

# Correction to MALDI-TOF-MS Platform for Integrated Proteomic and Peptidomic Profiling of Milk Samples Allows Rapid Detection of Food Adulterations

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Table 3 was missing two subheadings in the original publication. The corrected table appears below.

**Table 3. Marker Species Recognized during MALDI-TOF-MS Protein Profiling for Milk Speciation<sup>a</sup>**

DAve	description	exptl MH <sup>+</sup>	theor MH <sup>+</sup> (UniProt Code)
<b>Bovine Milk</b>			
36.26	$\alpha$ -lactalbumin	14181	14179 (P00711)
29.46	$\gamma$ 2-casein/ $\beta$ -casein f(106–209)	11827	11825 (P02666)
17.55	$\gamma$ 3-casein/ $\beta$ -casein f(108–209)	11560	11560 (P02666)
15.97	unknown	12006	
10.29	proteoso peptone p.p.8.1/ $\beta$ -casein f(29–105)	8640	8638 (P02666)
<b>Buffalo Milk</b>			
33.66	$\beta$ -casein f(69–209)	15749	15750 (Q9T5I0)
30.90	unknown	11991	
30.39	$\gamma$ 3-casein/ $\beta$ -casein f(108–209)	11521	11520 (Q9T5I0)
27.62	$\beta$ -casein f(1–68)P <sub>5</sub>	8251	8252 (Q9T5I0)
20.56	$\gamma$ 2-casein/ $\beta$ -casein f(106–209)	11786	11785 (Q9T5I0)
16.63	$\alpha$ -lactalbumin variant B	14236	14236
<b>Goat Milk</b>			
36.26	$\alpha$ -lactalbumin variant A	14186	14187 (P00712)
29.02	unknown	11882	
21.33	$\gamma$ 3-casein/ $\beta$ -casein f(108–207)	11288	11287 (Q9SL76)
16.48	unknown	11922	
15.17	unknown	5891	
14.06	$\gamma$ 2-casein/ $\beta$ -casein f(106–207)	11554	11553 (Q9SL76)
9.48	$\beta$ -casein f(98–207)	12466	12466 (Q9SL76)
8.66	$\beta$ -lactoglobulin	18185	18187 (P02756)
<b>Ovine Milk</b>			
36.25	$\gamma$ 2-casein/ $\beta$ -casein f(106–207)	11536	11535 (P11839)
31.26	$\gamma$ 3-casein/ $\beta$ -casein f(108–207)	11271	11270 (P11839)
22.59	unknown	8573	
14.40	$\beta$ -casein f(98–207)	12449	12448 (P11839)
9.48	unknown	9712	

<sup>a</sup>MS experiments were performed in linear mode as reported under Experimental Procedures. Difference value between the maximal and the minimal average peak/area intensity of all classes (DAve) (see ClinProt Tools software for details), protein/polypeptide name, and experimental/theoretical MH<sup>+</sup> (average) value are reported. Theoretical MH<sup>+</sup> values were calculated according to the amino acid sequence entries present in the UniProt Knowledge Database and the corresponding post-translational modifications. P, phosphate; f, fragment.  $\alpha$ -Lactalbumin variant B mass value was calculated according to dedicated studies.<sup>35</sup>

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