



SJTU-SOFTWARE



2022

The project aims to develop a modeling software to provide a feasible scheme for the reconstruction of ecGEM by actinomycetes.

At the same time, it combines deep learning to predict the conversion coefficient of metabolic enzymes Kcat to compensate for the lack of parameters. Protein three-dimensional structure constraints and proteolytic mutation hotspots identification tools were added to recommend the target of modification.

It uses the effects of modification on cell phenotypes which were verified by software modeling validating retrofitting scheme to provide the orientation of modification for enzyme engineering experiments and shorten the experimental period.

DL-ecGEM OF ACTINOMYCETES