Supplementary Table - Identification of murine ptx4 tryptic peptides by MALDI-TOF/TOF analysis

MALDI-MS $M+H^+$ obs	$M+H^+$ cal	Identification	Sequence
859.46	859.50	381-388	RLVATGSR
949.47	949.47	44-50	LEEQFQR
1002.52	1002.51	374-380	YWLHIDR
1013.55	1013.55	210-218	GPGSLQLWR
1093.55	1093.53	23-32	TPSQEAHPAR
1105.57	1105.56	43-50	RLEEQFQR
1125.55	1125.54*	296-304	ALSFCSWVR
1152.54	1152.48	469-478	AKCTCLEQCP
1209.57	1209.50*	469-478	AKCTCLEQCP
1284.61	1284.67	210-220	GPGSLQLWRDR
1423.70	1423.70	246-258	FQTPSSHQAAPPR
1431.75	1431.81	122-134	LQALDLSLSTKSR
1593.82	1593.82	305-319	MATSHLGTLLSYATK
1609.81	1609.82**	305-319	MATSHLGTLLSYATK
1721.82	1721.82	231-245	SSPHDVTVHVQEMQK
1737.82	1737.82**	231-245	SSPHDVTVHVQEMQK
1970.00	1970.01	331-348	NSLVPGSIHFVIGDPDFR
3139.66	3139.65	178-209	LAALEGQTQSASSGTVALGLTTAPTPTQLAQR

MALDIMS/MS $M+H^+$ obs	Sequence
1013.55	GPGSLQLWR (210-218)
1125.55	ALSFCSWVR (296-304)
1423.70	FQTPSSHQAAPPR (246-258)

The murine ptx4 purified protein was trypsinized and subjected to MALDI-TOF/TOF analysis. The analysis was limited to tryptic peptides with a molecular mass equal or more than 700 Da. For MALDI-MS analysis, the data in the first column are the mass value obtained experimentally (observed (obs)). The results in the second column are those calculated (cal) from the *in silico* tryptic fragmentation of the *ptx4* gene product. The third column indicates the amino acid positions of the identified ptx4 peptides. The fourth column shows the corresponding amino acid sequences. The single asterisk indicates carboxyamidomethylcysteine modification and the double asterisks indicate methionine sulfoxide modification. For MALDI-MS/MS analysis the data in the first column are the mass value obtained experimentally (observed (obs)) and the second column illustrates the sequencing results along with the residue positions.