

Supplementary Material

Inhibition effect of kaolinite on antibiotic resistance genes development in *Escherichia coli* induced by sublethal ampicillin and its molecular mechanism

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Protein extraction and digestion

Based on data of the antibiotic tolerance assay, the strains induced on the last day were selected for proteomic analysis. The strain was grown in LB media containing antibiotics at 37 ° C, and the antibiotic concentration was set as the 1/2 MIC value of the strains, and the strains were incubated in the LB media containing kaolinite. The strains were also incubated in kaolinite-free media as a control.

At the early stationary phase, the cells were harvested and washed twice with ice-cooled phosphate-buffered saline (PBS) solution and pelleted. The collected pellets were immediately stored at -80 °C and used for protein extraction. The mortar was pre-cooled, the sample was thoroughly ground and 1 ml of lysis buffer (1 mL/0.1 g; 7 M urea, 2 M thiourea, 4% CHAPS, and 1% Protease Inhibitor Cocktail) was added, dissolved and transferred to a 1.5 mL EP tube, sonicated (700w, 1.5s interval, 1s, ultrasonic 10min), 12000r / min, Centrifuge for 20 minutes and collect the supernatant. The supernatant was dispensed into 4 tubes of about 250 µL per tube and precipitated by adding 1 mL of acetone at -20 ° C overnight. The precipitated protein was centrifuged at 12000 r / min for 20 minutes at 4 ° C, the supernatant was decanted, and dried to obtain a processed protein mass. Add appropriate amount of lysis buffer (without SDS) to dissolve the protein. Ultrasonic dissolution (100 W, 0.8 sec, 0.8 sec, ultrasound, repeated once), after sonication at 4 ° C, 12000 r / min, centrifugation for 20 minutes, aspirate the supernatant and transfer to a new EP tube.

Characterization of E.coli-mineral complexes and minerals.

The X-ray diffraction patterns (XRD) of E.coli -mineral complexes or minerals were recorded by a powder diffractometer (Bruker, German) under Cu $\kappa\alpha$ radiation ($\lambda = 0.154$ nm, Ni-filter) with a scan range of 3° - 80° , a step size of 0.02° and a measuring time of 19.2 s per step.

The Fourier transform infrared (FTIR) spectra was recorded using a FTIR spectrometer Vertex-33 (Bruker, German) with the KBr pellet technique. Solid-state NMR spectra were collected on a Bruker Avance III HD 600 spectrometer. Al spectra were obtained at 104.26 MHz (14.095 T) with a 1s pulse delay. Si spectra were obtained at 79.49 MHz (14.095 T) with a 5s pulse delay. The spinning speed was 8 kHz.

The X-ray photoelectron spectra (XPS) were measured with an X-ray photoelectron spectrometer (Kratos, Axis Ultra DLD) and C1s (284.6 eV) was chosen as the reference. The pass energy was 40 eV and conventional Al K (1486.6 eV) anode radiation source was used as the excitation source. The C_{1s} and N_{1s} high resolution spectra and survey spectra of the samples were recorded. The C_{1s} and N_{1s} peak decomposition was performed using mixed Gaussian–Lorentzian (80/20) line shape with XPSPEAK software.

For SEM observation, after 48 h of incubation, the E.coli /mineral complexes or minerals were harvested and fixed with 2.5 % (v/v) glutaraldehyde in PBS at 4°C overnight, then E.coli /mineral complexes or minerals alone (without the addition of bacteria) were washed with 0.1 M PBS followed by 5 steps of dehydration with 30, 50,

70, 90 and 100 % ethanol solution for 10 min at each dehydration step. Thereafter, the pellets were resuspended in tertbutyl alcohol (TBA) for 20 min and then freeze-dried for at least 24 h. Dry specimens were gold coated for 90 s under vacuum in a JFC-1600 sputter coater (JEOL, Japan) to improve conductivity. The SEM images were obtained by a Zeiss EV0 LS10 scanning electron microscope (Carl Zeiss, Germany).

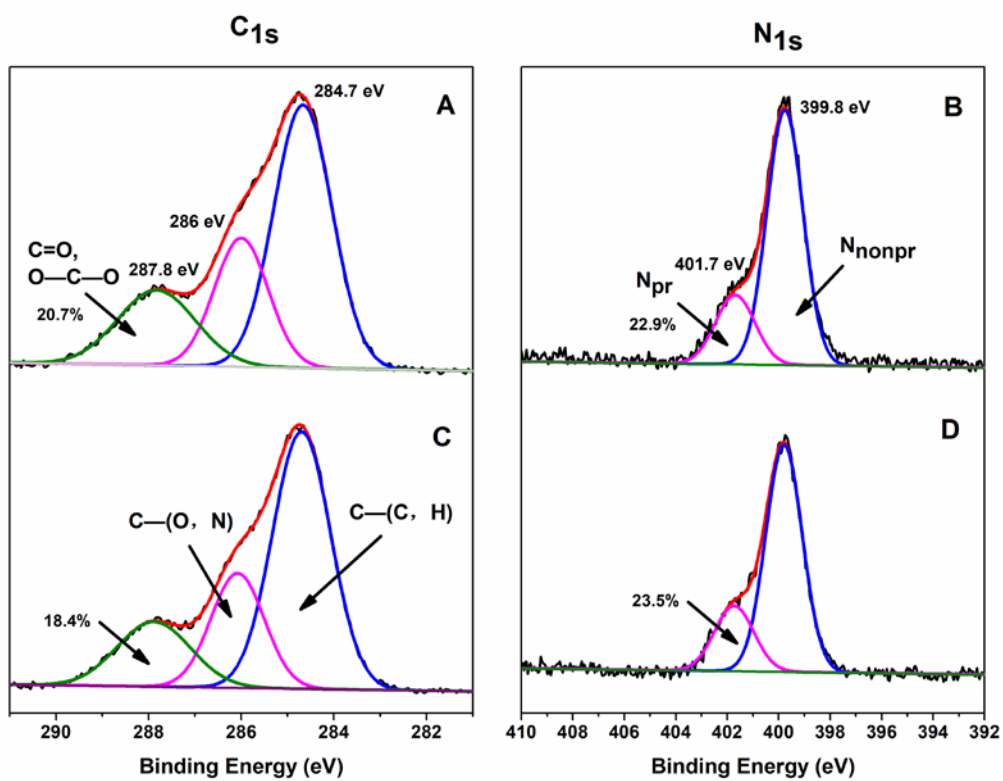


Fig. S1. High-resolution C 1s spectra of ampicillin + *E.coli* + kaolinite (A) and *E.coli* + kaolinite (C), and high-resolution N 1s spectra of ampicillin + *E.coli* + kaolinite (B) and *E.coli* + kaolinite (D).

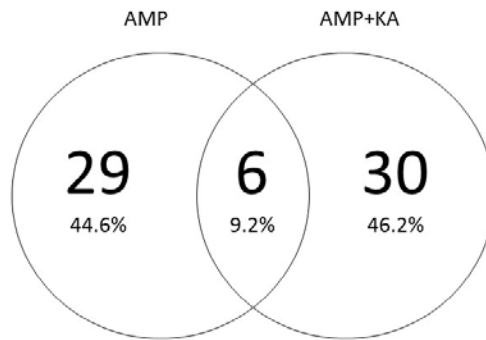


Fig. S2. Venn diagram showing the overlaps of the differentially expressed proteins in two experimental groups

Table S1. Targeted antibiotic resistance genes and their primer sequence

Targeted genes	Primers Sequence (5'to 3')	Annealing temperature (°C)
<i>acrA</i>	F:CAGATCACAACCGAGCTTCC	60
	R:GCTTCGATGTCGCTACCTTC	
<i>marA</i>	F:AATACATCCGCAGCCGTAAG	60
	R:TGAAGGTTCGGGTCAGAGTT	
<i>marR</i>	F:CAACCTTTCCACCCAGCCTT	60
	R:TGCTCTGCTCTATCCGCTGC	
<i>tetB</i>	F:ACGTGATAATACAGATACCGAA	60
	R:CACAAAGGCTTGGAATACTGA	
<i>blaTEM</i>	F:CCCCGAAGAACGTTTTTCAA	60
	R:TAGTGTATGCGGCGACCGAG	
<i>blaFOX</i>	F:AACATGGGGTATCAGGGAGATG	60
	R:CAAAGCGCGTAACCGGATTGG	
<i>tetE</i>	F:TTTGGTGGCGGTATGATTGC	60
	R:TGCCAGCCCGTTAATAGCAG	
<i>tetZ</i>	F:CCTTCTCGACCAGGTCGG	60
	R:ACCCACAGCGTGTCCGTC	
<i>tetA</i>	F: GCTACATCCTGCTTGCCTTC	60
	R:CATAGATCGCCGTGAAGAGG	

16S rRNA gene

F:ATGGYTGTCGTCAGCTCGTG

60

R:GGGTTGCGCTCGTTGC

Table S2. Fitting of kinetic models for the adsorption of tetracycline (TET), ampicillin (AMP) and mixed antibiotics by kaolinite in aqueous solutions at pH of 7.0, 37°C (initial antibiotic concentration, 16 mg L⁻¹; kaolinite dosage, 10 g L⁻¹).

Adsorbates	Pseudo-first-order model			$q_{e, \text{exp}}$ (mg g ⁻¹)	Pseudo-second-order model		
	k_1 (min ⁻¹)	q_e (mg g ⁻¹)	R^2		k_2 (g mg ⁻¹ min ⁻¹)	q_e (mg g ⁻¹)	R^2
TET	0.1492	0.9033	0.9328	0.9248	0.2898	0.9464	0.9998
AMP	0.3638	0.4602	0.9103	0.4672	1.0426	0.4721	0.9986
TET in mixed solution	0.3362	0.6875	0.9118	0.6912	1.0957	0.6981	0.9991
AMP in mixed solution	0.1838	`	0.9265	0.3472	1.1450	0.3532	0.9996

Table S3. A selection of proteins

Group	Citable	Gene	AVG.	FLAG
	Accession	Name		
AMP vs. control	P00370	<i>gdhA</i>	2.1289515	UP
AMP vs. control	P00448	<i>sodA</i>	0.25613	DOWN
AMP+KA vs. control	P00448	<i>sodA</i>	0.2697959	DOWN
AMP+KA vs. control	P00562	<i>metL</i>	1.995601	UP
AMP+KA vs. control	P00968	<i>carB</i>	0.663919	DOWN
AMP vs. control	P02918	<i>mrcA</i>	0.6340377	DOWN
AMP+KA vs. control	P07862	<i>ddlB</i>	1.599626	UP
AMP+KA vs. control	P08337	<i>mutT</i>	1.8709995	UP
AMP vs. control	P09155	<i>rnd</i>	0.6576648	DOWN
AMP+KA vs. control	P0A6L9	<i>hscB</i>	0.4659021	DOWN
AMP vs. control	P0A7A2	<i>gpmB</i>	1.513818	UP
AMP+KA vs. control	P0A7R5	<i>rpsJ</i>	0.5547198	DOWN
AMP+KA vs. control	P0A7W7	<i>rpsH</i>	0.6226237	DOWN
AMP+KA vs. control	P0A8B5	<i>ybaB</i>	0.5728507	DOWN
AMP+KA vs. control	P0A8K5	<i>yaeP</i>	0.5917874	DOWN
AMP vs. control	P0A908	<i>mipA</i>	0.3224485	DOWN
AMP vs. control	P0A968	<i>cspD</i>	1.729835	UP
AMP vs. control	P0A9H7	<i>cfa</i>	0.6670613	DOWN
AMP vs. control	P0A9M2	<i>hpt</i>	0.6166016	DOWN

AMP+KA vs. control	P0AA37	<i>rluA</i>	0.5889997	DOWN
AMP vs. control	P0AAC8	<i>iscA</i>	0.3500046	DOWN
AMP+KA vs. control	P0AAC8	<i>iscA</i>	0.6344143	DOWN
AMP+KA vs. control	P0AAD6	<i>sdaC</i>	11.912925	UP
AMP+KA vs. control	P0AAN9	<i>iraP</i>	0.6198615	DOWN
AMP vs. control	P0AB24	<i>efeO</i>	0.3383362	DOWN
AMP+KA vs. control	P0AB24	<i>efeO</i>	0.2977567	DOWN
AMP+KA vs. control	P0AB55	<i>yciI</i>	0.5579008	DOWN
AMP+KA vs. control	P0ABQ4	<i>folA</i>	0.6638064	DOWN
AMP vs. control	P0ABU9	<i>tolQ</i>	0.4609569	DOWN
AMP vs. control	P0AC33	<i>fumA</i>	2.3014665	UP
AMP vs. control	P0ACB2	<i>hemB</i>	0.5406323	DOWN
AMP vs. control	P0ACD4	<i>iscU</i>	0.1527631	DOWN
AMP vs. control	P0ADA1	<i>tesA</i>	0.6025851	DOWN
AMP vs. control	P0ADS9	<i>yggN</i>	0.5495642	DOWN
AMP+KA vs. control	P0AEJ4	<i>envZ</i>	2.5256486	UP
AMP vs. control	P0AEL0	<i>fdoI</i>	1.614427	UP
AMP vs. control	P0AFH2	<i>oppB</i>	1.535024	UP
AMP vs. control	P0AFL3	<i>ppiA</i>	0.6252788	DOWN
AMP vs. control	P0AFM2	<i>proX</i>	0.4529168	DOWN
AMP+KA vs. control	P0AG90	<i>secD</i>	3.7172824	UP
AMP+KA vs. control	P0DMC5	<i>rscC</i>	1.682692	UP

AMP+KA vs. control	P12282	<i>moeB</i>	1.698406	UP
AMP vs. control	P14175	<i>proV</i>	0.2040199	DOWN
AMP+KA vs. control	P14175	<i>proV</i>	0.5705512	DOWN
AMP vs. control	P15877	<i>gcd</i>	0.1455577	DOWN
AMP+KA vs. control	P15877	<i>gcd</i>	0.4864468	DOWN
AMP vs. control	P16703	<i>cysM</i>	0.497119	DOWN
AMP+KA vs. control	P17117	<i>nfsA</i>	2.4119754	UP
AMP vs. control	P21829	<i>ybhA</i>	2.0896505	UP
AMP vs. control	P24555	<i>ptrB</i>	0.6672593	DOWN
AMP vs. control	P28904	<i>treC</i>	3.3114514	UP
AMP vs. control	P31660	<i>prpC</i>	0.645661	DOWN
AMP vs. control	P33030	<i>yeiR</i>	0.6311982	DOWN
AMP vs. control	P33221	<i>purT</i>	3.0211049	UP
AMP+KA vs. control	P36672	<i>treB</i>	9.5069551	UP
AMP+KA vs. control	P37908	<i>yfjD</i>	1.5780295	UP
AMP+KA vs. control	P39180	<i>flu</i>	0.2929394	DOWN
AMP vs. control	P39451	<i>adhP</i>	0.3722012	DOWN
AMP+KA vs. control	P39451	<i>adhP</i>	0.4943579	DOWN
AMP+KA vs. control	P39830	<i>ybaL</i>	1.7952095	UP
AMP+KA vs. control	P45395	<i>kdsD</i>	0.6397416	DOWN
AMP vs. control	P63020	<i>nfuA</i>	0.6340377	DOWN
AMP+KA vs. control	P63177	<i>rlmB</i>	0.6368226	DOWN

AMP vs. control	P64534	<i>rcnB</i>	0.6698917	DOWN
AMP vs. control	P69874	<i>potA</i>	0.5155783	DOWN
AMP+KA vs. control	P76116	<i>yncE</i>	0.3435725	DOWN
AMP+KA vs. control	P76149	<i>sad</i>	2.4334674	UP
AMP+KA vs. control	P76217	<i>astD</i>	0.4024045	DOWN
AMP+KA vs. control	P76621	<i>csiD</i>	0.3362383	DOWN
AMP vs. control	P77252	<i>ykgE</i>	0.4051915	DOWN
AMP+KA vs. control	P77581	<i>astC</i>	0.2714537	DOWN

Table S4. GO analysis

Group	GO Classification	GO ID	GO Name	Gene ID	p-value
AMP vs. control	molecular_functio n	GO:004316 7	ion binding	P00448, P02918, P0AC33, P0ACB2, P15877, P39451, P69874, P0A9M2, P0ACD4, P33030, P63020, P0AAC8, P0AEL0, P14175, P16703, P33221, P21829, P64534, P00370, P00448, P15877, P39451, P0AEL0	0.002704
AMP vs. control	molecular_functio n	GO:001649 1	oxidoreductase activity	P39451, P0AEL0	0.014353
AMP vs. control	molecular_functio n	GO:000823 3	peptidase activity	P0ADA1, P24555, P0AC33, P0ACB2,	0.010377
AMP vs. control	molecular_functio n	GO:001682 9	lyase activity	P16703, P0AC33, P0AFL3,	0.071127
AMP vs. control	molecular_functio n	GO:001685 3	isomerase activity transmembrane	P0A7A2, P69874,	0.016657
AMP vs. control	molecular_functio n	GO:002285 7	transporter activity	P0AFM2, P14175	0.056572
AMP vs. control	molecular_functio n	GO:000367 7	DNA binding transferase activity,	P00448, P0A968	0.081616
AMP vs. control	molecular_functio n	GO:001674 6	transferring acyl groups	P31660, P0ADA1	0.040761

AMP vs. control	molecular_function	GO:001675 7	transferase activity, transferring glycosyl groups	P02918, P0A9M2 P69874,	0.027129
AMP vs. control	molecular_function	GO:001688 7	ATPase activity	P14175 P00448, P0AB24, P39451, P0AFM2, P63020, P0AEL0, P14175, P28904, P0A968,	0.016576
AMP vs. control	biological_process	GO:000695 0	response to stress	P64534 P00370, P02918, P0ACB2, P0A9H7, P0A9M2, P0A7A2, P16703, P33221, P0A908,	0.002064
AMP vs. control	biological_process	GO:000905 8	biosynthetic process	P0A968 P0AC33, P31660, P0A9H7, P0A9M2, P0A7A2, P0AEL0,	0.025641
AMP vs. control	biological_process	GO:004428 1	small molecule metabolic process	P33221 P69874, P0ABU9, P0AFM2, P0AFH2,	0.017633
AMP vs. control	biological_process	GO:000681 0	transport	P14175 P0ACB2, P09155, P0A9M2,	0.012210
AMP vs. control	biological_process	GO:003464 1	cellular nitrogen compound metabolic process	P33221, P0A968	0.073712
AMP vs.	biological_process	GO:005118	cofactor	P0ACB2,	0.008928

control		6	metabolic process	P0ACD4, P63020, P0A7A2, P0AAC8	
AMP vs. control	biological_process	GO:000609 1	generation of precursor metabolites and energy	P0AC33, P31660, P0A7A2, P0AEL0 P0ACD4, P63020,	0.004253
AMP vs. control	biological_process	GO:000679 0	sulfur compound metabolic process	P0AAC8, P16703 P31660,	0.002282
AMP vs. control	biological_process	GO:000662 9	lipid metabolic process	P0A9H7, P0ADA1 P0ACD4,	0.07657
AMP vs. control	biological_process	GO:002260 7	cellular component assembly	P63020, P0AAC8 P00370, P00448, P0AC33, P0ACB2, P0A9H7, P0A9M2, P0ACD4, P63020, P0AAC8, P28904, P33221, P77252, P0A968, P21829,	0.00228
AMP vs. control	cellular_componen t	GO:000582 9	cytosol	P64534 P00370, P00448, P31660, P09155, P0A9H7, P0A9M2, P16703, P28904,	0.002856
AMP vs. control	cellular_componen t	GO:000573 7	cytoplasm	P0A968, P24555	0.001548
AMP vs.	cellular_componen	GO:000588	plasma	P02918,	0.064852

control	t	6	membrane	P15877, P69874, P0ABU9, P0AFM2, P0AEL0, P0AFH2, P14175 P69874, P0AFM2,	
AMP vs. control	cellular_componen t	GO:003299 1	protein-containin g complex	P0AEL0, P14175	0.018925
AMP vs. control	cellular_componen t	GO:000562 2	intracellular external	P09155	0.036610
AMP vs. control	cellular_componen t	GO:003031 2	encapsulating structure	P0A908 P00562, P00968, P07862, P15877, P39451, P76621, P77581, P00448, P17117, P37908, P45395, P0AAC8, P0ABQ4, P0AEJ4, P0DMC5, P14175, P08337,	0.026043
AMP+K A vs. control	molecular_functio n	GO:004316 7	ion binding	P12282 P00562, P15877, P39451, P00448, P17117, P76149,	0.004116
AMP+K A vs. control	molecular_functio n	GO:001649 1	oxidoreductase activity	P0ABQ4, P76217	0.008817
AMP+K A vs.	molecular_functio n	GO:002285 7	transmembrane transporter	P0AG90, P36672,	0.021228

control			activity	P14175, P39830, P0AAD6 P0A7W7, P0A7R5, P63177, P0AA37	0.003005
AMP+K A vs. control	molecular_functio n	GO:000372 3	RNA binding	P00562, P36672, P0AEJ4, P0DMC5	0.014757
AMP+K A vs. control	molecular_functio n	GO:001630 1	kinase activity	P00448, P76116, P0A8B5	0.065263
AMP+K A vs. control	molecular_functio n	GO:000367 7	DNA binding	P0AEJ4, P0DMC5, P14175	0.001927
AMP+K A vs. control	molecular_functio n	GO:000487 1	signal transducer activity	P00968, P07862, P12282	0.009716
AMP+K A vs. control	molecular_functio n	GO:001687 4	ligase activity structural	P0A7W7, P0A7R5	0.011476
AMP+K A vs. control	molecular_functio n	GO:000373 5	constituent of ribosome	P45395, P0AA37 P00562, P00968, P07862, P77581, P0A7R5, P45395, P0ABQ4, P0DMC5, P08337, P0AAN9, P12282	0.017867
AMP+K A vs. control	biological_process	GO:000905 8	biosynthetic process	P39451, P76621, P00448, P0AB24, P0AEJ4, P0DMC5, P14175,	0.008636
AMP+K A vs. control	biological_process	GO:000695 0	response to stress		

AMP+K				P0A7R5, P17117, P63177, P0A6L9, P0A8B5, P0AAC8, P0ABQ4, P0AB55, P12282 P0AG90, P15877, P36672, P37908, P0AEJ4, P0DMC5, P14175, P39830,	
A vs. control	cellular_componen t	GO:000588 6	plasma membrane	P0AAD6 P00968, P07862, P00448, P63177, P0A8B5, P0AAN9	0.053972
AMP+K				P0AG90, P0A7R5, P0AEJ4, P0DMC5	
A vs. control	cellular_componen t	GO:000573 7	cytoplasm	P00968, P0A6L9, P14175	0.012118
AMP+K				P0A7W7, P0A7R5	
A vs. control	cellular_componen t	GO:000562 2	intracellular	P0A6L9, P14175	0.009071
AMP+K				P0A7W7, P0A7R5	
A vs. control	cellular_componen t	GO:003299 1	protein-containin g complex	P39180	0.039097
AMP+K					
A vs. control	cellular_componen t	GO:000584 0	ribosome		0.014418
AMP+K					
A vs. control	cellular_componen t	GO:000557 6	extracellular region		0.006644
AMP+K					
A vs. control	cellular_componen t	GO:003031 2	external encapsulating structure		0.027103

Table S5 KEGG Pathway

Group	KEGG Pathway	Pathway Name	Gene ID	p-value
			P69874	
			P0AFM2	
AMP vs. control	eco02010	ABC transporters	P14175 P0AFH2	0.011696
AMP vs. control	eco00550	Peptidoglycan biosynthesis	P02918	0.014547
AMP vs. control	eco00250	Alanine, aspartate and glutamate metabolism	P00370 P0AC33 P15877 P39451 P33221	0.02725
AMP vs. control	eco01130	Biosynthesis of antibiotics	P16703 P0A7A2 P0AC33 P0AEL0	0.001264
AMP vs. control	eco01200	Carbon metabolism	P16703 P0A7A2	0.0016
AMP vs. control	eco01501	beta-Lactam resistance	P02918 P0AFH2	0.000308
AMP vs. control	eco00030	Pentose phosphate pathway	P15877	0.025677
AMP vs. control	eco00640	Propanoate metabolism	P31660 P0ACB2 P0AC33 P15877 P39451 P0A9M2 P33221	0.039301
AMP vs. control	eco01110	Biosynthesis of secondary metabolites	P16703 P0A7A2	0.000524
AMP vs. control	eco00020	Citrate cycle (TCA cycle)	P0AC33	0.019777
AMP vs. control	eco00270	Cysteine and methionine metabolism	P16703	0.02725
AMP vs. control	eco01230	Biosynthesis of amino acids	P16703 P0A7A2	0.067943
AMP vs. control	eco00626	Naphthalene degradation	P39451	0.00038

AMP vs. control	eco00350	Tyrosine metabolism	P39451	0.002223
AMP vs. control	eco00010	Glycolysis / Gluconeogenesis	P39451 P0A7A2	0.005164
AMP vs. control	eco00071	Fatty acid degradation	P39451	0.006287
AMP vs. control	eco00500	Starch and sucrose metabolism	P28904	0.030512
AMP vs. control	eco00910	Nitrogen metabolism	P00370	0.015789
AMP vs. control	eco00230	Purine metabolism	P0A9M2 P33221	0.036567
AMP vs. control	eco01040	Biosynthesis of unsaturated fatty acids	P0ADA1	0.00094
AMP vs. control	eco00220	Arginine biosynthesis	P00370 P0ACB2 P0AC33 P15877 P02918 P39451 P00370 P0A9M2 P33221 P0AEL0 P16703	0.009023
AMP vs. control	eco01100	Metabolic pathways	P0A7A2	0.00838
AMP vs. control	eco00630	Glyoxylate and dicarboxylate metabolism	P0AEL0	0.044983
AMP vs. control	eco00860	Porphyrin and chlorophyll metabolism	P0ACB2	0.014547
AMP vs. control	eco00625	Chloroalkane and chloroalkene degradation	P39451	0.00038
AMP vs. control	eco01503	Cationic antimicrobial peptide (CAMP) resistance	P0AFL3 P0AEL0	0.033922
AMP vs. control	eco00680	Methane metabolism	P0A7A2	0.001253
AMP vs. control	eco02024	Quorum sensing	P0AFH2	0.099429
AMP vs. control	eco00260	Glycine, serine and threonine metabolism	P0A7A2	0.03568
AMP vs. control	eco01220	Degradation of aromatic compounds	P39451	0.008061
AMP vs.	eco00670	One carbon pool by folate	P33221	0.005477

control					
AMP vs.					
control	eco00620	Pyruvate metabolism	P0AC33	0.068139	
			P0ACB2		
			P0AC33		
			P39451		
			P0ABU9		
			P0AEL0		
AMP vs.		Microbial metabolism in diverse	P16703		
control	eco01120	environments	P0A7A2	0.000778	
			P00968		
			P15877		
			P39451		
			P77581		
			P00562		
			P07862		
			P76149		
AMP+KA			P45395		
vs.			P76217		
control	eco01100	Metabolic pathways	P0ABQ4	0.027714	
			P17117		
AMP+KA			P39451		
vs.		Microbial metabolism in diverse	P00562		
control	eco01120	environments	P76149	0.058375	
AMP+KA			P39180		
vs.			P0AEJ4		
control	eco02026	Biofilm formation - Escherichia coli	P0DMC5	0.001716	
AMP+KA			P15877		
vs.			P39451		
control	eco01110	Biosynthesis of secondary metabolites	P00562	0.246142	
AMP+KA			P15877		
vs.			P39451		
control	eco01130	Biosynthesis of antibiotics	P00562	0.096783	
AMP+KA					
vs.			P77581		
control	eco00330	Arginine and proline metabolism	P76217	0.001083	
AMP+KA					
vs.		Alanine, aspartate and glutamate	P00968		
control	eco00250	metabolism	P76149	0.002244	
AMP+KA					
vs.			P0A7W7		
control	eco03010	Ribosome	P0A7R5	0.026485	
AMP+KA			P0AEJ4		
vs.	eco02020	Two-component system	P0DMC5	0.131989	

control				
AMP+KA				
vs.		Chloroalkane and chloroalkene		
control	eco00625	degradation	P39451	0.000402
AMP+KA				
vs.				
control	eco02060	Phosphotransferase system (PTS)	P36672	0.047341
AMP+KA				
vs.				
control	eco00240	Pyrimidine metabolism	P00968	0.104275
AMP+KA				
vs.				
control	eco01502	Vancomycin resistance	P07862	0.001838
AMP+KA				
vs.				
control	eco02010	ABC transporters	P14175	0.424014
AMP+KA				
vs.				
control	eco00540	Lipopolysaccharide biosynthesis	P45395	0.027067
AMP+KA				
vs.				
control	eco03070	Bacterial secretion system	P0AG90	0.025452
AMP+KA				
vs.				
control	eco00790	Folate biosynthesis	P0ABQ4	0.019416
AMP+KA				
vs.				
control	eco00473	D-Alanine metabolism	P07862	0.000402
AMP+KA				
vs.				
control	eco00071	Fatty acid degradation	P39451	0.006644
AMP+KA				
vs.				
control	eco00270	Cysteine and methionine metabolism	P00562	0.028721
AMP+KA				
vs.				
control	eco00626	Naphthalene degradation	P39451	0.000402
AMP+KA				
vs.				
control	eco01230	Biosynthesis of amino acids	P00562	0.255403
AMP+KA				
vs.				
control	eco01220	Degradation of aromatic compounds	P39451	0.008516
AMP+KA	eco04122	Sulfur relay system	P12282	0.00953

vs.				
control				
AMP+KA				
vs.				
control	eco00350	Tyrosine metabolism	P39451	0.002351
AMP+KA				
vs.				
control	eco03060	Protein export	P0AG90	0.010596
AMP+KA				
vs.				
control	eco00300	Lysine biosynthesis	P00562	0.004988
AMP+KA				
vs.				
control	eco00633	Nitrotoluene degradation	P17117	0.001386
AMP+KA				
vs.		Glycine, serine and threonine		
control	eco00260	metabolism	P00562	0.037578
AMP+KA				
vs.				
control	eco00500	Starch and sucrose metabolism	P36672	0.03215
AMP+KA				
vs.				
control	eco00261	Monobactam biosynthesis	P00562	0.001838
AMP+KA				
vs.				
control	eco00550	Peptidoglycan biosynthesis	P07862	0.015353
AMP+KA				
vs.				
control	eco00030	Pentose phosphate pathway	P15877	0.027067
AMP+KA				
vs.				
control	eco00670	One carbon pool by folate	P0ABQ4	0.005788
AMP+KA				
vs.				
control	eco00010	Glycolysis / Gluconeogenesis	P39451	0.05148
AMP+KA				
vs.				
control	eco00650	Butanoate metabolism	P76149	0.037578
AMP+KA				
vs.				
control	eco00760	Nicotinate and nicotinamide metabolism	P76149	0.014091
