***One or two sentences providing a basic introduction to the field, comprehensible to a scientist in any discipline***

Photosynthesis is the primary function of leaves, and the ability of plants to perform this essential function is determined by their environment.

***Two to three sentences of more detailed background, comprehensible to scientists in related disciplines***

Several distinct biochemical processes are involved in photosynthesis, each facilitated by an associated set of leaf proteins with characteristic environmental optima. The abundance of these associated proteins reflects the capacity of the leaf to perform each process, so leaf protein abundances reveal important information about how plants photosynthesise under natural conditions.

***One sentence clearly stating the general problem being addressed by this particular study.***

Until now it has been has been impracticable to study the full set of individual proteins in leaves across many species and sites, and work on functional allocation in photosynthesis has progressed mostly through the use of proxies for protein amounts.

***One sentence summarising the main result (with the words “here we show” or their equivalent).***

Here we use quantitative protein extraction and mass spectrometry to quantify >1900 leaf proteins across 32 species of wild Eucalyptus, spanning continental-scale gradients of temperature and rainfall and in relation to key leaf traits.

***Two or three sentences explaining what the main result reveals in direct comparison to what was thought to be the case previously, or how the main result adds to previous knowledge.***

Two thirds (X%, SD X%) of eucalypt leaf proteins were associated with photosynthesis; the carbon fixing enzyme Rubisco was the most abundant single protein, accounting for 20% (SD X%) of leaf protein. Proteins associated with photosynthetic light capture are also highly abundant, representing X% (SD X%) of leaf protein.

The fraction of total protein in light capturing photosystems varied 2.5-fold, and declined by X% with an X% increase in incident radiation (x-y MJ/m2/year).

The fraction of protein in the Calvin-Benson cycle for photosynthetic carbon assimilation varied little (1.3-fold) and increased only X% in response to incident radiation. The amount of carbon-fixing protein per leaf area increased towards lower rainfall as expected, but this occurred via increasing leaf mass and leaf protein per area rather than by shifting proportions among different proteins.

Proportional abundance of Calvin-Benson cycle proteins involved in photosynthetic carbon assimilation was varied little (1.3-fold), and increased only X% in response to incident radiation. Unexpectedly, abundance of these proteins exhibited only minor changes in response to incident radiation (X% increase) proportionally, and no significant relationship with irradiance on a per area basis.

***One or two sentences to put the results into a more general context.***

Quantitative plant proteomics can answer many questions about adaptation of leaves and the photosynthetic apparatus in to environmental conditions.

The aaassociated data will be of interest to a broad scientific audience, including ecologists, plant physiologists, and terrestrial biosphere modellers.

To this end we have released our eucalypt data into the public domain.

***Two or three sentences to provide a broader perspective, readily comprehensible to a scientist in any discipline***

We believe this study is harbinger of a new wave of landscape proteomics, that will be able to assess wide-area environmental patterns of proteins with specific functions, and to express vegetation properties in kg of those proteins per km2.