

$^{12}_\Delta C$ with fidarc604

I tried to see if Hyp2006 analysis is "cured" with
newest reconstruction program
FIDAR_C604 (December production)

The prologue PLB 622

$-B_{\Lambda}$ (MeV) for the different "observed" peaks

#1 -10.94 ± 0.06

#2 -8.4 ± 0.2

#3 -5.9 ± 0.1

#4 -3.8 ± 0.1

#5 -1.6 ± 0.2

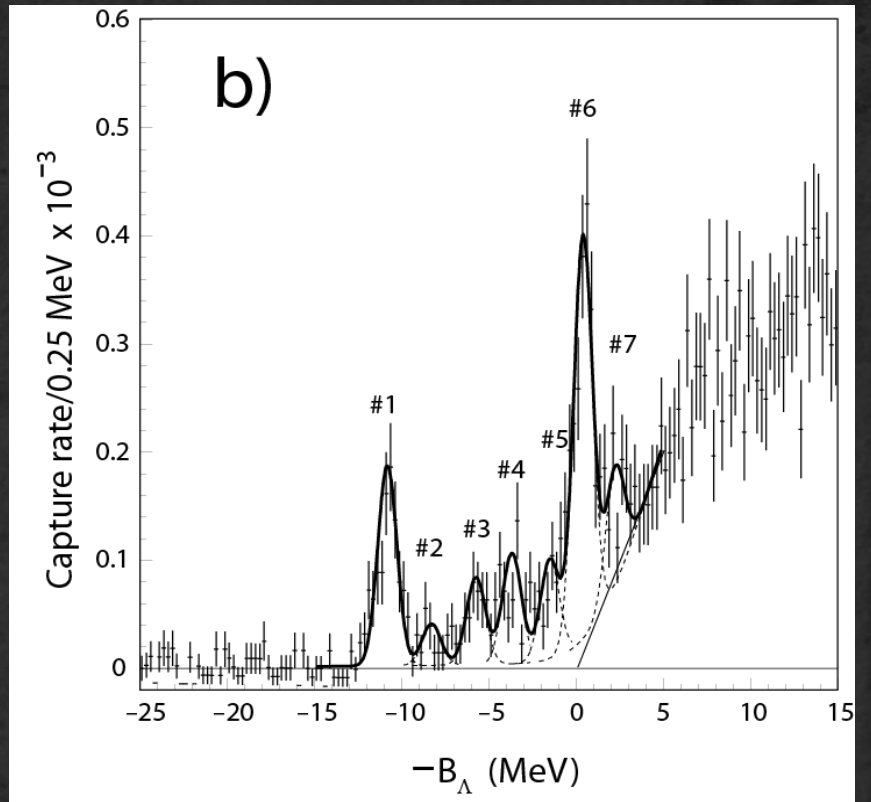
#6 0.27 ± 0.06

#7 2.1 ± 0.2

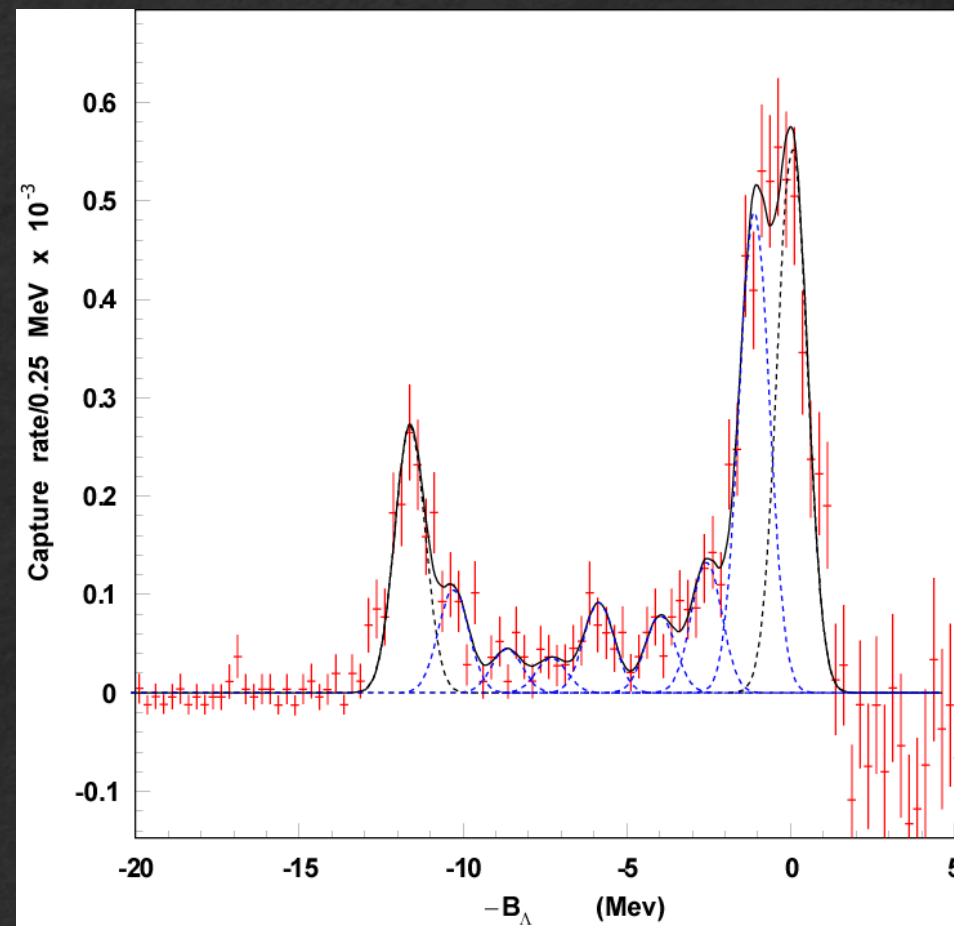
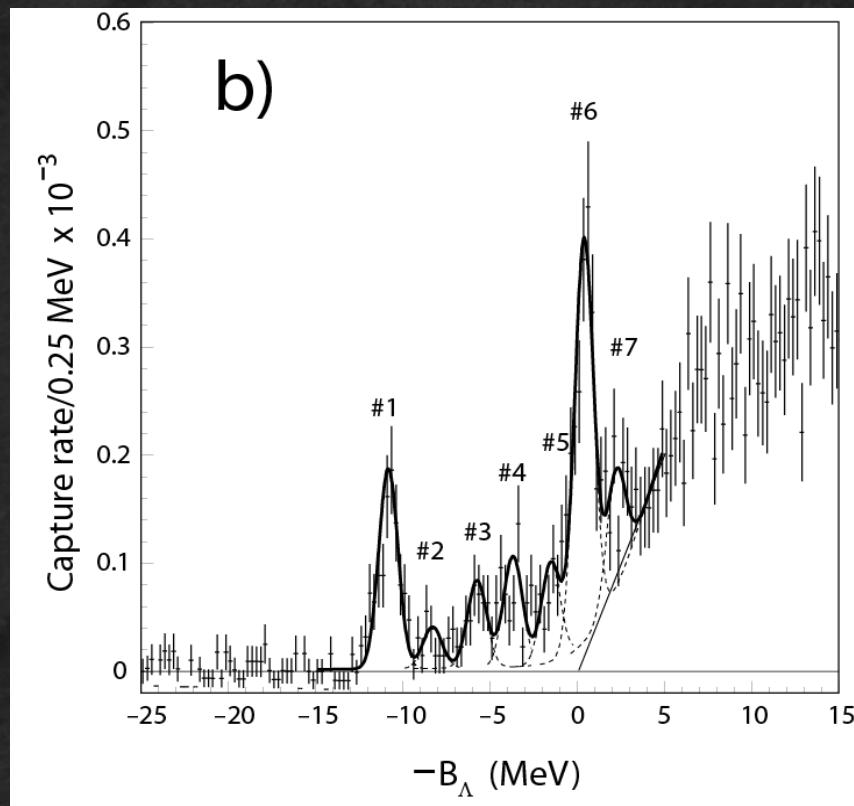
resolution 0.55 MeV (fixed and determined by an "ad hoc" fit on the S-state with "dedicated" cuts).

These results were obtained using data reconstructed by FIDARC v5lland with

only 2 of 3 ^{12}C targets (target 1 and 8) due to problem on alignment...



The prologue #YP2006

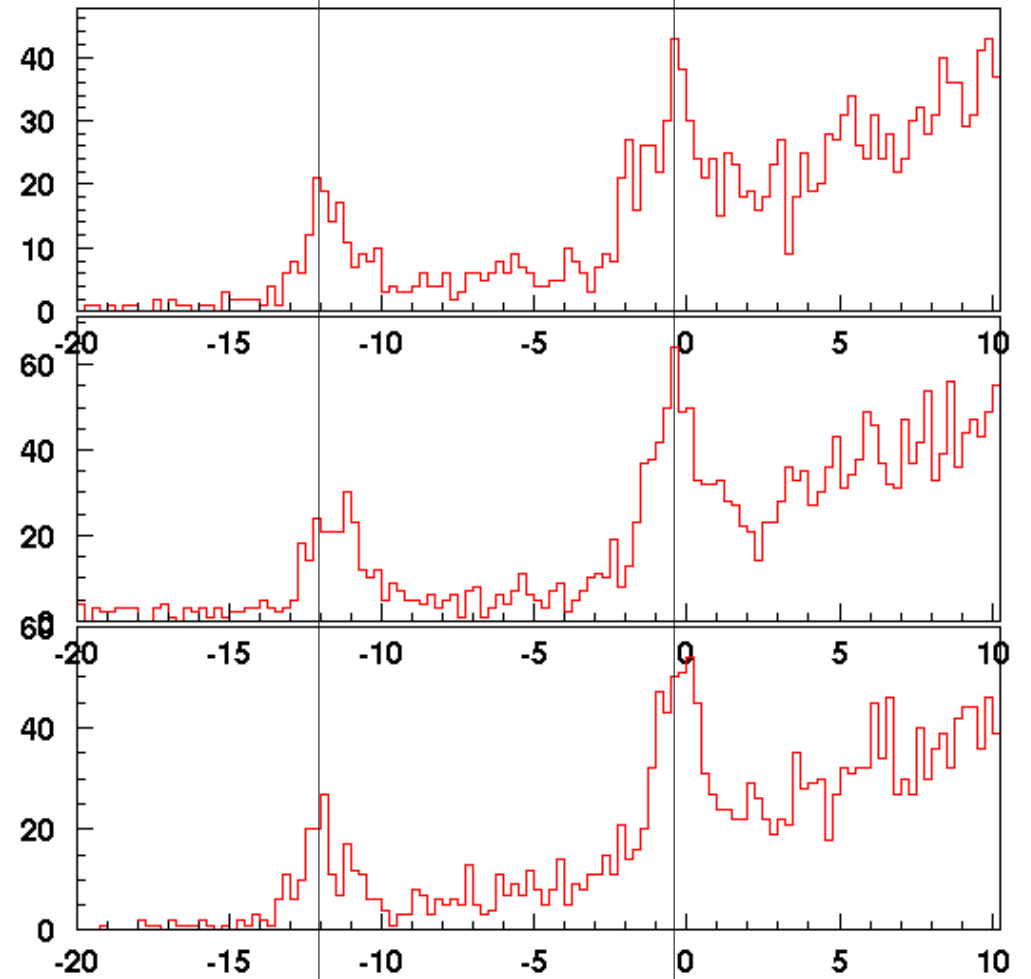
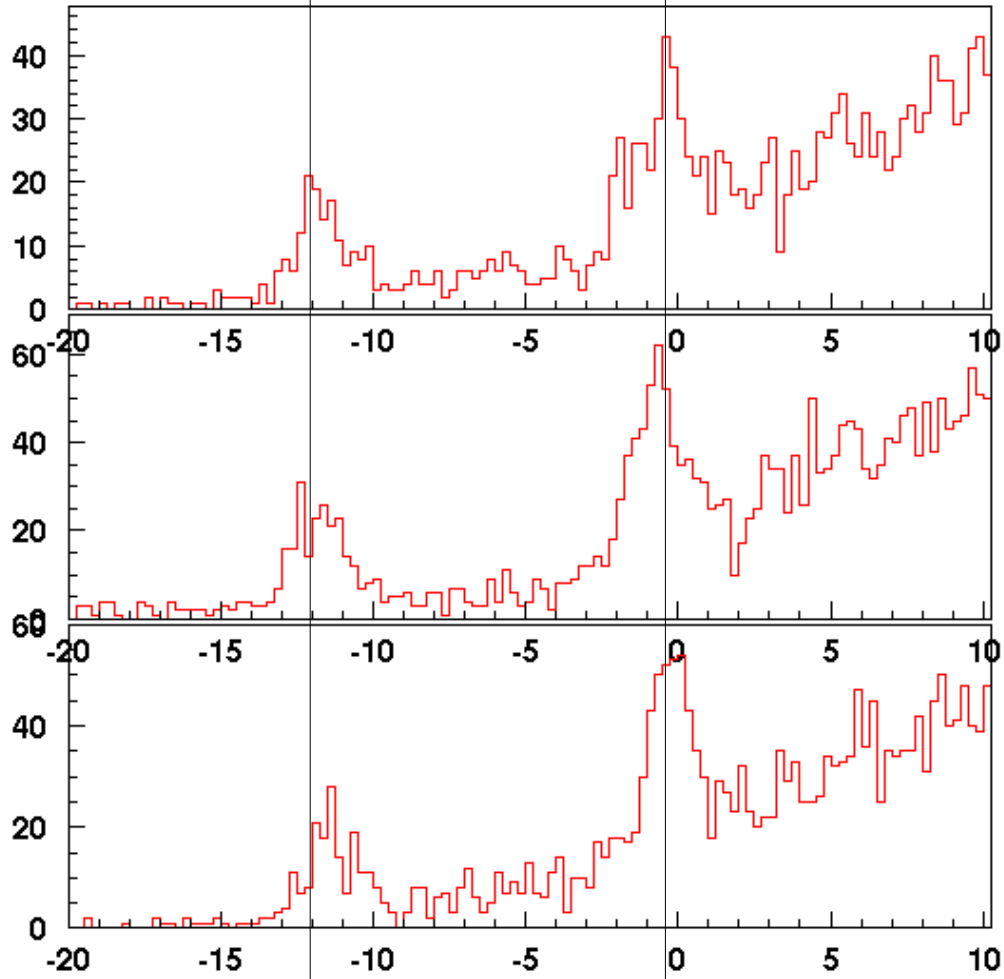


Hyp2006 analysis "opened" a discussion about the $1p$ level splitting w.r.t. PLB results

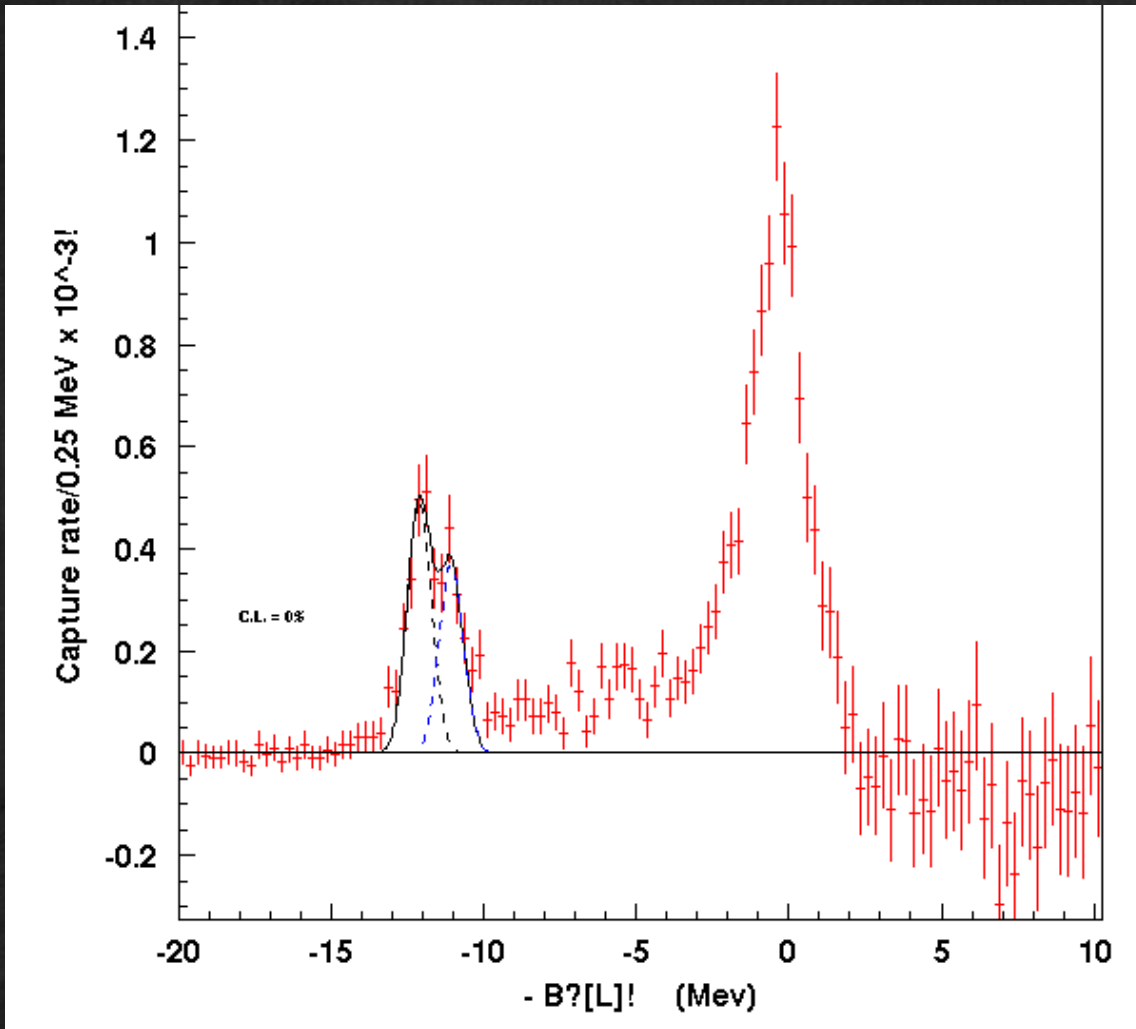
Now.....

$^{12}_{\Lambda}C$ is now analyzed with our
latest reconstruction program.
Optimized selection criteria

Now.....

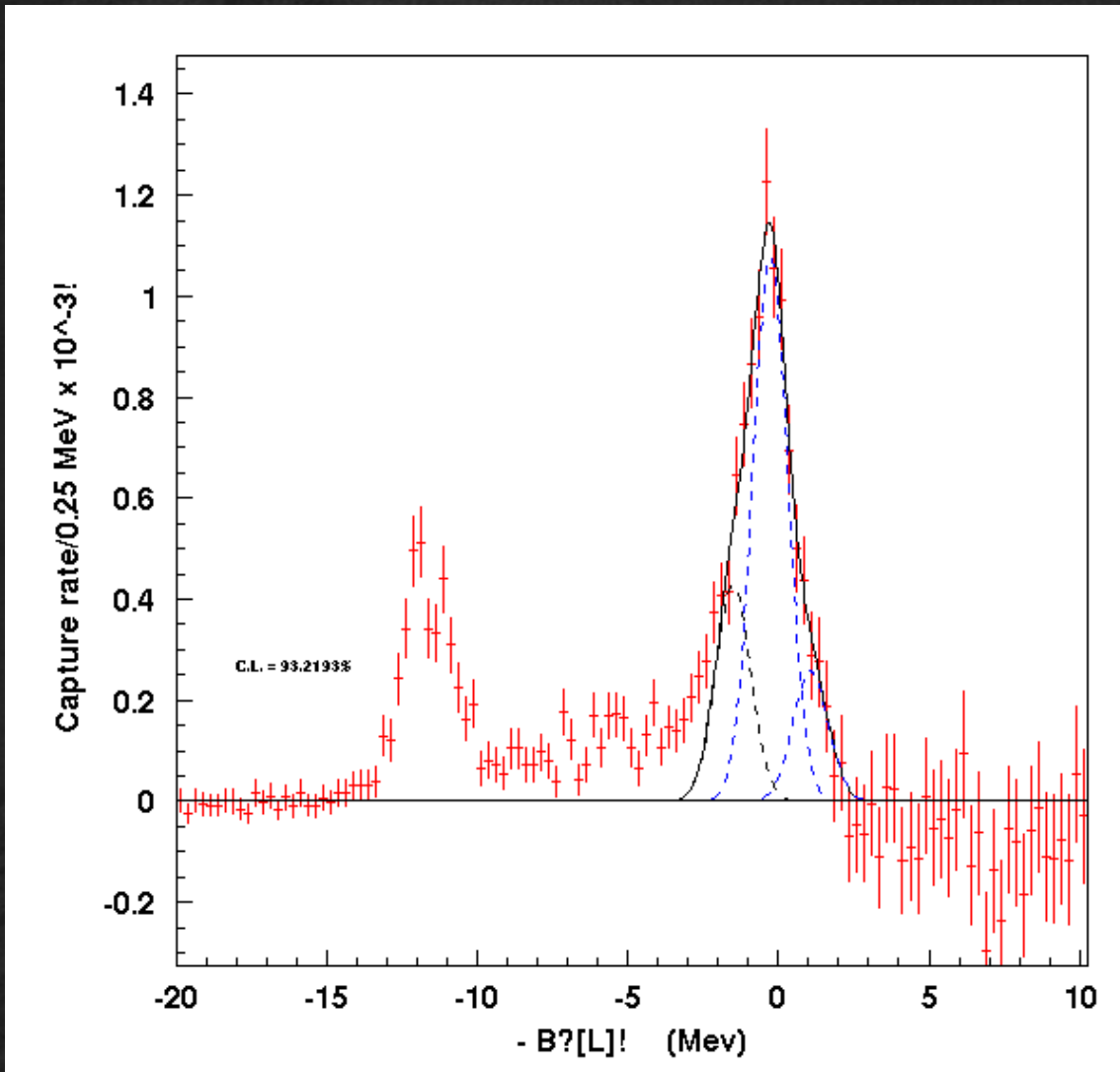


Now.....



1	Yieldgaus1	239.81	23.840	-0.49180E-03	0.27325E-02
2	Peak gaus1	-12.236	0.47437E-01	-0.34180E-03	0.28434E-01
3	Sigmatgaus	0.39528	0.48627E-01	-0.56457E-03	0.14234E-01
4	Yieldgaus2	180.14	19.719	0.89504E-04	0.10490E-01
5	Peak gaus2	-11.191	0.10370	0.10370	0.14855E-01

Now.....



1	Yieldgaus1	0.000000E+00	constant		
2	Peak gaus1	-12.400	constant		
3	Sigmatgaus	0.58502	0.64366E-01	0.30734E-02	-0.11966E-01
4	Yieldgaus2	0.000000E+00	constant		
5	Peak gaus2	-11.300	constant		
6	Yieldgaus3	0.000000E+00	constant		
7	Peak gaus3	-10.900	constant		
8	Yieldgaus4	0.000000E+00	constant		
9	Peak gaus4	-3.8000	constant		
10	Yieldgaus5	0.000000E+00	constant		
11	Peak gaus5	-0.60000	constant		
12	Yieldgaus6	0.000000E+00	constant		
13	Peak gaus6	-12.700	constant		
14	Yieldgaus7	771.44	87.510	-0.12850E-02	-0.13956E-01
15	Peak gaus7	-0.39336	0.93723E-01	0.13444E-03	-0.23781
16	Yieldgaus8	181.36	32.793	-0.10311E-02	-0.45736E-01
17	Peak gaus8	0.94905	0.11131	-0.21661E-03	0.33125E-01
18	Yieldgaus9	308.86	61.734	0.29284E-03	0.32879E-01
19	Peak gaus9	-16274	0.22913	0.22913	0.28001E-02

...??

Next steps:

- 1) make as soon as possible a new production without alignment
- 2) give up with carbon hyper-nuclear spectroscopy