

Using Genetically Incorporated Unnatural Amino Acids to Study and Control Protein Function

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Genetic code expansion (Figure 1) allows unnatural (non-canonical) amino acid incorporation into proteins of interest by repurposing the cellular translation machinery.¹ The development of this technique has enabled site-specific incorporation of many structurally and chemically diverse amino acids, facilitating a plethora of applications. Here I will show how genetic code expansion can be applied to regulate protein function in mammalian cells² and study protein post-translational modification.³

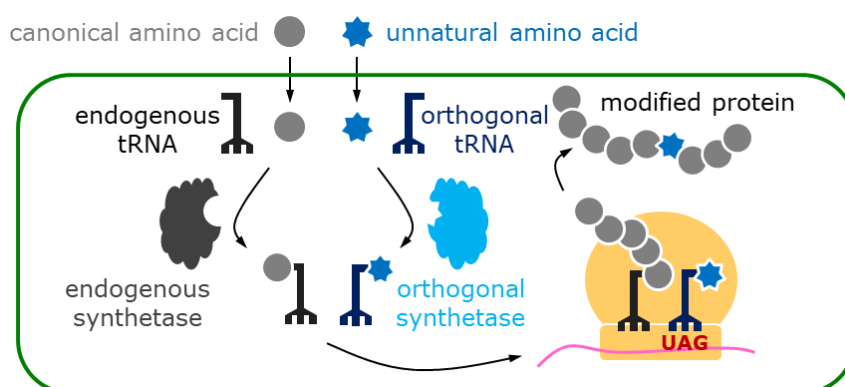


Figure 1. Concept of genetic code expansion.

1. A. R. Nödling, L. A. Spear, T. L. Williams, L. Y. P. Luk, and Y.-H. Tsai. Using genetically incorporated unnatural amino acids to control protein functions in mammalian cells. *Essays Biochem.* **2019**, 63, 237.
2. (a) Y.-H. Tsai, S. Essig, J. R. James, K. Lang, J. W. Chin*, Selective, rapid and optically switchable regulation of protein function in live mammalian cells. *Nat. Chem.* **2015**, 7, 554.
(b) T. Suzuki, M. Asami, S. G. Patel, L. Y. P. Luk, Y.-H. Tsai*, A. C. F. Perry*, Switchable genome editing via genetic code expansion. *Sci. Rep.* **2018**, 8, 10051.
3. J.-H. Liao, C.-H. Tsai, S. G. Patel, J.-T. Yang, I.-F. Tu, M. Lo Cicero, M. Lipka-Lloyd, W.-L. Wu, W.-J. Shen, M.-R. Ho, C.-C. Chou, G. R. Sharma, H. Okanishi, L. Y. P. Luk, Y.-H. Tsai*, S.-H. Wu*, Acetylome of *Acinetobacter baumannii* SK17 reveals a highly-conserved modification of histone-like protein HU. *Front. Mol. Biosci.* **2017**, 4, 77.