

Flowchart for database customization in LOBSTAHS, a multifunction R package for screening, annotation, and putative identification of mass spectral features in large, HPLC-MS lipid datasets

This flowchart was created to accompany the very detailed instructions in the [package vignette](#).

[Return to the LOBSTAHS vignette](#) (GitHub) | [Download the latest package user manual](#) (.pdf via Bioconductor) | [LOBSTAHS on GitHub](#) | [LOBSTAHS on Bioconductor](#)

