SI.Table3. Primer sequences for quantitative real-time PCR

Target gene	Gene Bank accession No.	Primer sequence (5'-3')	Product size (bp)
TNF-α (m)[b]	NM_013693.3	**F: 5'- CCACGCTCTTCTGTCTACTG -3'**	169
		R: 5'- ACTTGGTGGTTTGCTACGAC -3'	
IL-6 (m)	NM_031168.1	**F: 5'- GAGTCACAGAAGGAGTGGCTAAGGA-3**	106
		R:5'- CGCACTAGGTTTGCCGAGTAGATCT-3	
IL-8 (m)	NM_011339.2	**F:5'-TCTCGGTGTAGAGCAAGG-3**	146
		R:5'-TTCCCAAGTGCTGGTATT-3	
IL-10 (m)	NM_010548.2	**F: 5'- GGACCAGCTGGACAACATACTGCTA-3**	173
		R:5'- CCGATAAGGCTTGGCAACCCAAGT-3	
GAPDH (m)	NM_008084.3	**F: 5'- GAGAAACCTGCCAAGTATGATGAC -3**	212
		R: 5'- TAGCCGTATTCATTGTCATACCAG -3	
ZO-1 (m)	XM_006540786.1	**F: 5'-TCATCCCAAATAAGAACAGAGC-3**	198
		R: 5'-GAAGAACAACCCTTTCATAAGC-3	
ZO-2 (m)	XM_006526909.1	**F : 5'-GCTTTGGTGTGGACCAAGAT-3'**	269
		R: 5'-TCCATTATGGGTTTGCATGA-3'	
Occluding (m)	XM_006517566.1	**F: 5'-CTTTGGCTACGGAGGTGGCTAT-3'**	86
		R: 5'-CTTTGGCTGCTCTTGGGTCTG-3'	
Claudin-1 (m)	NM_016674.4	**F: 5'-GCTGGGTTTCATCCTGGCTTCT-3'**	110
		R: 5'-CCTGAGCGGTCACGATGTTGTC-3'	

Mucin1 (m)	NM_013605.2	**F: 5'-TGGATTGTTTCTGCAGATTTT-3'**	147
		R: 5'-CCTGACCTGAACTTGATGCT-3'	
Mucin2 (m)	NM_023566.3	**F: 5'-CCCAGAAGGGACTGTGTATG-3'**	134
		R: 5'-TGCAGACACACTGCTCACA-3'	
ZO-1 (h)[c]	XM_005254621.1	**F: 5'-CAGAGCCTTCTGATCATTCCAGCCA-3'**	69
		R: 5'-CATCTCTACTCCGGAGACTGC-3'	
Claudin-1 (h)	NM_021101.4	**F: 5'-GCGCGATATTTCTTCTTGCAGG-3'**	113
		R: 5'-TTCGTACCTGGCATTGACTGG-3'	
Occluding (h)	NM_001205255.1	**F: 5'-AAGCAAGTGAAGGGATCTGC-3'**	204
		R: 5'-GGGGTTATGGTCCAAAGTCA-3'	
GAPDH (h)	XM_005253678.1	**F:5'-GGTGGTCTCCTCTGACTTCAACA-3'**	127
		R: 5'-GTTGCTGTAGCCAAATTCGTTGT-3'	

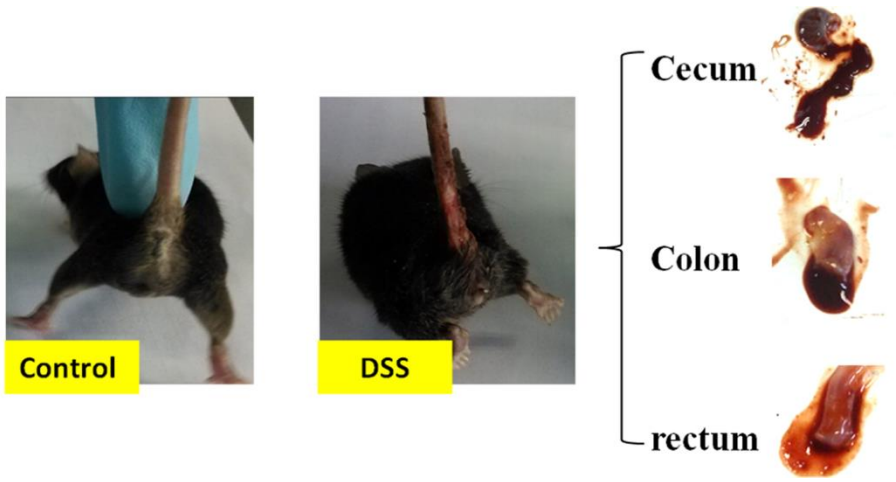
b: (m) = mouse; c: (h) = human. The amplification efficiency of all primers were verified before use.

SI.Table4. MIC and MBC of Cathelicidin-derived peptides against Gram negative and Gram positive bacterias

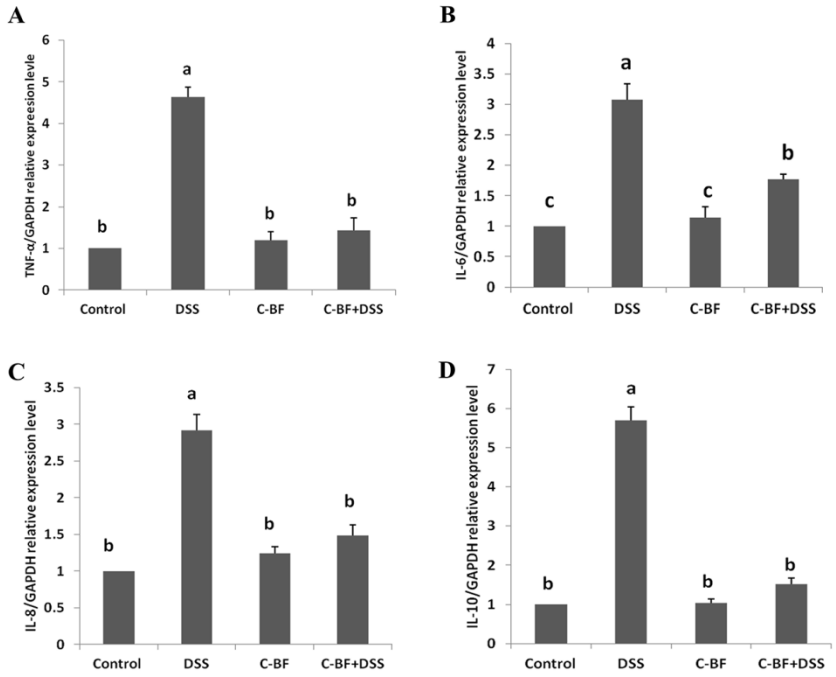
	MIC/MBC(μg/ml)						
	LL-37	**C-BF**	**PG-1**	**PMAP-23**	**IN**	**Aureomycin**	**Neomycin**
Gram-negative bacteria							
***E.coli* ATCC25922**	16/32	1/2	8/16	128/256	16/32	4/16	2/8
***E.coli* K88**	32/64	4/8	8/16	256/-	16/64	4/16	1/4
***E.coli* K12**	256/-	1/2	8/16	256/-	16/32	2/8	2/8
***E.coli* EPEC O78：K80**	-/-	16/32	32/64	-/-	16/32	64/256	1/4
***E.coli*EPEC O144:K26**	-/-	-/-	128/256	-/-	-/-	4/16	1/4
***E.coli EPEC* O44:K74**	-/-	64/128	64/128	-/-	-/-	64/256	16/64
S.choleraesuis	128/256	2/4	4/8	-/-	32/64	4/16	2/16
CMCC50020							
S.typhimurium	128/-	4/8	4/8	-/-	16/32	4/16	2/8
CMCC50013							
S.enteritidis	-/-	4/8	16/32	-/-	16/32	16/64	8/32
CMCC50041							
P.aeruginosa	128/-	4/8	8/16	-/-	128/-	2/16	4/16
CMCC27853							
Gram-positive bacteria							
***S.aureus* ATCC25923**	16/32	4/8	2/4	64/128	4/8	0.06/0.5	0.13/0.5
S.epidermidis	256/-	8/16	4/8	256/-	8/16	0.13/1	0.5/2
ATCC12228							

MIC: Minimal Inhibitory Concentration, MBC:Minimal Bactericidal Concentration

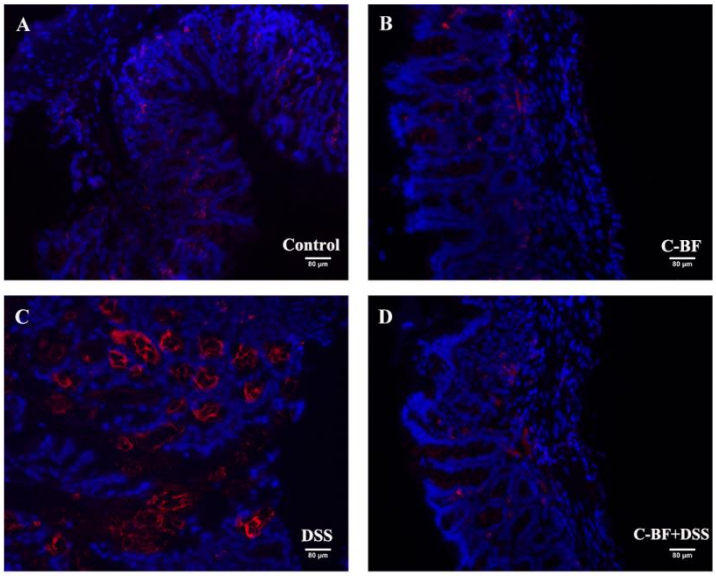
"-" Means no effect when tested within 256 μg/ml



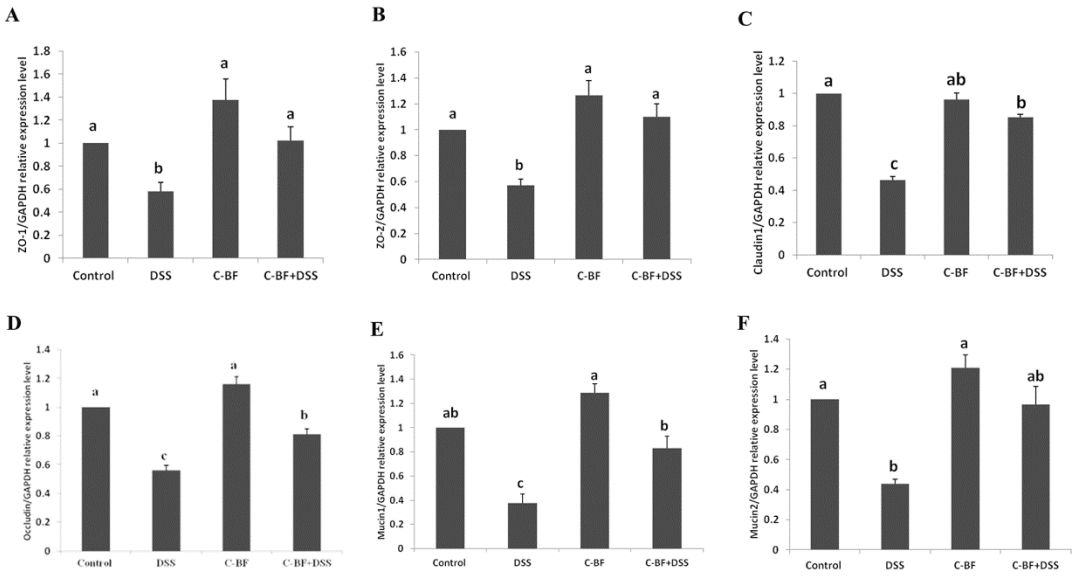
SI.Figure1. Bleeding status of the large intestine (cecum, colon, rectum). Photos were taken of the anus of representative mice at day 5 of the induction period. Samples of large intestine were also taken and photos of the three parts (cecum, colon, rectum) taken to evaluate the level of bleeding. There were at least six individuals showing the same bleeding status.



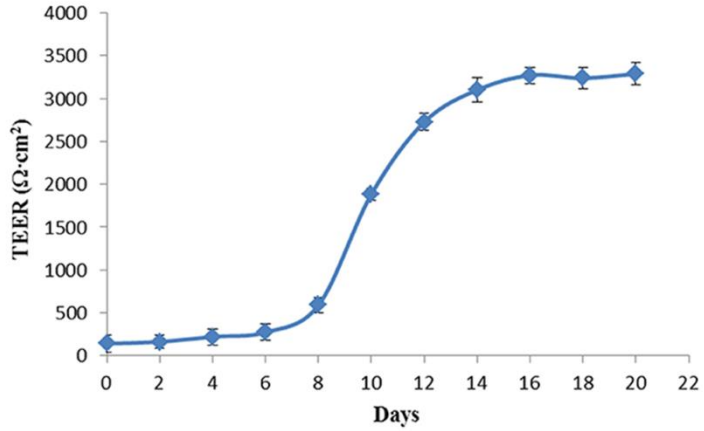
SI.Figure2. Gene expression level of cytokines in the colon of colitis mice. Total RNA isolation of colon and cDNA synthesis by reverse transcription were conducted using TRIzol reagent and M-MuLV reverse transcriptase. The mRNA levels of individual genes were measured by real-time PCR using a SYBR® Premix Ex TaqTM Kit in the ABI StepOne PlusTM Real-Time PCR system. Data were analyzed according to the comparative threshold cycle (Ct) method and normalized to an endogenous reference (GAPDH). The primers used were listed in Suppl.**Table3**. There were at least six repetitions in each group and the average values were calculated and multiple comparison test were carried out by Turkey HSD of one way analysis of variance (ANOVA) with SPSS 16.0, the final values were the means ± SEM and values without same letters are significantly different ($P < 0.05$).



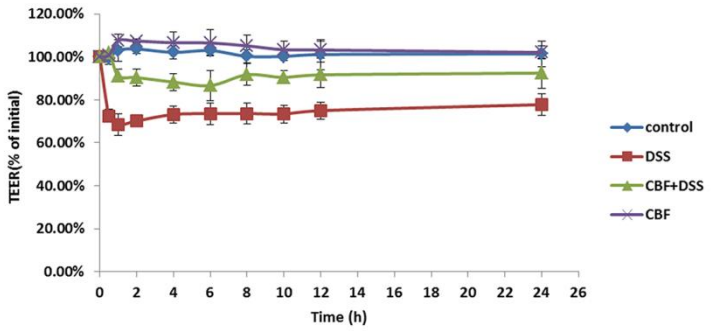
SI.Figure3. Immunofluorescence staining of mCRAMP in colon tissue (200×). Non-specific binding sites were blocked with 1% w/v BSA in PBS for 30 min, then 1:1000 rabbit anti-Cathelicidin polyclonal antibody in 1% w/v BSA in PBS added, and the sections incubated overnight at 4℃. PBS was used to wash the sections for 3 minutes for 5 times, then a 1:100 dilution of TRITC-conjugated goat anti-rabbit IgG was added and incubated at room temperature for 1 h in the dark. The secondary antibody was washed off as above, then DAPI was used to stain the nucleus. Unbound DAPI was washed off and glycerol used to mount the sections, the stained slides were observed under fluorescence microscope immediately at 200× magnification. (A) Control; (B) C-BF; (C) DSS; (D) C-BF+DSS. Scale bar = 80μm. The red represented positive of mCRAMP.



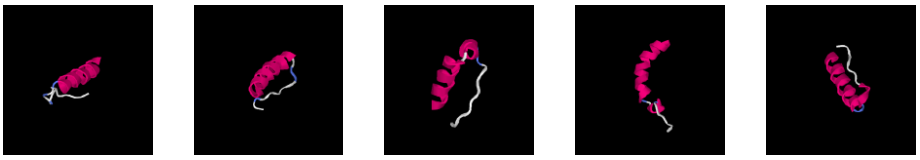
SI.Figure4. Gene expression level of barrier function related proteins. Total RNA isolation of colon RNA and cDNA synthesis by reverse transcription were conducted using TRIzol reagent and M-MuLV reverse transcriptase respectively. Data were analyzed according to the comparative threshold cycle (Ct) method and normalized to an endogenous reference (GAPDH). There were at least six repetitions in each group and the average values were calculated and multiple comparison test were carried out by Turkey HSD of one way analysis of variance (ANOVA) with SPSS 16.0. The final values were the means ± SEM and values without same letters are significantly different ($P < 0.05$).



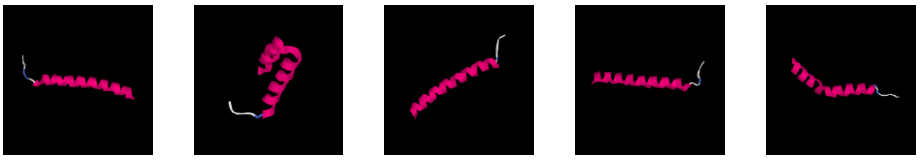
SI.Figure5. TEER value in Caco-2 cell monolayer during 21 days. Caco-2 cells were cultured in transwells at a density of 5×105 cells per well at a temperature of 37 ℃ with 5% CO2, and 95% humidity. The medium was changed every other day. The resistance value was tested by resistance meter every day, until the resistance value was stable. The values are expressed as the mean ± SEM.



SI.Figure6. Dynamic change (0–24 h) of TEER value in Caco-2 cell monolayers. After the resistance value was stable, the follow-up experiment was conducted. Adding 1.5 and 0.5 ml fresh medium to the upper well and basal well respectively, then C-BF was added to the upper well at the final concentration of 6.87μmol/L and incubated for 24 h. Then C-BF was washed out with PBS and DSS added in fresh medium at a final concentration of 3% (m/v) for 24 h. Cells were cultured in the incubator and the resistance per well was tested every other 2 h. There were at least four repetitions in each group and the average values were calculated and the values were expressed as the mean ± SEM.

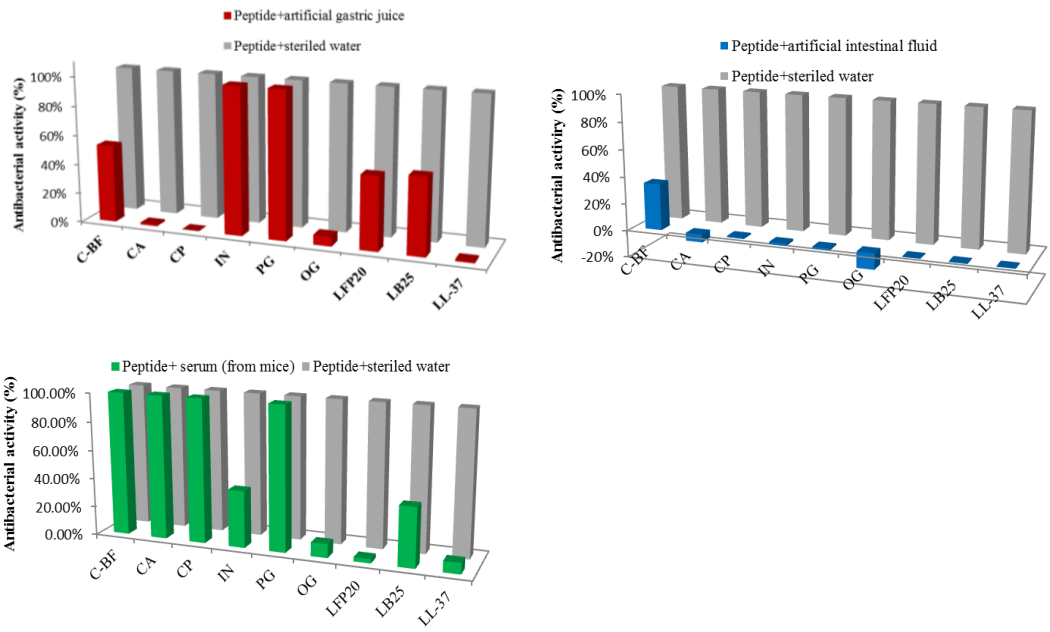


The peptide structure of C-BF predicted by I-TASSER

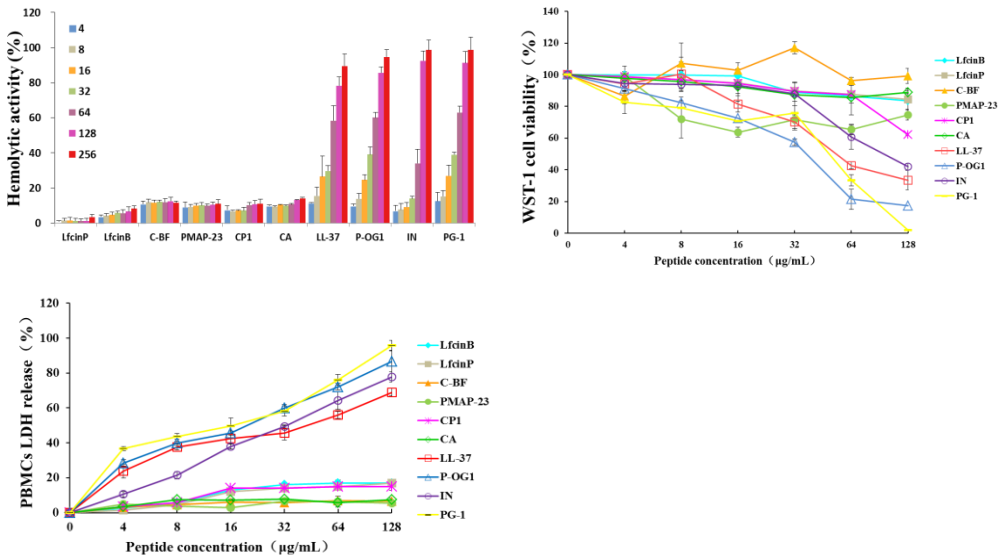


The peptide structure of LL-37 predicted by I-TASSER

SI.Figure7. The prediction of the structure of peptides (C-BF and LL-37). After submitting the sequence of C-BF (KFFRKLKKSV KKRAKEFFKK PRVIGVSIPF) and LL-37 (LLGDFFR KSK EKIGKEFKRI VQRIKDFLRN LVPRTES), the structural information could be obtained from http://zhanglab.ccmb.med.umich.edu/I-TASSER/.



SI.Figure8. The resistance ability of antimicrobial peptides to different enzymatic hydrolysis medium (artificial gastric juice、artificial intestinal fluid and serum from mice). nine different derived antimicrobial peptides were chemically derived and were incubated with artificial gastric juice, artificial intestinal fluid and serum (from mice) respectively for 4 h, after that their antibacterial activities were tested.



SI.Figure9. The cytotoxicity of antimicrobial peptides to porcine red blood cells and PBMCs. For hemolytic activity assay, 90 μl erythrocyte suspensions (final concentration: 1%) were mixed with 10 μl of tested peptides and incubated at 37℃ under 5% CO_2 for 24 h, after incubation, the supernatants were transferred into 96-well plates and the optical density was measured at 414 and 546 nm through Microplate Readers, there were four replicates for each test. For cell viability analysis, PBMCs (10^6 cells/well) were cultured in 96-well plates, and incubated with different peptides at the final concentrations of 4-128 μg/ml for 24 h (37℃ and 5% CO_2), after incubation, the following procedures were performed according to the manufactural instructions (Roche Molecular Biochemicals, Mannheim, Germany). For LDH release assay, the processes were similar to cell viability analysis, and after incubation, the following procedures were performed according to the manufacturer's instructions （Roche Molecular Biochemicals, Mannheim, Germany）.