

Pseudomonas aeruginosa Presents Multiple Vital Changes in Its Proteome in the Presence of 3-Hydroxyphenylacetic Acid, a Promising Antimicrobial Agent

Ozgun O. Ozdemir and Ferda Soyer*

Cite This: *ACS Omega* 2020, 5, 19938–19951

Read Online

ACCESS |



Metrics & More

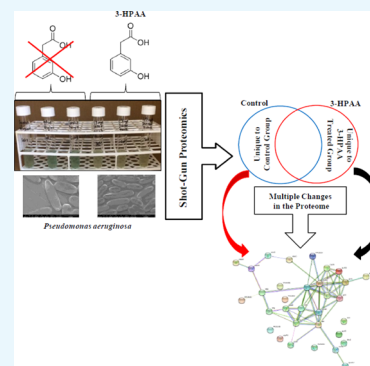


Article Recommendations



Supporting Information

ABSTRACT: *Pseudomonas aeruginosa*, a widely distributed opportunistic pathogen, is an important threat to human health for causing serious infections worldwide. Due to its antibiotic resistance and virulence factors, it is so difficult to combat this bacterium; thus, new antimicrobial agents are in search. 3-Hydroxyphenylacetic acid (3-HPAA), which is a phenolic acid mostly found in olive oil wastewater, can be a promising candidate with its dose-dependent antimicrobial properties. Elucidating the molecular mechanism of action is crucial for future examinations and the presentation of 3-HPAA as a new agent. In this study, the antimicrobial activity of 3-HPAA on *P. aeruginosa* and its action mechanism was investigated via shot-gun proteomics. The data, which are available via ProteomeXchange with identifier PXD016243, were examined by STRING analysis to determine the interaction networks of proteins. KEGG Pathway enrichment analysis via the DAVID bioinformatics tool was also performed to investigate the metabolic pathways that undetected and newly detected groups of the proteins. The results displayed remarkable changes after 3-HPAA exposure in the protein profile of *P. aeruginosa* related to DNA replication and repair, RNA modifications, ribosomes and proteins, cell envelope, oxidative stress, as well as nutrient availability. 3-HPAA showed its antimicrobial action on *P. aeruginosa* by affecting multiple bacterial processes; hence, it could be categorized as a multitarget antimicrobial agent.



1. INTRODUCTION

Pseudomonas aeruginosa, which is a Gram-negative bacterium, can colonize in soil, water, plant, and animal tissues in addition to the instruments and surfaces in the hospitals.^{1,2} Due to its highly diverse genotype and phenotype, it can switch the lifestyle according to the environmental conditions, leading to a rapid adaptation of broad changes in metabolism.^{3,4} These opportunistic pathogens are distributed extensively and accepted as one of the most critical agents in the nosocomial infections as well as the community-acquired ones, worldwide.⁵ They possess important virulence factors, including exotoxins and biofilm formation, in addition to their intrinsic and adaptive resistance abilities against various antibiotics.^{4,6} Their infections show high mortality and morbidity rates with a challenging treatment process, including extensive antibiotic therapy.⁷ Therefore, the effort for the development of new antimicrobial agents against *P. aeruginosa* is in progress. Phenolic acids, which can be accepted as promising antimicrobial agents, are secondary metabolites of the plants that function in various processes of the plant metabolism, including defense against predators and microorganisms.^{8,9} It is speculated that, because of their small size, phenolic acids can strongly interact with membranes or other targets in bacteria, such as easily cross through the outer membrane of Gram-negative bacteria,¹⁰ which can be an advantage in terms of antimicrobial effect. 3-Hydroxyphenylacetic acid (3-HPAA) is

a phenolic acid that showed a dose-dependent antimicrobial effect on *P. aeruginosa*, either static or cidal, according to the studies of our group (Figure 1 and Table 1). 3-Hydroxyphenylacetic acid has a small and simple structure with only one hydroxy group on its benzene ring. It belongs to the hydroxycinnamic acid group of phenolic acids since the carboxylic group is attached to the benzene ring via an ethylene group.¹¹ It is a water-soluble compound and mostly detected in olive oil wastewater, which is a byproduct of the olive oil extraction process.¹² Although various studies demonstrated the antimicrobial effects of phenolic compounds on pathogens,^{13–16} studies focusing on the molecular mechanisms of antimicrobial effects of phenolic acids are limited in the literature. These mechanisms can be examined by omics-studies, to be able to present them as new antimicrobial agents.¹⁷ Since protein production is the final state of the molecular cell process under particular conditions, investigation of protein profile changes is a useful approach for obtaining potential action mechanisms in the field of

Received: February 17, 2020

Accepted: July 21, 2020

Published: August 5, 2020



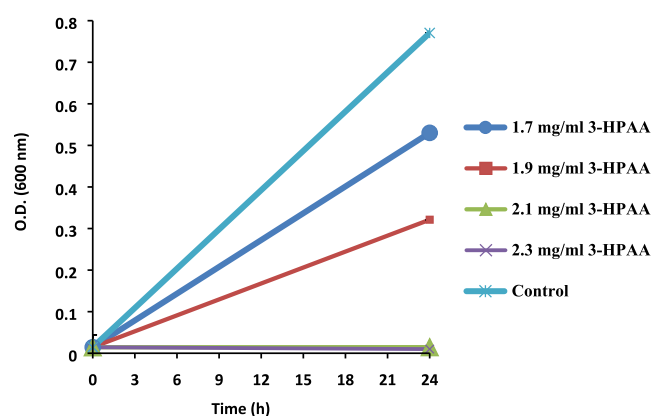


Figure 1. Growth of *P. aeruginosa* in the presence of various concentrations of 3-hydroxyphenylacetic acid (3-HPAA). The control group contains 0 mg/mL 3-HPAA. Optical density (OD) was measured at 600 nm.

Table 1. Percent Inhibition in Bacterial Growth and Cell Viability of *P. aeruginosa* in the Presence of 3-HPAA

3-HPAA concentrations (mg/mL)	percent inhibitions (%)	cell viability (cfu/mL)
1.7	31	5×10^6
1.9	58	3.4×10^6
2.1 ^a	98	1.9×10^5
2.3 ^b	99	no survivors

^aMinimum inhibitory concentration (MIC). ^bMinimum bacteriocidal concentration (MBC).

antimicrobial discovery.^{18,19} Mass spectrometry is accepted as a reliable technique to examine bacterial processes such as the proteome comparison of different bacterial strains, determination of proteomic changes in the same bacterial strain under stress conditions such as a toxic compound exposure or determination of the proteomic basis of antibiotic resistance of the bacteria.^{20–26}

Herein, we report the antimicrobial effect of 3-HPAA and the changes in the protein profile of *P. aeruginosa* after treatment with 3-HPAA by liquid chromatography electrospray ionization tandem mass spectrometry (LC-ESI-MS/MS) accompanied with STRING and KEGG analyses to evaluate the protein–protein interactions and related metabolic pathways, respectively. To the best of our knowledge, this would be the first study to show proteomic changes of *P. aeruginosa* following 3-HPAA exposure. Thus, it would aid in improving the information about the antimicrobial effects of phenolic acids at the molecular level. Our study can be a starting point in the determination of the molecular action mechanism of 3-HPAA, which can be developed as an effective antimicrobial agent against important pathogenic bacteria in the future.

2. RESULTS AND DISCUSSION

2.1. Antimicrobial Effect of 3-HPAA. The increasing concentrations of 3-HPAA resulted in a dose-dependent inhibition effect on the growth of *P. aeruginosa* (Figure 1). According to OD (600 nm) measurements, 1.9 mg/mL 3-HPAA showed a 58% inhibition, which is the subinhibitory concentration used in proteomic studies (Table 1). The minimum inhibitory concentration (MIC) was 2.1 mg/mL, with 98% inhibition. However, the enumeration studies demonstrated that 2.1 mg/mL had a bacteriostatic effect.

Application of 2.3 mg/mL resulted in no survivors of *P. aeruginosa*, which was determined as minimum bacteriocidal concentration (MBC) (Table 1).

The concentration of 3-HPAA that resulted in 58% inhibition of bacterial growth (1.9 mg/mL) was determined as the 3-HPAA concentration used in the protein profile studies. The results demonstrate the dose-dependent antimicrobial effect of 3-HPAA on *P. aeruginosa* (Table 1).

2.2. Overall Protein Profile. Bacterial response to changing environmental conditions such as exposure to toxic agents can be observed in their proteome.²⁶ The application of 3-HPAA resulted in various changes in the protein profile of *P. aeruginosa*. When the MASCOT data (FDR < 1.3%) were subjected to Venn diagram analysis, 312 proteins were detected as mutually unchanged in both the control group and 3-HPAA-treated groups (Figure 2A, region I; Table S17). Besides, the proteins which showed changes depending on 3-HPAA exposure were also detected: 203 undetected proteins (unique to control group) (Figure 2A, region II) and 95 newly detected proteins (unique to 3-HPAA-treated group) (Figure 2A, region III). Depending on their functions reported in the UniProt database, these undetected and newly detected proteins were categorized into eight main groups: DNA-, RNA-, ribosomes and protein-, cell wall and membrane-, metabolism-, redox and cell homeostasis-, and virulence-related, as well as uncharacterized proteins. All proteins are presented in Tables S1–S17.

The calculated percentage of the proteins in these groups (Figure 2B) showed that the lowest percentage of virulence-related proteins might demonstrate that 3-HPAA has a small effect on *P. aeruginosa* virulence. On the other hand, the highest percentage of metabolism-related proteins among these groups might be attributed to various changes in the protein profiles of general metabolism pathways for adaptation to the environment in the presence of 3-HPAA. Notable changes were recognized related to vital mechanisms of the bacteria after the exposure, which would be focused in this study as the basis of the antimicrobial effect of 3-HPAA (Tables 2 and 3).

The pathway enrichment analysis of changed proteins in the presence of 3-HPAA (Table S19) demonstrated that the bacteria manage the adaptation to environmental changes by altering the proteins related to metabolic pathways (Figure 3). The application of 3-HPAA resulted in the nondetection of proteins related to the biosynthesis of antibiotics, which validates the reduction in the virulence of *P. aeruginosa* (Figure 3A).

The newly detected proteins related to the carbon, pyruvate, and methane metabolism might demonstrate the changes in the use of energy pathways to adapt to the nonoptimal conditions due to 3-HPAA treatment. The changes in the microbial metabolism in diverse environments support these changes that occurred in the metabolism of *P. aeruginosa* in the presence of 3-HPAA (Figure 3B).

2.3. DNA-Related Protein Profile. The changes in the protein profile of *P. aeruginosa* after 3-HPAA exposure were mostly observed in the proteins functioned in DNA replication and repair (Tables S1 and S2), which showed strong interactions with each other in STRING analysis (Figure 4A). One of the remarkable results of this study was the nondetection of UvrABC system protein A (*uvrA*) and DNA mismatch repair protein (*mutS*) after 3-HPAA exposure. These proteins play roles in nucleotide excision repair (NER) and mismatch repair (MMR), respectively (Table 2). Since these

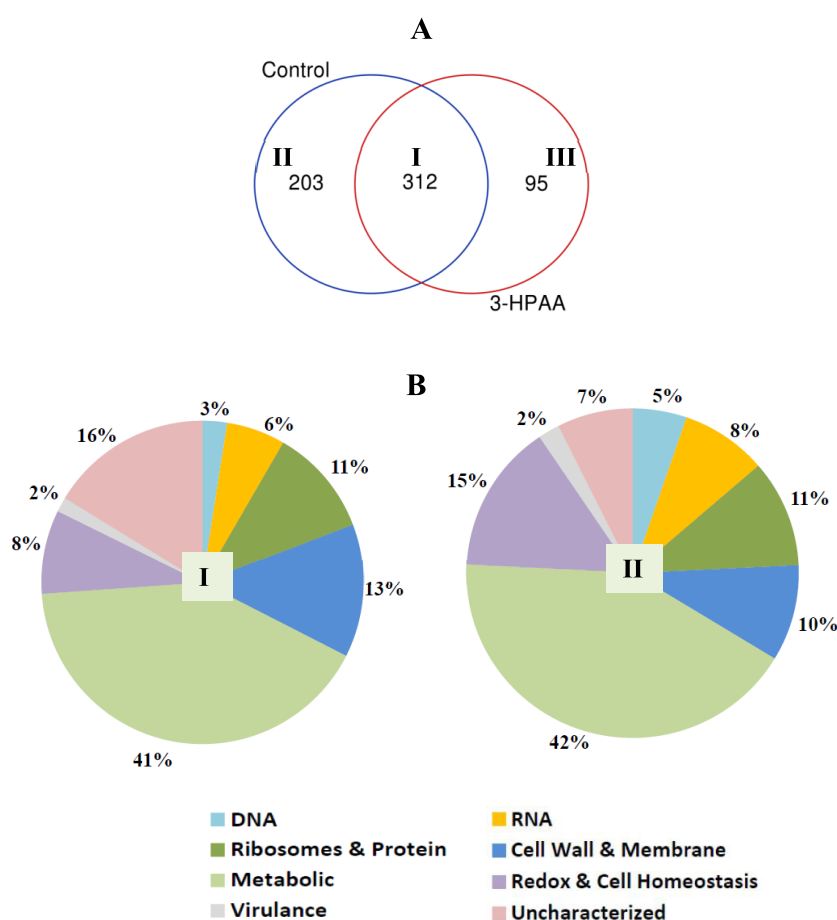


Figure 2. Overall protein profile of *P. aeruginosa* after 3-HPAA exposure. (A) Venn diagram representation of protein profile after 3-HPAA exposure: (I) mutual proteins of the control and 3-HPAA-treated groups (unchanged proteins), (II) unique proteins of the control group (undetected proteins after 3-HPAA exposure), and (III) unique proteins of the 3-HPAA-treated group (newly detected proteins after 3-HPAA exposure). (B) Percentages of proteins categorized based on their functions after 3-HPAA exposure: (I) undetected proteins and (II) newly detected proteins.

mechanisms are two of the primary DNA repair mechanisms in organisms,^{28–30} their impairment would cause the accumulation of mutations, leading to deterioration of the genome of *P. aeruginosa*, which eventually inhibits bacterial growth. Another significant result was the nondetection of DNA topoisomerase 4 subunit B (*parE*) and vitamin B12-dependent ribonucleotide reductase (*nrkJA*), which function in DNA replication (Table 2).

On the other hand, newly detected proteins, such as DNA polymerase III subunit α (*dnaE*) and β sliding clamp (*dnaN*), are functioned in DNA replication and repair (Table 3) and showed strong interactions with undetected proteins in STRING analysis (Figure 4A). It might be speculated that the bacteria managed to compensate for the unperformed functions in DNA replication and repair. The permanence of cell survival requires proper DNA replication and repair mechanisms,²⁹ and the results might display serious problems in the DNA metabolism of *P. aeruginosa* due to 3-HPAA exposure, which could be a reason for its antimicrobial activity.

2.4. RNA-Related Protein Profile. The undetected RNA-related proteins after 3-HPAA exposure were generally functioned in the regulation of transcription, RNA polymerase core enzyme binding, tRNA processing, and nutrient utilization (Table S3). The newly detected proteins were also functioned in transcriptional regulation in addition to transcription initiation and RNA polymerase transcriptional

activation (Table S4). The nondetection of an important sigma factor, the RNA polymerase sigma-54 factor (σ_{54}) (*rpoN*), would affect the function of σ_{54} -dependent promoters in *P. aeruginosa*. Therefore, it leads to problems in the expression of nitrogen metabolism-related proteins due to the role of σ_{54} in the transcription of nitrogen-related genes under stress conditions.³¹ Accordingly, DNA binding transcriptional regulator NtrC (*ntrC*), which has a role in nitrogen utilization, was also undetected, which might show the reduction in nitrogen assimilation in bacteria. The phosphate regulon transcriptional regulatory protein PhoB (*phoB*), which is the major transcription factor that functions in the phosphate limitation of the bacteria,³² was newly detected (Table 3). Since *rpoN*, *ntrC*, and *phoB* show strong interactions (Figure 4B), the treatment of *P. aeruginosa* with 3-HPAA might cause the bacteria to experience nitrogen and phosphate starvation and, eventually, bacterial growth inhibition. Fur proteins, which are crucial for bacterial survival but not found in eukaryotic cells, would be useful targets for antimicrobial action.³³ Therefore, 3-HPAA, which caused the nondetection of a Fur protein, ferric uptake regulation protein (*fur*), could be accepted as a promising antimicrobial agent. Depending on the metal chelation properties of the phenolic compounds,^{34,35} the presence of 3-HPAA in the growth environment of bacteria might result in the chelation of iron, which leads to iron limitation. Since this protein is functioned in iron limitation

Table 2. Significant Undetected Proteins of *P. aeruginosa* after 3-HPAA Exposure

protein ID ^a	protein name	gene name	function	group of protein profile ^b
Q9HWG0	UvrABC system protein A	uvrA PA4234	nucleotide excision repair, SOS response	DNA
Q9HY08	DNA mismatch repair protein	mutS PA3620	mismatch repair	DNA
Q9HUJ8	DNA topoisomerase 4 subunit B	parE PA4967	DNA topological change	DNA
Q9HT76	vitamin B12-dependent ribonucleotide reductase	nrdJA PA5497	DNA biosynthetic process, DNA replication	DNA
P49988	RNA polymerase sigma-54 factor	rpoN PA4462	transcription initiation, sigma factor activity	RNA
Q9HUS9	transcriptional regulator NtrC	ntrC PAS125	nitrogen fixation, regulation of nitrogen utilization, regulation of transcription	RNA
Q03456	ferric uptake regulation protein	fur PA4764	negative regulation of transcription	RNA
Q9HVY7	stringent starvation protein A	sspA PA4428	RNA polymerase core enzyme binding	RNA
Q9I382	tRNA 2-selenouridine/geranyl-2-thiouridine synthase	selU PA1643	tRNA seleno modification	RNA
Q9HY82	ribonuclease T	rnt PA3528	tRNA 3'-end processing	RNA
Q9I2U8	glutamine-tRNA ligase	glhS PA1794	glutamine-tRNA ligase activity	ribosomes and protein
Q9I2U7	cysteine-tRNA ligase	cysS PA1795	cysteine-tRNA ligase activity	ribosomes and protein
Q9HV58	30S ribosomal protein S15	rpsO PA4741	ribosome constituent, translation	ribosomes and protein
Q9HUS6	protein-export protein SecB	secB PAS128	protein tetramerization, protein transport	ribosomes and protein
Q9HZC5	aminopeptidase N	pepN PA3083	peptide catabolic process, proteolysis	ribosomes and protein
O68822	cytosol aminopeptidase	pepA phpA, PA3831	release of an N-terminal amino acid, processing and regular turnover of intracellular proteins.	ribosomes and protein
Q9HT06	membrane protein insertase YidC	yidC PAS568	membrane insertase activity, insertion and/or proper folding and/or complex formation of integral membrane proteins into the membrane	cell wall and membrane
Q9I6C1	signal recognition particle receptor FtsY	ftsY PA0373	cotranslational protein targeting to membrane	cell wall and membrane
Q9HV48	ATP-dependent zinc metalloprotease FtsH	ftsH PA4751	cell division, response to antibiotic	cell wall and membrane
P50598	Tol-Pal system protein TolQ	tolQ PA0969	cell cycle, cell division, bacteriocin transport	cell wall and membrane
P23189	glutathione reductase	gor PA2025	cell redox homeostasis, response to oxygen radical	redox and cell homeostasis
Q9I6Z2	alkyl hydroperoxide reductase	ahpF PA0140	response to reactive oxygen species	redox and cell homeostasis
P53652	superoxide dismutase [Mn]	sodA PA4468	removal of superoxide radicals	redox and cell homeostasis
Q9I5R7	S-adenosylmethionine decarboxylase proenzyme	speD PA0654	S-adenosylmethionine biosynthetic process, spermidine biosynthetic process	redox and cell homeostasis
Q9I5F9	lon protease	lon PA0779	response to antibiotic, response to stress, nitric oxide metabolic process, peptidase activity	redox and cell homeostasis

Table 2. continued

protein ID ^{a1}	protein name	gene name	function	group of protein profile ^b
Q9I2T9	lon protease	lon PA1803	response to antibiotics, response to drug, response to stress, pathogenesis, protein quality control for misfolded or incompletely synthesized proteins, single-species biofilm formation, type IV pilus-dependent motility, flagellum-dependent swarming motility	redox and cell homeostasis
Q9HTW6	aminopeptidase P	pepP PA5224	aminopeptidase activity	metabolism
Q9HWG9	5-methylphenazine-1-carboxylate 1-monooxygenase	phzS PA4217	pyocyanine biosynthetic process	metabolism
O69753	phenazine biosynthesis protein PhzB1	phzB1 PA4211	phenazine biosynthetic process	metabolism
Q7DC81	phenazine biosynthesis protein PhzE	phzE1 phzE2, PA1903, PA4214	glutamine metabolic process, tryptophan biosynthetic process, phenazine biosynthetic process	metabolism

^{a1}Information of protein IDs, protein names, gene names, and functions were obtained from the UniProt database. ^bGroup of protein profile was determined based on the function of the particular protein.

and oxidative stress adaptations of bacteria,³⁶ nondetection of this protein after 3-HPAA treatment (Table 2) might indicate iron starvation accompanying with oxidative stress in *P. aeruginosa*. Relatedly, newly detected protein OxyR (*oxyR*), which showed an interaction with Fur in STRING analysis (Figure 4B), is one of the main transcriptional regulators of oxidative stress defense by regulation of oxidative stress response genes (*kata*, *katB*, *ahpB*, and *ahpCF*), and the genes function in iron homeostasis in *P. aeruginosa*.^{37–39} These results indicate that the antimicrobial effect of 3-HPAA could be due to the oxidative stress and the failure of bacteria to adapt to iron limitation in the environment containing 3-HPAA. Another critical result related to the problems of bacteria in adaptation was the nondetection of an essential protein of stringent stress response, stringent starvation protein A (*sspA*). Under stress conditions, stringent response proteins aid the performance of alternative sigma factors,³⁸ which leads to the proper adaptation of bacteria to new environmental conditions for cell survival. The nondetection of this protein might show the deficiency of bacterial adaptation in the presence of 3-HPAA leading the bacterial inhibition.

After 3-HPAA exposure, tRNA 2-selenouridine/geranyl-2-thiouridine synthase (*selU*) and Ribonuclease T (*rnt*) were undetected as a vital result in terms of tRNA modification (Table 2). The protein SelU is the enzyme for geranylation of tRNA, which is a natural hydrophobic tRNA modification discovered in a few bacteria, including *P. aeruginosa*.⁴⁰ The geranylation provides increase in codon recognition fidelity and reduction in frameshift reading by taking action at the wobble position (U34) in the anticodon of lysine, glutamine, and glutamic acid.^{41,42} Protein Rnt is an incumbent in tRNA 3'-end processing, which is very important for tRNA biogenesis for editing and repairing of tRNAs.⁴³ The nondetection of these proteins might indicate the defects in tRNA biogenesis of the bacteria, which might lead to significant problems in bacterial RNA metabolism, depending on the 3-HPAA exposure.

2.5. Ribosomes and Protein-Related Protein Profile.

The nondetection of glutamine-tRNA ligase (*glnS*) and cysteine-tRNA ligase (*cysS*) (Table 2) could be indicated as important changes among the changes in tRNA ligase (aka aminoacyl-tRNA synthetase) profile due to 3-HPAA treatment. Since tRNA ligases are crucial for the growth of the peptide chain in protein translation by carrying the appropriate amino acids to the ribosomes,⁴⁴ targeting the tRNA ligase processes is accepted as one of the potent antimicrobial drug development approaches.^{45,46} For instance, the topical antibiotic Mupirocin, which is still in use against Gram-positive bacteria, takes effect by reversible inhibition of isoleucyl-tRNAs.⁴⁷ Likewise, the antibiotic purpurosmycin inhibits the bacterial translation by inhibiting the tRNA aminoacylation.⁴⁸ In this respect, it could be speculated that the nondetection of glutamine- and cysteine-tRNA ligases might be related to the antimicrobial effect of 3-HPAA on *P. aeruginosa*.

Besides the changes in the tRNA ligase profile, 3-HPAA resulted in changes in the structural components of ribosomal subunits, which might lead to an improper ribosome structure of the bacteria (Tables S5 and S6). One notable result on this subject was the nondetection of 30S ribosomal protein S15 (*rpsO*), which was also validated by our group via real-time quantitative PCR (Supporting Information 3, Figure S4 and Table S18).^{49,50} The subunits of prokaryotic ribosomes, 30S small subunit, and 50S large subunit, consist of ribosomal

Table 3. Significant Newly Detected Proteins of *P. aeruginosa* after 3-HPAA Exposure

protein ID ^a	protein name	gene name	function (UniProt)	protein profile group ^b
Q9HXZ1	DNA polymerase III subunit α	dnaE PA3640	DNA replication	DNA
Q9I7C4	β sliding clamp	dnaN PA0002	DNA strand elongation involved in DNA replication, 3'-5' exonuclease activity, DNA-directed DNA polymerase activity	DNA
P23620	phosphate regulon transcriptional regulatory protein PhoB	phoB PA5360	flagellum-dependent swarming motility, phosphate-ion transport, positive regulation of cellular response to phosphate starvation, transcription	RNA
Q9HTL4	OxyR	oxyR PA5344	RNA polymerase transcription activator, transcription regulatory region DNA binding source, negative regulation of secondary metabolite biosynthetic process, cell motility, lipid biosynthesis, response to reactive oxygen species	RNA
Q9HUN0	30S ribosomal protein S18	rpsR PA4934	structural constituent of ribosome, translation	ribosomes and protein
P33641	outer membrane protein assembly factor BamD	bamD PA4545	cell envelope organization, protein insertion into membrane	cell wall and membrane
G3XDB2	cell division coordinator CpoB	cpoB PA0974	FtsZ-dependent cytokinesis	cell wall and membrane
Q9HUF1	peptide methionine sulfoxide reductase MsrA	msrA PA5018	response to oxidative stress, response to hypochlorite	redox and cell homeostasis
Q9I619	spermidine/putrescine import ATP-binding protein PotA	spuF_potA, PA0302	spermidine transport, putrescine transport	redox and cell homeostasis
Q9HUX1	biosynthetic arginine decarboxylase	speA PA4839	arginine catabolic process, putrescine biosynthetic process, spermidine biosynthetic process	redox and cell homeostasis
Q9X6R0	polyamine aminopropyltransferase 1	speE1_speE, PA1687	spermidine biosynthetic process	redox and cell homeostasis

^aInformation of protein IDs, protein names, gene names, and functions were obtained from the UniProt database. ^bGroup of protein profile was determined based on the function of the particular protein.

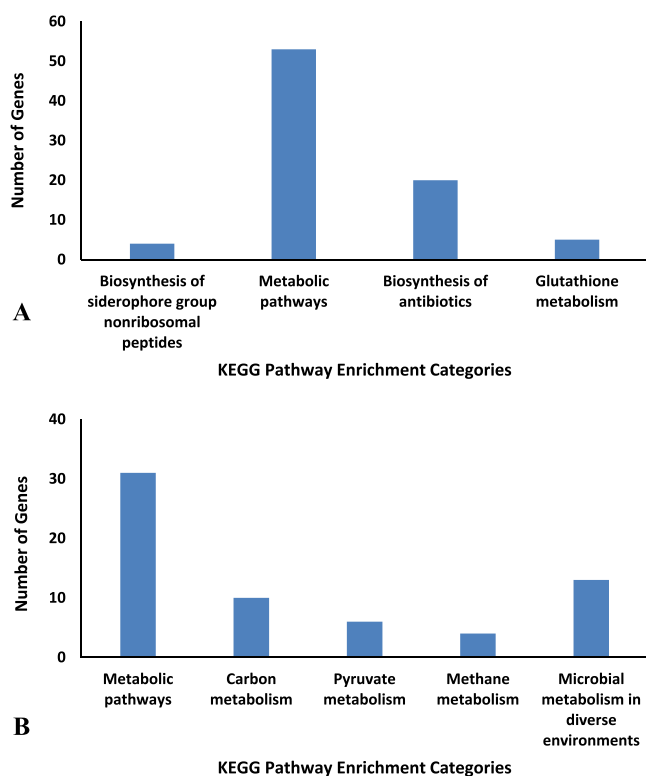


Figure 3. KEGG pathway enrichment analysis of the genes of changed proteins. (A) Genes of undetected proteins and (B) genes of newly detected proteins (for all categories, P value < 0.05).

RNAs and various ribosomal proteins.⁵¹ In ribosomal assembly, small and large subunits are connected by intersubunit bridges.⁵² The 30S ribosomal protein is crucial for proper bacterial ribosome assembly and translation due to its location in one of these bridges: Bridge B4.⁵² It also plays a role in the binding of proteins S6, S18, S11, and S21 in vitro.⁵³ When Bubunenko et al. examined in vivo function of the 30S ribosomal protein S15 in the binding of these proteins in *E. coli*, they have shown that the deletion of the *rpsO* gene did not keep them from binding in vivo.⁵⁴ Nevertheless, they also pointed out that the mutant bacteria had a weaker 70S ribosomal structure, and it had a cold-sensitive phenotype. They concluded that under nonoptimal conditions, S15 protein is required for cell survival of *Escherichia coli*.⁵⁴ Depending on the outcome of that study, it could be speculated that, for the survival of the bacteria, some other bacterial ribosomal assembly pathways might exist for use in the absence of S15 in vivo.⁵³ According to STRING analysis, a newly detected protein, 30S ribosomal protein S18 (*rpsR*), showed strong interactions to protein S15 (Figure 4), which might be an alternative protein for the assembly of ribosomes in *P. aeruginosa* to compensate the function of undetected protein S15. All in all, 3-HPAA exposure formed an unideal condition for *P. aeruginosa*, and it might lead to detrimental effects by restraining the proper ribosomal assembly due to the nondetection of protein S15. Some antibiotics, such as gentamicin and kanamycin, show their antimicrobial effects by mainly targeting the small subunit of the bacterial ribosome.⁵⁵ Since 3-HPAA displayed significant changes in the small ribosomal subunit of *P. aeruginosa*, its antimicrobial effect might be related to the aforementioned changes in small subunit. Besides the effects on the small subunit structure, 3-

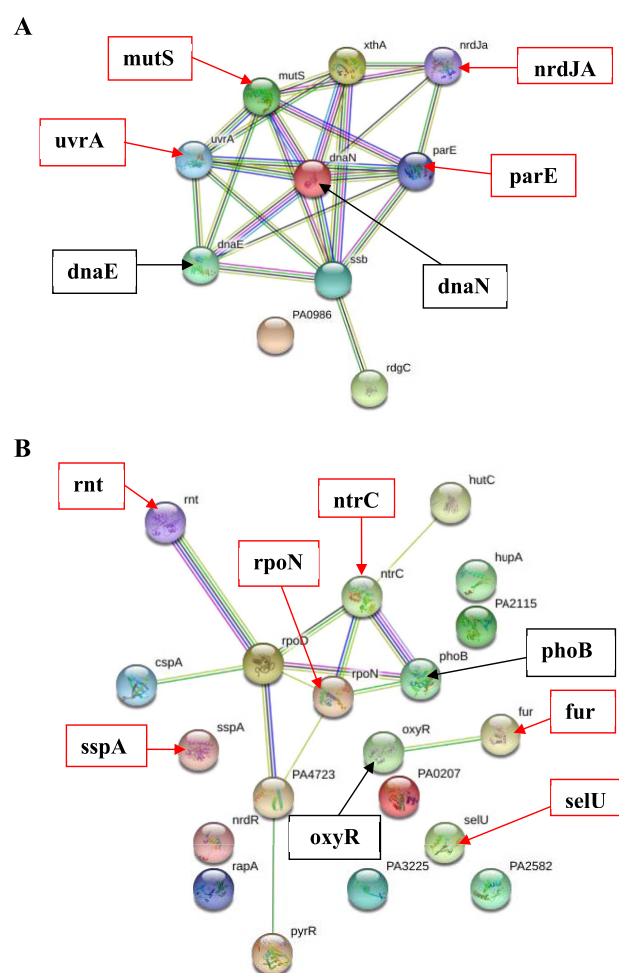


Figure 4. Interaction networks of DNA-related and RNA-related proteins after 3-HPAA exposure by STRING. Proteins are represented as nodes. The undetected and newly detected significant proteins are shown with their names in bold by the red and black arrows, respectively. (A) DNA-related protein profile; (B) RNA-related protein profile.

HPAA also resulted in changes in the large subunit assembly and RNA structure, translational initiation, and translational fidelity due to the nondetection of proteins that function in these processes (Table S5). These results demonstrate that the antimicrobial effect of 3-HPAA might be not only due to the defects in ribosomal structure and assembly but also due to the problems in protein translation. The protein modification processes were also affected by 3-HPAA exposure. For instance, protein-export protein SecB (*secB*), aminopeptidase N (*pepN*), and cytosol aminopeptidase (*pepA*) were undetected after the treatment (Table 2). According to the interaction network, aminopeptidase N interacted with cytosol aminopeptidase and protein-export protein SecB (Figure 5). The cleavage of the amino-terminal (N-terminal) of the peptides or proteins, which determine their structure and function, is carried out by the aminopeptidase enzymes.⁵⁶ The role of the molecular chaperone SecB is to recognize the precursor proteins with the N-terminal signal sequences for their translocation during the bacterial growth.^{57,58} The nondetection of these proteins after 3-HPAA exposure caused defects in the modification and translocation of precursor proteins with N-terminal signals, which might eventually lead to serious consequences for the overall metabolism of *P.*

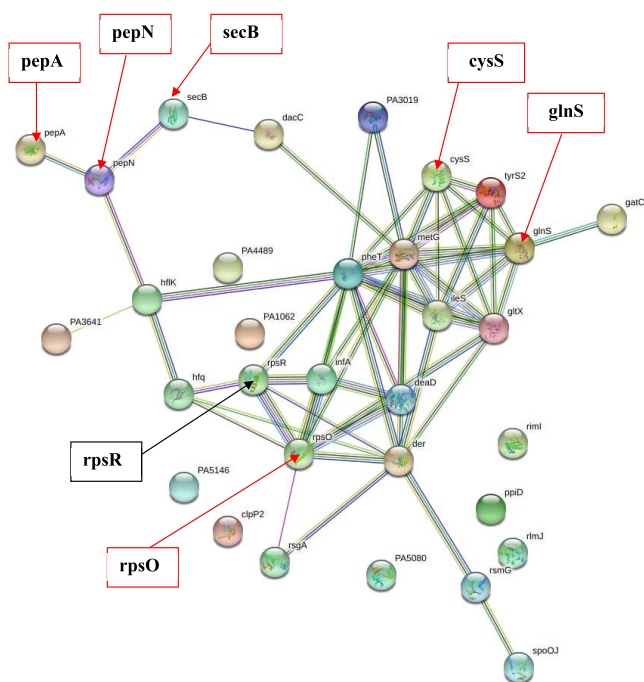


Figure 5. Interaction network of ribosomes and protein-related undetected and newly detected proteins after 3-HPAA exposure by STRING. Proteins are represented as nodes. The undetected and newly detected significant proteins are shown with their names in bold by the red and black arrows, respectively.

aeruginosa. Thus, the inhibition of *P. aeruginosa* after 3-HPAA exposure might be attributed to the notable effects of this phenolic acid on tRNA loading, ribosomal structure, and assembly as well as protein translation and modification.

2.6. Cell Wall and Membrane-Related Protein Profile.

The treatment of *P. aeruginosa* with 3-HPAA resulted in remarkable changes in the profile of cell wall and membrane proteins, which function in cell envelope structure composition and organization, cell division, motility, and chemotaxis (Tables S7 and S8). Since cell envelope functions as the protective component for bacterial cell,⁵⁷ these vital changes in the proteome of cell envelope might be related to the mode of growth inhibition effect of 3-HPAA on *P. aeruginosa*. The proteins that showed strong interactions in STRING analysis, membrane protein insertase YidC (*yidC*), signal recognition particle receptor FtsY (*ftsY*), ATP-dependent zinc metalloprotease FtsH (*ftsH*), and Tol-Pal system protein TolQ (*tolQ*) were undetected due to 3-HPAA exposure (Figure 6). YidC protein is one of the major proteins for bacteria, which functions in the insertion/integration of small membrane proteins into the membrane by working together with Sec proteins.⁵⁹ On the other hand, FtsY protein plays a role in the transfer of the newly formed proteins to the cytoplasmic region of the membrane since it targets the nascent polypeptide chains to the membrane.⁶⁰ Therefore, 3-HPAA resulted in problems in the membrane protein targeting and insertion into the membrane, which might lead to membrane weakness and damage. The other undetected protein, FtsH, which is universally conserved among prokaryotes, is a protease for rapid control of the regulation of cell metabolism in the presence of environmental stress.²⁷ It is the only one protease that is attached to the inner membrane, and it is responsible for quality control of membrane proteins as well as post-

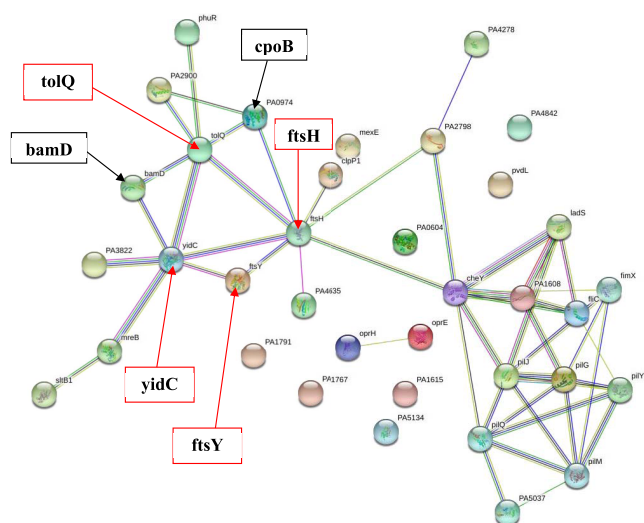


Figure 6. Interaction network of the cell wall and membrane-related undetected and newly detected proteins after 3-HPAA exposure by STRING. Proteins are represented as nodes. (The undetected and newly detected significant proteins are shown by the red and black arrows, respectively, with their names indicated in bold).

translation of transcription factors and enzymes.²⁷ The nondetection of FtsH might cause defects in the regulation of these transcription factors, leading to problems in transcription processes of *P. aeruginosa*. Among the transcription factors, it also plays a role in the post-translational regulation of RpoN (σ^{54}) in *E. coli*,⁶¹ which was also undetected after 3-HPAA exposure (Figure 4B). Therefore, we speculate that 3-HPAA treatment caused serious changes in the regulation of transcription in addition to the defects in the cell envelope structure of *P. aeruginosa*. Besides, the Tol-Pal system protein TolQ, which plays a role in cell cycle and division, was also undetected (Table 2). The Tol-Pal system is vital for Gram-negative bacteria for maintaining the outer membrane integrity.^{62,63} This system is structurally conserved among Gram-negative bacteria,⁶² which consists of seven genes in *Pseudomonas*: *orf1*, *tolQ*, *tolR*, *tolA*, *tolB*, *oprL*, and *orf2*.⁶⁴ Since the generated mutations in the genes of the Tol-Pal system result in damages in the outer membrane,⁶² the nondetection of TolQ after 3-HPAA exposure might cause problems in the cell envelope integrity. The newly detected proteins, outer membrane protein assembly factor BamD (*bamD*), and cell division coordinator CpoB (*PA0974*) also showed interactions with YidC, FtsH, and TolQ (Figure 6). Since the lipoprotein BamD is crucial for outer membrane biogenesis⁶⁴ and CpoB is important for peptidoglycan synthesis control and outer membrane construction,^{65,66} these might be used for the maintenance of the integrity of the cell envelope, especially the outer membrane, for survival. In our preliminary studies, we have determined the defects on *P. aeruginosa* cell morphology as the invagination lines throughout the surfaces of bacteria in the presence of 3-HPAA (TOC graphic). These morphological changes could be explained by the differences in the aforementioned proteome in the cell envelope. The cell envelope is the barrier against many unfavorable environmental conditions, such as the presence of antimicrobial agents. The notable results of our study could display that 3-HPAA seriously affected the structure and integrity of the *P. aeruginosa* cell wall and

antimicrobial target since it is highly conserved among pseudomonads and played a role in the virulence of the bacteria.⁷⁷ Therefore, the nondetection of this protein might be meaningful in terms of the 3-HPAA antimicrobial action mechanism. The profile of lipid metabolism-related proteins also changed 3-HPAA exposure.

The main change was the nondetection of proteins functioned in fatty acid β -oxidation, while the proteins functioned in lipid biosynthesis, phosphate transport, and phospholipase synthesis were newly detected (Tables S11 and S12). These changes demonstrated the increase in lipid biosynthesis and the decrease in fatty acid degradation of *P. aeruginosa*, which might indicate the effort of the bacteria to maintain the integrity of cell envelope in the presence of 3-HPAA. During the 3-HPAA exposure, the distinct greenish-blue color of *P. aeruginosa* culture was not observed (TOC graphic). The proteomic basis of this color change was due to the nondetection of the proteins functioned in phenazine biosynthesis (Table 2). The pyocyanin pigment, called phenazine produced by *P. aeruginosa*, is responsible for the specific blue color.⁷⁸ Phenazine is an extracellular, water-soluble, heterocyclic pigment that can produce ROS and be toxic to other microorganisms and eukaryotes.^{78–80} It also elevates the virulence of *P. aeruginosa* by playing the leading role in the quorum sensing mechanism.^{80,81} Nowadays, the antimicrobial strategies which target quorum sensing, such as inhibiting the phenazine production, catch attention in combatting against pathogens.^{81,82} Thereby, the nondetection of 5-methylphenazine-1-carboxylate 1-monooxygenase (*phzS*), phenazine biosynthesis protein PhzB1 (*phzB1*), and phenazine biosynthesis protein PhzE (*phzE1*, *phzE2*) (Table 2) could make 3-HPAA a favorable antimicrobial agent candidate against *P. aeruginosa* in terms of reduction of phenazine synthesis.

3. CONCLUSIONS

Our study demonstrated that, when 3-HPAA, a dose-dependent antimicrobial agent, was present, notable changes in the protein profile of *P. aeruginosa* were determined. These might lead to serious problems to bacteria not only in maintaining the proper RNA and protein metabolism but also in shape, cell division, nutrient transport, motility, and chemotaxis, which might be stated as the basis of the antimicrobial effect. The other vital problems were in DNA repair mechanisms, which might cause deleterious results for bacteria due to the accumulation of mutations. Additionally, it could be stated that high oxidative stress and defected stress response of bacteria that 3-HPAA caused might be another reason for bacterial inhibition. Moreover, bacteria encountered iron, phosphate, and sulfate starvations in the presence of 3-HPAA, which might eventually damage the overall metabolism of the bacteria. Depending upon all of the results, we conclude that the antimicrobial activity of 3-HPAA on *P. aeruginosa* has occurred by more than one route, and it could be entitled as a multitarget antimicrobial agent. Our study could be elucidated as the starting point of further studies in examining the mechanisms of antimicrobial action of phenolic acids against pathogenic bacteria.

4. EXPERIMENTAL SECTION

4.1. Bacterial Growth Conditions. *P. aeruginosa* (ATCC 27853) were maintained on Mueller Hinton (Sigma-Aldrich)

agar plates by overnight incubation at 37 °C. The stock cultures of bacteria were kept in glycerol at –80 °C. In each experiment, the overnight culture of *P. aeruginosa* was obtained by a single-colony inoculation in Mueller Hinton broth (MHB) following incubation at 37 °C for 18 h without shaking. The optical density (OD) of the overnight culture was determined at 600 nm.

4.2. Determination of MIC of 3-HPAA. 3-HPAA was obtained commercially (Sigma-Aldrich). The solutions of 3-HPAA were prepared at the time of the experiment in sterile double-distilled water and added to MHB. The final bacterial load of 10⁶ cfu/mL from overnight culture was inoculated into MHB, containing 3-HPAA, and incubated at 37 °C for 18 h without shaking. The OD of the treated and control cultures were measured at 600 nm at 0th and 24th hour time points of the growth. At the same time, the cell viabilities of the cultures grown for 24 h were tested by the enumeration method on MHA.

4.3. 3-HPAA Exposure for Protein Studies. The final bacterial load of 10⁶ cfu/mL was inoculated from overnight culture into MHB (Sigma-Aldrich) containing subinhibitory concentration (1.9 mg/mL) of 3-HPAA for the treated group and incubated at 37 °C for 18 h without shaking. The same procedure was simultaneously applied for control bacteria without 3-HPAA addition.

4.4. Total Protein Isolation. The protocol of Sianglum et al. was used with minor modifications in the total protein isolation from the 3-HPAA-treated and the control bacteria.⁸³ The cells were harvested at 10 000g for 20 min at 4 °C. They were washed twice with NaCl (0.85%) and centrifuged at 20 000g for 20 min at 4 °C. The pellet was dissolved in phosphate-buffered saline (PBS, pH 7.4) and sonicated for 9 s with 9 s intervals for 15 min. After centrifugation at 20 000g for 20 min at 4 °C, the supernatant was collected and kept at –80 °C until usage.

4.5. Peptide Sample Preparation. Acetone precipitation of the protein samples was performed: acetone (ice-cold) was added on the protein samples and mixed by a vortex. They were kept at –20 °C for overnight precipitation. The concentrations of the proteins were determined by Bradford assay ($R^2 > 0.98$) and adjusted to 0.4 mg. The solution digestion protocol of Carrera et al. was used with minor modifications.²³ It was initiated by a three-step procedure with dithiothreitol (DTT) (10/50 mM Tris–HCl, pH 7.8), iodoacetamide (20/50 mM Tris–HCl, pH 7.8) and DTT (20/50 mM Tris–HCl, pH 7.8) consecutively. The procedure was performed for 50 min each step in the dark at room temperature. The samples were cleaned by centrifugation at 14 000 rpm for 30 min in 10 K cutoff filters and washed with 50 mM Tris–HCl (pH 7.8). Each protein sample was treated with trypsin (in 50 mM Tris–HCl, pH 7.8) at the final concentration of 0.04 μ g/mL and incubated overnight at 37 °C for trypsin digestion. The volume of each sample was decreased below 100 μ L in a SpeedVac concentrator and kept at –20 °C.

4.6. LC-ESI-MS/MS. Fractionation of peptide samples was carried out by high-performance liquid chromatography (HPLC) (Shimadzu, LC20AD) via high-pH reversed-phase chromatography (reverse phase C18 Column, 25 cm \times 0.46 cm, 5 μ m) with fraction concatenation.⁸⁴ The phases in fractionation were used as phase A (10 mM ammonium formate/double-distilled H₂O (ddH₂O), pH 10) and phase B (a mixture of 90% acetonitrile and 10 mM ammonium

formate/ddH₂O, pH 10). Peptide samples, which were adjusted to 100 μ L with phase A, were fractionated by LC-solution software and collected by MALDI-Spotter (SunChrome, SunCollect System). Randomly collected fractions were completely dried in a SpeedVac concentrator, and zip-tip was applied to each sample. In the zip-tip process, each sample was prepared by the addition of an acetonitrile (20%) and formic acid (0.1%) mixture in ddH₂O following ultrasonication in a bath (15 s) and vortexing (5 s) alternately for three times. After centrifugation at 14 000 rpm for 10 min, zip-tip was carried out for 10–15 cycles for each sample via the ZipTip column (C18), which was conditioned by acetonitrile (100%) and formic acid (1%) previously. The column was washed by formic acid (1%). Then, the peptides were collected by treatment with increasing concentrations of acetonitrile (twice with 50% and once with 75%). Each sample was mixed with 25 μ L of formic acid (0.1%) and transferred into the insert tubes. These samples were analyzed by LC-ESI-MS/MS (Dionex Ultimate 3000) HPLC equipped with an LTQ XL mass spectrometer with electrospray ion source (Thermo Scientific). Chromeleon software (version 6.80) and low-pH column (Sigma Supelco Ascentis, 15 cm \times 500 μ m, 2.7 μ m) were used for the analysis of peptides.⁸⁴ The phases used were phase A (0.1% formic acid/ddH₂O) and phase B (0.1% formic acid/acetonitrile) during the process (initiated by 98% phase A and 2% phase B; increasing phase B up to 90%). Ion trap electrospraying was carried out using helium gas, and the peaks of the peptide samples were collected twice as raw data by the LTQ Tune software.

4.7. Data Analysis. Proteome Discoverer software (version 1.4) and Mass Matrix MS Data File Conversion software were used for transferring the raw data into MGF format and merging the data of fractions, respectively. The reference protein database of *P. aeruginosa* was downloaded from UniProt proteomes (Proteome ID: UP000002438). It was used in search of merged data in MASCOT MS/MS ions software. Conditions in MASCOT (version 2.3) were: fixed modifications, carbamidomethyl; variable modifications, oxidation; peptide tolerance, +1.2 Da; MS/MS tolerance, +0.6 Da; peptide charge +2 and +3; instrument, ESI-TRAP; MASCOT percolator activated. Two biological repeats were analyzed, and the obtained protein data of two individual analyses were combined prior to comparison in the Draw Venn Diagram tool (<http://bioinformatics.psb.ugent.be/webtools/Venn/>) to determine the mutual or unique proteins of the control and 3-HPAA-treated groups. The proteins that were unique to the control group (undetected proteins after 3-HPAA exposure) or unique to the 3-HPAA-treated group (newly detected proteins after 3-HPAA exposure) were investigated in terms of functions using UniProt Retrieve/I.D. Mapping with their protein IDs. The functions of uncharacterized proteins in UniProt were estimated by searching in the Protein BLAST tool. All proteins were grouped according to their functions in UniProt, and the interaction networks of the proteins in these groups were determined by STRING (Search Tool for the Retrieval of Interacting Genes/Proteins) software version 10.5 (https://version-10-5.string-db.org/cgi/input.pl?sessionId=6mlAzREKIVnK&input_page_show_search=on).⁸⁵ The significant metabolic pathways of the genes of these proteins were elucidated by the KEGG pathway enrichment analysis using the DAVID bioinformatics database (version 6.8). The gene IDs of the proteins which were determined in UNIPROT were converted to Entrez Gene IDs by Gene ID Conversion

tool, and these were used for the functional annotation analysis tool. The determined categories that have a p-value below 0.05 were demonstrated in the bar chart.

■ ASSOCIATED CONTENT

Supporting Information

The Supporting Information is available free of charge at <https://pubs.acs.org/doi/10.1021/acsomega.0c00703>.

All protein tables showing the proteins categorized based on functions in Uniprot and the list of unchanged mutual proteins (Supporting Information 1); validation of protein data of 30S ribosomal protein S15 (*rpsO*) by real-time quantitative polymerase chain reaction (qPCR) (Supporting Information 2); STRING representations of metabolism-related, virulence-related, and uncharacterized proteins (Supporting Information 3); and names of the genes in the categories of KEGG pathway enrichment analysis (Supporting Information 4) (PDF)

■ AUTHOR INFORMATION

Corresponding Author

Ferda Soyer – Department of Molecular Biology and Genetics, Izmir Institute of Technology, 35430 Urla Izmir, Turkey;
orcid.org/0000-0001-8307-1258;
Phone: +902327507307; Email: ferdasoyer@iyte.edu.tr

Author

Ozgun O. Ozdemir – Department of Molecular Biology and Genetics, Izmir Institute of Technology, 35430 Urla Izmir, Turkey

Complete contact information is available at:
<https://pubs.acs.org/doi/10.1021/acsomega.0c00703>

Author Contributions

O.O.O. and F.S. contributed to the design of this study, interpretation of data, and writing of the manuscript. O.O.O. performed the experiments and analyses.

Notes

The authors declare no competing financial interest. The mass spectrometry proteomics data have been deposited to the ProteomeXchange Consortium via the PRIDE partner repository with the dataset identifier PXD016243.

■ ACKNOWLEDGMENTS

The authors thank Prof. Dr. Talat Yalcin for generously providing his expertise and support for LC-ESI-MS/MS and MASCOT analyses. This work was funded by the Izmir Institute of Technology Research Fund (Project # 2014IYTE22) to F.S., and a Ph.D. grant to O.O.O. by the Izmir Institute of Technology. The mass spectrometry proteomics data have been deposited to the ProteomeXchange Consortium via the PRIDE^{86,87} partner repository.

■ REFERENCES

- (1) Valentini, M.; Gonzalez, D.; Al Mavridou, D.; Filloux, A. Lifestyle transitions and adaptive pathogenesis of *Pseudomonas aeruginosa*. *Curr. Opin. Microbiol.* **2018**, *41*, 15–20.
- (2) Ha, D.-G.; O'Toole, G. A. c-di-GMP and its effects on biofilm formation and dispersion: a *Pseudomonas aeruginosa* review *Microbiol. Spectrum* **2015**, *32* DOI: [10.1128/microbiolspec.MB-0003-2014](https://doi.org/10.1128/microbiolspec.MB-0003-2014).

- (3) Silby, M. W.; Winstanley, C.; Godfrey, S. A. C.; Levy, S. B.; Jackson, R. W. *Pseudomonas* genomes: diverse and adaptable. *FEMS Microbiol. Rev.* **2011**, *35*, 652–680.
- (4) Morita, Y.; Tomida, J.; Kawamura, Y. Responses of *Pseudomonas aeruginosa* to antimicrobials. *Front. Microbiol.* **2014**, *4*, No. 422.
- (5) Klockgether, J.; Tümmler, B. Recent advances in understanding *Pseudomonas aeruginosa* as a pathogen [version 1; referees: 3 approved]. *F1000Research* **2017**, *6*, No. 1261.
- (6) Pang, Z.; Raudonis, R.; Glick, B. R.; Lin, T.-J.; Cheng, Z. Antibiotic resistance in *Pseudomonas aeruginosa*: mechanisms and alternative therapeutic strategies. *Biotechnol. Adv.* **2019**, *37*, 177–192.
- (7) Wagner, S.; Sommer, R.; Hinsberger, S.; Lu, C.; Hartmann, R. W.; Empting, M.; Titz, A. Novel Strategies for the Treatment of *Pseudomonas aeruginosa* Infections. *J. Med. Chem.* **2016**, *59*, 5929–5969.
- (8) Silva, L. N.; Zimmer, K. R.; Macedo, A. J.; Trentin, D. S. Plant Natural Products Targeting Bacterial Virulence Factors. *Chem. Rev.* **2016**, *116*, 9162–9236.
- (9) Kärllund, A.; Salminen, J.-P.; Koskinen, P.; Ahern, J. R.; Karonen, M.; Tiilikkala, K.; Karjalainen, R. O. Polyphenols in Strawberry (*Fragaria × ananassa*) Leaves Induced by Plant Activators. *J. Agric. Food Chem.* **2014**, *62*, 4592–4600.
- (10) Lima, M. C.; de Sousa, C. P.; Fernandez-Prada, C.; Harel, J.; Dubreuil, J. D.; de Souza, E. L. A review of the current evidence of fruit phenolic compounds as potential antimicrobials against pathogenic bacteria. *Microb. Pathog.* **2019**, *130*, 259–270.
- (11) Miklasińska-Majdanik, M.; Kepa, M.; Wojtyczka, R. D.; Idzik, D.; Wasik, T. J. Phenolic Compounds Diminish Antibiotic Resistance of *Staphylococcus aureus* Clinical Strains. *Int. J. Environ. Res. Public Health* **2018**, *15*, 2321–2338.
- (12) Zafra, A.; Juarez, M. J. B.; Blanc, R.; Navalon, A.; Gonzalez, J.; Vilchez, J. L. Determination of polyphenolic compounds in wastewater olive oil by gas chromatography-mass spectrometry. *Talanta* **2006**, *70*, 213–218.
- (13) Albano, M.; Crulhas, B. P.; Alves, F. C. B.; Pereira, A. F. M.; Andrade, B. F. M. T.; Barbosa, L. N.; Furlanetto, A.; da Silveira Lyra, L. P.; Rall, V. L. M.; Júnior, A. F. Antibacterial and anti-biofilm activities of cinnamaldehyde against *S. epidermidis*. *Microb. Pathog.* **2019**, *126*, 231–238.
- (14) Keman, D.; Soyer, F. Antibiotic-Resistant *Staphylococcus aureus* Does Not Develop Resistance to Vanillic Acid and 2-Hydroxycinnamic Acid after Continuous Exposure in Vitro. *ACS Omega* **2019**, *4*, 15393–15400.
- (15) Gutiérrez-Larrazar, M.; Rúa, J.; Caro, I.; de Castro, C.; de Arriaga, D.; García-Armesto, M. R.; del Valle, P. Evaluation of antimicrobial and antioxidant activities of natural phenolic compounds against foodborne pathogens and spoilage bacteria. *Food Control* **2012**, *26*, 555–563.
- (16) Karaosmanoglu, H.; Soyer, F.; Ozen, B.; Tokatli, F. Antimicrobial and antioxidant activities of Turkish extra virgin olive oils. *J. Agric. Food Chem.* **2010**, *58*, 8238–8245.
- (17) Gutierrez, D. B.; Gant-Branum, R. L.; Romer, C. E.; Farrow, M. A.; Allen, J. L.; Dahal, N.; Nei, Y.-W.; Codreanu, S. G.; Jordan, A. T.; Palmer, L. D.; Sherrod, S. D.; McLean, J. A.; Skaar, E. P.; Norris, J. L.; Caprioli, R. M. An Integrated, High-Throughput Strategy for Multiomic Systems Level Analysis. *J. Proteome Res.* **2018**, *17*, 3396–3408.
- (18) Navare, A. T.; Chavez, J. D.; Zheng, C.; Weisbrod, C. R.; Eng, J. K.; Siehnel, R.; Singh, P. K.; Manoel, C.; Bruce, J. E. Probing the protein interaction network of *Pseudomonas aeruginosa* cells by chemical cross-linking mass spectrometry. *Structure* **2015**, *23*, 762–773.
- (19) François, P.; Scherl, A.; Hochstrasser, D.; Schrenzel, J. Proteomic approaches to study *Staphylococcus aureus* pathogenesis. *J. Proteomics* **2010**, *73*, 701–708.
- (20) Nilsson, J. F.; Castellani, L. G.; Draghi, W. O.; Perez-Gimenez, J.; Tejerizo, G. A. T.; Pistorio, M. Proteomic Analysis of *Rhizobium favelukesii* LPU83 in Response to Acid Stress. *J. Proteome Res.* **2019**, *18*, 3615–3629.
- (21) Sharma, D.; Garg, A.; Kumar, M.; Khan, A. U. Proteome profiling of carbapenem-resistant *K. pneumoniae* clinical isolate (NDM-4): Exploring the mechanism of resistance and potential drug targets. *J. Proteomics* **2019**, *200*, 102–110.
- (22) Li, W.; Zhang, S.; Wang, X.; Yu, J.; Li, Z.; Lin, W.; Lin, X. Systematically integrated metabolomic-proteomic studies of *Escherichia coli* under ciprofloxacin stress. *J. Proteomics* **2018**, *179*, 61–70.
- (23) Carrera, M.; Böhme, K.; Gallardo, J. M.; Barros-Velazquez, J.; Canas, B.; Calo-Mata, P. Characterization of foodborne strains of *Staphylococcus aureus* by shot-gun proteomics: Functional networks, virulence factors and species-specific peptide biomarkers. *Front. Microbiol.* **2017**, *8*, No. 2458.
- (24) Heunis, T.; Deane, S.; Smit, S.; Dicks, L. M. T. Proteomic Profiling of the Acid Stress Response in *Lactobacillus plantarum* 423. *J. Proteome Res.* **2014**, *13*, 4028–4039.
- (25) Lee, J. Y.; Pajarillo, E. A. B.; Kim, M. J.; Chae, J. P.; Kang, D.-K. Proteomic and Transcriptional Analysis of *Lactobacillus johnsonii* PF01 during Bile Salt Exposure by iTRAQ Shotgun Proteomics and Quantitative RT-PCR. *J. Proteome Res.* **2013**, *12*, 432–443.
- (26) Santos, P. M.; Benndorf, D.; Sa-Correia, I. Insights into *Pseudomonas putida* KT2440 response to phenol-induced stress by quantitative proteomics. *Proteomics* **2004**, *4*, 2640–2652.
- (27) Langklotz, S.; Baumann, U.; Narberhaus, F. Structure and function of the bacterial AAA protease FtsH. *Biochim. Biophys. Acta* **2012**, *1823*, 40–48.
- (28) Lakhani, B.; Thayer, K. M.; Hingorani, M. M.; Beveridge, D. L. Evolutionary Covariance Combined with Molecular Dynamics Predicts a Framework for Allostery in the MutS DNA Mismatch Repair Protein. *J. Phys. Chem. B* **2017**, *121*, 2049–2061.
- (29) Peng, X.; Ghosh, A. K.; Van Houten, B.; Greenberg, M. M. Nucleotide Excision Repair of a DNA Interstrand Cross-Link Produces Single- and Double-Strand Breaks. *Biochemistry* **2010**, *49*, 11–19.
- (30) Sidorenko, J.; Ukkivi, K.; Kivisaar, M. NER enzymes maintain genome integrity and suppress homologous recombination in the absence of exogenously induced DNA damage in *Pseudomonas putida*. *DNA Repair* **2015**, *25*, 15–26.
- (31) Erickson, K. E.; Winkler, J. D.; Nguyen, D. T.; Gill, R. T.; Chatterjee, A. The Tolerome: A Database of Transcriptome-Level Contributions to Diverse *Escherichia coli* Resistance and Tolerance Phenotypes. *ACS Synth. Biol.* **2017**, *6*, 2302–2315.
- (32) Fontaine, B. M.; Duggal, Y.; Weinert, E. E. Exploring the Links between Nucleotide Signaling and Quorum Sensing Pathways in Regulating Bacterial Virulence. *ACS Infect. Dis.* **2018**, *4*, 1645–1655.
- (33) Mathieu, S.; Cisse, C.; Vitale, S.; Ahmadova, A.; Degardin, M.; Perard, J.; Colas, P.; Miras, R.; Boturny, D.; Coves, J.; Crouzy, S.; Michaud-Soret, I. From peptide aptamers to inhibitors of FUR, bacterial transcriptional regulator of iron homeostasis and virulence. *ACS Chem. Biol.* **2016**, *11*, 2519–2528.
- (34) Mazzone, G. On the Inhibition of Hydroxyl Radical Formation by Hydroxycinnamic Acids: The Case of Caffeic Acid as a Promising Chelating Ligand of a Ferrous Ion. *J. Phys. Chem. A* **2019**, *123*, 9560–9566.
- (35) Andjelic, M.; Camp, J. V.; De Meulenaer, B.; Depaemelaere, G.; Socaciu, C.; Verloo, M.; Verhe, R. Iron-chelation properties of phenolic acids bearing catechol and galloyl groups. *Food Chem.* **2006**, *98*, 23–31.
- (36) Pinochet-Barros, A.; Helmann, J. D. Redox sensing by Fe²⁺ in bacterial Fur family metalloregulators. *Antioxid. Redox Signaling* **2018**, *29*, 1858–1871.
- (37) Kim, S. Y.; Park, C.; Jang, H.-J.; Kim, B.-o.; Bae, H.-W.; Chung, I.-Y.; Kim, E. S.; Cho, Y.-H. Antibacterial strategies inspired by the oxidative stress and response Networks. *J. Microbiol.* **2019**, *57*, 203–212.
- (38) Wei, Q.; Le Minh, P. N.; Dotsch, A.; Hildebrand, F.; Panmanee, W.; Elfarash, A.; Schulz, S.; Plaisance, S.; Charlier, D.; Hassett, D.; Haussler, S.; Cornelis, P. Global regulation of gene expression by OxyR in an important human opportunistic pathogen. *Nucleic Acids Res.* **2012**, *40*, 4320–4333.

- (39) Swiecilo, A.; Zych-Wezyk, I. Bacterial stress response as an adaptation to life in a soil environment. *Pol. J. Environ. Stud.* **2013**, *22*, 1577–1587.
- (40) Wang, R.; Vangaveti, S.; Ranganathan, S. V.; Basanta-Sanchez, M.; Haruehanroengra, P.; Chen, A.; Sheng, J. Synthesis, base pairing and structure studies of geranylated RNA. *Nucleic Acids Res.* **2016**, *44*, 6036–6045.
- (41) Sierant, M.; Leszczynska, G.; Sadowska, K.; Dziergowska, A.; Rozanski, M.; Sochacka, E.; Nawrot, B. S-Geranyl-2-thiouridine wobble nucleosides of bacterial tRNAs; chemical and enzymatic synthesis of S-geranylated-RNAs and their physicochemical characterization. *Nucleic Acids Res.* **2016**, *44*, 10986–10998.
- (42) Dumelin, C. E.; Chen, Y.; Leconte, A. M.; Chen, Y. G.; Liu, D. R. Discovery and biological characterization of geranylated RNA in bacteria. *Nat. Chem. Biol.* **2012**, *8*, 913–919.
- (43) Rammelt, C.; Rossmann, W. Repairing tRNA termini: News from the 3' end. *RNA Biol.* **2016**, *13*, 1182–1188.
- (44) Ferro, I.; Chelysheva, I.; Ignatova, Z. Competition for amino acid flux among translation, growth and detoxification in bacteria. *RNA Biol.* **2018**, *15*, 991–994.
- (45) Ho, J. M.; Bakkalbasi, E.; Söll, D.; Miller, C. A. Drugging tRNA aminoacylation. *RNA Biol.* **2018**, *15*, 667–677.
- (46) Lee, E.-Y.; Kim, S.; Kim, M. H. Aminoacyl-tRNA synthetases, therapeutic targets for infectious diseases. *Biochem. Pharmacol.* **2018**, *154*, 424–434.
- (47) Parenti, M. A.; Hatfield, S. M.; Leyden, J. J. Mupirocin: a topical antibiotic with a unique structure and mechanism of action. *Clin. Pharm.* **1987**, *6*, 761–770.
- (48) Kirillov, S.; Vitali, L. A.; Goldstein, B. P.; Monti, F.; Semenov, Y.; Makhno, V.; Ripa, S.; Pon, C. L.; Gualerzi, C. O. Purpurosmycin: An antibiotic inhibiting tRNA aminoacylation. *RNA* **1997**, *3*, 905–913.
- (49) Dumas, J.-L.; van Delden, C.; Perron, K.; Köhler, T. Analysis of antibiotic resistance gene expression in *Pseudomonas aeruginosa* by quantitative real-time-PCR. *FEMS Microbiol. Lett.* **2006**, *254*, 217–225.
- (50) Llanes, C.; Hocquet, D.; Vogne, C.; Benali-Baitich, D.; Neuwirth, C.; Plesiat, P. Clinical strains of *Pseudomonas aeruginosa* overproducing MexAB-OprM and MexXY efflux pumps simultaneously. *Antimicrob. Agents Chemother.* **2004**, *48*, 1797–1802.
- (51) Al-Majdoub, Z. M.; Carroll, K. M.; Gaskell, S. J.; Barber, J. Quantification of the Proteins of the Bacterial Ribosome Using QconCAT Technology. *J. Proteome Res.* **2014**, *13*, 1211–1222.
- (52) Liu, Q.; Fredrick, K. Intersubunit bridges of the bacterial ribosome. *J. Mol. Biol.* **2016**, *428*, 2146–2164.
- (53) Shajani, Z.; Sykes, M. T.; Williamson, J. R. Assembly of bacterial ribosomes. *Annu. Rev. Biochem.* **2011**, *80*, 501–26.
- (54) Bubunencko, M.; Korepanov, A.; Court, D. L.; Jagannathan, I.; Dickinson, D.; Chaudhuri, B. R.; Garber, M. B.; Culver, G. M. 30S ribosomal subunits can be assembled in vivo without primary binding ribosomal protein S15. *RNA* **2006**, *12*, 1229–1239.
- (55) Sutcliffe, J. A. Improving on nature: antibiotics that target the ribosome. *Curr. Opin. Microbiol.* **2005**, *8*, 534–542.
- (56) Nandan, A.; Nampoothri, K. Molecular advances in microbial aminopeptidases. *Bioresour. Technol.* **2017**, *245*, 1757–1765.
- (57) Kedrov, A.; Kusters, I.; Driessen, A. J. M. Single-Molecule Studies of Bacterial Protein Translocation. *Biochemistry* **2013**, *52*, 6740–6754.
- (58) Meyer, K.; Addy, C.; Akashi, S.; Roper, D. I.; Tame, J. R. H. The crystal structure and oligomeric form of *Escherichia coli* L₁D-carboxypeptidase A. *Biochem. Biophys. Res. Commun.* **2018**, *499*, 594–599.
- (59) Hennon, S. W.; Dalbey, R. E. Cross-Linking-Based Flexibility and Proximity Relationships between the T.M. Segments of the *Escherichia coli* YidC. *Biochemistry* **2014**, *53*, 3278–3286.
- (60) Dalbey, R. E.; Wang, P.; Kuhn, A. Assembly of bacterial inner membrane proteins. *Annu. Rev. Biochem.* **2011**, *80*, 161–87.
- (61) Carmona, M.; de Lorenzo, V. Involvement of the FtsH (HflB) protease in the activity of σ 54 promoters. *Mol. Microbiol.* **1999**, *31*, 261–270.
- (62) Schwechheimer, C.; Sullivan, C. J.; Kuehn, M. J. Envelope Control of Outer Membrane Vesicle Production in Gram-Negative Bacteria. *Biochemistry* **2013**, *52*, 3031–3040.
- (63) Sturgis, J. N. Organisation and evolution of the tol-pal gene cluster. *J. Mol. Microbiol. Biotechnol.* **2001**, *3*, 113–122.
- (64) Llamas, M. A.; Ramos, J. L.; Rodriguez-Herva, J. J. Transcriptional organization of the *Pseudomonas putida* tol-oprL genes. *J. Bacteriol.* **2003**, *185*, 184–195.
- (65) Mori, N.; Ishii, Y.; Tateda, K.; Kimura, S.; Kouyama, Y.; Inoko, H.; Mitsunaga, S.; Yamaguchi, K.; Yoshihara, E. A peptide based on homologous sequences of the b-barrel assembly machinery component BamD potentiates antibiotic susceptibility of *Pseudomonas aeruginosa*. *J. Antimicrob. Chemother.* **2012**, *67*, 2173–2181.
- (66) Gray, A. N.; Egan, A. J. F.; van't Veer, I. L.; Verheul, J.; Colavin, A.; Koumoutsis, A.; Biboy, J.; Altelaar, A. F. M.; Damen, M. J.; Huang, K. C.; Simorre, J.-P.; Breukink, E.; den Blaauwen, T.; Typas, A.; Gross, C. A.; Vollmer, W. Coordination of peptidoglycan synthesis and outer membrane constriction during *Escherichia coli* cell division. *eLife* **2015**, DOI: 10.7554/eLife.07118.
- (67) Kamariah, N.; Manimekalai, M. S. S.; Nartey, W.; Eisenhaber, F.; Eisenhaber, B.; Gruber, G. Crystallographic and solution studies of NAD(+) and NADH-bound alkylhydroperoxide reductase subunit F (AhpF) from *Escherichia coli* provide insight into sequential enzymatic steps. *Biochim. Biophys. Acta, Bioenerg.* **2015**, *1847*, 1139–1152.
- (68) Smirnova, G. V.; Oktyabrsky, O. N. Glutathione in bacteria. *Biochemistry* **2005**, *70*, 1199–1211.
- (69) Surya, A.; Liu, X.; Miller, M. J. Glutathione Utilization in *Lactobacillus fermentum* CECT 5716. *J. Agric. Food Chem.* **2018**, *66*, 12651–12656.
- (70) Ogasawara, Y.; Funakoshi, M.; Ishii, K. Determination of reduced nicotinamide adenine dinucleotide phosphate concentration using high-performance liquid chromatography with fluorescence detection: Ratio of the reduced form as a biomarker of oxidative stress. *Biol. Pharm. Bull.* **2009**, *32*, 1819–1823.
- (71) Davis, N. K.; Greer, S.; Jones-Mortimer, M. C.; Perham, R. N. Isolation and Mapping of Glutathione Reductase-negative Mutants of *Escherichia coli* K 12. *J. Gen. Microbiol.* **1982**, *128*, 1631–1634.
- (72) Iiyama, K.; Chieda, Y.; Lee, J. M.; Kusakabe, T.; Yasunaga-Aoki, C.; Shimizu, S. Effect of superoxide dismutase gene inactivation on virulence of *Pseudomonas aeruginosa* PAO1 toward the silkworm, *Bombyx mori*. *Appl. Environ. Microbiol.* **2007**, *73*, 1569–1575.
- (73) Fernández, L.; Breidenstein, E. B. M.; Taylor, P. K.; Bains, M.; de la Fuente-Núñez, C.; Fang, Y.; Foster, L. J.; Hancock, R. E. W. Interconnection of posttranscriptional regulation: The RNA-binding protein Hfq is a novel target of the Lon protease in *Pseudomonas aeruginosa*. *Sci. Rep.* **2016**, *6*, No. 26811.
- (74) Han, A.-r.; Kim, M.-J.; Kwak, G.-H.; Son, J.; Hwang, K. Y.; Kim, H.-Y. Essential Role of the Linker Region in the Higher Catalytic Efficiency of a Bifunctional MsrA-MsrB Fusion Protein. *Biochemistry* **2016**, *55*, 5117–5127.
- (75) Johnson, L.; Mulcahy, H.; Kanevets, U.; Shi, Y.; Lewenza, S. Surface-localized spermidine protects the *Pseudomonas aeruginosa* outer membrane from antibiotic treatment and oxidative stress. *J. Bacteriol.* **2012**, *194*, 813–826.
- (76) Bandounas, L.; Ballerstedt, H.; de Winde, J. H.; Ruijsenaars, H. J. Redundancy in putrescine catabolism in solvent tolerant *Pseudomonas putida* S12. *J. Biotechnol.* **2011**, *154*, 1–10.
- (77) Peng, C.-T.; Liu, L.; Li, C.-C.; He, L.-H.; Li, T.; Shen, Y.-L.; Gao, C.; Wang, N.-Y.; Xia, Y.; Zhu, Y.-B.; Song, Y.-J.; Lei, Q.; Yu, L.-T.; Bao, R. Structure-Function Relationship of Aminopeptidase P from *Pseudomonas aeruginosa*. *Front. Microbiol.* **2017**, *8*, No. 2385.
- (78) Rada, B.; Leto, T. L. Pyocyanin effects on respiratory epithelium: relevance in *Pseudomonas aeruginosa* airway infections. *Trends Microbiol.* **2013**, *21*, 73.

(79) El-Fouly, M. Z.; Sharaf, A. M.; Shahin, A. A. M.; El-Bialy, H. A.; Omara, A. M. A. Biosynthesis of pyocyanin pigment by *Pseudomonas aeruginosa*. *J. Radiat. Res. Appl. Sci.* **2015**, *8*, 36–48.

(80) Dietrich, L. E. P.; Price-Whelan, A.; Petersen, A.; Whiteley, M.; Newman, D. K. The phenazine pyocyanin is a terminal signaling factor in the quorum sensing network of *Pseudomonas aeruginosa*. *Mol. Microbiol.* **2006**, *61*, 1308–1321.

(81) Ugurlu, A.; Karahasan Yagci, A.; Ulusoy, S.; Aksu, B.; Bosgelmez-Tinaz, G. Phenolic compounds affect production of pyocyanin, swarming motility and biofilm formation of *Pseudomonas aeruginosa*. *Asian Pac. J. Trop. Biomed.* **2016**, *6*, 698–701.

(82) Lu, H. D.; Pearson, E.; Ristroph, K. D.; Duncan, G. A.; Ensign, L. M.; mSuk, J. S.; Hanes, J.; Prudhomme, R. K. *Pseudomonas aeruginosa* pyocyanin production reduced by quorum-sensing inhibiting nanocarriers. *Int. J. Pharm.* **2018**, *544*, 75–82.

(83) Sianglum, W.; Srimanote, P.; Wonglumsom, W.; Kittiniyom, K.; Voravuthikunchai, S. P. Proteome Analyses of Cellular Proteins in Methicillin-Resistant *Staphylococcus aureus* Treated with Rhodomyrone, a Novel Antibiotic Candidate. *PLoS One* **2011**, *6*, No. e16628.

(84) Dinç, M. Proteomic Analyses of Biological Samples by Using Different Mass Spectrometric Strategies. Ph.D. Dissertation, Izmir Institute of Technology: Izmir, Turkey, 2018.

(85) Szklarczyk, D.; Morris, J. H.; Cook, H.; Kuhn, M.; Stefan Wyder, S.; Simonovic, M.; Santos, A.; Doncheva, N. T.; Roth, A.; Bork, P.; Jensen, L. J.; von Mering, C. The STRING database in 2017: quality-controlled protein-protein association networks, made broadly accessible. *Nucleic Acids Res.* **2017**, *45*, D362–D368.

(86) Perez-Riverol, Y.; Csordas, A.; Bai, J.; Bernal-Llinares, M.; Hewapathirana, S.; Kundu, D. J.; Inuganti, A.; Griss, J.; Mayer, G.; Eisenacher, M.; Pérez, E.; Uszkoreit, J.; Pfeuffer, J.; Sachsenberg, T.; Yilmaz, S.; Tiwary, S.; Cox, J.; Audain, E.; Walzer, M.; Jarnuczak, A. F.; Ternent, T.; Brazma, A.; Vizcaíno, J. A. The PRIDE database and related tools and resources in 2019: improving support for quantification data. *Nucleic Acids Res.* **2019**, *47*, D442–D450.

(87) Deutsch, E. W.; Csordas, A.; Sun, Z.; Jarnuczak, A.; Perez-Riverol, Y.; Ternent, T.; Campbell, D. S.; Bernal-Llinares, M.; Okuda, S.; Kawano, S.; Moritz, R. L.; Carver, J. J.; Wang, M.; Ishihama, Y.; Bandeira, N.; Hermjakob, H.; Vizcaíno, J. A. The ProteomeXchange Consortium in 2017: supporting the cultural change in proteomics public data deposition. *Nucleic Acids Res.* **2017**, *54*, D1100–D1106.