

## Erratum

# Erratum to: APOE4 Copy Number-Dependent Proteomic Changes in the Cerebrospinal Fluid

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On page 515 in Table 3; the data from Figure 4 was incorrectly copied into Figure 3, meaning that Figure 3 and 4 have the exact same data numbers in the published article. Below is the correct data for Figure 3.

Table 3

Expression for the Top 20 Peptides and for all complement peptides/proteins by APOE4 copy number in multivariate models accounting for age and gender (Model 1)

### Model 1

Top 20 Protein/Peptides whose expression differed as function of APOE4 copy number, controlling for age and gender.

Protein	UniProt ID	Peptide	Log Fold Change	Average Expression	t statistic	P Value	FDR Corrected P Value
APOE	P02649	LGADMEDVR	3.597	9.193	28.182	0.000	0.000
CRP	P02741	ESDTSYVSLK	-0.624	15.228	-4.177	0.000	0.006
CH3L1	P36222	ILGQQVPYATK	0.136	23.114	3.926	0.000	0.008
FABPH	P05413	SIVTLDDGGK	0.157	14.664	3.968	0.000	0.008
CH3L1	P36222	SFTLASSETGVGAPISGPGIPGR	0.133	18.225	3.800	0.000	0.010
FABPH	P05413	SLGVGFATR	0.133	15.706	3.775	0.000	0.010
CH3L1	P36222	VTIDSSYDIAK	0.130	21.303	3.580	0.000	0.017
ALDOA	P04075	ALQASALK	0.129	19.168	3.439	0.001	0.025
APOE	P02649	CLAVYQAGAR	-0.691	8.715	-3.321	0.001	0.027
APOE	P02649	LAVYQAGAR	0.275	25.410	3.351	0.001	0.027
APOE	P02649	LGPLVEQGR	0.256	22.419	3.317	0.001	0.027
ALDOA	P04075	QLLLTADDR	0.113	16.246	3.124	0.002	0.048
APOE	P02649	AATVGSLAGQPLQER	0.222	20.145	2.835	0.005	0.111
ENOG	P09104	GNPTVEVDLYTAK	0.083	11.624	2.723	0.007	0.144
AMBP	P02760	FLYHK	-0.142	11.800	-2.604	0.010	0.190
KNG1	P01042	TVGSDTFYSFK	-0.156	15.118	-2.533	0.012	0.204
PRDX1	Q06830	DISLSDYK	0.088	14.604	2.533	0.012	0.204
PRDX2	P32119	IGKPAPDFK	0.208	12.992	2.514	0.012	0.204
CFAB	P00751	VSEADSSNADWVTK	-0.105	16.220	-2.440	0.015	0.229
KPYM	P14618	LDIDSPPTAR	0.100	18.520	2.433	0.016	0.229

*CSF Complement Protein/Peptides Expression as a function of APOE4 copy number, controlling for age and gender.*

Protein	UniProt ID	Peptide	Log Fold Change	Average Expression	t statistic	P Value	FDR Corrected P Value
C1QB	P02746	LEQGENVFLQATDK	-0.035	17.128	-1.071	0.285	0.690
C1QB	P02746	VPGLYYFTYHASSR	-0.055	17.604	-1.215	0.225	0.643
CFAB	P00751	DAQYAPGYDK	-0.117	16.401	-2.207	0.028	0.290
CFAB	P00751	VSEADSSNADWVTK	-0.105	16.220	-2.440	0.015	0.229
CFAB	P00751	YGLVTYATYPK	-0.122	22.532	-2.335	0.020	0.259
CO2	P06681	DFHINLFR	-0.055	18.691	-1.086	0.279	0.690
CO2	P06681	HAIILLTDGK	-0.064	15.695	-1.540	0.125	0.542
CO2	P06681	SSGQWQTPGATR	-0.069	15.922	-1.556	0.121	0.542
CO3	P01024	IHWESASLLR	-0.206	14.006	-1.707	0.089	0.454
CO3	P01024	TELRPGETLNVNFLLR	-0.057	10.150	-1.448	0.149	0.590
CO4A	P0C0L4	DHAVDLIQK	-0.029	22.142	-0.591	0.555	0.891
CO4A	P0C0L4	GSFEFPVGDVAVSK	-0.024	25.297	-0.446	0.656	0.931
CO4A	P0C0L4	LGQYASPTAK	-0.031	21.701	-0.599	0.549	0.891
CO4A	P0C0L4	NVNFQK	-0.013	18.387	-0.281	0.779	0.948
CO4A	P0C0L4	VLSLAQEQVGGVGSPEK	-0.037	19.989	-0.813	0.417	0.793
CO4A	P0C0L4	VTASDPLDTLGSEGALSPGGVASLLR	-0.026	18.008	-0.650	0.516	0.868
CO5	P01031	DINYVNPVIK	-0.035	16.181	-0.512	0.609	0.908
CO5	P01031	TLLPVSKPEIR	-0.037	17.209	-0.575	0.566	0.891
CO5	P01031	VFQFLEK	-0.031	18.210	-0.481	0.631	0.917
CO6	P13671	ALNHLPLEYNSALYSR	-0.093	16.297	-1.515	0.131	0.550
CO6	P13671	SEYGAALAWEK	-0.098	15.760	-1.793	0.074	0.449
CO8B	P07358	IPGIFELGISSQSDR	-0.029	14.476	-0.399	0.690	0.948
CO8B	P07358	SDLEVAHYK	-0.063	13.090	-1.071	0.285	0.690
CO8B	P07358	YEFILK	-0.052	18.883	-0.876	0.382	0.758

Log Fold Change - log<sub>2</sub> fold change of peptide expression with each additional APOE4 allele copy in multivariate models for all analyzed CSF samples; Average expression – average peptide expression in all analyzed CSF samples; t statistic – hypothesis test statistic estimating the mean peptide expression (population mean) from the sampling distribution for each peptide in all analyzed CSF samples.