Stanford

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Ph.D. Student in Computer Science, admitted Autumn 2020

Bio

INSTITUTE AFFILIATIONS

- Member (Student), Cardiovascular Institute

Publications

PUBLICATIONS

- **DeepLoc 2.1: multi-label membrane protein type prediction using protein language models.** *Nucleic acids research*
  Ødum, M. T., Teufel, F., Thumuluri, V., Almagro Armenteros, J. J., Johansen, A. R., Winther, O., Nielsen, H.
  2024

- **GraphPart: homology partitioning for biological sequence analysis.** *NAR genomics and bioinformatics*
  Teufel, F., Gíslason, M. H., Almagro Armenteros, J. J., Johansen, A. R., Winther, O., Nielsen, H.
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- **DeepLoc 2.0: multi-label subcellular localization prediction using protein language models.** *Nucleic acids research*
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  2022

- **SignalP 6.0 predicts all five types of signal peptides using protein language models.** *Nature biotechnology*
  Teufel, F., Almagro Armenteros, J. J., Johansen, A. R., Gislason, M. H., Pihl, S. I., Tsirigos, K. D., Winther, O., Brunak, S., von Heijne, G., Nielsen, H.
  1800

- **NetSolP: predicting protein solubility in Escherichia coli using language models.** *Bioinformatics (Oxford, England)*
  Thumuluri, V., Martiny, H. M., Almagro Armenteros, J. J., Salomon, J., Nielsen, H., Johansen, A. R.
  2022; 38 (4): 941-946

- **NetSolP: predicting protein solubility in E. coli using language models.** *Bioinformatics (Oxford, England)*
  Thumuluri, V., Martiny, H., Armenteros, J. J., Salomon, J., Nielsen, H., Johansen, A. R.
  2021

- **Prediction of GPI-anchored proteins with pointer neural networks** *CURRENT RESEARCH IN BIOTECHNOLOGY*
  Gislason, M., Nielsen, H., Armenteros, J., Johansen, A.
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- **Deep protein representations enable recombinant protein expression prediction.** *Computational biology and chemistry*
  Martiny, H. M., Armenteros, J. J., Johansen, A. R., Salomon, J., Nielsen, H.
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