

Metabolomics



Nowadays, gene discovery has been made very efficient with the combination of deep sequencing and the exploitation of natural variation. Just in *Arabidopsis*, hundreds of genetic loci have been identified as influencing a wide variety of processes, and we aim to go from gene-of-interest to characterized protein product using approaches to “take a picture” of the comprehensive metabolome of the plant.

The IPB is currently operating a wide range of NMR and mass spectrometry instruments for metabolomics across all four departments, which are integrated into our Metabolomics Platform.

The experimental work is complemented by extensive Cheminformatics and Bioinformatics research to process and interpret the huge amounts of data. The IPB is operating the first European MassBank server, and hosts several online tools for metabolite identification.

Contact partner for all interests concerning the metabolomics platform is [Dr. Steffen Neumann](#).