(A)

(B)

1 MPNFFIDRPI FAWVIAIIIM LAGGLAILKL PVAQYPTIAP PAVTISASYP 51 GADAKTVQDT VTQVIEQNMN GIDNLMYMSS NSDSTGTVQI TLTFESGTDA
101 DIAQVQVQNK LQLAMPLLPQ EVQQQGVSVE KSSSSFLMVV GVINTDGTMT
151 QEDISDYVAA NMKDAISRTS GVGDVQLFGS QYAMRIWMNP NELNKFQLTP
201 VDVITAIKAQ NAQVAAGQLG GTPPVKGQQL NASIIAQTRL TSTEEFGKIL
251 LKVNQDGSRV LLRDVAKIEL GGENYDIIAE FNGQPASGLG IKLATGANAL
301 DTAAAIRAEL AKMEPFFPSG LKIVYPYDTT PFVKISIHEV VKTLVEAIIL
351 VFLVMYLFLQ NFRATLIPTI AVPVVLLGTF AVLAAFGFSI NTLTMFGMVL
401 AIGLLVDDAI VVVENVERVM AEEGLPPKEA TRKSMGQIQG ALVGIAMVLS
451 AVFVPMAFFG GSTGAIYRQF SITIVSAMAL SVLVALILTP ALCATMLKPI
501 AKGDHGEGKK GFFGWFNRMF EKSTHHYTDS VGGILRSTGR YLVLYLIIVV
551 GMAYLFVRLP SSFLPDEDQG VFMTMVQLPA GATQERTQKV LNEVTHYYLT
601 KEKNNVESVF AVNGFGFAGR GQNTGIAFVS LKDWADRPGE ENKVEAITMR
651 ATRAFSQIKD AMVFAFNLPA IVELGTATGF DFELIDQAGL GHEKLTQARN
701 QLLAEAAKHP DMLTSVRPNG LEDTPQFKID IDQEKAQALG VSINDINTTL
751 GAAWGGSYVN DFIDRGRVKK VYVMSEAKYR MLPDDIGDWY VRAADGQMVP
801 FSAFSSSRWE YGSPRLERYN GLPSMEILGQ AAPGKSTGEA MELMEQLASK
851 LPTGVGYDWT GMSYQERLSG NQAPSLYAIS LIVVFLCLAA LYESWSIPFS
901 VMLVVPLGVI GALLAATFRG LTNDVYFQVG LLTTIGLSAK NAILIVEFAK
951 DLMDKEGKGL IEATLDAVRM RLRPILMTSL AFILGVMPLV ISTGAGSGAQ
1001 NAVGTGVMGG MVTATVLAIF FVPVFFVVVR RRFSRKNEDI EHSHTVDHH

Figure 1. Identification of the purified AcrB protein. (A) SDS-PAGE. M: protein molecular weight marker; FT: flow through; W1: wash by 30 mM imidazole; W2: wash by 50 mM imidazole; E: elution by 500 mM imidazole. The black arrow indicated overexpressed AcrB. (B) AcrB sequence coverage determined by MS. Taxonomy: E. coli K-12. Sequence coverage: $41 \%$. Identified peptides were shown in red.

Table S1. The IC 50 $_{50}$ of Kam3, and Kam3-AcrB against dyes and drugs.

| Drug group and drug | IC50 $(\mu \mathrm{g} / \mathrm{mL})$ |  |  |
| :---: | :---: | :---: | :---: |
|  | Kam3 | Relative <br> resistance |  |
| Erythromycin | Macrolide |  |  |
| Clarithromycin | 7.812 | 250 | 32 |
|  | 10.937 | 87.5 | 8 |
| Norfloxacin | Quinolone |  |  |
|  | 0.78 | 1.56 | 2 |
| Tetracycline | Tetracycline |  | 4 |
| Rifampicin | 0.098 | 0.39 | 2 |
| Dyes | 0.625 | 1.25 | 2 |
| Hoechst 33342 | 7.812 |  | 4 |
| Ethidium bromide | 25 | 15.625 | 4 |
| Nile red | $>16$ | $>16$ | 1 |

(C)


Increased substrates in the extracellular space monitored by using MALDI-TOF.

Fewer substrates in the extracellular space as compared with the no EPI group.
(A)


At time $=0$, substrates started to get across the cell membrane by passive diffusion. The influx rate was much greater than the efflux rate.
(B)


Substrates influx gradually reached a plateau within 5 min.

Figure S2. The influx and efflux of the substrates when they are incubated with the E. coli cells.
(A)

(B)

(C)


Figure S3. The calibration curves of dyes (A) Hoechst 33342 (B) EtBr (C) Nile red. Values were expressed as mean $\pm$ standard deviation (SD) $(n=3)$.
(A)

(B)


Figure S4. The calibration curves of dyes (A) Erythromycin (B) Rifampicin. Values were expressed as mean $\pm$ standard deviation (SD) $(n=3)$.

