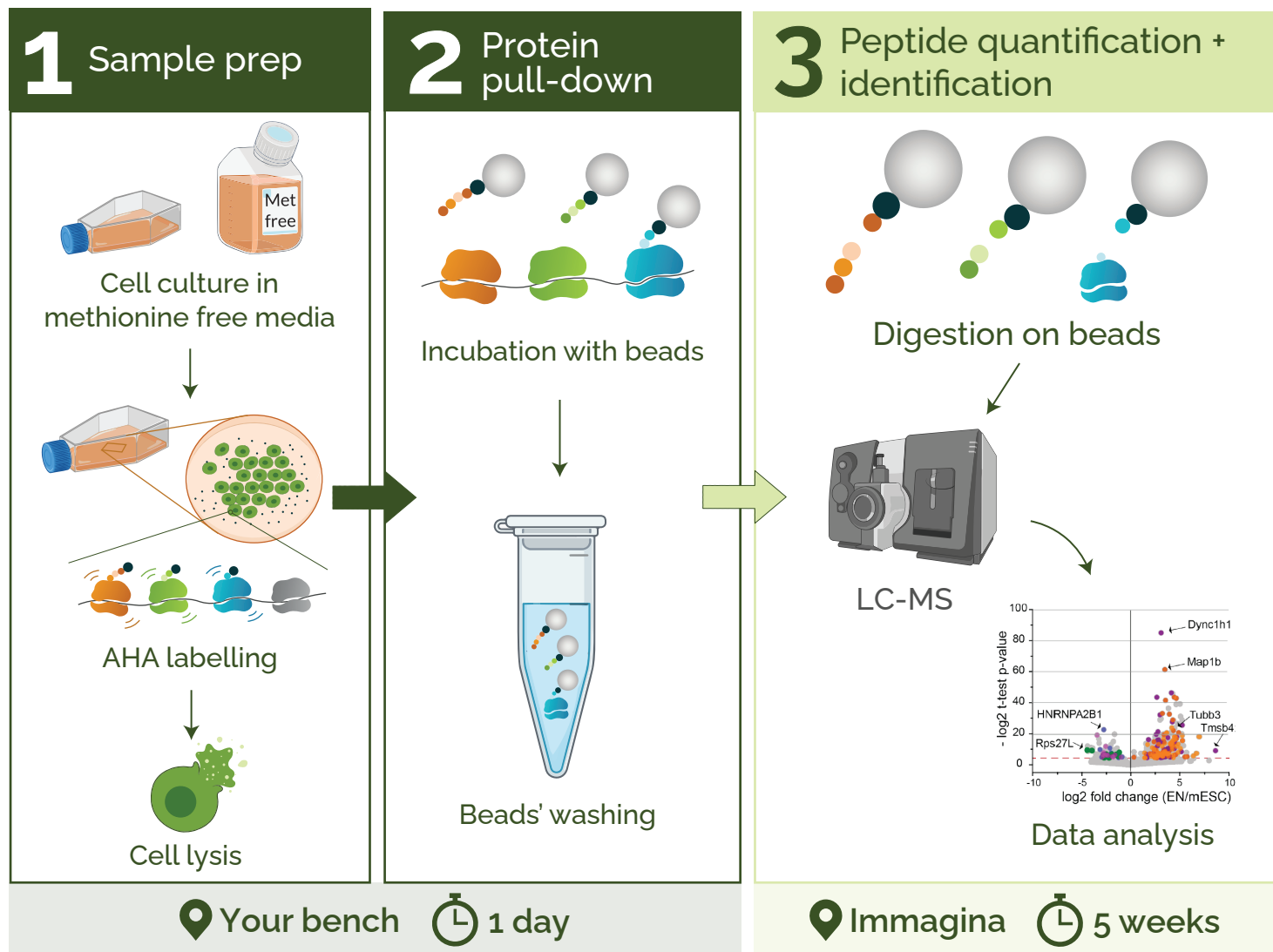


AHARIBO Protein 360

Identify and quantify *de-novo* synthesized protein

Introducing AHARIBO Protein 360: for fast **isolation and analysis** of ***de novo*** synthesized proteins. With AHARIBO Protein 360, you label **nascent proteins** with azidohomoalanine (AHA) during active translation and **isolate them** using magnetic beads. Then, simply send the preparation to us, and we will conduct **LC-MS identification**. In a matter of weeks, you will be provided with a **comprehensive report** with all *de novo* synthesized proteins detected in your sample.



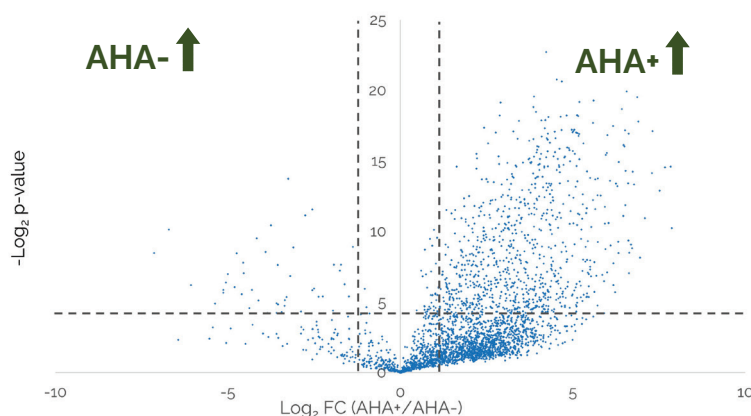
Specifications

Species	Eukaryotic cell lines	Kit size	12 rxns	Catalogue number
Minimum input	100k cells	Outputs	Data reports to publish	#AHA360PS



Proof-of-concept studies

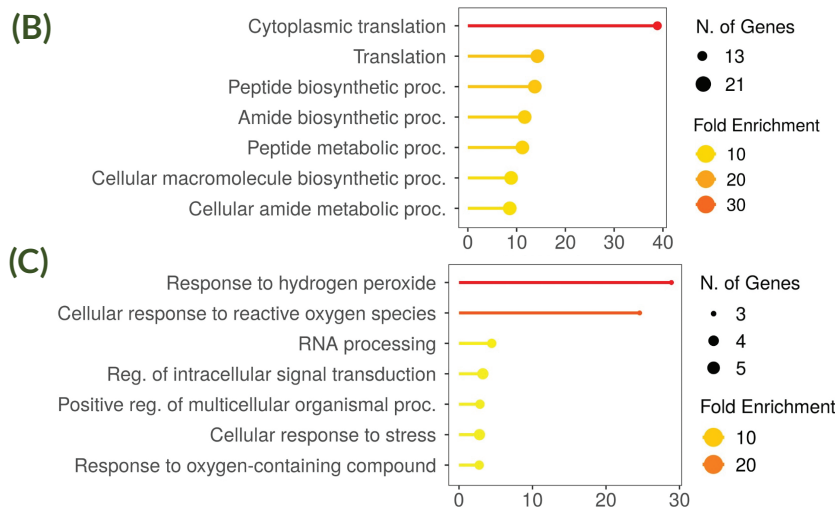
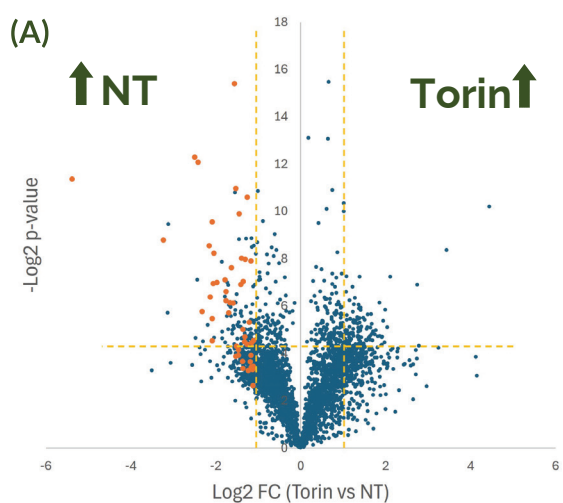
AHARIBO protein 360 successfully isolates AHA-labelled peptides



Comparison of pulldown efficiency between K562 cells treated with AHA (AHA+) and untreated (AHA-). In the graph generated by LC-MS, we observe a significant enrichment of signal in AHA+ samples, demonstrating that AHARIBO-mediated pulldown is highly specific for AHA-labelled peptides.

Case study: Torin 2 treatment

Torin 2 is a chemical inhibitor of mTOR, a transcription factor responsible for the regulation of *de novo* protein synthesis. We used AHARIBO Protein to test whether we could detect Torin2-induced inhibition of translation. K562 cells were treated with Torin 2 for 1 hour during AHA incubation, whereas controls were incubated only with AHA. After peptide pull-down, the samples were analysed by LC-MS and data analysis was conducted. The volcano plot (A) represents the fold change in Torin treated (Torin) vs. non-treated (NT) cells. Orange dots represent proteins involved in translation, whereas blue dots represent all other proteins. Translation-associated proteins (B) and proteins responsive to reactive oxygen species (C) were significantly enriched in comparison with their expected frequency.



Highlights



Low input



Highly specific for
de-novo synthesized
proteins



Full streamlined
workflow
From samples to data



Fast workflow
1 day from cells
to peptides



Imagine what you can discover. Immagina.