# Article information:

Adaptor protein complex interaction map in Arabidopsis identifies P34 as a common stability regulator | Nature Plants  
<https://www.nature.com/articles/s41477-022-01328-2>

# Article summary:

1. The transport of integral membrane proteins from one compartment to another within the endomembrane system is essential for all living eukaryotic cells and is mediated by adaptor protein (AP) complexes.

2. Five AP complexes have been identified in higher eukaryotes, and some functions of AP-1 to AP-4 have been characterized in the model plant Arabidopsis thaliana.

3. Using AP–MS and proximity labelling (PL) coupled to MS (PL–MS), a comprehensive interactome of the six AP complexes in Arabidopsis was generated, revealing two interconnected networks and identifying the adaptin binding-like protein P34 as a common stability regulator.

# 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:

This article provides an overview of the transport of integral membrane proteins from one compartment to another within the endomembrane system, which is essential for all living eukaryotic cells and is mediated by adaptor protein (AP) complexes. The article discusses five AP complexes that have been identified in higher eukaryotes, as well as some functions of AP-1 to AP-4 that have been characterized in the model plant Arabidopsis thaliana. The authors then describe their use of AP–MS and PL–MS to generate a comprehensive interactome of the six AP complexes in Arabidopsis, revealing two interconnected networks and identifying the adaptin binding-like protein P34 as a common stability regulator.

The article appears to be reliable overall, with its claims supported by evidence from experiments conducted by the authors themselves or other researchers referenced throughout the text. The authors provide detailed descriptions of their methods used for generating their interactome data, which adds credibility to their findings. Furthermore, they discuss potential limitations associated with their work such as incomplete coverage due to technical difficulties or lack of available antibodies for certain proteins. This indicates that they are aware of potential biases or errors that could arise from their research and are taking steps to address them.

The only potential issue with this article is that it does not present any counterarguments or alternative perspectives on its findings; however, this may be due to space constraints rather than bias or partiality on behalf of the authors. All in all, this article appears trustworthy and reliable overall, providing an informative overview on adaptor protein complex interaction maps in Arabidopsis thaliana while also highlighting potential areas for further research.

# Topics for further research:

* Adaptor protein complex structure
* Adaptor protein complex function
* Adaptor protein complex interactome
* Adaptor protein complex regulation
* Arabidopsis thaliana adaptor protein complexes
* Adaptin binding-like protein P34

# Report location:

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