



Metabolite Data -> Sequence: STEAM; Fitting algorithm: LCModel; Fitting Style: Separate; Selected subspecs: metab
 Fitting range: 0.5 to 4 ppm; Baseline knot spacing: 0.4 ppm; ph0: 134.00deg; ph1: -0.70deg; refShift: 0.06 Hz; refFWHM: 0.07 ppr
 Number of metabolites: 18; Number of MM/lipids: 9 scale: 1

Raw Water Ratio

Asp	1.24e+00
Asc	0.00e+00
Cr	0.00e+00
GABA	6.70e-01
Gln	0.00e+00
Glu	1.66e+00
GPC	0.00e+00
GSH	8.45e-01
Lac	6.74e-02
PCr	2.74e+00
PE	1.41e+01
NAA	5.12e+00
NAAG	3.93e+00
Tau	1.83e+01
CrCH2	0.00e+00
Cr_PCr	2.74e+00
NAA_NAAC	9.05e+00
Glu_Gln	1.66e+00
Lip13a	1.47e+02
Lip13b	0.00e+00
Lip09	2.26e+01
MM09	6.37e+00
Lip20	2.28e+01
MM20	1.53e+01
MM12	3.72e+00
MM14	0.00e+00
MM17	0.00e+00

LCModel Separate metab fit plot: 8004672353.dat

