

Supplementary Materials

Table S1. The oligonucleotide primers designed and used in the RT-qPCR assay.

Strain	Primer	Sequence (5'→3')
<i>S. aureus</i> ATCC25923	KQ76_04230-F	GGTATTATTGATTCTTTCCAAAC
	KQ76_04230-R	TCGTAACCTCTTCTAATGCTTC
	KQ76_12495-F	GTACGAGATGTTTGGACTAGA
	KQ76_12495-R	GCATGATGTTTCACTCCTTTT
	KQ76_05765-F	GAAGTTTGGTCATCGTGGTG
	KQ76_05765-R	ATCTGACGGTCCTGGATTG
	KQ76_05755-F	ATTGATTGTGGCGACATT
	KQ76_05755-R	AATCCAAGCATTGCGGCTA
	KQ76_09185-F	CCTTATGGCGATGATTGGT
	KQ76_09185-R	TAAGCCAGCAGGTTTCACA
	KQ76_11910-F	AAAATACAGGAGATCGACCAA
	KQ76_11910-R	CCATACCACGAAAACCAAA
	KQ76_09200-F	CGGTAGGTTTGGTGGACAT
	KQ76_09200-R	ACGCCTCGTTTCTGGAATA
	KQ76_00500-F	CACATTCATCGGTTTCAGA
	KQ76_00500-R	CAACAATAACTTCGCATTA
<i>V. parahaemolyticus</i> ATCC17802	WU75_19785-F	GATGACAGGTGAGAAGGCTAT
	WU75_19785-R	GTCCTGACCAGAAATACGG
	WU75_00290-F	TATCGCTGAAGCCGATTTT
	WU75_00290-R	ACATGGCGGTAATCAATCA
	WU75_20180-F	GTGAGCGTGTTGCTATTGTC
	WU75_20180-R	GTAAGCGTCGGTATGGATG
	WU75_22235-F	CCAGGCTTTGGTGGTTGTG
	WU75_22235-R	TGAGTGTCAGTGGCGAGGT
	WU75_16140-F	CTCGCCGCACTGGATAACT
	WU75_16140-R	CGCTGCTTCTGCCTTTCAC
	WU75_08850-F	GGCGTGGTTAGGCACAGAT
	WU75_08850-R	GCCGAAGGTCGTAGTTTCA
	WU75_10815-F	AGTGTCAGTGAACGCAAAC
	WU75_10815-R	CAGAAGTAACGACGAGGAG
	WU75_14960-F	TTGTTGCGACGCTATTTACG
	WU75_14960-R	GCTGTCTGAACCCATGTTGTT

Table S2. The relative expression of the representative DEGs by the RT-qPCR assay.

Sample	Gene	Predicted protein	Fold change	
			RNA-Seq.	RT-PCR
<i>S. aureus</i> ATCC25923	KQ76_04230	Alanine-phosphoribitol ligase	28.924	29.731
	KQ76_12495	Nitrate reductase	10.404	8.465
	KQ76_05765	Carbamoyl phosphate synthase small subunit	3.084	6.324
	KQ76_05755	Aspartate carbamoyltransferase	3.213	12.109
	KQ76_09185	Proline dehydrogenase	0.109	0.101
	KQ76_11910	Urease subunit beta	0.412	0.472
	KQ76_09200	Riboflavin synthase subunit alpha	0.373	1.237
	KQ76_00500	Capsular biosynthesis protein	0.373	0.369
<i>V. parahaemolyticus</i> ATCC17802	WU75_19785	2-oxoglutarate dehydrogenase	0.146	0.475
	WU75_00290	Malate synthase	0.315	0.331
	WU75_20180	3-ketoacyl-CoA thiolase	0.305	0.643
	WU75_22235	Multifunctional fatty acid oxidation complex subunit alpha	0.151	0.149
	WU75_16140	Diaminobutyrate--2-oxoglutarate aminotransferase	0.222	25.317
	WU75_08850	Hydroxylamine reductase	63.107	59.973
	WU75_10815	Nitrate reductase	6.27	6.86
	WU75_14960	PTS fructose transporter subunit IIBC	5.096	5.755

Table S3. Bacterial strains and media used in this study

Bacterial Strain	Culture Medium	Source
<i>Aeromonas hydrophila</i> ATCC35654	TSB	ATCC, United States
<i>Bacillus cereus</i> A1-1	TSB	LS-SHOU, China
<i>Bacillus cereus</i> A2-	TSB	LS-SHOU, China
<i>Enterobacter cloacae</i> ATCC13047	TSB	Biobw, China
<i>Enterobacter cloacae</i> C1-1	LB	LS-SHOU, China
<i>Escherichia coli</i> ATCC8739	TSB	Biobw, China
<i>Escherichia coli</i> ATCC25922	LB	ATCC, United States
<i>Escherichia coli</i> K12	TSB	IIM, China
<i>Enterobacter sakazakii</i> CMCC45401	TSB	Biobw, China
<i>Klebsiella pneumoniae</i> 8-2-10-8	EE	LS-SHOU, China
<i>Klebsiella pneumoniae</i> 8-2-10-8	EE	LS-SHOU, China
<i>Pseudomonas aeruginosa</i> ATCC9027	TSB	Biobw, China
<i>Pseudomonas aeruginosa</i> ATCC27853	TSB	Biobw, China
<i>Salmonella enterica</i> subsp. <i>enterica</i> (ex Kauffmann and Edwards) Le Minor and Popoff serovar Choleraesuis ATCC13312	TSB	ATCC, United States
<i>Salmonella paratyphi</i> -A CMCC50093	TSB	GCCC, China
<i>Salmonella enterica</i> subsp. <i>enterica</i> (ex Kauffmann and Edwards) Le Minor and Popoff serovar Vellore ATCC15611	TSB	ATCC, United States
<i>Salmonella</i> E1-1	LB	LS-SHOU, China
<i>Shigella dysenteriae</i> CMCC 51252	TSB	GCCC, China
<i>Shigella flexneri</i> CMCC51572	TSB	GCCC, China
<i>Shigella flexneri</i> ATCC12022	TSB	ATCC, United States
<i>Shigella flexneri</i> CMCC51574	TSB	GCCC, China
<i>Shigella sonnei</i> ATCC25931	TSB	ATCC, United States
<i>Shigella sonnet</i> CMCC51592	TSB	GCCC, China
<i>Staphylococcus aureus</i> ATCC 25923	TSB	ATCC, United States
<i>Staphylococcus aureus</i> ATCC 8095	TSB	ATCC, United States
<i>Staphylococcus aureus</i> ATCC29213	TSB	ATCC, United States
<i>Staphylococcus aureus</i> ATCC6538	TSB	ATCC, United States
<i>Staphylococcus aureus</i> D1-1	TSB	LS-SHOU, China
<i>Vibrio alginolyticus</i> ATCC17749	TSB	ATCC, United States
<i>Vibrio alginolyticus</i> ATCC33787	TSB	ATCC, United States
<i>Vibrio cholerae</i> GIM1.449	TSB	GCCC, China
<i>Vibrio cholerae</i> Q10-54	TSB	LS-SHOU, China
<i>Vibrio fluvialis</i> ATCC33809	Marine 2216	ATCC, United States
<i>Vibrio harvey</i> ATCC BAA-1117	Marine 2216	ATCC, United States
<i>Vibrio harveyi</i> ATCC33842	Marine 2216	ATCC, United States
<i>Vibrio mimicus</i> bio-56759	TSB	Biobw, China
<i>Vibrio parahaemolyticus</i> ATCC17802	TSB	ATCC, United States
<i>Vibrio parahaemolyticus</i> ATCC33847	TSB	ATCC, United States
<i>Vibrio parahaemolyticus</i> B3-13	TSB	LS-SHOU, China
<i>Vibrio parahaemolyticus</i> B4-10	TSB	LS-SHOU, China
<i>Vibrio parahaemolyticus</i> B5-29	TSB	LS-SHOU, China
<i>Vibrio parahaemolyticus</i> B9-35	TSB	LS-SHOU, China
<i>Vibrio parahemolyticus</i> A1-1	TSB	LS-SHOU, China
<i>Vibrio vulnificus</i> ATCC27562	TSB	Biobw, China

ATCC: American Type Culture Collection, United States; GCCC, Guangdong Culture Collection Center, Guangzhou, China; IIM, Institute of Industrial Microbiology, Shanghai, China; LS-SHOU, Laboratory stock, Shanghai Ocean University, Shanghai, China.

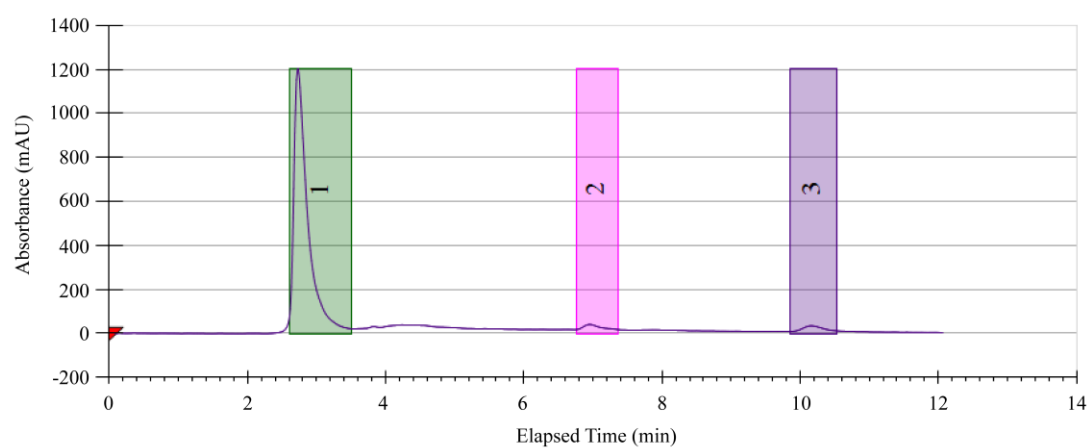


Figure S1. The Prep-HPLC diagram of purifying the methanol-phase crude extract from *P. kleiniana* Wight et Arn.