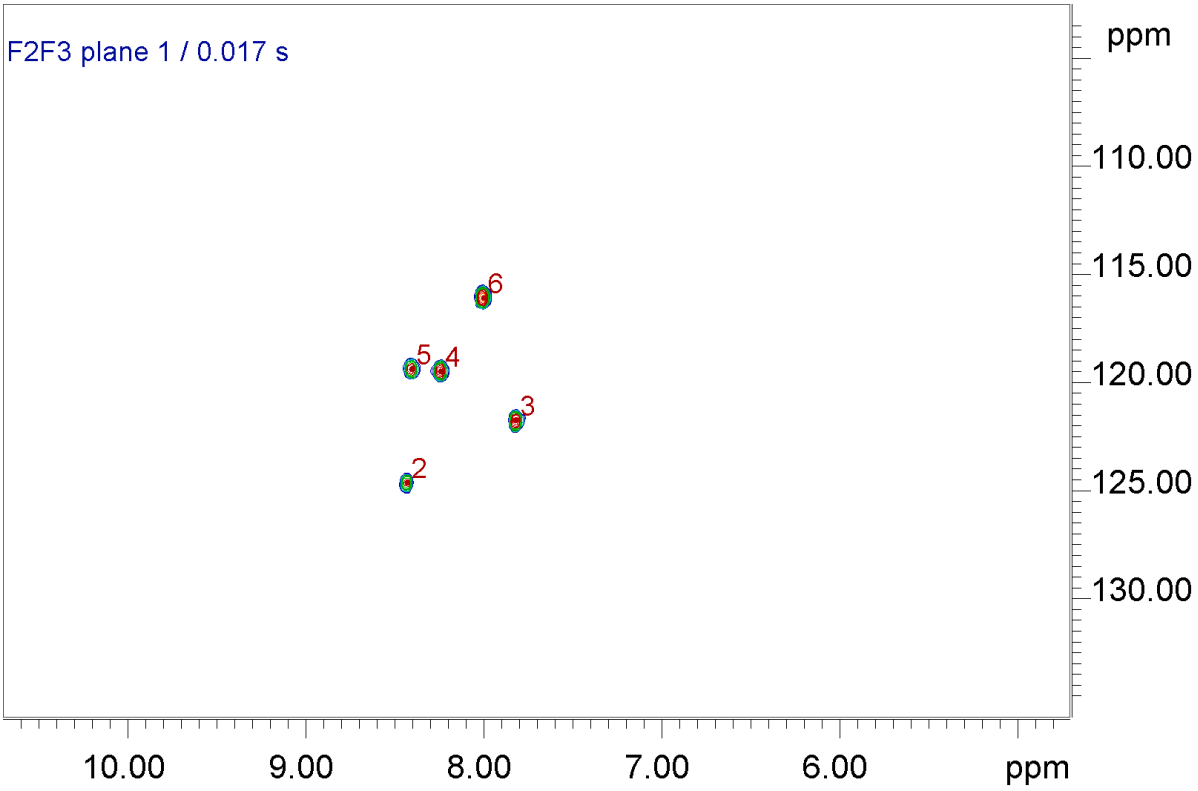
• T2 Analysis

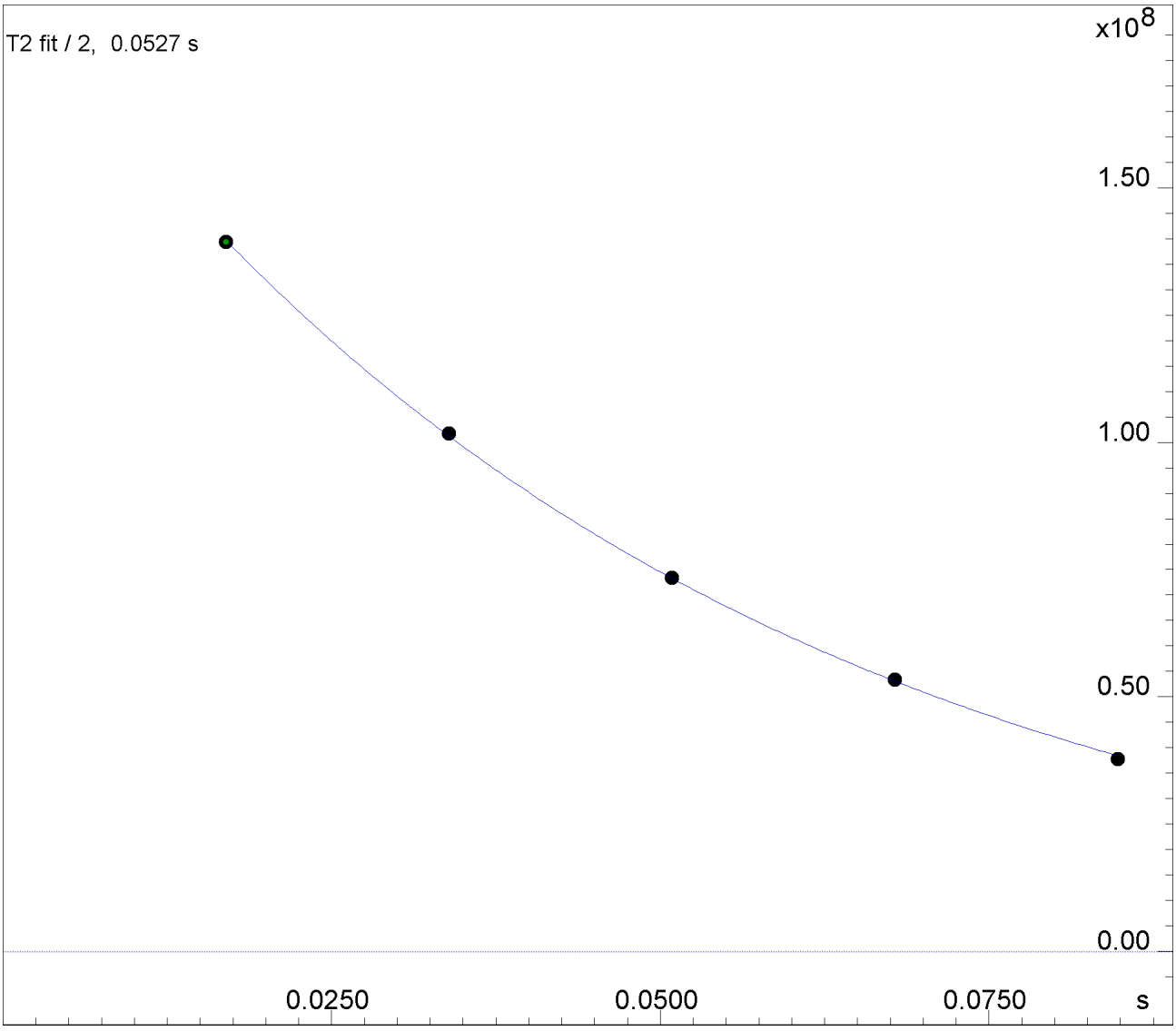
sample name:	ubiquitine
Description/Title:	standard demo sample
Origin:	in-house
Date of preparation:	06 / 2005
Solvent:	D2O
pH:	7.0
Sample tube:	normal
Tube diameter (mm):	3
Concentration (mM):	10.00
Temperature (K):	308.0
Weight (Daltons):	8900
Correlation time (ns):	12.40
Labelling:	15N
AminoAcid storage:	SEQ file
AminoAcid file:	/opt/data/nmrsu/nmr/sample/ubiquitine.seq
PDB file:	/opt/data/nmrsu/nmr/sample/ubiquitine.pdb

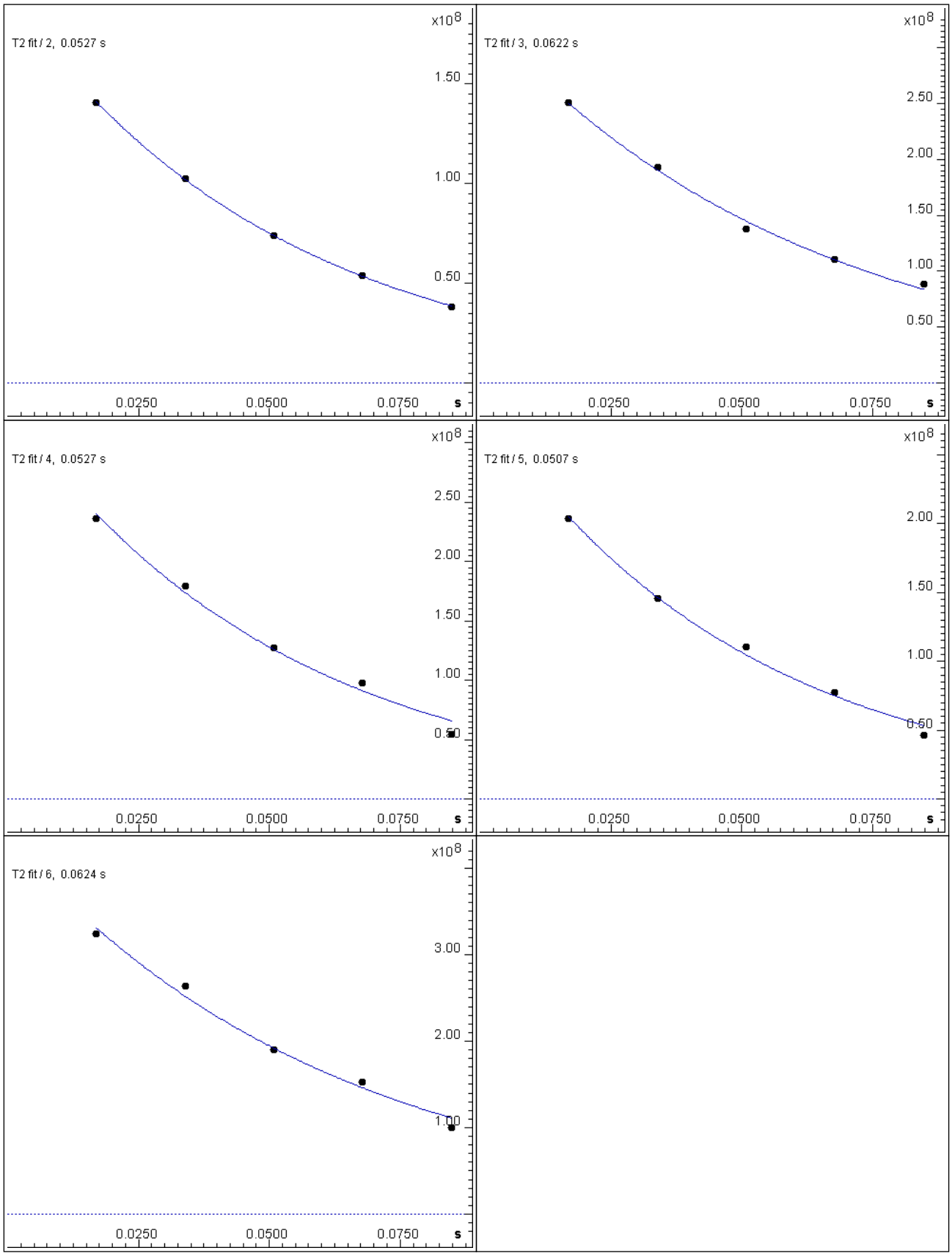

F2F3 plane 1 / 0.017 s
ppm
110.00
115.00
120.00
125.00
130.00
6
5
4
3
2
10.00
9.00
8.00
7.00
6.00
ppm

Fitted function:	f(t) = Io * exp (-t/T)
Random error estimation of data:	RMS per spectrum (or trace/plane)
Systematic error estimation of data:	worst case per peak scenario
Fit parameter Error estimation method:	from fit using arbitray y uncertainties
Confidence level:	95%
Used peaks:	automatically picked peaks
Used integrals:	peak intensities
Used Time:	all values (including replicates) used

Peak name	F1 [ppm]	F2 [ppm]	T2 [s]	error	fitInfo
2	124.625	8.425	0.0527	0.001285	Done
3	121.756	7.816	0.0622	0.008432	Done
4	119.467	8.238	0.0527	0.01155	Done
5	119.371	8.402	0.0507	0.008522	Done
6	116.083	7.998	0.0624	0.01382	Done

Current fit display




T2 fit / 2, 0.0527 s
x10^8
1.50
1.00
0.50
0.0250
0.0500
0.0750
s
T2 fit / 3, 0.0622 s
x10^8
2.50
2.00
1.50
1.00
0.50
0.0250
0.0500
0.0750
s
T2 fit / 4, 0.0527 s
x10^8
2.50
2.00
1.50
1.00
0.50
0.0250
0.0500
0.0750
s
T2 fit / 5, 0.0507 s
x10^8
2.00
1.50
1.00
0.50
0.0250
0.0500
0.0750
s
T2 fit / 6, 0.0624 s
x10^8
3.00
2.00
1.00
0.0250
0.0500
0.0750
s