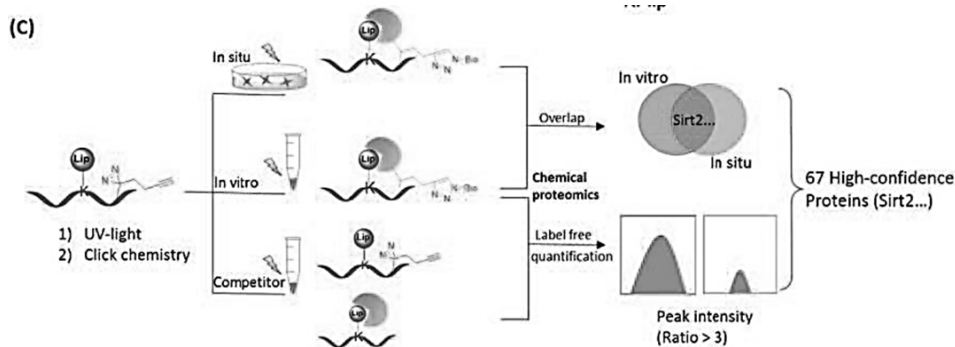


A Set of Affinity Probes for Dissecting the Proteomics of Lysine Lipoylation



Health & Wellness

Biomedical and Genetic Engineering



IP Status

Patent filed



Opportunity

Posttranslational modifications (PTMs) of lysine residues are highly prevalent in living organisms and play important roles in regulating diverse biological processes such as gene transcription, DNA repair, chromatin structure modulation, and metabolism. Lysine lipoylation is a highly conserved lysine PTM found in organisms ranging from bacteria to mammals. Lipoylated lysine is known to act as an essential cofactor for maintaining the activity of essential metabolic multimeric enzyme complexes. Dysregulation of lysine lipoylation leads to malfunctions of metabolic complexes and numerous diseases.

Biological regulations of lysine lipoylation depend on proteins that function as the “writers”, “readers”, and “erasers” of lysine lipoylation. Dissecting lysine lipoylation at the proteomic level can reveal potential drug targets in the dynamic regulation of cellular metabolism. As no affinity probe yet exists to identify proteins that bind/remove lysine lipoylation, an opportunity exists for the development of such a tool.

Technology

The inventors developed a series of affinity probes of lysine lipoylation that are highly efficient and reliable in detecting “reader” and “eraser” proteins of lysine lipoylation in native cellular conditions. All the probes can be used to perform the binding and pull-down experiments in living cells and cell lysates. Using this set of probes, the inventors identified that Sirt2 is a novel “eraser” of lysine lipoylation. Thus, this invention may serve as a useful chemical tool for profiling the proteomic regulation of lysine lipoylation in different cellular contexts to identify therapeutic targets.

Technology Readiness Level (TRL) ?

5

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Develop
Concept

Proof
Concept

Follow-on
Funding

Build Value

Advantages

- The invention is advantageous in profiling binding proteins of lysine lipoylation with high sensitivity and by a simple procedure.
- The probes can operate in both cell lysates and living cells.
- The toolset includes a control probe and a competing probe, which ensures the high specificity of the identification of “readers” and “erasers” of lysine lipoylation.

Applications

- The toolset can be used to identify “readers” and “erasers” of lysine lipoylation using a proteomic approach, and thereby uncover new biology related to lipoylation.
- A tentative application of the probes is profiling the changes of “readers” and “erasers” of lysine lipoylation in different disease models.
- The probes can be used to evaluate the potential of small compounds as inhibitors of lipoylated lysine-binding proteins.

