

NEW DATABASE FOR IDENTIFYING FUNCTIONS OF PLANT GENES

A team led by Tetsuya Sakurai from RIKEN Research developed a new database that will aid scientists in identifying the unknown functions of plant genes. This was done through analyzing protein structures encoded by the unknown genes.



Using six plants representative of plant species, *Arabidopsis thaliana*, *Glycine max* (soybean), *Populus trichocarpa* (poplar), *Oryza sativa* (rice), *Physcomitrella patens* (moss) and *Cyanidioschycon merolae* (algae), the researchers conducted a computational modeling to predict the physicochemical and structure properties of their genome's proteins. The features of the three dimensional structure specific to protein with its function were analyzed, and were subject to further analysis which led to the identification of the regions in the proteins that were functional.

An estimated total of 52,000 functional regions of the proteins was identified from the six plants. This result becomes the basis for their new database Plant Protein Annotation Suite or Plant-PrAs.

Read the full details of the study at [RIKEN website](#).