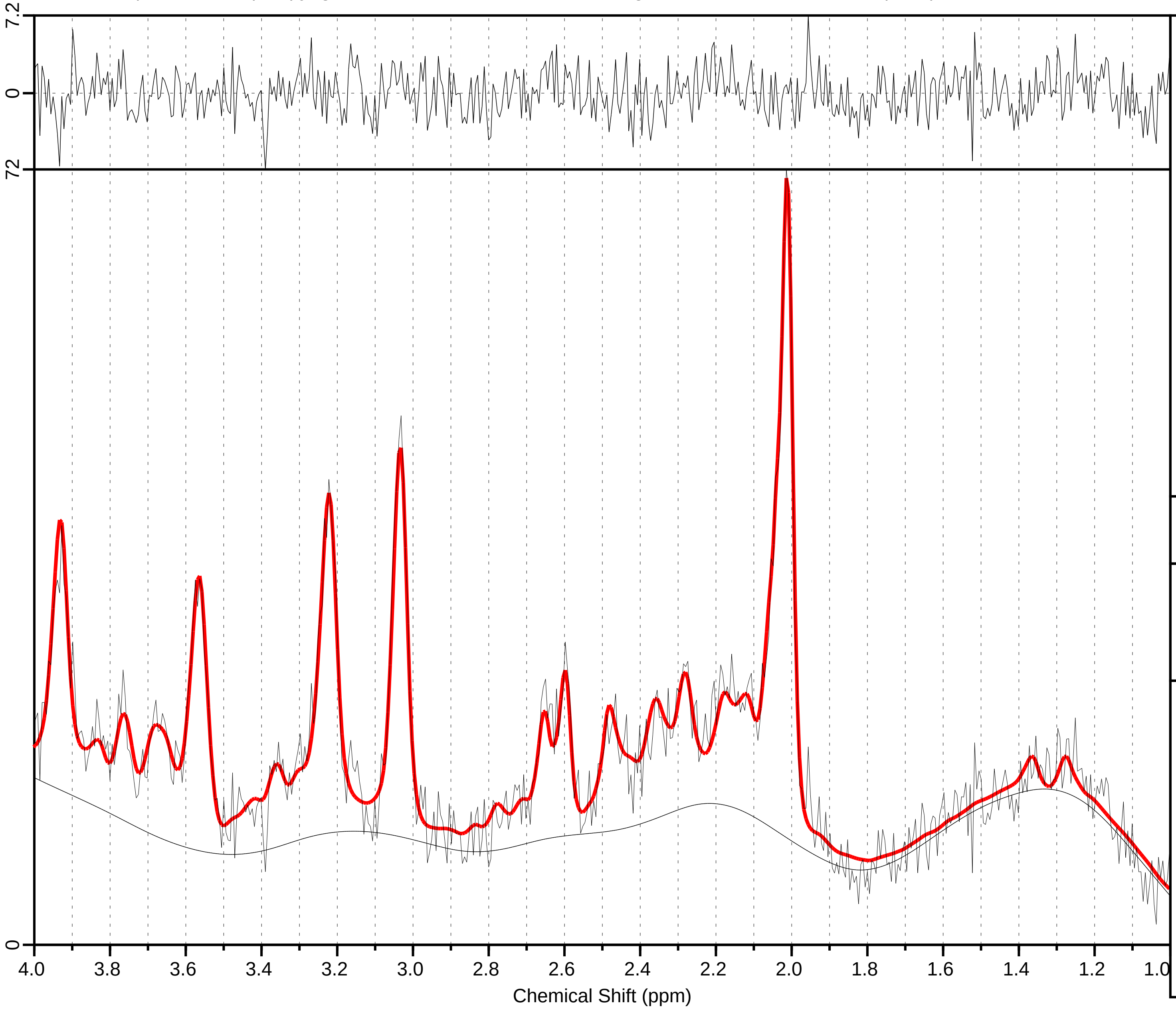
FIGURE 1: Test Data (also used for Fig. 1 in Ref. [1]).

Data of: Biomedizinische NMR Forschungs GmbH, Goettingen

LCModel (Version 5.2-0) Copyright: S.W. Provencher. *Ref.: Magn. Reson. Med. 30:672-679 (1993).* *08-December-1999 23:20*



Conc.	%SD	/Cr	Metab.
0.000	999%	0.000	Ala
1.055	71%	0.154	Asp
6.872	**5%**	**1.000**	**Cr**
0.000	999%	0.000	GABA
0.000	999%	0.000	Glc
2.888	33%	0.420	Gln
8.158	**13%**	**1.187**	**Glu**
0.981	34%	0.143	GPC
1.000	35%	0.145	PCh
6.251	**8%**	**0.910**	**Ins**
1.078	38%	0.157	Lac
7.844	**4%**	**1.142**	**NAA**
2.915	**15%**	**0.424**	**NAAG**
0.075	157%	0.011	Scyllo
2.144	39%	0.312	Tau
10.759	**4%**	**1.566**	**NAA+NAAG**
1.981	**6%**	**0.288**	**GPC+PCh**
11.046	**13%**	**1.607**	**Glu+Gln**

DIAGNOSTICS

```
1 info       RFALSI 11
```

MISCELLANEOUS OUTPUT

```
FWHM = 0.043 ppm      S/N = 13
Data shift = 0.006 ppm
Ph:  45 deg          -16 deg/ppm
```

INPUT CHANGES

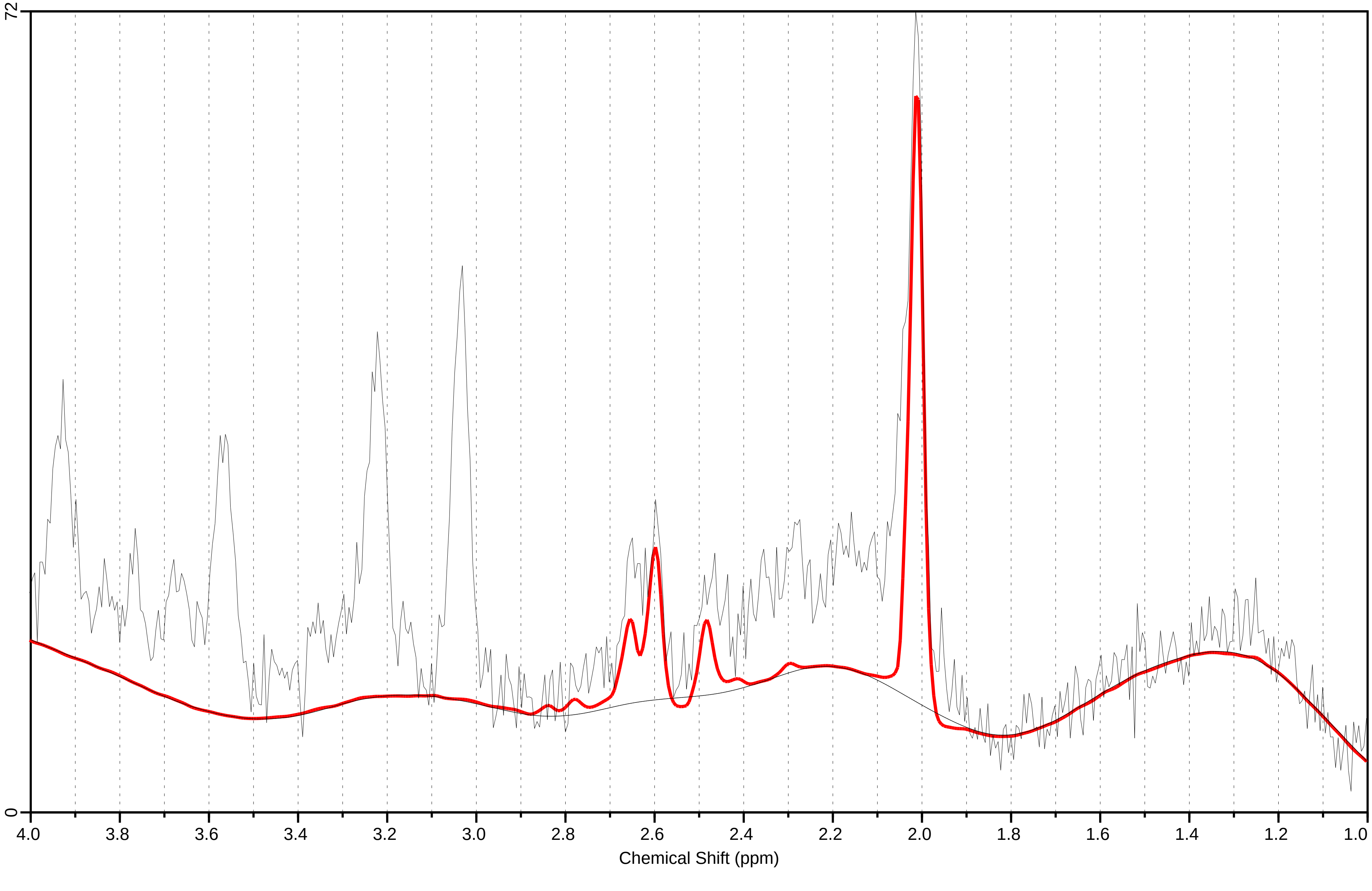
```
HZPPPM=84.47
NUNFIL=2048, DELTAT=.0005
NEACH=2, NAMEAC(1)='NAA'
NAMEAC(2)='NAAG'
FILPS='ps/fig_MRM1.PS'
FILRAW='../../../doc/manual/f
  igures/raw/Test.RAW'
FILBAS='../../../doc/manual/f
  igures/Test.BASIS'
degppm=-15., sddegp=5.
degzer=40., sddegz=15.
```

FIGURE 2: Test Data (also used for Fig. 1 in Ref. [1]).

NAA Conc. = 7.84E+00

Data of: Biomedizinische NMR Forschungs GmbH, Goettingen

LCModel (Version 5.2-0) Copyright: S.W. Provencher. *Ref.: Magn. Reson. Med. 30:672-679 (1993).* *08-December-1999 23:20*



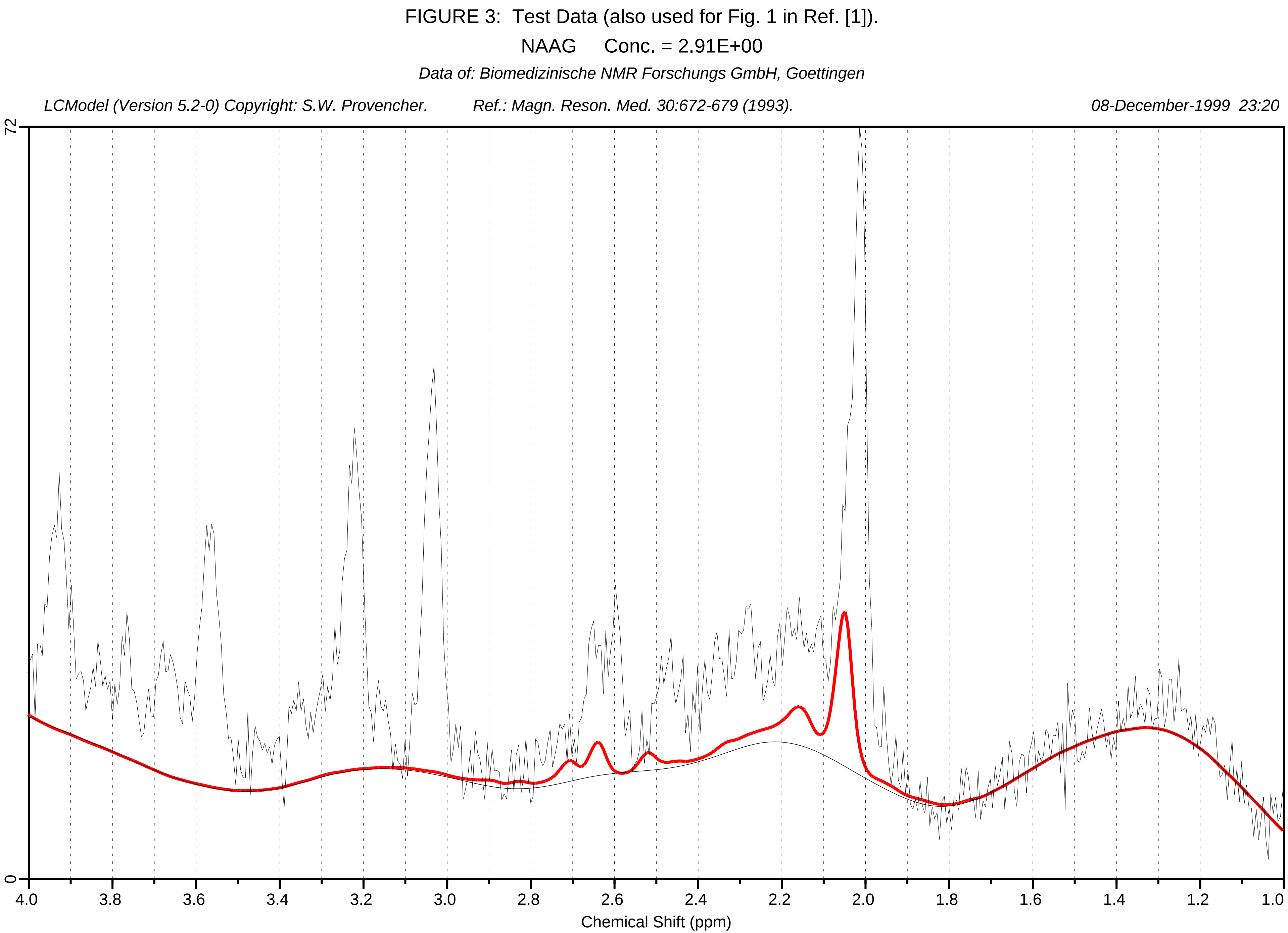


FIGURE 3: Test Data (also used for Fig. 1 in Ref. [1]).
NAAG Conc. = 2.91E+00
Data of: Biomedizinische NMR Forschungs GmbH, Goettingen
LCModel (Version 5.2-0) Copyright: S.W. Provencher.
Ref.: Magn. Reson. Med. 30:672-679 (1993).
08-December-1999 23:20
72
0
4.0
3.8
3.6
3.4
3.2
3.0
2.8
2.6
2.4
2.2
2.0
1.8
1.6
1.4
1.2
1.0
Chemical Shift (ppm)

FIGURE 4: Abort with FATAL diagnostic and Absolute-Value Plot due to unreasonable input.

Data of: Biomedizinische NMR Forschungs GmbH, Goettingen

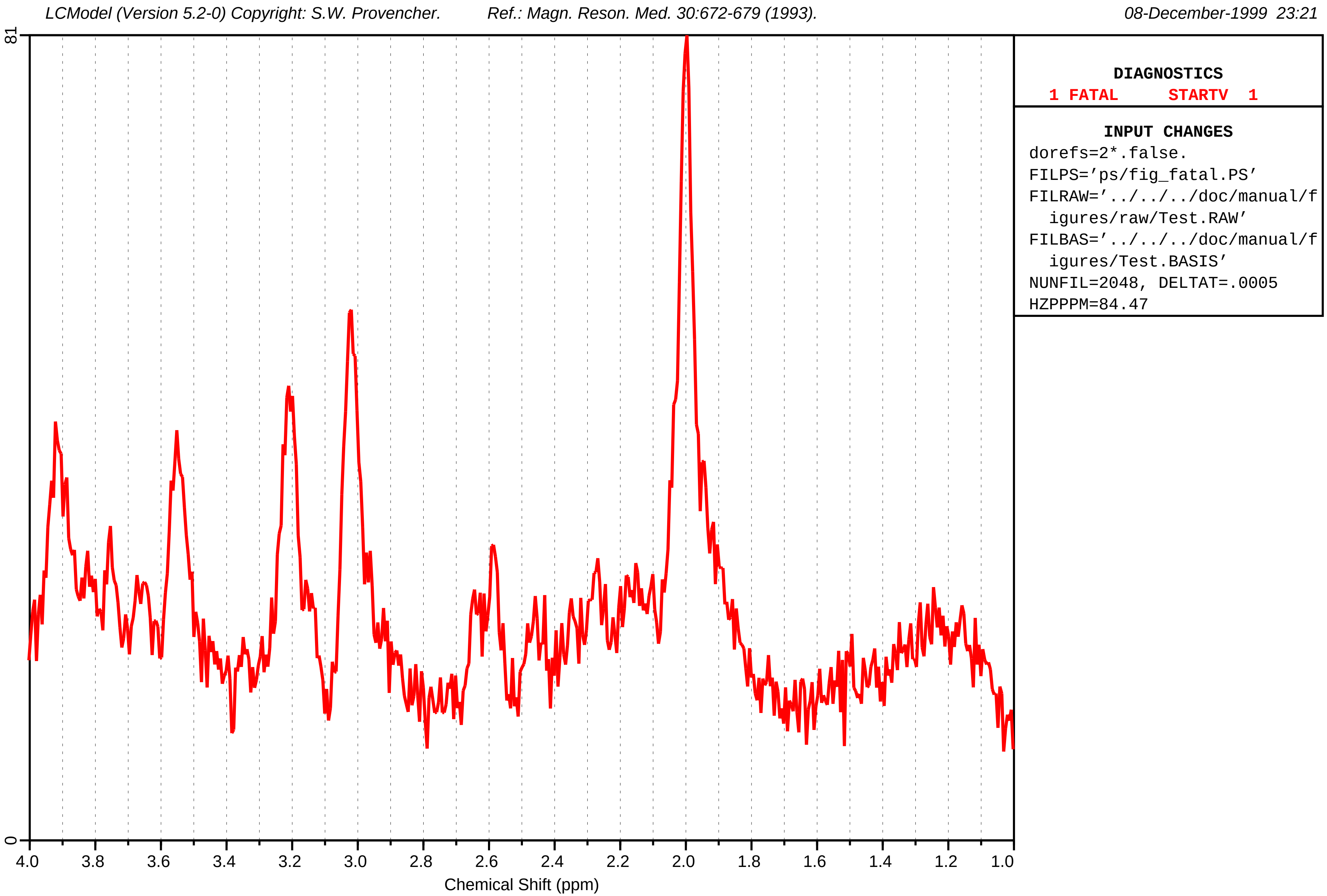
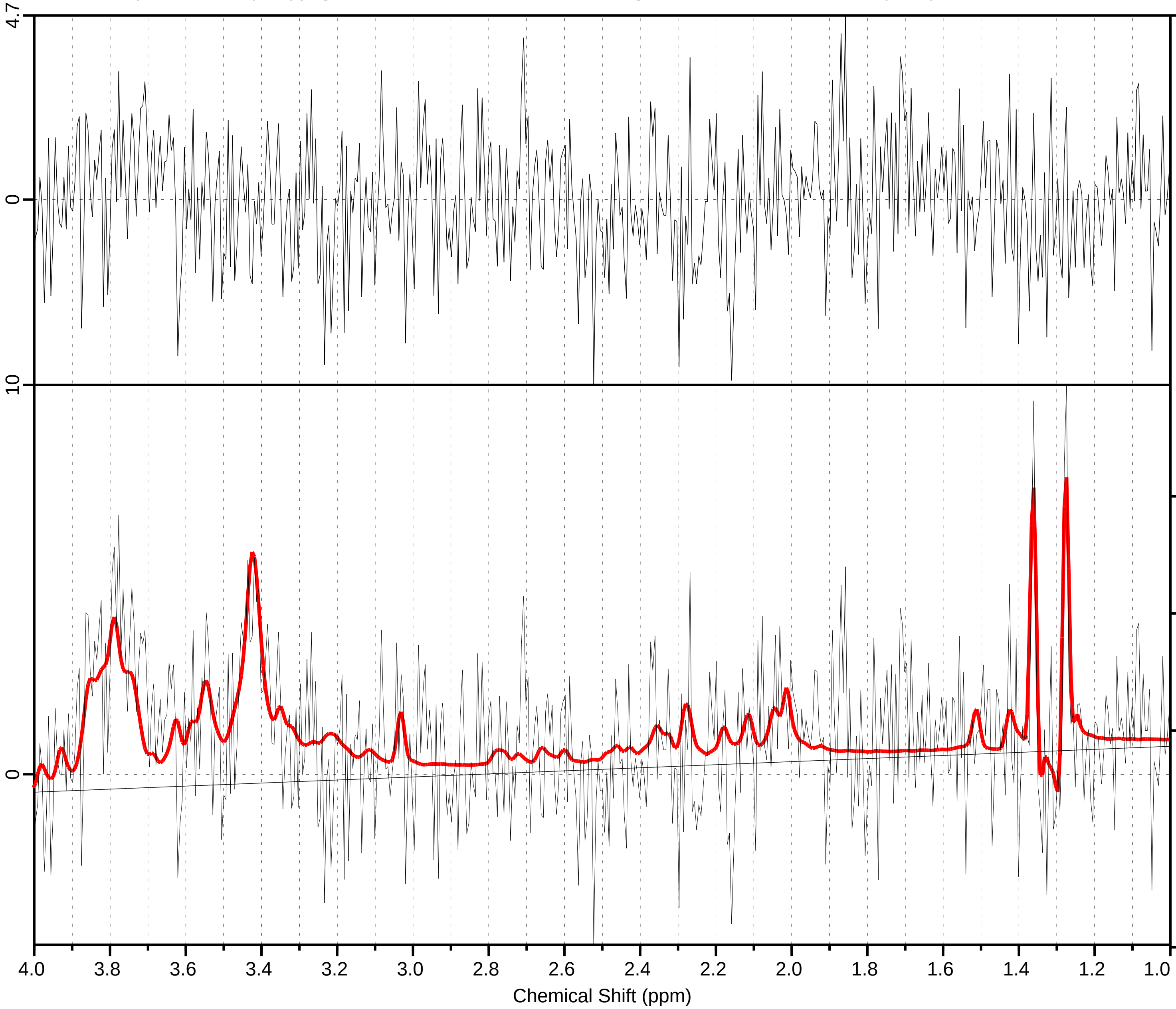


FIGURE 5: Borderline case with poor S/N and missing landmark peaks (CSF).

Data of: Biomedizinische NMR Forschungs GmbH, Goettingen

LCModel (Version 5.2-0) Copyright: S.W. Provencher. Ref.: Magn. Reson. Med. 30:672-679 (1993). *08-December-1999 23:21*



Conc.	**%SD**	**/Cr**	**Metab.**
0.233	79%	1.674	Ala
0.226	159%	1.622	Asp
0.139	68%	1.000	Cr
0.000	999%	0.000	GABA
2.955	**12%**	**21.240**	**Glc**
0.087	469%	0.628	Gln
0.796	45%	5.722	Glu
0.000	999%	0.000	GPC
0.000	999%	0.000	PCh
0.268	66%	1.925	Ins
1.094	**18%**	**7.864**	**Lac**
0.152	72%	1.095	NAA
0.077	165%	0.555	NAAG
0.024	225%	0.170	Scyllo
0.000	999%	0.000	Tau
0.230	68%	1.650	NAA+NAAG
0.000	999%	0.000	GPC+PCh
0.883	46%	6.351	Glu+Gln

DIAGNOSTICS

1 info	STARTV 20
2 info's	RFALSI 4
1 info	TWOREG 8

MISCELLANEOUS OUTPUT

```
FWHM = 0.014 ppm     S/N =  2
Data shift = 0.000 ppm
Ph:  16 deg          -5 deg/ppm
```

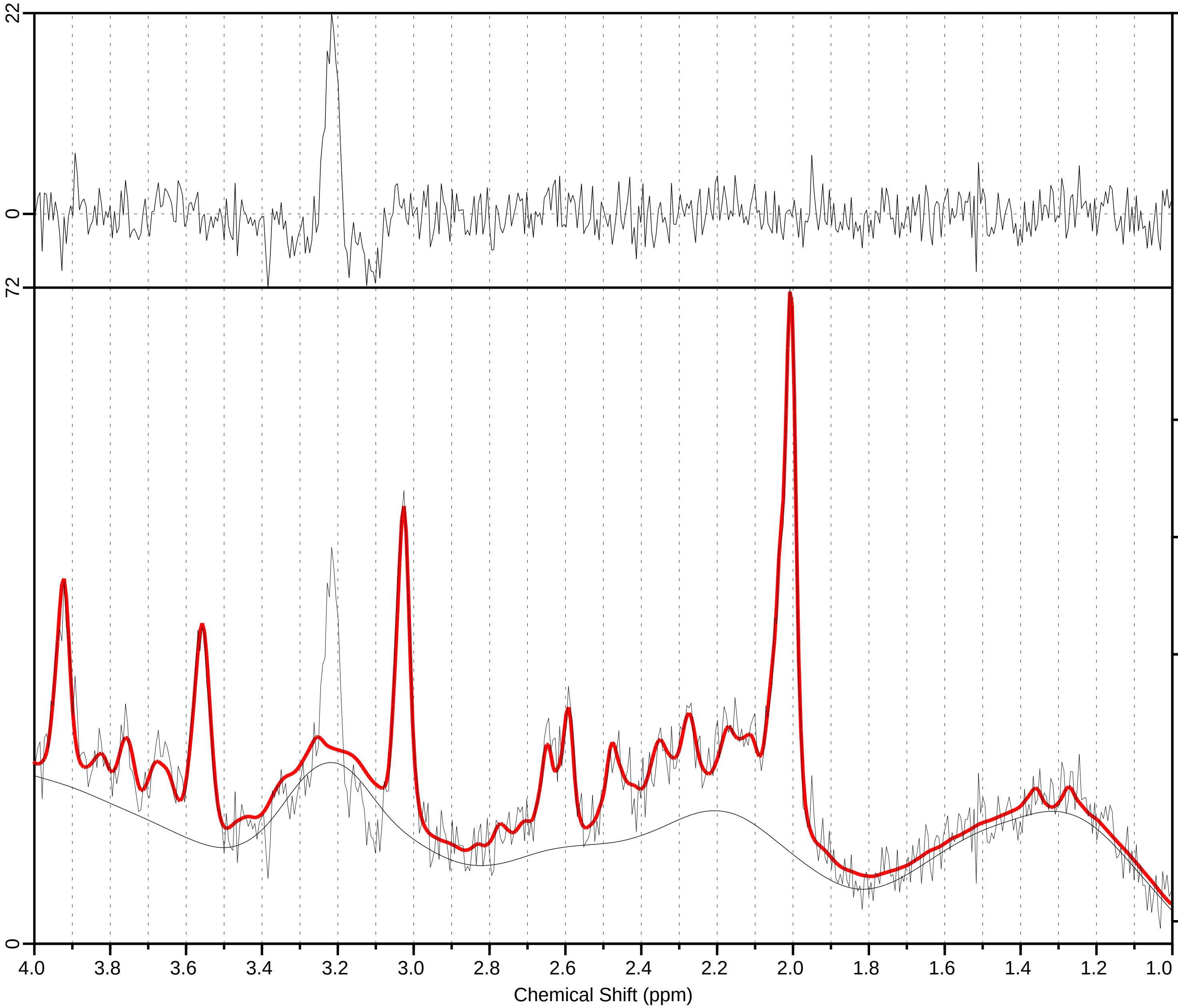
INPUT CHANGES

```
FILPS='ps/fig_csf.PS'
FILRAW='../../../doc/manual/f
  igures/raw/pat_535_116.RAW'
FILBAS='../../../doc/manual/f
  igures/Test.BASIS'
NUNFIL=2048, DELTAT=.0005
HZPPPM=84.47
```

FIGURE 6: Reject, because of the large artifact (simulated by removing choline compounds from the Basis Set).

Data of: Biomedizinische NMR Forschungs GmbH, Goettingen

LCModel (Version 5.2-0) Copyright: S.W. Provencher. *Ref.: Magn. Reson. Med. 30:672-679 (1993).* *08-December-1999 23:22*



Conc.	%SD	/Cr	Metab.
0.000	999%	0.000	Ala
1.298	88%	0.216	Asp
5.996	**8%**	**1.000**	**Cr**
0.000	999%	0.000	GABA
0.000	999%	0.000	Glc
2.552	55%	0.426	Gln
7.055	21%	1.177	Glu
6.519	**11%**	**1.087**	**Ins**
0.819	70%	0.137	Lac
8.024	**9%**	**1.338**	**NAA**
2.810	26%	0.469	NAAG
0.000	999%	0.000	Scyllo
0.000	999%	0.000	Tau
10.833	**6%**	**1.807**	**NAA+NAAG**
9.607	22%	1.602	Glu+Gln

DIAGNOSTICS

```
1 info      MYBASI  8
1 info      RFALSI 12
1 info      RFALSI 11
```

MISCELLANEOUS OUTPUT

```
FWHM = 0.044 ppm      S/N =  9
Data shift = 0.000 ppm
Ph:  44 deg          -15 deg/ppm
```

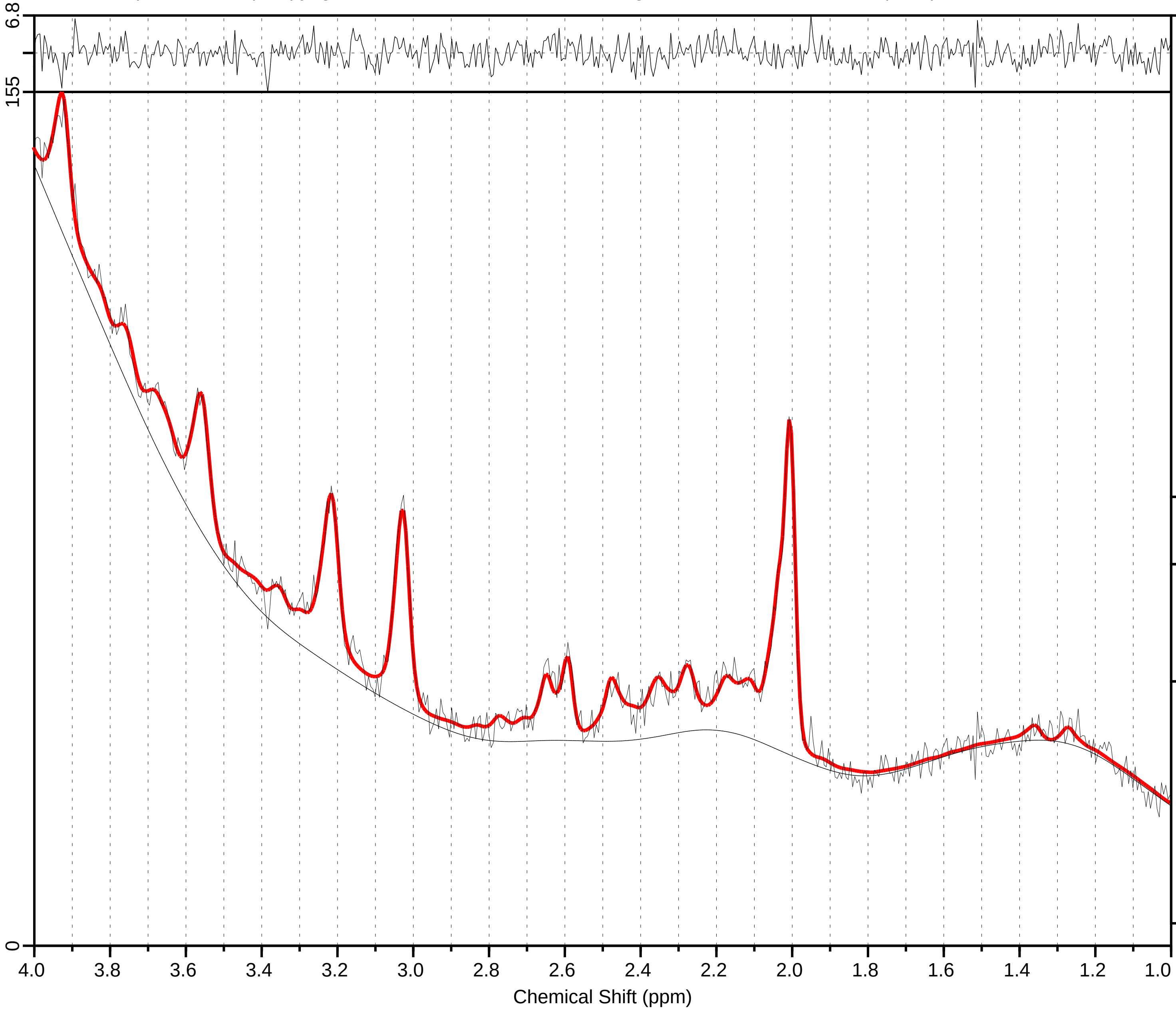
INPUT CHANGES

```
nomit=2, chomit(1)='PCh'
chomit(2)='GPC'
FILPS='ps/fig_no_cho.PS'
FILRAW='../../../doc/manual/f
  igures/raw/Test.RAW'
FILBAS='../../../doc/manual/f
  igures/Test.BASIS'
NUNFIL=2048, DELTAT=.0005
HZPPPM=84.47
```

FIGURE 7: LCModel can handle weak water suppression very well.

Data of: Biomedizinische NMR Forschungs GmbH, Goettingen

LCModel (Version 5.2-0) Copyright: S.W. Provencher.   *Ref.: Magn. Reson. Med. 30:672-679 (1993).*   *08-December-1999 23:24*



Conc.	%SD	/Cr	Metab.
0.000	999%	0.000	Ala
1.337	57%	0.191	Asp
6.989	**5%**	**1.000**	**Cr**
0.000	999%	0.000	GABA
0.000	999%	0.000	Glc
2.824	34%	0.404	Gln
7.803	**14%**	**1.117**	**Glu**
0.964	35%	0.138	GPC
1.006	34%	0.144	PCh
6.110	**9%**	**0.874**	**Ins**
0.963	42%	0.138	Lac
7.894	**4%**	**1.129**	**NAA**
2.819	**17%**	**0.403**	**NAAG**
0.081	144%	0.012	Scyllo
2.024	42%	0.290	Tau
10.713	**4%**	**1.533**	**NAA+NAAG**
1.970	**6%**	**0.282**	**GPC+PCh**
10.628	**14%**	**1.521**	**Glu+Gln**

DIAGNOSTICS

1 info   RFALSI 11

MISCELLANEOUS OUTPUT

FWHM = 0.043 ppm   S/N = 13
Data shift = 0.000 ppm
Ph: 44 deg   -16 deg/ppm

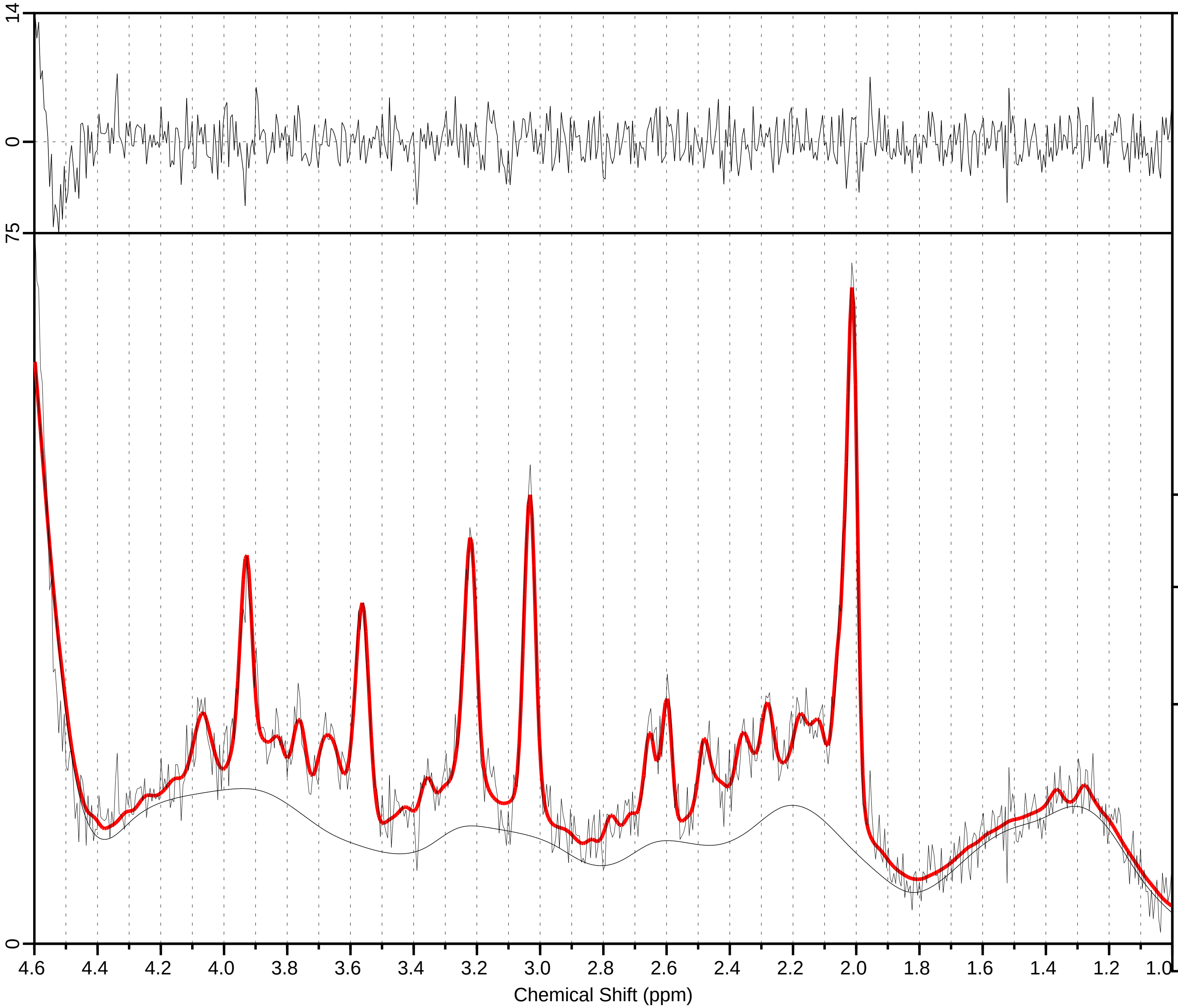
INPUT CHANGES

FILPS='ps/fig_water_ok.PS'
FILRAW='../../../doc/manual/figures/raw/fig_water_ok.RAW'
FILBAS='../../../doc/manual/figures/Test.BASIS'
NUNFIL=2048, DELTAT=.0005
HZPPPM=84.47

FIGURE 8: Reject, because the bend in the Baseline around 4.4 ppm is much too sharp, as seen in Residuals there.

Data of: Biomedizinische NMR Forschungs GmbH, Goettingen

LCModel (Version 5.2-0) Copyright: S.W. Provencher. Ref.: Magn. Reson. Med. 30:672-679 (1993). *08-December-1999 23:27*



Conc.	%SD	/Cr	Metab.
0.000	999%	0.000	Ala
1.697	64%	0.259	Asp
6.547	**7%**	**1.000**	**Cr**
0.323	331%	0.049	GABA
0.356	256%	0.054	Glc
3.021	46%	0.461	Gln
7.407	**19%**	**1.131**	**Glu**
1.105	37%	0.169	GPC
0.761	55%	0.116	PCh
6.435	**10%**	**0.983**	**Ins**
0.656	72%	0.100	Lac
7.873	**4%**	**1.203**	**NAA**
2.568	20%	0.392	NAAG
0.127	113%	0.019	Scyllo
1.588	85%	0.243	Tau
10.441	**5%**	**1.595**	**NAA+NAAG**
1.866	**8%**	**0.285**	**GPC+PCh**
10.428	**18%**	**1.593**	**Glu+Gln**

DIAGNOSTICS

2 info's RFALSI 12
1 info RFALSI 11

MISCELLANEOUS OUTPUT

FWHM = 0.043 ppm S/N = 11
Data shift = 0.006 ppm
Ph: 52 deg -13 deg/ppm

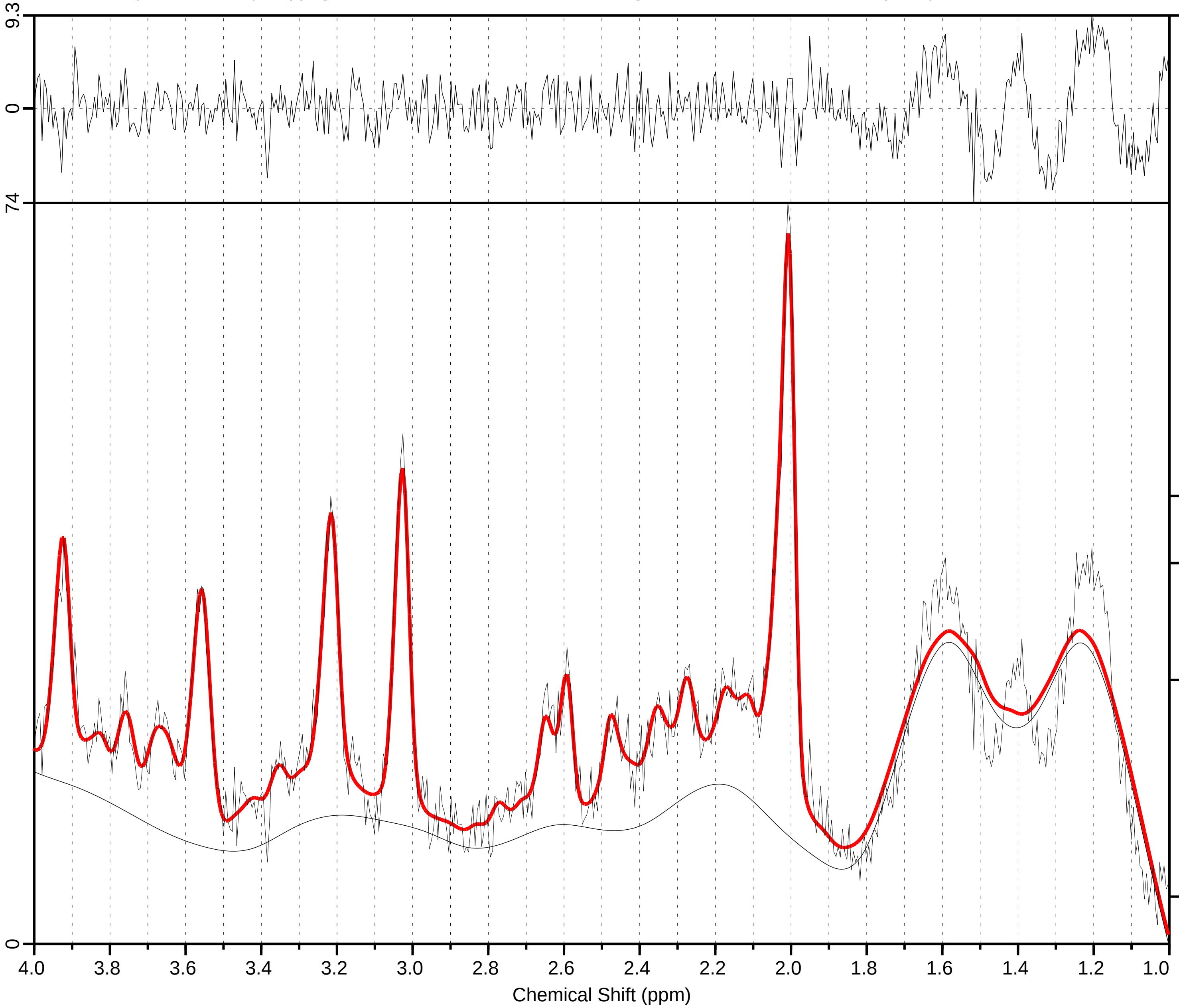
INPUT CHANGES

```
ppmst=4.6
FILPS='ps/fig_water_too_sharp
  .PS'
FILRAW='../../../doc/manual/f
  igures/raw/Test.RAW'
FILBAS='../../../doc/manual/f
  igures/Test.BASIS'
NUNFIL=2048, DELTAT=.0005
HZPPPM=84.47
```

FIGURE 9: Reject, because the 3 simulated lipid peaks are much too sharp to be accounted for by the Baseline.

Data of: Biomedizinische NMR Forschungs GmbH, Goettingen

LCModel (Version 5.2-0) Copyright: S.W. Provencher. *Ref.: Magn. Reson. Med. 30:672-679 (1993).* *08-December-1999 23:30*



Conc.	%SD	/Cr	Metab.
0.236	254%	0.036	Ala
1.139	117%	0.174	Asp
6.547	**8%**	**1.000**	**Cr**
0.000	999%	0.000	GABA
0.390	298%	0.060	Glc
3.365	48%	0.514	Gln
7.933	21%	1.212	Glu
1.017	52%	0.155	GPC
0.879	61%	0.134	PCh
6.665	**12%**	**1.018**	**Ins**
0.000	999%	0.000	Lac
8.466	**5%**	**1.293**	**NAA**
2.309	28%	0.353	NAAG
0.108	168%	0.017	Scyllo
1.712	97%	0.261	Tau
10.774	**6%**	**1.646**	**NAA+NAAG**
1.896	**9%**	**0.290**	**GPC+PCh**
11.299	21%	1.726	Glu+Gln

DIAGNOSTICS

1 info RFALSI 12

MISCELLANEOUS OUTPUT

FWHM = 0.048 ppm S/N = 9
Data shift = 0.000 ppm
Ph: 45 deg -15 deg/ppm

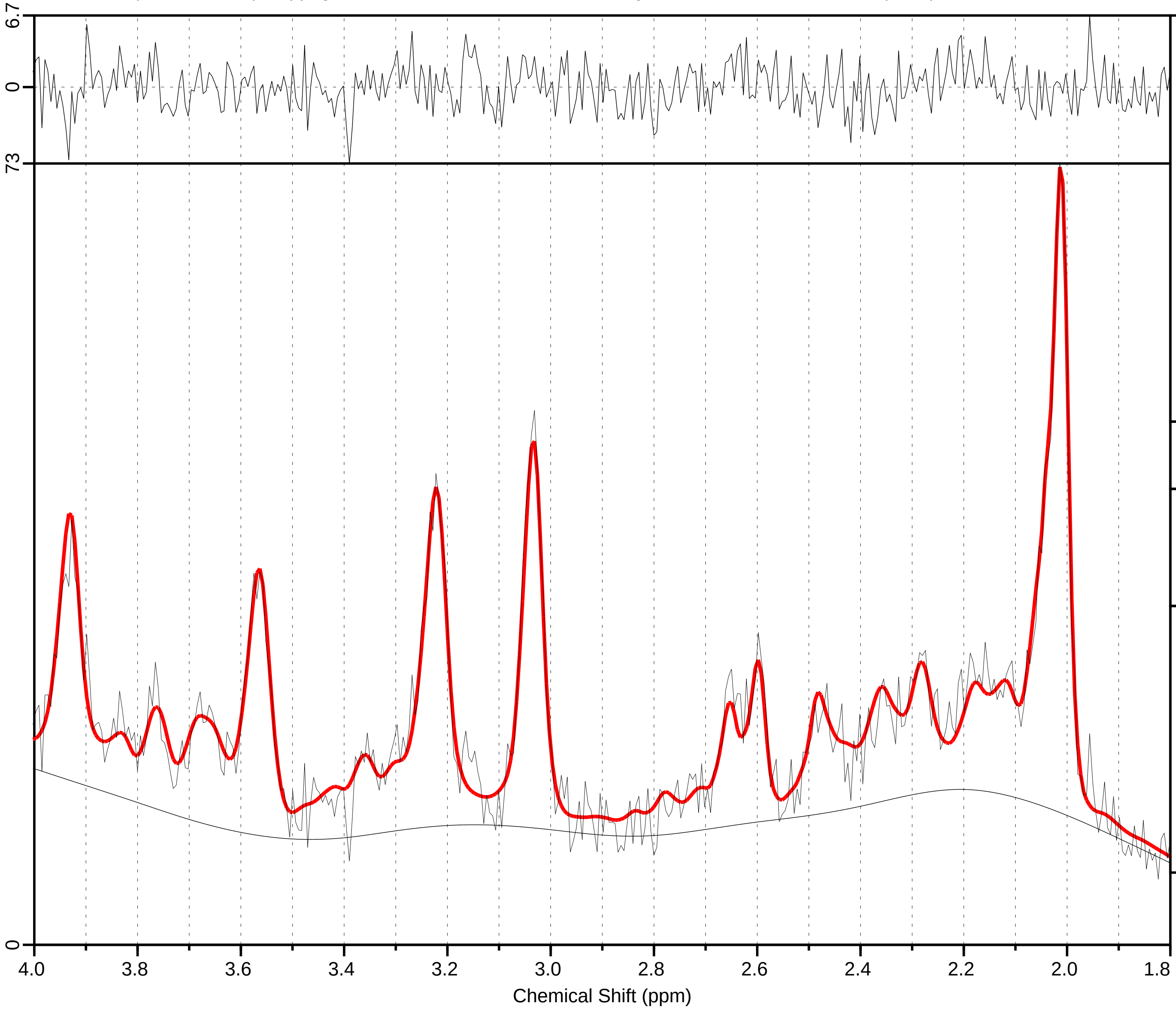
INPUT CHANGES

```
FILPS='ps/fig_lipid3.PS'
FILRAW='../../../doc/manual/f
  igures/raw/fig_lipid3.RAW'
FILBAS='../../../doc/manual/f
  igures/Test.BASIS'
NUNFIL=2048, DELTAT=.0005
HZPPPM=84.47
```

FIGURE 10: As Fig. #lipid3, but with the problematic lipid region truncated from the Analysis Window using PPMEND.

Data of: Biomedizinische NMR Forschungs GmbH, Goettingen

LCModel (Version 5.2-0) Copyright: S.W. Provencher. *Ref.: Magn. Reson. Med. 30:672-679 (1993).* *08-December-1999 23:32*



Conc.	%SD	/Cr	Metab.
0.901	80%	0.128	Asp
7.055	5%	1.000	Cr
0.000	999%	0.000	Glc
2.639	35%	0.374	Gln
8.047	13%	1.141	Glu
0.969	34%	0.137	GPC
1.082	32%	0.153	PCh
6.004	8%	0.851	Ins
7.737	4%	1.097	NAA
2.796	16%	0.396	NAAG
0.071	168%	0.010	Scyllo
2.113	37%	0.299	Tau
10.532	4%	1.493	NAA+NAAG
2.051	6%	0.291	GPC+PCh
10.686	12%	1.515	Glu+Gln

DIAGNOSTICS

```
1 info       MYBASI   8
```

MISCELLANEOUS OUTPUT

```
FWHM = 0.042 ppm     S/N = 13
Data shift = 0.006 ppm
Ph:  45 deg         -17 deg/ppm
```

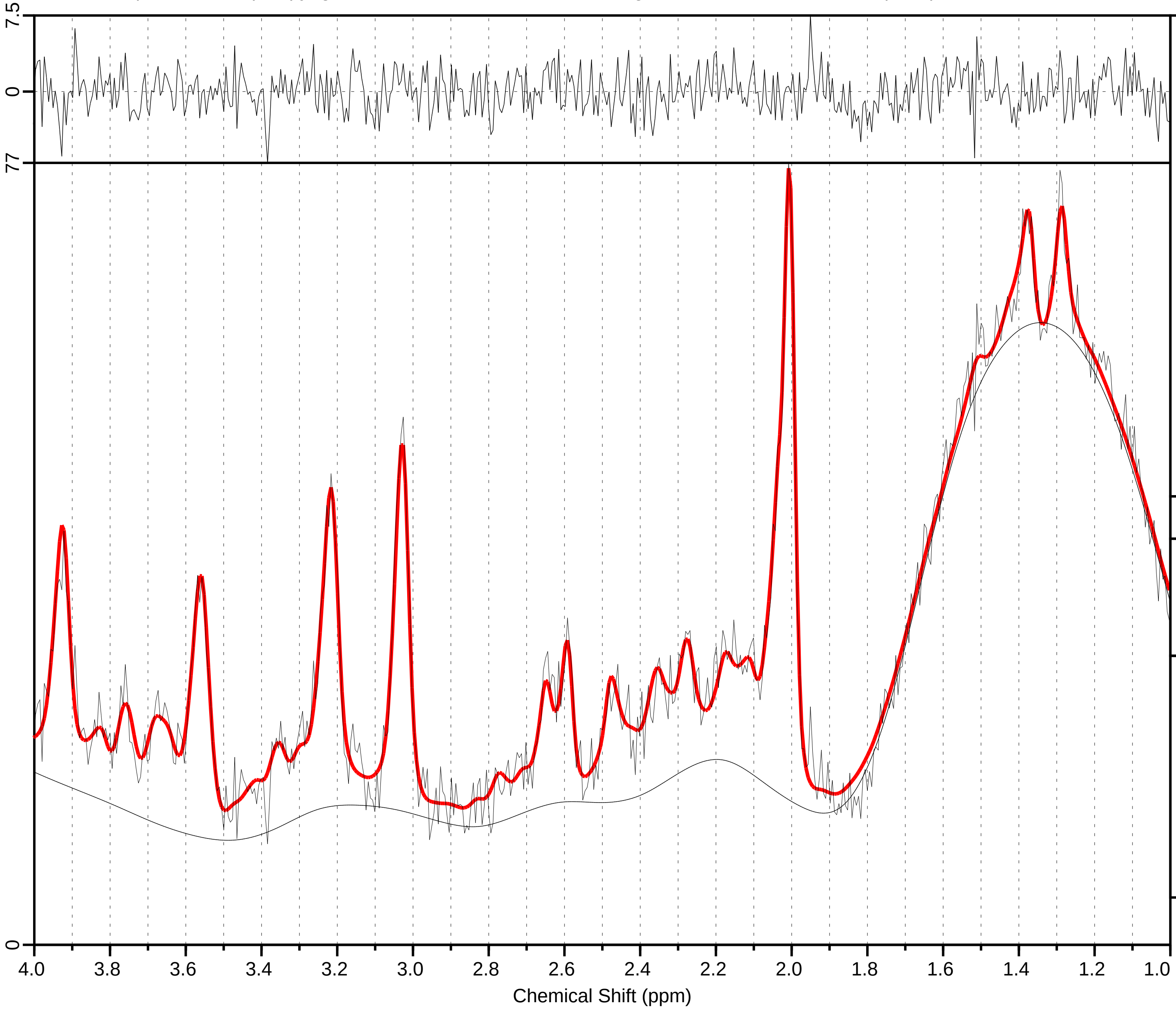
INPUT CHANGES

```
ppmend=1.8
FILPS='ps/fig_lipid3_ppmend.P
  S'
FILRAW='../../../doc/manual/f
  igures/raw/fig_lipid3.RAW'
FILBAS='../../../doc/manual/f
  igures/Test.BASIS'
NUNFIL=2048, DELTAT=.0005
HZPPPM=84.47
```

FIGURE 11: LCModel can resolve lactate from lipid very well.

Data of: Biomedizinische NMR Forschungs GmbH, Goettingen

LCModel (Version 5.2-0) Copyright: S.W. Provencher. Ref.: Magn. Reson. Med. 30:672-679 (1993). *08-December-1999 23:34*



Conc.	%SD	/Cr	Metab.
0.838	51%	0.122	Ala
1.265	67%	0.184	Asp
6.861	**6%**	**1.000**	**Cr**
0.000	999%	0.000	GABA
0.000	999%	0.000	Glc
3.279	33%	0.478	Gln
8.285	**15%**	**1.207**	**Glu**
0.900	39%	0.131	GPC
1.040	35%	0.152	PCh
6.467	**9%**	**0.943**	**Ins**
4.068	**14%**	**0.593**	**Lac**
8.421	**6%**	**1.227**	**NAA**
2.493	22%	0.363	NAAG
0.092	131%	0.013	Scyllo
2.333	43%	0.340	Tau
10.914	**4%**	**1.591**	**NAA+NAAG**
1.940	**7%**	**0.283**	**GPC+PCh**
11.563	**14%**	**1.685**	**Glu+Gln**

NO DIAGNOSTICS

MISCELLANEOUS OUTPUT

FWHM = 0.045 ppm S/N = 13

Data shift = 0.000 ppm

Ph: 39 deg -18 deg/ppm

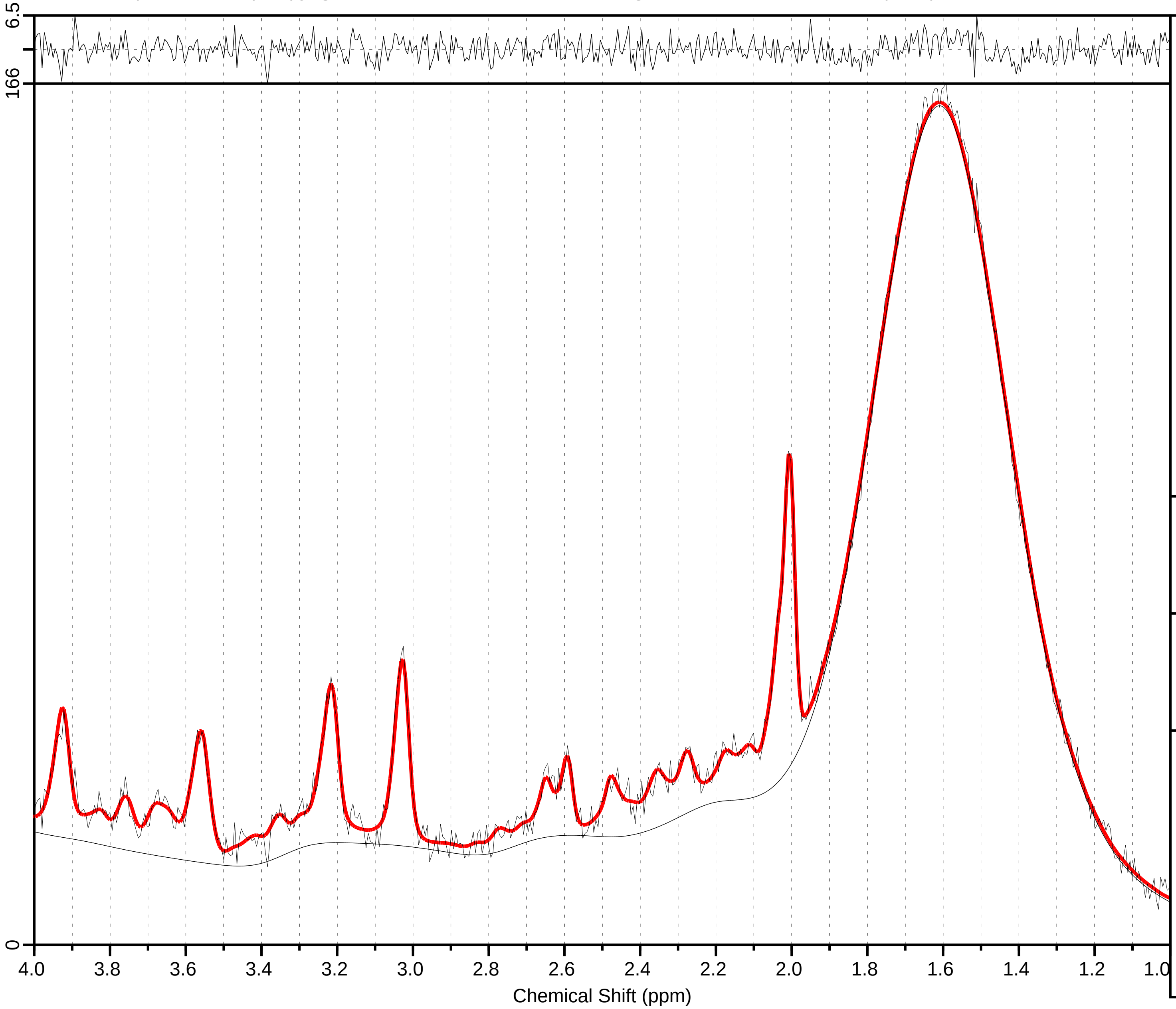
INPUT CHANGES

```
FILPS='ps/fig_lipid_ok.PS'
FILRAW='../../../doc/manual/f
  igures/raw/fig_lipid_ok.RAW
  '
FILBAS='../../../doc/manual/f
  igures/Test.BASIS'
NUNFIL=2048, DELTAT=.0005
HZPPPM=84.47
```

FIGURE 12: Borderline case: Baseline can just barely compensate for the huge simulated lipid peak.

Data of: Biomedizinische NMR Forschungs GmbH, Goettingen

LCModel (Version 5.2-0) Copyright: S.W. Provencher. *Ref.: Magn. Reson. Med. 30:672-679 (1993).* *08-December-1999 23:36*



Conc.	%SD	/Cr	Metab.
0.000	999%	0.000	Ala
1.260	75%	0.185	Asp
6.795	**7%**	**1.000**	**Cr**
0.000	999%	0.000	GABA
0.426	197%	0.063	Glc
3.165	36%	0.466	Gln
7.799	**17%**	**1.148**	**Glu**
0.844	45%	0.124	GPC
1.019	38%	0.150	PCh
6.357	**10%**	**0.936**	**Ins**
0.000	999%	0.000	Lac
8.113	**4%**	**1.194**	**NAA**
2.146	23%	0.316	NAAG
0.117	106%	0.017	Scyllo
2.100	59%	0.309	Tau
10.259	**4%**	**1.510**	**NAA+NAAG**
1.863	**7%**	**0.274**	**GPC+PCh**
10.963	**16%**	**1.613**	**Glu+Gln**

DIAGNOSTICS

2 info's	STARTV 6
1 warning	**STARTV 7**
1 info	PLINLS 7

MISCELLANEOUS OUTPUT

```
FWHM = 0.050 ppm      S/N = 13
Data shift = 0.000 ppm
Ph:  40 deg         -17 deg/ppm
```

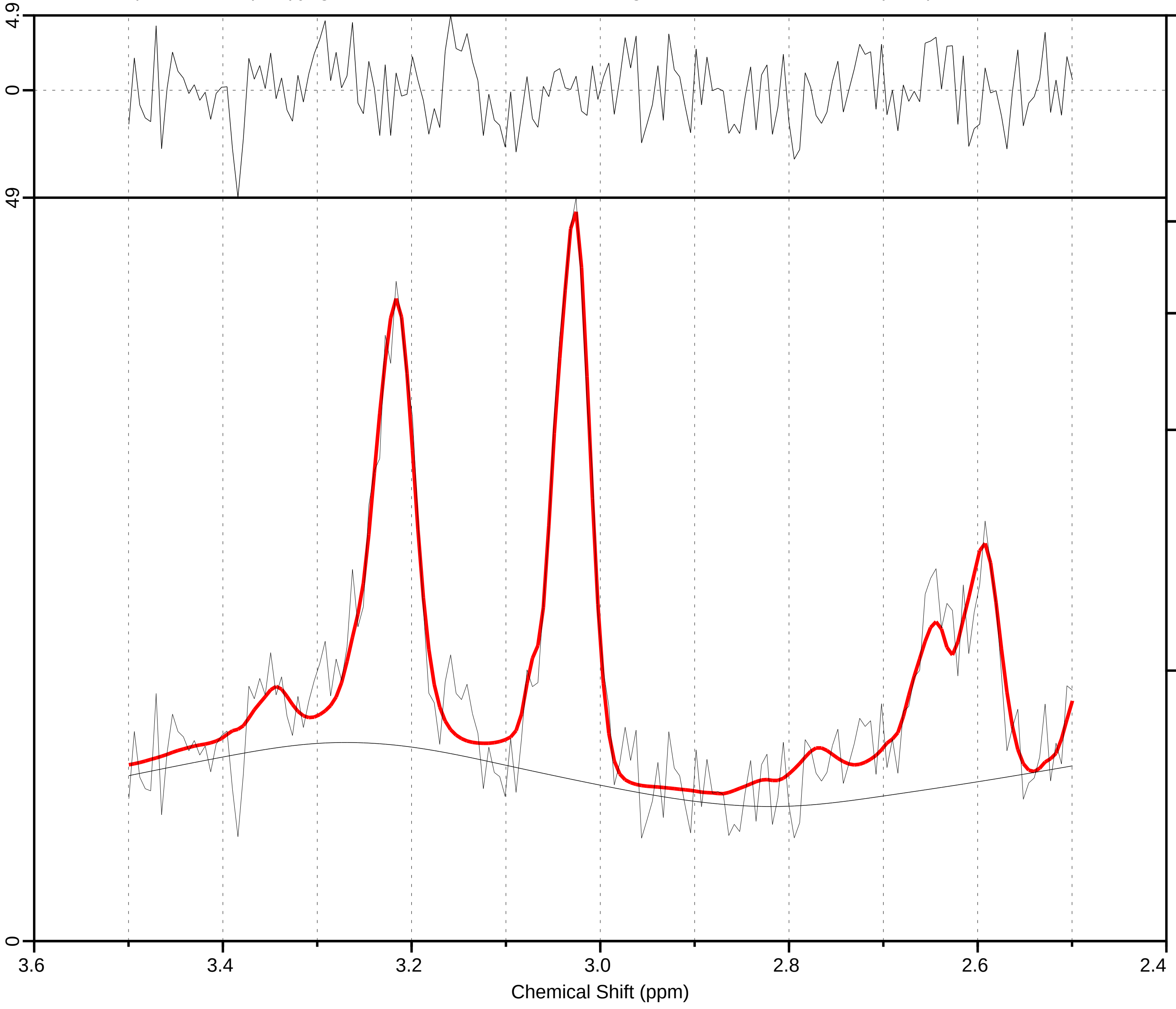
INPUT CHANGES

```
FILPS='ps/fig_lipid_borderlin
  e.PS'
FILRAW='../../../doc/manual/f
  igures/raw/fig_lipid_border
  line.RAW'
FILBAS='../../../doc/manual/f
  igures/Test.BASIS'
NUNFIL=2048, DELTAT=.0005
HZPPPM=84.47
```

FIGURE 13: Few peaks, very low information content.

Data of: Biomedizinische NMR Forschungs GmbH, Goettingen

LCModel (Version 5.2-0) Copyright: S.W. Provencher. *Ref.: Magn. Reson. Med. 30:672-679 (1993).* *08-December-1999 23:41*



Conc.	%SD	/Cr	Metab.
1.225	81%	0.185	Asp
6.616	**6%**	**1.000**	**Cr**
2.155	**7%**	**0.326**	**GPC**
0.000	999%	0.000	PCh
11.593	**11%**	**1.752**	**NAA**
0.268	49%	0.041	Scyllo
2.155	**7%**	**0.326**	**GPC+PCh**

DIAGNOSTICS

1 warning		**MYBASI**	**8**
1 info		FINOUT	9

MISCELLANEOUS OUTPUT

```
FWHM = 0.044 ppm      S/N =  7
Data shift = 0.000 ppm
Ph:  53 deg          -11 deg/ppm
```

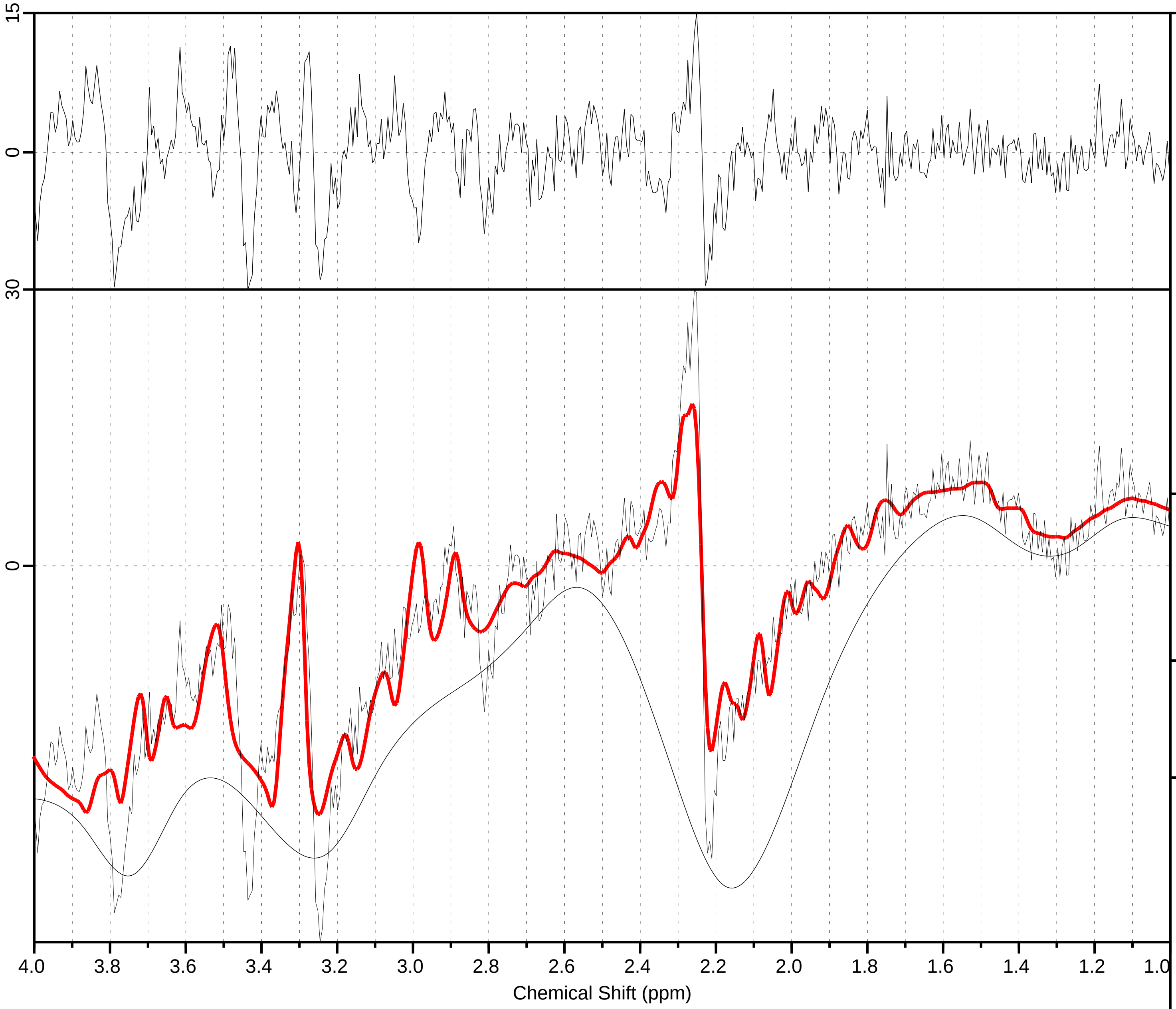
INPUT CHANGES

```
ppmst=3.5, ppmend=2.5
FILPS='ps/fig_narrow_ppm.PS'
FILRAW='../../../../doc/manual/f
  igures/raw/Test.RAW'
FILBAS='../../../../doc/manual/f
  igures/Test.BASIS'
NUNFIL=2048, DELTAT=.0005
HZPPPM=84.47
```

FIGURE 14: Total failure (due to grossly incorrect referencing constraint with PPMSHF).

Data of: Biomedizinische NMR Forschungs GmbH, Goettingen

LCModel (Version 5.2-0) Copyright: S.W. Provencher. Ref.: Magn. Reson. Med. 30:672-679 (1993). *08-December-1999 23:41*



Conc.	%SD	/Cr	Metab.
0.838	126%	0.000	Ala
2.313	86%	0.000	Asp
0.000	999%	0.000	Cr
16.894	**16%**	**0.000**	**GABA**
0.000	999%	0.000	Glc
0.000	999%	0.000	Gln
25.335	**10%**	**0.000**	**Glu**
0.577	36%	0.000	GPC
0.000	999%	0.000	PCh
4.639	21%	0.000	Ins
0.000	999%	0.000	Lac
0.225	245%	0.000	NAA
0.470	146%	0.000	NAAG
3.479	**12%**	**0.000**	**Scyllo**
0.000	999%	0.000	Tau
0.695	107%	0.000	NAA+NAAG
0.577	36%	0.000	GPC+PCh
25.335	**10%**	**0.000**	**Glu+Gln**

DIAGNOSTICS

9 info's	RFALSI 11
2 info's	TWOREG 8
1 info	RFALSI 12
1 warning	**FINOUT 7**
1 warning	**FINOUT 8**

MISCELLANEOUS OUTPUT

FWHM = 0.054 ppm S/N = 4
Data shift = 0.237 ppm
Ph: 235 deg -62 deg/ppm

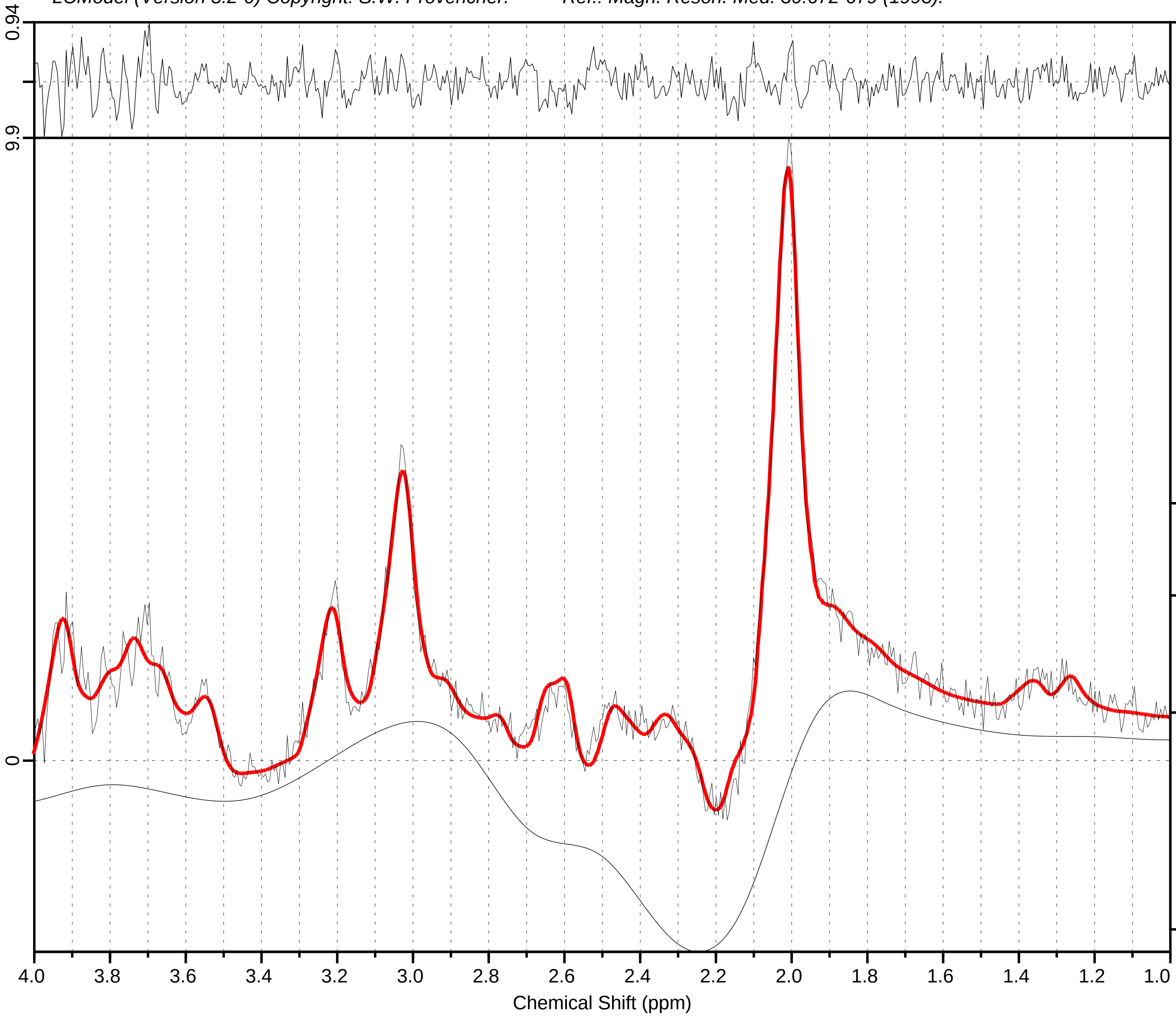
INPUT CHANGES

```
ppmshf=.4
FILPS='ps/fig_failure.PS'
FILRAW='../../../doc/manual/f
  igures/raw/Test.RAW'
FILBAS='../../../doc/manual/f
  igures/Test.BASIS'
NUNFIL=2048, DELTAT=.0005
HZPPPM=84.47
```

FIGURE 15: Sagging Baseline due to incompatibility between the data (TE=270 ms) and the Basis Set (TE=20 ms).

Data of: Biomedizinische NMR Forschungs GmbH, Goettingen

LCModel (Version 5.2-0) Copyright: S.W. Provencher. *Ref.: Magn. Reson. Med. 30:672-679 (1993).* *08-December-1999 23:46*



Conc.	%SD	/Cr	Metab.
0.000	999%	0.000	Ala
0.707	23%	0.700	Asp
1.009	**7%**	**1.000**	**Cr**
0.739	39%	0.732	GABA
0.000	999%	0.000	Glc
1.609	**17%**	**1.594**	**Gln**
2.527	**11%**	**2.504**	**Glu**
0.215	**10%**	**0.213**	**GPC**
0.000	999%	0.000	PCh
0.548	**14%**	**0.543**	**Ins**
0.385	28%	0.382	Lac
2.350	**4%**	**2.328**	**NAA**
0.000	999%	0.000	NAAG
0.000	999%	0.000	Scyllo
0.000	999%	0.000	Tau
2.350	**4%**	**2.328**	**NAA+NAAG**
0.215	**10%**	**0.213**	**GPC+PCh**
4.136	**10%**	**4.098**	**Glu+Gln**

DIAGNOSTICS

```
1 info      STARTV 24
6 info's    RFALSI 11
```

MISCELLANEOUS OUTPUT

```
FWHM = 0.076 ppm     S/N = 17
Data shift = 0.006 ppm
Ph: 233 deg        -17 deg/ppm
```

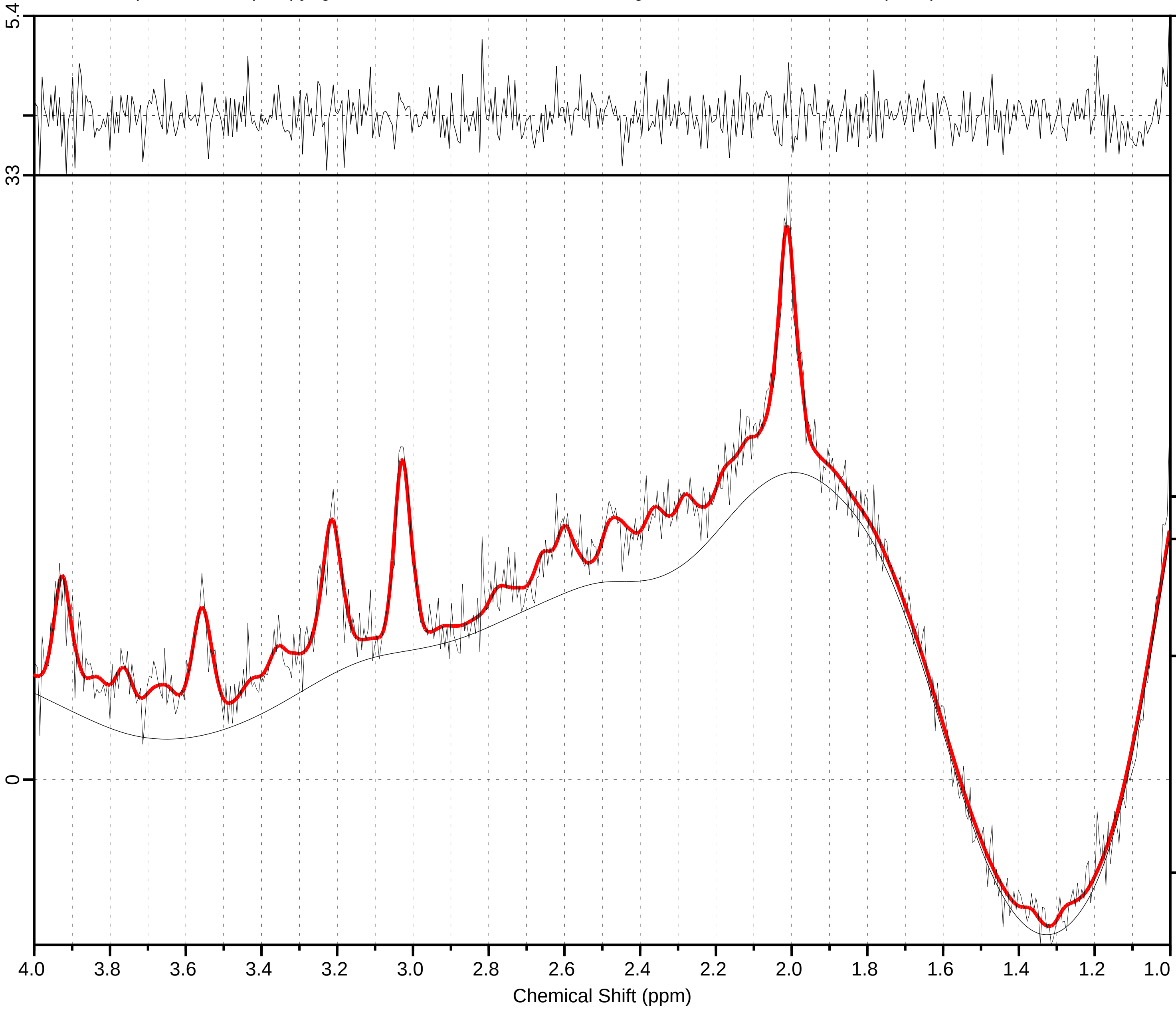
INPUT CHANGES

```
FILPS='ps/fig_sag.PS'
FILRAW='../../../doc/manual/f
  igures/raw/vol_339_128.RAW'
FILBAS='../../../doc/manual/f
  igures/Test.BASIS'
NUNFIL=2048, DELTAT=.0005
HZPPPM=84.47
```

FIGURE 16: Reject: Strong dip in the data (and Baseline) due to an artifact in the data.

Data of: Biomedizinische NMR Forschungs GmbH, Goettingen

LCModel (Version 5.2-0) Copyright: S.W. Provencher. Ref.: Magn. Reson. Med. 30:672-679 (1993). *08-December-1999 23:49*



Conc.	%SD	/Cr	Metab.
0.000	999%	0.000	Ala
0.960	57%	0.474	Asp
2.023	**7%**	**1.000**	**Cr**
0.489	120%	0.242	GABA
0.313	143%	0.155	Glc
1.866	40%	0.922	Gln
2.406	27%	1.189	Glu
0.203	54%	0.100	GPC
0.386	30%	0.191	PCh
1.865	**12%**	**0.922**	**Ins**
0.371	77%	0.184	Lac
2.263	**7%**	**1.119**	**NAA**
0.200	118%	0.099	NAAG
0.110	73%	0.054	Scyllo
0.778	86%	0.385	Tau
2.463	**9%**	**1.217**	**NAA+NAAG**
0.589	**10%**	**0.291**	**GPC+PCh**
4.272	24%	2.111	Glu+Gln

NO DIAGNOSTICS

MISCELLANEOUS OUTPUT

```
FWHM = 0.053 ppm     S/N =  6
Data shift = 0.017 ppm
Ph: 192 deg         -13 deg/ppm
```

INPUT CHANGES

```
FILPS='ps/fig_dip.PS'
FILRAW='../../../doc/manual/f
  igures/raw/pat_528_89.RAW'
FILBAS='../../../doc/manual/f
  igures/Test.BASIS'
NUNFIL=2048, DELTAT=.0005
HZPPPM=84.47
```

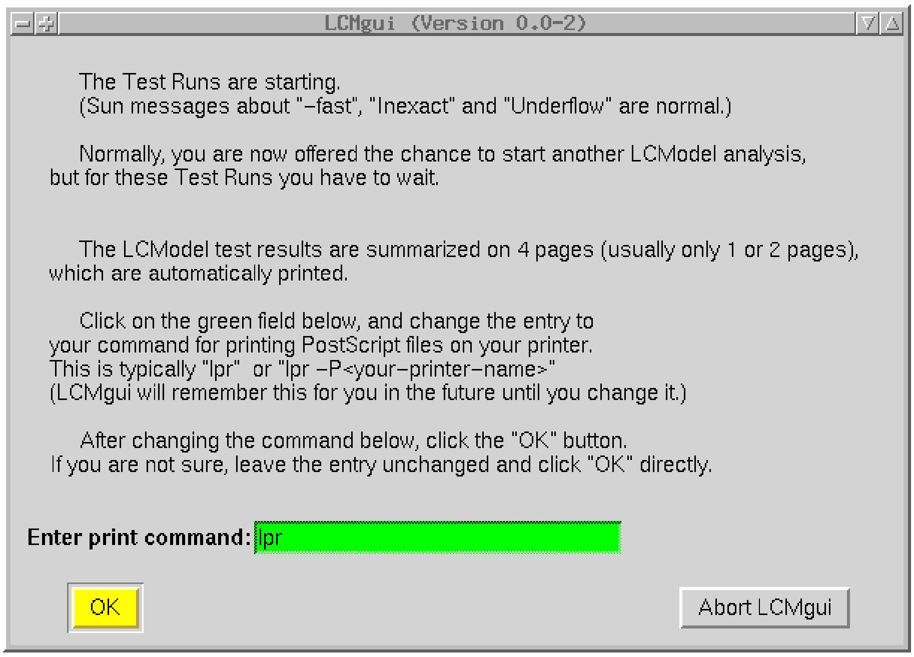


Figure 3.1: Here you enter your command for printing PostScript files.

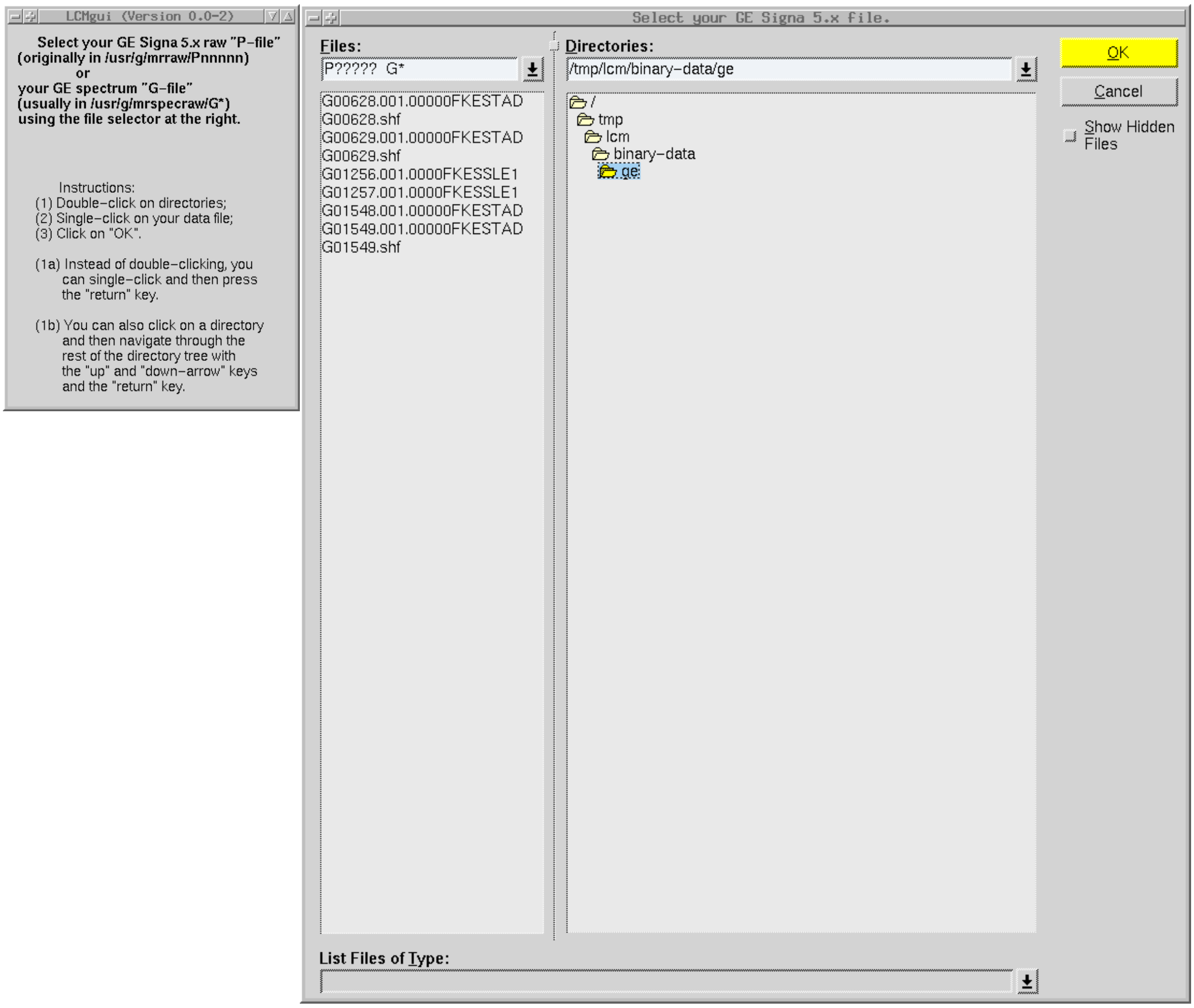


Figure 6.1: The File Selector

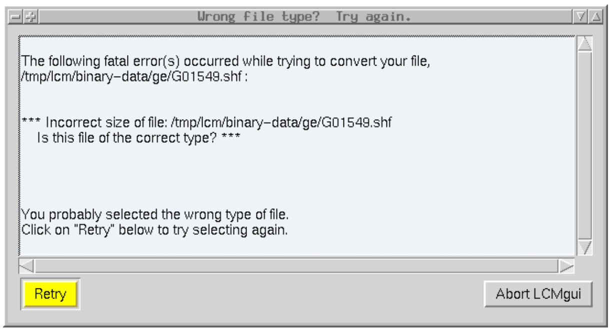


Figure 6.2: You selected a file of the wrong type in the File Selector

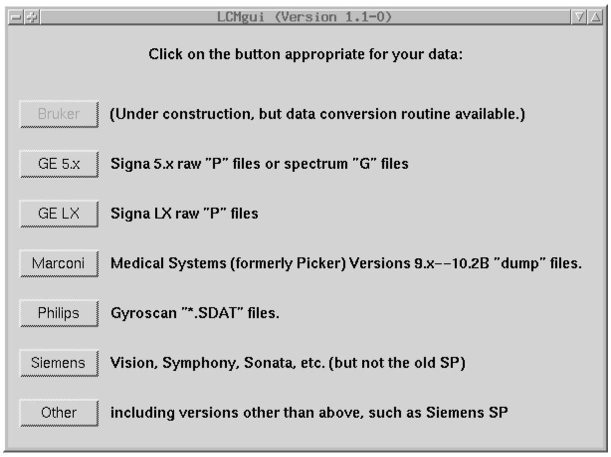


Figure 6.3: Note that GE Signa 5.x & LX have distinct buttons.

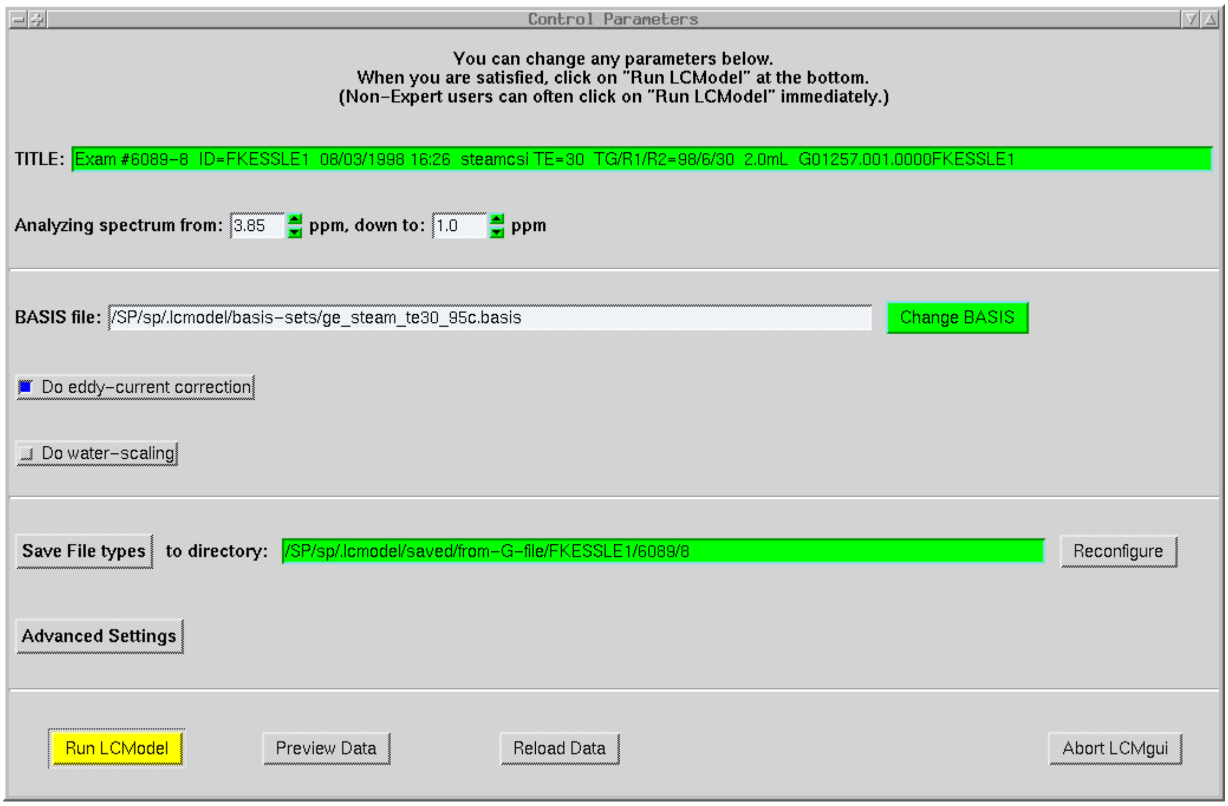


Figure 6.4: The Control Parameters Window

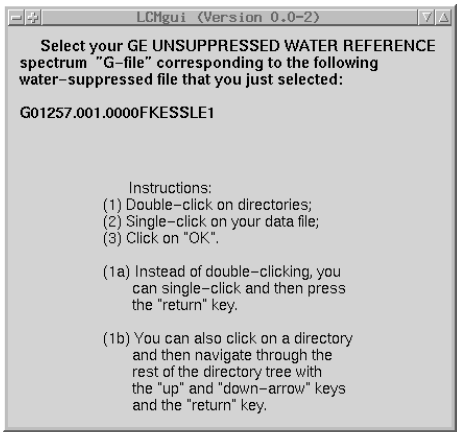


Figure 6.5: The instructions-part of the File Selector for the unsuppressed water reference.

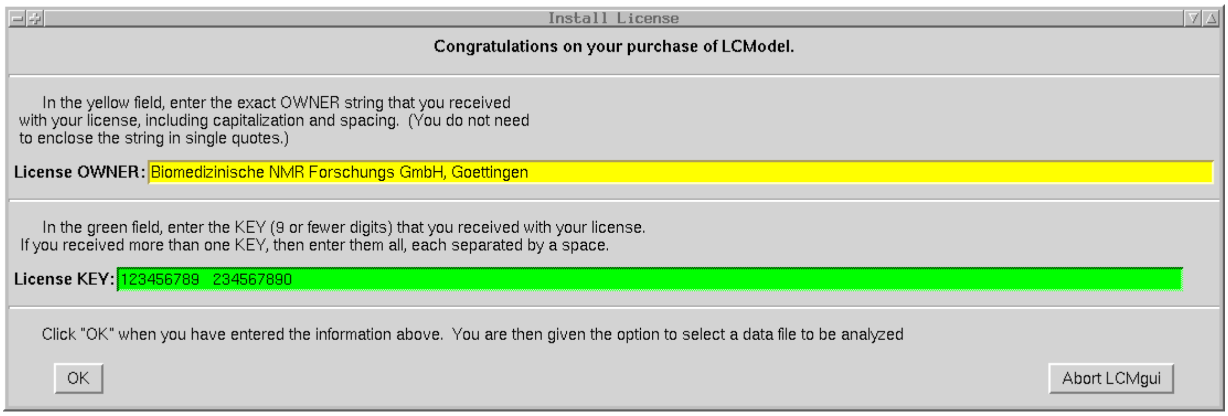


Figure 7.1: The Install License Window

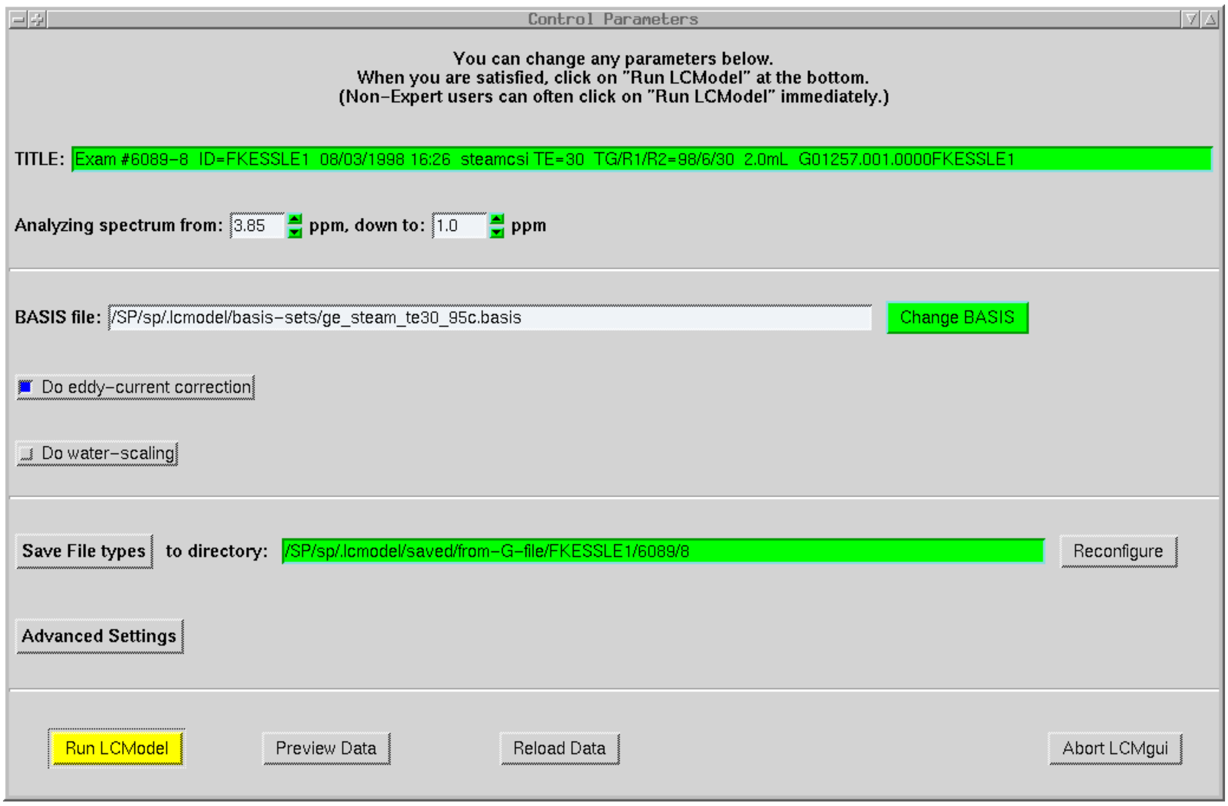


Figure 7.2: The Control Parameters Window

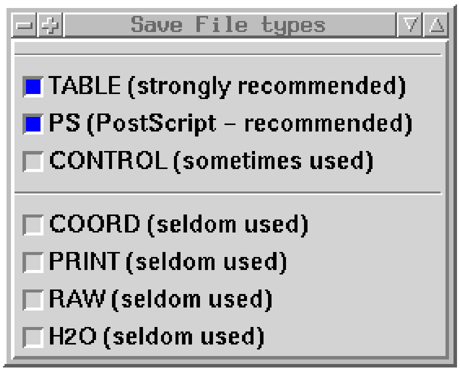


Figure 7.3: You get this menu when you click the “Save File Types” button in Fig. 7.2.

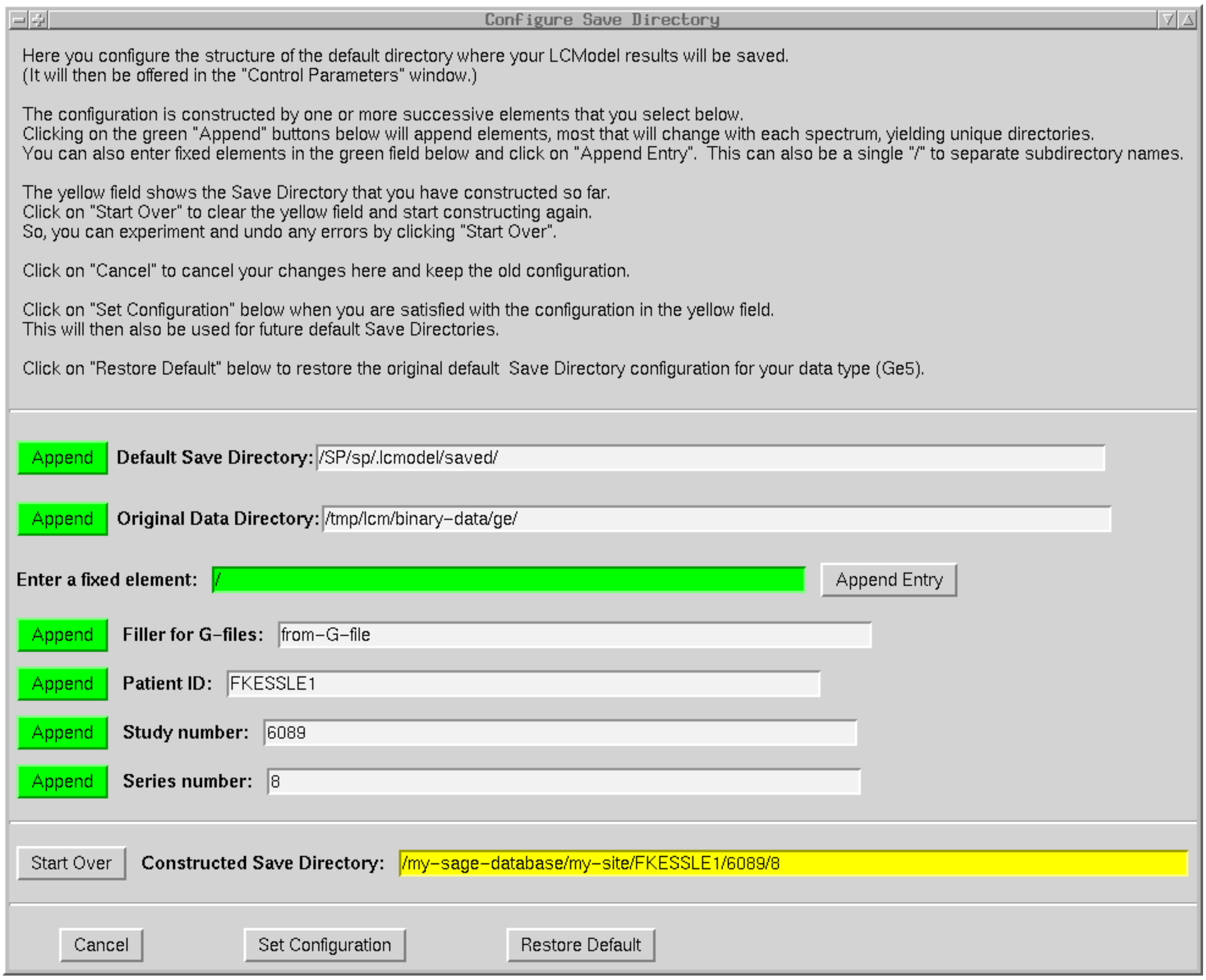


Figure 7.4: The window for permanently reconfiguring the structure of the archive directories.

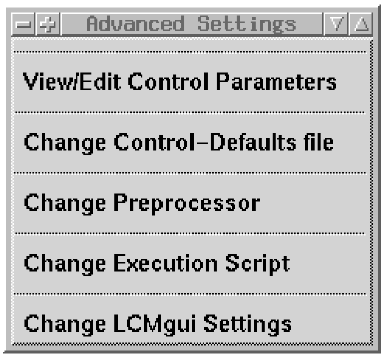


Figure 7.5: You get this menu when you click the "Advanced Settings" button in Fig. 7.2
.

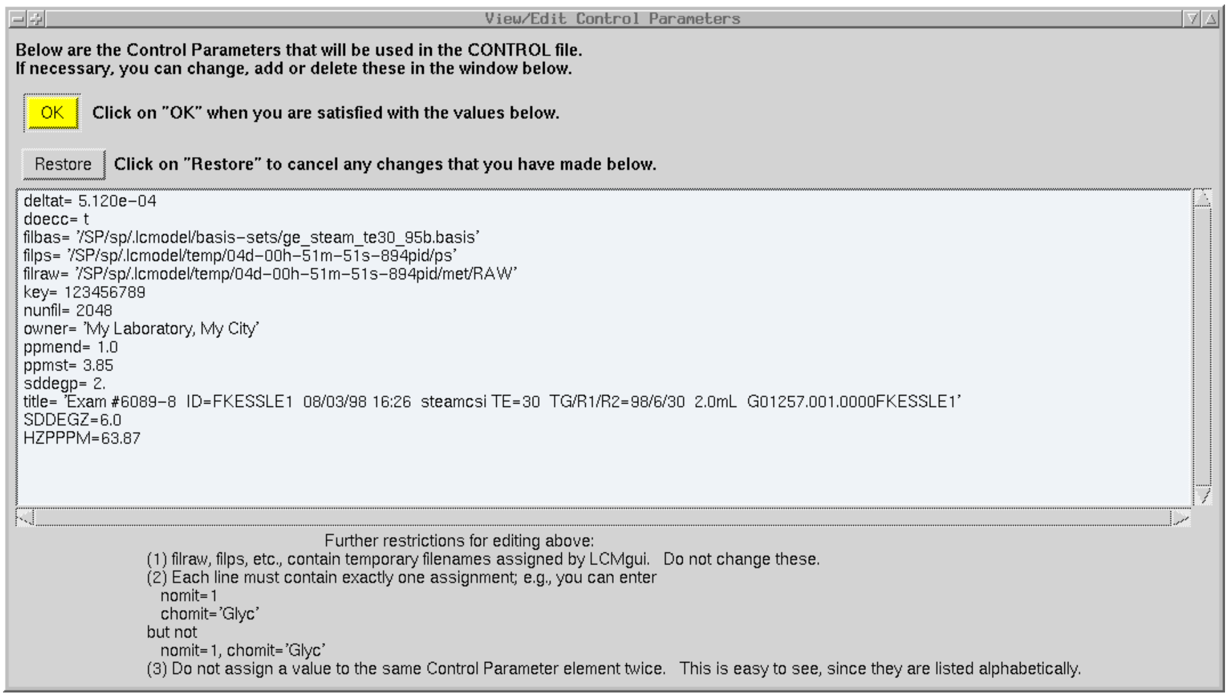


Figure 7.6: You can view, edit, delete or add all Control Parameters here.

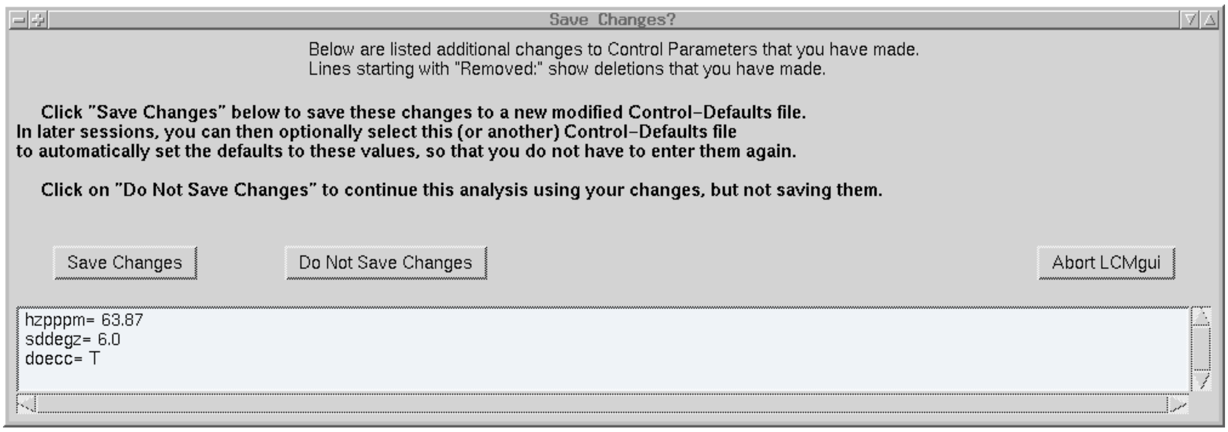


Figure 7.7: You can save all the Control Parameters, including your modifications, for optional use as starting defaults in the future.

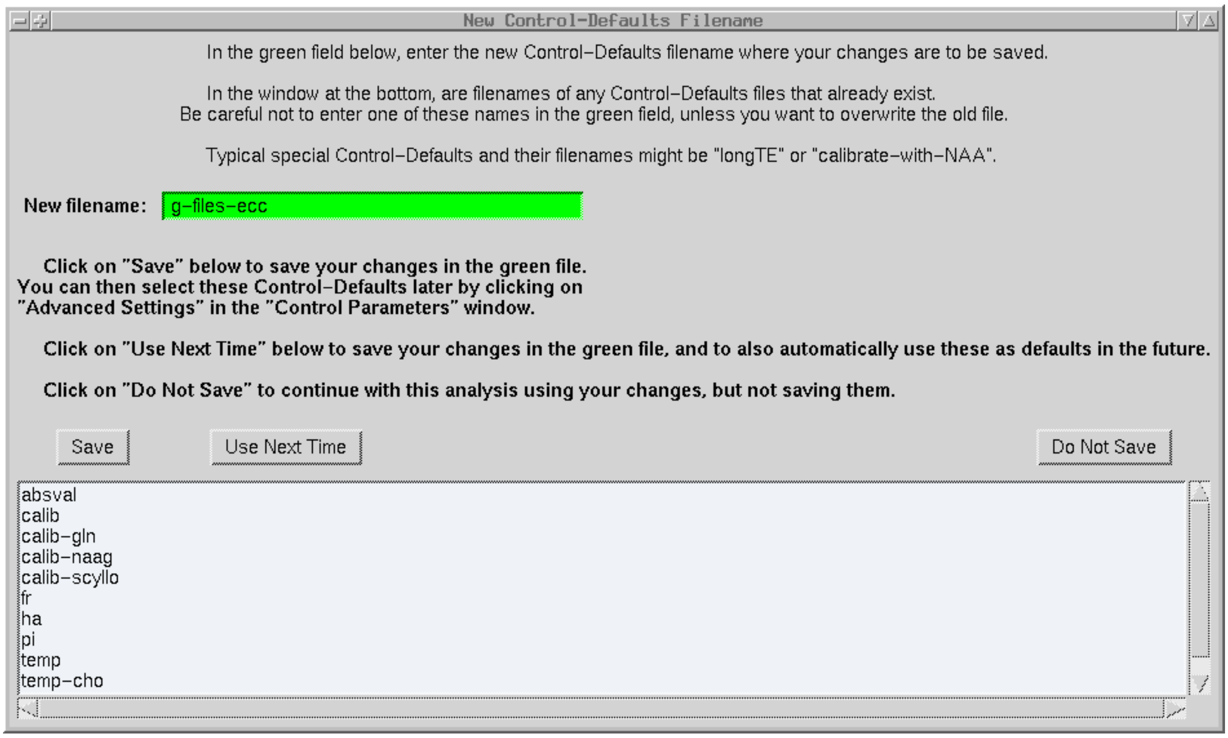


Figure 7.8: Here you enter a name for the file which will store your Control Parameters for optional future use.

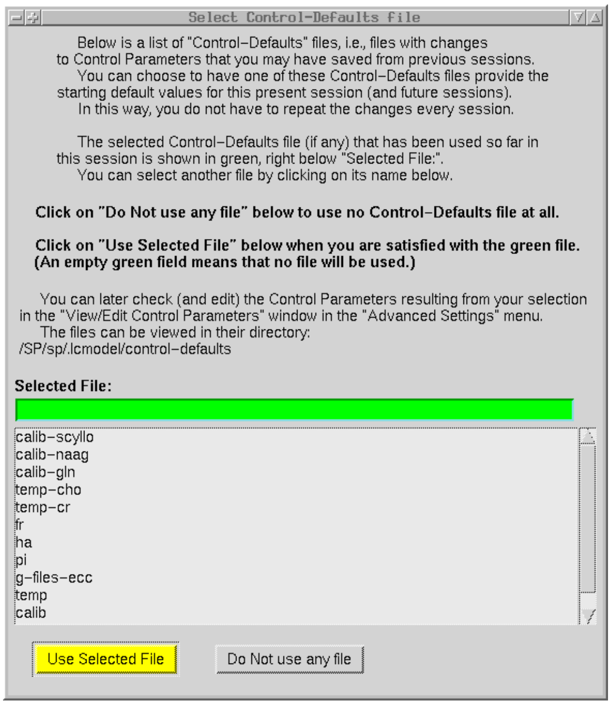


Figure 7.9: Here you select the Control-Defaults file to be used now and in the future.

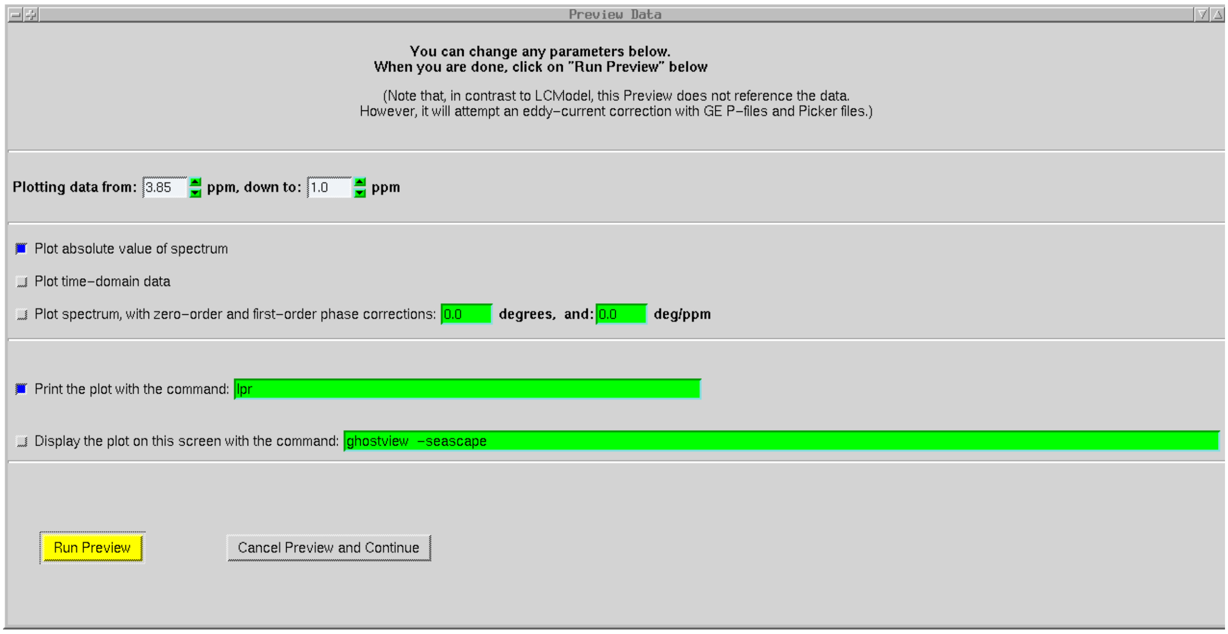


Figure 7.10: Here you can set and execute your commands for printing and/or plotting previews of your data.

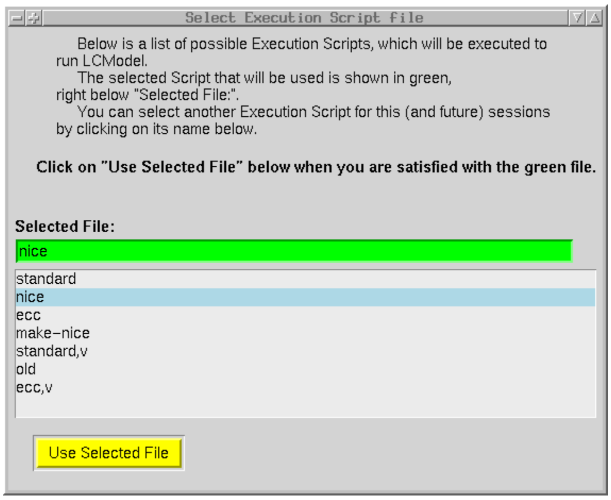


Figure 7.11: Here you can view and/or change the Execution Script that will be started by LCMgui.

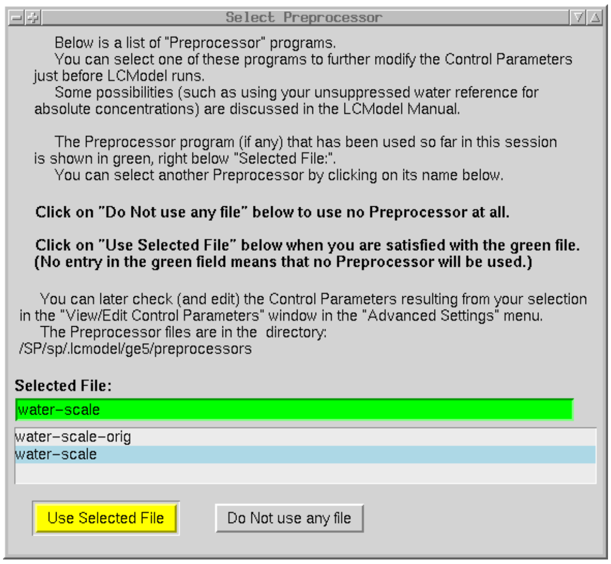


Figure 7.12: Here you can view and/or change the Preprocessor that will be used by LCMgui.