Table 2

Predicted antimicrobial peptides from the *in vitro* simulated neonatal digestion of human colostrum (*n*= 24) by using the AMPA bioinformatic tool (tcoffee.crg.cat/apps/ampa): experimental exact mass, isoelectric point (*pI*), and hydrophobicity, according to the phase of digestion in which they were observed.

Precursor Protein	Peptide[a]	Phase of simulated digestion (t, min)	Probability of antimicrobial activity %	Exact mass (Da)	Net charge	pI	Hydrophobicity (kcal * mol^{-1})
Tenascin, isoform 4	FSTFD**K**DTDSAITNCALSY**K**GAFWY**R**NCH**R**VN (2122-2153)	Gastric (65)	2	3729.7039	+ 1	8.21	+ 26.19
	FD**K**DTDSAITNCALSY**K**GAFWYRNCH**R**VN (2125-2153)	Gastric (35)	2	3394.5563	+ 1	8.21	+ 27.19
b-2-Microglobulin	IQ**R**TP**K**IQVYS**R**HPAENG**K**SNF (21-42)	Gastric (35 and 65)	19	2569.3474	+ 3	10.8	+ 24.3
C3 Complement	Y**R**IFTVNH**K**LLPVG**R**TVM (147-164)	Gastric (65)	13	2143.2053	+ 3	11.4	+ 11.2
S100-A8 Protein	SIIDVYH**K**YSLI**K**GNF (11-26)	Gastric (35 and 65)	4	1896.0114	+ 1	9.34	+ 14.19
C3 Complement	Y**R**IFTVNH**K**LLPVG**R** (147-161)	Gastric (65)	13	1812.0493	+ 3	11.4	+ 12.08
	Y**R**IFTVNH**K**LLPVG (147-160)	Gastric (35 and 65)	16	1655.9484	+ 2	10.4	+ 10.27

[a]Numbers between parentheses indicate the initial and final position of the peptide in the primary sequence of the precursor protein, considering the signal peptide. Codes used for identification of amino acid residues' properties in the peptide sequences: **bold font** was used for arginine and lysine (R and K, respectively), which have positively charged side chains; red font was used for amino acids with hydrophobic side chains; green font was used for cysteine residues, indicating potential sites of disulfide bonds.