

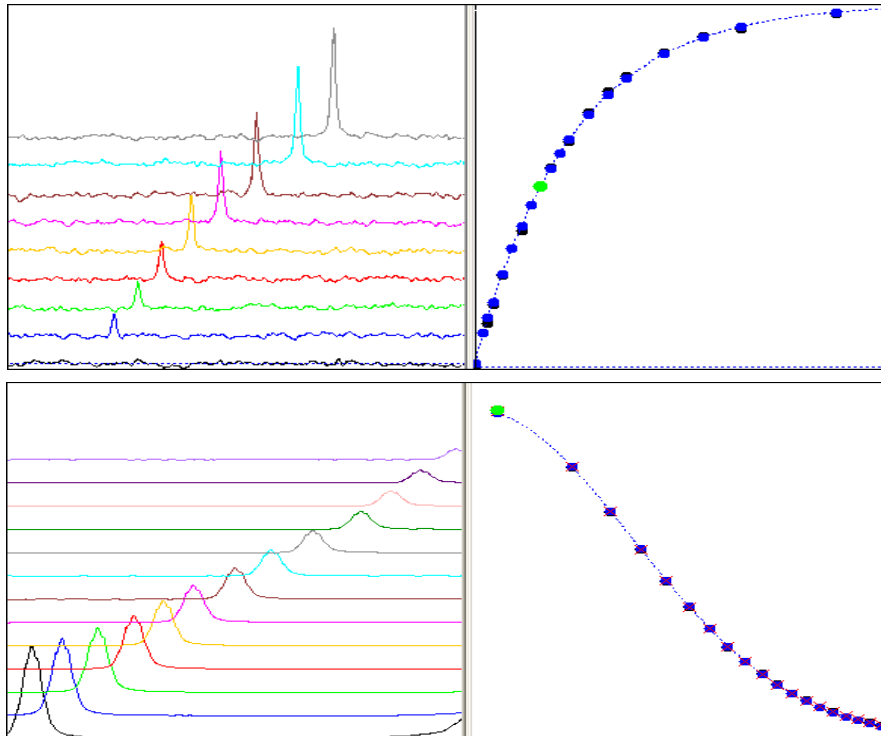
Dynamics Center

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Symposium on Frontiers in Biomolecular NMR
Vanderbilt University
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As “dynamics experiments” we regard a wide range of experiments where:

Series of spectra measured with dependence on **at least one variable** that is **not Fourier transformed**, e.g.



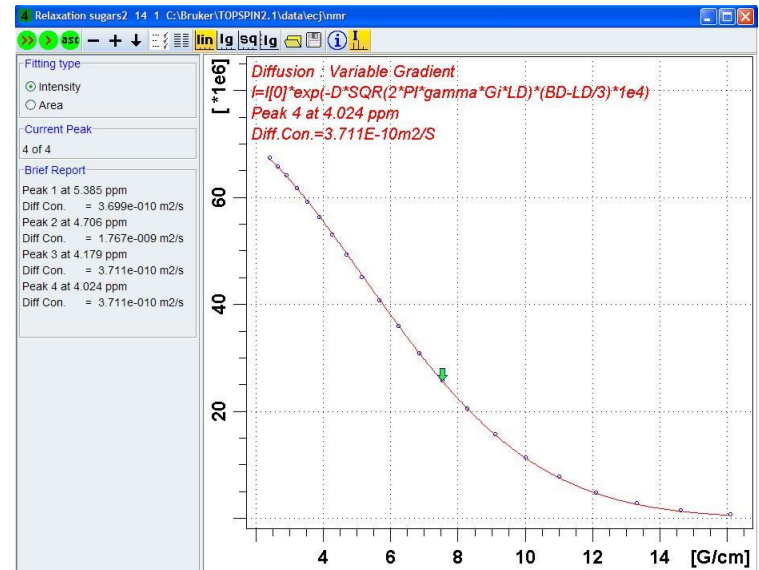
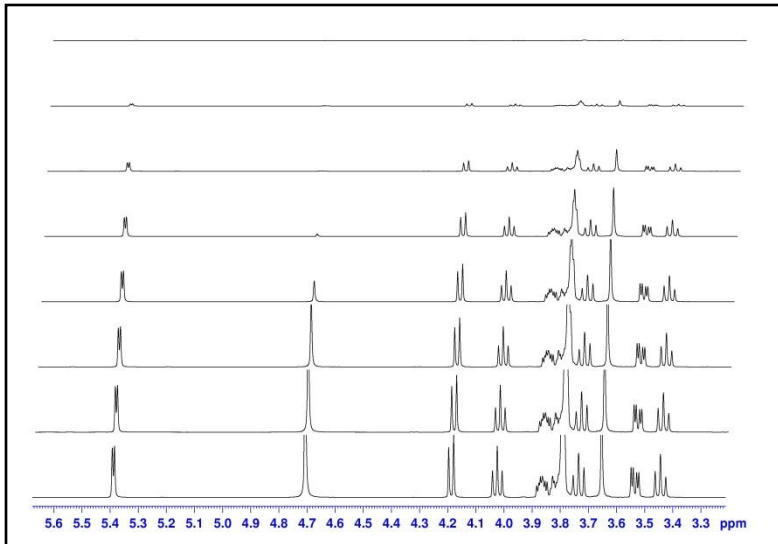
Relaxation:

signal amplitude as a function of mixing time

Diffusion:

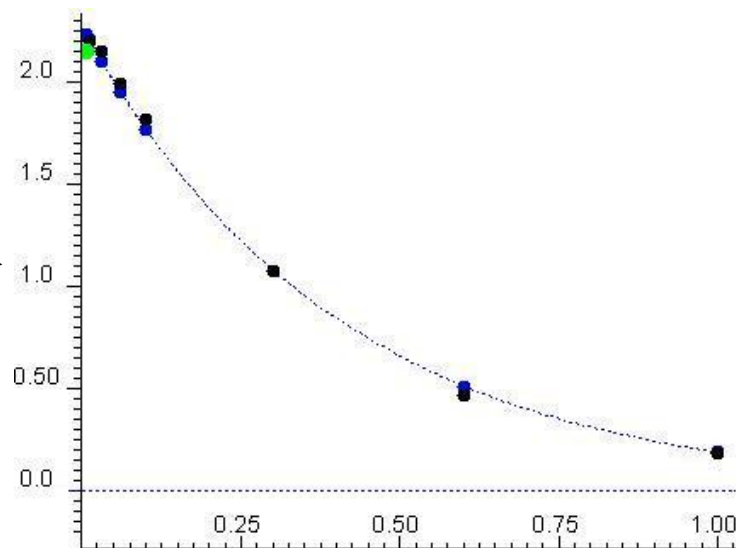
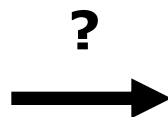
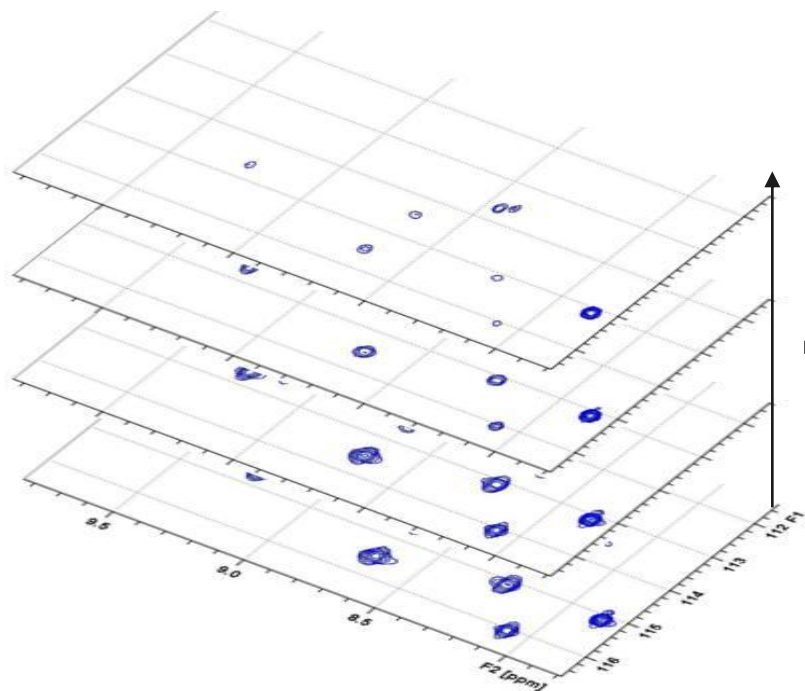
signal amplitude as a function of gradient strength

Analysis of small molecule relaxation data



T1/T2 Relaxation Guide has long been part of Topspin

Analysis of protein relaxation data



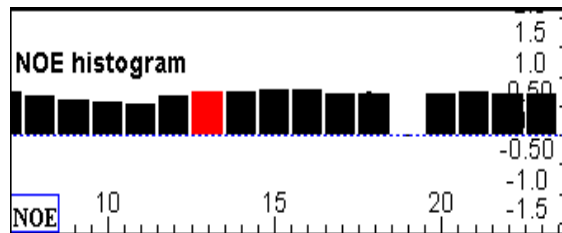
How do we go from 2D spectra (or pseudo-3D) to curve fitting?

Hetero nuclear relaxation experiments



method pulse program

NOE hsqcnoef3gpsi



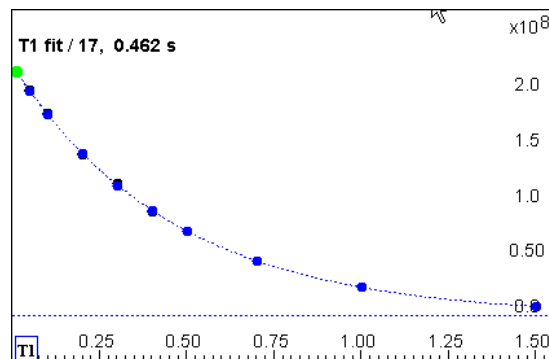
ratio

$$NOE^i = \frac{I_s^i}{I_u^i}$$

T_1 hsqct1etf3gpsi3d

T_2 hsqct2etf3gpsi3d

$T_{1\rho}$ hsqctretf3gpsi3d



fit

$$I(t) = A * e^{-t/B}$$

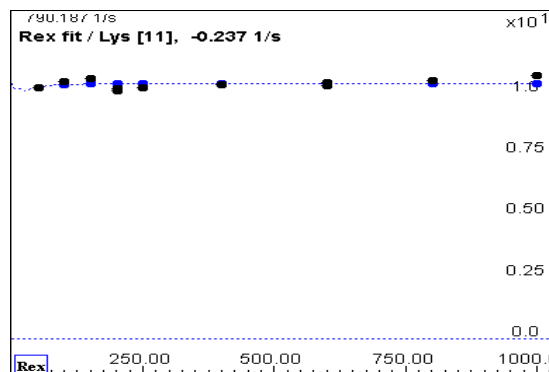
add. calculation

(T_2 from T_1 , $T_{1\rho}$)

R_{ex} hsqcrexetf3gpsi3d

JACS 123, 11341, 2001

(2 sites, slow exchange)



fit

$$R^{eff}(\tau_{cp}) = R_0 + K_{ex} * \left(1 - \frac{\sin(\delta\omega \tau_{cp})}{\delta\omega \tau_{cp}}\right)$$

model selection

Bruker BioSpin

From Relaxation to Dynamics



NOE, R_1 , R_2

$J(0), J(\omega_H), J(\omega_N),$
 $J(\omega_H + \omega_N), J(\omega_H - \omega_N)$

Model free Analysis
 global | local motion
 $J \sim f(S^2, \tau_c, \tau_e, \dots)$

reduced spectral density mapping
 $J(0), J(0.87 \omega_H), J(\omega_N),$

$\rho \sim f(R_2^{sel} / R_1^{sel}) \sim D_{||}, D_{\perp}$
 magnitude of diffusion tensor

$J(0), J(\omega_N)$ ↓ dynamics ↑
 $J(0.87 \omega_H)$ ↑ dynamics ↑
 $J(0)$ ↑↑ exchange ↑
 estimation of S^2, R_{ex}

$D_{||} / D_{\perp} < 1.2 ?$

structure not needed

structure needed

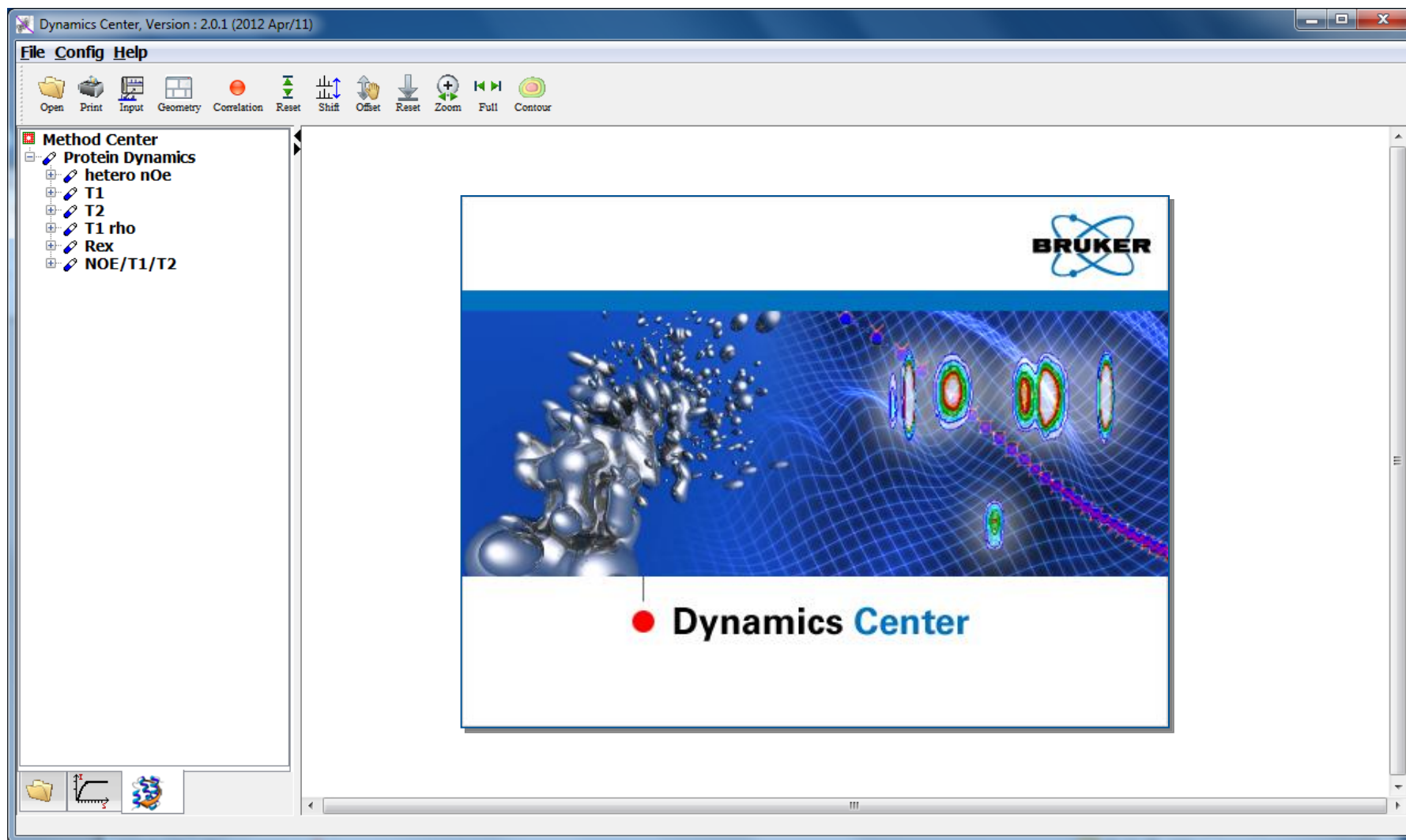
$\tau_c \sim f(R_2^{sel} / R_1^{sel})$

fit dynamic parameters
 via up to 5 models

minimize $f(\rho - \rho')$, get
 full diffusion tensor

fit dynamic parameters
 via up to 5 anisotropic
 models

The New Dynamics Center...



The New Dynamics Center...

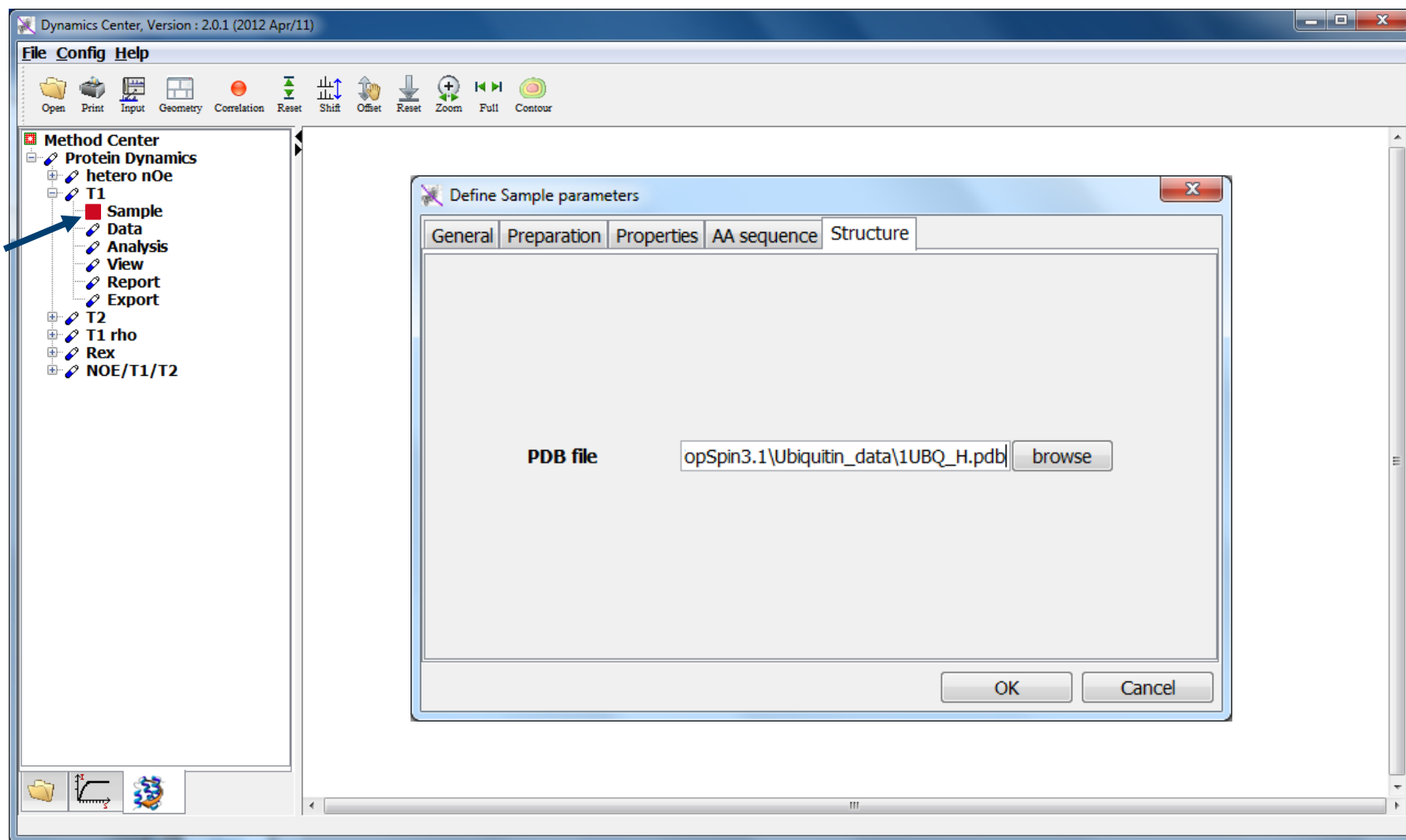


The screenshot displays the Dynamics Center software interface (Version 2.0.1, 2012 Apr/11). The main window features a menu bar (File, Config, Help) and a toolbar with icons for Open, Print, Input, Geometry, Correlation, Reset, Shift, Offset, Reset, Zoom, Full, and Contour. On the left, the 'Method Center' tree is visible, with 'Protein Dynamics' expanded to show 'hetero nOe', 'T1', and 'T2'. The 'T1' method is selected, and a blue arrow points to its 'Sample Data' sub-item. A 'Define Sample parameters' dialog box is open in the foreground, showing the 'General' tab with the following fields:

Field	Value
Sample/Protein name	ubiquitine
Description/Title	standard demo sample
Origin	in-house
Date of preparation	06 / 2005

The dialog box also includes 'Preparation', 'Properties', 'AA sequence', and 'Structure' tabs, and 'OK' and 'Cancel' buttons at the bottom.

The New Dynamics Center...



The New Dynamics Center...



The screenshot displays the Dynamics Center software interface. On the left, the 'Method Center' tree is visible, with a blue arrow pointing to the 'Data' folder under the 'T1' method. The main window shows the 'Select Data for T1 method' dialog box, which is currently open. The dialog has three tabs: 'Spectra', 'Peaks', and 'Lists'. The 'Spectra' tab is active, showing options for 'Select spectra type' (pseudo 3D (N planes) is selected) and a list of spectra configurations. The 'pseudo 3D spectrum' is set to 'Ubiquitin_data\1065-T1\1\pdata\1\3rrr'. The 'number of spectra' is set to 8. Below this, there are nine rows for '2D spectrum' (1-9), each with a 'browse' button and a 'Mixing time [s]' value ranging from 0.000 to 0.400. The 'OK' and 'Cancel' buttons are at the bottom right.

2D spectrum	File Path	Mixing time [s]
2D spectrum 1	Ubiquitin_data\1065-T1\1\pdata\1\3rrr	0.000
2D spectrum 2	???	0.050
2D spectrum 3	???	0.100
2D spectrum 4	???	0.150
2D spectrum 5	???	0.200
2D spectrum 6	???	0.250
2D spectrum 7	???	0.300
2D spectrum 8	???	0.350
2D spectrum 9	???	0.400

The New Dynamics Center...

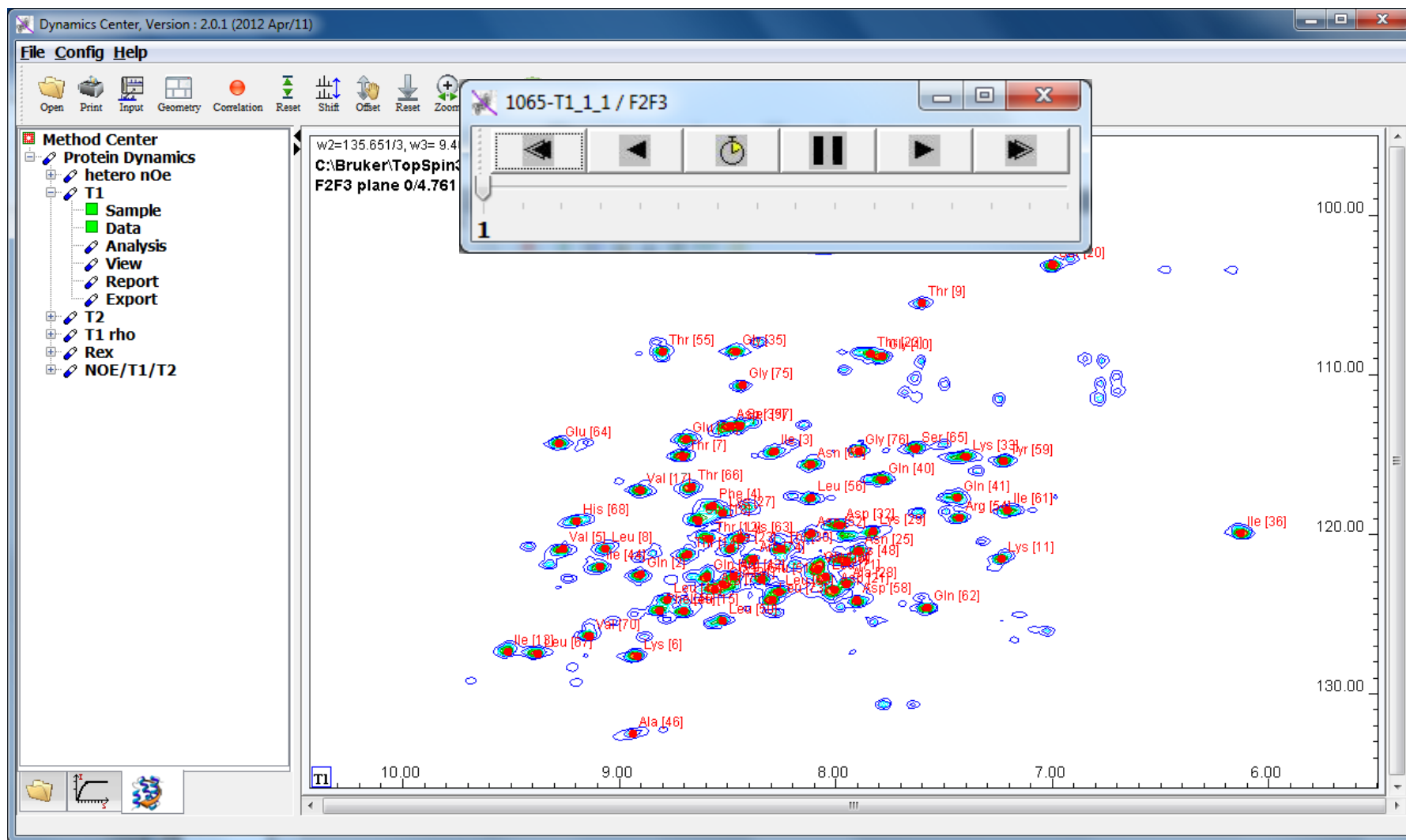


The screenshot displays the Dynamics Center software interface (Version 2.0.1, 2012 Apr/11). The main window features a menu bar (File, Config, Help) and a toolbar with icons for Open, Print, Input, Geometry, Correlation, Reset, Shift, Offset, and another Reset. A tree view on the left, titled 'Method Center', shows a hierarchy: Protein Dynamics, hetero nOe, T1, Sample, Data (highlighted with a red square and a blue arrow), Analysis, View, Report, Export, T2, T1 rho, Rex, and NOE/T1/T2. A dialog box titled 'Select Data for T1 method' is open, showing three tabs: Spectra, Peaks, and Lists. The 'Lists' tab is active, displaying the following options:

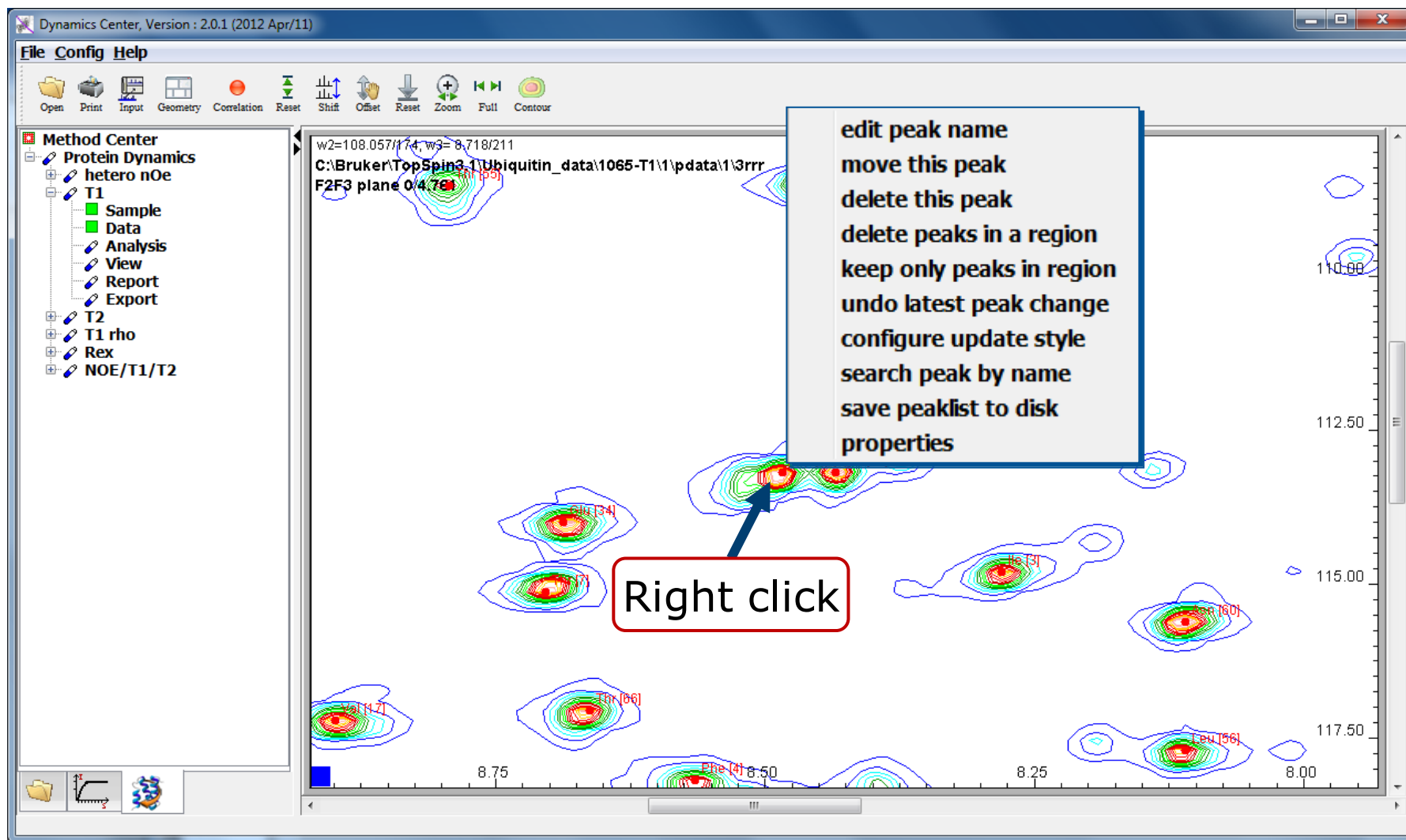
- Select peak type:**
 - do an automated peak picking
 - use peak list at spectrum (peaklist.xml)
 - use any other peak list (peaklist.xml)
- Peak list file:** tin_data\2D-Ref\1\data\1\peaklist.xml
- perform automated peak snapping
- Select integral type:**
 - use peak intensities
 - use peak area integrals
 - use peak shape integrals
 - use deconvoluted peak integrals
- Available functions:**
 - lorentzian
 - gaussian
 - fixed gaussian/lorentzian
 - variable gaussian/lorentzian
- Default line width (Hz) in F1:** 25.0

At the bottom of the dialog box are 'OK' and 'Cancel' buttons.

The New Dynamics Center...



The New Dynamics Center...



The New Dynamics Center...



Dynamics Center, Version : 2.0.1 (2012 Apr/11)

File Config Help

Open Print Input Geometry Correlation Reset Shift Offset Reset Zoom

Method Center

- Protein Dynamics
 - hetero nOe
 - T1
 - Sample
 - Data
 - Analysis
 - View
 - Report
 - Export
 - T2
 - T1 rho
 - Rex
 - NOE/T1/T2

w2=135.651/3, w3= 9.400
C:\Bruker\TopSpin3.1
F2F3 plane 0/4.761

10.00

100.00
110.00
120.00
130.00

Ile [36]

6.00

Select the details of analysis

Select T1 fit function

- $f(t) = I_0 * e^{-t/T1}$
- $f(t) = I_0 * [1 - e^{-t/T1}]$, Saturation Recovery
- $f(t) = I_0 * [1 - 2 * e^{-t/T1}]$, Inversion Recovery

The quality of Fits usually increases if good start parameters are chosen.

start value for T1 (e.g. 0.5) s

Fit parameter error estimation can be based on different methods

Select error estimation method

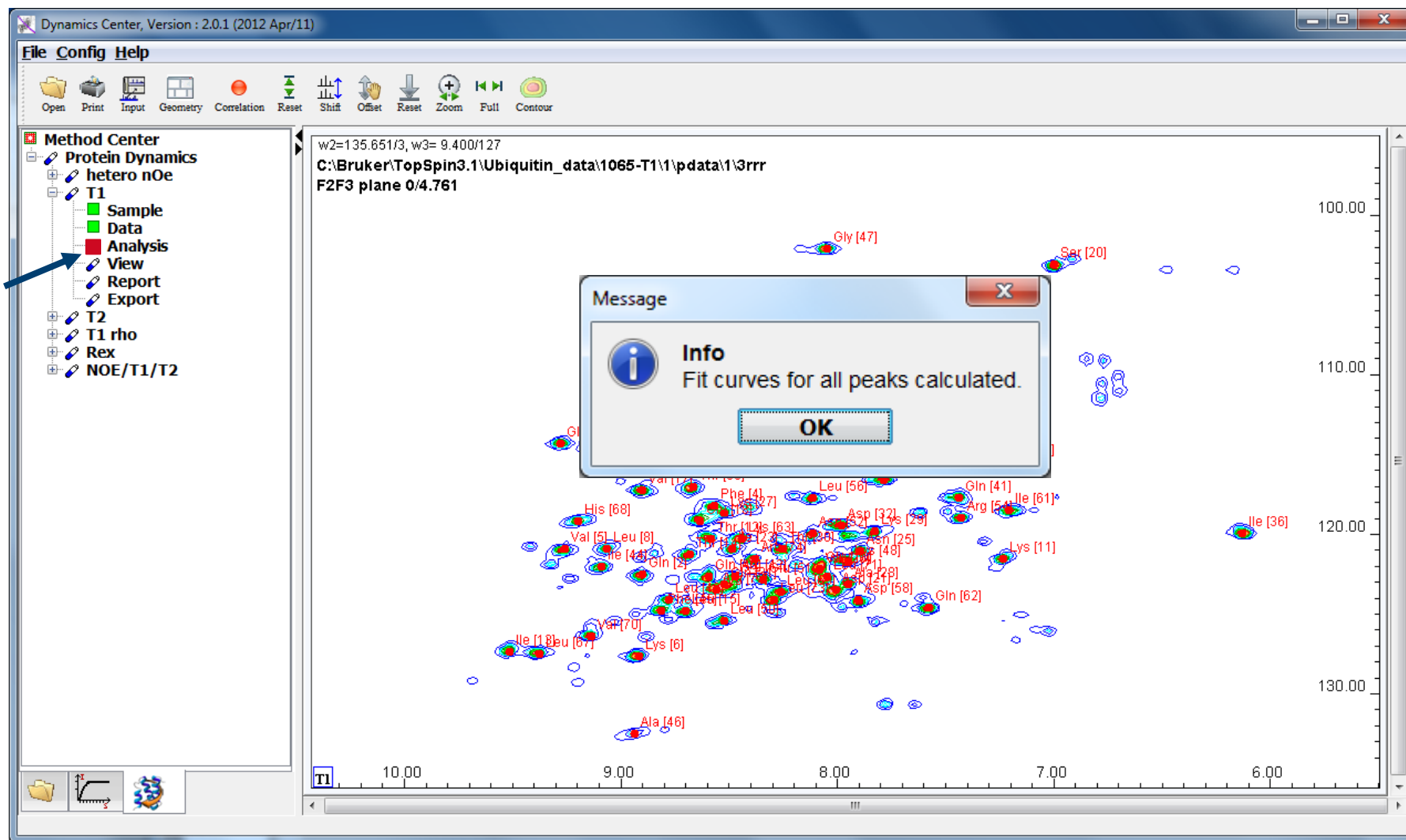
- error estimation by fit
- error estimation by weighted fit
- error estimation by Monte Carlo simulation

Fitted parameters are calculated and given with a confidence interval

Confidence level %

OK Cancel

The New Dynamics Center...



The New Dynamics Center...

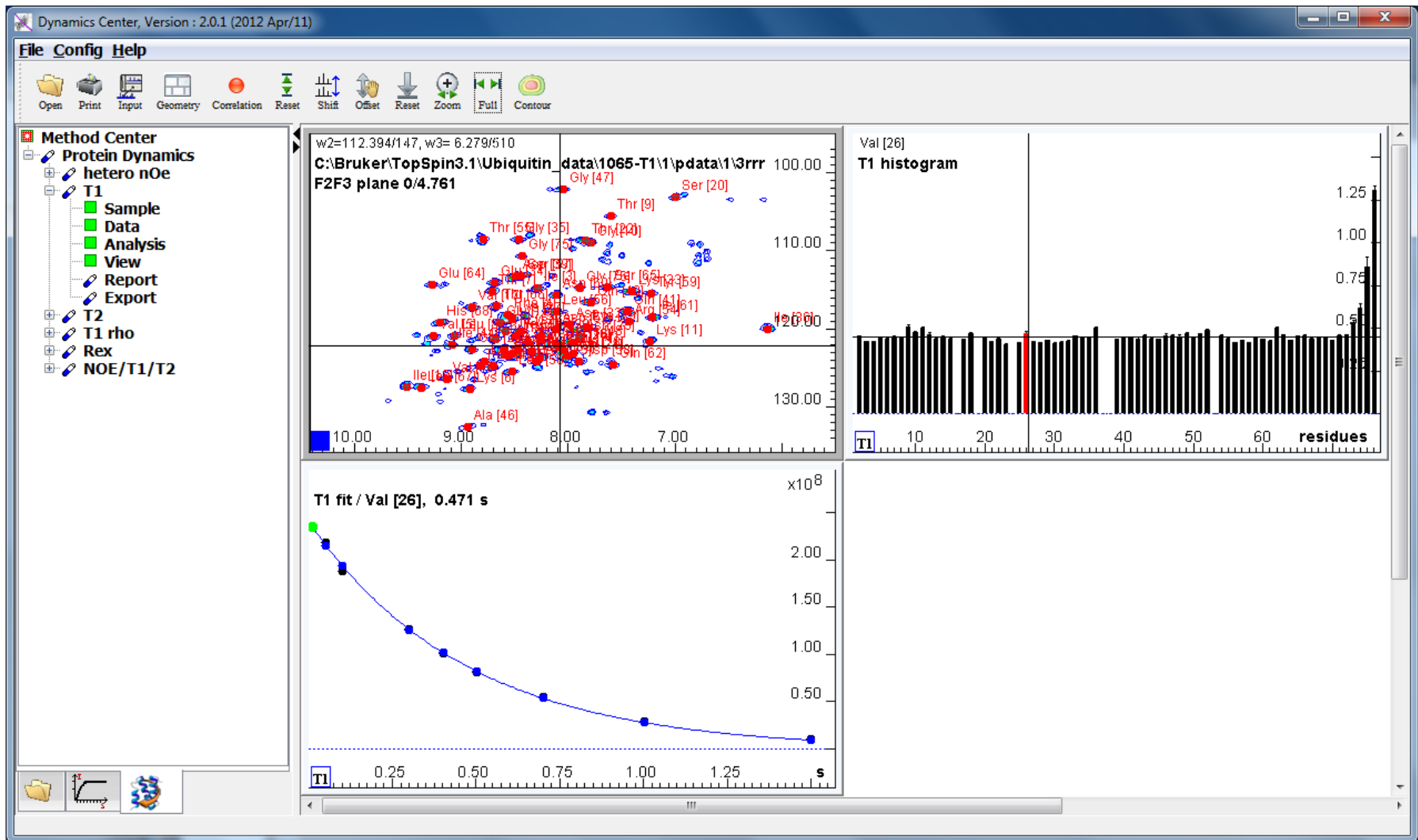


The screenshot displays the Dynamics Center software interface. On the left is a 'Method Center' tree with a blue arrow pointing to the 'View' option. The main window shows a 2D NMR spectrum with peaks labeled 'Ser [20]' and 'Ile [36]'. A dialog box titled 'Details of result viewing' is open, containing the following options:

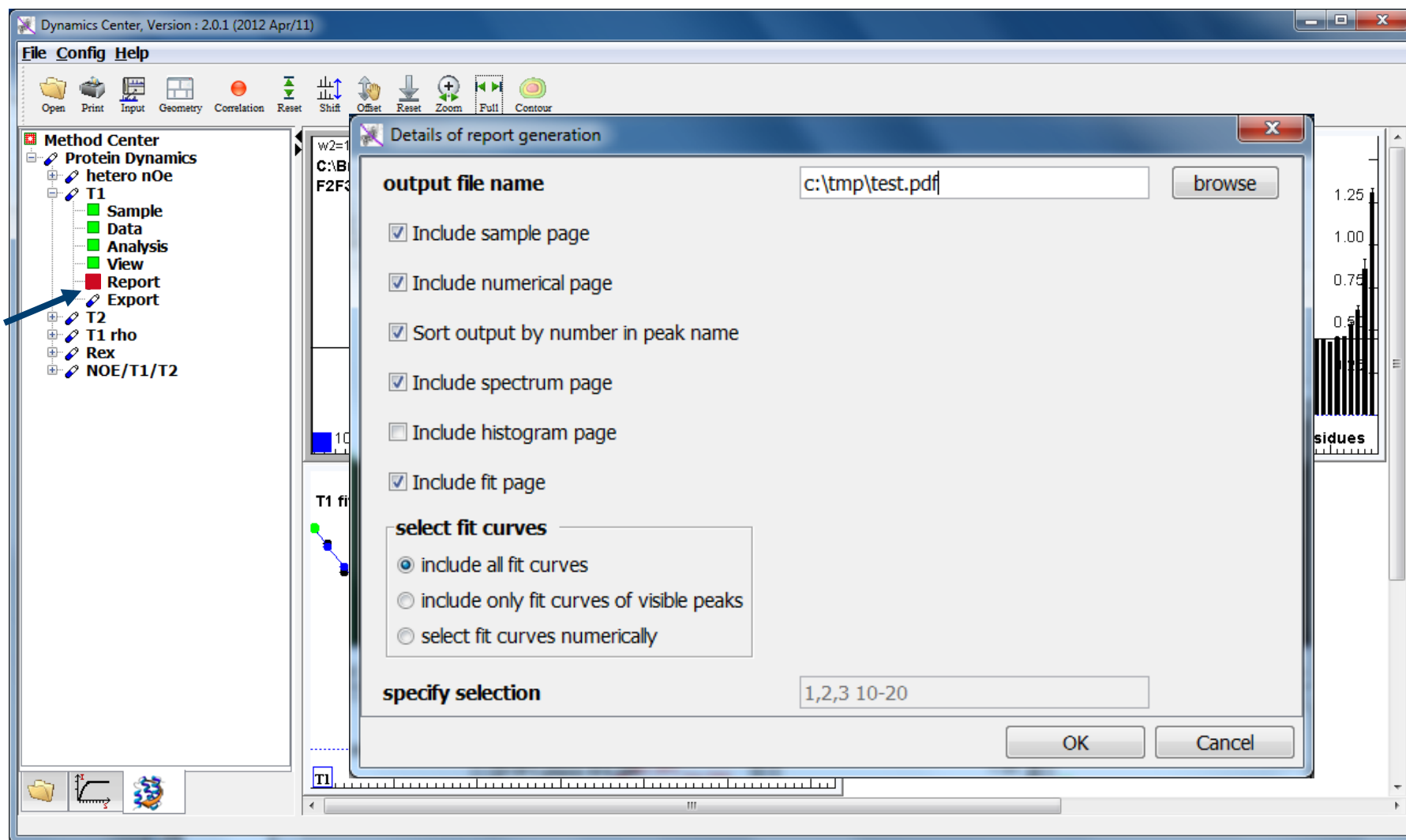
- Select how Fit gets displayed**
 - no interactive fit display
 - show T1 fit in separate internal window
 - show T1 fit in separate external window
- Select how Fit gets selected**
 - if cursor is moved close to peak
 - if left mouse button is clicked near peak
- Show error bars of integrals
- Logarithmic display of fit curve
- Show T1/Sequence histogram
- Show error bars of of Fit on histogram
- Show normalized Chi2/Sequence histogram

Buttons for 'OK' and 'Cancel' are at the bottom of the dialog box.

The New Dynamics Center...



The New Dynamics Center...



The New Dynamics Center...



Dynamics Center, Version : 2.0.1 (2012 Apr/11)

File Config Help

Open Print Input Geometry Correlation Reset Shift Offset Reset Zoom Full Contour

Method Center
Protein Dynamics
hetero nOe
T1
T2
T1 rho
Rex
NOE/T1/T2

w2=112.394/147, w3= 6.279/510
C:\Bruker\TopSpin3.1\Ubiquitin...data\1065-T1\1\pdata\1\3rrr
E2E3 plane 0/4.761
Gly [47] Ser [20]

Val [26]
T1 histogram

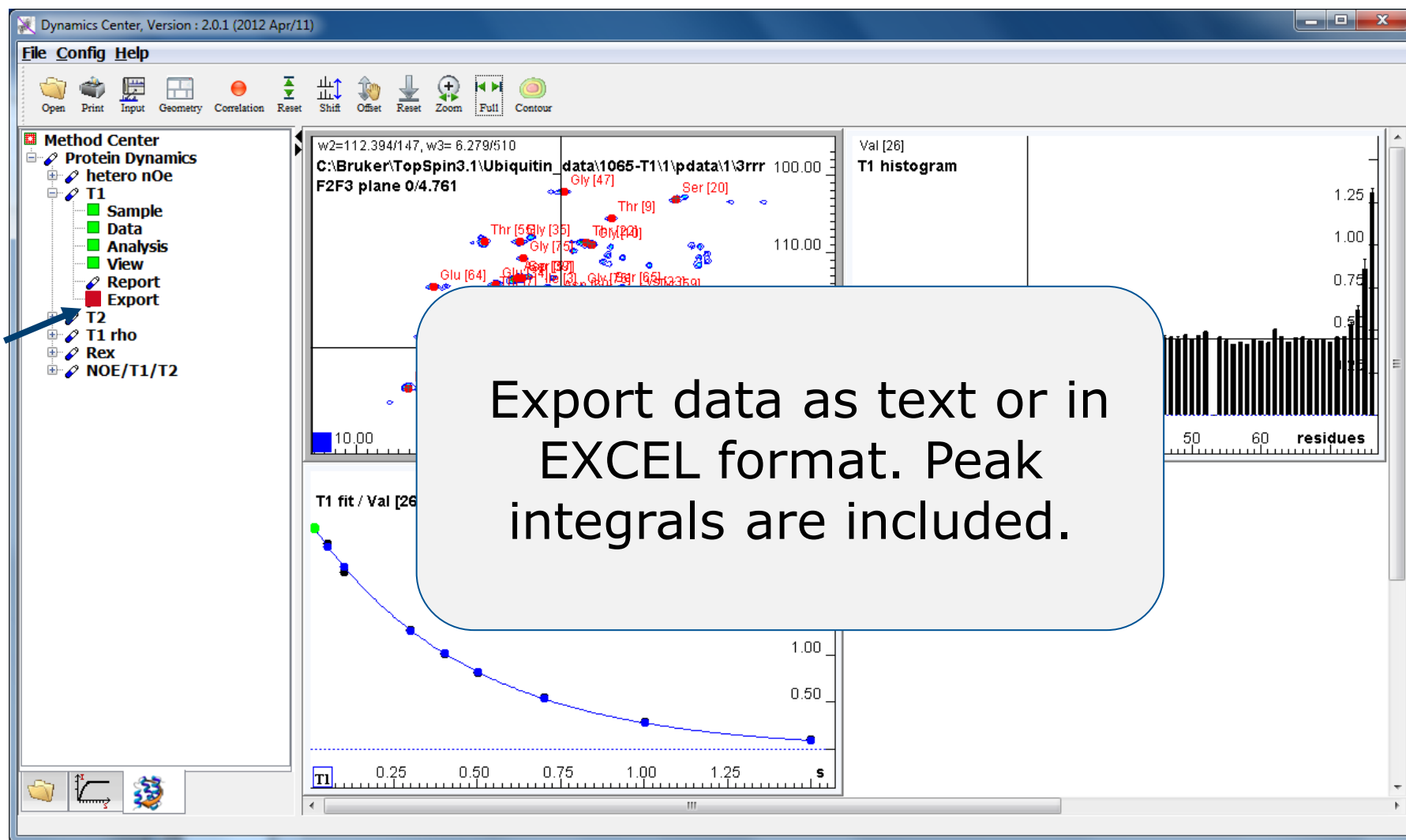
T1 Analysis
E:\data\dynamic\nmr\sample_ber561\pdata\1\3rrr

E:\data\dynamic\nmr\sample_ber561\pdata\1\3rrr
F2F3 plane 1/4.759, t = 0.500 s

T1 histogram

name	F1 [ppm]	F2 [ppm]	T1 [s]	Error [s]
GLN 2	122.669	8.898	0.466	0.029
ILE 3	114.800	8.288	0.435	0.036
PHE 4	118.172	8.565	0.423	0.020
VAL 5	121.063	9.264	0.449	1.1
LYS 6	127.647	8.931	0.431	0.035
THR 7	115.121	8.703	0.451	0.029
LEU 8	121.545	9.126	0.458	0.098
THR 9	105.488	7.605	0.505	0.097
GLY 10	108.858	7.792	0.475	0.052
LYS 11	121.545	7.238	1.26	0.026
THR 12	120.260	8.581	0.464	0.039
ILE 13	127.326	9.517	0.446	0.023
THR 14	121.223	8.679	0.456	0.0097
LEU 15	124.917	8.703	0.446	0.032
GLU 16	121.868	8.182	0.420	0.038
VAL 17	117.209	8.906	0.438	0.022
GLU 18	119.136	8.638	0.461	0.016
SER 20	103.237	7.002	0.449	0.012
ASP 21	123.472	8.011	0.417	0.0081
THR 22	108.537	7.881	0.431	0.091
ILE 23	120.902	8.483	0.417	0.011
ASN 25	121.063	7.889	0.415	0.0093
VAL 26	122.187	8.085	0.478	0.033
LYS 27	118.975	8.589	0.408	1.7
ALA 28	123.359	8.017	0.00	0.0
LYS 29	119.839	7.832	0.424	0.013

The New Dynamics Center...



The New Dynamics Center...



The screenshot displays the Dynamics Center software interface. On the left, the 'Method Center' tree shows a project named 'hetero nOe' with sub-items for 'Sample', 'Data', 'Analysis', 'View', 'Report', and 'Export'. Below this, there are sections for 'T1' and 'T2', each with similar sub-items. A red square icon is visible under the 'NOE/T1/T2' section, and a blue arrow points to it.

The central dialog box, titled 'Select (NOE, T1, T2) project files for multi-field modelling', is open. It features a 'number of field strengths' input field set to '1'. Below this, there are five groups of project files, each corresponding to a field strength. Each group contains three rows: 'NOE project file', 'T1 project file', and 'T2 project file'. The first group (field 1) has file paths: '\\Users\ecj\Documents\uqi_hetnoe.proj', 'C:\Users\ecj\Documents\uqi_t1.proj', and 'C:\Users\ecj\Documents\uqi_t2.proj'. The subsequent groups (fields 2-5) have '???' in the file path fields. Each row includes a 'browse' button.

On the right side of the screenshot, two plots are visible. The top plot is a 'histogram' showing the distribution of 'residues' on the x-axis (ranging from 0 to 60) and a y-axis ranging from 0 to 1.50. The bottom plot is a 'fit / Gln [62], 0.507 s' showing a decay curve with data points and a fitted line. The x-axis is labeled 's' and ranges from 0 to 1.50, with a scale factor of $\times 10^8$.

The New Dynamics Center...



The screenshot shows the Dynamics Center software interface with a dialog box titled "Select details for modelling relaxation parameters". The dialog box has four tabs: "Settings", "TauC", "Reduced SD", and "Isotropic modelling". The "Settings" tab is active, showing the following options:

- Enter NH bond length: 1.02 Angstrom
- Enter chemical shift anisotropy: -160.0 ppm
- Improved model fitting may be done with multiple (e.g. 1000) random selections of the start parameters.
- Number of iterations (>= 0): 0
- Depending on previous fits and availability of repetition experiments, errors of T1, T2 and NOE might be quite small
- This may lead to problems during mdl fitting.
- Override calculated errors with defaults
- Default error of T1 values: 2.0 %
- Default error of T2 values: 2.0 %
- Default error of NOE values: 2.0 %

The background shows the Dynamics Center interface with a file menu, a toolbar, and a tree view on the left. A blue arrow points to the "Analysis" option under the "NOE/T1/T2" category in the tree view. The main window displays two plots: a 2D correlation plot and a 1D plot showing a peak at 1.00 s.

The New Dynamics Center...



Dynamics Center, Version : 2.0.1 (2012 Apr/11)

File Config Help

Open Print Input Geometry Correlation Reset Shift Offset Re

Method Center

- Protein Dynamics
 - hetero nOe
 - Sample
 - Data
 - Analysis
 - View
 - Report
 - Export
 - T1
 - Sample
 - Data
 - Analysis
 - View
 - Report
 - Export
 - T2
 - Sample
 - Data
 - Analysis
 - View
 - Report
 - Export
 - T1 rho
 - Rex
 - NOE/T1/T2
 - Data
 - Analysis
 - View
 - Report
 - Export

W2=125.476163
C:\Bruker\TopSp
F2F3 plane 0/4.7

W2=125.476163
C:\Bruker\TopSp
F2F3 plane 0/4.7

T2⁰⁰

Select details for modelling relaxation parameters

Settings **TauC** Reduced SD Isotropic modelling Anisotropic modelling

Calculation of global isotropic TauC can be restricted to certain ranges of values of T1, T2 and NOE

Residues with NOEs smaller than a given value (including negative) can be excluded

Check NOE values

Lowest NOE value (e.g. 0.65)

Residues with T2 smaller than mean - n * stdev can be excluded

Check T2 values

Number of stdev (e.g. 1)

Residues with T2 too large compared to T1 $(T2 - T2_{\text{mean}}) / T2 > n * (T1 - T1_{\text{mean}}) / T1$ can be excluded

Check T1 and T2 values

Number of ratios (e.g. 3)

OK Cancel

1.50
1.25
1.00
0.75
0.50

40 residues

507 s $\times 10^8$

2.00
1.50
1.00
0.50

1.00 s

The New Dynamics Center...



The screenshot displays the Dynamics Center software interface. On the left, a tree view under 'Method Center' shows 'Protein Dynamics' expanded to 'hetero nOe', with 'Analysis' selected. A blue arrow points to this 'Analysis' option. The main window shows two NMR spectra plots. A dialog box titled 'Select details for modelling relaxation parameters' is open, with the 'Reduced SD' tab selected. The dialog contains the following text:

With the available T1, T2 and NOE values reduced spectral densities $J(0)$, $J(0.87\omega_H)$, $J(\omega_N)$ are calculated and $D_{||} / D_{\perp}$ of the diffusion tensor is estimated.

Furthermore, R_{ex} and S_2 can be estimated.

- Calculate spectral densities & estimate $D_{||} / D_{\perp}$
- Estimate R_{ex} from reduced spectral densities
- Estimate S_2 from reduced spectral densities

The dialog box also features 'OK' and 'Cancel' buttons at the bottom. In the background, a plot shows a histogram of residues (0 to 40) with a peak at approximately 35 residues, and a curve showing a decay over time (0 to 1.00 s) with a value of 507×10^8 .

The New Dynamics Center...



The screenshot displays the Dynamics Center software interface. On the left, a tree view shows the project structure under 'Method Center' and 'Protein Dynamics', with 'NOE/T1/T2' selected. The main window shows two NMR spectra plots. A dialog box titled 'Select details for modelling relaxation parameters' is open, featuring tabs for 'Settings', 'TauC', 'Reduced SD', 'Isotropic modelling', and 'Anisotropic modelling'. The 'Isotropic modelling' tab is active, showing five models (M1-M5) with their respective spectral density functions and checkboxes for 'order parameter fit'. The 'NOE/T1/T2' item in the tree view is highlighted with a blue arrow.

Select details for modelling relaxation parameters

Settings | TauC | Reduced SD | **Isotropic modelling** | Anisotropic modelling

With the available T1, T2 and NOE values and the calculated overall TauC, order parameters can be fitted to various models assuming isotropic tumbling.

M1: spectral density ~ S2 (TauC fixed)

order parameter fit of Model M1

M2: spectral density ~ TauE, S2 (TauC fixed)

order parameter fit of Model M2

M3: spectral density ~ S2, Kex (TauC fixed)

order parameter fit of Model M3

M4: spectral density ~ TauE, S2, Rex (TauC fixed)

order parameter fit of Model M4

M5: spectral density ~ TauS, Ss², Sf² (TauC fixed, TauF=0)

order parameter fit of Model M5

OK Cancel

Method Center
Protein Dynamics
hetero noe
Sample
Data
Analysis
View
Report
Export
T1
Sample
Data
Analysis
View
Report
Export
T2
Sample
Data
Analysis
View
Report
Export
T1 rho
Rex
NOE/T1/T2
Data
Analysis
View
Report
Export

w2=12E.476'63
C:\Bruker\TopSp
F2F3 plane 0/4.7

C:\Bruker\TopSp
F2F3 plane 0/4.7

residues

507 s

1.00 s

The New Dynamics Center...



The screenshot displays the Dynamics Center software interface. On the left, a tree view under 'Method Center' shows 'Protein Dynamics' expanded to 'hetero nOe', with 'Analysis' selected. A blue arrow points to this 'Analysis' item. The main window shows two NMR spectra plots. A dialog box titled 'Select details for modelling relaxation parameters' is open, with the 'Anisotropic modelling' tab selected. The dialog contains the following text and options:

The assumption of isotropic tumbling is not valid in many cases. If the protein structure is available the anisotropic diffusion tensor can be calculated.

- Fit diffusion tensor to T1/T2 values

Local motions can be modelled assuming overall anisotropic diffusion

TM1: spectral density $\sim S^2$

- order parameter fit of Model TM1

TM2: spectral density $\sim \text{TauE}, S^2$

- order parameter fit of Model TM2

TM3: spectral density $\sim S^2, \text{Kex}$

- order parameter fit of Model TM3

TM4: spectral density $\sim S^2, \text{TauE}, \text{Kex}$

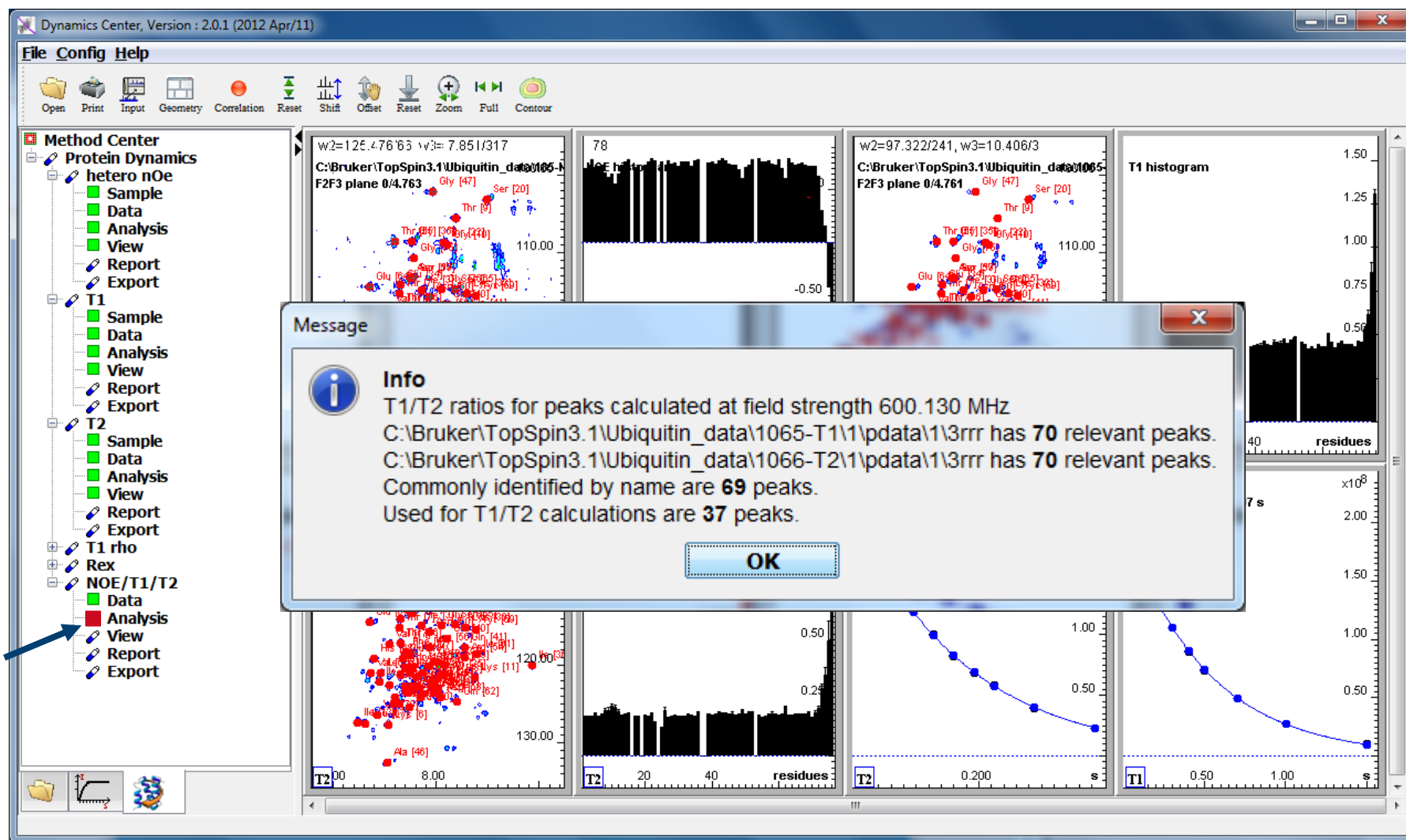
- order parameter fit of Model TM4

TM5: spectral density $\sim S^2, \text{Sf2}, \text{TauS}$

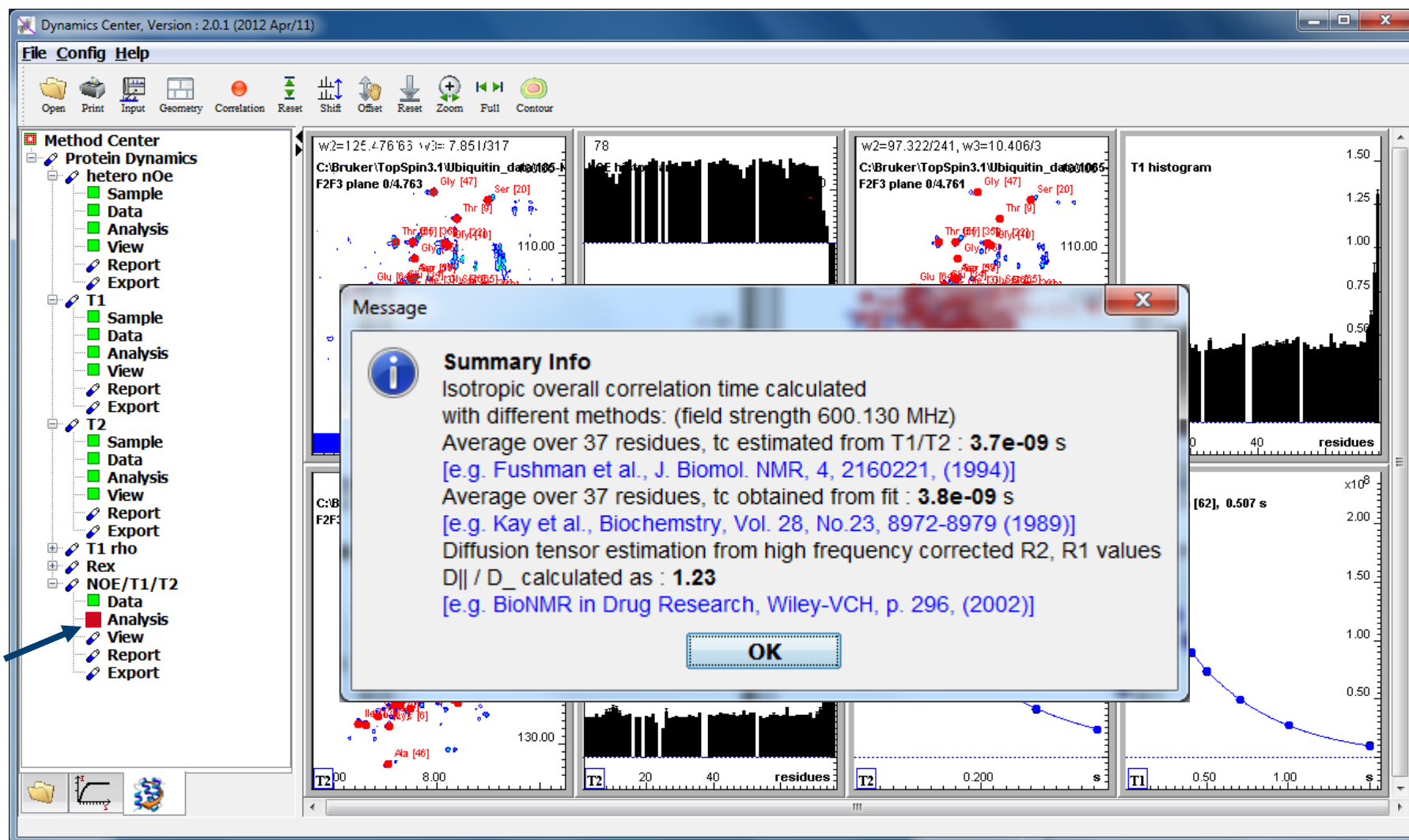
- order parameter fit of Model TM5

At the bottom of the dialog are 'OK' and 'Cancel' buttons. To the right of the dialog, a plot shows a histogram of residues (0-40) with a peak at approximately 1.50. Below it, a plot shows a curve of relaxation times (0-1.00 s) with a peak at approximately 507 s.

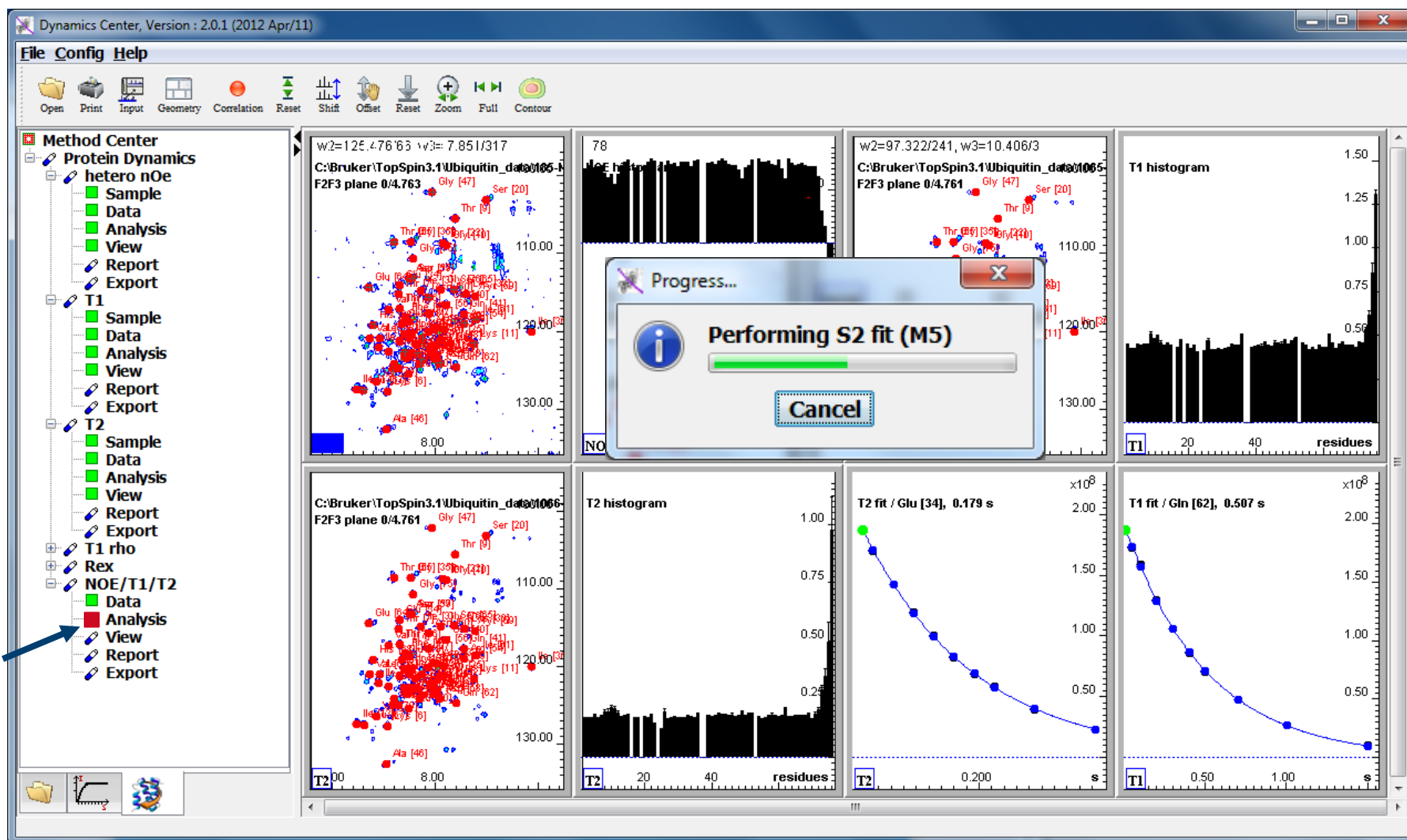
The New Dynamics Center...



The New Dynamics Center...



The New Dynamics Center...



The New Dynamics Center...



The screenshot displays the Dynamics Center software interface (Version 2.0.1, 2012 Apr/11). The interface includes a menu bar (File, Config, Help), a toolbar with icons for Open, Print, Input, Geometry, Correlation, Reset, Shift, Offset, Zoom, Full, and Contour, and a left-hand navigation pane. The navigation pane is organized into sections: Method Center, Protein Dynamics, hetero nOe, T1, T2, Rex, and NOE/T1/T2. A blue arrow points to the 'Analysis' option under the NOE/T1/T2 section.

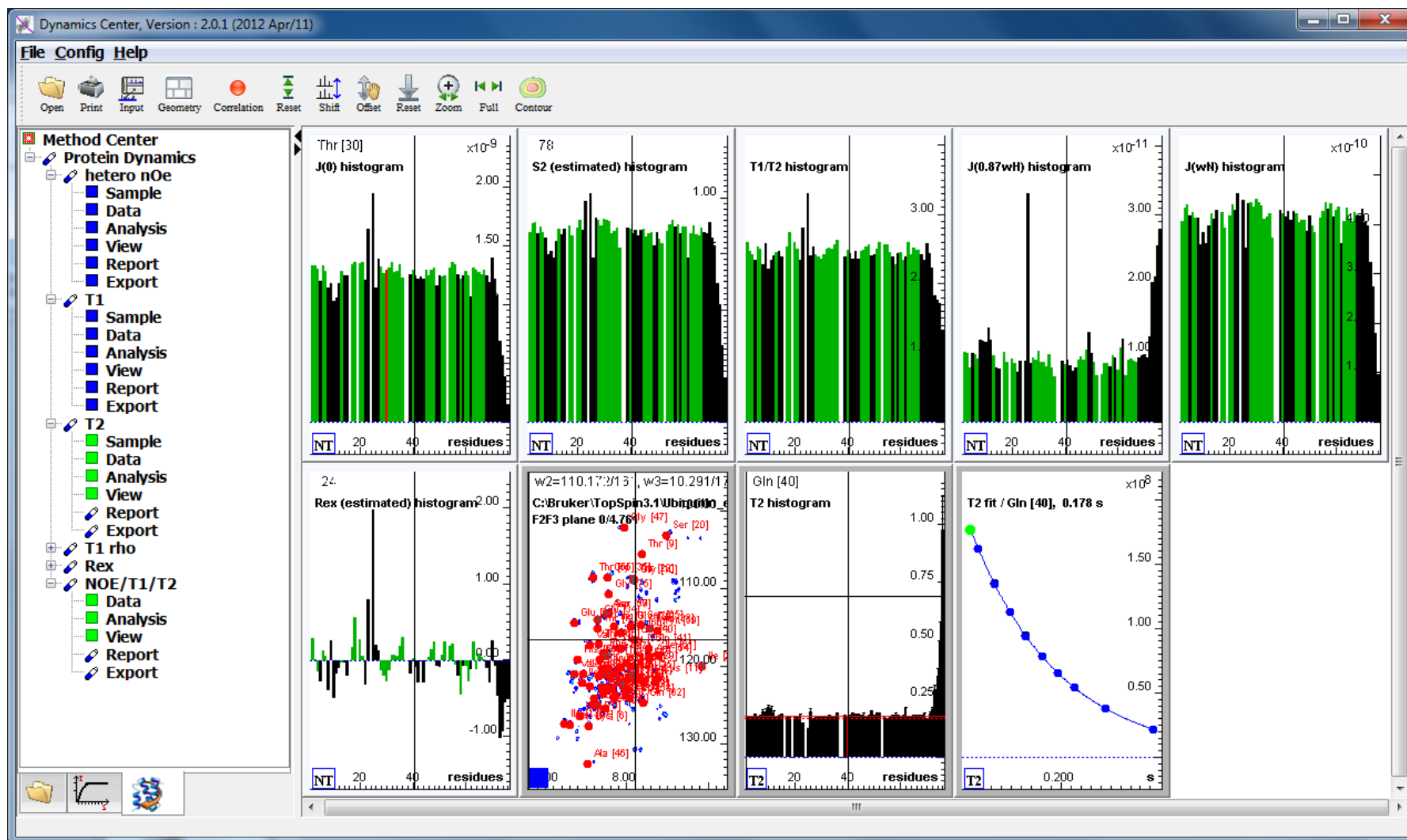
The main workspace contains several plots: two 2D F2F3 planes (w2=125.476/63, w3=7.851/317 and w2=97.322/241, w3=10.406/3), a T1 histogram, and a T1 fit plot for Gln [62] at 0.507 s. A central message dialog box is open, displaying the following information:

Message

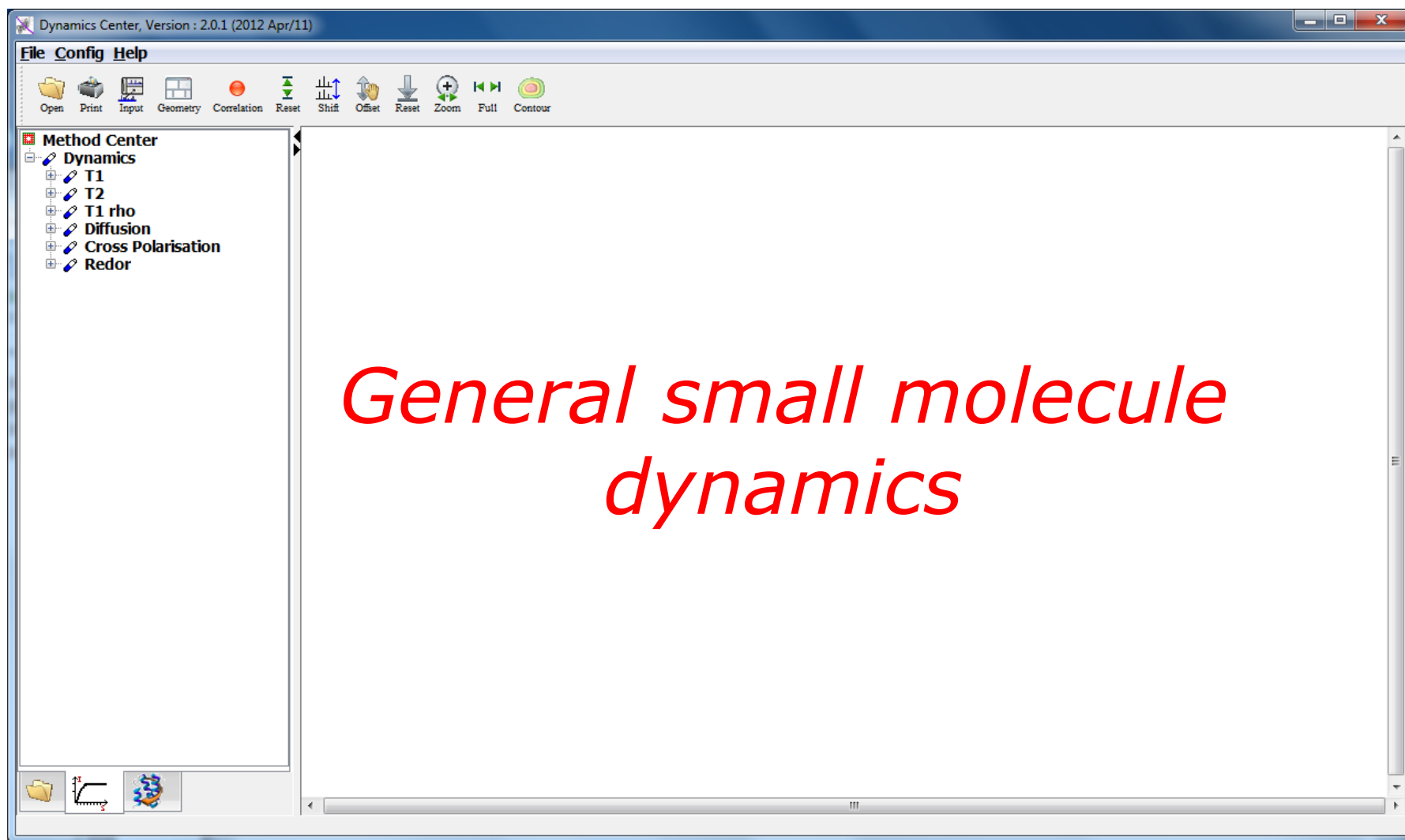
Info
Fit of the full anisotropic diffusion tensor yields
[\[e.g. Ghose et al., J. Mag. Res., 149, 204-217 \(2001\)\]](#)
alpha = 82 +/- 0.152 1/s
beta = 29 +/- 0.0636 1/s
gamma = 13 +/- 0.383 1/s
Dxx = 4.09e+07 +/- 5.04e+05 1/s
Dyy = 4.21e+07 +/- 4.94e+05 1/s
Dzz = 4.86e+07 +/- 5.91e+05 1/s
anisotropy = 1.17
rhombicity = 0.243
tc = 1/6Diso = 3.80e-09 s

OK

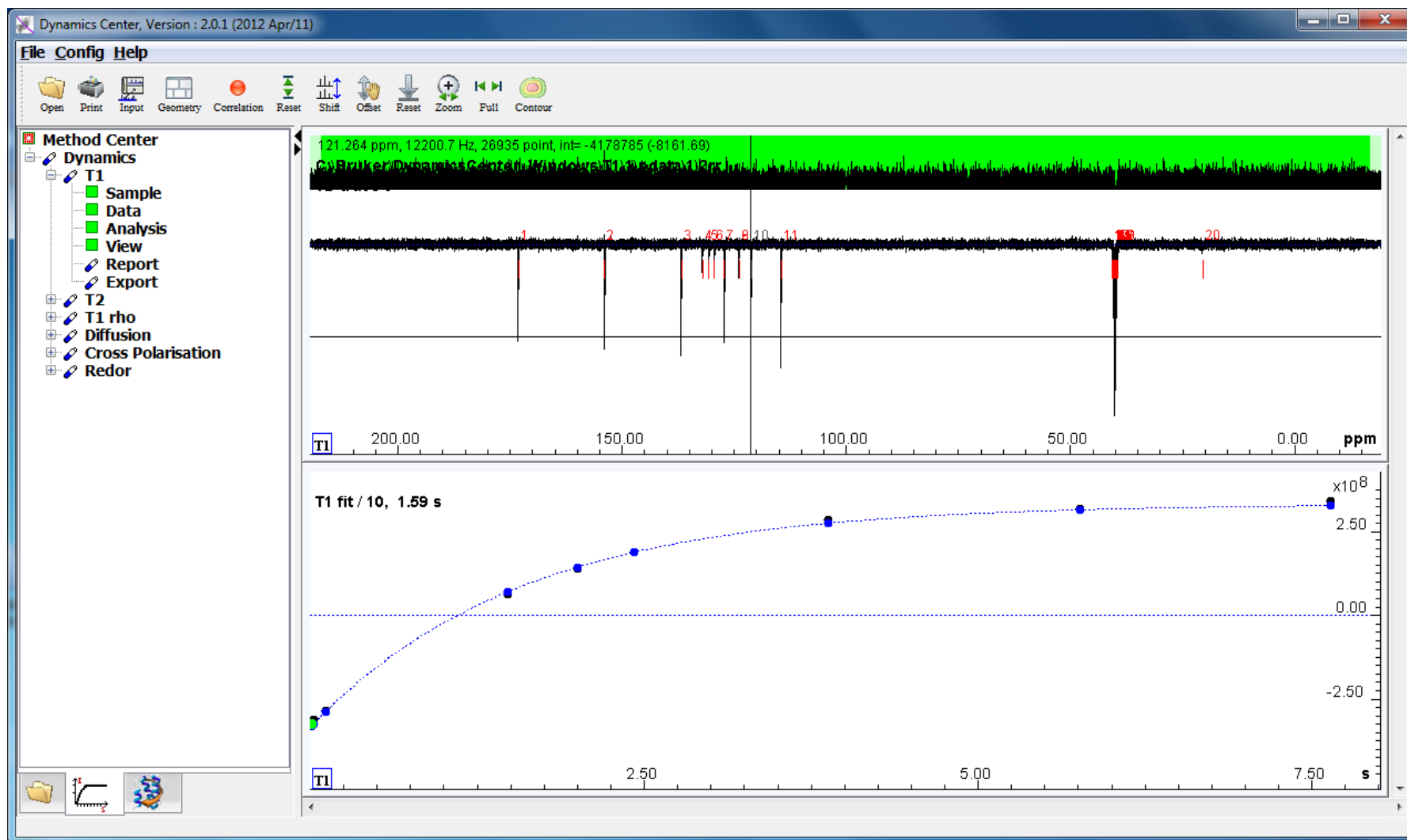
The New Dynamics Center...



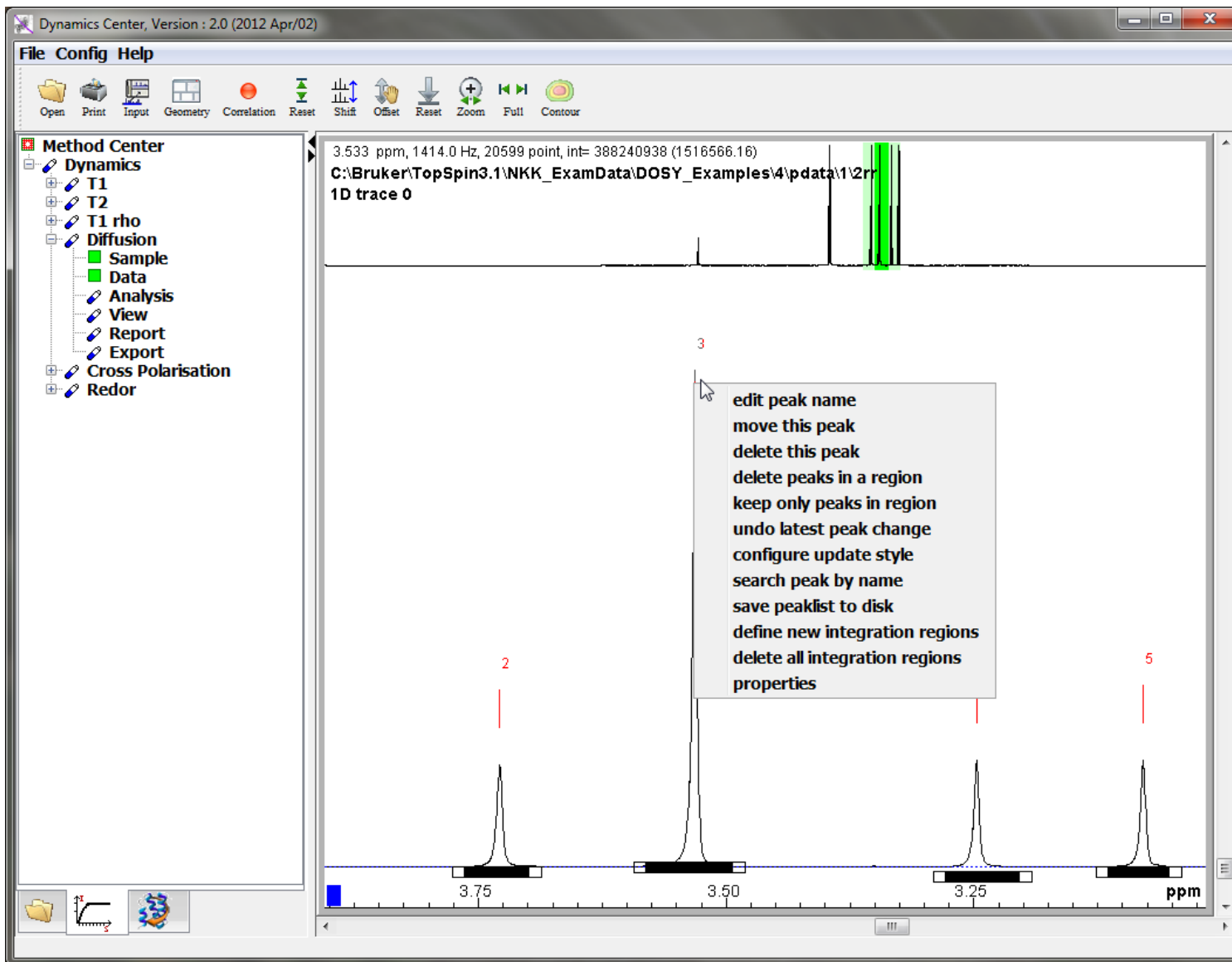
New in Dynamics Center v2.0



New in Dynamics Center v2.0



Inclusion of Diffusion analysis



Inclusion of Diffusion analysis

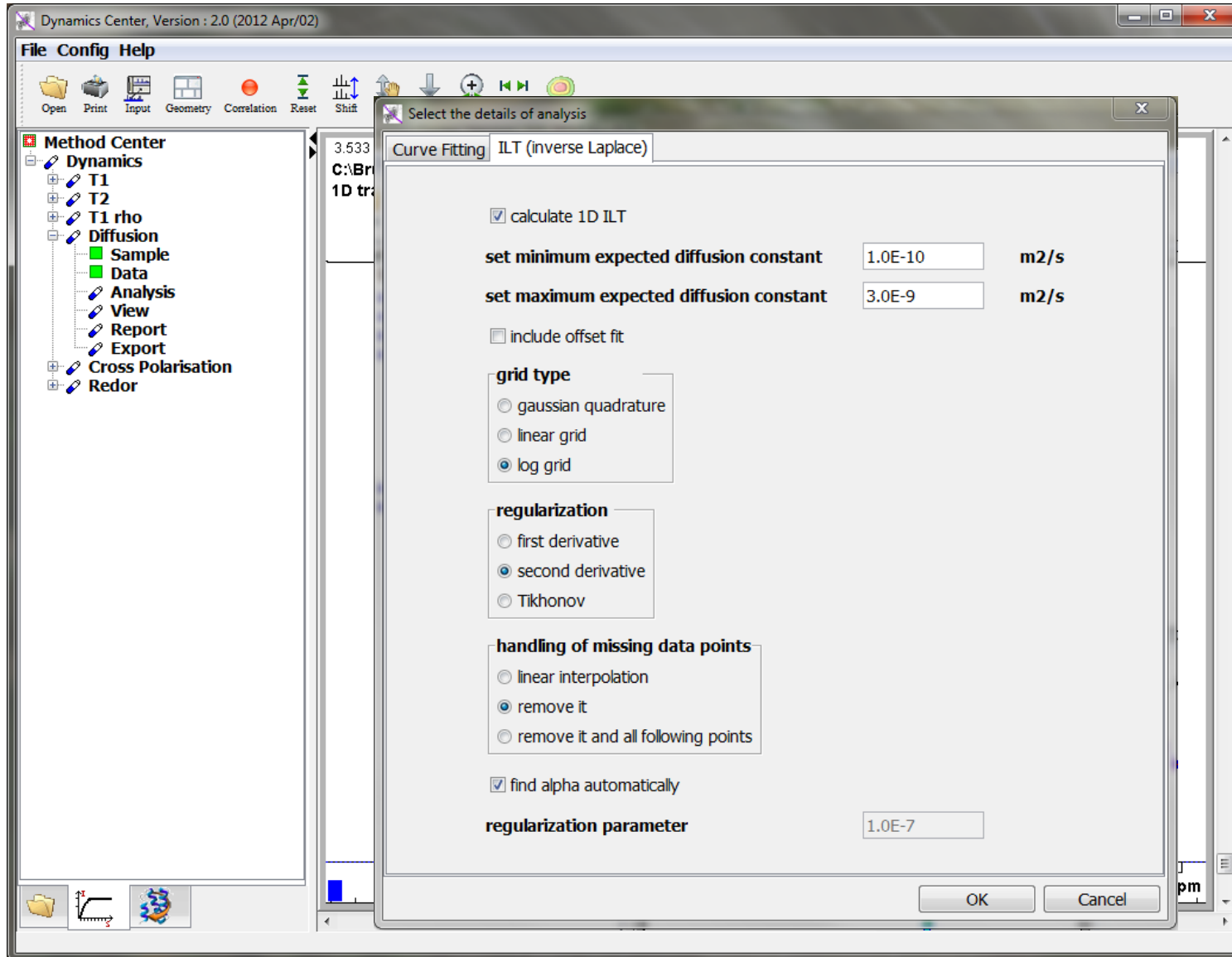


The screenshot displays the Bruker Dynamics Center software interface. The main window shows a file explorer on the left with a tree view containing 'Method Center', 'Dynamics', 'T1', 'T2', 'T1 rho', 'Diffusion', 'Sample', 'Data', 'Analysis', 'View', 'Report', 'Export', 'Cross Polarisation', and 'Redor'. The central pane shows a 1D trace at 3.533 ppm, 1414.0 Hz, with the file path 'C:\Bruker\TopSpin3\1D trace 0'. A dialog box titled 'Select the details of analysis' is open, showing the 'Curve Fitting' tab with the 'ILT (inverse Laplace)' method selected. The dialog includes the following settings:

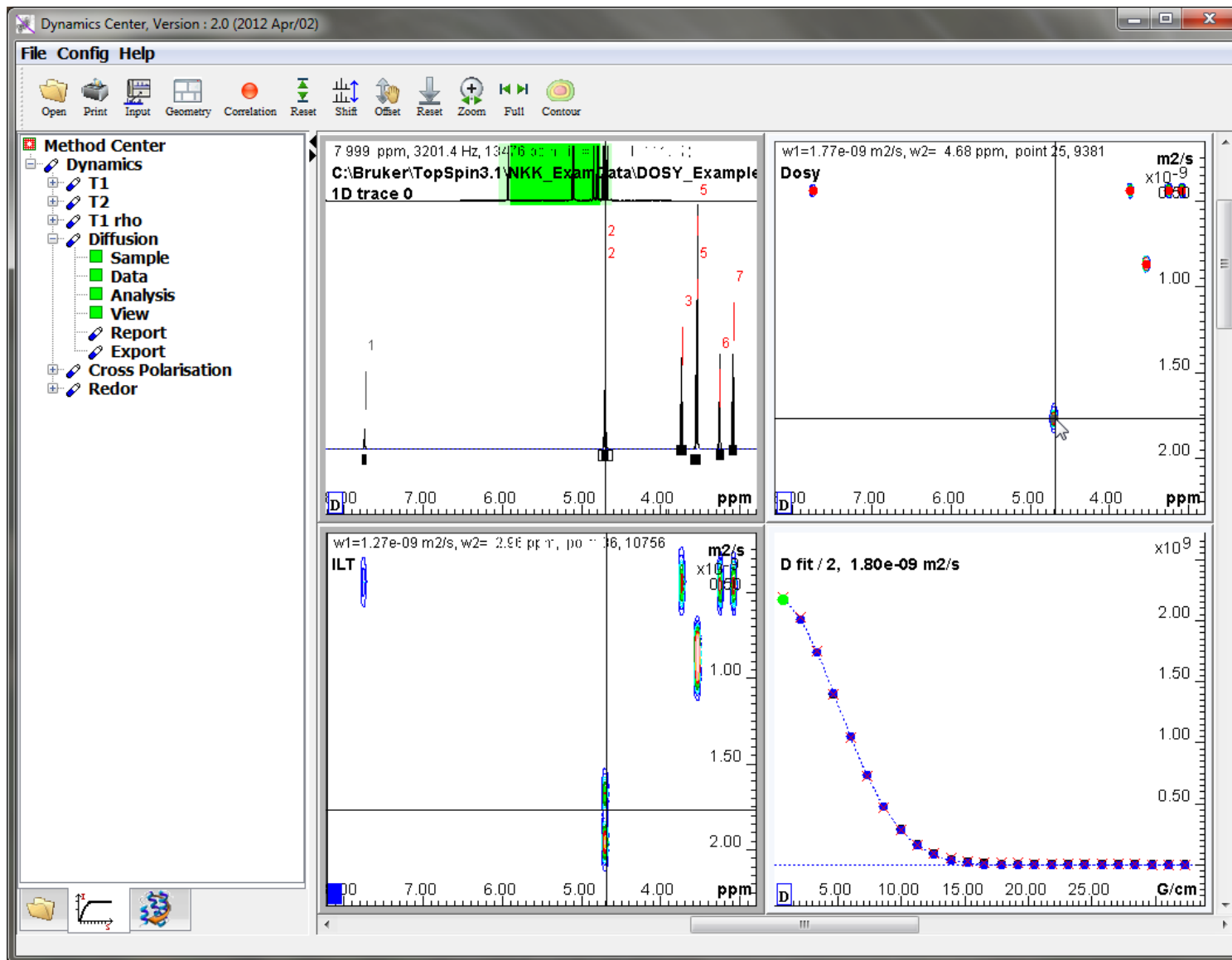
- Select Diffusion fit function:** $f(g) = I_0 * e^{(-\gamma^2 * g^2 * \delta^2 * (\Delta-\delta/3)*D)}$ is selected.
- number of function components:** 1
- assume constant offset term
- Use the notation $y = p[0]*func(x...$ with parameters $p[0], p[1], ...$ variable called x , and func like sin, exp, log, ...**
- number of parameters:** 1
- function equation:** $y = p[0]*exp(-p[1]*x*x)$
- Provide comma separated default parameters**
- default values (comma separated):** 0.0, 0.0
- Provide comma separated parameter units e.g. s, m, none**
- parameter units (comma separated):** s, m
- Fit parameter error estimation can be based on different methods**
- Select error estimation method:** error estimation by fit is selected.
- Fitted parameters are calculated and given with a confidence interval**
- Confidence level:** 95.0 %

The dialog box has 'OK' and 'Cancel' buttons at the bottom. A small plot of the 1D trace is visible in the background on the right side of the dialog.

Inclusion of diffusion analysis



Inclusion of diffusion analysis



Availability



PC Dynamics Center | Bruker BioSpin - Mozilla Firefox

Datei Bearbeiten Ansicht Chronik Lesezeichen Extras Hilfe

PC Dynamics Center | Bruker BioS... +

www.bruker-biospin.com/sw_nmr_win_protein.html

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 - PC TopSpin
 - PC TopSpin Processing Only
 - PC XWIN-NMR
 - PC IconNMR
 - PC XWIN-PLOT
 - PC AUREMOL
 - PC MOLMOL
 - PC Dynamics Center**
 - Linux Amix/Aurelia
 - Linux TopSpin
 - Linux TopSpin Processing Only
 - Linux XWIN-NMR
 - Linux IconNMR
 - Linux XWIN-PLOT
 - Linux Dynamics Center
 - Mac OS X TopSpin Processing Only

Dynamics Center

2.0 for Windows XP/Vista/Win 7

To download the current Dynamics Center version, click on the link and follow the instructions provided in the Readme file. Please store the file on your hard disk and start the installation when the download is complete.

PC Dynamics Center -- Release Download

For Bruker intranet users:
You need to [log in on the Web site](#) in order to see the release downloads.

License information

- The Dynamics Center contains a general dynamics part which is free to use if a TOPSPIN_1D or PROTEIN_DYNAMIC2 license is available. The Dynamics Center also contains the former Protein Dynamics Center. It requires a PROTEIN_DYNAMIC2 license.

Free demo licenses can be obtained by filling out the **license form**. Supply the host ID of the machine on which the demo license should be installed.

PC Dynamics Center -- Tutorial Download

For Bruker intranet users:
You need to [log in on the Web site](#) in order to see the release downloads.

Tutorial information

- Two tutorials (one for protein dynamics, one for general dynamics) are available. Both contain sample spectra and a pdf which describes the various exercises.

Language: select language

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Dynamics Center 2.0 now available

- On http://www.bruker-biospin.com/sw_nmr_win_protein.html
- On Bruker software DVD TS 3.1 PL6
- Directly in TS (starting TS 3.2)

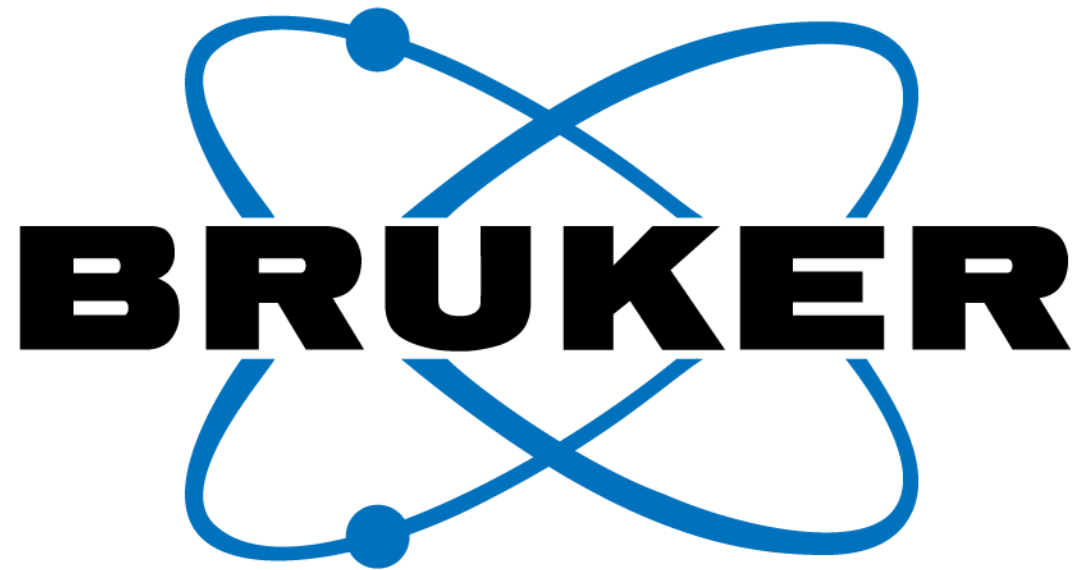
Licenses

- General dynamics is free.
- Protein dynamics needs license PROTEIN_DYNAMIC2

Platforms

- Windows XP/Vista/7
- Linux CentOS 5

**Thank
You**



www.bruker-biospin.com