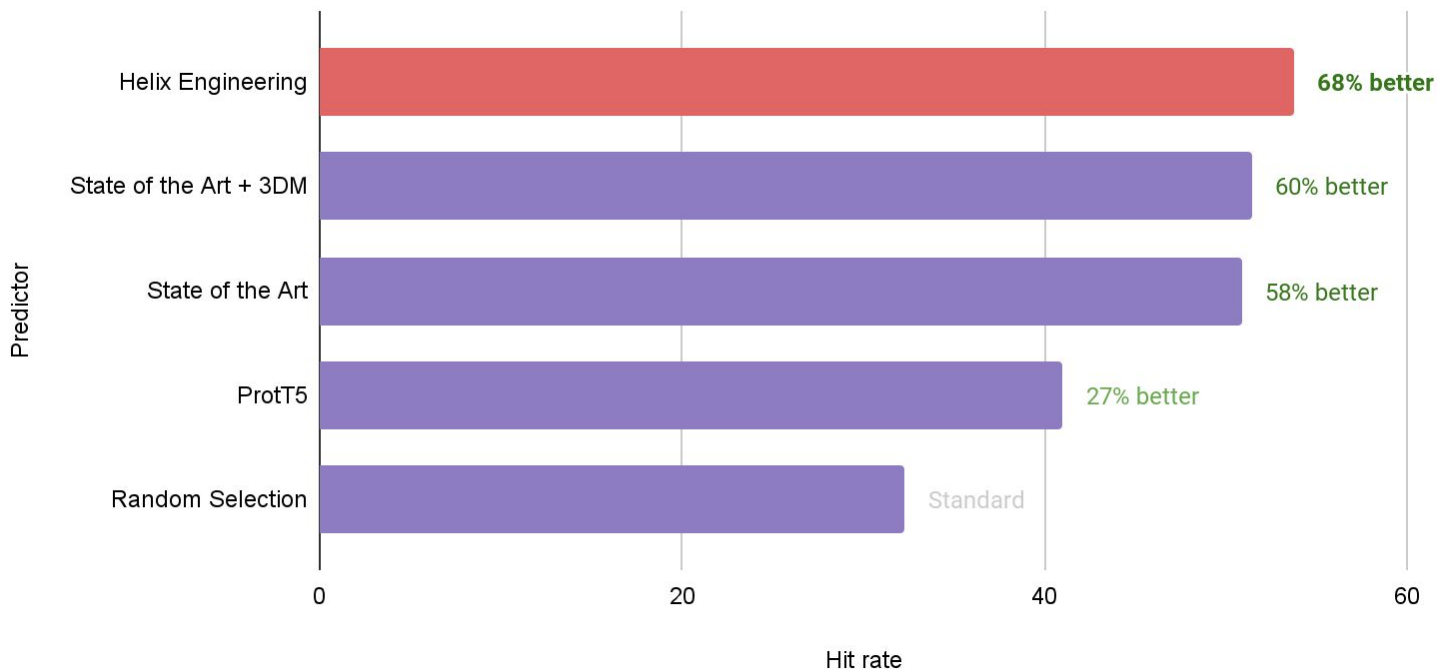


Bio-Product 3DM + AI

- Our next frontier: **Helix Engineering**
- Use Helix Pathogenicity strategy to enable AI based Protein Engineering
 - 56 number of tests have been performed with public data and several pilots are currently being run using customer data.
 - Low number of mutations needed (50 to 100) for the prediction of a high quality second round of evolution.
 - Can be applied to different protein features, such as activity, stability, co-factor binding, and many others.
- **Helix Engineering is a generic solution that boosts Protein Engineering with 3DM and AI insights**

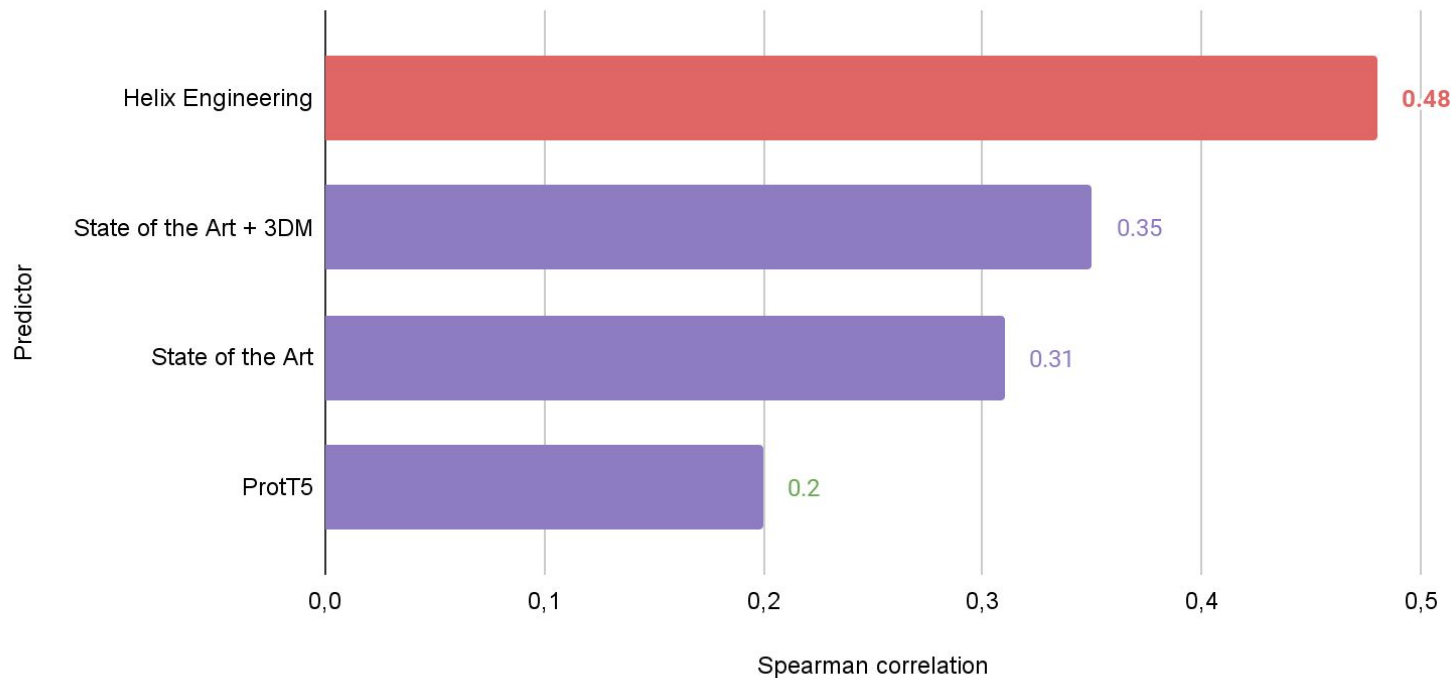
Prediction performance

Measure the number of hits (better than wild-type) per experiment on average, compared to random selection in 56 test sets.



Prediction performance

Spearman Correlation (ranking performance) with true fitness of all variants in 56 test sets



Conclusion

- Using modern machine learning techniques, we can increase fitness prediction performance by **>60%** over legacy techniques, like random selection or one-hot encoding.
- By intelligently selecting training variants using a generic 3DM based search strategy, we are able to increase this up to **100%**
- In a collaborative approach we combine domain expertise to get the most out of each evolutionary run using a minimum of mutations to measure.
- We offer a full-service package for protein engineering with low turnaround times and low overhead
- The result: **Faster and better protein engineering results**

Q&A

More information:

www.bio-product.nl
helixlabs.ai

Whitepaper: <https://arxiv.org/abs/2104.01033>

