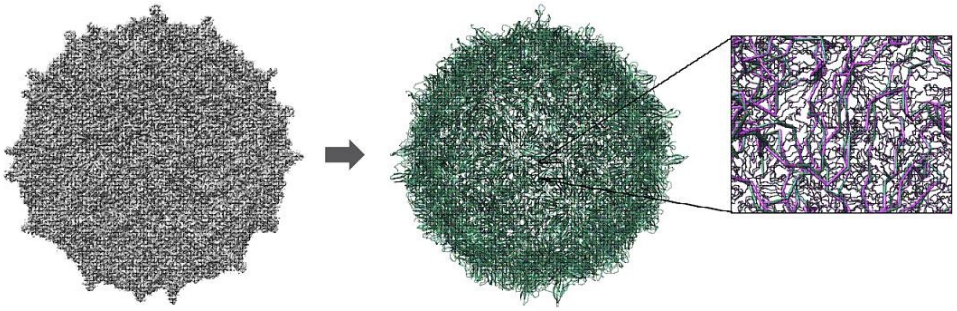
DeepTracer™

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://deeptracer.uw.edu



Technology ID

49069,49151,8133

Category

Software/Bioinformatics

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References

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