

**Supplementary Table 1**

Predictive	scoring	of	peptide	activity	and	its	related	information.
Number	Peptides	Probability of activity	Homologous proteins	Molecular mass (Da)				
1	PFKFF	0.9861	A0A445CPR7_ARAHY	684.3635				
2	NPFKFF	0.9783	A0A445CPR7_ARAHY	798.4064				
3	NNPFKFF	0.9730	A0A445CPR7_ARAHY	912.4493				
4	LLRFF	0.9678	CASA1_BOVIN	694.4166				
5	QPPSPPPFL	0.9665	A0A444X8W9_ARAHY	1075.5702				
6	LIRFF	0.9587	A0A444XJY2_ARAHY	694.4166				
7	PPPPP	0.9561	A0A444ZWK8_ARAHY	503.2744				
8	RGPPF	0.9559	CASB_BOVIN	572.3071				
9	NPFKF	0.9481	A0A445CPR7_ARAHY	651.338				
10	NNPFKF	0.9380	A0A445CPR7_ARAHY	765.3809				
11	FLPYPY	0.9361	CASK_BOVIN	798.3952				
12	MPFPK	0.9331	CASB_BOVIN	618.3199				
13	TWDFPLP	0.9319	A0A3Q1N1W0_BOVIN	874.4225				
14	FYFPSR	0.9298	NING13_ARAHY	815.3966				
15	FYFPSRR	0.9254	NING13_ARAHY	971.4977				
16	QPSYFPF	0.9173	EIBKM4_BOVIN	834.3912				
17	NNNPFKF	0.9104	A0A445CPR7_ARAHY	879.4239				
18	FLPYPHY	0.9094	CASK_BOVIN	961.4585				
19	FVAPFP	0.9075	CASA1_BOVIN	676.3584				
20	LKNNNPFKFF	0.8953	A0A445CPR7_ARAHY	1267.6713				
21	FYPELFR	0.8943	CASA1_BOVIN	970.4912				
22	GGGYGPPPPP	0.8894	A0A444YDJ3_ARAHY	894.4235				
23	FPKYP	0.8861	CASB_BOVIN	650.3428				
24	VYPFP	0.8845	CASB_BOVIN	621.3162				
25	MPFPKYP	0.8841	CASB_BOVIN	878.436				
26	VYPFPGP	0.8792	CASB_BOVIN	775.3904				

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27	GPVRGPF	0.8779	CASB_BOVIN	728.3969
28	AMKPW	0.8777	CASA2_BOVIN	631.3152
29	APFPEVF	0.8744	CASA1_BOVIN	805.401
30	PFPKYP	0.8741	CASB_BOVIN	747.3955
31	DGPSSKDWRGGR	0.8738	A0A445DWQ9_ARAHY	1316.6221
32	FPGPIH	0.8685	A0A452DHW7_BOVIN	666.3489
33	GPVRGPF	0.8676	CASB_BOVIN	825.4497
34	APFPEVFG	0.8612	CASA1_BOVIN	862.4225
35	LNYPYAPFP	0.8526	A0A3Q1LX31_BOVIN	1177.5807
36	QFLPYPPY	0.8515	CASK_BOVIN	1089.5171
37	LHRFL	0.8454	F1MI39_BOVIN	684.4071
38	VRGPF	0.8439	CASB_BOVIN	671.3755
39	PVRGPF	0.8436	CASB_BOVIN	768.4282
40	YFPGPIH	0.8436	A0A452DHW7_BOVIN	926.465
41	GRQPGDYDDRRQP	0.8414	NING13_ARAHY	2514.1819
	RREEGGR			
42	SLVYFP	0.8400	CASB_BOVIN	821.4323
43	FVAPFPEVFGK	0.8368	CASA1_BOVIN	1236.6542
44	YFPSRR	0.8365	NING13_ARAHY	824.4293
45	FPKYPVEPF	0.8316	CASB_BOVIN	1122.575
46	FGRLF	0.8301	B3IXL2_ARAHY	767.3966
47	APFPEVFGK	0.8298	CASA1_BOVIN	990.5174
48	QFRPR	0.8242	A6QLC0_BOVIN	702.3925
49	QEPVLGPVRGPFPIV	0.8187	CASB_BOVIN	1716.9926
50	GPVRGPFPIV	0.8185	CASB_BOVIN	1150.6862
51	MPIQAF	0.8181	CASB_BOVIN	818.436
52	PGPSPTR	0.8181	A0A3Q1MTR8_BOVIN	807.4239
53	GPFPPIV	0.8150	CASB_BOVIN	741.4425
54	NENLLRFF	0.8146	CASA1_BOVIN	1051.545

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55	IPPLR	0.8077	A0A445DCJ9_ARAHY	594.3853
56	DQFPRR	0.8040	A0A445CPR7_ARAHY	817.4194
57	WAKYLGRSFR	0.8013	A0A445DSD6_ARAHY	1282.6935
58	LPYPYY	0.8002	CASK_BOVIN	814.3901

### Supplementary Table 2

Pathways involved in differential proteins.

Number	ID	Pathways	Number of proteins
1	path:bta04611	Platelet activation	7
2	path:bta03010	Ribosome	7
3	path:bta04612	Antigen processing and presentation	7
4	path:bta04141	Protein processing in endoplasmic reticulum	7
5	path:bta05417	Lipid and atherosclerosis	7
6	path:bta04810	Regulation of actin cytoskeleton	6
7	path:bta00010	Glycolysis / Gluconeogenesis	6
8	path:bta04144	Endocytosis	6
9	path:bta04971	Gastric acid secretion	5
10	path:bta04142	Lysosome	5
11	path:bta04015	Rap1 signaling pathway	5
12	path:bta04613	Neutrophil extracellular trap formation	5
13	path:bta05418	Fluid shear stress and atherosclerosis	5
14	path:bta03320	PPAR signaling pathway	5
15	path:bta00052	Galactose metabolism	5
16	path:bta04670	Leukocyte transendothelial migration	5
17	path:bta04151	PI3K-Akt signaling pathway	5
18	path:bta04066	HIF-1 signaling pathway	4
19	path:bta04010	MAPK signaling pathway	4
20	path:bta04961	Endocrine and other factor-regulated calcium reabsorption	4
21	path:bta04270	Vascular smooth muscle contraction	3

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22	path:bta04022	cGMP-PKG signaling pathway	3
23	path:bta00380	Tryptophan metabolism	3
24	path:bta04979	Cholesterol metabolism	3
25	path:bta04146	Peroxisome	3
26	path:bta04068	FoxO signaling pathway	3
27	path:bta00562	Inositol phosphate metabolism	3
28	path:bta04722	Neurotrophin signaling pathway	3
29	path:bta04120	Ubiquitin mediated proteolysis	3
30	path:bta04261	Adrenergic signaling in cardiomyocytes	2
31	path:bta04911	Insulin secretion	2
32	path:bta00561	Glycerolipid metabolism	2
33	path:bta04978	Mineral absorption	2
34	path:bta04024	cAMP signaling pathway	2
35	path:bta00310	Lysine degradation	2
36	path:bta00980	Metabolism of xenobiotics by cytochrome P450	2
37	path:bta04080	Neuroactive ligand-receptor interaction	2
38	path:bta04110	Cell cycle	2
39	path:bta04974	Protein digestion and absorption	2
40	path:bta00051	Fructose and mannose metabolism	2
41	path:bta04514	Cell adhesion molecules	2
42	path:bta04070	Phosphatidylinositol signaling system	2
43	path:bta04152	AMPK signaling pathway	2
44	path:bta00620	Pyruvate metabolism	2
45	path:bta04973	Carbohydrate digestion and absorption	2
46	path:bta00330	Arginine and proline metabolism	2
47	path:bta04724	Glutamatergic synapse	2
48	path:bta04972	Pancreatic secretion	2
49	path:bta04925	Aldosterone synthesis and secretion	2
50	path:bta00030	Pentose phosphate pathway	2

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51	path:bta03013	Nucleocytoplasmic transport	2
52	path:bta04910	Insulin signaling pathway	2
53	path:bta04620	Toll-like receptor signaling pathway	2
54	path:bta05415	Diabetic cardiomyopathy	2
55	path:bta04064	NF-kappa B signaling pathway	2
56	path:bta00500	Starch and sucrose metabolism	2
57	path:bta00410	beta-Alanine metabolism	1
58	path:bta04020	Calcium signaling pathway	1
59	path:bta04512	ECM-receptor interaction	1
60	path:bta04933	AGE-RAGE signaling pathway in diabetic complications	1
61	path:bta04062	Chemokine signaling pathway	1
62	path:bta04750	Inflammatory mediator regulation of TRP channels	1
63	path:bta04672	Intestinal immune network for IgA production	1
64	path:bta04260	Cardiac muscle contraction	1
65	path:bta00280	Valine, leucine and isoleucine degradation	1
66	path:bta04960	Aldosterone-regulated sodium reabsorption	1
67	path:bta04662	B cell receptor signaling pathway	1
68	path:bta04728	Dopaminergic synapse	1
69	path:bta04310	Wnt signaling pathway	1
70	path:bta00270	Cysteine and methionine metabolism	1
71	path:bta04927	Cortisol synthesis and secretion	1
72	path:bta00520	Amino sugar and nucleotide sugar metabolism	1
73	path:bta04071	Sphingolipid signaling pathway	1
74	path:bta04726	Serotonergic synapse	1
75	path:bta04666	Fc gamma R-mediated phagocytosis	1
76	path:bta00601	Glycosphingolipid biosynthesis - lacto and neolacto series	1
77	path:bta00340	Histidine metabolism	1
78	path:bta04371	Apelin signaling pathway	1
79	path:bta04610	Complement and coagulation cascades	1

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80	path:bta04926	Relaxin signaling pathway	1
81	path:bta00040	Pentose and glucuronate interconversions	1
82	path:bta00020	Citrate cycle (TCA cycle)	1
83	path:bta04924	Renin secretion	1
84	path:bta04659	Th17 cell differentiation	1
85	path:bta04922	Glucagon signaling pathway	1
86	path:bta00260	Glycine, serine and threonine metabolism	1
87	path:bta04657	IL-17 signaling pathway	1
88	path:bta00480	Glutathione metabolism	1

### Supplementary Table 3

Complete results for molecular docking affinity and property prediction.

Number	Peptides	Affinity	Isoelectric point	Hydrophilic	Hydrophobicity	SVM
1	LNYPPAYPPF	-11.0	5.52	-0.41	5.43	-0.47
2	QPPSPPPFL	-10.9	5.52	-0.73	7.01	-0.62
3	FLPYPY	-10.9	5.52	0.133	3.8	-0.77
4	YFPGPIH	-10.8	6.74	-0.3	8.26	-0.74
5	GGGYGPPPPP	-10.6	5.52	-1.09	12.49	-0.31
6	APFPEVFGK	-10.6	6.05	0.067	12.38	-1.17
7	QEPVLGPVRGPFPIIV	-10.2	6.00	0.594	10.39	-1.02
8	VYFPGP	-10.1	5.49	0.071	6.59	-0.66
9	NNPKFF	-10.0	8.75	-0.586	7.41	-0.47
10	APFPEVF	-9.9	4.00	0.7	8.43	-1.11
11	APFPEVFG	-9.9	4.00	0.562	9.58	-1.19
12	QPSYPPF	-9.8	5.52	-1.086	7.13	-0.86
13	QFRPR	-9.8	12	-2.26	10.72	-0.87
14	WAKYLGRSFR	-9.8	11	-0.79	10.67	-1.09
15	RGPF	-9.7	9.75	-1.06	9.43	-0.81
16	PFPKYP	-9.7	9.01	-1.2	8.70	-0.6

17	QFLPYPPY	-9.7	5.52	-0.5	3.86	-0.46
18	SLVYPPF	-9.7	5.24	0.786	4.51	-0.87
19	DQFPRR	-9.6	9.6	-2.467	14.36	-0.93
20	NPFKFF	-9.5	8.75	-0.1	6.56	-0.56
21	LKNNNPFKFF	-9.5	10	-0.77	9.81	-0.62
22	TWDFPLP	-9.4	3.8	-0.243	7.02	-0.9
23	NNNPFKF	-9.4	8.75	-1.486	9.97	-0.65
24	MPFPKYP	-9.4	8.34	-0.757	8.03	-0.9
25	PGPSPTPR	-9.4	10.18	-1.6	12.13	-0.94
26	LLRFF	-9.3	9.75	1.74	3.79	-0.94
27	LIRFF	-9.3	9.75	1.88	3.92	-0.73
28	FYFPSRR	-9.3	10.84	-1.014	7.99	-1.06
29	PVRGPF	-9.3	10.18	-0.386	9.11	-0.95
30	IPPLR	-9.3	9.75	0.12	7.62	-0.46
31	PFKFF	-9.2	9.18	0.58	5.71	-0.73
32	FYPELFR	-9.2	6	-0.214	8.1	-1.07
33	FPKYP	-9.2	8.59	-1.12	8.56	-0.57
34	VYPPF	-9.2	5.49	0.5	5.3	-0.8
35	FPGPIH	-9.2	6.74	0.083	8.83	-0.79
36	GRQPGDYDDRRQPRREGGR	-9.2	6.27	-2.91	46.29	-0.81
37	FGRLF	-9.1	6.00	0.167	9.82	-0.71
38	YFPSRR	-9	10.84	-1.65	9.7	-0.92
39	PPPPP	-8.9	5.96	-1.6	8.6	-0.55
40	NPFKF	-8.9	8.75	-0.68	8.27	-0.67
41	DGPSSKDWRGGR	-8.9	8.75	-2.1	24.02	-0.55
42	NNPFKF	-8.8	8.75	-1.15	9.12	-0.58
43	FYFPSR	-8.8	8.75	-0.433	6.18	-0.91
44	VRGPF	-8.8	9.72	-0.183	8.97	-0.88
45	NENLLRFF	-8.8	6.00	-0.225	9.12	-0.88

46	FPKYPVEPF	-8.6	6.00	-0.411	10.16	-0.78
47	MPFPK	-8.4	8.5	-0.48	8.60	-1.09
48	AMKPW	-8.4	8.8	-0.54	8.58	-0.72
49	LHRFL	-8.1	9.76	0.54	7.83	-0.48

#### Supplementary Table 4

Molecular docking affinity and property prediction results

Number	peptides	affinity	Isoelectric point	Hydrophilic	Hydrophobicity	SVM <sup>1</sup>
1	LNYPAYPFP	-11.0	5.52	-0.41	5.43	-0.47
2	QPPSPPPFL	-10.9	5.52	-0.73	7.01	-0.62
3	FLPYPY	-10.9	5.52	0.133	3.8	-0.77
4	YFPFGPIH	-10.8	6.74	-0.3	8.26	-0.74
5	GGGYGPPPPP	-10.6	5.52	-1.09	12.49	-0.31
6	APFPEVFGK	-10.6	6.05	0.067	12.38	-1.17

\* The lower the value of the affinity, the more stable the conformation of the complex formed after binding. SVM shows a negative value for non-toxic and a positive value for toxic.

#### Supplementary Table 5

Screening peptides for ACEI activity

Number	Smple	Molecular mass (Da)	Amino acid number	ACEI rate (%)
1	Captopril	/	/	93.5
2	APFPEVFGK	990.52	9	84
3	QPPSPPPFL	1075	10	77
4	FLPYPY	798.4	6	71



