

- [ScienceWatch Home](#)
- [Inside This Month...](#)
- [Interviews](#)

- Featured Interviews
- Author Commentaries
- Institutional Interviews
- Journal Interviews
- Podcasts

Analyses

- Featured Analyses
- What's Hot In...
- Special Topics

Data & Rankings

- Sci-Bytes
- Fast Breaking Papers
- New Hot Papers
- Emerging Research Fronts
- Fast Moving Fronts
- Corporate Research Fronts
- Research Front Maps
- Current Classics
- Top Topics
- Rising Stars
- New Entrants
- Country Profiles

About Science Watch

- Methodology
- Archives
- Contact Us
- RSS Feeds

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TRACKING TRENDS & PERFORMANCE IN BASIC RESEARCH

[Interviews](#)[Analyses](#)[Data & Rankings](#)

2009 : November 2009 - Fast Moving Fronts : Joshua Heazlewood on the Arabidopsis Subcellular Database

FAST MOVING FRONTS - 2009

November 2009



Joshua Heazlewood talks with *ScienceWatch.com* and answers a few questions about this month's Fast Moving Front in the field of Plant & Animal Science.



Article: SUBA: The *Arabidopsis* subcellular database

Authors: Heazlewood, JL; Verboom, RE; Tonti-Filippini, J; Small, I; Millar, AH

Journal: NUCL ACID RES, 35: D213-D218 Sp. Iss. SI JAN 2007
Univ Western Australia, ARC Ctr Excellence Plant Energy Biol, 35
Stirling Highway, CMS Bldg, M316, Crawley, WA 6009, Australia.
Univ Western Australia, ARC Ctr Excellence Plant Energy Biol, Crawley,
WA 6009, Australia.

SW: Why do you think your paper is highly cited?

The *Arabidopsis thaliana* genome was sequenced nearly 10 years ago and, in the time since, a significant worldwide investment has been made to determine the function of the ~30,000 proteins encoded by this model plant.

Knowing the subcellular location of a protein provides a researcher with clues that assist in the discovery of function, interaction partners, and biochemical pathways for a protein of interest. SUBA has thus served as a starting point for many researchers seeking to discover biological mechanisms from within a collection of unknown proteins.

SW: Does it describe a new discovery, methodology, or synthesis of knowledge?

The SUBA database brings together thousands of individual pieces of information from a collection of both experimental and predicted subcellular protein localizations in *Arabidopsis thaliana*. The database provides a web-based, dynamic query construction tool that allows researchers to query subcellular information in a powerful way.

SW: Would you summarize the significance of your paper in layman's terms?

Plants (and animals) are built from billions of individual cells and each one of these cells has its own internal structure complete with organelles that are responsible for doing specific jobs at a subcellular level. For example, within the cells of a plant's leaves are plastids, organelles that act as tiny solar cells, converting solar energy into chemical energy for the cell (and the entire plant) to survive.

Being able to reverse engineer and describe how these tiny biological machines work

"...we plan to expand SUBA, which currently only houses data from the model dicot *Arabidopsis*, to the model monocot, rice."

is of great scientific interest and sometimes leads to useful technological applications. Within a cell, proteins are assembled together to build more complex biological machines (or may function entirely on their own).

SUBA provides information about where proteins are located within a single cell and therefore gives researchers important information about which proteins may be working together to perform specific biological roles.

SW: How did you become involved in this research and were any particular problems encountered along the way?

Our initial research involved using mass spectrometry to discover proteins found within plant mitochondria. While describing the proteome of this organelle, it was important to assess potential contamination from other components within the cell.

We subsequently commenced curation of our findings and that of others to build an Excel spreadsheet that later evolved into SUBA. In the process, we added fluorescent protein localization data, subcellular prediction data, and subcellular annotation information.

SW: Where do you see your research leading in the future?

The SUBA database is an extremely useful resource for the community and is continually updated as new research is undertaken and published. There is currently a considerable effort by the *Arabidopsis* community to produce a protein-protein interaction network and it is likely that the information in SUBA will provide useful validation as interacting proteins would presumably localize to the same subcellular location.

Finally, we plan to expand SUBA, which currently only houses data from the model dicot *Arabidopsis*, to the model monocot, rice.

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KEYWORDS: MITOCHONDRIAL PROTEOME; THALIANA CHLOROPLASTS; DRAFT SEQUENCE; SWISS-PROT; GENOME; PREDICTION; LOCATION; ELECTROPHORESIS; CLASSIFICATION; LOCALIZATION.

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 PDF

[back to top](#) 

2009 : [November 2009 - Fast Moving Fronts](#) : Joshua Heazlewood on the Arabidopsis Subcellular Database