Dynamic mapping of proteome trafficking within and between living cells by TransitID

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The ability to map trafficking for thousands of endogenous proteins at once in living cells would reveal biology currently invisible to both microscopy and mass spectrometry. Here we report TransitID, a method for unbiased mapping of endogenous proteome trafficking with nanometer spatial resolution in living cells. Two proximity labeling (PL) enzymes, TurboID and APEX, are targeted to source and destination compartments, and PL with each enzyme is performed in tandem via sequential addition of their small-molecule substrates. Mass spectrometry identifies the proteins tagged by both enzymes. Using TransitID, we mapped proteome trafficking between cytosol and mitochondria, cytosol and nucleus, and nucleolus and stress granules, uncovering a role for stress granules in protecting the transcription factor JUN from oxidative stress. TransitID also identifies proteins that signal intercellularly between macrophages and cancer cells. TransitID introduces a powerful approach for distinguishing protein populations based on compartment or cell type of origin.

References

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Wei Qin. Beijing Institute of Technology (BS, 2014), Peking University (Ph.D., 2019, Prof. Chu Wang and Prof. Xing Chen), Stanford University (Postdoc, 2019-2023, Prof. Alice Y. Ting), Tsinghua University (professor, 2023-present). [Field of research] Proximity labeling, Chemoproteomics, Post-translational modifications.