

NEWS

Recent proteomic study(1) enforced the interest of LC-MS/MS quantitative proteomics in understanding heterosis. The proteome of leaves of one sunflower hybrid and its parental inbred lines was analyzed by label free LC-MS/MS and biostatistics. It could help to better determine what mechanisms are involved in heterosis of sunflower leaves and what happens at proteome level.

(1)Heterosis profile of sunflower leaves: a label free proteomics approach. Mohayeji and all.

2014 <http://www.ncbi.nlm.nih.gov/pubmed/24508334>

High-resolution nano LC-MS/MS quantitative proteomics and CORAVALID™ data processing: The efficient tool

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