Supplementary Materials

A rapid and specific antimicrobial resistance detection of *Escherichia coli* via magnetic nanoclusters

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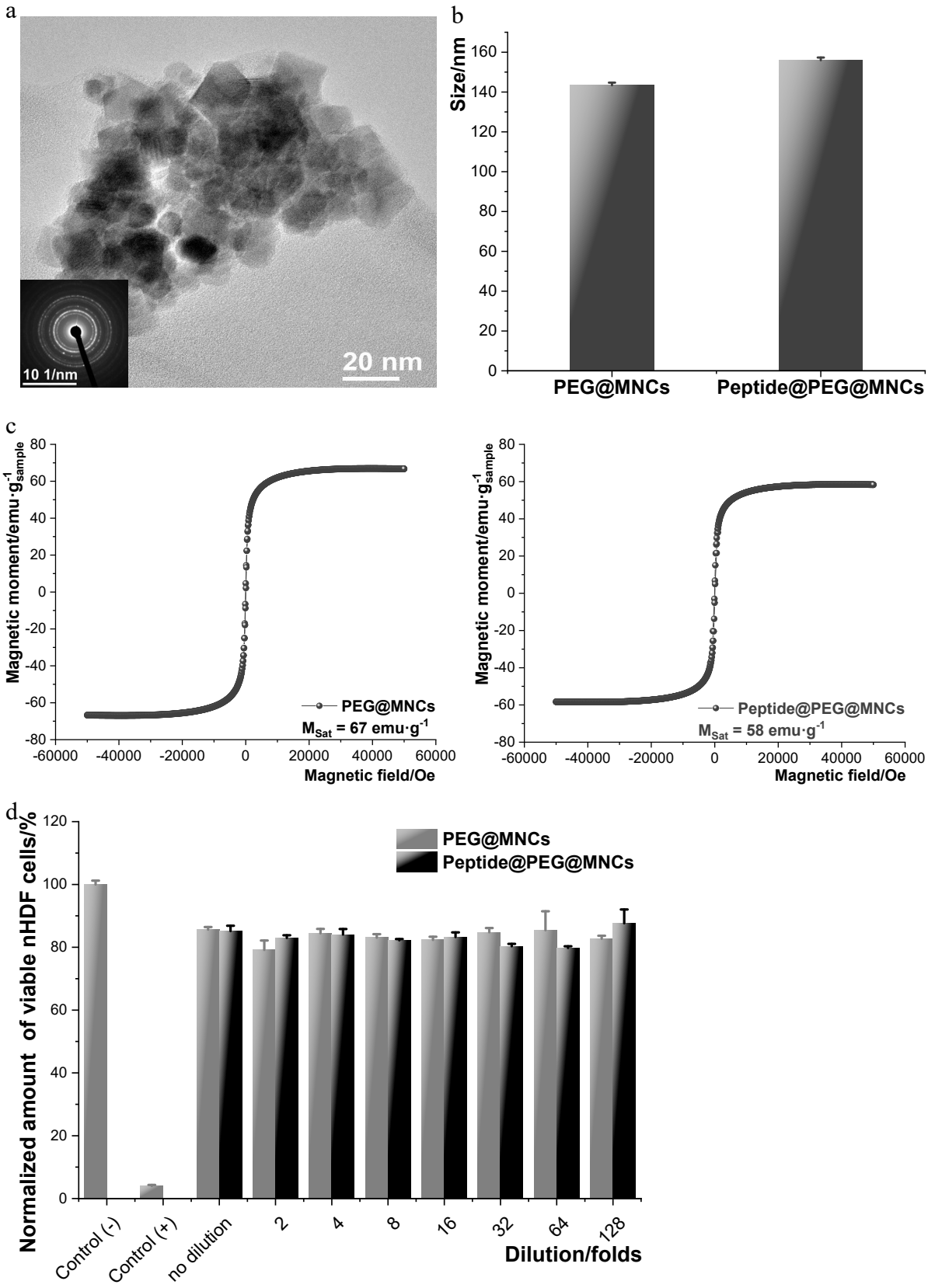
a
20 nm
10 1/nm
b
Size/nm
PEG@MNCs
Peptide@PEG@MNCs
c
Magnetic moment/emu·g-1sample
PEG@MNCs
MSat = 67 emu·g-1
Magnetic field/Oe
Peptide@PEG@MNCs
MSat = 58 emu·g-1
Magnetic field/Oe
d
PEG@MNCs
Peptide@PEG@MNCs
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2
4
8
16
32
64
128
Dilution/folds

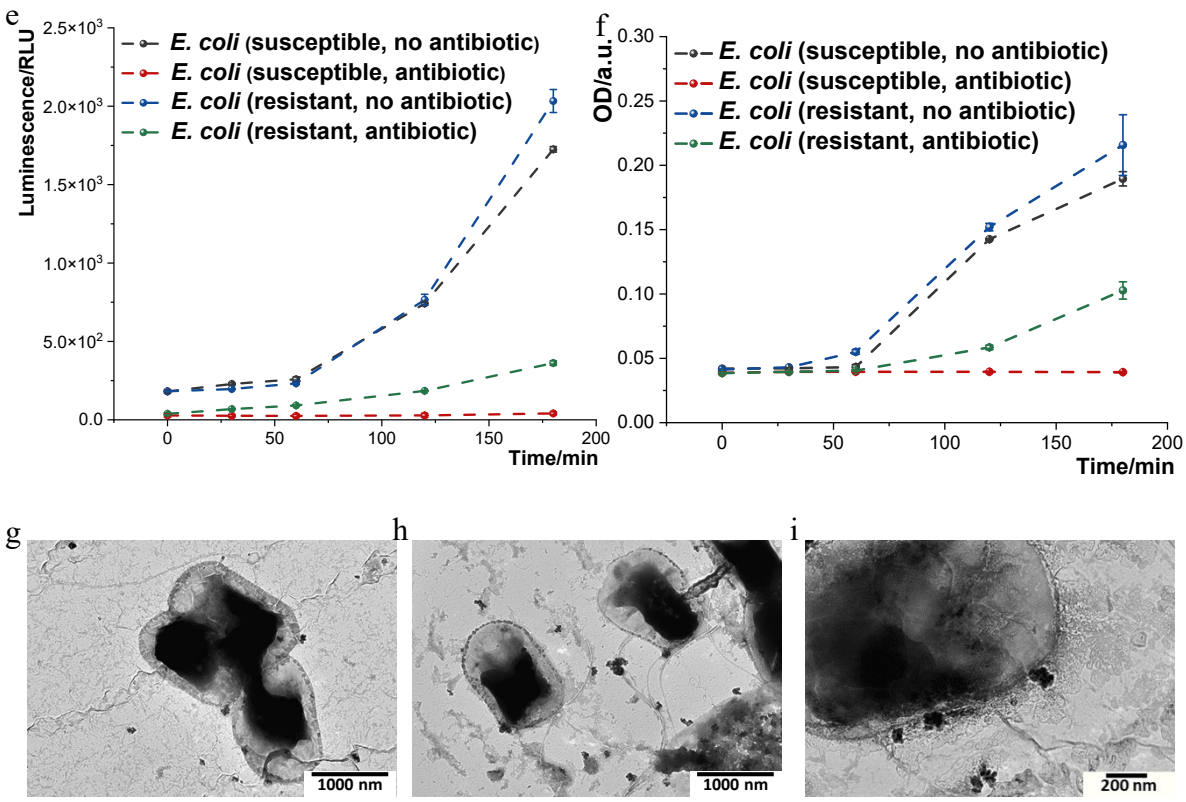


Figure S1. Bacterial capture in PBS towards *E. coli*. (a) PEGylated MNCs before functionalization was imaged by applying a scanning transmission electron microscope (STEM), manifesting a cluster structure. (b) The size of PEG@MNCs before and after functionalization was analyzed by employing a dynamic light scattering (DLS). (c) Analysis of vibrating sample magnetometry (VSM) hysteresis was performed at room temperature towards PEG@MNCs and peptide@ PEG@MNCs, including the relative values of saturation magnetization (M_{sat}). (d) The viability of the normal human dermal fibroblasts (nHDFs) was measured after incubation for 24h at 37°C with PEG@MNCs and peptide@PEG@MNCs in DMEM containing 1 % penicillin/streptomycin/neomycin (PSN) at pH 7.4. The cytotoxic cut-off was determined as 70 % viability of the nHDFs measured from the negative control (empty wells). 1 % Triton X-100 in DMEM containing 5 % FCS was regarded as a positive control. No cytotoxicity was observed for all samples aligned with the negative control. Error bars denoted the standard deviations calculated from 8 measurements. The growth analysis of the captured susceptible and resistant *E. coli* without a rinsing process was performed in the presence of 300 $\mu g \cdot mL^{-1}$ ampicillin through the utilization of AquaSpark® beta-D-glucuronide (e) and optical density (f). (g)-(i) The interaction between susceptible *E. coli* and peptide@ PEG@MNCs was analyzed through a transmission electron microscope (TEM). n = 3 (biological repeats), mean ± SD shown.

Table S1. Affinity evaluation was analyzed using single bacterial adhesion force spectroscopies between bacteria and various nanoclusters (MNCs, peptide@MNCs, PEG@MNCs, and peptide@PEG@MNCs). Every type of nanoclusters was deposited on glass petri dishes coated by polydopamine according to published methods(*1*). Every measurement was carried out at least ten times to derive the average value and standard deviation.

Single bacterial adhesion force between different bacterial pathogens and various surfaces/nN					
	S. aureus	*P. aeruginosa*	*S. epidermidis*	Susceptible *E. coli*	Resistant *E. coli*
Glass	1.35 ± 0.43	1.39 ± 0.65	0.77 ± 0.57	1.04 ± 0.42	0.66 ± 0.30
polydopamine@Glass	6.25 ± 1.79	8.25 ± 2.39	8.37 ± 1.40	8.17 ± 1.62	2.99 ± 0.59
MNCs	1.47 ± 0.40	1.15 ± 0.68	1.11 ± 0.54	1.81 ± 0.52	1.25 ± 0.44
Peptide@MNCs	1.68 ± 0.86	1.28 ± 0.72	1.23 ± 0.28	1.82 ± 0.57	1.48 ± 0.56
PEG@MNCs	0.61 ± 0.32	0.48 ± 0.24	0.61 ± 0.19	0.42 ± 0.14	0.60 ± 0.32
Peptide@PEG@MNCs	0.77 ± 0.37	1.60 ± 0.44	1.48 ± 0.68	24.44 ± 5.0	23.56 ± 3.84

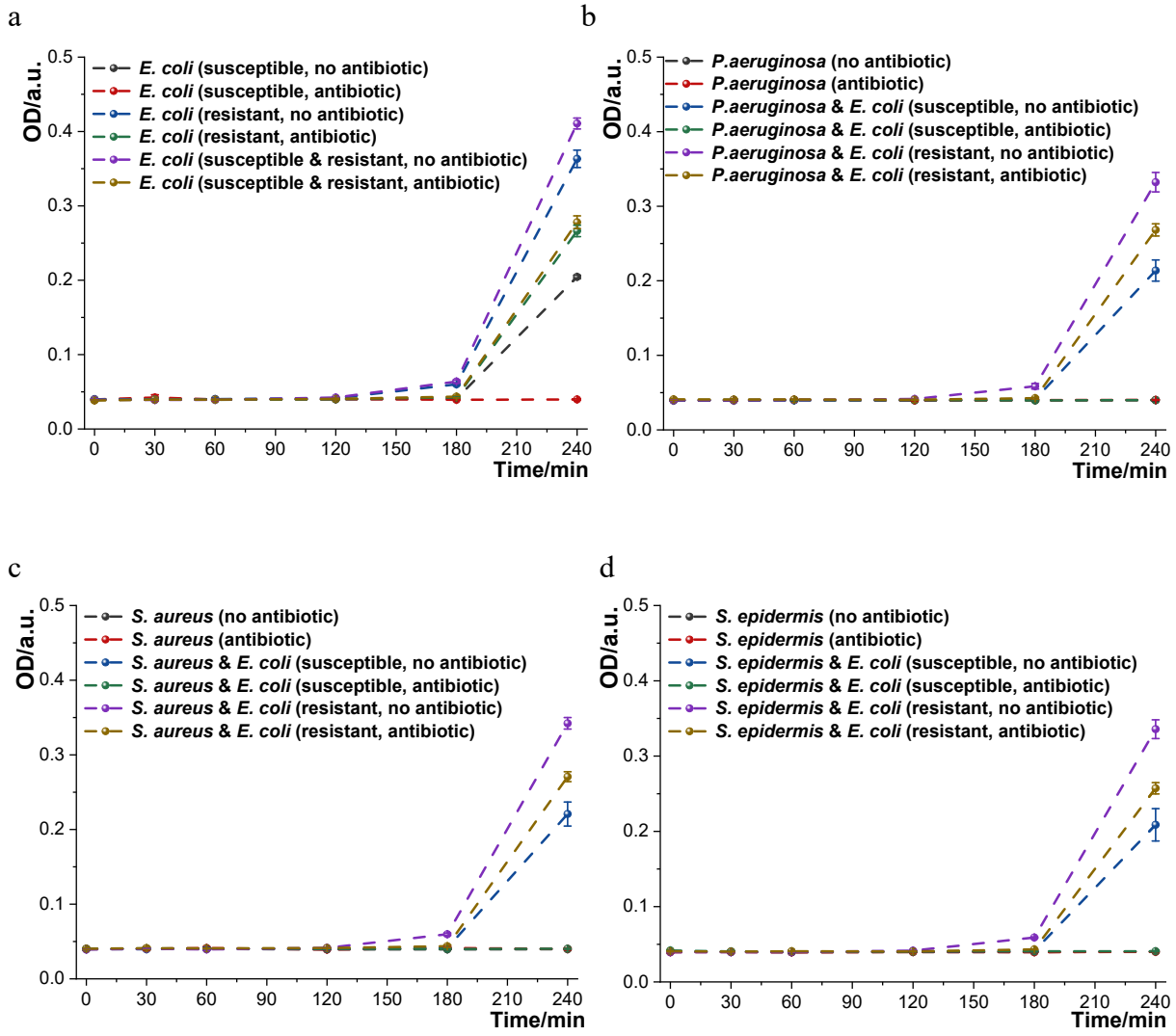
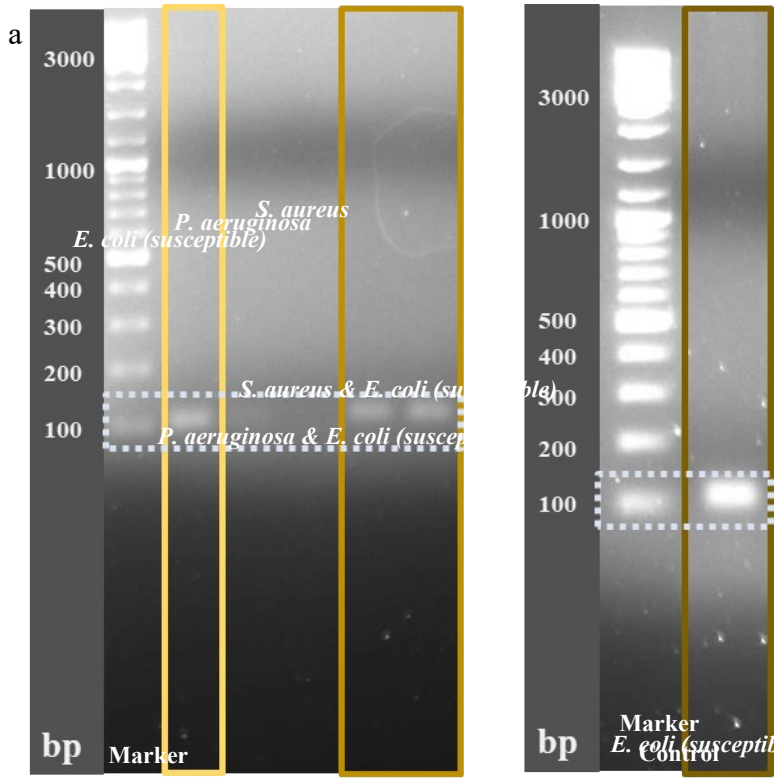


Figure S2. Bacterial capture in artificial urine. (a)-(d) The growth analysis of the captured susceptible and resistant *E. coli* with a rinsing process was performed in the presence of 300 $\mu g \cdot mL^{-1}$ ampicillin through applying AquaSpark® beta-D-glucuronide and the relative optical density, from a suspension of every single bacterial strain or a mixture of bacterial strains. Single bacterial strain: susceptible and resistant *E. coli*, *P. aeruginosa*, *S. aureus,* and *S. epidermidis*; mixed bacterial strains: susceptible and resistant *E. coli* respectively with *P. aeruginosa*, *S. aureus,* and *S. epidermidis*, and a mixture of susceptible and resistant *E. coli*. n = 3 (biological repeats), mean ± SD shown.



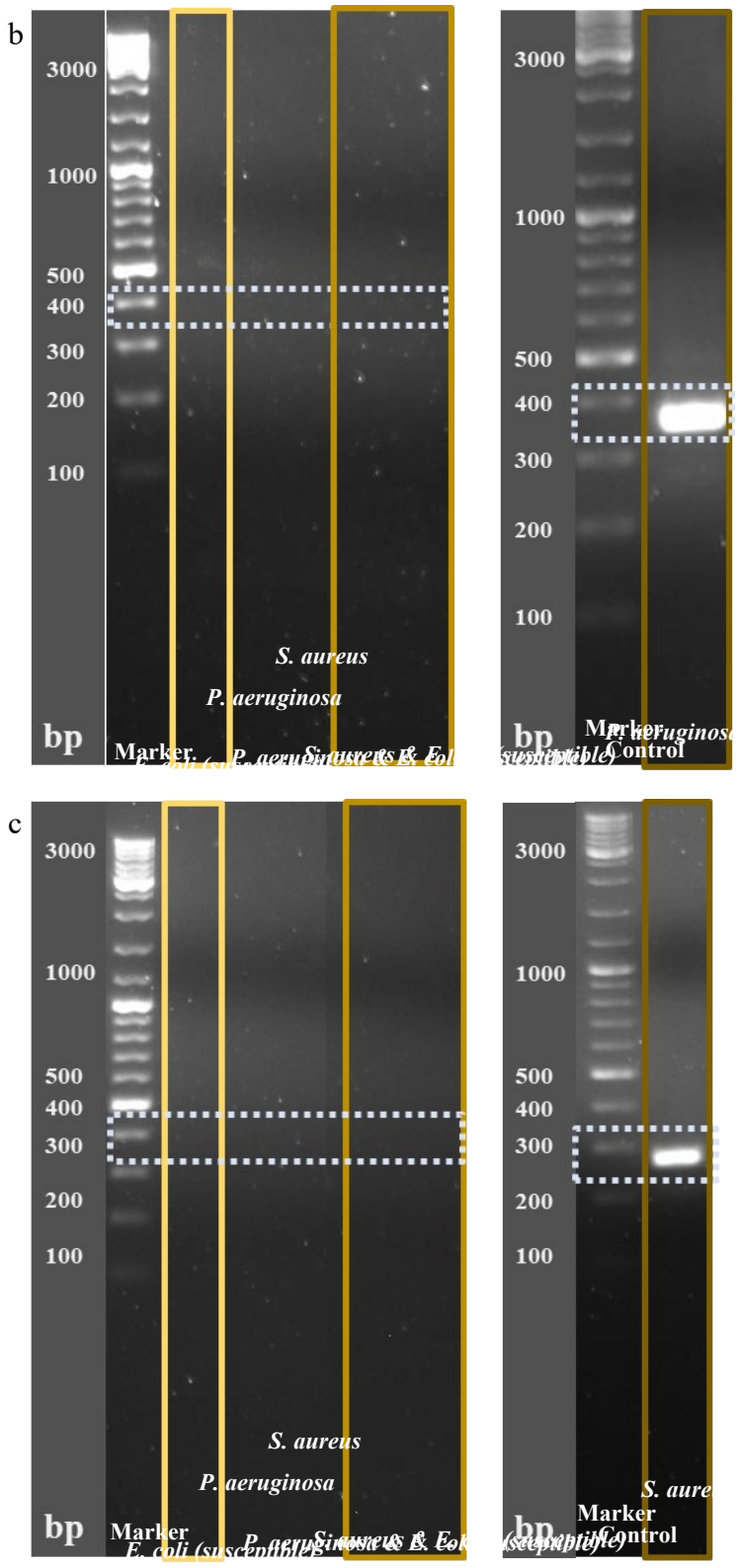


Figure S3. Capture specificity to *E. coli*. Polymerase chain reaction (PCR) analysis was conducted to understand the specificity of the fabricated peptide@PEG@MNCs to *E. coli*. Thereby, the lacY gene of *E. coli* (a), the toxA gene of *P. aeruginosa* (b), and the 16 rRNA gene of *S. aureus* (c) were respectively targeted. Moreover, we respectively applied susceptible *E. coli, P. aeruginosa,* and *S. aureus* as the positive controls. The analyzed peptide@PEG@MNCs were separated after the interaction and rinsing process from the

artificial urine spiked by susceptible *E. coli*, *P. aeruginosa*, *S. aureus*, and susceptible *E. coli*, mixed with *P. aeruginosa*, and *S. aureus*, respectively. Only the samples isolated from artificial urine spiked by susceptible *E. coli* and the bacterial mixtures containing susceptible *E. coli* lead to distinctive bands, revealing the existence of *E. coli*. Hence, the fabricated peptide@PEG@MNCs have the specificity to capture *E. coli* from the infected media.

Reference

1. M. Mittelviefhaus, D. B. Müller, T. Zambelli, J. A. Vorholt, A modular atomic force microscopy approach reveals a large range of hydrophobic adhesion forces among bacterial members of the leaf microbiota. *The ISME journal* **13**, 1878-1882 (2019).