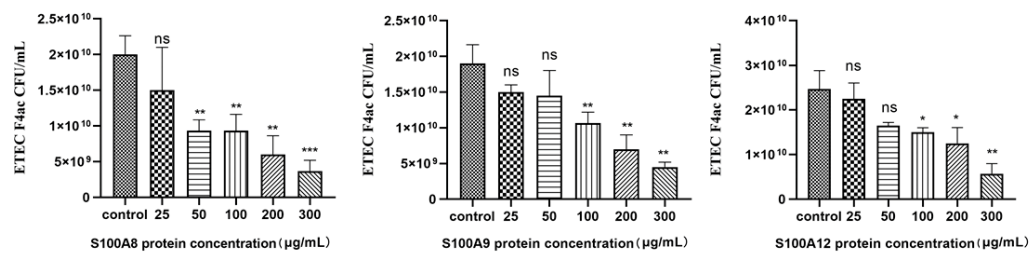
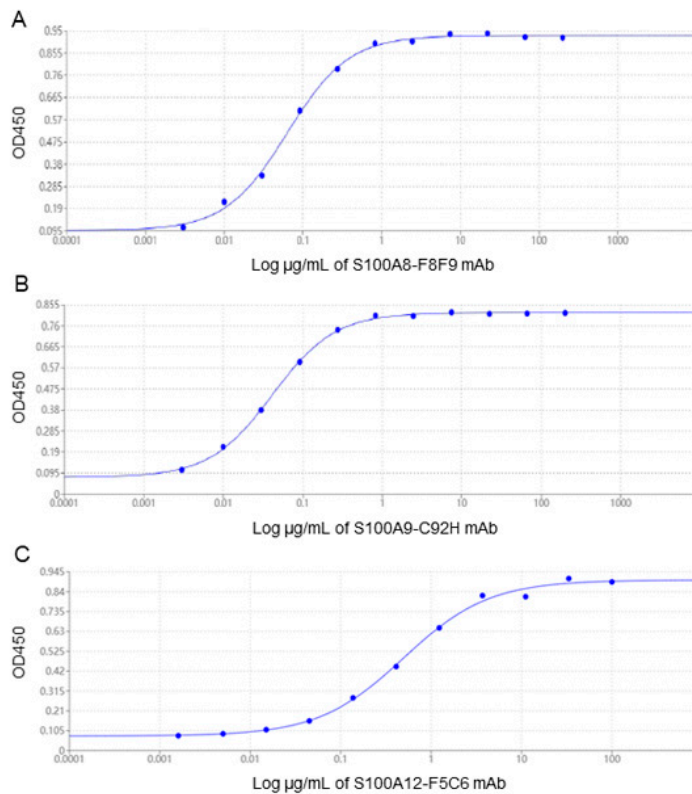


## Supplementary Materials



**Figure S1.** Bacterial load statistics of different concentrations of S100A8, S100A9, and S100A12 proteins (25, 50, 100, 200, and 300 µg/mL) co-cultured with F4ac for 48 h (the relative value between different groups and the control (without protein treatment) were analyzed by SPSS 16.0 software (SPSS Inc., USA) using student's t-test, and ns represents no statistical difference between the data, \* represents  $P < 0.05$ , \*\* represents  $P < 0.01$ , \*\*\* represents  $P < 0.001$  and there are significant statistical differences between the data). All proteins expressed by the prokaryotic expression system in this experiment can perform an antimicrobial function *in vitro* and the bacteriostatic effects on the F4ac ETEC strain were dose-dependent in a certain range.



**Figure S2.** Determination of S100A8-F8F9, S100A9-C92H, and S100A12-F5C6 mAbs antibody relative binding affinities using the ELISA assay. The binding curve was plotted using a four-parameter logistic curve fit, the X-axis shows the logarithmic concentration of antibodies, and the y-axis shows the absorbance at 450 nm.

**S100A8**

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<-----FR1-IMGT-----
L L Q L N L W R R A S Y G R C Q M T Q S H K F M S T S V G D
271 CTG CTG CAG TTG AAC CTC TGG AGG CGC GCA AGC TAC GGC CGA TGT CAG ATG ACC CAG TCT CACAAA TTC ATG TCC ACATCA GTA GGA GAC 360

R V S I T C K A S Q D V G T A V A W Y Q Q K P G Q S P K L L
361 AGG GTC AGC ATC ACC TGC AAG GCC AGT CAG GAT GTG GGT ACT GCT GTA GCC TGG TAT CAA CAG AAA CCAGGG CAATCT CCT AAACTA CTG 450

I Y W A S T R H T G V P D R F T G S G S G T D F T L T I S N
451 ATT TAC TGG GCATCC ACC CGG CACACT GGA GTC CCT GAT CGC TTC ACA GGC AGT GGA TCT GGG ACAGAT TTC ACT CTC ACCATT AGCAAT 540

V Q S E D L A D Y F C Q Q Y S S Y P L T F G A G T K L E L K
541 GTG CAG TCT GAA GAC TTG GCA GAT TAT TTC TGT CAG CAATAT AGC AGC TAT CCT CTC ACG TTC GGT GCT GGG ACCAAG CTG GAG CTG AAA 630

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**S100A9**

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<-----FR1-IMGT-----
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310 GCT ACG GCC GAT GTC CTG TGG GGA CAT TGT GAT GTC ACA GTC TCC ATC CTC CCT AGC TGT GTC AGT TGG AGA GAA GGT TAC TAT GAG CTG 399

K S S Q S L L Y S S N Q K N Y L A W Y Q Q K P G Q S P K L L
400 CAA GTC CAG TCA GAG CCT TTT ATA TAG TAG CAATCAAAA GAA CTA CTT GGC CTG GTA CCAGCA GAA GCC AGG GCA GTC TCC TAA ACT GCT 489

I Y W A S T R E S G V P D R F T G S G S G T D F T L T I S S
490 GAT TTA CTG GGC ATC CAC TAG GGAATC TGG GGT CCC TGA TCG CTT CACAGG CAG TGG ATC TGG GAC AGA TTT CACTCT CAC CAT CAG CAG 579

V K A E D L A V Y Y C Q Q Y Y S Y P Y T F G G G T K L E I K
580 TGT GAA GGC TGA AGA CCT GTC AGT TTA TTA CTG TCA GCA ATA TTA TAG CTA TCC TTA CAC GTT CGG AGG GGG GAC CAA GCT GGA AAT AAA 669

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**S100A12**

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<-----FR1-IMGT-----
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S C R A S E S V D S Y G N S F M H W Y Q Q K P G Q P P K L L
382 TCC TGC AGA GCC AGT GAAAGT GTT GAT AGT TAT GGC AAT AGT TTT ATG CAC TGG TAC CAG CAG AAA CCA GGA CAG CCA CCCAAA CTC CTC 471

I Y R A S N L E S G I P A R F S G S G S R T D F T L T I N P
472 ATC TAT CGT GCATCC AAC CTA GAATCT GGG ATC CCT GCC AGG TTC AGT GGC AGT GGG TCT AGG ACAGAC TTC ACC CTC ACCATT AAT CCT 561

V E A D D V A T Y Y C Q Q S N E D P Y T F G G G T K L E I K
562 CCT GTG GAG GCT GAT GAT GTT GCAACC TAT TAC TGT CAG CAAAGT AAT GAG GAT CCG TAC ACG TTC GGA GGG GGG ACCAAG CTG GAAATA 651

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**Figure S3.** The sequences encoding the framework regions (FR) and CDR of the S100A8-F8F9, S100A9-C92H, and S100A12-F5C6 mAbs. The CDR1, CDR2, and CDR3 regions are highlighted in red, blue, and green, respectively.