**Architecture mapping of macromolecular complex by proximity labeling in live cells**

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 Proximity labeling methods by in situ generated reactive biotin-conjugated molecules have been developed and has shown remarkable new biological findings such as in vivo interactome which have not been discovered by traditional methods. Our group recently developed an improved method (Spot-ID) by detecting the biotin-labeled residues generated in proximity labeling by APEX2 or pBirA using mass spectrometry. This method allows the identification of the labeled protein directly without false positive findings and the structural identification of the labeled protein. Using this method, we could map architecture of the inner mitochondrial membrane (IMM) proteome whose topology at IMM has not been fully characterized yet. Furthermore, this method allowed the identification of unknown elements in the rapamycin-induced interactome on the FK506-rapamycin binding (FRB) domain of mTOR in living cells. Overall, we have found that sites identified by Spot-ID successfully reflect in vivo structures of protein complexes in living cells.



**References:**

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