# Article information:

A versatile new tool derived from a bacterial deubiquitylase to detect and purify ubiquitylated substrates and their interacting proteins | PLOS Biology  
<https://journals.plos.org/plosbiology/article?id=10.1371/journal.pbio.3001501>

# Article summary:

1. Researchers have developed a novel tool for ubiquitin detection and purification based on OtUBD, a high-affinity ubiquitin-binding domain (UBD) derived from an Orientia tsutsugamushi deubiquitylase (DUB).

2. This tool can be used to purify both monoubiquitylated and polyubiquitylated substrates from yeast and human tissue culture samples.

3. The tool was used to profile the ubiquitylome and ubiquitin-associated proteome of the budding yeast Saccharomyces cerevisiae, identifying potential substrates for the E3 ligases Bre1 and Pib1.

# Article rating:

Appears well balanced: The article presents the information in a reliable and balanced way, without biases and prejudices. The claims made in the article are well supported and, where applicable, all sides of the argument are given opportunity to present their point of view. The article appears trustworthy and reliable.

# Article analysis:

The article is generally reliable and trustworthy, as it is a peer-reviewed open access publication in PLOS Biology. The authors provide detailed information about their methods, results, and discussion, which allows readers to evaluate the validity of their claims. Furthermore, they provide supporting information such as raw images for all gels and blots, as well as mass spectrometry proteomics data deposited to the ProteomeXchange Consortium via the PRIDE partner repository.

The article does not appear to contain any biases or one-sided reporting; rather, it presents both sides of the argument equally by discussing existing methods alongside their newly developed tool. Additionally, all claims are supported with evidence from experiments conducted by the authors or other sources cited in the references section. There are no missing points of consideration or unexplored counterarguments that could affect readers’ understanding of the topic.

The article does not contain any promotional content or partiality towards any particular method or product; rather, it provides an objective comparison between existing methods and their newly developed tool. Possible risks associated with using this new tool are noted in the discussion section of the article.

In conclusion, this article is reliable and trustworthy due to its peer-reviewed open access publication in PLOS Biology, detailed information about methods used, evidence provided for claims made, lack of bias or one-sided reporting, absence of promotional content or partiality towards any particular method or product, noting possible risks associated with using this new tool, and presenting both sides of the argument equally.

# Topics for further research:

* Proteomics data analysis
* Mass spectrometry proteomics
* ProteomeXchange Consortium
* PRIDE partner repository
* Protein quantification methods
* Protein quantification tools

# Report location:

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