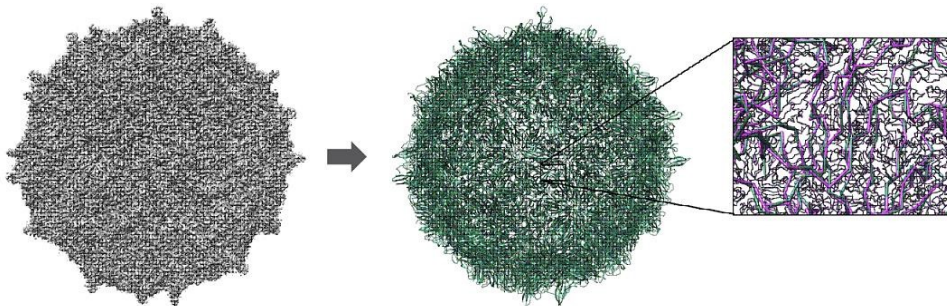


DeepTracer™

A software tool for ultra-fast, fully automated, and accurate de novo protein large complex structure prediction from 3D electron microscopy map. DeepTracer uses deep learning methods and optimization techniques to predict the locations of the atoms, secondary structure elements, and amino acid types. It targets the ab initio all-atom protein structure prediction problem for extremely large complexes, such as viruses, bacteria, and other molecular machines. The work has been featured on PNAS research highlights and Nature Computational Science research highlights.

For more information: <https://deepttracer.uw.edu>



International Requests:

University of Washington agreements require additional review if the requesting entity is located in, or affiliated with the government of, China (Including Hong Kong; not including Taiwan), Iran, North Korea, Russia, or Syria. For requests from these countries, please **allow for an additional month of processing time** for a response.

Available Licenses

Academic License:

See right panel to license this product.

References

1. Jonas Pfab, Nhut Minh Phan, and Dong Si ,
<https://www.pnas.org/content/118/2/eiti0221118#sec-9>
2. Fernando Chirigati , <https://www.nature.com/articles/s43588-021-00035-w>

Technology ID

49069,49151,8133

Category

Software/Bioinformatics

Learn more

