Correction to: Exploring the peptide retention mechanism in molecularly imprinted polymers

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The authors would like to call the reader's attention to the fact that unfortunately due to the file formatting during the exporting of the data matrix from the program Unscrambler (used for the development of the statistical model) to the Word office file, the negative signs of the GRAVY index variable were lost. The authors apologize for the mistake.

Below please find the corrected version of Table 1:

The online version of the original article can be found at <https://doi.org/10.1007/s00216-017-0520-6>

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Table 1 Extracted peptides and their molecular descriptors: number of amino acids, number of negative charges, number of positive charges, number of aromatic residues, molecular weight (*MW*), grand average of hydropathicity (*GRAVY*) index, isoelectric point (*pI*), aliphatic index (*AI*)

and the percentage of acetonitrile (*MeCN*) required to achieve 50% recovery in the molecularly imprinted polymer (*MIP*) cartridge and the nonimprinted polymer (*NIP*) cartridge

Peptides	No. of amino acids ^a	No. of negative charge ^a	No. of positive charge ^a	No. of aromatic residues ^a	<i>MW</i> ^a	<i>GRAVY</i> index ^b	<i>pI</i> ^b	<i>AI</i> ^b	MeCN (%)	
									MIP	NIP
LCVLHEKTPVSEK	13	2	2	0	1482.75	−0.20	6.75	104.62	1.5	4.0
NECFLSHKDDSPDLPK	16	4	3	1	1845.00	−1.28	4.31	48.75	4.0	0.0
VPQVSTPTLVEVSR	14	1	1	0	1511.72	0.21	6.84	110.71	13.0	13.0
RPCFSALTPDETYVPK	16	2	2	2	1824.06	−0.54	6.18	48.75	8.0	8.0
SLHTLFGDELCK	12	2	2	1	1362.55	0.06	5.17	97.50	4.0	4.5
YNGVFQECQAEDKGACLLPK	21	3	2	2	2316.6	−0.32	4.32	60.48	2.5	4.5
LVNELTEFAKTCVADESHAGCEK	23	5	3	1	2494.76	−0.23	4.24	72.17	0.0	2.0
TCVADESHAGCEK	13	3	2	0	1349.45	−0.52	4.31	37.69	0.0	0.0
FKDLGEEHFK	10	3	3	2	1249.39	−1.25	5.34	39.00	3.5	4.5
YICDNQDTISSK	12	2	1	1	1386.50	−0.83	3.88	65.00	1.5	2.0
HLVDEPQNLIK	11	2	2	0	1305.50	−0.58	5.21	132.73	12.5	4.5
YLYEIAR	7	1	1	2	927.07	−0.07	6.82	125.71	15.0	15.0
YNGVFQECQAEDK	14	3	1	2	1633.78	−0.91	3.83	27.86	1.0	2.0
KVPQVSTPTLVEVSR	15	1	2	0	1639.91	−0.07	10.09	103.33	16.5	18.5
KQTALVELLK	10	1	2	0	1142.41	0.19	9.88	156.00	16.5	18.5
LVVSTQTALA	10	0	0	0	1002.18	1.39	6.01	156.00	9.0	7.0
LVNELTEFAK	10	2	1	1	1163.34	0.13	4.26	117.00	5.0	5.0
QTALVELLK	9	1	1	0	1014.23	0.64	6.94	173.33	13.5	14.0
LFTFHADICTLPDTEK	16	3	2	2	1851.11	0.04	4.30	79.38	5.0	8.0
LGEYGFQNALIVR	13	1	1	2	1479.70	0.29	6.89	120.00	18.0	21.0
NLLGLIEAK	9	1	1	0	978.60	0.71	6.94	184.44	17.0	16.0

^a <http://pepcalc.com>

^b <http://web.expasy.org/protparam>