

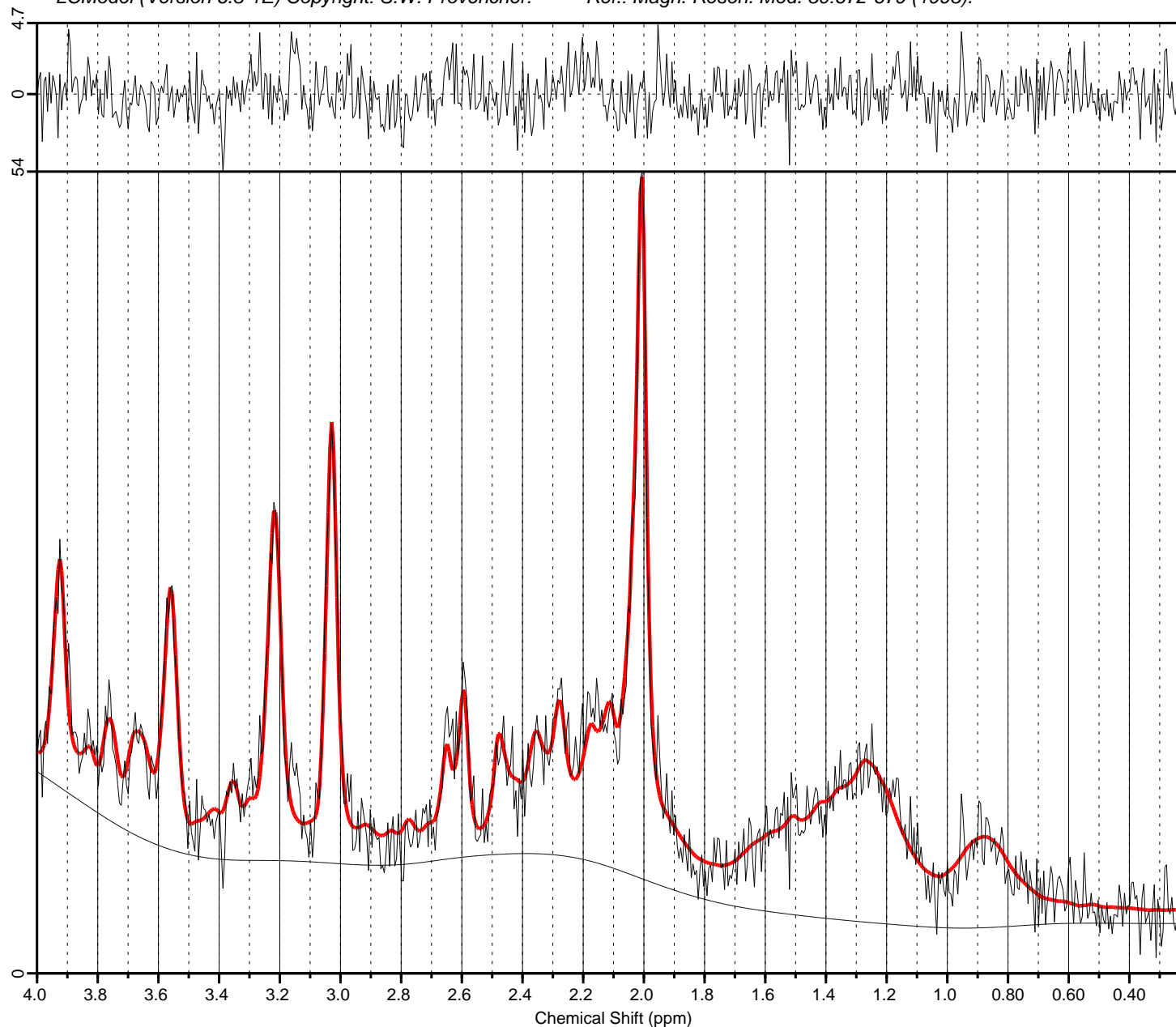
PLOT 1: Page 1 of test run output

Data of: Biomedizinische NMR Forschungs GmbH, Goettingen

LCModel (Version 6.3-1E) Copyright: S.W. Provencher.

Ref.: Magn. Reson. Med. 30:672-679 (1993).

16-November-2013 19:39



Conc.	%SD	/Cr	Metabolite
0.205	147%	4.0E-02	Ala
0.372	116%	7.2E-02	Asp
5.133	4%	1.000	Cr
0.518	77%	0.101	GABA
0.000	999%	0.000	Glc
1.730	38%	0.337	Gln
5.311	11%	1.035	Glu
0.815	24%	0.159	GPC
0.687	29%	0.134	PCh
4.227	6%	0.823	Ins
0.178	174%	3.5E-02	Lac
6.071	4%	1.183	NAA
1.142	24%	0.223	NAAG
6.90E-02	108%	1.3E-02	Scyllo
1.441	29%	0.281	Tau
1.016	28%	0.198	-CrCH2
0.259	97%	5.1E-02	Gua
1.502	5%	0.293	GPC+PCh
7.213	4%	1.405	NAA+NAAG
7.041	12%	1.372	Glu+Gln
14.054	19%	2.738	Lip13a
0.000	999%	0.000	Lip13b
0.000	999%	0.000	Lip09
4.860	18%	0.947	MM09
1.440	79%	0.280	Lip20
8.283	19%	1.614	MM20
1.687	32%	0.329	MM12
6.002	26%	1.169	MM14
3.125	32%	0.609	MM17
14.054	19%	2.738	Lip13a+Lip13b
21.743	13%	4.236	MM14+Lip13a+L
4.860	18%	0.947	MM09+Lip09
9.723	17%	1.894	MM20+Lip20

DIAGNOSTICS

1 info RFALSI 11

MISCELLANEOUS OUTPUT

FWHM = 0.035 ppm S/N = 14
Data shift = 0.006 ppm
Ph: 48 deg -17.0 deg/ppm

INPUT CHANGES

NEACH=2
NAMEAC(1)='NAA'
NAMEAC(2)='NAAG'
hzpppm=84.47

PLOT 2: Page 2 of test run output
Data of: Biomedizinische NMR Forschungs GmbH, Goettingen

LCModel (Version 6.3-1E) Copyright: S.W. Provencher.

Ref.: Magn. Reson. Med. 30:672-679 (1993).

16-November-2013 19:39

Conc.	%SD	/Cr	Metabolite	NAMEAC(2)='NAAG'
0.205	147%	4.0E-02	Ala	hzpppm=84.47
0.372	116%	7.2E-02	Asp	ratipm = 2.0
5.133	4%	1.000	Cr	nunfil=2048 deltat=.0005
0.518	77%	0.101	GABA	FILPS='ps/fig_mrml.ps'
0.000	999%	0.000	Glc	FILRAW='../../../../doc/manual/figures/raw/test.RAW'
1.730	38%	0.337	Gln	,
5.311	11%	1.035	Glu	FILBAS='../../../../doc/manual/figures/test.basis'
0.815	24%	0.159	GPC	
0.687	29%	0.134	PCh	
4.227	6%	0.823	Ins	
0.178	174%	3.5E-02	Lac	
6.071	4%	1.183	NAA	
1.142	24%	0.223	NAAG	
6.90E-02	108%	1.3E-02	Scyllo	
1.441	29%	0.281	Tau	
1.016	28%	0.198	-CrCH2	
0.259	97%	5.1E-02	Gua	
1.502	5%	0.293	GPC+PCh	
7.213	4%	1.405	NAA+NAAG	
7.041	12%	1.372	Glu+Gln	
14.054	19%	2.738	Lip13a	
0.000	999%	0.000	Lip13b	
0.000	999%	0.000	-Lip09	
4.860	18%	0.947	MM09	
1.440	79%	0.280	Lip20	
8.283	19%	1.614	MM20	
1.687	32%	0.329	MM12	
6.002	26%	1.169	MM14	
3.125	32%	0.609	MM17	
14.054	19%	2.738	Lip13a+Lip13b	
21.743	13%	4.236	MM14+Lip13a+Lip13b+MM12	
4.860	18%	0.947	MM09+Lip09	
9.723	17%	1.894	MM20+Lip20	
DIAGNOSTICS				
1	info	RFALSI	11	
MISCELLANEOUS OUTPUT				
FWHM = 0.035 ppm S/N = 14				
Data shift = 0.006 ppm				
Ph: 48 deg -17.0 deg/ppm				
INPUT CHANGES				
NEACH=2				
NAMEAC(1)='NAA'				

PLOT 3: Page 3 of test run output

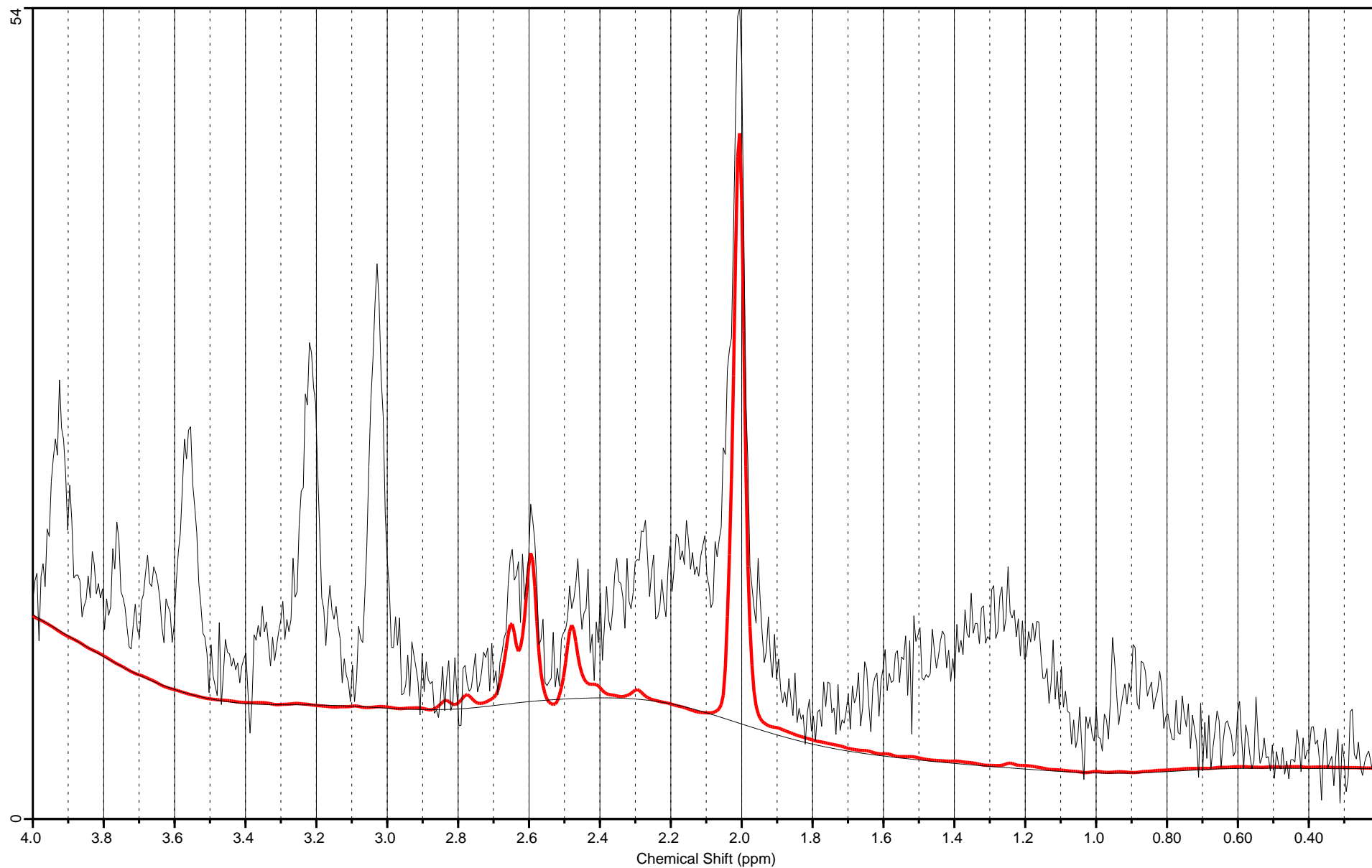
NAA Conc. = 6.07E+00

Data of: Biomedizinische NMR Forschungs GmbH, Goettingen

LCModel (Version 6.3-1E) Copyright: S.W. Provencher.

Ref.: Magn. Reson. Med. 30:672-679 (1993).

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PLOT 4: Page 4 of test run output

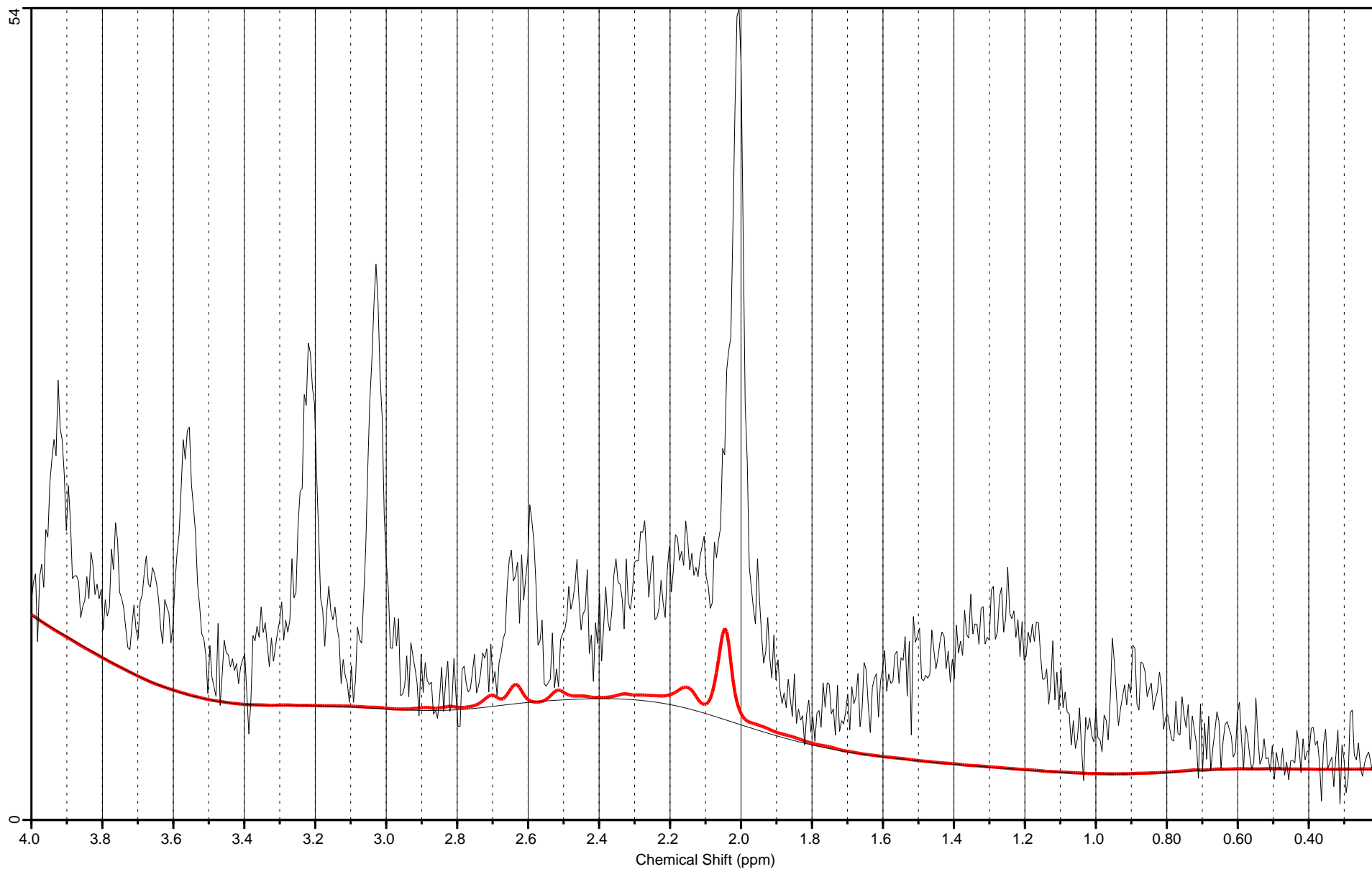
NAAG Conc. = 1.14E+00

Data of: Biomedizinische NMR Forschungs GmbH, Goettingen

LCModel (Version 6.3-1E) Copyright: S.W. Provencher.

Ref.: Magn. Reson. Med. 30:672-679 (1993).

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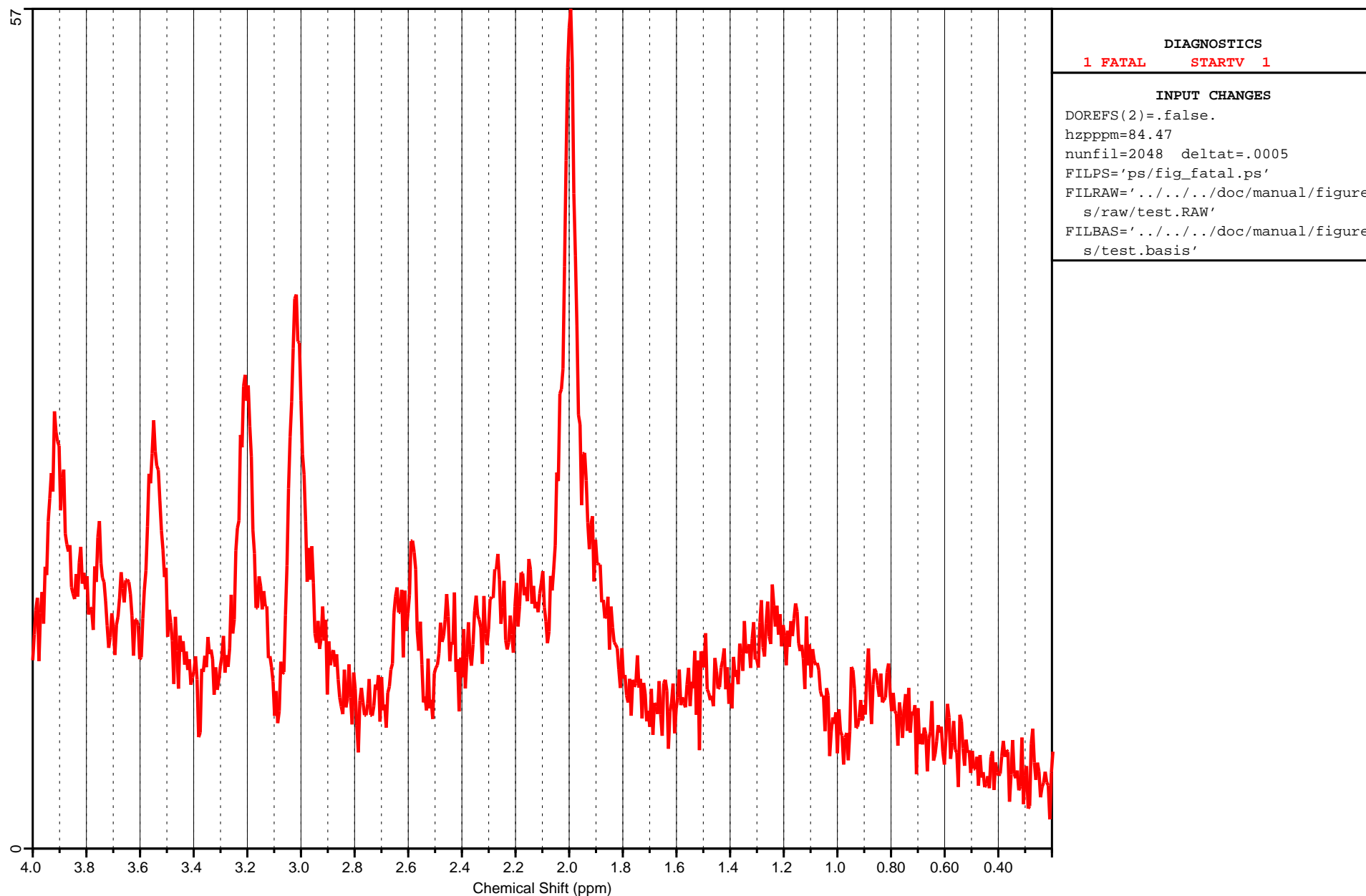
PLOT 5: Abort with FATAL diagnostic and Absolute-Value Plot due to unreasonable input.

Data of: Biomedizinische NMR Forschungs GmbH, Goettingen

LCModel (Version 6.3-1E) Copyright: S.W. Provencher.

Ref.: Magn. Reson. Med. 30:672-679 (1993).

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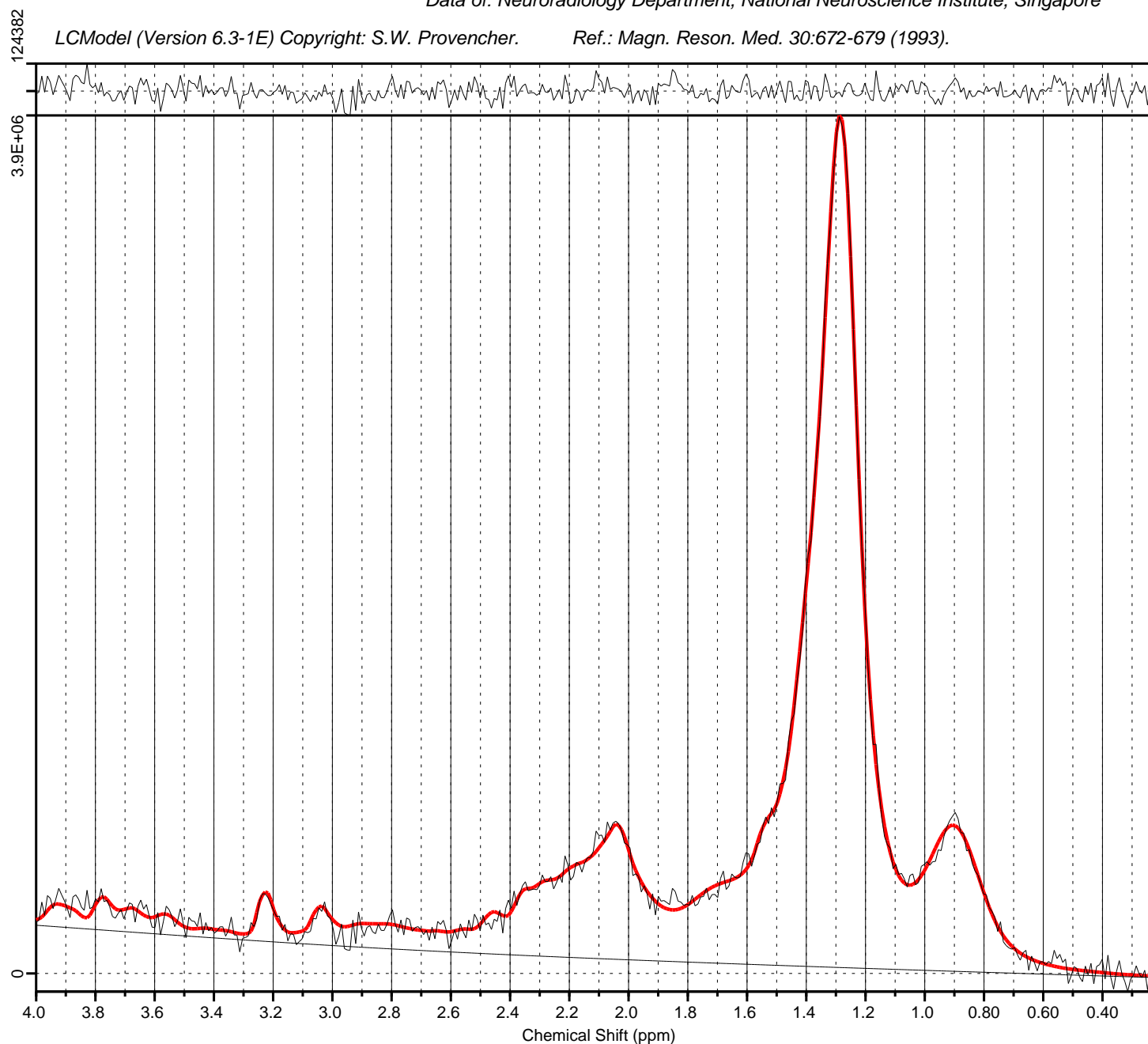
PLOT 6: Use SPTYPE='tumor' when NAA could be weaker than lipid or macromolecule signals.

Data of: Neuroradiology Department, National Neuroscience Institute, Singapore

LCModel (Version 6.3-1E) Copyright: S.W. Provencher.

Ref.: Magn. Reson. Med. 30:672-679 (1993).

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Conc.	%SD	/GPC+PC	Metabolite
2.049	30%	3.064	Ala
0.101	346%	0.152	Asp
0.431	172%	0.645	Cr
0.530	144%	0.792	PCr
0.152	142%	0.227	GABA
0.458	45%	0.684	Glc
5.263	26%	7.871	Gln
3.467	30%	5.185	Glu
0.669	14%	1.000	GPC
0.000	999%	0.000	PCh
0.391	84%	0.585	GSH
0.800	40%	1.196	Ins
0.000	999%	0.000	Lac
0.929	33%	1.389	NAA
0.160	44%	0.240	NAAG
4.56E-02	145%	6.8E-02	Scyllo
3.71E-02	704%	5.6E-02	Tau
0.000	999%	0.000	-CrCH2
0.669	14%	1.000	GPC+PCh
1.089	33%	1.628	NAA+NAAG
0.961	25%	1.437	Cr+PCr
8.731	10%	13.055	Glu+Gln

137.592	9%	205.744	Lip13a
34.850	38%	52.111	Lip13b
13.225	48%	19.776	Lip09
12.061	49%	18.035	MM09
11.780	25%	17.616	Lip20
17.312	15%	25.887	MM20
3.341	98%	4.996	MM12
23.183	33%	34.666	MM14
15.367	19%	22.979	MM17
172.442	6%	257.855	Lip13a+Lip13b
198.966	2%	297.517	MM14+Lip13a+L
25.286	8%	37.811	MM09+Lip09
29.092	8%	43.502	MM20+Lip20

DIAGNOSTICS	
Doing Water-Scaling	
MISCELLANEOUS OUTPUT	
FWHM = 0.057 ppm	S/N = 43
Data shift = 0.019 ppm	
Ph: -2 deg	1.2 deg/ppm

INPUT CHANGES	
SPTYPE='tumor'	
hzzppm=63.929 ipage2=0	

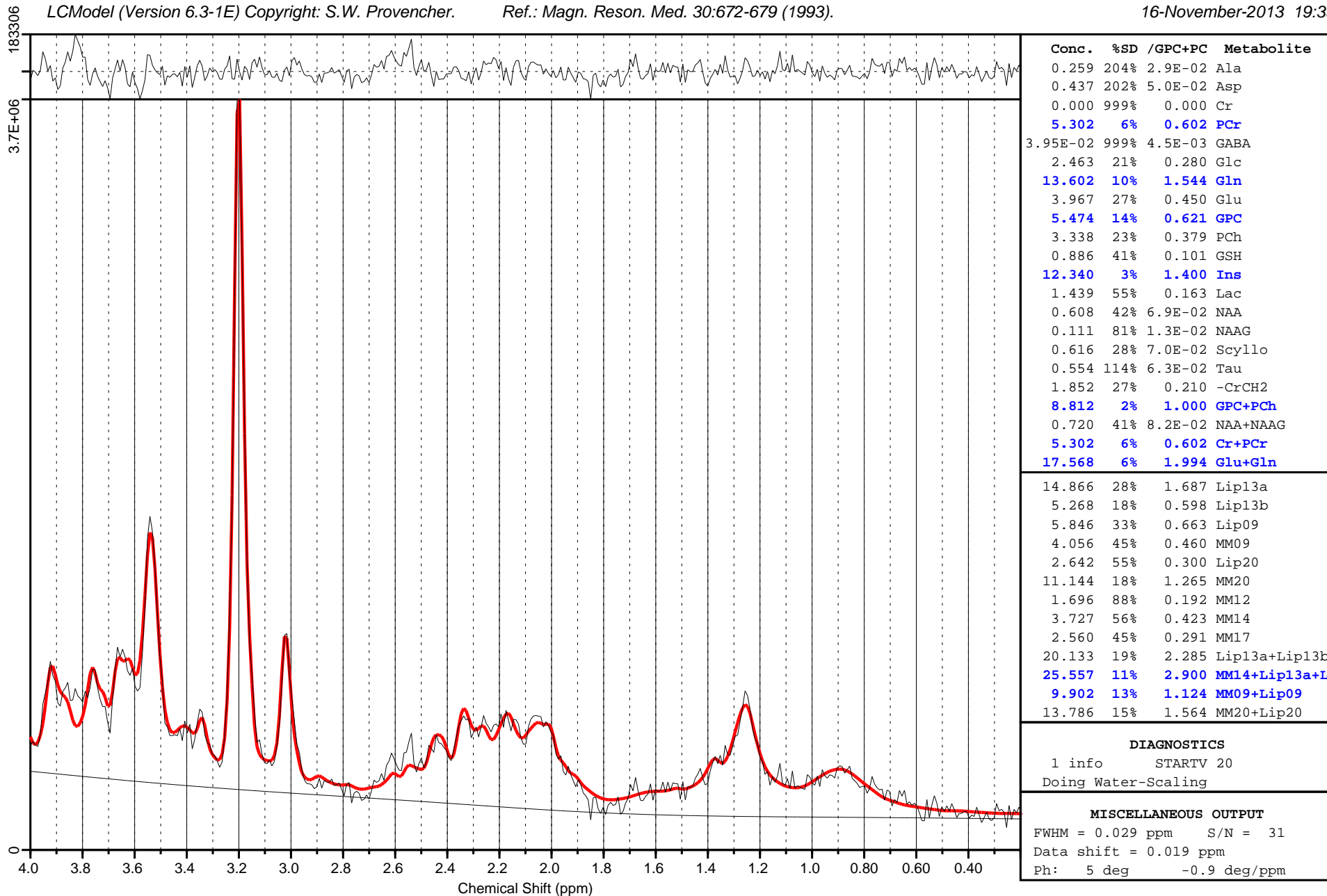
PLOT 7: Use SPTYPE='tumor' whenever the NAA signal may be weak (not just for strong lipid signals).

Data of: Department of Radiology, Childrens Hospital of Los Angeles

LCModel (Version 6.3-1E) Copyright: S.W. Provencher.

Ref.: Magn. Reson. Med. 30:672-679 (1993).

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PLOT 8: Muscle spectrum using SPTYPE='muscle-5'.

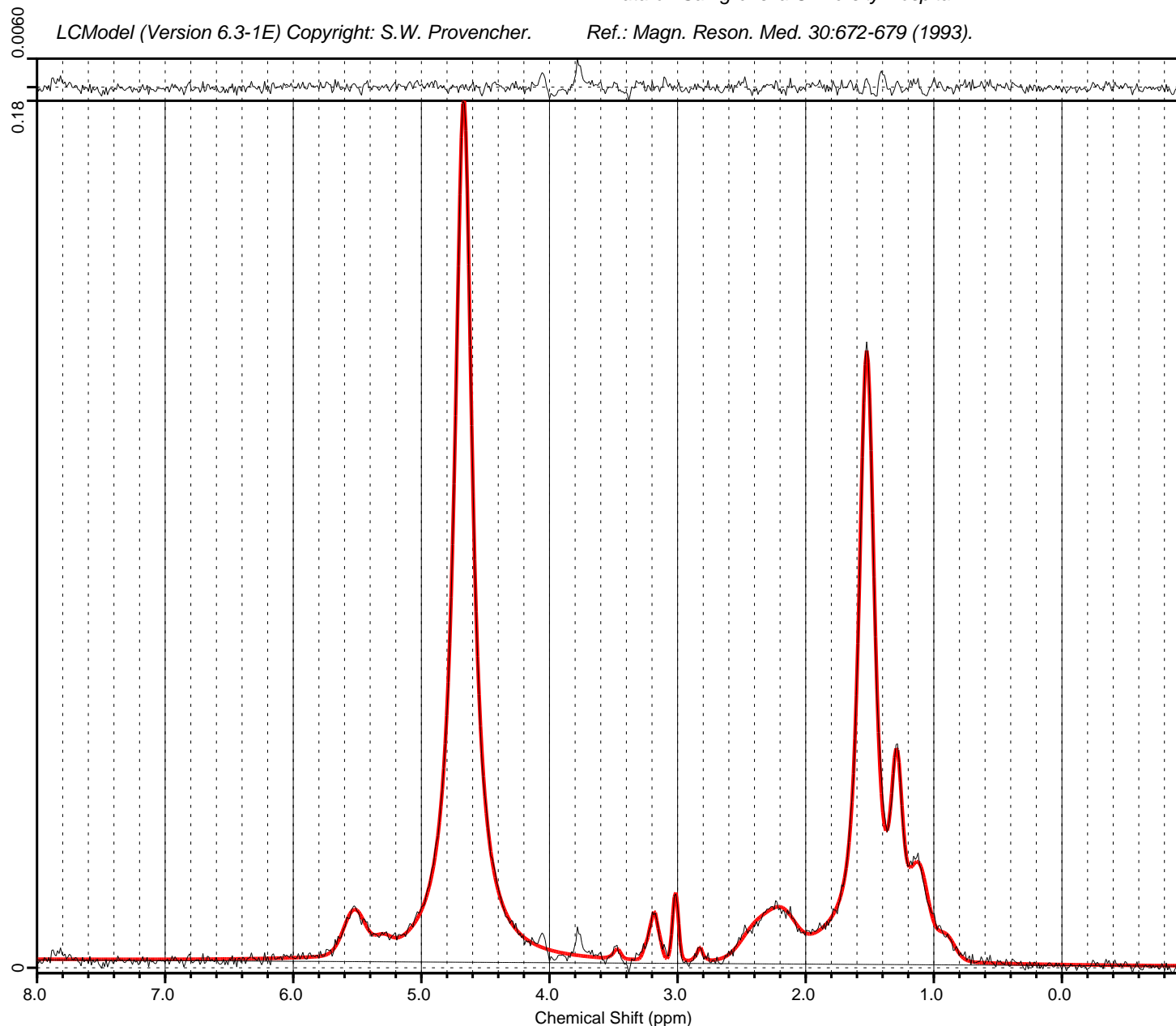
"Conc." values in the top table are ratios of the metabolite resonance area to the unsuppressed water resonance area.

Data of: Sahlgremska University Hospital

LCModel (Version 6.3-1E) Copyright: S.W. Provencher.

Ref.: Magn. Reson. Med. 30:672-679 (1993).

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Conc.	%SD	/Cr	Metabolite
5.08E-03	4%	6.140	IMCL13
2.43E-02	1%	29.364	EMCL15
8.27E-04	7%	1.000	Cr
9.10E-04	12%	1.100	I09
3.24E-03	5%	3.919	E11
4.71E-02	0%	56.981	Water
3.94E-04	19%	0.476	I53
1.94E-03	5%	2.339	E55
2.33E-03	4%	2.815	I53+E55
1.01E-03	6%	1.216	cho
3.46E-03	9%	4.182	I21
4.01E-03	8%	4.841	E23
1.48E-04	32%	0.179	tau
0.000	999%	0.000	cr39
1.72E-04	28%	0.208	cr28

DIAGNOSTICS

Doing Water-Scaling

MISCELLANEOUS OUTPUT

FWHM = 0.176 ppm S/N = 78

Data shift = 0.011 ppm

Ph: -3 deg 0.7 deg/ppm

INPUT CHANGES

SPTYPE='muscle-4'

ppmst=8.0 ppmend=-1.0

doecc=T, dows=T

hzpppm=63.897

nunfil=1024 deltat=6.667e-4

FILPS='ps/fig_muscle.ps'

FILh2o='../../../../doc/manual/figure
s/raw/IMCL11-1R.h2o'

FILRAW='../../../../doc/manual/figure
s/raw/IMCL11-1A.raw'

PLOT 9: Bone marrow spectrum (with no water suppression) using SPTYPE='lipid-8': For water & lipids only (no choline).

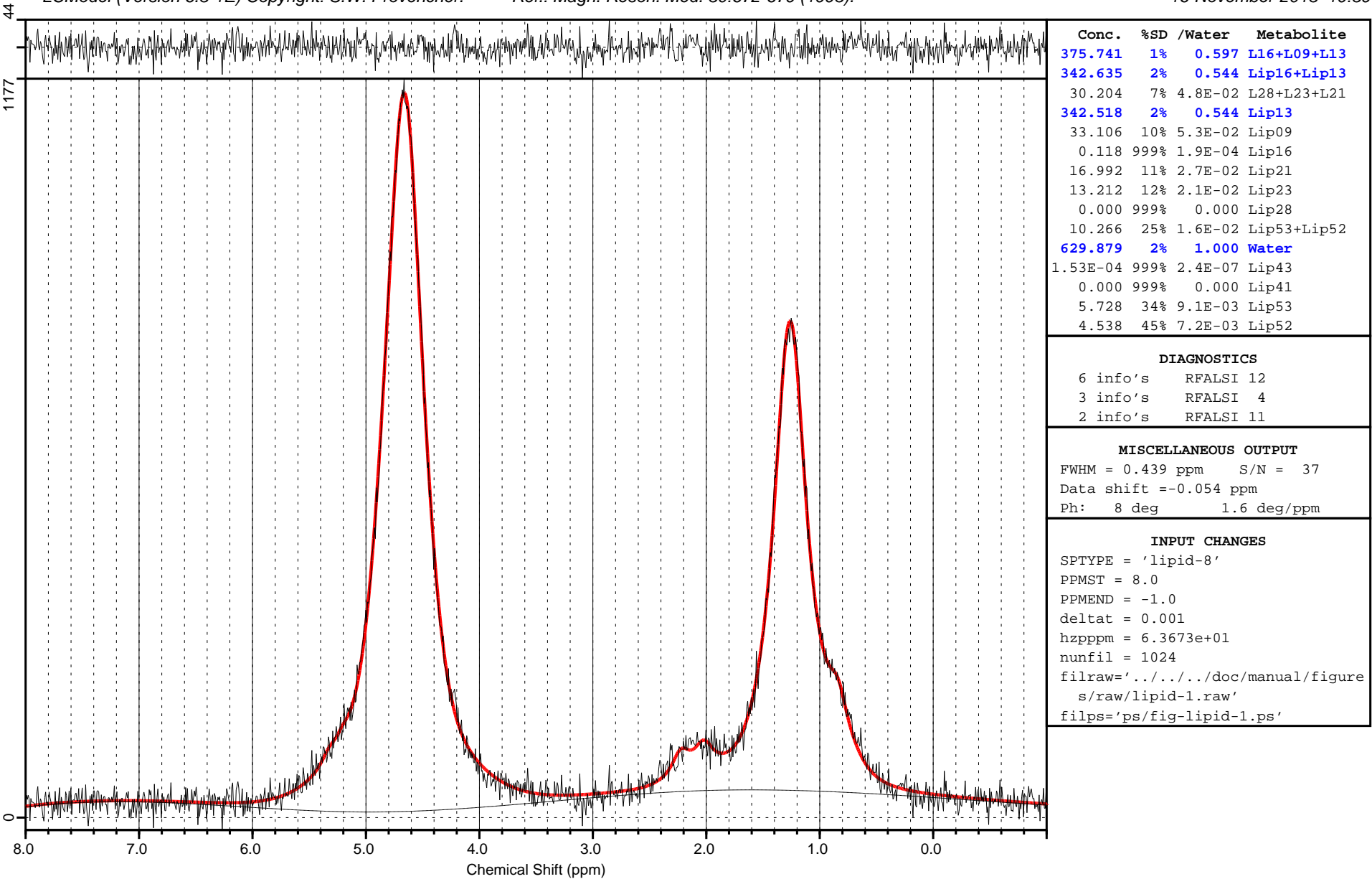
"/Water" values in the top table are ratios of the metabolite resonance area to the water resonance area.

Data of: Department of Diagnostic Radiology, Singapore General Hospital

LCModel (Version 6.3-1E) Copyright: S.W. Provencher.

Ref.: Magn. Reson. Med. 30:672-679 (1993).

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PLOT 10: Breast spectrum using SPTYPE='breast-8' (for water & lipids plus possibly choline).

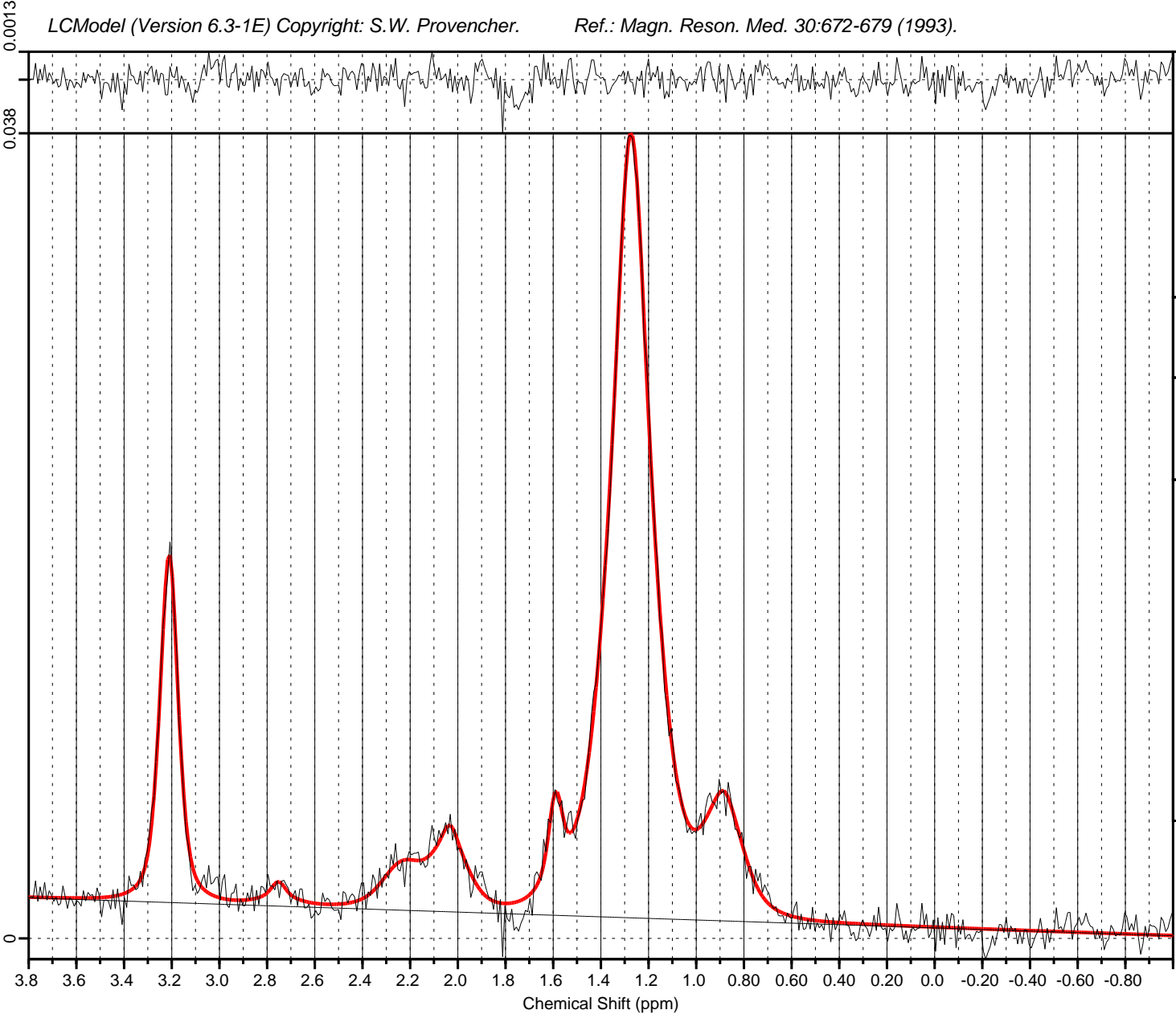
"Conc." values in the top table are ratios of the metabolite resonance area to the unsuppressed water resonance area.

Data of: Centre of MR Investigations, University of Hull

LCModel (Version 6.3-1E) Copyright: S.W. Provencher.

Ref.: Magn. Reson. Med. 30:672-679 (1993).

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Conc.	%SD	/L16+L0	Metabolite
1.06E-02	1%	1.000	L16+L09+L13
9.37E-03	1%	0.885	Lip16+Lip13
1.32E-03	6%	0.125	L28+L23+L21
8.91E-03	1%	0.842	Lip13
1.21E-03	7%	0.115	Lip09
4.58E-04	13%	4.3E-02	Lip16
6.90E-04	8%	6.5E-02	Lip21
4.85E-04	10%	4.6E-02	Lip23
1.48E-04	24%	1.4E-02	Lip28
1.84E-03	3%	0.174	Cho

DIAGNOSTICS		
2 info's	RFALSI	4
Doing Water-Scaling		

MISCELLANEOUS OUTPUT		
FWHM = 0.205 ppm	S/N =	32
Data shift = 0.029 ppm		
Ph: 2 deg	-0.3 deg/ppm	

INPUT CHANGES		
SPTYPE = 'breast-8'		
ppmst = 3.8		
PPMEND = -1.0		
DOWS=T		
DOECC=T		
deltat = 4.000e-04		
hzpppm = 63.862		
nunfil = 2048		
sddegp=1. sddegz=3.		
filh2o='../../../../doc/manual/figure		
s/raw/breast-1.h2o'		
filraw='../../../../doc/manual/figure		
s/raw/breast-1.raw'		
filps='ps/fig-breast-1.ps'		

PLOT 11: Liver spectrum using SPTYPE='liver-11'

"/Water" values in the top table are ratios of the metabolite resonance area to the water resonance area.

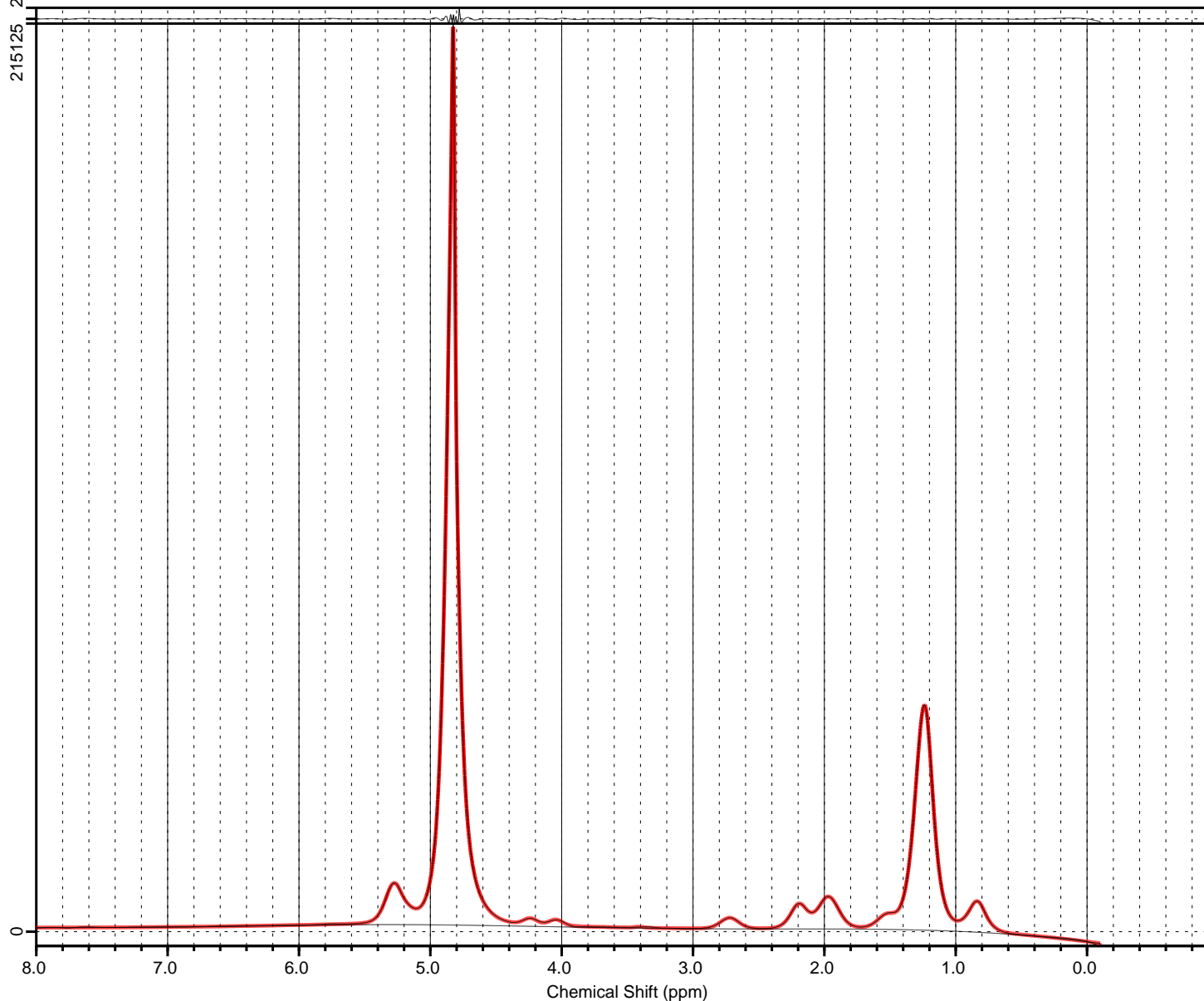
Data of: AMIR, Medical Physics, Dept. of Radiology, University Medical Center Freiburg

LCModel (Version 6.3-1E) Copyright: S.W. Provencher.

Ref.: Magn. Reson. Med. 30:672-679 (1993).

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215125 2626



Conc.	%SD	/Water	Metabolite
1.19E+04	0%	0.466	L16+L09+L13
1.06E+04	1%	0.416	Lip16+Lip13
2.99E+03	1%	0.117	L28+L23+L21
1.01E+04	1%	0.397	Lip13
1.29E+03	2%	5.1E-02	Lip09
488.562	6%	1.9E-02	Lip16
1.56E+03	1%	6.1E-02	Lip21
963.345	2%	3.8E-02	Lip23
464.685	3%	1.8E-02	Lip28
1.76E+03	1%	6.9E-02	Lip53+Lip52
2.55E+04	0%	1.000	Water
0.504	843%	2.0E-05	Cho
235.842	3%	9.2E-03	Lip43
234.290	3%	9.2E-03	Lip41
676.109	16%	2.7E-02	Lip53
1.09E+03	10%	4.3E-02	Lip52
30.341	25%	1.2E-03	Glycg

DIAGNOSTICS

1 warning MYCONT 17
1 info RFALSI 12
2 info's RFALSI 11

MISCELLANEOUS OUTPUT

FWHM = 0.115 ppm S/N = 740
Data shift = -0.015 ppm
Ph: 145 deg -0.7 deg/ppm

INPUT CHANGES

sptype = 'liver-11'
ppmend = -0.1 PPMST = 8.0
DELTAT = 2.496e-04
hzpppm = 400.3316
NUNFIL = 2048
roomt = T
filraw='../../doc/manual/figure
s/raw/liver-1.raw'
FILPS='ps/fig-liver-1.ps'

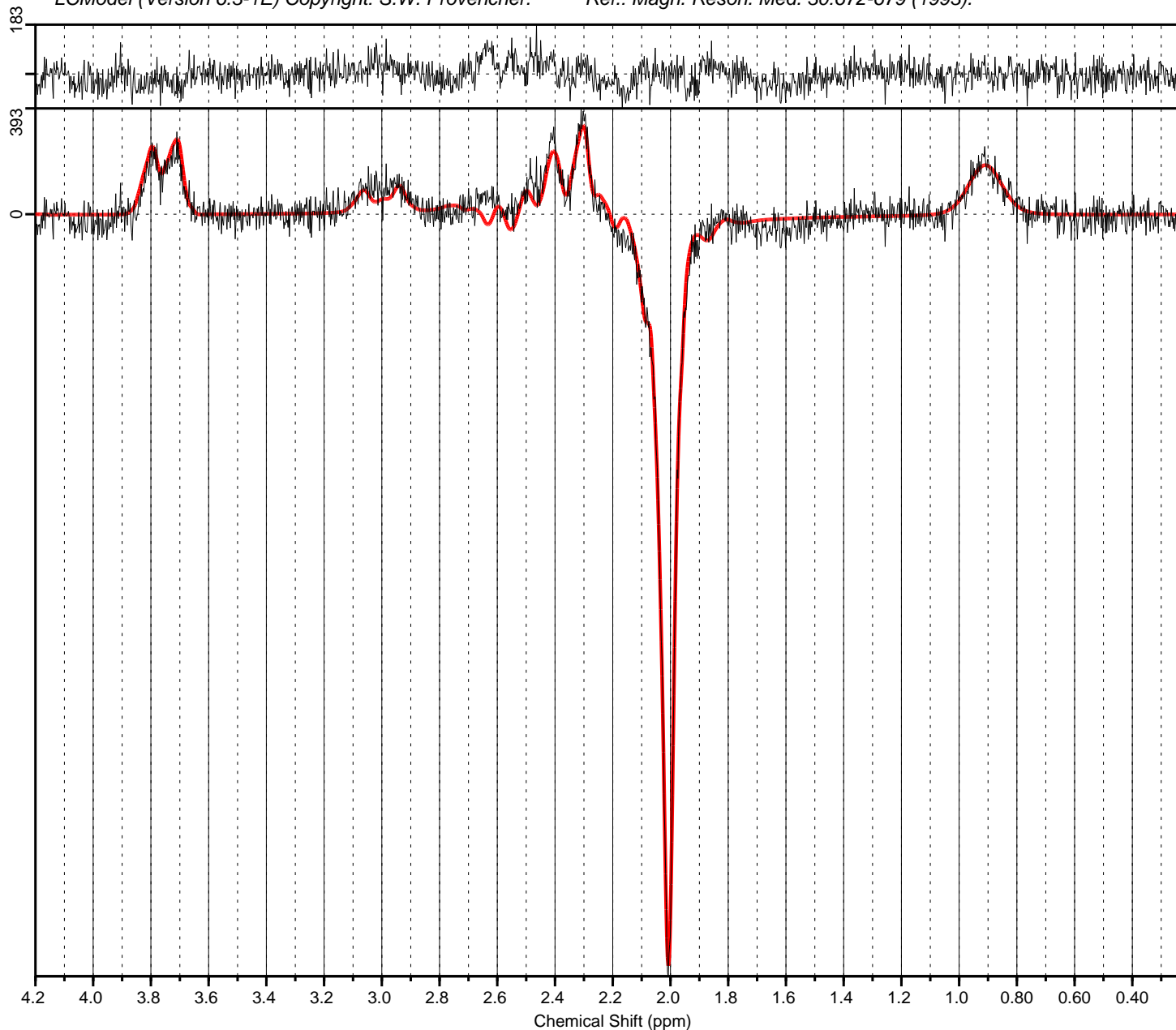
PLOT 12: Use SPTYPE='mega-press-3' for estimating GABA with MEGA-PRESS

Data of: Department of Psychiatry, MIND Research Network, University of New Mexico

LCModel (Version 6.3-1E) Copyright: S.W. Provencher.

Ref.: Magn. Reson. Med. 30:672-679 (1993).

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Conc.	%SD	/NAA+NA	Metabolite
0.898	6%	0.124	GABA
1.645	9%	0.228	Gln
3.053	4%	0.423	Glu
1.089	8%	0.151	GSH
6.505	1%	0.900	NAA
0.719	6%	0.100	NAAG
7.225	1%	1.000	NAA+NAAG
4.697	3%	0.650	Glu+Gln
5.786	2%	0.801	GSH+Glu+Gln

1.184	6%	0.164	MM09
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DIAGNOSTICS

1 info STARTV 24
 4 info's RFALSI 12
 1 info FINOUT 9
 Doing Water-Scaling

MISCELLANEOUS OUTPUT

FWHM = 0.038 ppm S/N = 32
 Data shift = 0.052 ppm
 Ph: -2 deg 1.0 deg/ppm

INPUT CHANGES

sptype = 'mega-press-3'
 PPMST = 4.2
 ppmend = 0.2
 DOWS = T
 DELTAT = 8.33e-04
 hzpppm = 123.26
 NUNFIL = 2048
 FILPS='ps/fig-mega.ps'
 filraw='../../../../doc/manual/figure
 s/raw/mega.raw'
 filh2o='../../../../doc/manual/figure
 s/raw/mega.h2o'
 filbas = '/home/sp/tmp/new-mexico-
 u/mega-press-3t-1.basis'

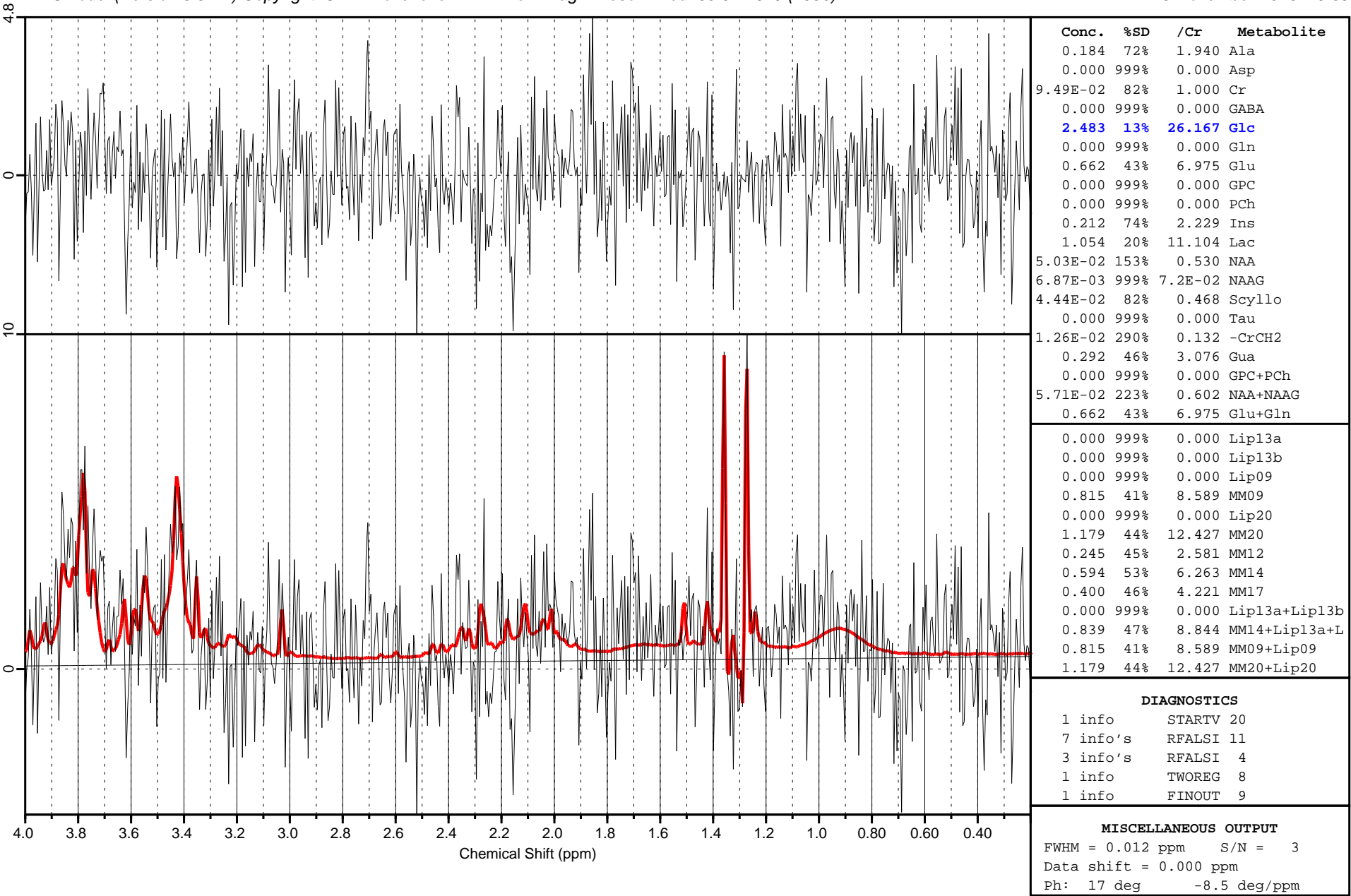
PLOT 13: Use SPTYPE='csf' with mainly cerebrospinal fluid, when the usual landmarks (NAA, cholines & Cr) are weaker than Lac & Glc

Data of: Biomedizinische NMR Forschungs GmbH, Goettingen

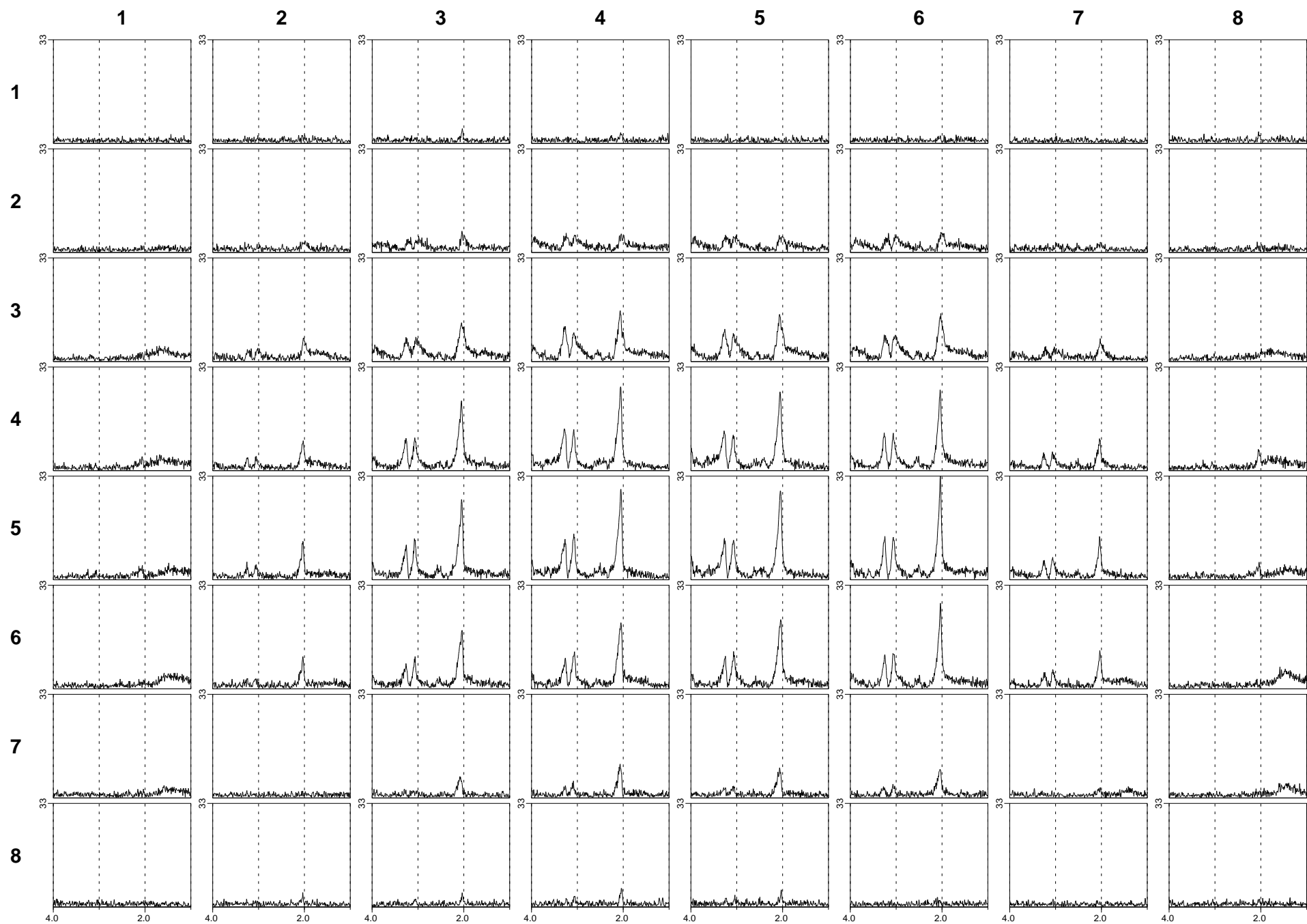
LCModel (Version 6.3-1E) Copyright: S.W. Provencher.

Ref.: Magn. Reson. Med. 30:672-679 (1993).

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PLOT 14: LCMgui display of a full slice of CSI data (from the Montreal Neurological Institute)



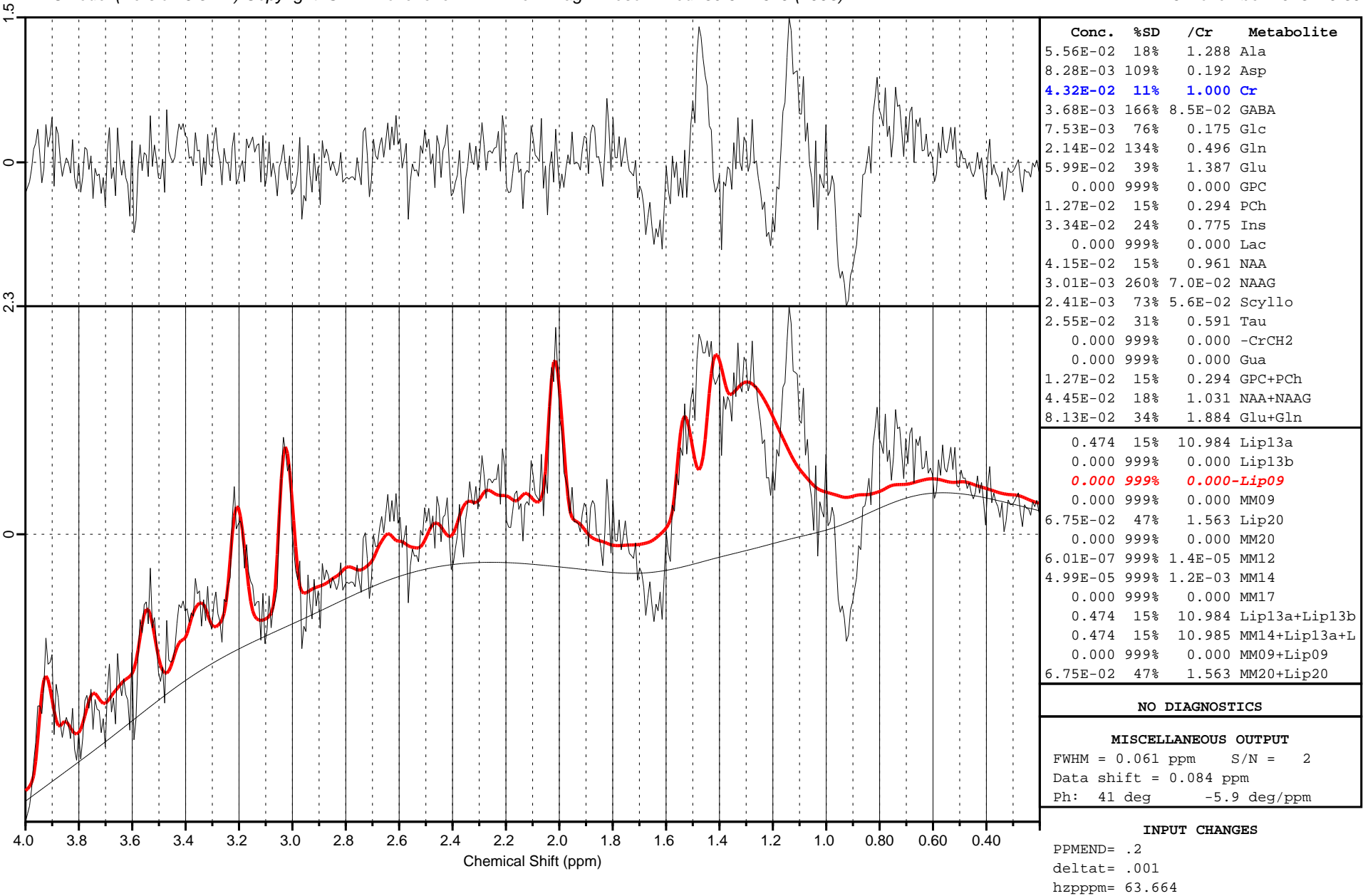
Row#9 Col#10 PLOT 15: Strong artifact signals from outside the voxel ruin the quantification (at least below 1.8 ppm). These artifacts must be avoided by using PPMEND=1.8 (in PLOT 16).

Data of: LCModel Users

LCModel (Version 6.3-1E) Copyright: S.W. Provencher.

Ref.: Magn. Reson. Med. 30:672-679 (1993).

16-November-2013 19:39



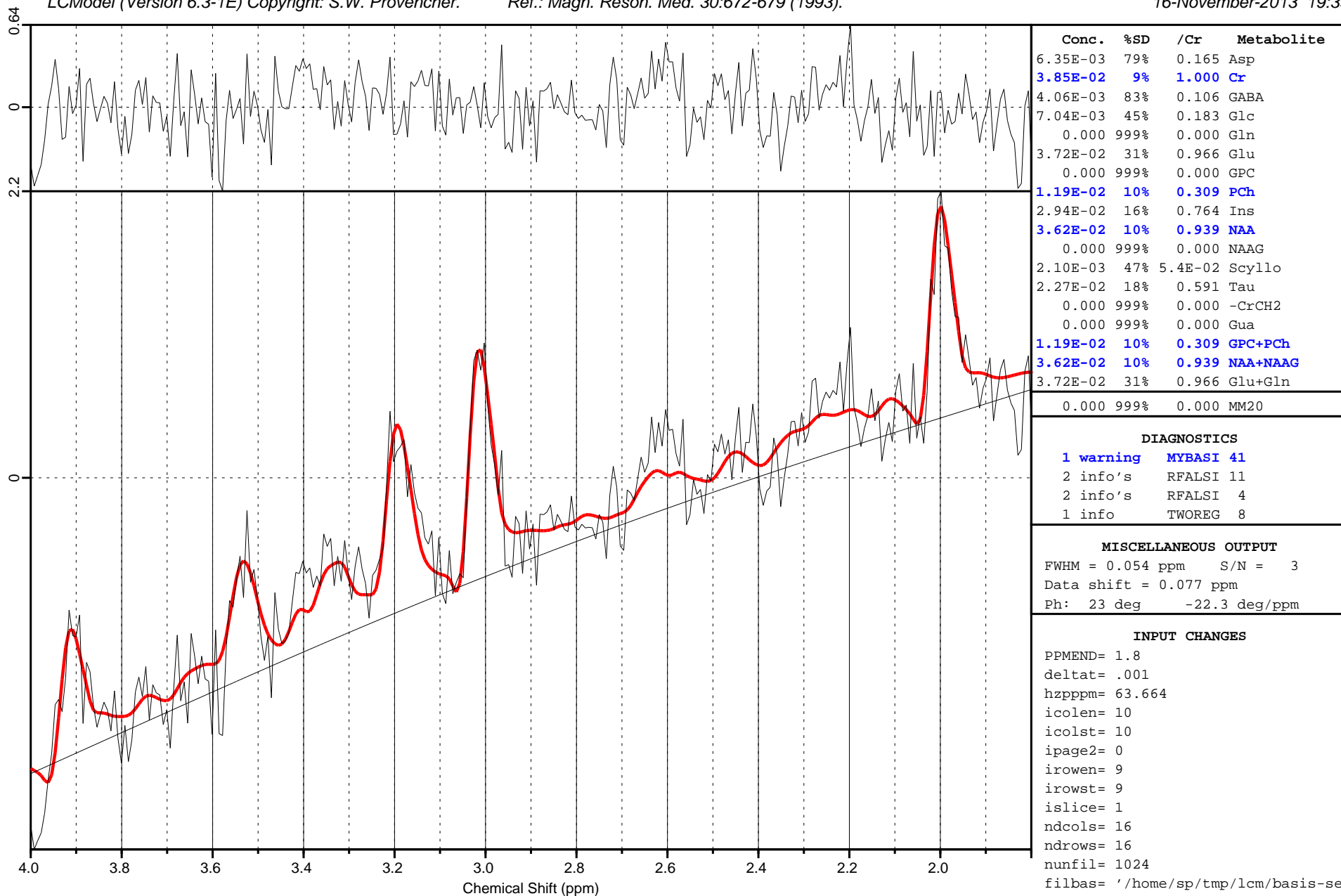
Row#9 Col#10 PLOT 16: Same data as in PLOT 15, but with PPMEND=1.8 to avoid the strong artifacts.

Data of: LCModel Users

LCModel (Version 6.3-1E) Copyright: S.W. Provencher.

Ref.: Magn. Reson. Med. 30:672-679 (1993).

16-November-2013 19:39



Conc.	%SD	/Cr	Metabolite
6.35E-03	79%	0.165	Asp
3.85E-02	9%	1.000	Cr
4.06E-03	83%	0.106	GABA
7.04E-03	45%	0.183	Glc
0.000	999%	0.000	Gln
3.72E-02	31%	0.966	Glu
0.000	999%	0.000	GPC
1.19E-02	10%	0.309	PCh
2.94E-02	16%	0.764	Ins
3.62E-02	10%	0.939	NAA
0.000	999%	0.000	NAAG
2.10E-03	47%	5.4E-02	Scyllo
2.27E-02	18%	0.591	Tau
0.000	999%	0.000	-CrCH2
0.000	999%	0.000	Gua
1.19E-02	10%	0.309	GPC+PCh
3.62E-02	10%	0.939	NAA+NAAG
3.72E-02	31%	0.966	Glu+Gln
0.000	999%	0.000	MM20

DIAGNOSTICS

1 warning MYBASI 41
 2 info's RFALSI 11
 2 info's RFALSI 4
 1 info TWOREG 8

MISCELLANEOUS OUTPUT

FWHM = 0.054 ppm S/N = 3
 Data shift = 0.077 ppm
 Ph: 23 deg -22.3 deg/ppm

INPUT CHANGES

PPMEND= 1.8
 deltat= .001
 hzpppm= 63.664
 icolen= 10
 icolst= 10
 ipage2= 0
 irowen= 9
 irowst= 9
 islice= 1
 ndcols= 16
 ndrows= 16
 nunfil= 1024
 filbas= '/home/sp/tmp/lcm/basis-se
 ts/steam/siemens_steam_te20_tm10
 _99c.basis'

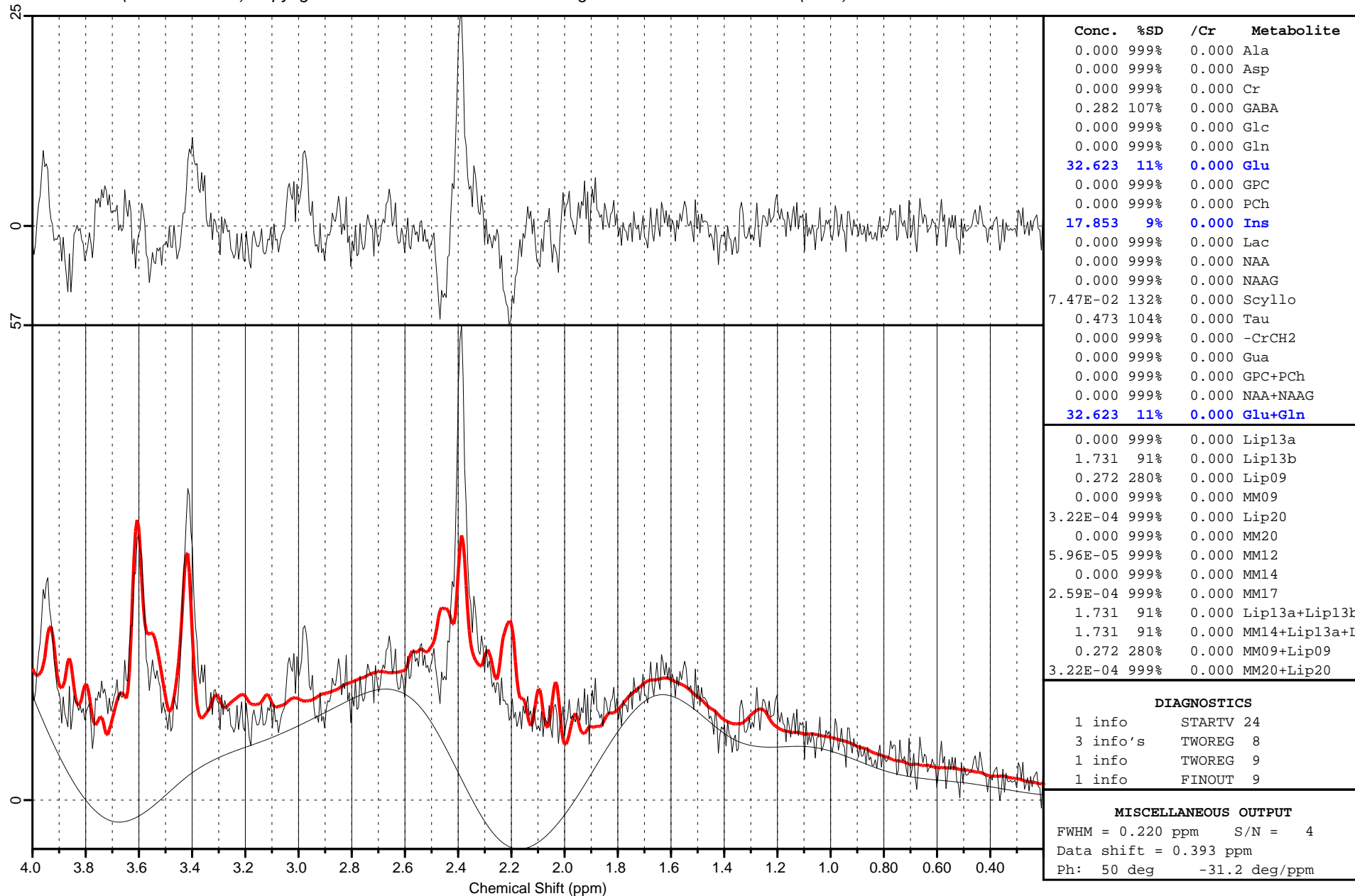
PLOT 17: Total failure (due to grossly incorrect referencing constraint with PPMShf).

Data of: Biomedizinische NMR Forschungs GmbH, Goettingen

LCModel (Version 6.3-1E) Copyright: S.W. Provencher.

Ref.: Magn. Reson. Med. 30:672-679 (1993).

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INPUT CHANGES

PPMSHF=.4

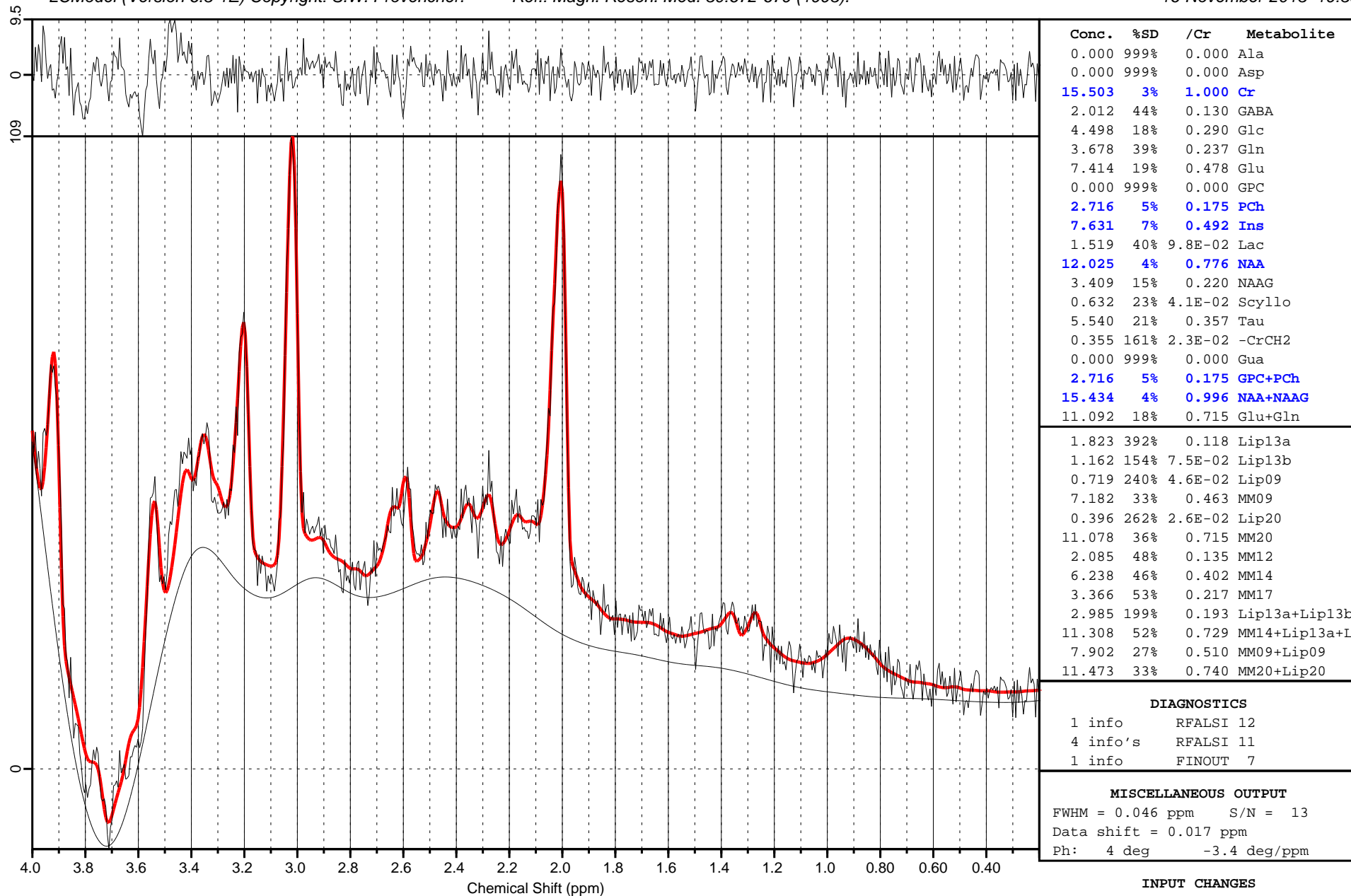
PLOT 18: Reject spectra with strongly bent baselines.

Data of: Biomedizinische NMR Forschungs GmbH, Goettingen

LCModel (Version 6.3-1E) Copyright: S.W. Provencher.

Ref.: Magn. Reson. Med. 30:672-679 (1993).

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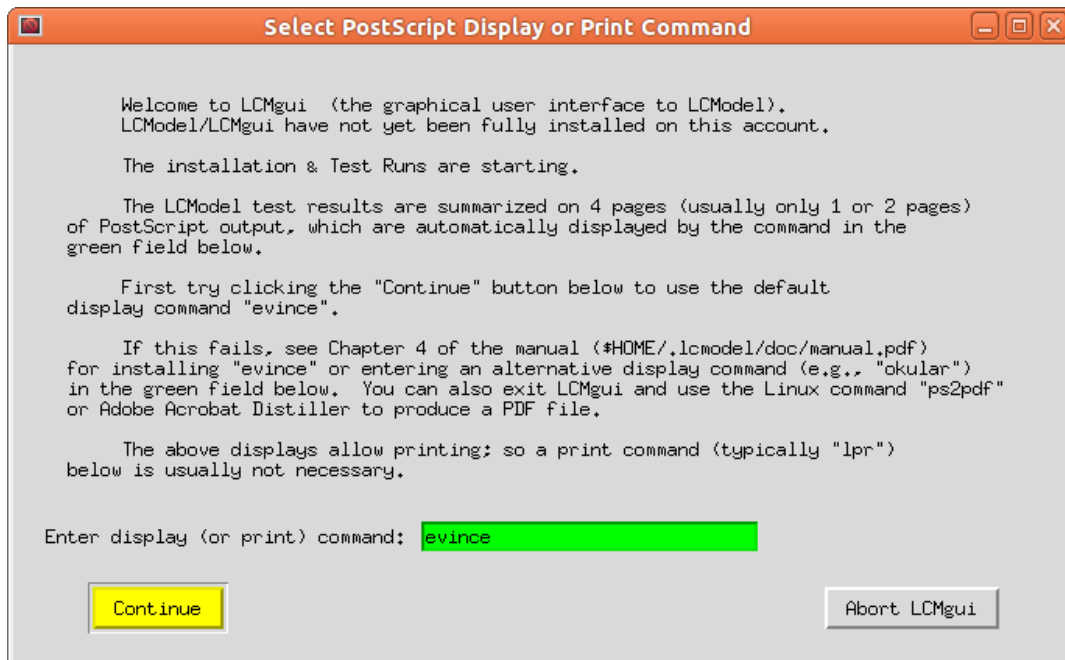


Figure 4.1: Here you enter your command for displaying or printing PostScript files.

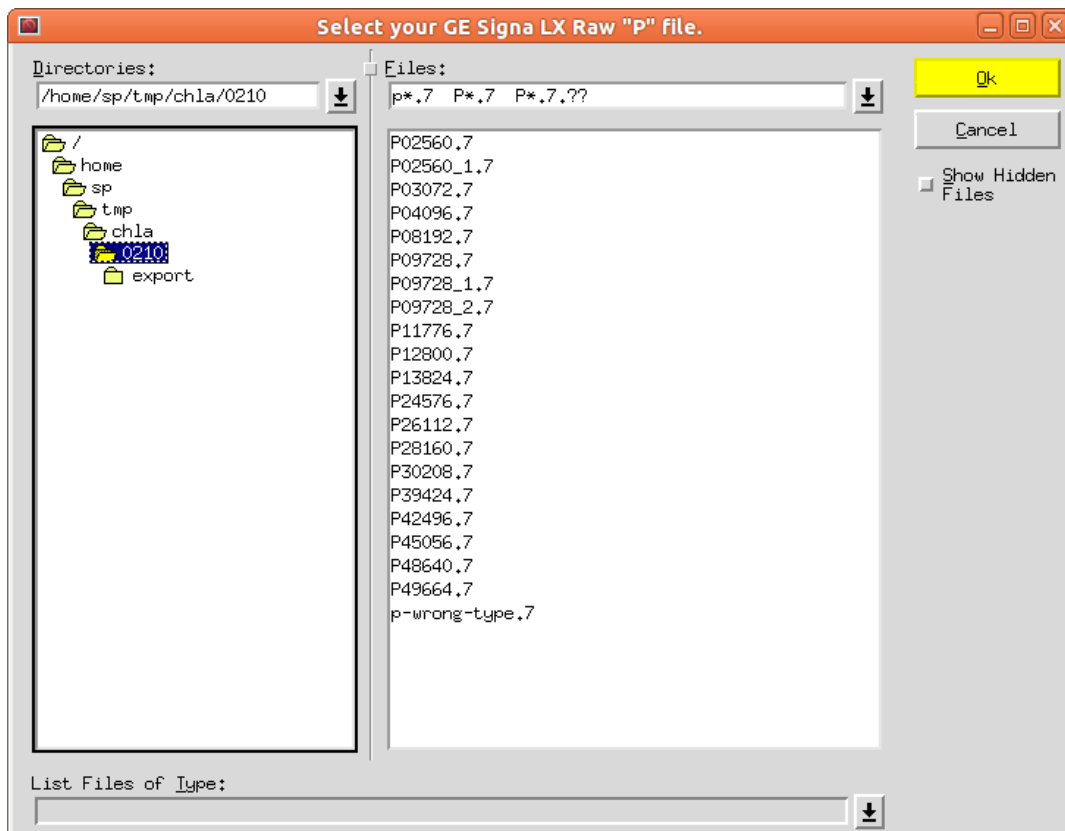


Figure 6.1: The File Selector, shown here for GE LX files

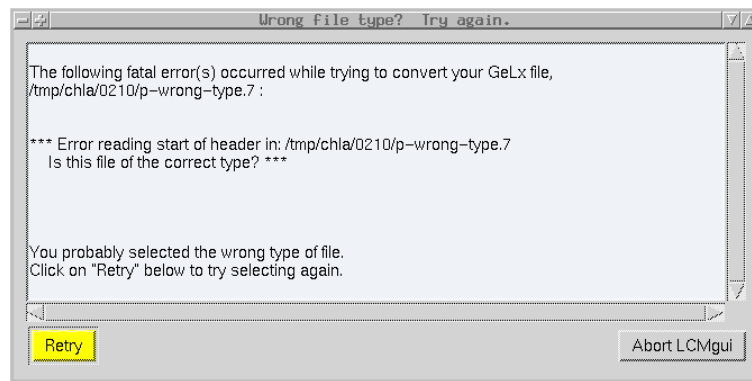


Figure 6.2: You selected a file of the wrong type in the File Selector



Figure 6.3: Note that GE Signal 5.x and LX have distinct buttons.

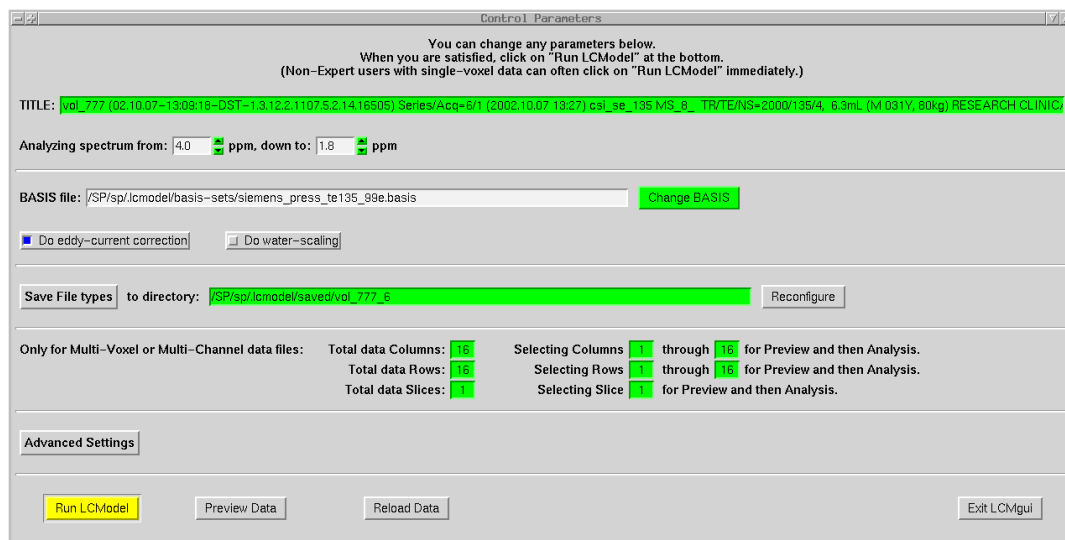


Figure 6.4: The Control Parameters Window

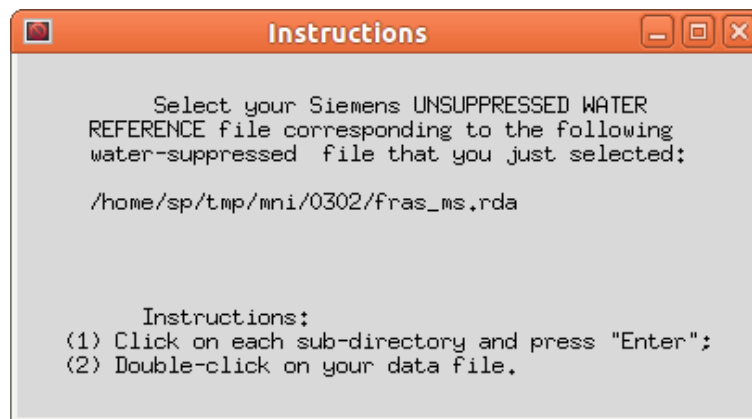


Figure 6.5: The instructions-part of the File Selector for the unsuppressed water reference.



Figure 6.6: Here you decide how to save the settings from this session.

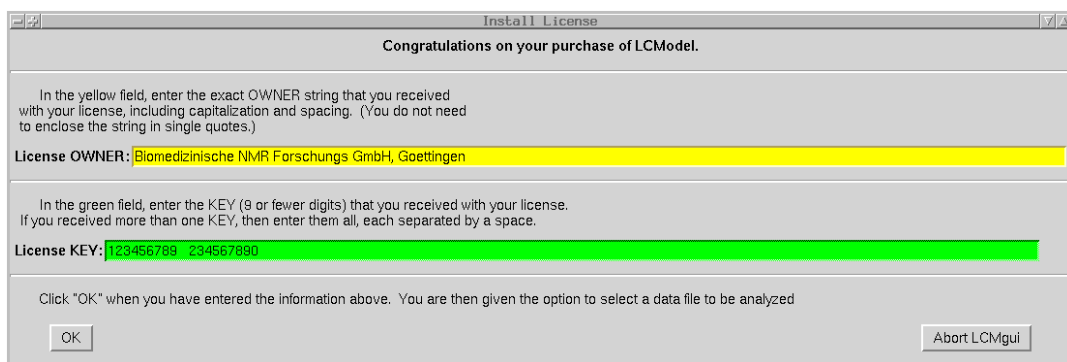


Figure 7.1: The Install License Window (with Sun, SGI or DEC/Compaq)

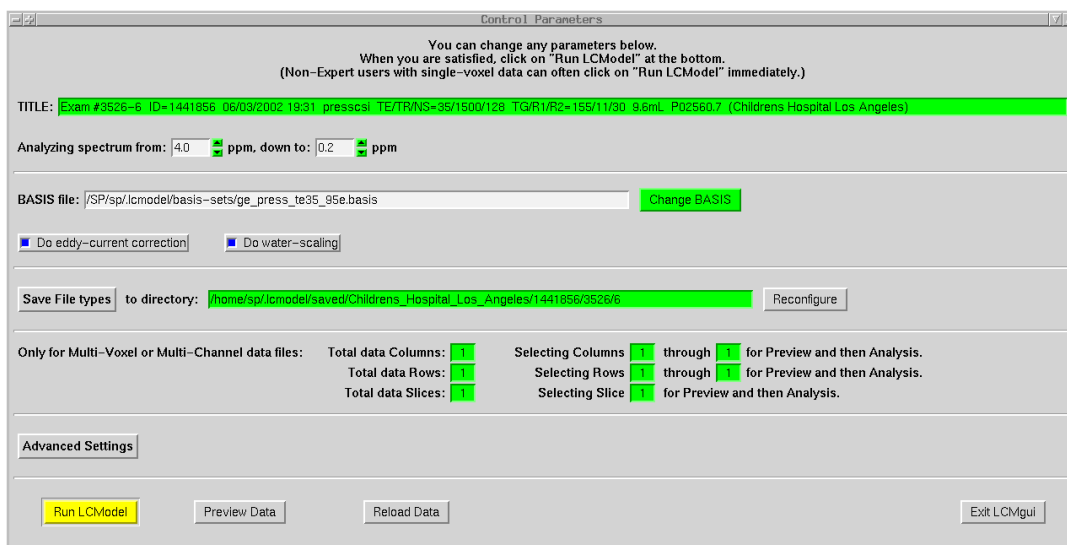


Figure 7.2: The Control Parameters Window

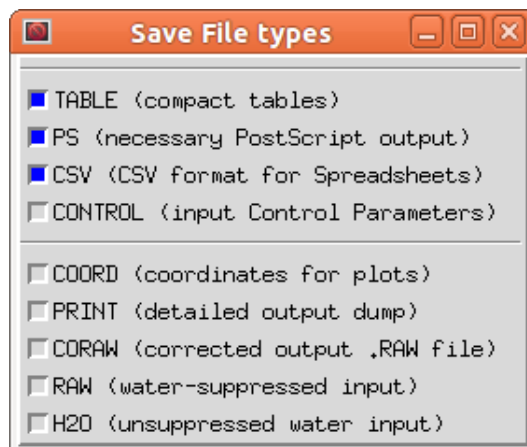


Figure 7.3: You get this menu when you click the “Save File Types” button in Fig. 7.2.

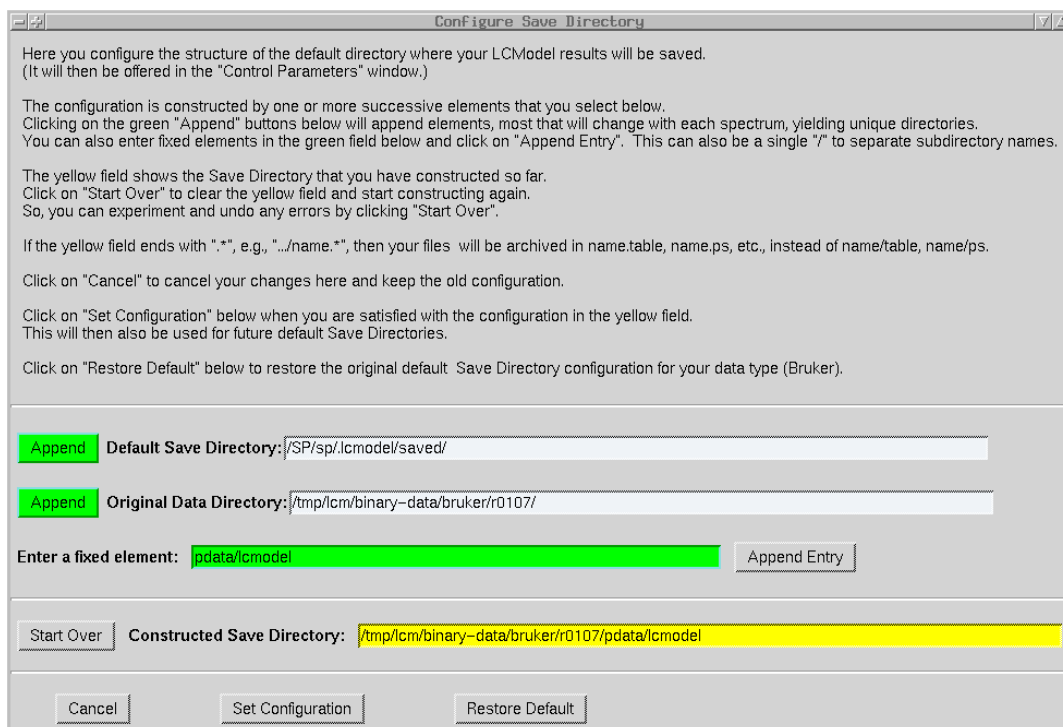


Figure 7.4: The window for permanently reconfiguring the structure of (Bruker) Archive Directories.

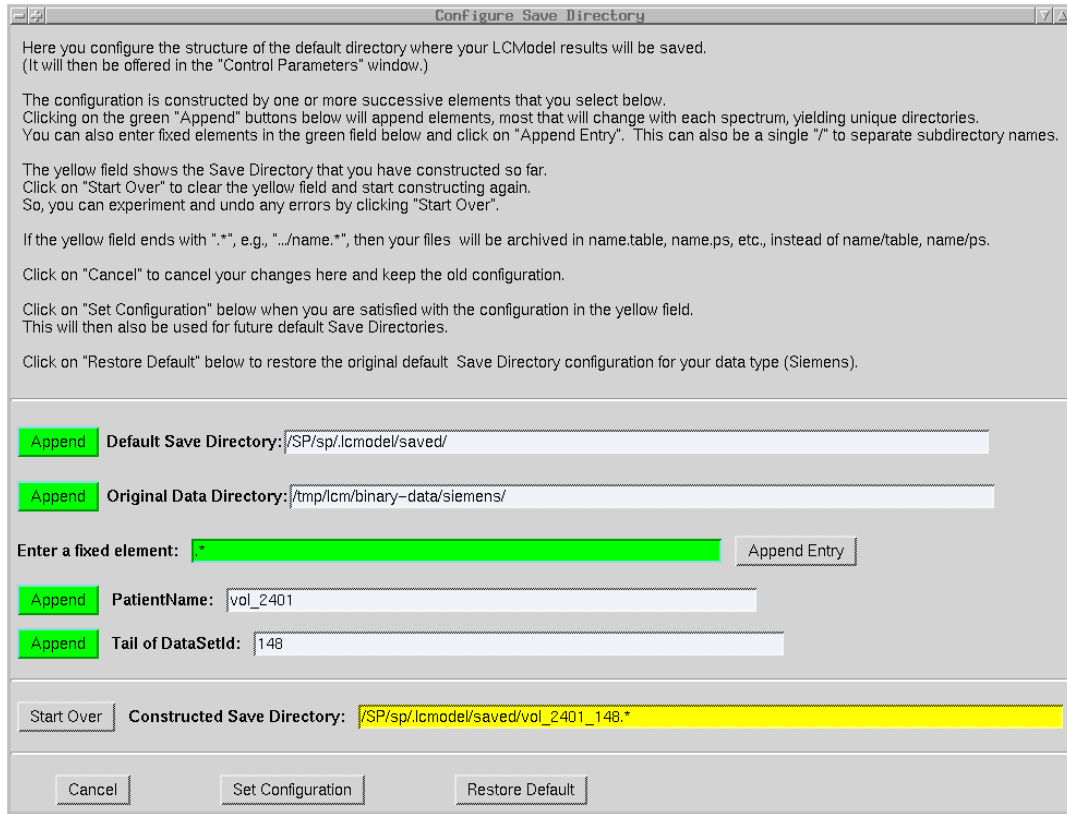


Figure 7.5: The window for permanently reconfiguring the structure of (Siemens) Archive Directories.

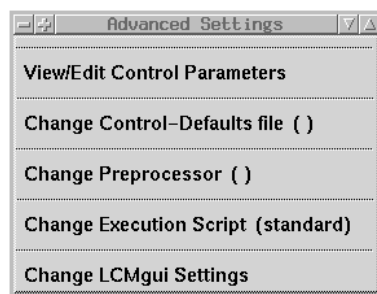


Figure 7.6: You get this menu when you click the "Advanced Settings" button in Fig. 7.2.

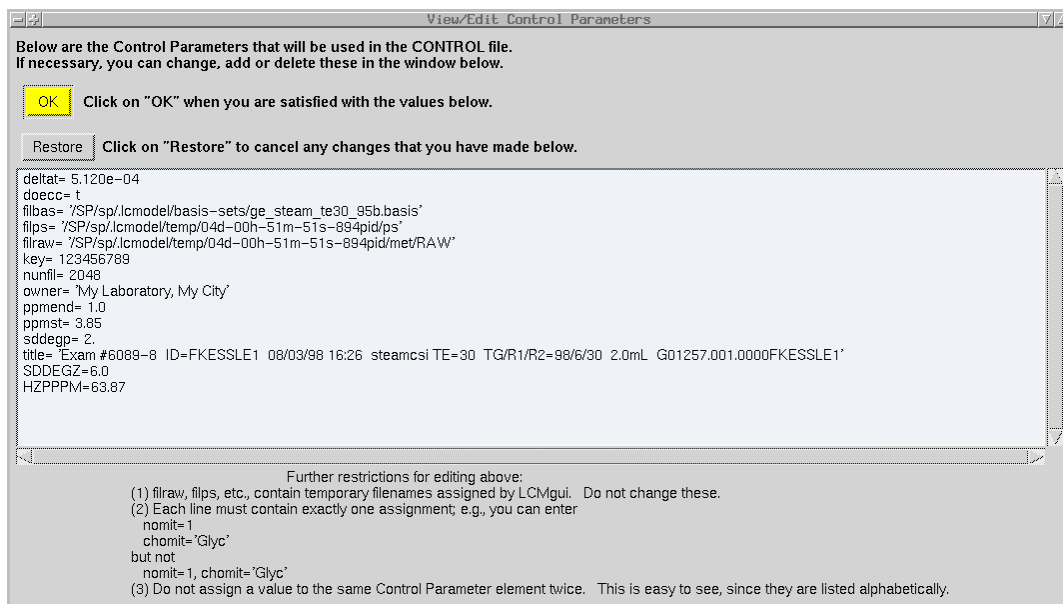


Figure 7.7: You can view, edit, delete or add all Control Parameters here.

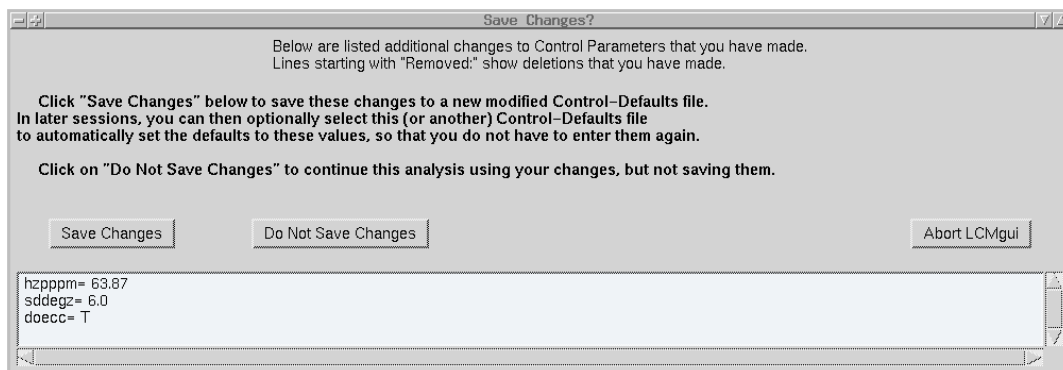


Figure 7.8: You can save all the Control Parameters, including your modifications, for optional use as starting defaults in the future.

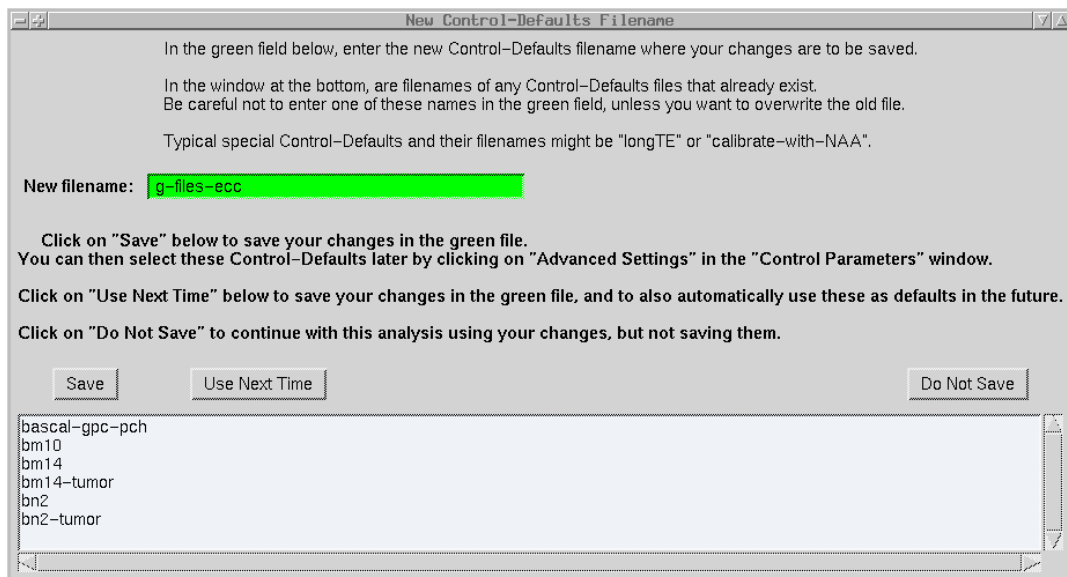


Figure 7.9: Here you enter a name for the file which will store your Control Parameters for optional future use.

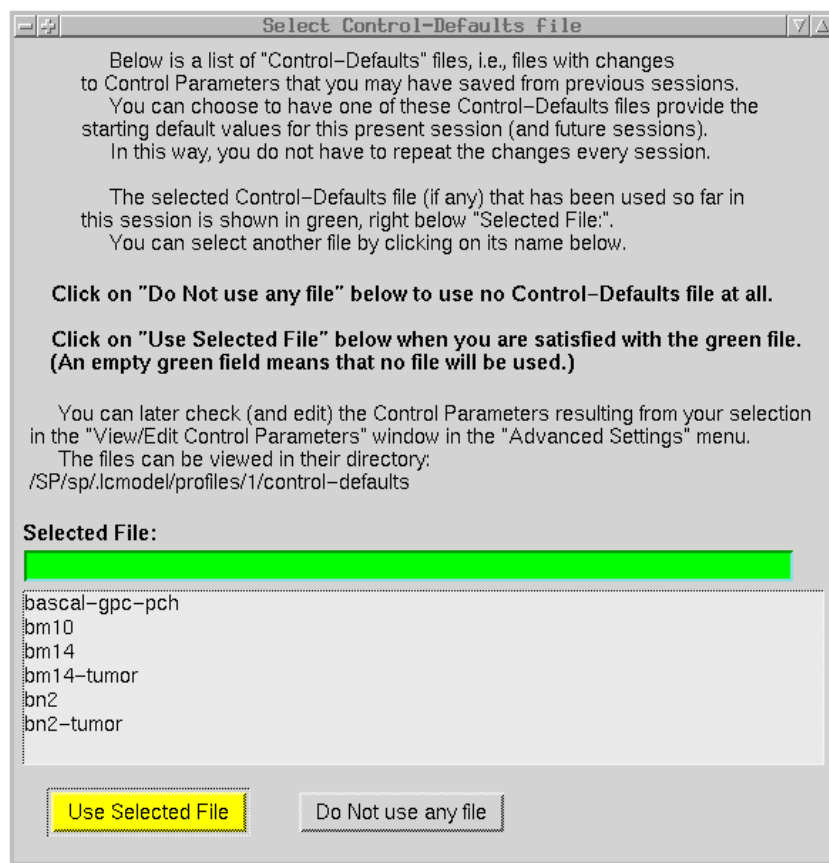


Figure 7.10: Here you select the Control-Defaults file to be used now and in the future.

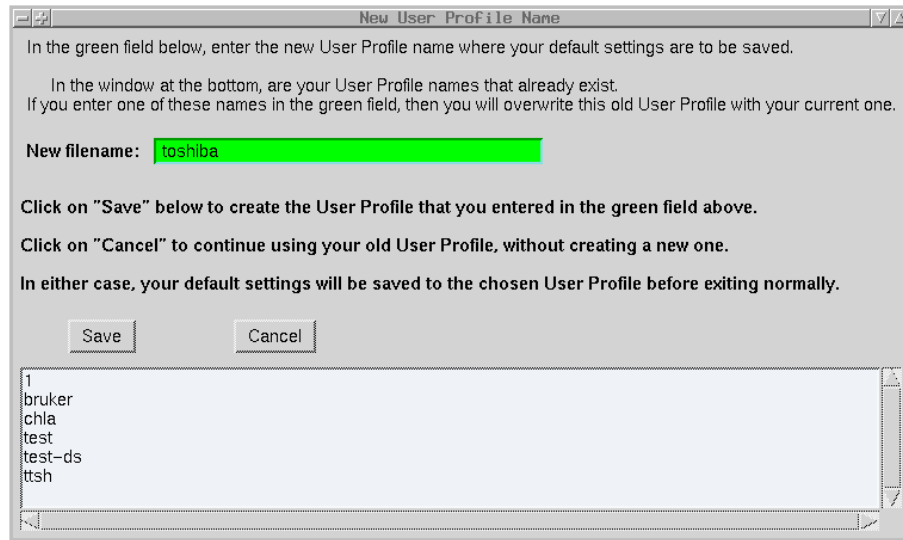


Figure 7.11: At the end of a session, you can select a new User Profile where all of your settings from the session will be saved.

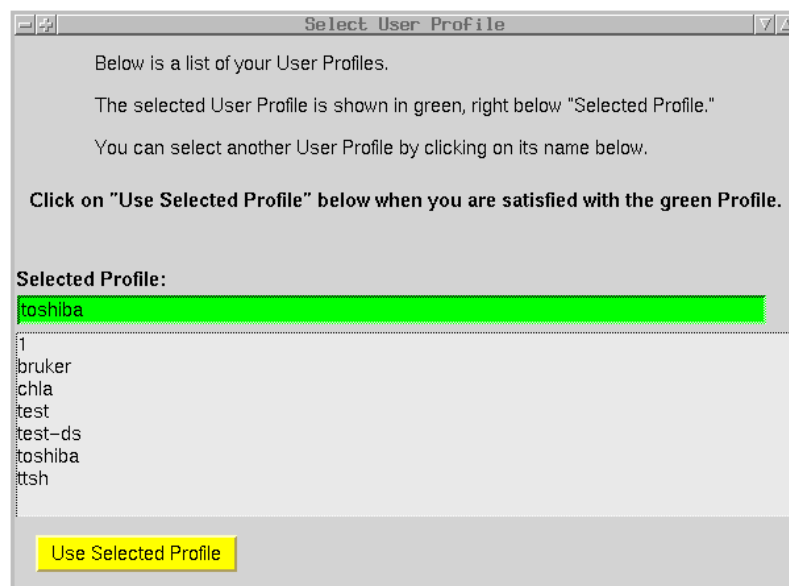


Figure 7.12: At the start of a session, you select the User Profile to be used.

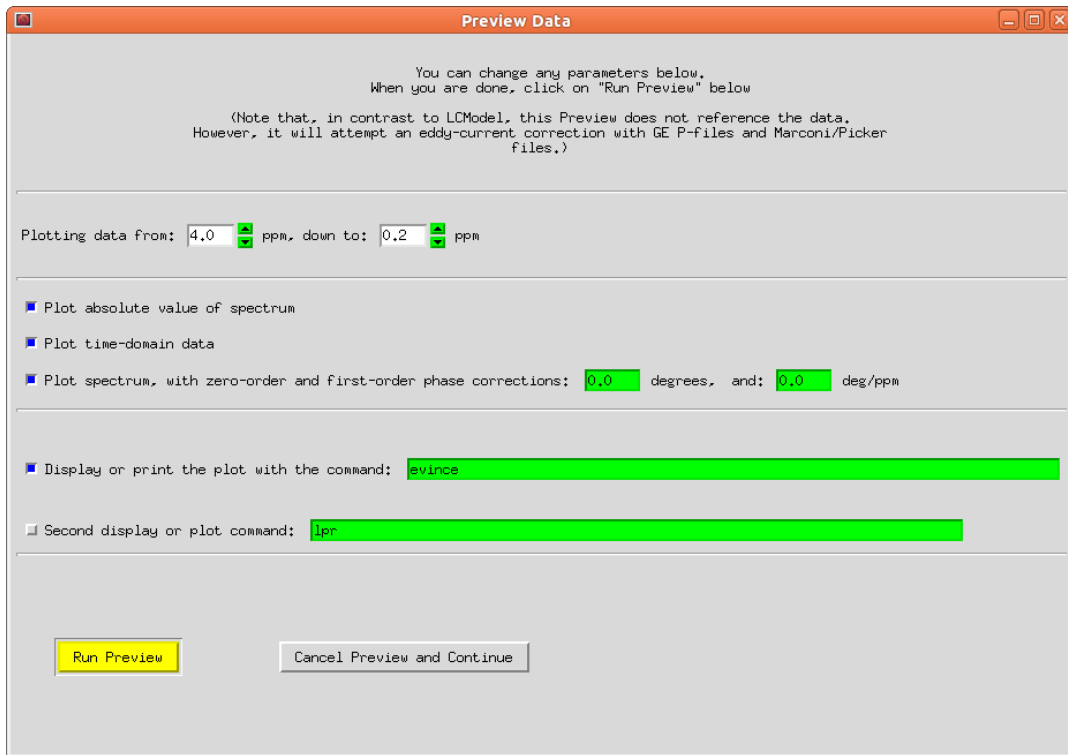


Figure 7.13: Here you can set and execute your commands for printing and/or plotting previews of your data.

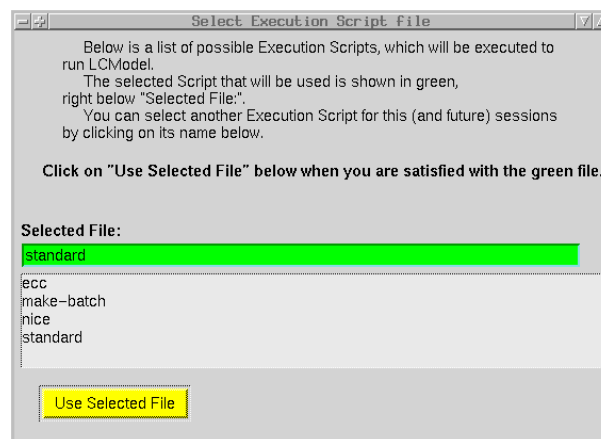


Figure 7.14: Here you can select the Execution Script that will be started by LCMgui.

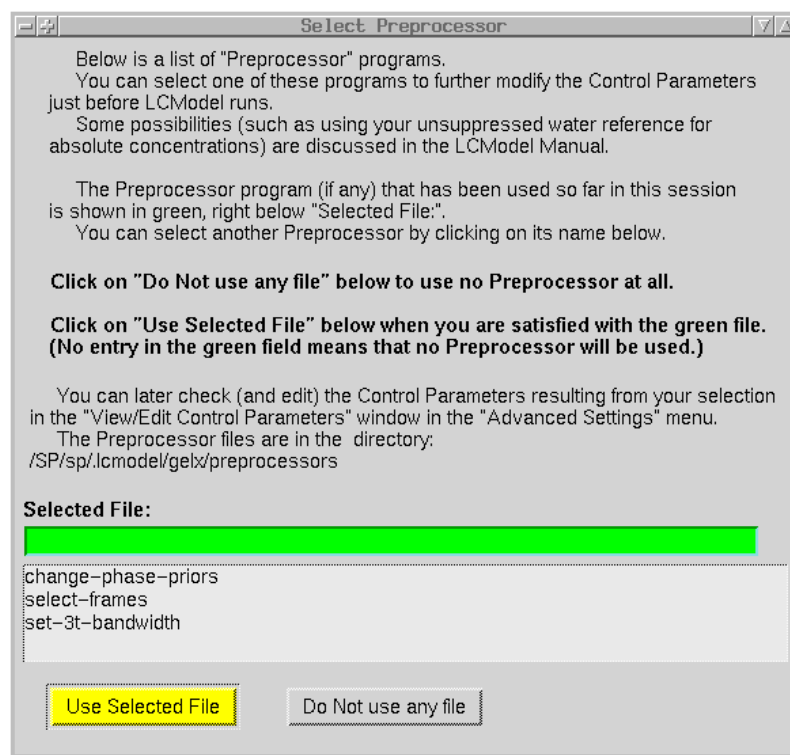


Figure 7.15: Here you can view and/or change the Preprocessor that will be used by LCMgui.