

Jason NMR Data Software



JASON, JEOL Analytical Network

[What's new on version 3.1](#)

Features based on feedback and experiences from NMR labs around the world

[**DOSY Transform – Easy and intuitive**](#)

Process your DOSY data easily

[**Create multiplet reports quickly, and in the format you need**](#)

New NMR processing capabilities

- Improved automatic processing of PureShift and SAPPHIRE experiments
- Backward linear Interpolation for the data acquired by cryogenic probe
- Better parameter handling for sine apodisation
- Improved 1D inverse FT
- A processing function to remove group delay points
- Spectrum width scaling (e.g. as needed for solid-state CRAMPS experiments)
- Improvements in backward linear prediction in basic mode
- A processing function to calculate sum of rows from pseudo-2D/2D data

DOSY processing

User-customisable multiplet reports

- Improvements for annotation selection and handling
- A setting for the spectrum line width for printing
- Opening processed Delta JDF files show the applied processing
- A processing function to calculate sum of rows from pseudo-2D/2D data
- “Locked” mode for NMR spectra. Clean-up of the NMR context toolbar
- “Square” cursors for homonuclear 2D in the “Lock” mode to help see COSY-like correlations
- Improved customisation for all tables. Custom columns and data could be added to tables
- Automatically fit spectra when dragged to a new page on the canvas
- Performance tuning and numerous bug fixes

[MAGRES \(plugin\): can generate synthetic 2D spectra](#)

[Improved JCAMP-DX import/export](#)

[Watermarks on NMR spectra](#)

[Open multiple files from a directory by drag&drop of the directory](#)

Three options to start optimizing your NMR data

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lab

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smileq
Spectral Management Interface
Launching Engine for Q-NMR