Electronic Supplementary Material (ESI) for Food & Function.

Supplementary Table S1. Peptides identified in the digests obtained from the lunasin:IBB1 mixtures at different ratios after the gastric and intestinal phases of digestive process simulating gastrointestinal conditions. The peak (number or letter) corresponds to the peptide peaks and sequences shown in Figures 1, 2, and 3 (number for lunasin-derived peptides and letter for IBB1-derived peptides).

Peak	**Protein fragment**	**Amino acid sequences**	**Ion *m/z* (charge)**	**Simulated gastric digests**				**Simulated gastrointestinal digests**			
				1:0	**1:1**	**1:2**	**1:2i**	**1:0**	**1:1**	**1:2**	**1:2i**
1	f(29-35)	KIQGRGD	773.5(+1)	+	+	+	-	-	-	-	-
2	f(29-36)	KIQGRGDD	888.5(+1)	+	+	+	+	-	-	+	-
3	f(29-37)	KIQGRGDDD	1003.6(+1)	+	+	-	+	-	-	+	-
4	f(29-38)	KIQGRGDDDD	1118.6(+1)	+	+	-	+	-	-	-	-
5	f(29-39)	KIQGRGDDDDD	1233.7(+1)	+	+	+	+	-	-	+	-
6	f(28-33)	EKIQGR	729.7(+1)	+	+	+	+	+	+	+	+
7	f(29-41)	KIQGRGDDDDDDD	1463.7(+1)	+	+	+	-	-	+	+	-
8	f(29-40)	KIQGRGDDDDDD	1348.6(+1)	-	-	+	+	-	+	+	+
9	f(29-43)	KIQGRGDDDDDDDDD	1694.0(+1)	+	+	+	+	+	+	+	+
10	f(11-18)	RKQLQGVN	942.7(+1)	+	+	+	+	-	+	+	+
11	f(24-28)	KHIME	657.5(+1)	+	+	+	-	+	+	+	-
12	f(1-8)	SKWQHQQD	1056.6(+1)	+	+	+	-	-	+	+	-
13	f(1-10)	SKWQHQQDSC	1246.7(+1)	+	+	+	+	-	+	+	+
14	f(19-23)	LTPCE	562.3(+1)	+	-	-	-	-	-	-	-
15	f(21-28)	PCEKHIME	986.6(+1)	+	-	-	-	-	-	-	-
16	f(20-28)	TPCEKHIME	1087.6(+1)	+	-	-	-	-	-	-	-
17	f(1-18)	SKWQHQQDSCRKQLQGVN	1085.8(+2)	+	+	+	+	-	+	+	-
18	f(19-28)	LTPCEKHIME	1200.8(+1)	+	+	+	+	-	+	+	+
19	f(11-19)	RKQLQGVNL	1055.8(+1)	+	+	+	+	-	+	+	+
20	LUNASIN: SKWQHQQDSCRKQLQGVNLTPCEKHIMEKIQGRGDDDDDDDDD		1677.2(+3) 1258.0(+4)	+	+	+	+	+	+	+	+
21	f(17-28)	VNLTPCEKHIME	1413.9(+1)	+	-	-	-	-	-	-	-
22	f(11-28)	RKQLQGVNLTPCEKHIME	1062.8(+2)	+	-	-	+	-	-	-	+
23	f(11-20)	RKQLQGVNLT	1156.7(+1)	-	+	+	-	-	+	+	-
24	f(28-37)	EKIQGRGDDD	1133.4(+1)	-	-	-	-	+	-	-	-
25	f(4-10)	QHQQDSC	845.5(+1)	-	-	-	-	+	-	-	-
26	f(34-43)	GDDDDDDDDD	1111.4(+1)	-	-	-	-	+	-	-	-
27	f(29-33)	KIQGR	601.5(+1)	-	-	-	-	+	-	-	-
28	f(4-11)	QHQQDSCR	1001.6(+1)	-	-	-	-	+	-	-	-
29	f(28-32)	EKIQG	573.4(+1)	-	-	-	-	+	-	-	-
30	f(28-34)	EKIQGRG	786.6(+1)	-	-	-	-	+	-	-	-
31	f(19-24)	LTPCEK	690.5(+1)	-	-	-	-	+	-	-	-
32	f(25-28)	HIME	529.4(+1)	-	-	-	-	+	-	-	-
33	f(29-34)	KIQGRG	658.5(+1)	-	-	-	-	+	-	-	-
34	f(27-38)	MEKIQGRGDDDD	1378.7(+1)	-	-	-	-	+	-	-	-
35	f(1-3)	SKW	420.4(+1)	-	-	-	-	+	-	-	-
36	f(17-24)	VNLTPCEK	903.7(+1)	-	-	-	-	+	-	-	-
37	f(16-24)	GVNLTPCEK	960.6(+1)	-	-	-	-	+	-	-	-
38	f(15-24)	QGVNLTPCEK	1088.7(+1)	-	-	-	-	+	-	-	-
39	f(28-43)	EKIQGRGDDDDDDDDD	911.9(+2)	-	-	-	-	-	+	-	-
40	f(31-43)	QGRGDDDDDDDDD	1451.5(+1)	-	-	-	-	-	-	+	-
A	f(19-26)	PPQCRCSD	1019.5(+1)	-	-	-	+	-	-	-	+
B	f(14-26)	CTKSNPPQCRCSD	1609.8(+1)	-	-	-	+	-	-	-	+
C	f(1-13)	DDESSKPCCDQCA	1571.7(+1)	-	-	-	+	-	-	-	+
D	f(1-15)	DDESSKPCCDQCACT	1832.8(+1)	-	-	-	+	-	-	-	+
E	f(16-27)	KSNPPQCRCSDM	1479.7(+1)	-	-	-	+	-	-	-	+
F	f(24-35)	CSDMRLNSCHSA	719.3(+2)	-	-	-	+	-	-	-	-
G	f(30-42)	NSCHSACKSCICA	1554.7(+1)	-	-	-	+	-	-	-	+
H	f(58-71)	CYEPCKPSEDDKEN	885.9(+2)	-	-	-	+	-	-	-	-
I	f(58-66)	CYEPCKPSE	1169.6(+1)	-	-	-	+	-	-	-	+

J	f(51-56)	CVDITD	722.4(+1)	-	-	-	+	-	-	-	+
K	f(46-50)	PAQCF	622.4(+1)	-	-	-	+	-	-	-	+
L	f(43-49)	LSYPAQC	838.4(+1)	-	-	-	+	-	-	-	-
M	f(57-71)	FCYEPCKPSEDDKEN	959.5(+2)	-	-	-	+	-	-	-	+
N	f(61-71)	PCKPSEDDKEN	1318.7(+1)	-	-	-	+	-	-	-	-
O	f(27-29)	MRL	419.3(+1)	-	-	-	+	-	-	-	+
P	f(57-67)	FCYEPCKPSED	1431.7(+1)	-	-	-	+	-	-	-	+
Q	f(57-66)	FCYEPCKPSE	1316.7(+1)	-	-	-	+	-	-	-	+
R	f(43-50)	LSYPAQCF	985.5(+1)	-	-	-	+	-	-	-	+
S	f(51-57)	CVDITDF	869.4(+1)	-	-	-	+	-	-	-	+
T	IBB1: DDESSKPCCDQCACTKSNPPQCRCSDMRLNSCHSACKSCIAL SYPAQCFCVDITDFCYEPCKPSEDDKEN		1572.8(+5) 1310.7(+6)	-	+	+	+	-	+	+	-
U	f(2-7)	DESSKP	661.3(+1)	-	-	-	-	-	-	-	+
V	f(16-22)	KSNPPQC	830.5(+1)	-	-	-	-	-	-	-	+
W	f(17-23)	SNPPQCR	858.4(+1)	-	-	-	-	-	-	-	+
X	f(16-23)	KSNPPQCR	986.6(+1)	-	-	-	-	-	-	-	+
Y	f(17-26)	SNPPQCRCSD	1220.6(+1)	-	-	-	-	-	-	-	+
Z	f(31-42)	SCHSACKSCICA	1440.7(+1)	-	-	-	-	-	-	-	+
α	f(28-42)	RLNSCHSACKSCICA	912.5(+2)	-	-	-	-	-	-	-	+
β	f(46-49)	PAQC	475.2(+1)	-	-	-	-	-	-	-	+
γ	f(54-57)	ITDF	495.2(+1)	-	-	-	-	-	-	-	+