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KIMBLE (KNIME-based Integrated MetaBoLomics Environment) is a flexible, expandable and self-documenting workflow for transforming raw time-domain NMR data into biologically meaningful information. KIMBLE is designed to address the problem of the data reproducibility in the field of NMR metabolomics. The workflow handles both 1D and 2D-JRES spectra and it provides both targeted and non-targeted analysis of metabolomics data. KIMBLE is free open-source software, it provides all necessary software libraries, and can be easily shared with others.