

Development of new tools to study proteins in live cells

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Abstract

Cells are composed of highly interconnected networks of proteins, nucleic acids and metabolites. To better understand how proteins modulate cell function, we use mass spectrometry based proteomics to identify proteins and quantify their abundance in cells. However, traditional proteomics experiments are fundamentally limited by temporal resolution.

In collaboration with the chemistry department, we have developed a strategy to synthesize a heavy isotope molecule that can be used to add temporal resolution to proteomics.

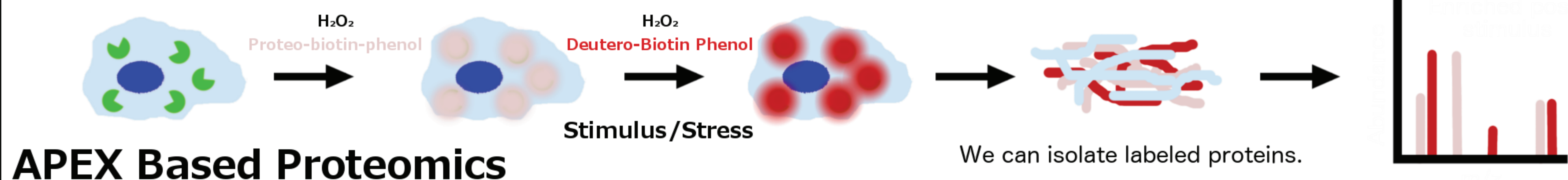
Objective: To develop a strategy to synthesize deuterated biotin-phenol.

APEX is a promiscuous enzyme that is used to add spatial resolution to proteomics experiments.

APEX labels proteins with a molecule that we can identify.

A second round of APEX labeling can be used to label new proteins with a different molecule.

Mass Spectrometry can be used to identify the proteins that were labeled by APEX at each timepoint. Therefore, we can add temporal resolution to our experiments.



APEX Based Proteomics

1. Develop Synthesis Strategy

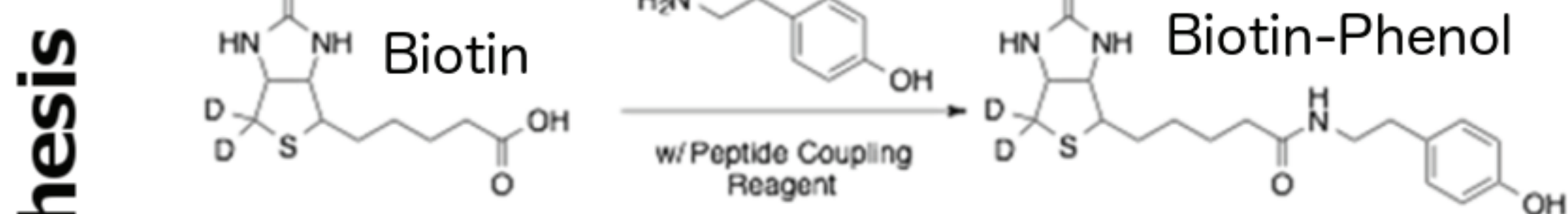
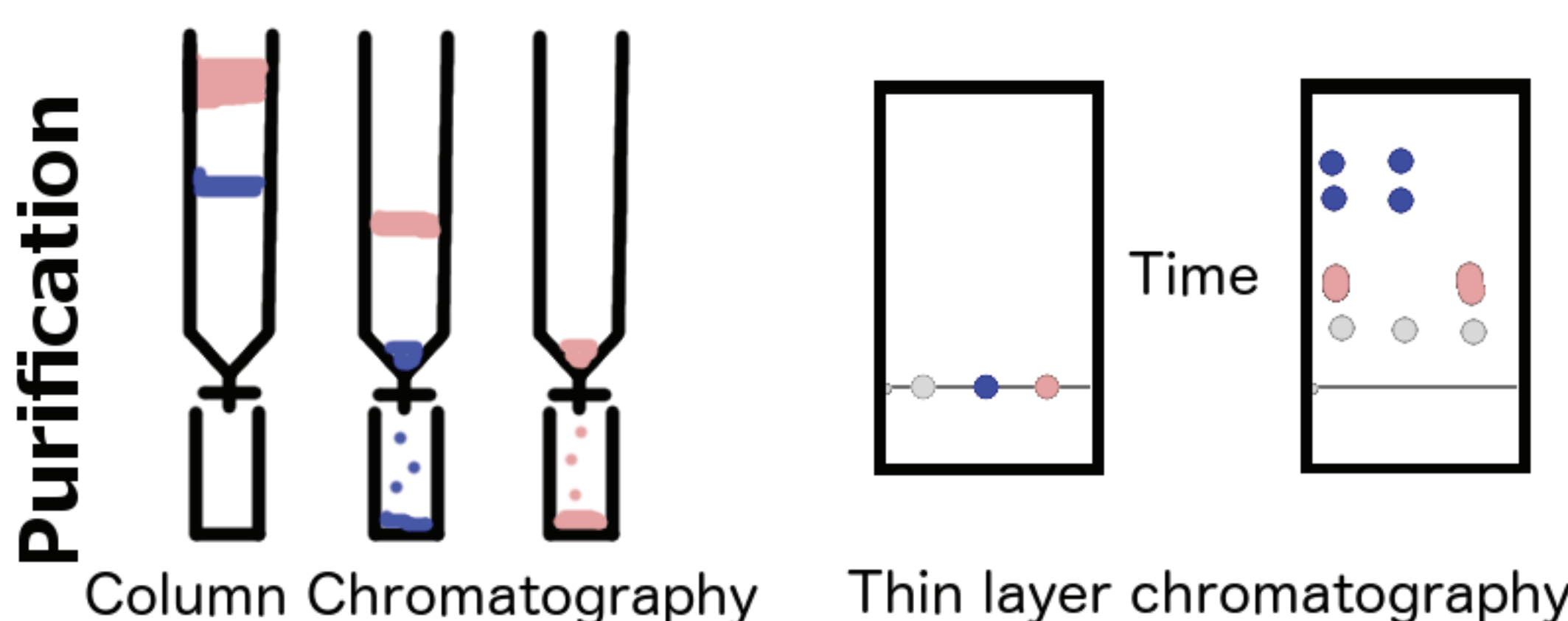


Figure 1: Organic synthesis strategy. Replace select hydrogens (H) on biotin with deuterium (D). Deuterium is a heavier isotope of hydrogen. It has the same molecular properties however is slightly heavier.



2. Confirm Compound

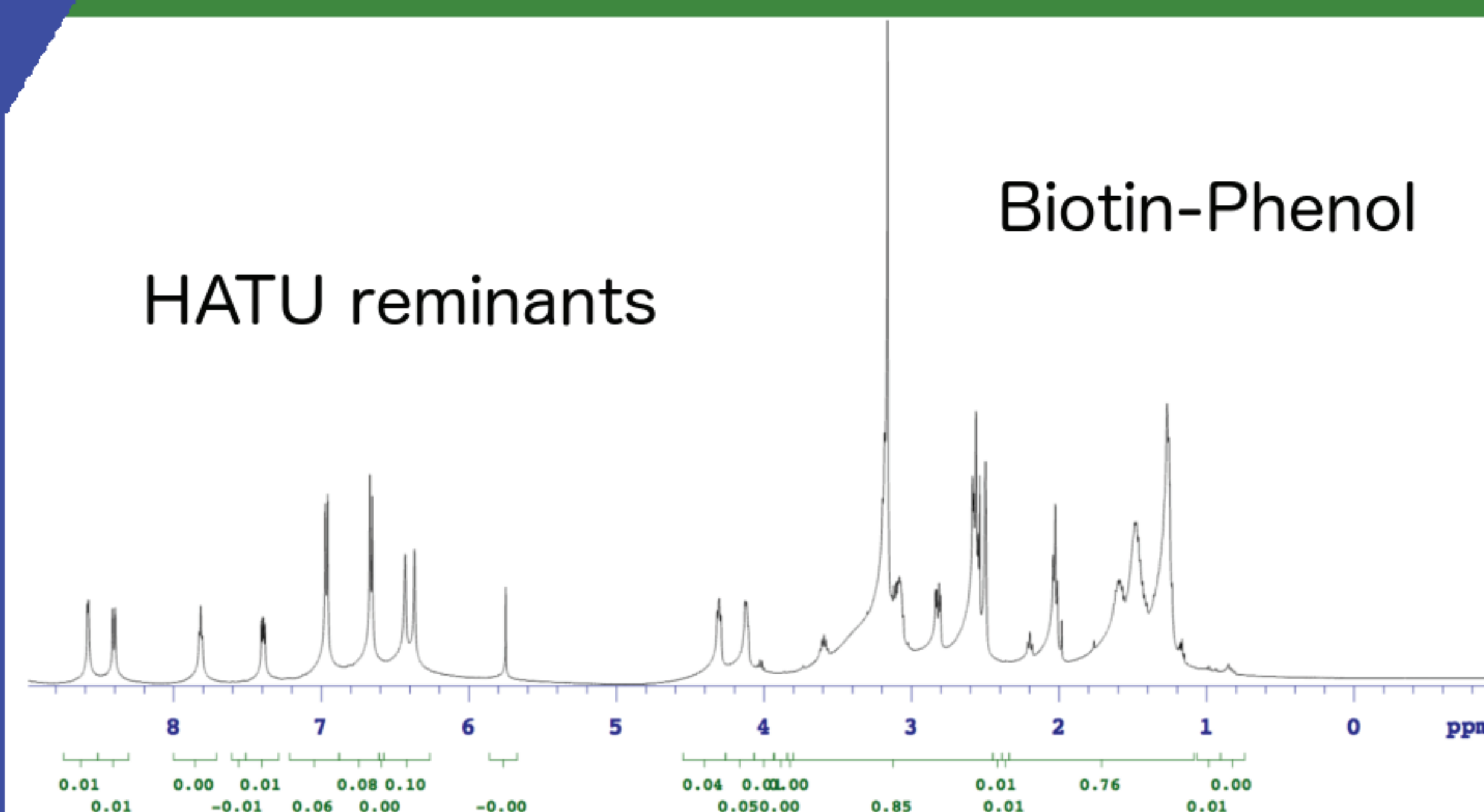


Figure 2: NMR synthesized biotin-phenol. Nuclear Magnetic Resonance (NMR) was used to determine the structure of synthesized compound fractions. Our successfully purified compound was 93% by mass biotin-phenol and 7% HATU.

3. Test in Live Cells

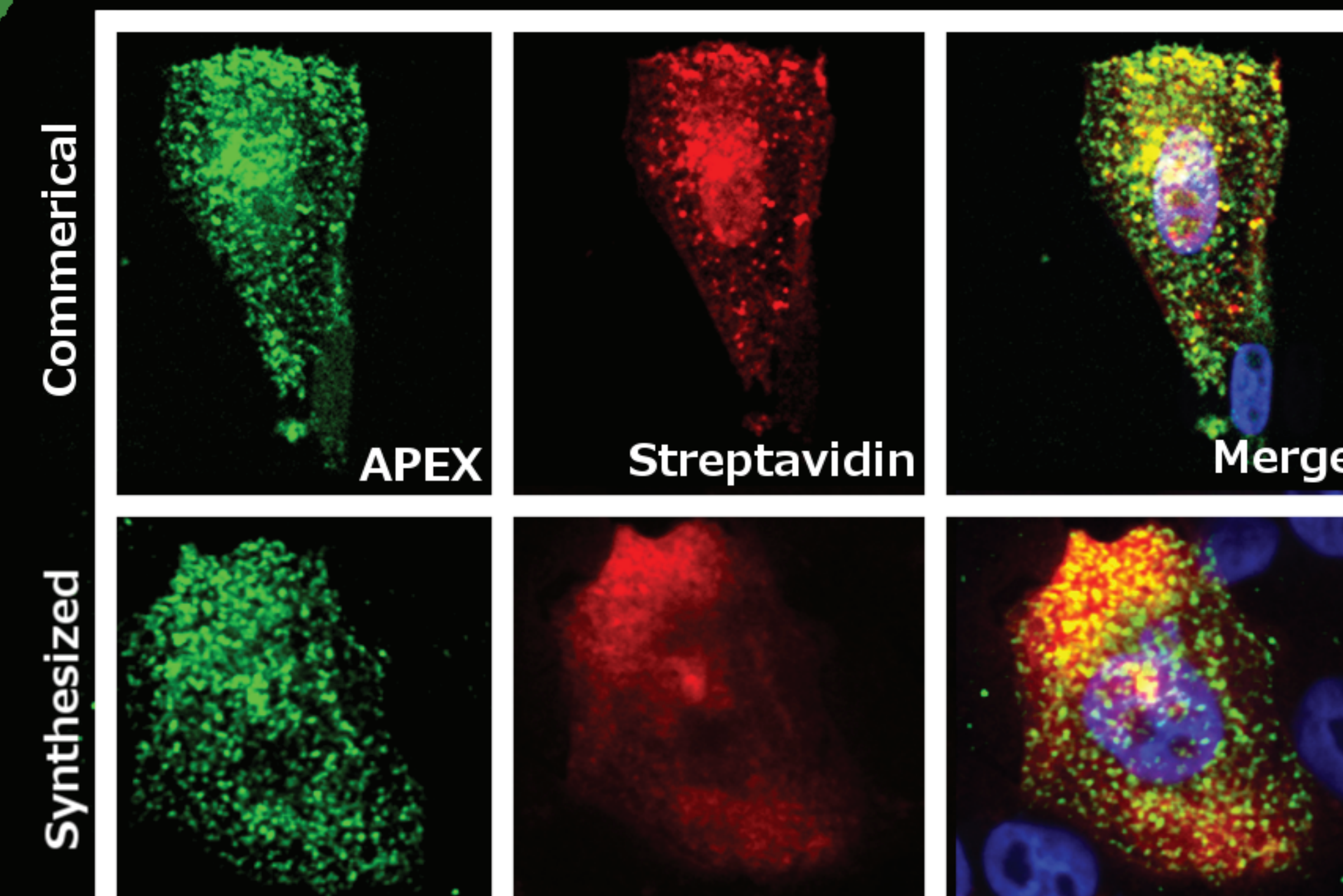
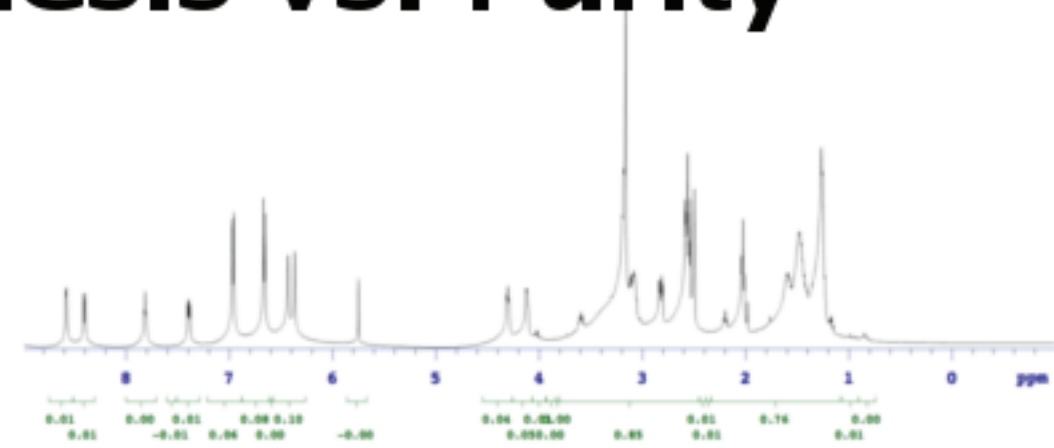


Figure 3: APEX can use both commercial and synthesized biotin-phenol to biotinylate endogenous proteins.

What We Learned

Synthesis vs. Purity



New Technologies

- Organic synthesis, column and thin layer chromatography
- Applications of organic synthesis to answer biological questions

Real Life impacts

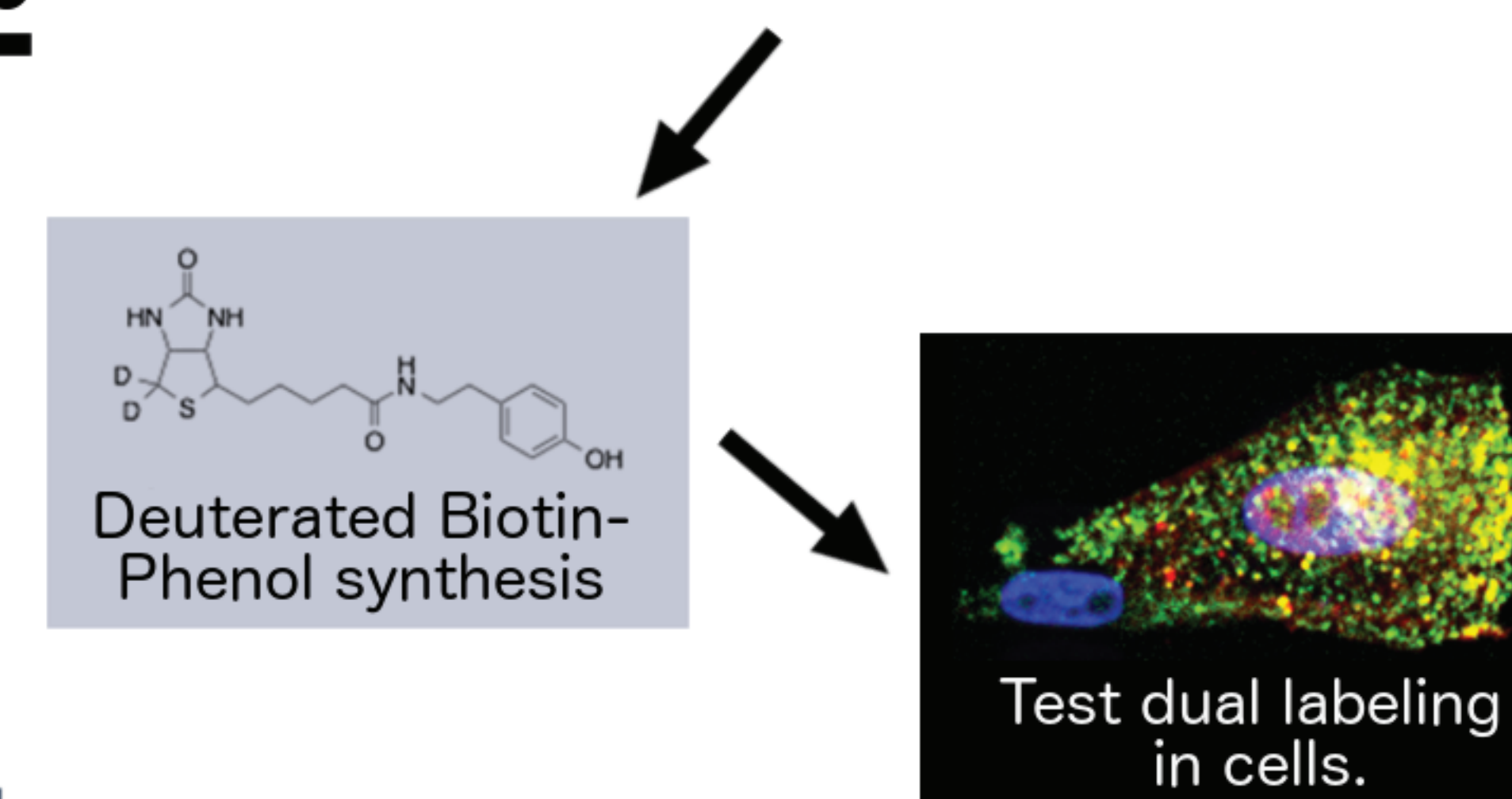
- Forge New Collaboration
- Interdisciplinary Research
- Development of a new technology that enables temporal resolution and dual labeling proteomics experiments.



Library Partnership

- Financial support
- Accelerated Collaboration
- Reference Management
- Reaxys Database Searching

Future directions



Acknowledgements and References

1. Rhee, H.; Zou, R.; Udeshi, N.D.; Martell, J.D.; Mootha, V.K.; Carr, S.A.; Ting, A.Y. Science. 2013, 339, 6125, 1328.
2. This project is sponsored by a 2015-2016 mini-grant awarded through the university Library's Student Chemistry Librarian, Engagement Program. As part of the mini-grant, I was paired with Ye Li, Chemistry Librarian.
3. NSF Graduate Research Fellowship