# Article information:

D-SCRIPT translates genome to phenome with sequence-based, structure-aware, genome-scale predictions of protein-protein interactions - ScienceDirect  
<https://www.sciencedirect.com/science/article/pii/S2405471221003331?via%3Dihub>

# Article summary:

1. D-SCRIPT is a deep-learning model that predicts protein-protein interactions from primary amino acid sequences.

2. D-SCRIPT maintains high accuracy with limited training data and across species, enabling improved functional characterization of proteins in less studied organisms.

3. D-SCRIPT can be used to predict PPIs de novo from the genome of a newly sequenced organism, allowing for functional gene modules to be identified and gene function to be annotated at scale.

# Article rating:

May be slightly imbalanced: The article presents the information in a generally reliable way, but there are minor points of consideration that could be explored further or claims that are not fully backed by appropriate evidence. Some perspectives may also be omitted, and you are encouraged to use the research topics section to explore the topic further.

# Article analysis:

The article “D-SCRIPT translates genome to phenome with sequence-based, structure-aware, genome-scale predictions of protein-protein interactions” is an informative and well written piece that provides an overview of the new deep learning model D-SCRIPT and its potential applications in predicting protein interactions from sequence data. The article is clear in its description of the model’s architecture and how it works, as well as providing evidence for its efficacy in cross species prediction tasks.

The article does not appear to have any major biases or one sided reporting, as it presents both sides of the argument fairly and objectively. It also does not contain any unsupported claims or missing points of consideration; all claims are backed up by evidence provided in the form of experiments conducted on the model itself or other studies cited throughout the article. Furthermore, there is no promotional content present in the article; instead it focuses solely on providing an objective overview of D-SCRIPT’s capabilities and potential applications.

The only potential issue with this article is that it does not explore any counterarguments or possible risks associated with using D-SCRIPT for predicting protein interactions from sequence data. While this may not be necessary for such an overview piece, it would have been beneficial to include some discussion on these topics so as to provide a more comprehensive view on the implications of using this model for such tasks.

# Topics for further research:

* Protein-protein interaction prediction risks
* Potential drawbacks of deep learning models for protein-protein interaction prediction
* Cross species protein-protein interaction prediction accuracy
* Challenges of predicting protein-protein interactions from sequence data
* Advantages of using D-SCRIPT for protein-protein interaction prediction
* Applications of D-SCRIPT in genomics research

# Report location:

<https://www.fullpicture.app/item/9fd401b564477d46f256d7a6dad9b606>