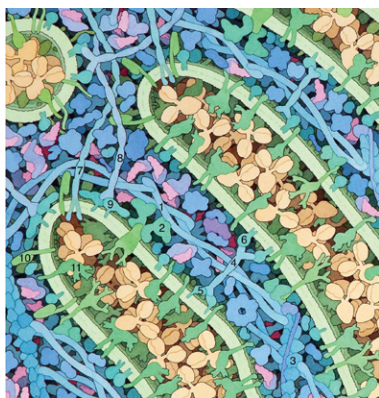


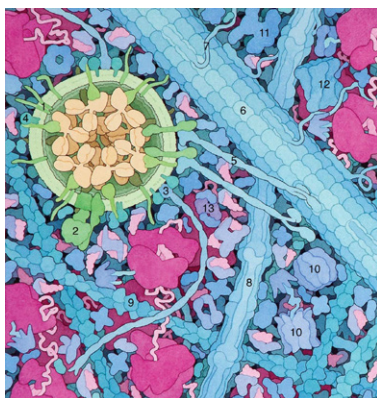
The Problem With Traditional Tagging

Unlike what we were taught, biology is not empty space. The panorama below, drawn to scale from structural and molecular data, shows the coordinated complexity of eukaryotic cells. Every region is densely packed with interacting proteins. No empty space. No isolation.

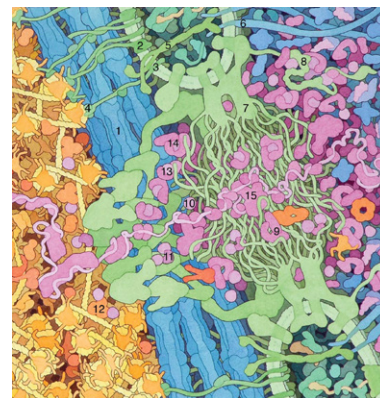
A. Protein Sorting Golgi



B. Vesicle Transport



C. Nuclear Pore Transport



Protein Sorting Golgi: Dense enzymatic network regulating modification and trafficking. Vesicle Transport: Coat proteins, motors, and adaptors orchestrating directional cargo flow. Nuclear Pore Transport: Massive protein assemblies controlling selective nuclear exchange.
 Source: *Eukaryotic Cell Panorama* from David S. Goodsell, *Biochemistry and Molecular Biology Education* Vol. 39, No. 2 pp. 91-101, 2011

The EditCo Standard: Native Biology, Preserved

EditCo engineers genome edits that preserve physiological context through native promoter control, physiological protein expression, correct subcellular localization, and authentic interaction networks. This creates models that reflect true biology, from discovery through translation.

The EditCo Solution: Endogenous Tagging, Done Right



Visualization

See proteins in their native environment

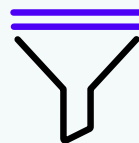
Recommended tags:
GFP, RFP, mCherry



Quantification

Turn cellular behavior into dynamic data

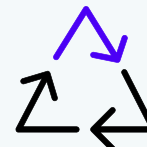
Recommended tags:
HiBiT, GFP, NanoLuc



Purification

Pull down proteins that matter

Recommended tags:
HA, FLAG, HaloTag



Degradation

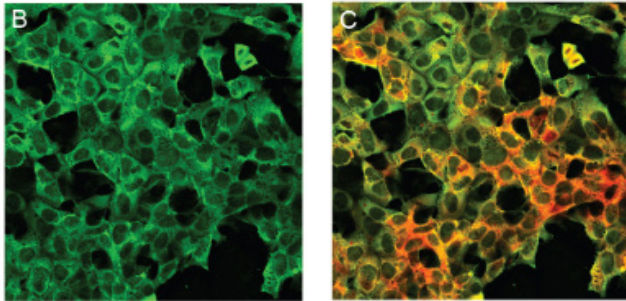
Control protein stability with precision

Recommended tags:
dTAG, AID2

Data That Reflects Real Biology

Visualization

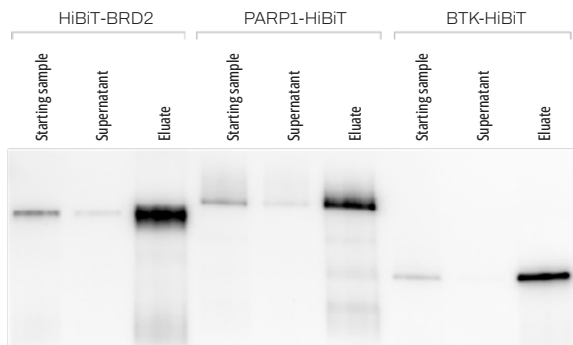
Eliminate artifacts and mislocalization to observe proteins in real time in their native environment (nucleus, membrane, or cytoplasm) with fluorescent tags.



High-resolution visualization of protein localization within the crowded, highly structured cellular environment using fluorescent and covalent tags.

Purification

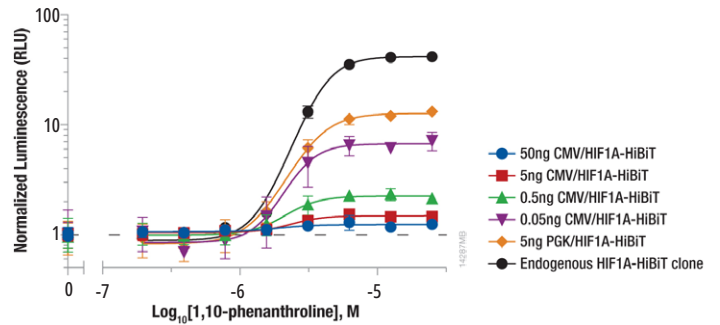
Use endogenously added affinity tags (His, GST, Strep) to isolate a target protein from complex cell lysates for downstream biochemical analysis.



High-affinity immunoprecipitation of natively expressed, endogenously tagged BRD2, PARP1, and BTK with Anti-HiBiT Magne® Beads. Enrichment of tagged proteins in the eluate preserves natural stoichiometries and interactions for IP, co-IP, Western blotting, and proteomics. Source: <https://www.promega.com/products/protein-purification/protein-purification-kits/anti-hihibit-magnetic-beads-and-elution-peptide/>

Quantification

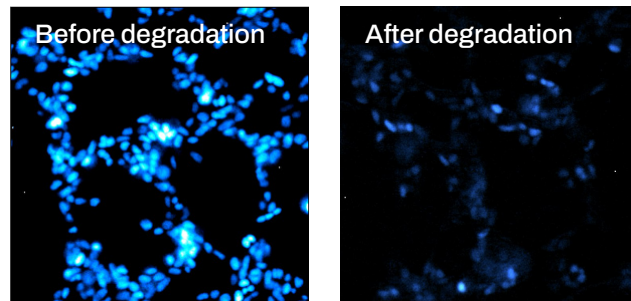
Enable accurate, real-time dose-response analysis with kinetic, stability, and degradation measurements across conditions or cell types—without using protein-specific antibodies.



Protein abundance is constantly and quickly tuned in response to environmental cues. This graph illustrates how endogenous luminescent tagging with HiBiT enables highly sensitive, quantitative measurement of these dynamics. Source: <https://www.promega.com/resources/pubhub/2017/quantifying-protein-abundance-at-endogenous-levels/>

Degradation

Degron tags enable rapid, on-demand protein degradation, giving researchers precise temporal control and the ability to compare knockout versus degradation effects.



In response to environmental cues, cells rapidly degrade some proteins while preserving others. Endogenous tagging enables direct visualization of degradation over time, with fluorescence intensity decreasing over time as the tagged protein is selectively depleted.

What you get

- ✓ Assay-ready edited cell lines
- ✓ Sequence-verified endogenous integration
- ✓ Models designed for real biology
- ✓ Scalability across discovery and translational workflows

