Erratum to: Porcine P2 myelin protein primary structure and bound fatty acids determined by mass spectrometry

Gianluca Maddalo · Mohammadreza Shariatgorji ·
Christopher M. Adams · Eva Fung · Ulrika Nilsson ·
Roman A. Zubarev · Jan Sedzik · Leopold L. Ilag

Published online: 5 October 2010
© Springer-Verlag 2010

Erratum to: Anal Bioanal Chem
DOI 10.1007/s00216-010-3762-0

Regrettably, there was a mistake in Fig. 1 of this article. The corrected Fig. 1 is given below. In Fig. 2a the label in the spectrum should correctly read $[M+3H]^{3+}$. In the electronic supplementary material, in Fig. S2, the label in the spectrum should correctly read $[M+2H]^{2+}$.

The online version of the original article can be found at <http://dx.doi.org/10.1007/s00216-010-3762-0>.

G. Maddalo · M. Shariatgorji · U. Nilsson · L. L. Ilag (✉)
Department of Analytical Chemistry, Stockholm University,
Svante Arrhenius väg 16,
10691 Stockholm, Sweden
e-mail: leopold.ilag@anchem.su.se

C. M. Adams · E. Fung · R. A. Zubarev
Institute for Cell and Molecular Biology, Uppsala University,
75124 Uppsala, Sweden

C. M. Adams · E. Fung · R. A. Zubarev
Division of Molecular Biometry,
Institute for Medicinal Biochemistry and Biophysics,
Karolinska Institutet,
Scheeles väg 2,
17177 Stockholm, Sweden

J. Sedzik
Department of Neurobiology, Health Care and Society,
Protein Crystallization Facility, Karolinska Institute, NOVUM,
14186 Stockholm, Sweden

J. Sedzik
Department of Chemical Engineering and Technology,
Protein Crystallization Facility,
Royal Institute of Technology, KTH,
Teknikringen 28,
10044 Stockholm, Sweden

J. Sedzik
Division of Neurobiology and Bioinformatic,
National Institute of Physiological Science,
Nishigonaka Myadaiji,
Okazaki 444-8585 Aichi, Japan

J. Sedzik
Department of Applied Chemistry, School of Engineering 7-3-1,
The University of Tokyo,
Hongo, Bunkyo 113-8656 Tokyo, Japan

	1	10	20	30	40	50	60
PORCINE	SNKFLGTWKLVSSEN	FDDYMKALGVGL	ATRKLG	NLAKPRVI	ISKKGDI	ITIRTEST	FKNT
BOVINE	SNKFLGTWKLVSSEN	FDEYMKALGVGL	ATRKLG	NLAKPRVI	ISKKGDI	ITIRTESP	FKNT
HUMAN	SNKFLGTWKLVSSEN	FDDYMKALGVGL	ATRKLG	NLAKPTVI	ISKKGDI	ITIRTEST	FKNT
MOUSE	SNKFLGTWKLVSSEH	FDDYMKALGVGL	ANRKL	GNLAKPTVI	ISKKGDI	ITIRTESA	FKNT
RABBIT	SNKFLGTWKLVSSEN	FDDYMKALGVGL	ATRKLG	NLAKPNVI	ISKKGDI	ITIRTEST	FKNT
HORSE	SNKFLGTWKLTSSEN	FDEYMKALGVGL	GTRSL	GNLAGPTVI	ISKSGDV	ITIRTESG	FKNT

	61	70	80	90	100	110	120
PORCINE	EISFKLGQEFEE	TTADNRKA	KS	VVTLAR	GS	LNQVQK	WDGKET
BOVINE	EISFKLGQEFEE	TTADNRKTK	STVTLAR	GS	LNQVQK	WDGNET	TIKRKLVDGKMVVECKMK
HUMAN	EISFKLGQEFEE	TTADNRKTK	SIVTLQR	GS	LNQVQK	WDGKET	TIKRKLVDGKMVAECKMK
MOUSE	EISFKLGQEFDE	TTADNRKA	KSIVTLER	GS	LNQVQK	WDGKET	AI RRTLLDGRMVVECKIMK
RABBIT	EISFKLGQEFEE	TTADNRKTK	SIITLER	GALN	QVQK	WDGKET	TIKRKLVDGKMVVECKMK
HORSE	EISFKLGQEFEE	TTADNRKTK	STVTLA	GGKLN	QVQK	WNGNET	TIKRELVDGKMVVECSMA
	121	131					
PORCINE	DVVCTRIYE	KV					
BOVINE	DVVCTRIYE	KV					
HUMAN	GVVCTRIYE	KV					
MOUSE	GVVCTRIYE	KV					
RABBIT	GVVCTRIYE	KV					
HORSE	SVVCTRIYE	QV					

Fig. 1 Multiple sequence alignment of porcine myelin P2 protein with homologs from five other species. The porcine sequence is indicated in *bold*. Highlighted in *boxes* are the amino acid

substitutions between porcine and bovine sequences determined in this study. The lipid-binding domain as defined by the software ScanProsite [40] is *underlined*