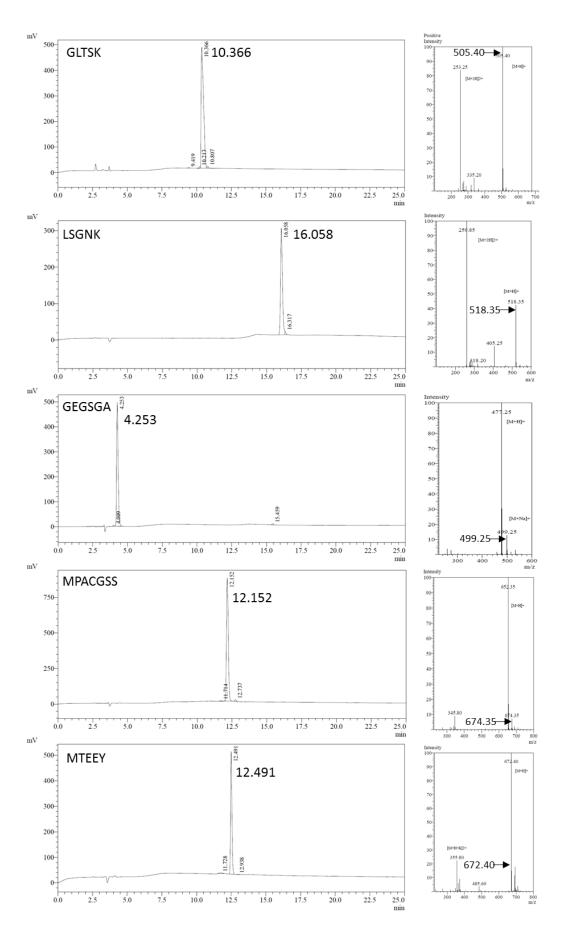
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**Supplementary Figure 1** Chromatograms (left) and mass/mass spectra (right) of pure peptides originally found in bean NDF.

Supplementary Figure 2 Chemical structure of the peptides studied and captopril used in the molecular docking analysis.

Supplementary Figure 3 Representative chromatograms of peptides A) before the incubation and B) post incubation with gastric enzymes. C) Peak areas and retention times of the peptides before and after incubation with pepsin and pancreatin. The results are expressed as the mean  $\pm$  standard deviation of three independent experiments. Different letters by pairs in the same row means significant difference as determined by Student's t test.

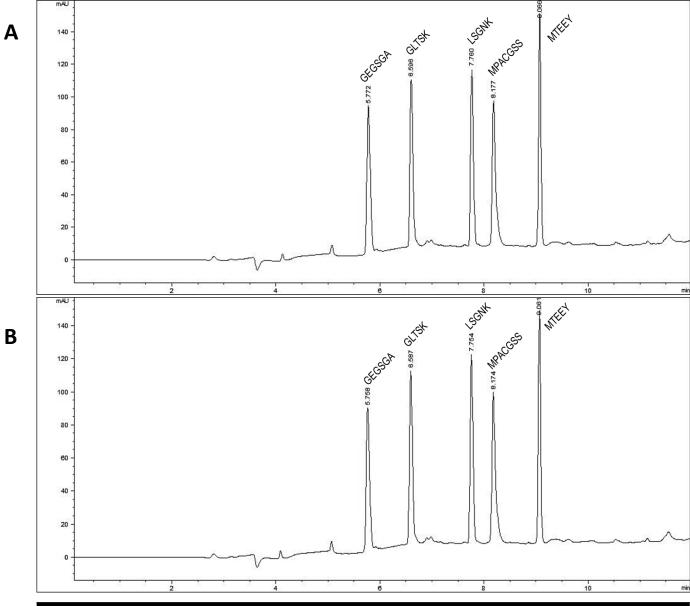
## **Supplementary figure 1.**



## **Supplementary Figure 2**

## **Supplementary Figure 4**

C



Peptide	Peak area (mAU)		Retention time (min)	
	Pre-incubation	Post-incubation	Pre-incubation	Post-incubation
GLTSK	420.13 ± 19.03°	410.27 ± 13.24 <sup>a</sup>	6.59 ± 0.02 <sup>A</sup>	6.52 ± 0.03 <sup>A</sup>
LSGNK	440.97 ± 7.04°	439.27 ± 8.51 <sup>a</sup>	7.79 ± 0.04 <sup>A</sup>	7.75 ± 0.08 <sup>A</sup>
GEGSGA	422.40 ± 13.43°	413.67 ± 18.56 <sup>a</sup>	5.77 ± 0.02 <sup>A</sup>	5.69 ± 0.01 <sup>A</sup>
MPACGSS	437.23 ± 7.09 <sup>a</sup>	434.13 ± 11.57 <sup>a</sup>	$8.17 \pm 0.02^{A}$	8.17 ± 0.03 <sup>A</sup>
MTEEY	463.57 ± 14.43 <sup>a</sup>	440.77 ± 1.78 <sup>a</sup>	9.05 ± 0.04 <sup>A</sup>	9.06 ± 0.01 <sup>A</sup>