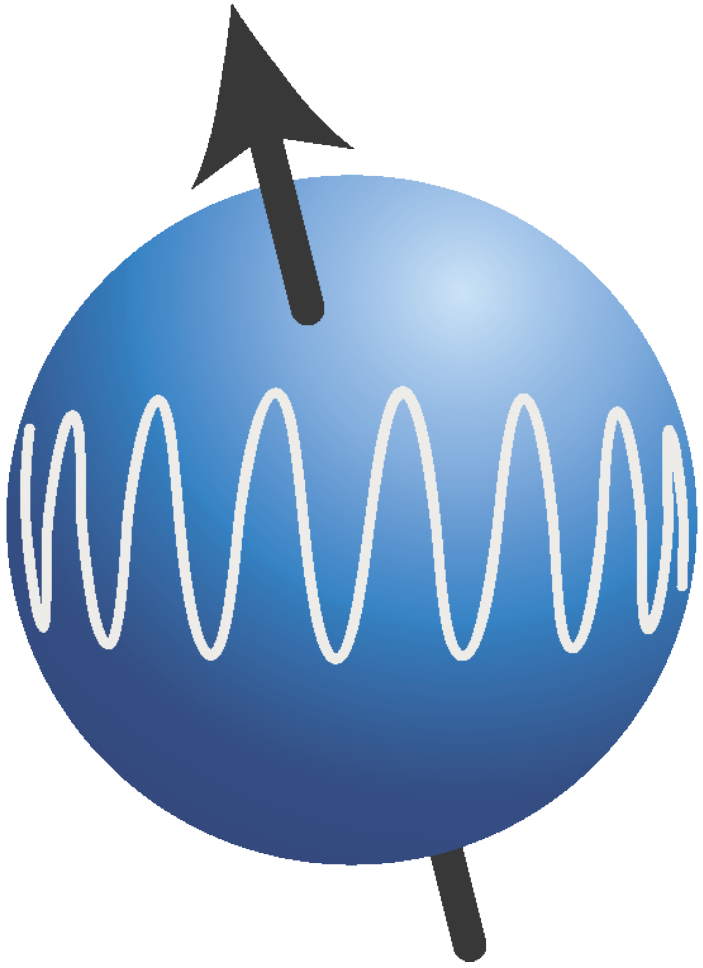


TopSpin

Data Analysis

Contents

Contents continued on next page

→ *Please click on a topic to view page*

Contents (cont.)

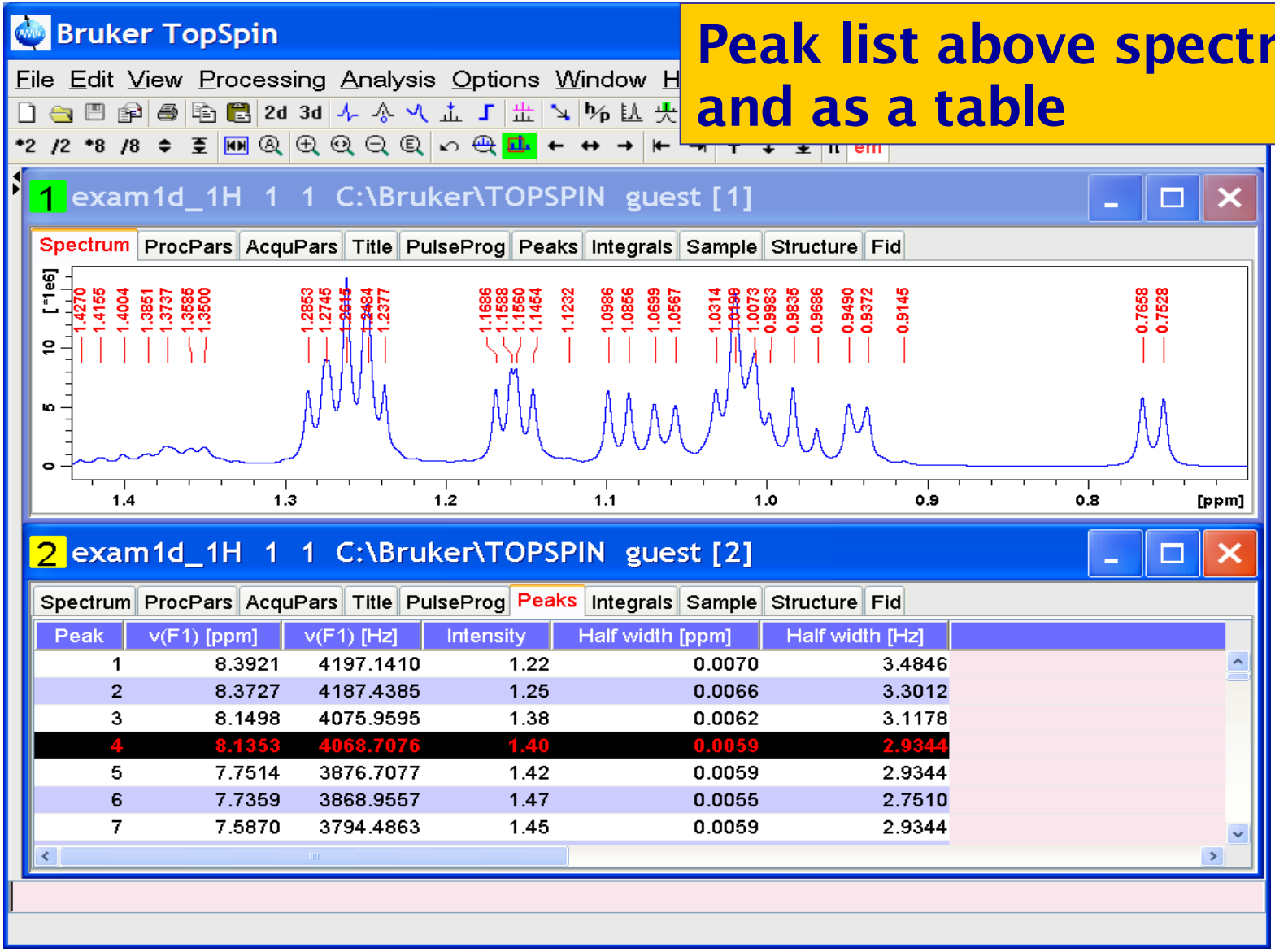
Peak Picking

Features:

- Automatic peak picking of 1D-3D spectra
- Interactive peak picking of 1D and 2D spectra
- Editable peak list
- Annotation support
- Several peak table display and sorting modes
- Peak table export in various formats
- Corrlation of peak table with cursor position in spectrum

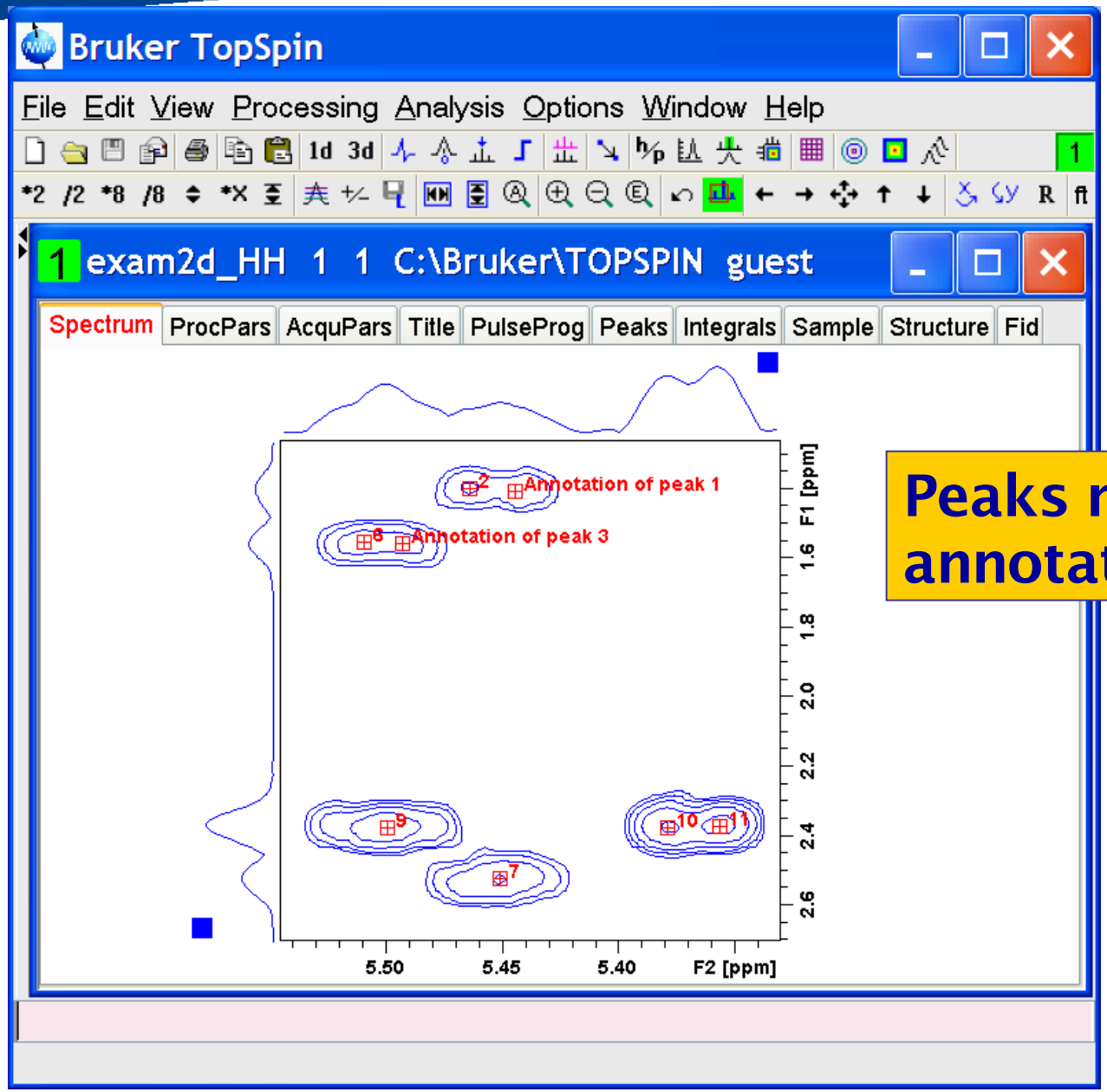
Peak Picking

Peak list above spectrum and as a table



Peak	v(F1) [ppm]	v(F1) [Hz]	Intensity	Half width [ppm]	Half width [Hz]
1	8.3921	4197.1410	1.22	0.0070	3.4846
2	8.3727	4187.4385	1.25	0.0066	3.3012
3	8.1498	4075.9595	1.38	0.0062	3.1178
4	8.1353	4068.7076	1.40	0.0059	2.9344
5	7.7514	3876.7077	1.42	0.0059	2.9344
6	7.7359	3868.9557	1.47	0.0055	2.7510
7	7.5870	3794.4863	1.45	0.0059	2.9344

Peak Picking



Peaks numbered or annotated

Integration

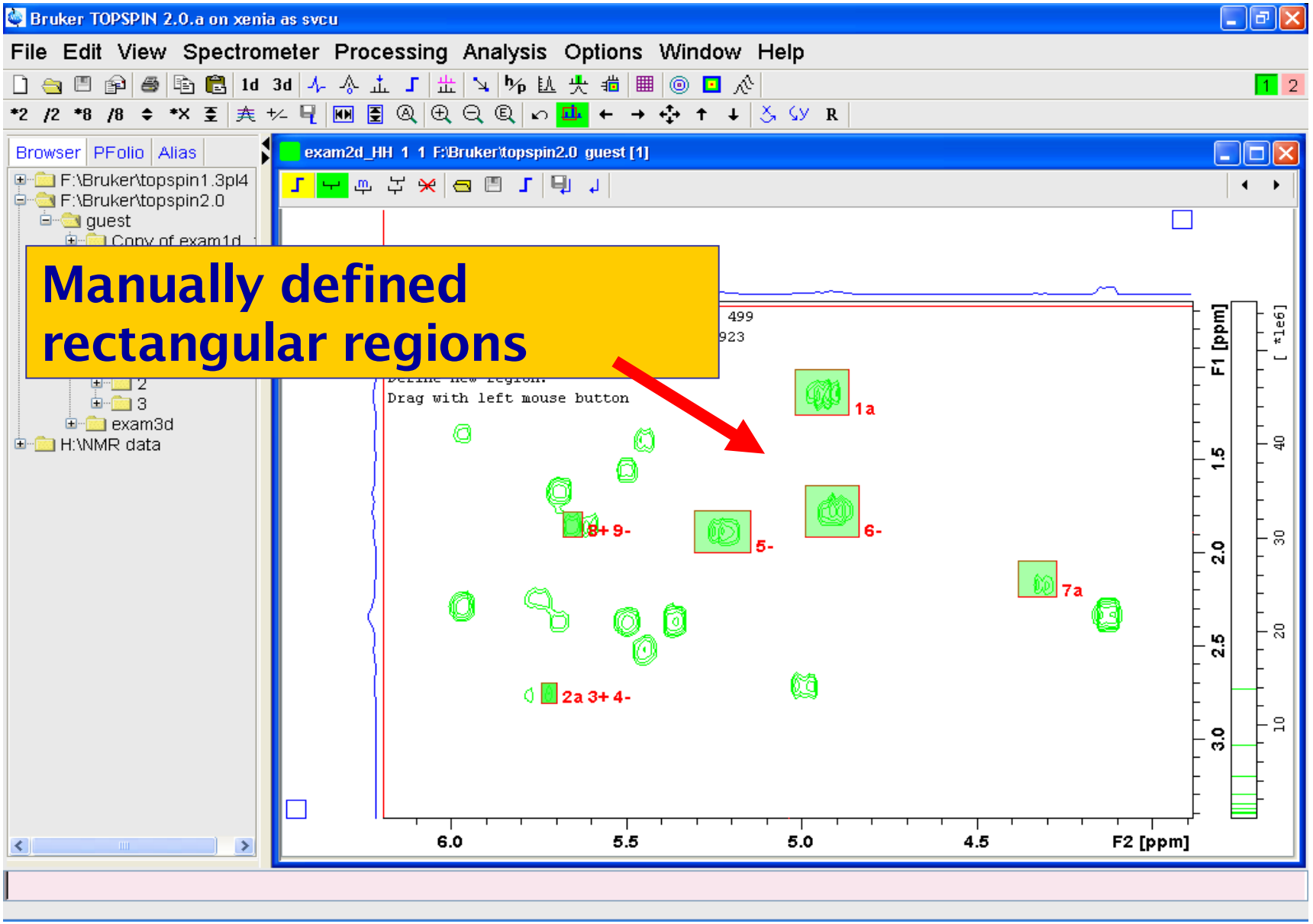
TopSpin provides automatic and interactive integration of 1D and 2D spectra

2D Integration Features:

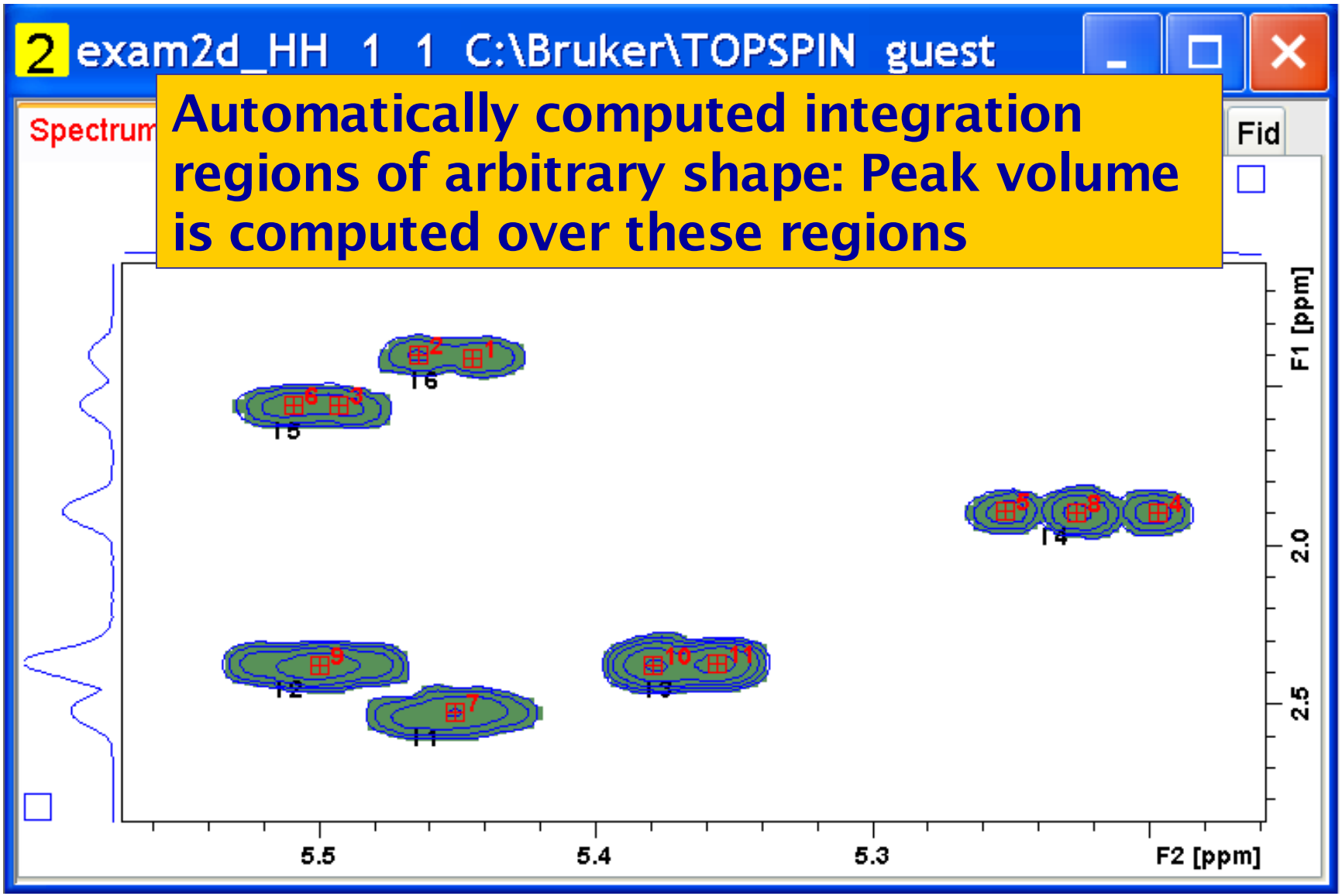
- Manual definition of integration regions:
User draws rectangles around peak / groups

- Automatic definition of integration regions:
TopSpin computes the regions of arbitrary shape, following the lowest contour level

Integration: 2D



Integration: 2D



Integration: 2D

**Integration result table,
including involved peaks:
Table can be sorted, edited, exported, …**

2 exam2d_HH 1 1 C:\Bruker\TOPSPIN guest

Spectrum | ProcPars | AcquPars | Title | PulseProg | Peaks | Integrals | Sample | Structure | Fid

Object	Integral [abs]	Integral [rel]	Type	Mode	Peaks	v(F2) [ppm]	v(F1) [ppm]	Intensity
Integral 6	245761882.62	0.2295	Automatic		2			
Integral 5	350632932.50	0.3274	Automatic		2			
Integral 4	579831496.88	0.5414	Automatic		3			
Peak 4						5.1970	1.8905	978056.63
Peak 5						5.2523	1.8873	1013835.75
Peak 8						5.2263	1.8905	1599931.13
Integral 3	1071031180.25	1.0000	Automatic		2			
Peak 10						5.3792	2.3722	2472559.00
Peak 11						5.3564	2.3689	2868560.50
Integral 2	731963384.75	0.6834	Automatic		1			
Peak 9						5.4996	2.3754	2123102.00
Integral 1	494250739.75	0.4615	Automatic		1			
Peak 7						5.4508	2.5219	1347464.63

Serial Integration

Problem Definition:

Integrating a series of 1D- oder 2D spectra (e.g. monitoring progression of variable temperature / chemical reaction)

Given:

Integral Regions, List of Spectra

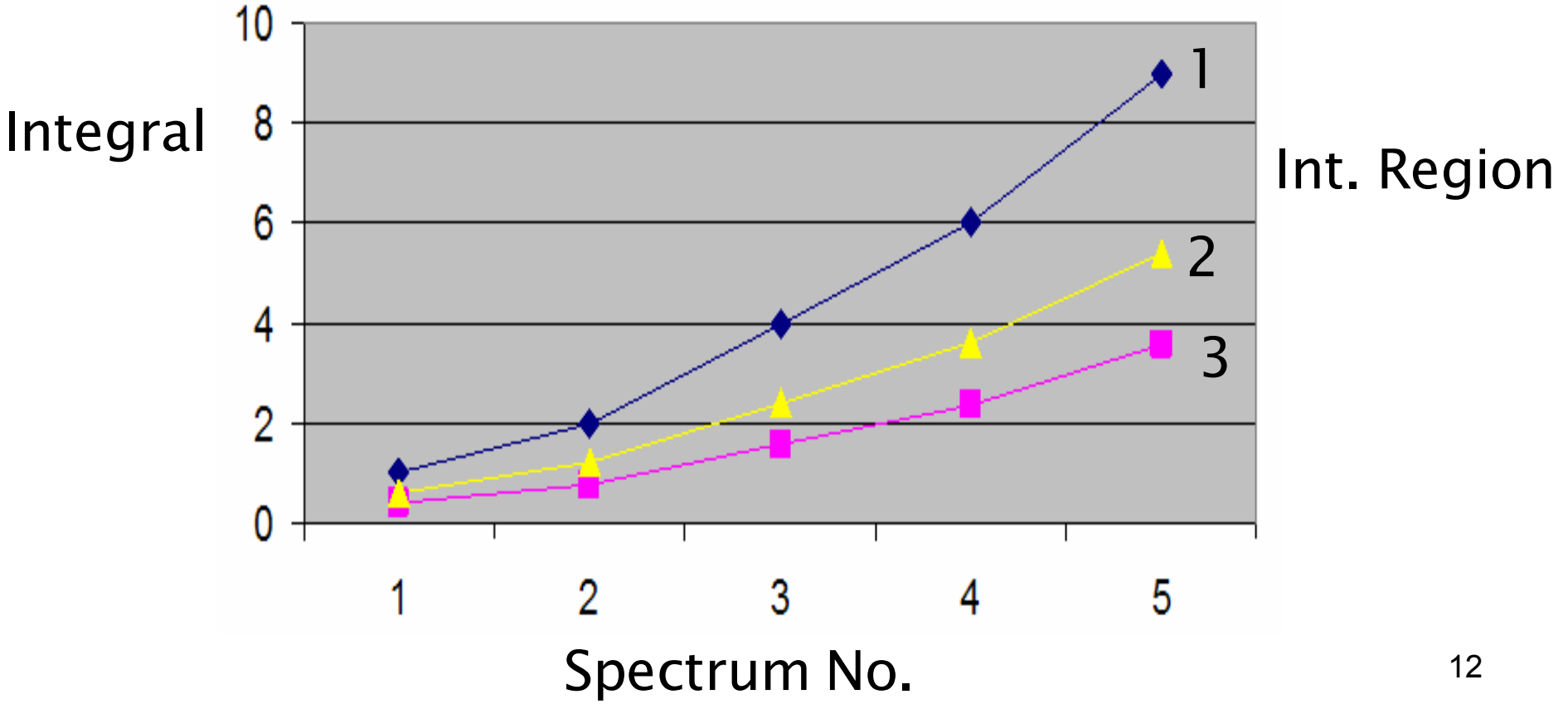
Solution:

Serial integration command intser:

- *Loops over all spectra in the specified list*
- *Integrates each spectrum according to the regions*
- *Writes the result in a CSV file (=Excel compatible)*
- *Provides several scaling options*

Serial Integration

Graphical presentation of a serial intergration run *(here: 5 spectra/3 regions)*
- Read result file into Excel or OpenOffice
- Display as diagram

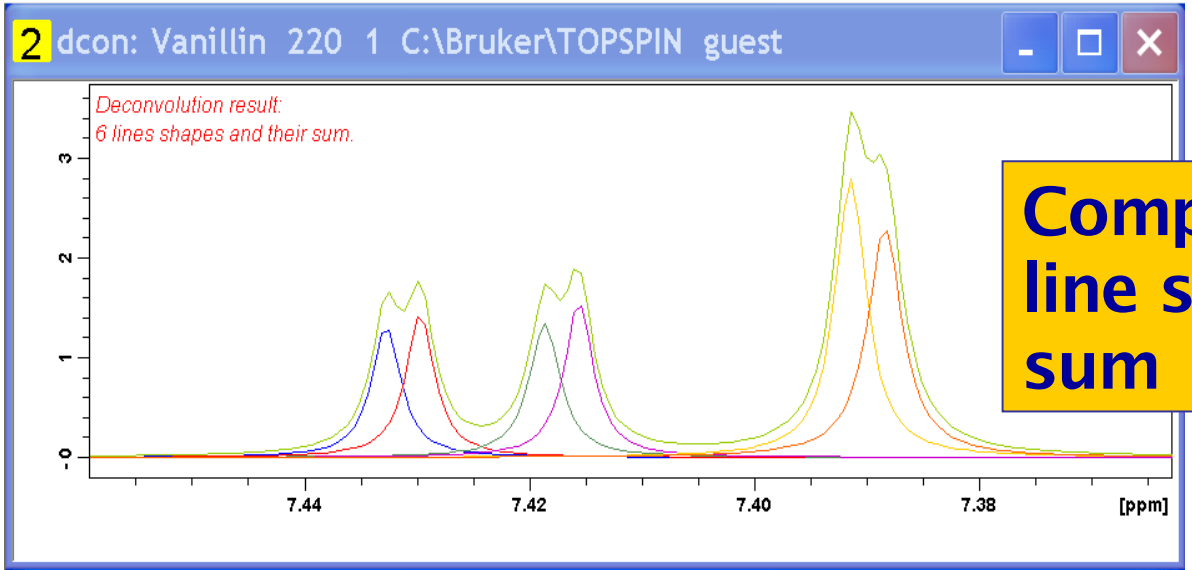


Deconvolution

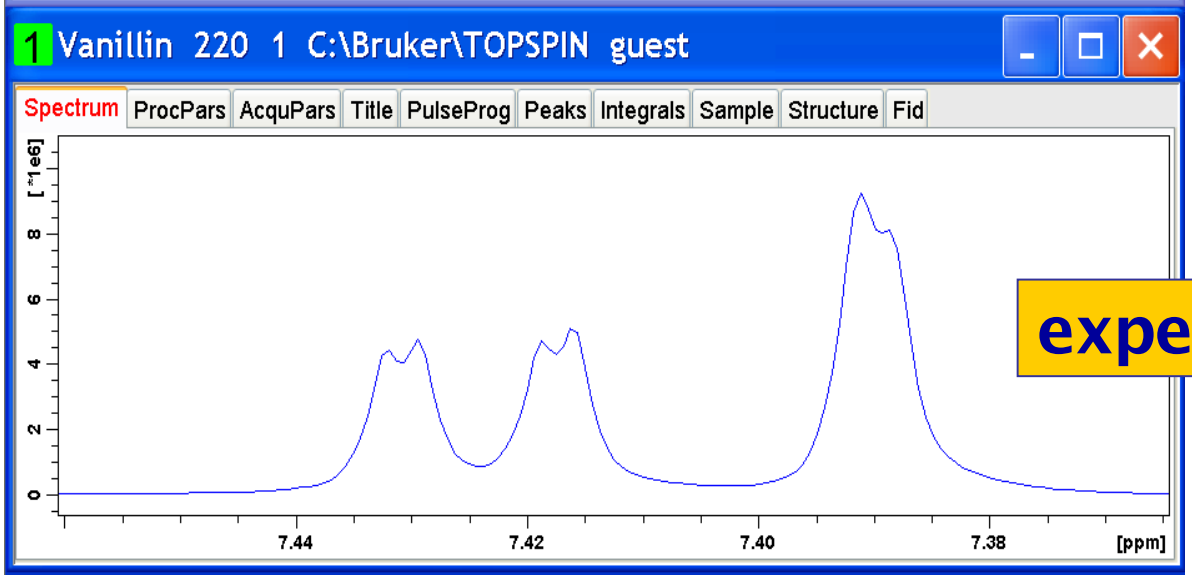
Features:

- Deconvolution of 1D and 2D line shapes
- Types: Lorentz, Gaussian, mixed shapes

Deconvolution: 1D



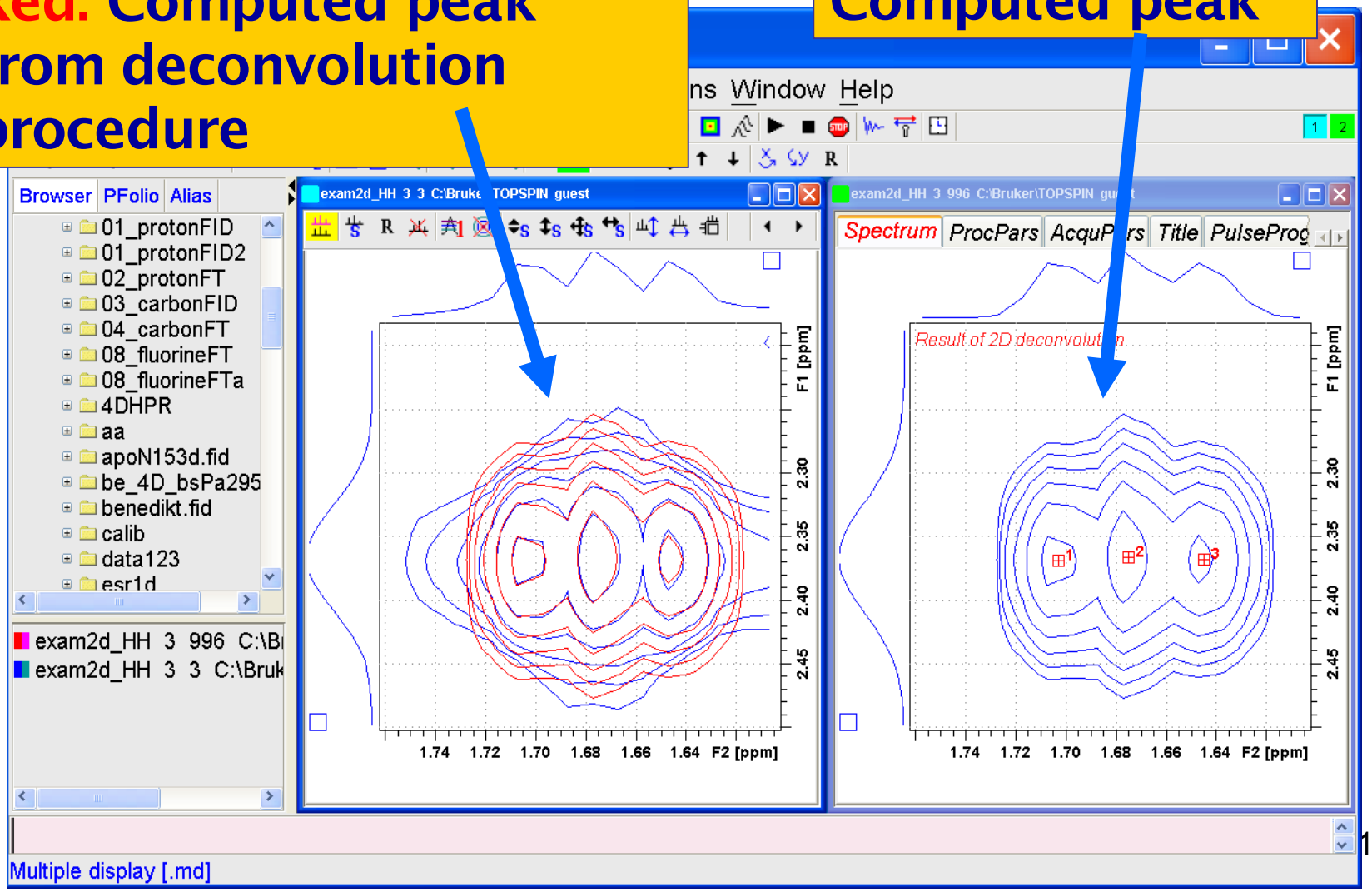
Computed Lorentzian line shapes and their sum



experimental

Deconvolution: 2D

Blue: Experimental peak
Red: Computed peak from deconvolution procedure



Deconvolution: 2D

Numeric deconvolution result

Data set: exam2d_HH 3 3 C:\Bruker\TOPSPIN guest

Fit shape type: Gaussian

Chi square: 2.31063657E15

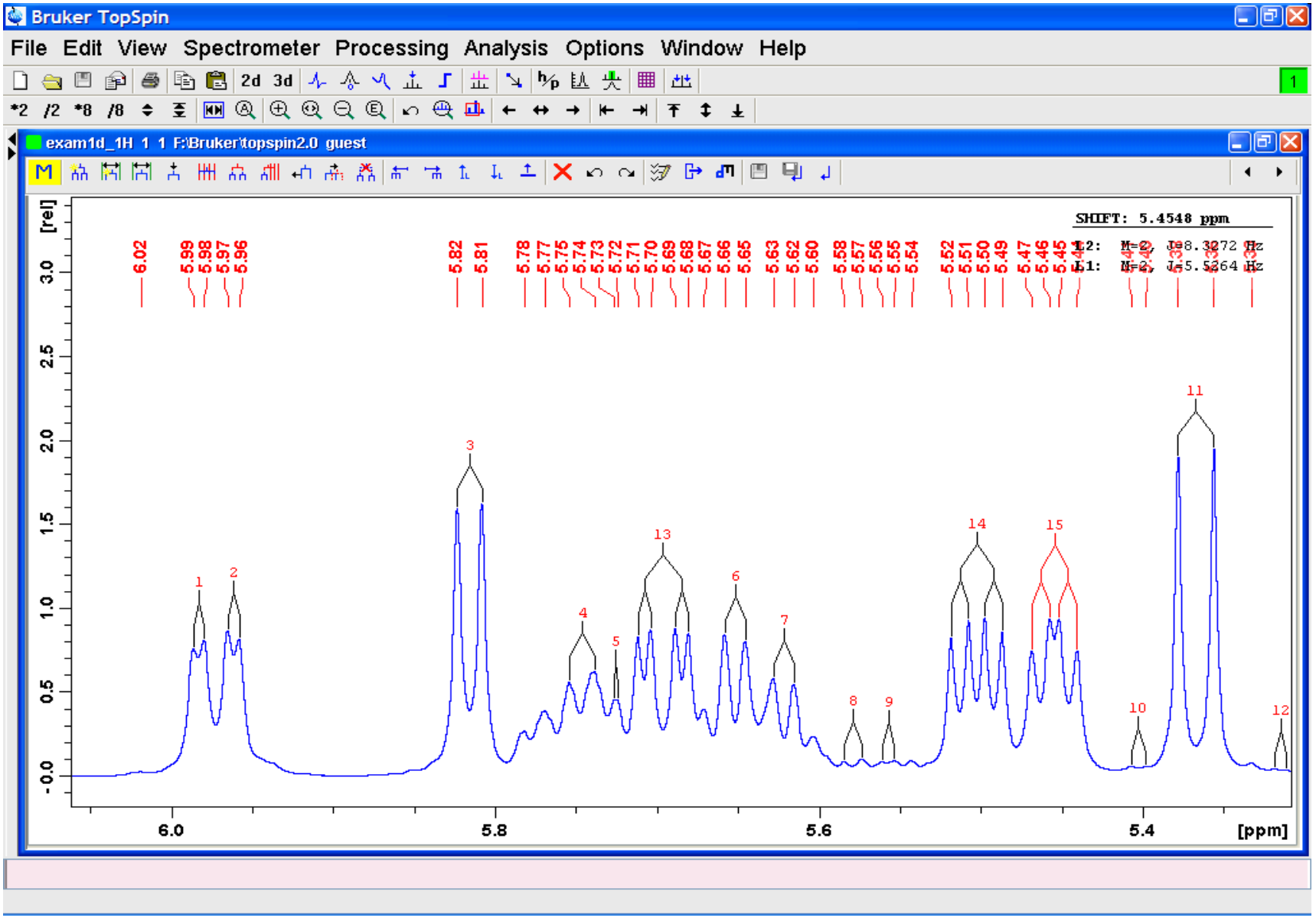
Peak	Frequency ppm		Full Width ppm		Intensity	Integral
	F1	F2	F1	F2		
1	2.368	1.703	0.091	0.024	1582982.641	861.242
2	2.365	1.675	0.106	0.020	1778635.966	924.190
3	2.367	1.645	0.090	0.028	1468825.100	942.954

Multiplet Analysis

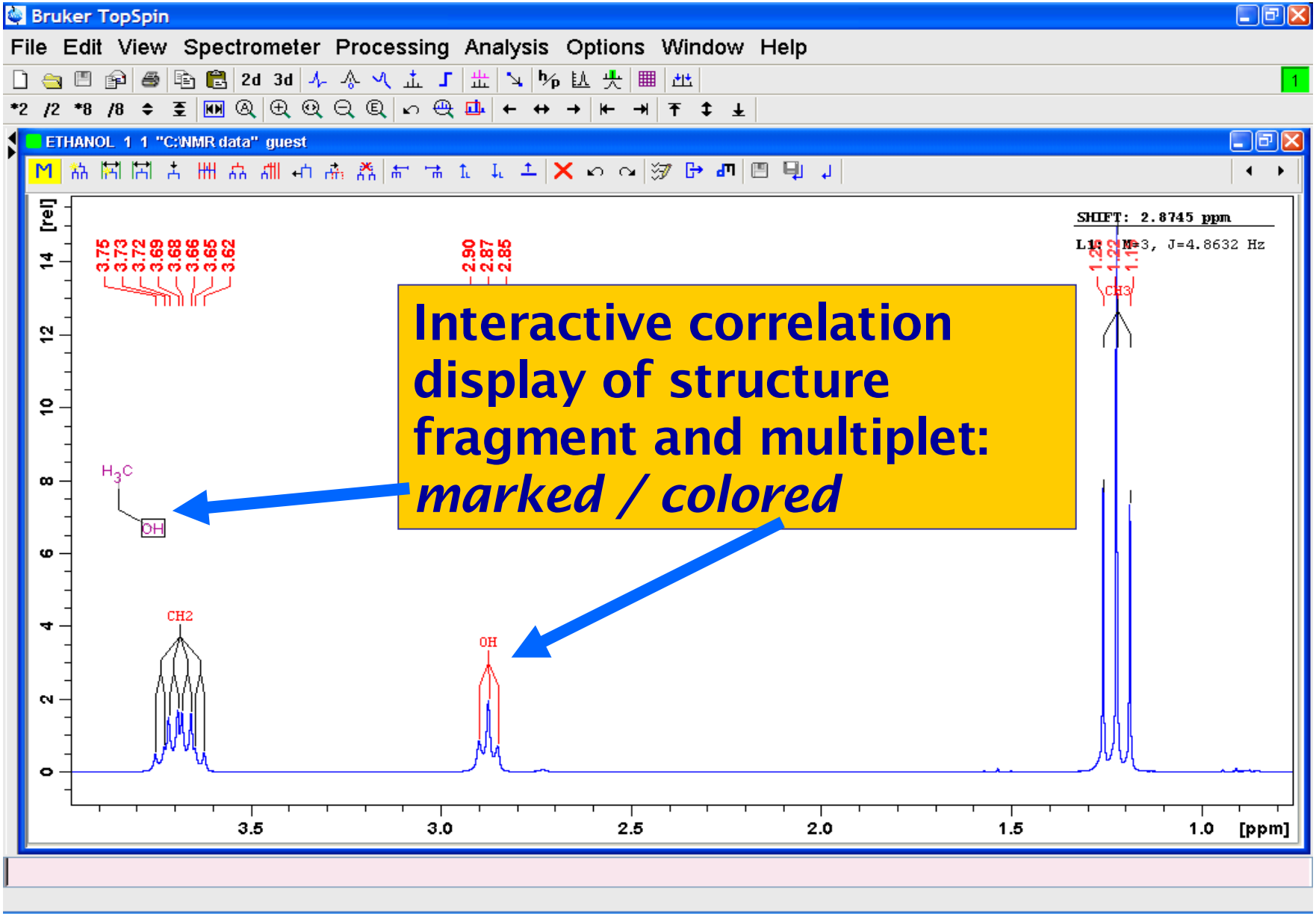
Features:

- Interactive and automatic multiplet definition
- Flexible multiplet tree manipulation
- Simultaneous structure display
- Structure ←→ multiplet correlation display
- JMR and Japanese patent report formats

Multiplet Analysis



Multiplet Analysis



1D Spectrum Simulation & Iteration

BRUKER

Features of Simulation:

- Spectrum simulation is based on the solution of the time-independent Schroedinger equation to calculate the energy levels.
- Chemical equivalence, magnetic equivalence, fragment factorizing are taken into account for Hamiltonian factorization
- Up to 10 nuclei or groups with I>= 1/2 can be treated with one fragment
- The Lorentzian lineshape is calculated by application of global or individual linewidths to the transitions of as many fragments as are defined.

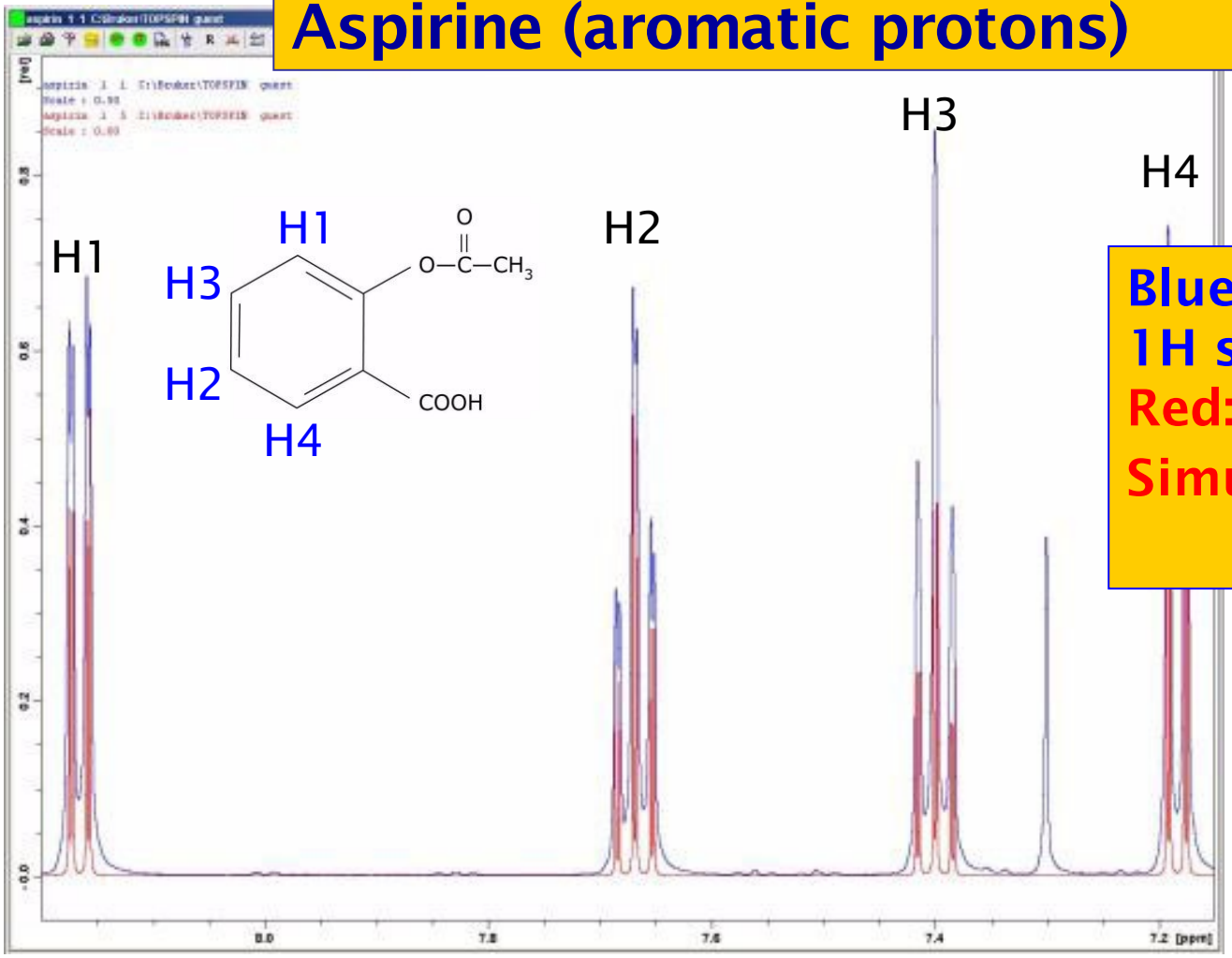
1D Spectrum Simulation & Iteration

Features of Iteration:

- Spectrum Iteration uses the method of *total-lineshape fitting*
- Adjustable parameters are resonance frequencies, scalar coupling constants and linewidths
- The program uses the current experimental spectrum as its input data.

1D Spectrum Simulation & Iteration

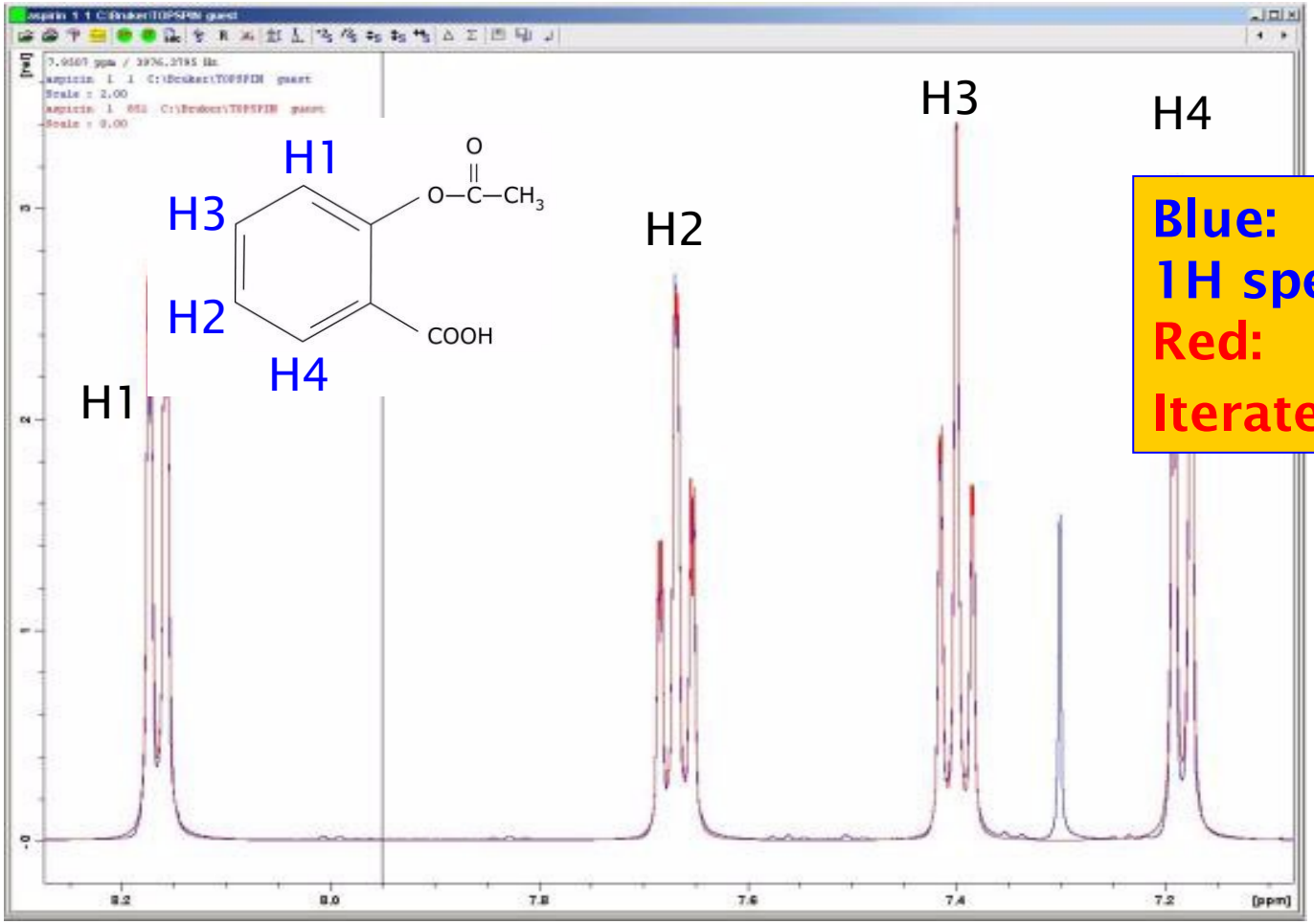
Example:
Simulation of the 1H spectrum of Aspirine (aromatic protons)



Blue:
1H spectrum
Red:
Simulated spectrum

1D Spectrum Simulation & Iteration

Example:
Iteration of the 1H spectrum of Aspirine (aromatic protons)



Blue:
1H spectrum
Red:
Iterated spectrum

1D Spectrum Simulation & Iteration

Iteration protocol

Parameters before and after iteration

Parameters to be iterated

==========

Fragment	Type	starting value	lower limit	upper limit
1	F(1)	4083.59000	4073.58640	4093.58640
1	F(2)	3835.02000	3825.02180	3845.02180
1	F(3)	3700.91000	3690.91190	3710.91190
1	F(4)	3592.55000	3582.55880	3602.55880
1	J(1, 2)	1.55040	-0.44960	3.55040
1	J(1, 3)	7.75200	5.75200	9.75200
1	J(2, 3)	7.92100	5.90000	9.90000
1	J(2, 4)	7.92100	5.90000	9.90000
1	J(3, 4)	1.00000	-0.45000	3.55000
1	H(1)	0.30000	0.00100	2.00000
1	H(2)	0.30000	0.00100	2.00000
1	H(3)	0.30000	0.00100	2.00000
1	H(4)	0.30000	0.00100	2.00000

Iteration 21 rms = 1.78270396

Index	Parameter Type	Parameter Value	neg. Grad.	GN-Corr.
0	F(1)	4083.65011	2.891e-004	2.952e-004
1	F(2)	3834.98820	-2.802e-004	-2.614e-004
2	F(3)	3700.91634	3.834e-004	3.713e-004
3	F(4)	3592.53425	3.880e-004	3.802e-004
4	J(1, 2)	1.69580	7.011e-004	1.503e-003
5	J(1, 3)	7.87206	-6.621e-004	-3.382e-004
6	J(2, 3)	7.39957	2.575e-003	1.005e-003
7	J(2, 4)	8.09810	-5.682e-004	1.634e-004
8	J(3, 4)	1.08665	-9.393e-004	2.475e-004
9	H(1)	1.54867	-4.263e-003	-4.733e-003
10	H(2)	1.34961	-5.573e-003	-5.830e-003
11	H(3)	1.29116	-3.844e-003	-3.774e-003
12	H(4)	1.71547	-7.271e-004	-1.068e-003

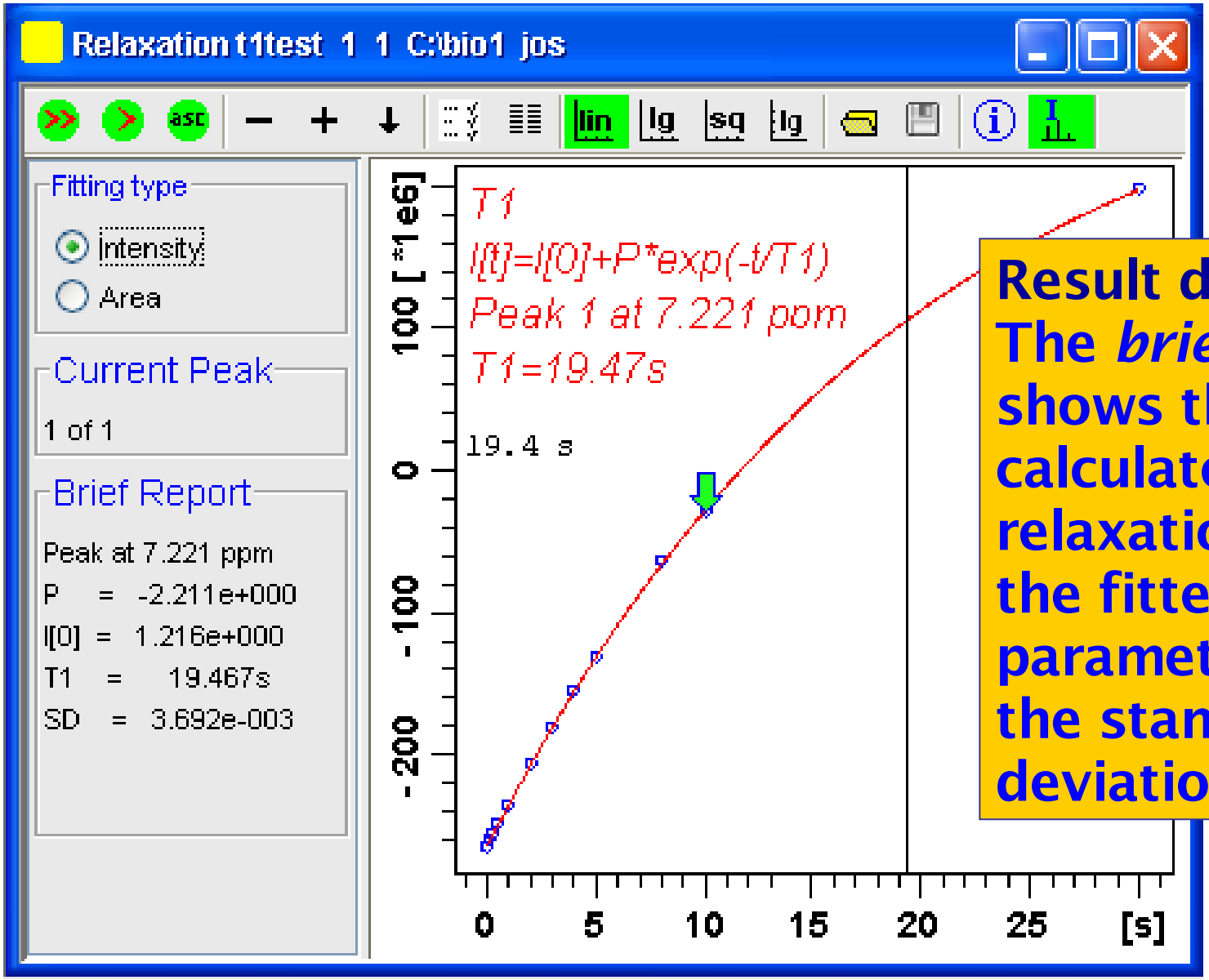
Relaxation Analysis

Features:

Intensity or area fitting, fitting types for:

- → **One-component T1 experiments.**
  *I(t) = I(0) + P*exp(t/T1)*
- → **One-component T2 experiments**
  *I(t) = P*exp(t/T2)*
- → **Experiments with 3 or 4 components:**
  cpt1rho, lorgauss
- → **Experiments with up to 6 components:**
  invrec, satrec,, expdec, gaussdec, varbigdel, varlitdel, vargrad, vardamp

Relaxation Analysis

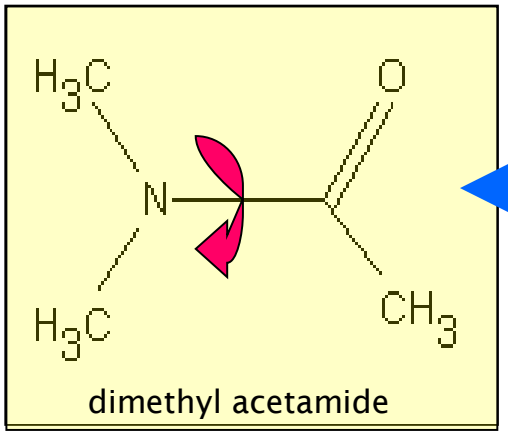


Result display. The *brief report* shows the calculated relaxation value, the fitted parameters and the standard deviation

Dynamic NMR Line Shape Analysis

Features:

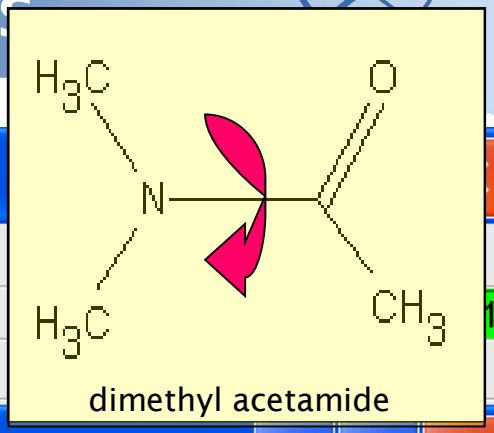
- Simulation of temperature-dependent spectra
- Iteratively refine model parameters
- Computation based on Liouville/von Neumann Form of Schrödinger equation
- Superposition of DNMR spectra of more than one spin system



dimethyl acetamide

Example: **Restricted rotation about amide bond, exchange of Nitrogen methyl groups at high temperature**

Dynamic NMR Line Shape Analysis



dimethyl acetamide

Bruker TopSpin

File Edit View Processing Analysis Options Window Help

1 exam_DNMR_Me2NCOMe 320 1 C:\Bruker\TOPSPIN guest

420K

370K

350K

320K

Fast rotation: 1 signal

Slow rotation: 2 sharp Nitrogen methyl signals

[*1e6]

15

10

5

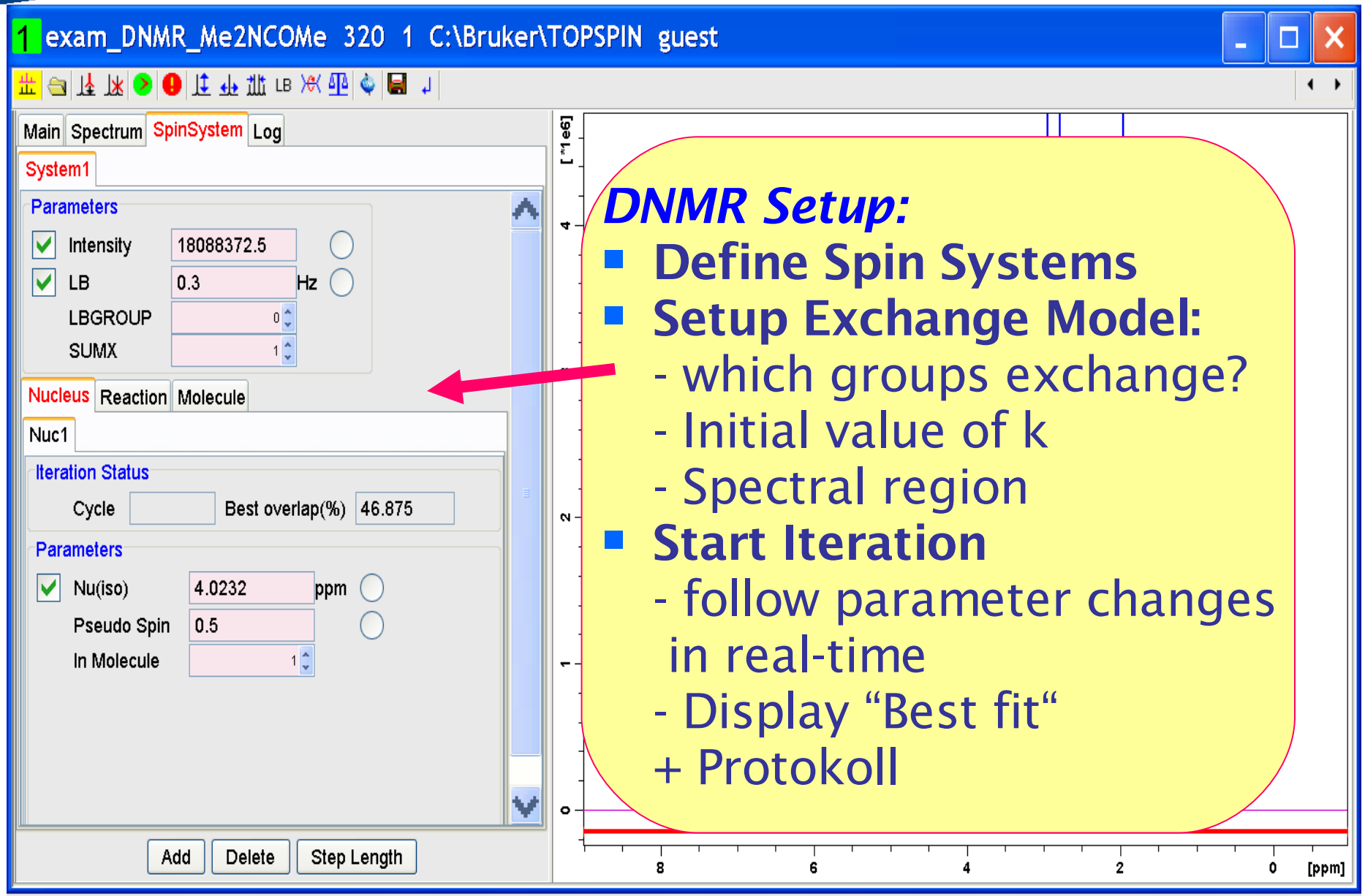
3.5

3.0

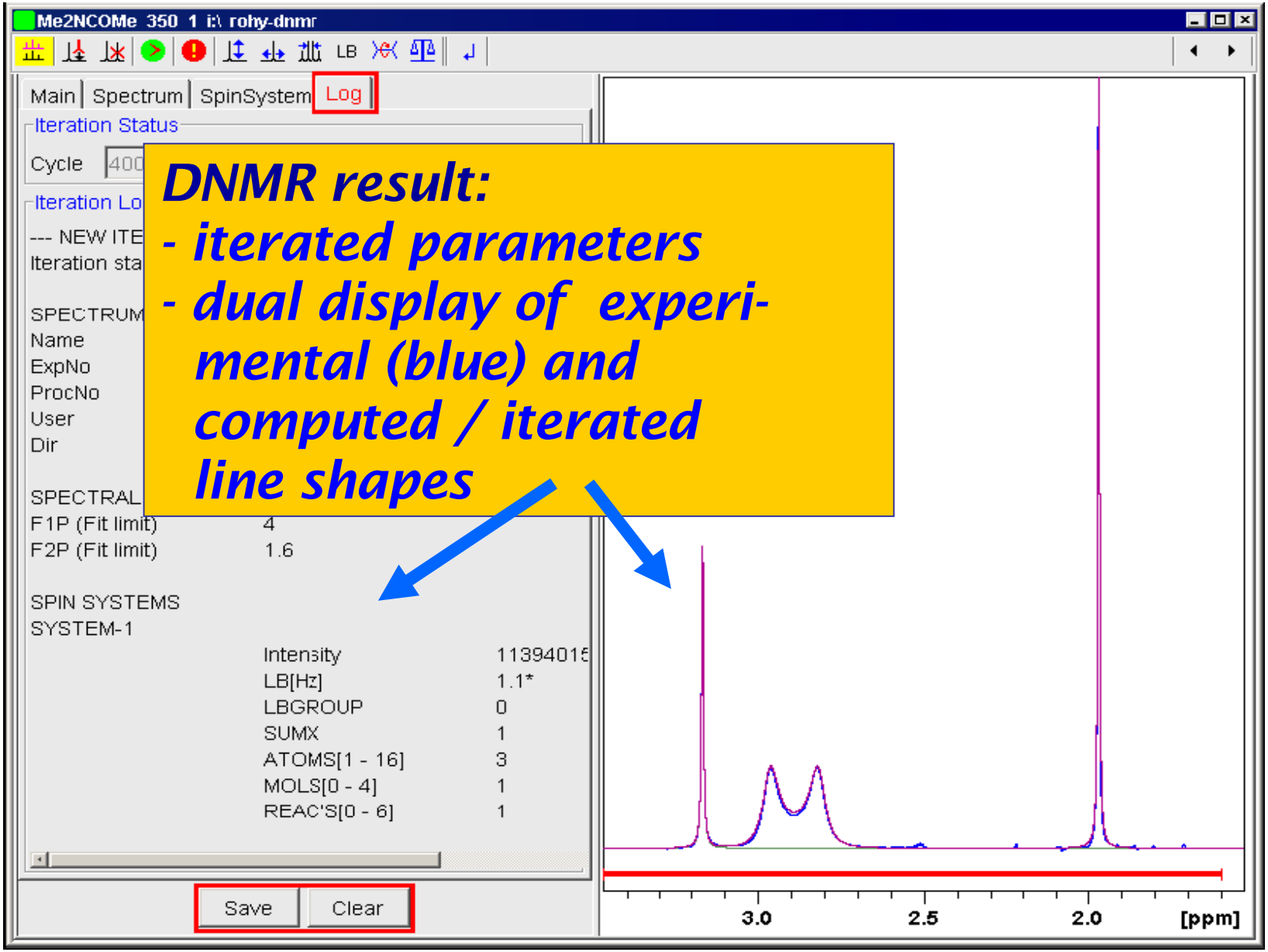
2.5

[ppm]

Dynamic NMR Line Shape Analysis



Dynamic NMR Line Shape Analysis



DNMR result:
- iterated parameters
- dual display of experi-mental (blue) and computed / iterated line shapes

Solids Line Shape Analysis

Features:

Simulates 1D solids NMR spectra and fits them to experimental spectra using the following line shape models:

- **Gauss / Lorentz**
- **Chemical shift anisotropy**
- **Quadrupolar central peak of the +/- ½ transition of a quadrupolar nucleus**
- **All quadrupolar transitions of a quadrupolar nucleus**
- **Combination of chemical shift anisotropy and quadrupolar interaction**

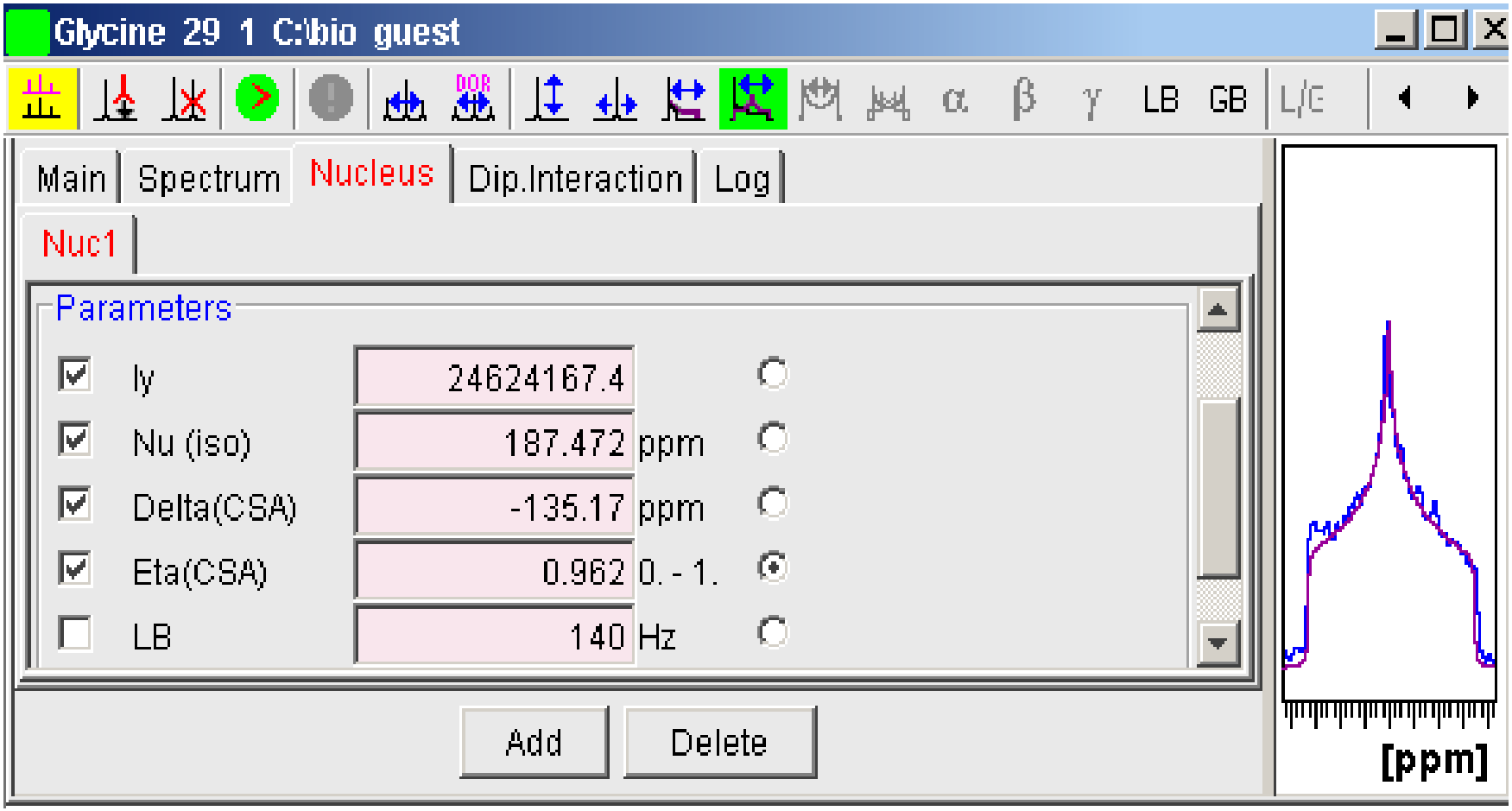
Solids Line Shape Analysis

Features (continued):

- Powder spectra of static or rotating samples
- 10 rotation and 5 DOR side bands definable
- Up to 25 observable nuclei (i.e. 25 nucleus sites)
- 10 dipolar coupling partners for the observed nucleus definable

Solids Line Shape Analysis

- Solids line shape analysis set up window
- Dual display of experimental (blue) and fitted (red) line shape



Structure Editor / Viewer

TopSpin comes with a
- 2D structure editor and a
- 3D structure viewer

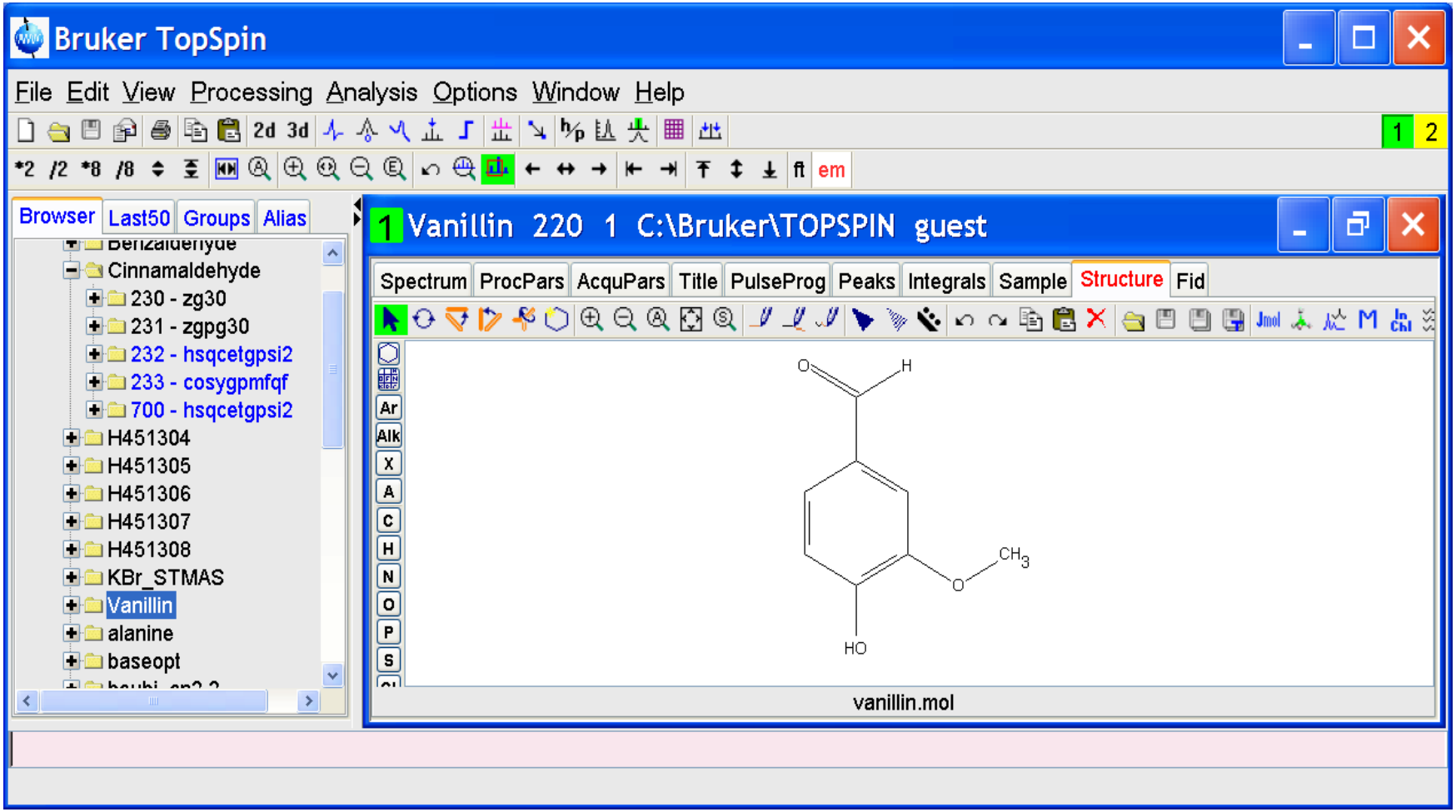
Structure Editor

Features:

2D structure editor

- **Drawing chains, stereo bonds, aromatic bonds**
- **View spectrum correlation when spectrum displayed simultaneously**
- **Zoom / rotate / flip / refine**
- **Show mass information / INCHI identifier**
- **save a mol file, read mol file**

Structure Editor



Structure Viewer: Jmol

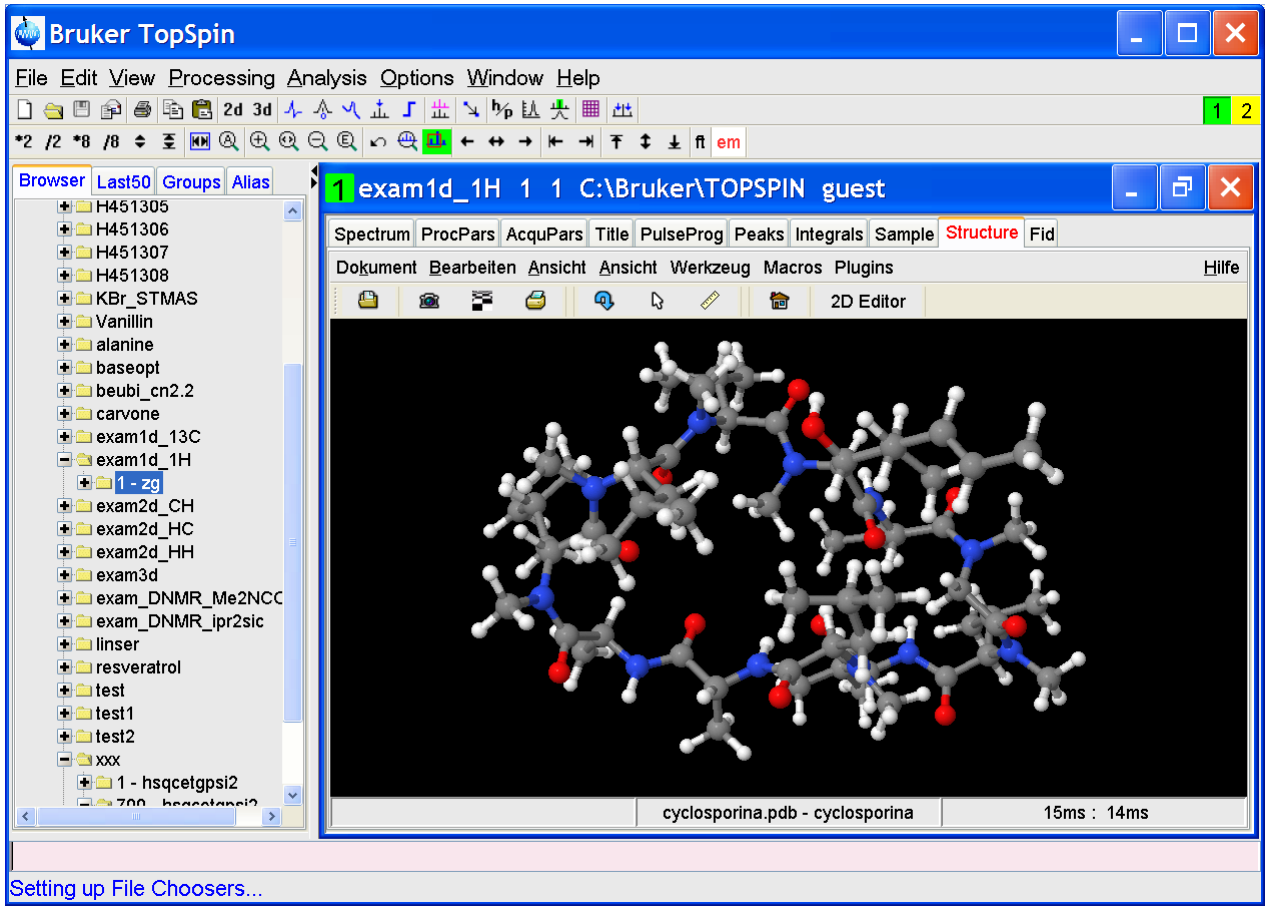
Features:

3D structure viewer

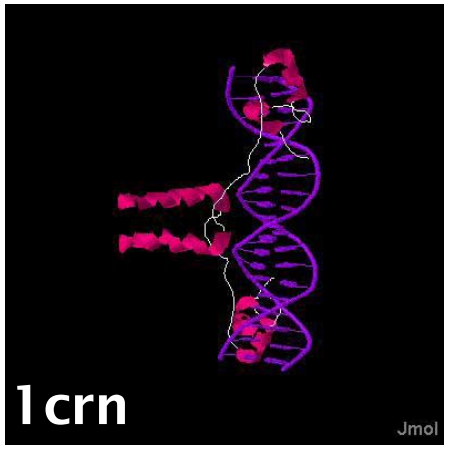
- **TopSpin-Implementation of the open source Jmol viewer** *(jmol.sourceforge.net)*
- **High-performance 3D rendering**
- **Can read many file formats!**
- **Distance / angle / torsion angle measurements**
- **RasMol/Chime scripting language support**
- **Displays secondary structure elements (schematic shapes)**
- **Exports .png, .jpg, .ppm, .pdf, Povray**

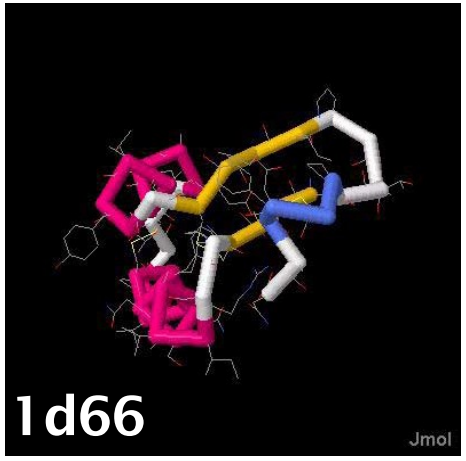
Structure Viewer : Jmol

Cyclosporine display using Jmol Viewer



Other examples: Secondary structure display





Shift Prediction

Features:

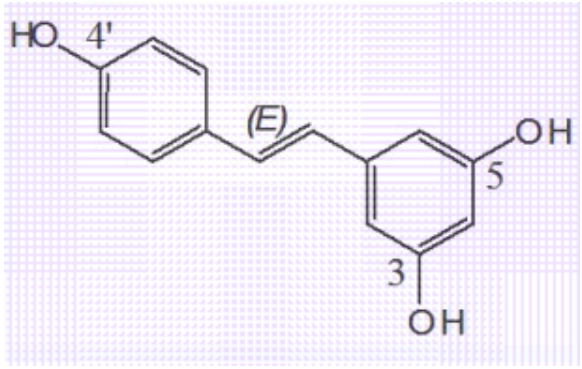
TopSpin includes a 1H / 13C shift prediction module of company PERCH, Kuopio, Finland

- **Shift prediction can be operated directly from the TopSpin (or Amix) user interface**
- **Shift prediction is based on Molecular Mechanics/ Dynamics**
- **Takes into account solvent, pH, ionic strength, concentration**
- **Computes a 1D spectrum via quantum mechanical methods from the prediction**
- **Prediction result in text form and as a spectrum**

Shift Prediction

Shift prediction workflow in TopSpin

Input



.mol - File

Predict Software

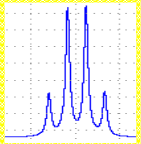
Result

δ(1H)
δ (13C)

As:
Text File

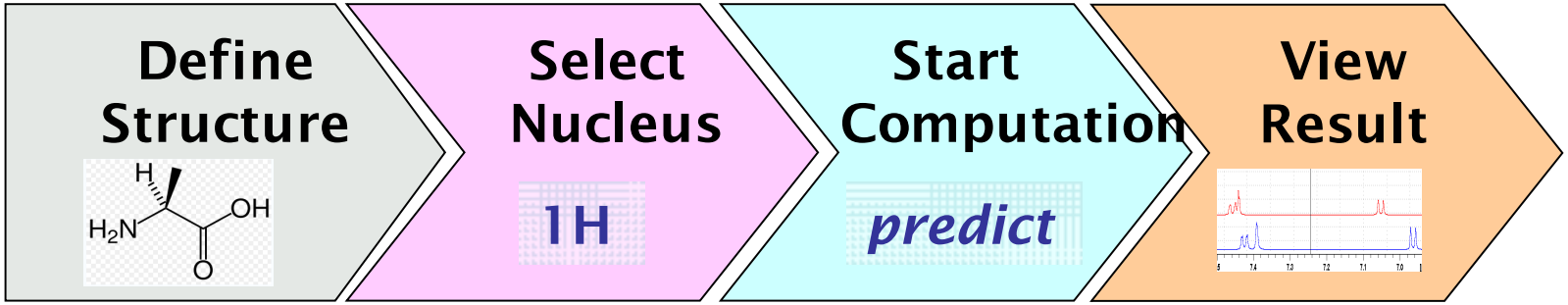
```
ATOM INFORMATION:
    0 H "" 0 0 0 1*1 ND
    1 C "" 2 1 1 1*1 ND
      0 H "" 0 0 0 1*
     33 H "" 0 29 29
    2 C "" 1 2 2 1*1 ND
     34 H "" 0 30 30
```

Calculated
Spectrum



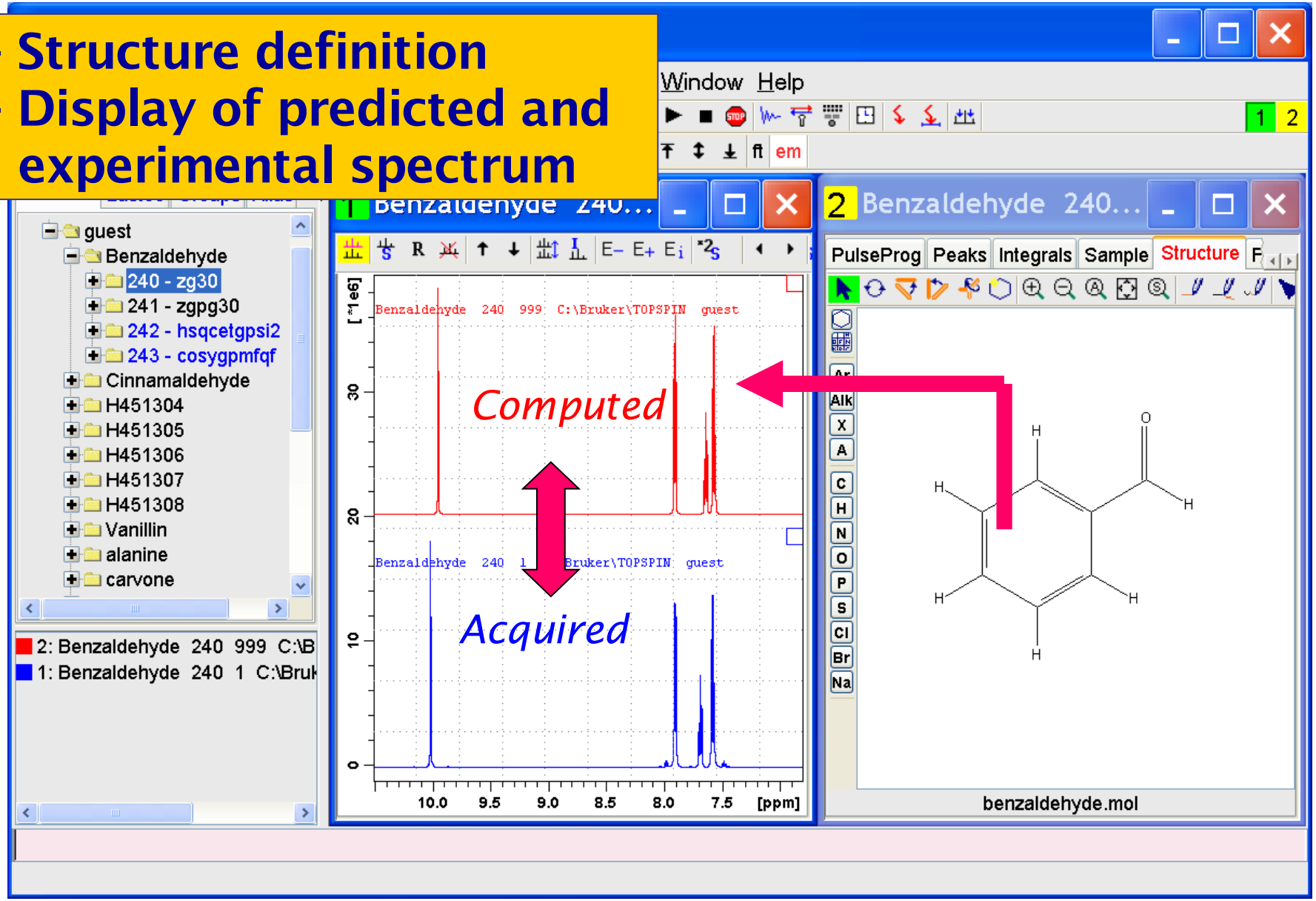
Shift Prediction

Shift prediction workflow in TopSpin



Shift Prediction

- Structure definition
- Display of predicted and experimental spectrum



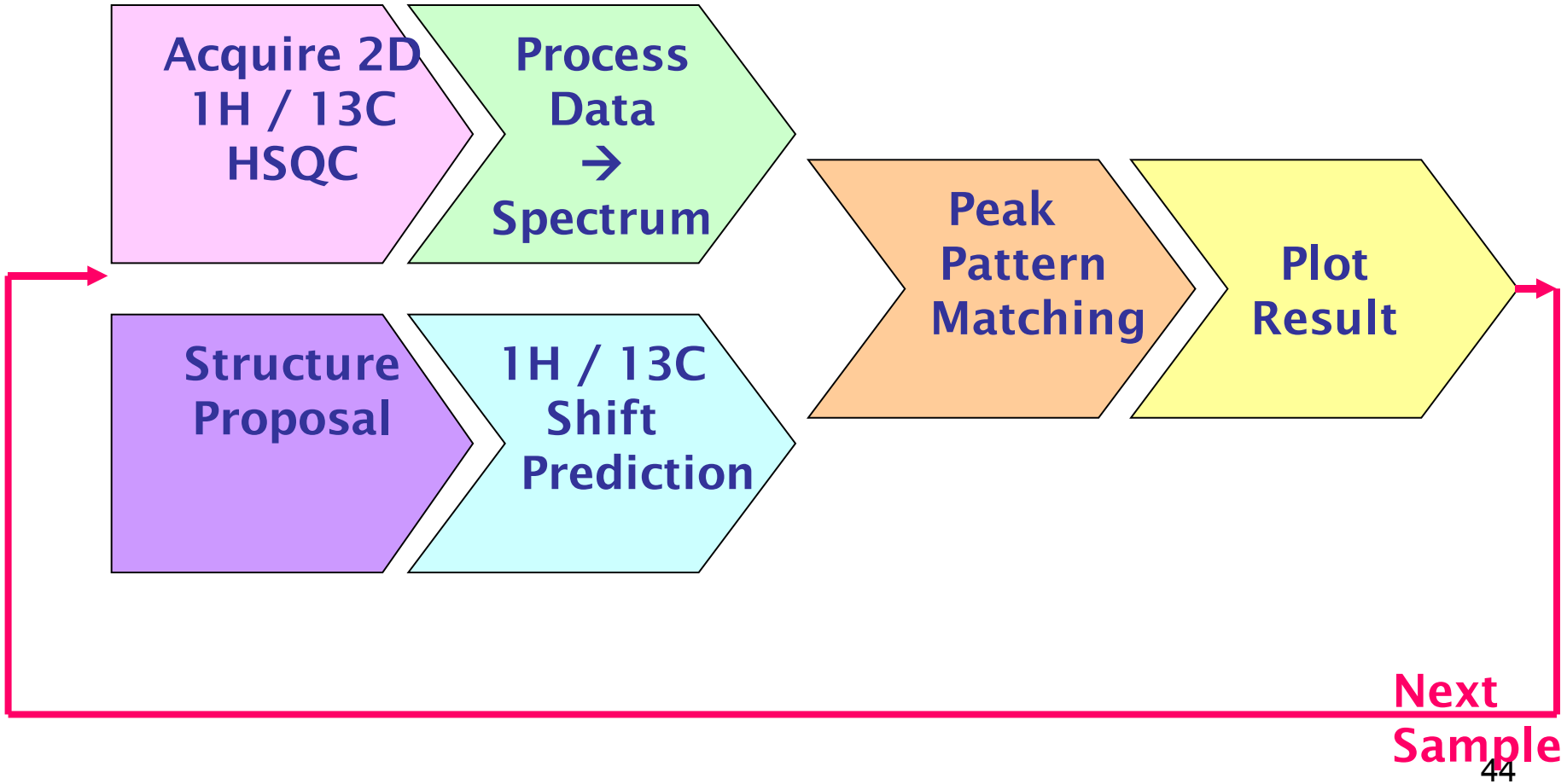
Structure Verification

Features:

TopSpin (from 2.1) includes a Structure Verification Module based on 1H / 13C shift prediction and a respective HSQC spectrum.

Structure Verification

Based on 1H + 13C Shift Prediction and acquired HSQC



Structure Verification

Result Plot, spectrum/prediction consistent

ps-hsqc-5m DMSO /u ps-ddmso 32

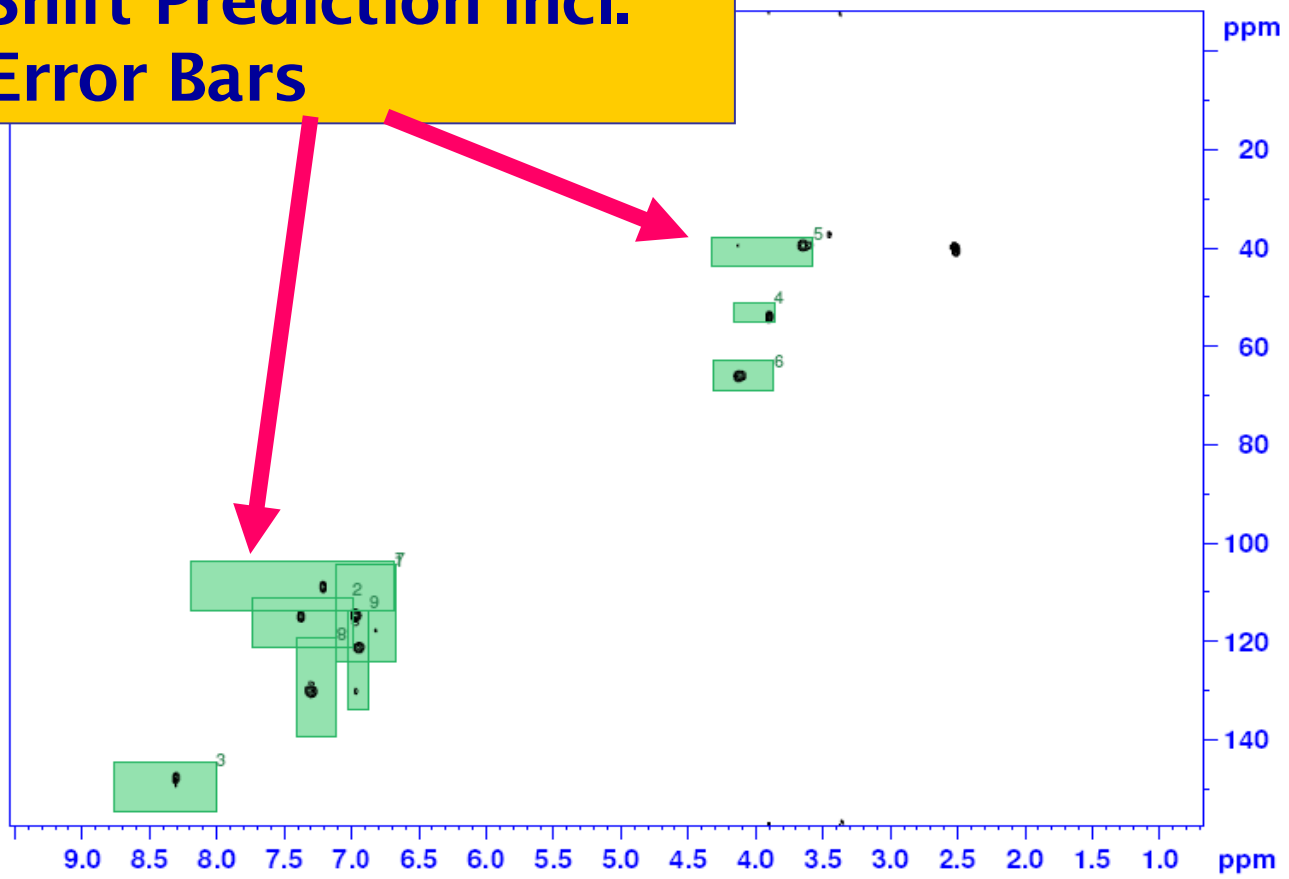
Electronic Signature:
USER ID prs
USER NAME prs
MEANING review
2006-10-31 11:22:06.792 +0100

Current Data Parameters

Current Data Parameters
NAME 20094
EXPNO 5
PROCNO 1

HSQC Structure Verification Summary
TOPSPIN 2.1, verification module 1.1 $, 2006-09-31 11:30:29
MOL file C:/bruker/TS20/data/perch/nmr/20094/5/pdata/1/bru20094.mol
prediction by PERCH NMR TOOLS 2006.1017 BUILD125615R
pattern matching by AURELIA/AMIX : Wed Oct 25 14:49:12 2006
15 of 15 patterns verified (0 empty)
51 of 66 peaks inside patterns (15 outside)

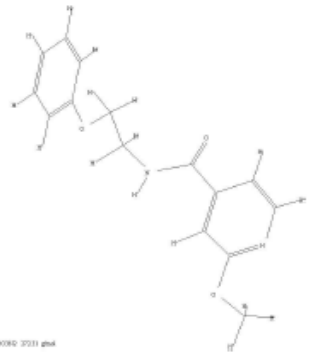
Shift Prediction incl. Error Bars



BRUKER

4009285 004907

Structure

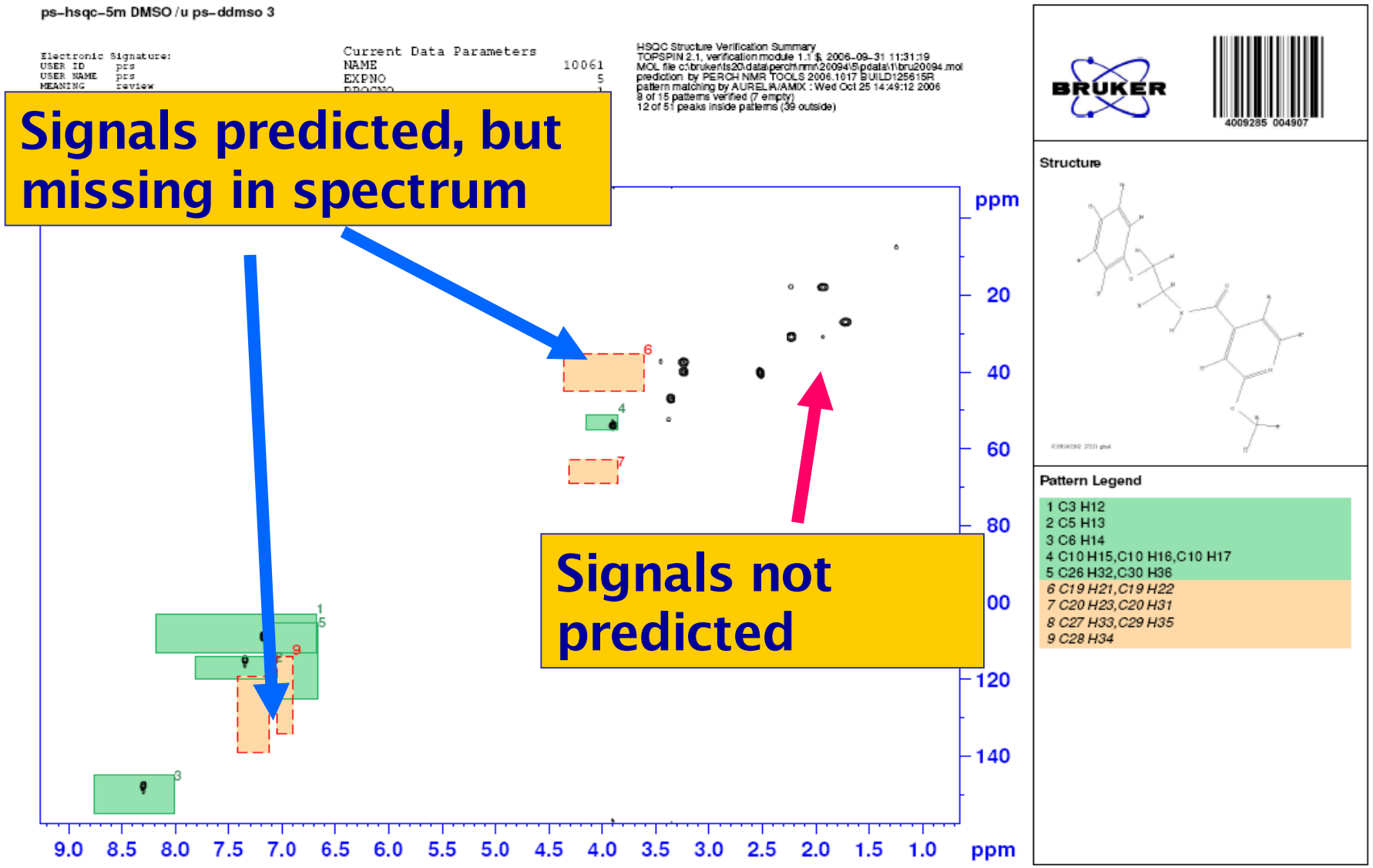


Pattern Legend

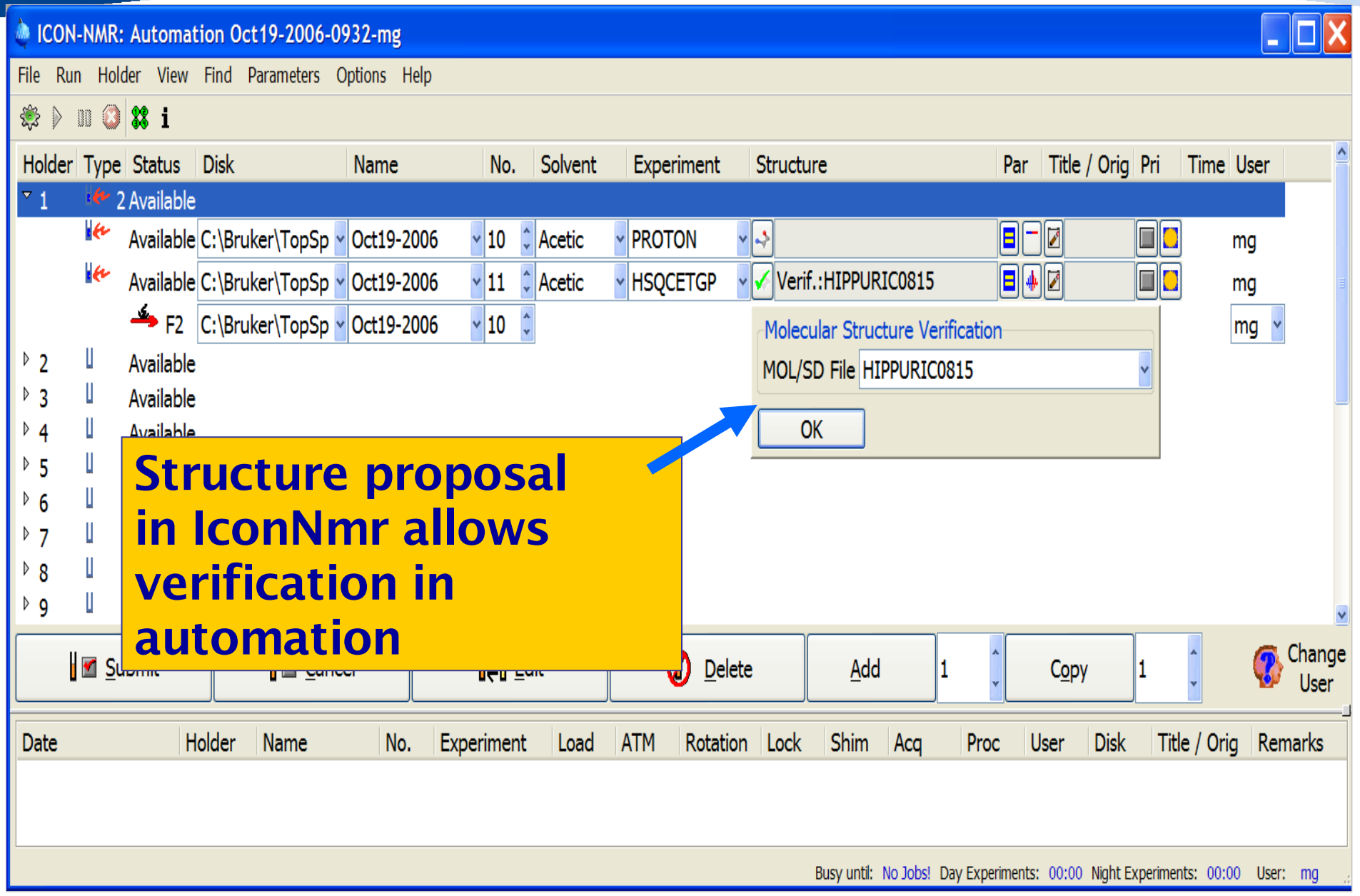
1 C3 H12
2 C5 H13
3 C6 H14
4 C10 H15,C10 H16,C10 H17
5 C19 H21,C19 H22
6 C20 H23,C20 H31
7 C26 H32,C30 H36
8 C27 H33,C29 H35
9 C28 H34

Structure Verification

Result Plot, spectrum/prediction inconsistent



Structure Verification



DOSY

TopSpin provides several DOSY processing algorithms:

- 3-component fit
- Decra
- CONTIN
- DOSY*m*
- Fitting diffusion decays with the relaxation package

DOSY

Example spectrum

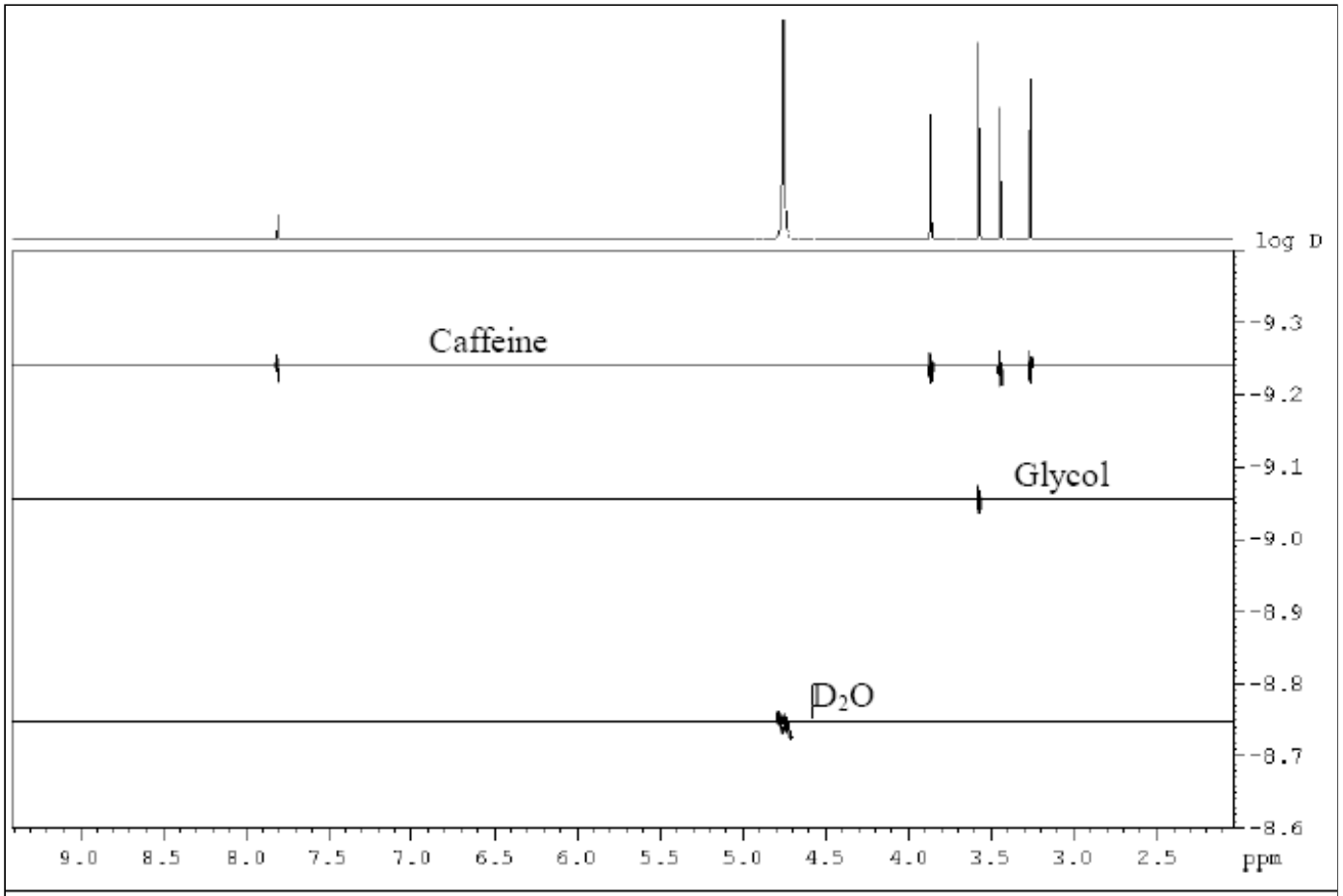


Figure 3.2: Example of a DOSY spectrum showing the different diffusion behavior of Ethylenglycol and Caffeine dissolved in D_2O.

DOSY

3-component fit
- Fits up to 3 exponentially decaying curves

Decra *(direct exponential curve resolution algorithm)*

- Easy to use
- Fool-proof results
- But: Data acquistion requires variable gradient strength and with the square ramp option

Fitting diffusion decays using the relaxation package

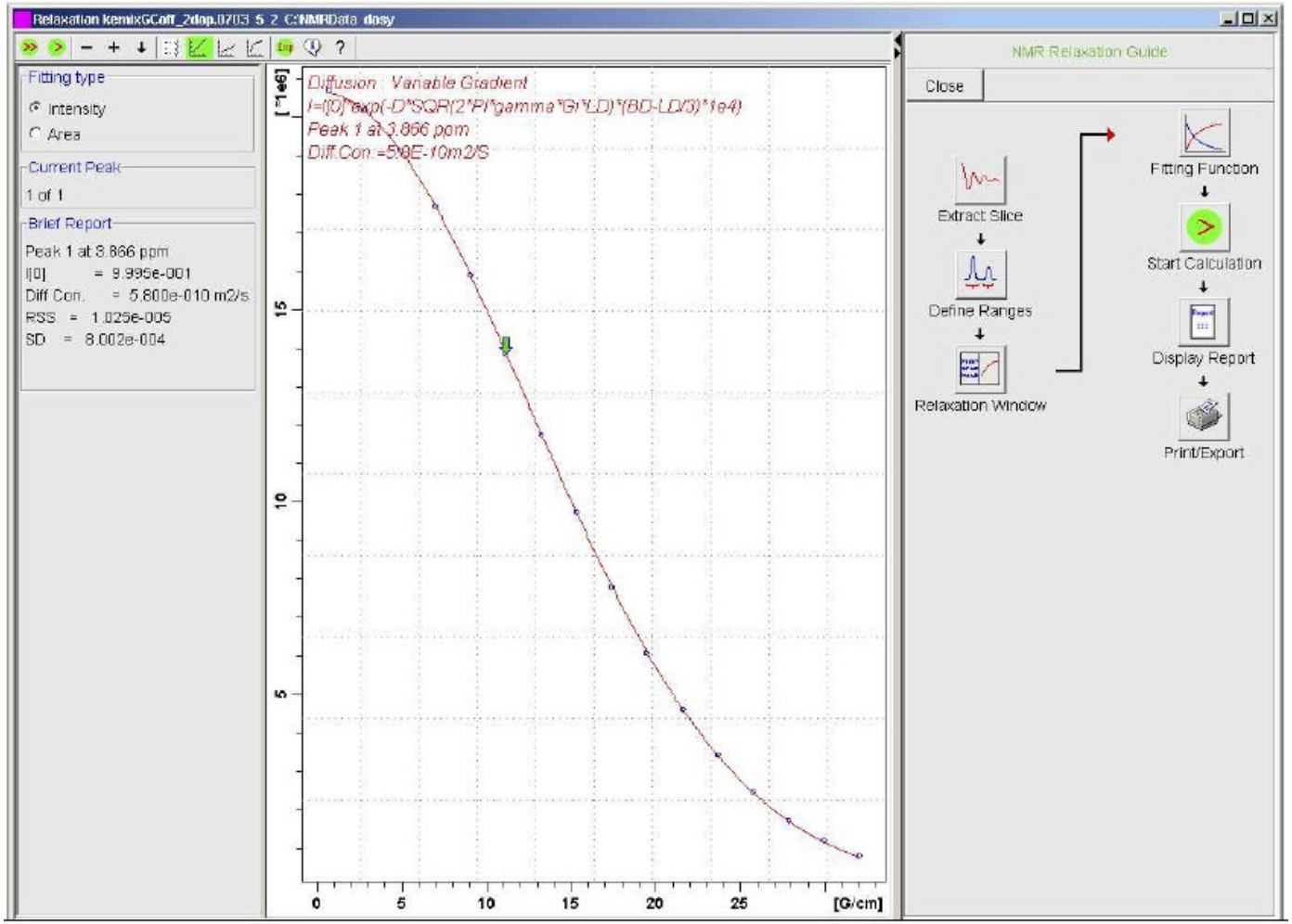


Figure 3.4: TopSpin display after fitting with SimFit (T1/T2 Analysis). The fitting curve for the peak at 3.87 ppm (Caffeine) is shown.

DOSY

CONTIN
- Based on algorithm of *Provencher*
- Intended for a complex mixture of small molecules with highly overlapping signals

DOSY*m*™
- Based on maximum entropy mathematics
- Intended for a complex mixture of small molecules with highly overlapping signals
- Third-party module directly interfaced to TopSpin
- Requires separate license

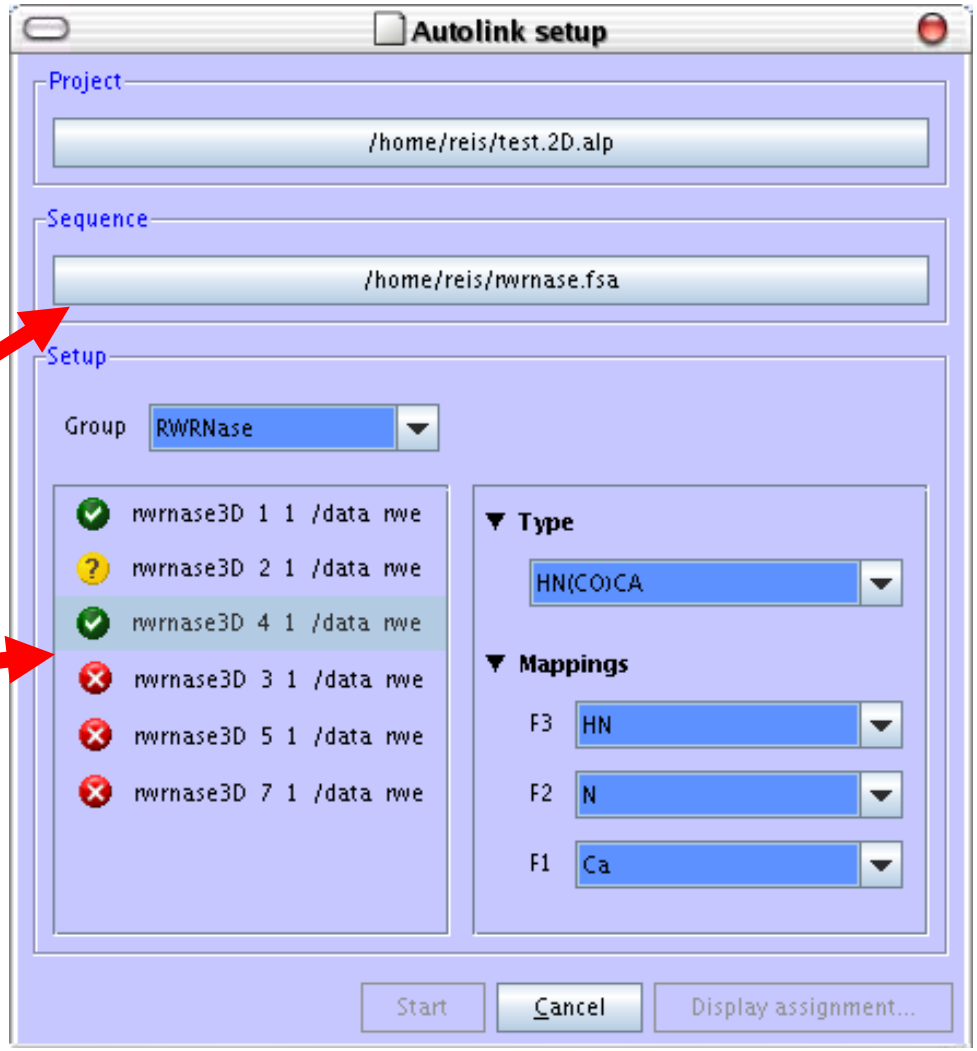
Protein Backbone Assignment

TopSpin includes the *AutoLink* backbone assignment algorithm

AutoLink setup dialog

Amino Acid sequence

Input spectra



Protein Backbone Assignment

Assignment result display