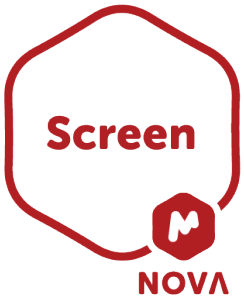
Mnova Screen

Automatic analysis tool for fragment-based drug screening by NMR



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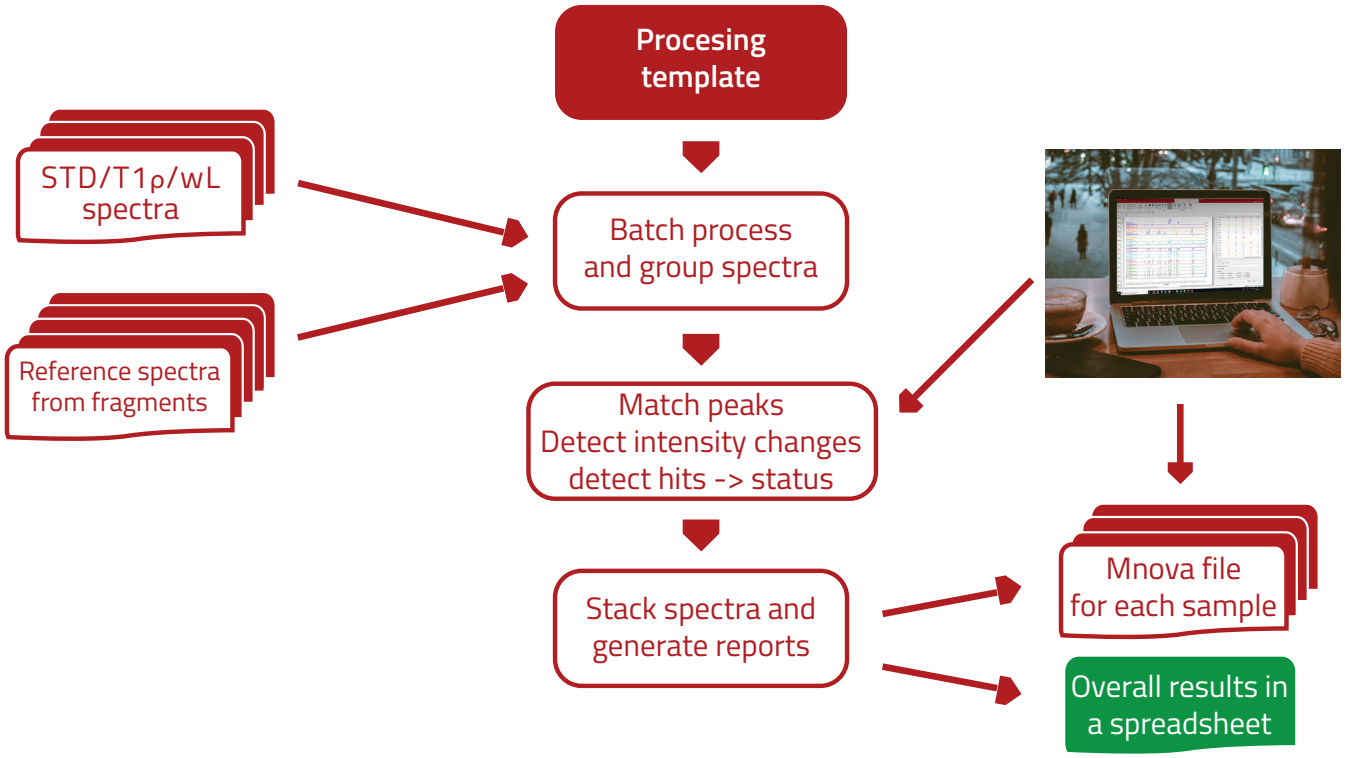
Mnova Screen: Automatic analysis tool for fragment-based drug screening by NMR

An automation software for fast and efficient hit detection in fragment-based drug discovery campaigns using ligand detected NMR data.

Highlights

- ✓ Pattern recognition algorithms map your experimental data.
- ✓ Considers the use of STD, wLOGSY, T1ρ, CMPG experiments.
- ✓ Uses deconvolution to effectively pick peak, even weak signals.
- ✓ Results viewer to quickly inspect your hits.
- ✓ Exports metrics of your analysis into your favorite statistical package.

Mnova Screen: from data to hits



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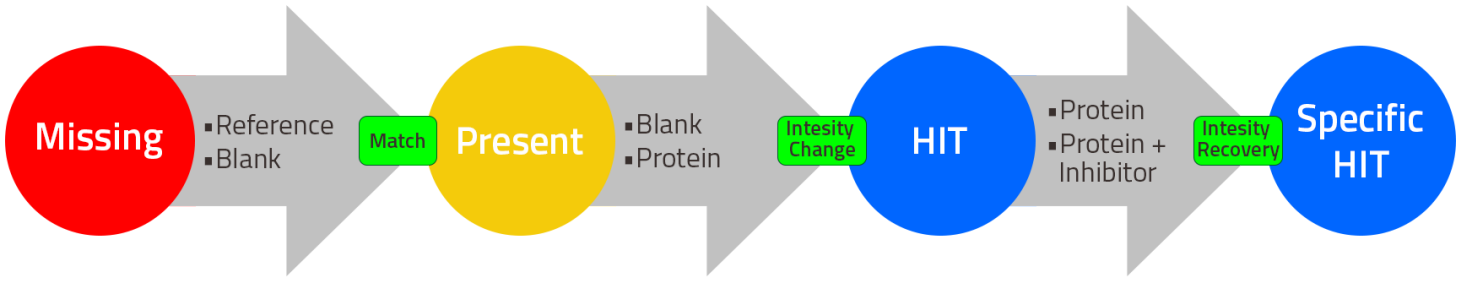
Data Types

Mnova Screen can handle all data from the following screening experiments:

- ^{1}H or ^{19}F
- Single compounds or mixtures
- With or without reference spectra
- Single or multiple types of spectra (STD, T1ρ, wLOGSY, CPMG)
- Use of Blank, w/ Protein, & w/ Protein+ Inhibitors
- Automatic hit specificity detection based on results of Protein + Inhibitor experiments

The spectral data can be raw or processed data from various vendors (Bruker, Varian/Agilent, JEOL, JCAMP etc.)

Workflow illustrating how Mnova Screen detects hits based on the evaluation of the different spectra



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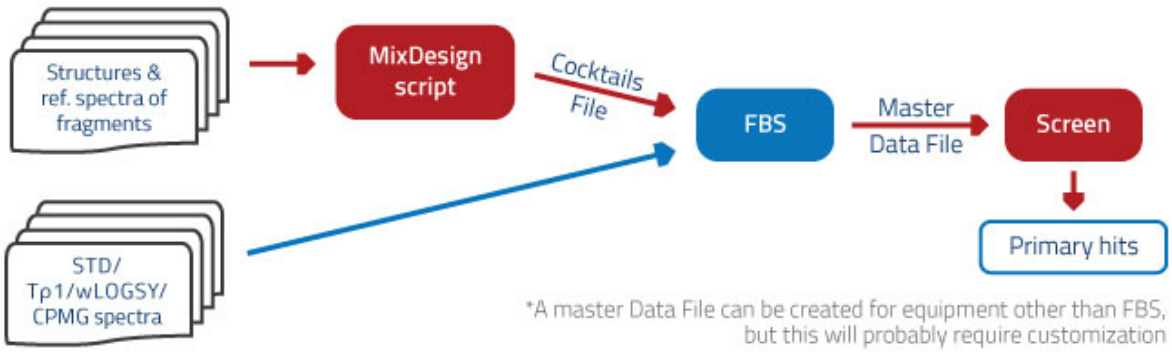
Data Organization for batch processing

Data organization is critical for batch processing. Mnova Screen needs to:

— find the mixture/screen data for each sample, and recognize their type correctly
— find the reference spectra and associate with the mixture data properly

Screen uses a Master Data File that brings together all necessary information in the right format. Mestrelab often writes customized scripts to re-organize customers' data and will be happy to assist your company in this. If you are using FBS, a Master Data File (JSON format) for Screen can now be generated automatically, making the import of raw data effortless:



REFERENCES
- ✓ location (e.g. file)
- ✓ Id
- ✓ name
- ✓ peaklist

SPECTRA
- ✓ location (e.g. file)
- ✓ subtype
- ✓ content
- ✓ type

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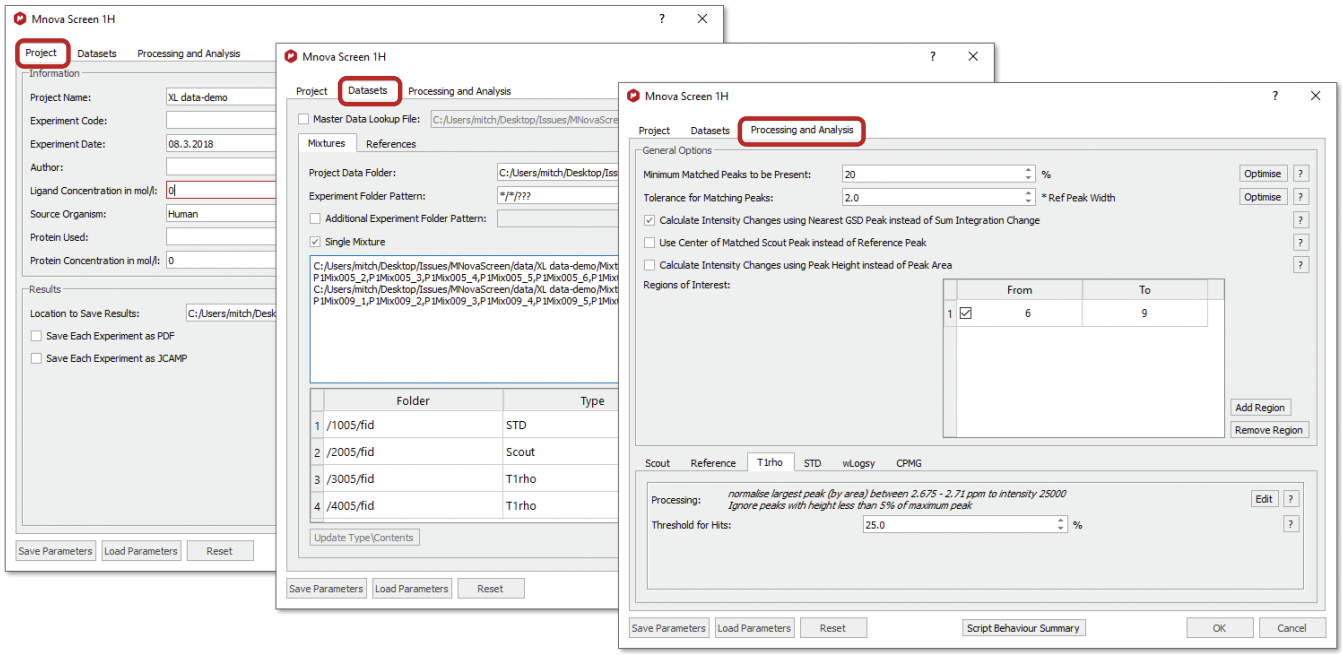
New Screen User Interface

Redesigned GUI allows the easy configuration of all input parameters required for the execution of the automation.



- **'Project':** Contains general information and the output

- **'Datasets':** Includes the input reference and screening experiment spectra with definition

- **'Processing & Analysis':** Processing configuration, hit and status definition parameters

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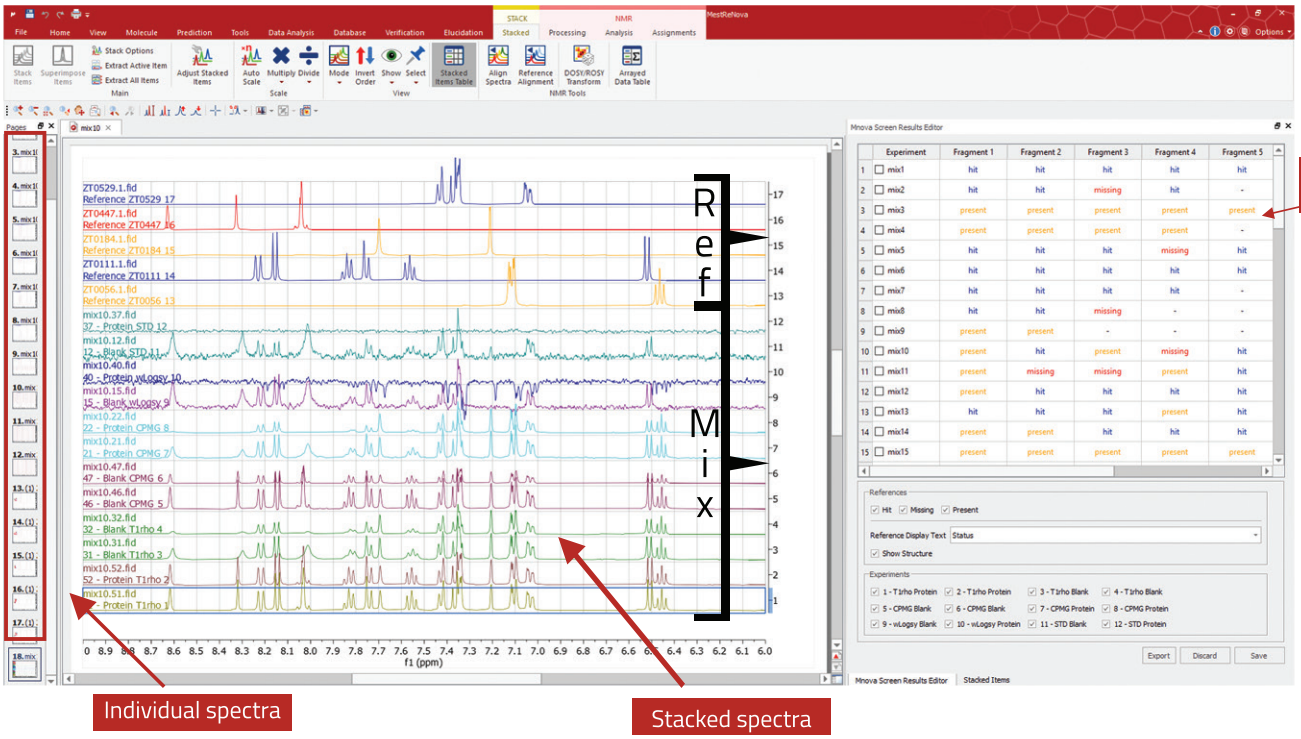
Reviewing ^{1}H Screen Results



The evaluation output can be readily reviewed using a Results Editor, with access to all spectral information in separated Mnova Files.

Data courtesy of Bruker, Faellanden: Human serum albumin, Zenobia Fragment Library

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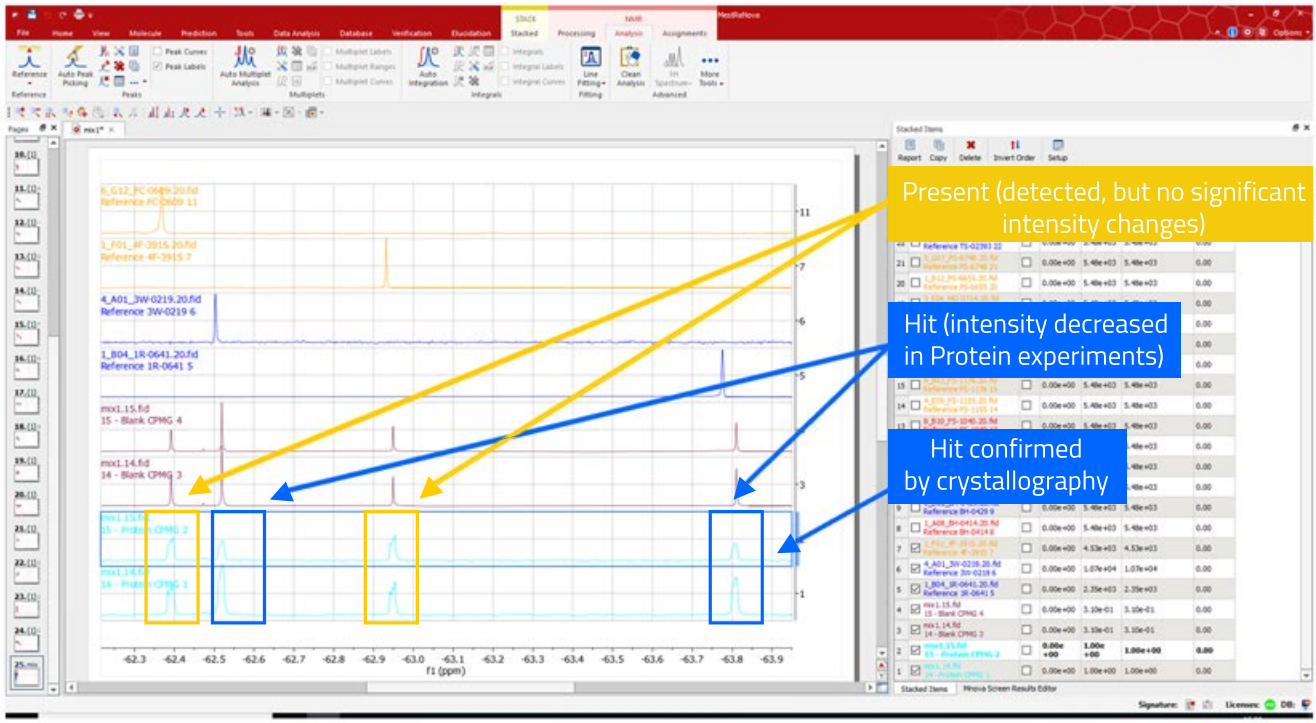
^{19}F Automatic hit detection based on intensity changes



Example of hit detection in a ^{19}F Screen using CPMG experiments:

– Fragments in blue were identified as hits, based on CPMG intensity decrease from short to long mixing time in Protein sample.

– Fragments in yellow were detected in the mixtures, but show no intensity decrease, and were assigned as 'Present'.

Data courtesy of Yuliya Dubianok Structural Genomics Consortium, Nuffield Department of Medicine, University of Oxford. NUDT5, BIONET Fragment library, measured at Bruker, Faellanden.

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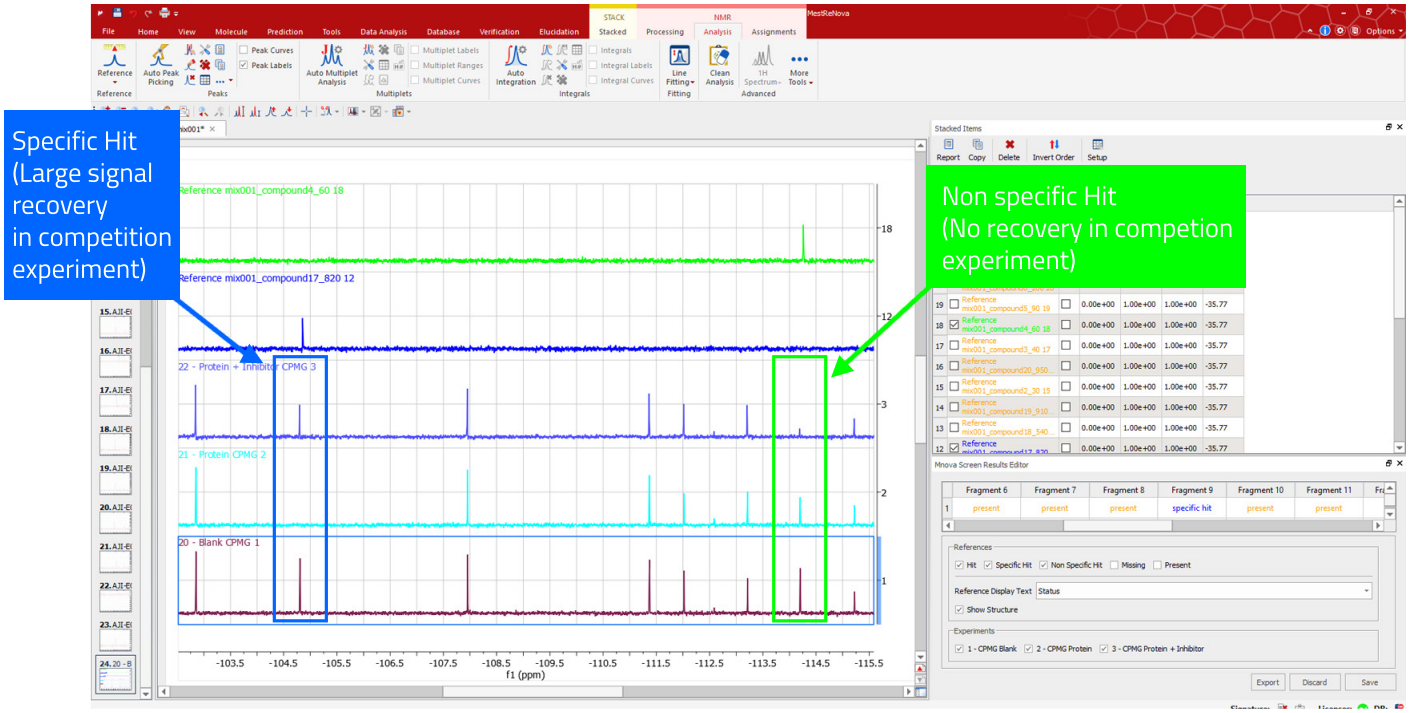
Specificity test with Screen



Example of Fragment specificy detection by Screen: based on Intensity recovery from Protein to Protein+Inhibitor Sample. The software identifies the first fragment (blue) as a specific hit, while the second (green) is non specific hit.

With Mnova Screen you can evaluate specificity with CPMG, T1rho or waterLOGSY data.

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Mnova Screen Summary - Top features & benefits

— Includes analysis using the four most common methods (WaterLOGSY, STD, T1ρ, CPMG)

✓ *Versatility in choice of experiments*

— Choice of 1H and/or 19F nuclei as a probe

✓ *Reduce risk of missing hits*

— Uses deconvolution to effectively pick peak even weak signals

✓ *Improve resolution of overlap peaks, i.e. increase accuracy*

— Access to various reporting and output format

✓ *Flexibility*

— Export metrics of your analysis into your favorite statistical package

✓ *Gives you more choice with post processing operatations*

— Ability to read Bruker FBS output (master data filer) for seamless data input exchange

✓ *Improvement of batch processing process organizing/processing customer's data*

Who should be using Mnova Screen?

Companies/institution involved in high throughput methods for the detection of lead compounds for biological targets, more specifically those involved in Fragment-Based Screening using NMR such as:

✓ Structural biology, biophysics and NMR groups in pharmaceutical companies.

✓ Target based drug discovery and NMR groups in academic and research institutions.

✓ CRO's and service providers for target based lead detection and lead optimization.

Mnova Screen streamlines the lead discovery and optimisation process and reduce the necessary time for data analysis by automating the processes allowing structural biology experts to focus on other tasks.

Mscreen Suite together with Bruker FBS improves the workflow by facilitating the acquisition and performing druggability assessments on the fly.

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