

SUPPORTING INFORMATION

***Pseudomonas aeruginosa* Presents Multiple Vital Changes in its Proteome in the Presence of 3-Hydroxyphenylacetic acid, a Promising Antimicrobial Agent**

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Supporting Information 1

Table S1. The undetected DNA-related proteins after 3-HPAA exposure

Protein ID	Protein Name	Gene Name	Function
<u>Q9HUU8</u>	DNA topoisomerase 4 subunit B	parE PA4967	DNA topological change
<u>Q9HT76</u>	Vitamin B12-dependent ribonucleotide reductase	nrdJa PA5497	DNA biosynthetic process, DNA replication
<u>Q9HWG0</u>	UvrABC system protein A	uvrA PA4234	Nucleotide excision repair, SOS response
<u>Q9HY08</u>	DNA mismatch repair protein MutS	mutS PA3620	Mismatch repair
<u>Q914Y3</u>	Uncharacterized protein	PA0986	Transposase activity, transposition

Table S2. The newly detected DNA-related proteins after 3-HPAA exposure

Protein ID	Protein Name	Gene Name	Function
<u>Q910T9</u>	Exodeoxyribonuclease III	xthA PA2545	Endonuclease activity, DNA repair
<u>Q9HXZ1</u>	DNA polymerase III subunit alpha	dnaE PA3640	DNA replication
<u>Q9HYX7</u>	Recombination-associated protein RdgC	rdgC PA3263	DNA recombination
<u>Q917C4</u>	Beta sliding clamp	dnaN PA0002	DNA strand elongation involved in DNA replication, 3'-5' exonuclease activity, DNA-directed DNA polymerase activity
<u>P40947</u>	Single-stranded DNA-binding protein	ssb PA4232	DNA recombination, DNA repair, DNA replication

Table S3. The undetected RNA-related proteins after 3-HPAA exposure

Protein ID	Protein Name	Gene Name	Function
<u>P49988</u>	RNA polymerase sigma-54 factor	rpoN PA4462	Transcription initiation, sigma factor activity
<u>Q9HVV7</u>	Stringent starvation protein A	sspA PA4428	RNA-polymerase core enzyme binding
<u>Q9X6W6</u>	Bifunctional protein PyrR	pyrR PA0403	Nucleoside metabolic process, regulation of transcription
<u>Q910Q4</u>	RNA chaperone ProQ	PA2582	RNA strand exchange activity, RNA strand annealing activity, posttranscriptional regulation of gene expression
<u>Q9I200</u>	Probable transcriptional regulator	PA2115	Transcription
<u>Q9HZ15</u>	Probable transcriptional regulator	PA3225	Transcription
<u>Q9I382</u>	tRNA 2-selenouridine/geranyl-2-thiouridine synthase	selU PA1643	tRNA seleno modification

<u>Q9HY82</u>	Ribonuclease T	rnt PA3528	tRNA 3'-end processing
<u>Q9HU78</u>	Histidine utilization repressor	hutC PA5105	Negative regulation of transcription, histidine catabolic process
<u>Q9HU59</u>	DNA-binding transcriptional regulator NtrC	ntrC PA5125	Nitrogen fixation, regulation of nitrogen utilization, regulation of transcription
<u>Q9HWX1</u>	Transcriptional repressor NrdR	nrdR PA4057	Transcription, negative regulation of oxidoreductase activity,
<u>Q03456</u>	Ferric uptake regulation protein	fur PA4764	Negative regulation of transcription

Table S4. The newly detected RNA-related proteins after 3-HPAA exposure

<u>Protein ID</u>	<u>Protein Name</u>	<u>Gene Name</u>	<u>Function</u>
<u>P95459</u>	Major cold shock protein CspA	cspA PA3266	Regulation of transcription
<u>Q916T1</u>	Probable transcriptional regulator	PA0207	Transcription, DNA binding transcription factor activity
<u>P23620</u>	Phosphate regulon transcriptional regulatory protein PhoB	phoB PA5360	Flagellum-dependent swarming motility, phosphate ion transport positive regulation of cellular response to phosphate starvation, transcription
<u>Q9HTL0</u>	DNA-binding protein HU-alpha	hupA PA5348	Chromosome condensation, regulation of nucleic acid templated transcription
<u>Q9HTL4</u>	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
<u>Q9HYT6</u>	RNA polymerase-associated protein RapA	rapA hepA, PA3308	Transcription, Helicase activity
<u>G3XD14</u>	RNA polymerase-binding transcription factor DksA	dksA PA4723	RNA polymerase binding, negative regulation of rRNA expression and positive regulation of several amino acid biosynthesis promoters
<u>P26480</u>	RNA polymerase sigma factor RpoD	rpoD rpoDA, PA0576	DNA binding transcription factor activity, sigma factor activity, transcription initiation

Table S5. The undetected ribosome and protein-related proteins after 3-HPAA exposure

<u>Protein ID</u>	<u>Protein Name</u>	<u>Gene Name</u>	<u>Function</u>
<u>P65116</u>	Translation initiation factor IF-1	infA PA2619	Ribosome binding, rRNA binding, translation initiation factor activity
<u>Q9HVT9</u>	Glutamyl-tRNA(Gln) amidotransferase subunit C	gatC PA4482	Regulation of translational fidelity, translation
<u>Q9HUM0</u>	RNA-binding protein Hfq	hfq PA4944	mRNA translational regulation
<u>Q9HUL3</u>	Small ribosomal subunit biogenesis GTPase RsgA	rsgA PA4952	Ribosome biogenesis
<u>Q9HV58</u>	30S ribosomal protein S15	rpsO PA4741	ribosome constituent, translation
<u>Q9HT10</u>	Ribosomal RNA small subunit methyltransferase G	rsmG PA5564	rRNA (guanine-N7)-methylation

<u>Q9I003</u>	ATP-dependent RNA helicase DeaD	deaD PA2840	ribosomal large subunit assembly, RNA catabolic process, RNA secondary structure unwinding
<u>Q9HUF0</u>	Ribosomal RNA large subunit methyltransferase J	rlmJ PA5019	rRNA base methylation
<u>Q9I2U8</u>	Glutamine--tRNA ligase	glnS PA1794	Glutamine--tRNA ligase activity
<u>Q9I2U7</u>	Cysteine--tRNA ligase	cysS PA1795	Cysteine--tRNA ligase activity
<u>Q9I4R2</u>	Uncharacterized protein	PA1062	Protein acetylation
<u>Q9HVB7</u>	Ribosomal-protein-alanine acetyltransferase	rimI PA4678	N-terminal protein amino acid acetylation
<u>Q9I2T8</u>	Peptidylprolyl isomerase	ppiD PA1805	peptidyl-prolyl cis-trans isomerase activity
<u>Q9HT12</u>	Chromosome partitioning protein Spo0J	spoOJ PA5562	Identical protein binding, protein homopolymerization
<u>Q9HU56</u>	Protein-export protein SecB	secB PA5128	Protein tetramerization, protein transport
<u>O68822</u>	Cytosol aminopeptidase	pepA phpA, PA3831	Release of an N-terminal amino acid, processing and regular turnover of intracellular proteins.
<u>Q9HU38</u>	Uncharacterized protein	PA5146	Regulation of protein targeting to membrane
<u>Q9HXZ0</u>	Probable amino acid permease	PA3641	Alanine:sodium symporter activity
<u>Q9HYR9</u>	ATP-dependent Clp protease proteolytic subunit 2	clpP2 PA3326	Endopeptidase activity
<u>Q9HVT2</u>	Alpha-2-macroglobulin homolog	PA4489	Endopeptidase inhibitor activity
<u>Q9HUM2</u>	Protein HflK	hflK PA4942	Peptidase activity
<u>Q9HZC5</u>	Aminopeptidase N	pepN PA3083	Peptide catabolic process, proteolysis

Table S6. The newly detected ribosome and protein-related proteins after 3-HPAA exposure

Protein ID	Protein Name	Gene Name	Function
<u>Q9HYC7</u>	Methionine--tRNA ligase	metG PA3482	Elongation of protein synthesis and initiation of all mRNA translation through initiator tRNA (fMet) aminoacylation.
<u>Q9XC6</u>	Glutamate--tRNA ligase	gltX PA3134	Glutamate-tRNA ligase activity
<u>Q9I5Q3</u>	Tyrosine--tRNA ligase 2	tyrS2 PA0668	Tyrosine-tRNA ligase activity
<u>Q9HVM4</u>	Isoleucine--tRNA ligase	ileS PA4560	Isoleucine--tRNA ligase activity
<u>Q9I0A4</u>	Phenylalanine--tRNA ligase beta subunit	pheT PA2739	Phenylalanine--tRNA ligase activity
<u>Q9HZI7</u>	Probable ATP-binding component of ABC transporter	PA3019	Valine-tRNA ligase activity, ATPase activity
<u>Q9HUA3</u>	Proline iminopeptidase	PA5080	Aminopeptidase activity
<u>Q9HXJ8</u>	GTPase Der	der engA, PA3799	GTP binding, ribosome biogenesis
<u>Q9HUN0</u>	30S ribosomal protein S18	rpsR PA4934	Structural constituent of ribosome, translation
<u>G3XD74</u>	D-ala-D-ala-carboxypeptidase	dacC PA3999	Carboxypeptidase activity

Table S7. The undetected cell wall and membrane-related proteins after 3-HPAA exposure

Protein ID	Protein Name	Gene Name	Function
<u>Q9HT06</u>	Membrane protein insertase YidC	yidC PA5568	Membrane insertase activity, insertion and/or proper folding and/or complex formation of integral membrane proteins into the membrane
<u>Q9I6C1</u>	Signal recognition particle receptor FtsY	ftsY PA0373	Cotranslational protein targeting to membrane
<u>Q9I157</u>	PvdL	pvdL PA2424	Pyoverdine biosynthetic process
<u>Q9HVM8</u>	Type IV pilus biogenesis factor PilY1	pilY1 PA4554	Type IV-pilus dependent motility
<u>P34750</u>	Fimbrial assembly protein PilQ	pilQ PA5040	Type IV-pilus biogenesis
<u>G3XD28</u>	Type 4 fimbrial biogenesis protein PilM	pilM PA5044	Type IV pilus biogenesis, cell cycle,
<u>P50598</u>	Tol-Pal system protein TolQ	tolQ PA0969	Cell cycle, cell division, bacteriocin transport
<u>Q9I0Y9</u>	Resistance-Nodulation-Cell Division (RND) multidrug efflux membrane fusion protein MexE	mexE PA2493	Cell division, response to antibiotic
<u>Q9HV48</u>	ATP-dependent zinc metalloprotease FtsH	ftsH PA4751	Cell division, response to antibiotic
<u>Q9HVV0</u>	Rod shape-determining protein MreB	mreB PA4481	Cell morphogenesis
<u>Q9HWC2</u>	Uncharacterized protein	PA4278	Peptidoglycan binding
<u>Q51455</u>	Chemotaxis protein CheY	cheY PA1456	Flagellum dependent cell motility, chemotaxis, phosphorelay signal transduction system
<u>Q9I2U1</u>	ATP-dependent Clp protease proteolytic subunit 1	clpP1 PA1801	Flagellum dependent cell motility, single species biofilm formation, response to antibiotic
<u>Q9I3B3</u>	Probable chemotaxis transducer	PA1608	Chemotaxis
<u>G3XDA5</u>	Anaerobically-induced outer membrane porin OprE	oprE PA0291	Integral component of membrane
<u>Q9I5T4</u>	Probable binding protein component of ABC transporter	PA0604	Membrane transport
<u>Q9I2X2</u>	Uncharacterized protein	PA1767	Transmembrane component
<u>Q9HUW8</u>	Uncharacterized protein	PA4842	Integral component of membrane
<u>Q9I3A7</u>	Probable lipase	PA1615	Integral component of membrane
<u>Q9HXI0</u>	Uncharacterized protein	PA3822	Integral component of membrane
<u>Q9I2V1</u>	Uncharacterized protein	PA1791	Integral component of membrane
<u>G3XD11</u>	PhoP/Q and low Mg ²⁺ inducible outer membrane protein H1	oprH PA1178	Integral component of membrane, cell outer membrane
<u>Q9HV88</u>	Heme/hemoglobin uptake outer membrane receptor PhuR	phuR PA4710	Integral component of membrane, response to iron ion, heme transport
<u>P46384</u>	Protein PilG	pilG PA0408	Phosphorelay signal transduction system, pilus biosynthesis and twitching motility
<u>Q9I045</u>	Probable two-component response regulator	PA2798	Phosphorelay transduction system
<u>Q9HX42</u>	Lost Adherence Sensor, LadS	ladS PA3974	Phosphorelay sensor kinase activity
<u>Q9HUK6</u>	FimX	fimX PA4959	Phosphorelay transduction system

Table S8. The newly detected cell wall and membrane-related proteins after 3-HPAA exposure

Protein ID	Protein Name	Gene Name	Function
<u>Q9HX24</u>	Soluble lytic transglycosylase B	sltB1 PA4001	Lytic transglycosylase activity
<u>Q9HUD4</u>	Uncharacterized protein	PA5037	Peptidoglycan binding
<u>Q9HVF6</u>	Uncharacterized protein	PA4635	Integral component of membrane
<u>P42257</u>	Protein PilJ	pilJ PA0411	Chemotaxis, transmembrane signaling receptor activity
<u>P72151</u>	B-type flagellin	fliC PA1092	Flagellum dependent cell motility, Flagellum organization
<u>Q9HU50</u>	Probable carboxyl-terminal protease	PA5134	Cell envelope organization, cell wall biogenesis, pathogenesis, endopeptidase activity
<u>G3XDB2</u>	Cell division coordinator CpoB	cpoB PA0974	FtsZ-dependent cytokinesis
<u>Q9HZU7</u>	Probable outer membrane protein	PA2900	Integral component of membrane, cell outer membrane
<u>P33641</u>	Outer membrane protein assembly factor BamD	bamD PA4545	Cell envelope organization, protein insertion into membrane

Table S9. The undetected redox and cell homeostasis-related proteins after 3-HPAA exposure

Protein ID	Protein Name	Gene Name	Function
<u>Q915F9</u>	Lon protease	lon PA0779	Response to antibiotic, response to stress, nitric oxide metabolic process, peptidase activity
<u>Q912T9</u>	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
<u>Q9HZ19</u>	Universal stress protein	PA3017	Response to stress
<u>Q9I2V3</u>	Uncharacterized protein	PA1789	Response to stress
<u>Q9HW73</u>	Uncharacterized protein	PA4328	Response to stress
<u>Q9HUK9</u>	Thiosulfate sulfurtransferase	rhdA PA4956	Response to toxic substance (Contributes to P. aeruginosa survival under cyanogenic conditions)
<u>Q916Z2</u>	Alkyl hydroperoxide reductase subunit F	ahpF PA0140	Response to reactive oxygen species
<u>P23189</u>	Glutathione reductase	gor PA2025	Cell redox homeostasis, response to oxygen radical
<u>P0C2B2</u>	Thiol:disulfide interchange protein DsbA	dsbA PA5489	Cell redox homeostasis

<u>Q9HYY4</u>	Probable oxidoreductase	PA3256	Oxidoreductase activity
<u>P53652</u>	Superoxide dismutase [Mn]	sodA PA4468	Removal of superoxide radicals
<u>Q911F8</u>	Probable oxidoreductase	PA2317	Oxidoreductase activity
<u>Q91067</u>	Uncharacterized protein	PA2776	Oxidoreductase activity
<u>Q9HVG5</u>	Glycerate dehydrogenase	hprA PA4626	Oxidoreductase activity
<u>Q910T4</u>	Probable acyl-CoA dehydrogenase	PA2550	Oxidoreductase activity
<u>Q915R7</u>	S-adenosylmethionine decarboxylase proenzyme	speD PA0654	S-adenosylmethioninamine biosynthetic process, spermidine biosynthetic process

Table S10. The newly detected redox and cell homeostasis-related proteins after 3-HPAA exposure

<u>Protein ID</u>	<u>Protein Name</u>	<u>Gene Name</u>	<u>Function</u>
<u>Q91578</u>	Probable oxidoreductase	PA0863	Oxidoreductase activity
<u>Q910T0</u>	Probable short-chain dehydrogenase	PA2554	Oxidoreductase activity
<u>Q9HV44</u>	Chaperone protein DnaJ	dnaJ PA4760	Response to hyperosmotic and heat shock
<u>Q912C4</u>	NAD ⁺ dependent aldehyde dehydrogenase ExaC	exaC PA1984	Oxidoreductase activity
<u>Q915A2</u>	Glutathione peroxidase	PA0838	Response to oxidative stress
<u>Q9HZZ3</u>	Organic hydroperoxide resistance protein	ohr PA2850	Response to oxidative stress
<u>Q912R2</u>	Probable oxidoreductase	PA1833	Oxidoreductase activity
<u>Q9HUF1</u>	Peptide methionine sulfoxide reductase MsrA	msrA PA5018	Response to oxidative stress, response to hypochlorite
<u>Q9HUQ6</u>	Probable short-chain dehydrogenase	PA4907	Oxidoreductase activity
<u>Q910Z1</u>	Probable oxidoreductase	PA2491	Oxidoreductase activity, Negative regulation of secondary metabolite biosynthetic process
<u>Q9HWP5</u>	Probable major facilitator superfamily (MFS) transporter	PA4136	Drug transmembrane transporter activity
<u>Q91619</u>	Spermidine/putrescine import ATP-binding protein PotA	spuF potA, PA0302	Spermidine transport, putrescine transport
<u>Q9HUX1</u>	Biosynthetic arginine decarboxylase	speA PA4839	Arginine catabolic process, putrescine biosynthetic process, spermidine biosynthetic process
<u>Q9X6R0</u>	Polyamine aminopropyltransferase 1	speE1 speE, PA1687	Spermidine biosynthetic process

Table S11. The undetected metabolism-related proteins after 3-HPAA exposure

Protein ID	Protein Name	Gene Name	Function
<u>Q9I700</u>	Beta-alanine--pyruvate aminotransferase	bauA PA0132	Beta-alanine biosynthetic process
<u>Q9I2S7</u>	Lysine-specific pyridoxal 5'-phosphate-dependent carboxylase, LdcA	ldcA PA1818	Amino acid metabolic process
<u>Q9HTW6</u>	Aminopeptidase P	pepP PA5224	Aminopeptidase activity
<u>Q9I4W3</u>	4-hydroxy-tetrahydrodipicolinate synthase	dapA PA1010	Diaminopimelate biosynthetic process, Lysine biosynthetic process
<u>P19572</u>	Diaminopimelate decarboxylase	lysA PA5277	Lysine biosynthetic process
<u>Q5I375</u>	3-isopropylmalate dehydrogenase	leuB PA3118	Leucine biosynthetic process
<u>O86428</u>	Branched-chain-amino-acid aminotransferase	ilvE PA5013	Leucine biosynthetic process, Isoleucine biosynthetic process, valine biosynthetic process
<u>Q9HXI8</u>	Cysteine desulfurase IscS	iscS PA3814	Cysteine desulfurase activity
<u>Q9I583</u>	UPF0176 protein PA0858	PA0858	Cysteine persulfate intermediate
<u>Q9I6A1</u>	Cystathionine beta-synthase	PA0399	Cysteine biosynthetic process
<u>Q9HXE4</u>	NAD(P)H-dependent anabolic L-arginine dehydrogenase DauB	dauB PA3862	Arginine catabolic process
<u>Q9HZ67</u>	Bifunctional chorismate mutase/prephenate dehydratase	pheA PA3166	L-phenylalanine biosynthesis, Prephenate biosynthesis
<u>Q9HU83</u>	Urocanate hydratase	hutU PA5100	Histidine catabolic process
<u>Q9I2A2</u>	Fumarylacetoacetase	fahA PA2008	Aromatic amino acid family metabolic process
<u>P32722</u>	Porin D	oprD PA0958	Amino acid transport
<u>Q9HUP4</u>	Nicotinate phosphoribosyltransferase 1	pncB1 PA4919	NAD biosynthetic process
<u>Q9HTK1</u>	Probable chorismate pyruvate-lyase	ubiC PA5357	Ubiquinone biosynthetic process
<u>Q9HTW9</u>	Probable FAD-dependent monooxygenase	PA5221	Ubiquinone biosynthetic process
<u>Q9I187</u>	Probable dipeptidase	PA2393	Biyoverdine biosynthetic process
<u>Q5I507</u>	Isochorismate pyruvate lyase	pchB PA4230	Salicylate biosynthetic process
<u>Q9HWG9</u>	5-methylphenazine-1-carboxylate 1-monooxygenase	phzS PA4217	Pyocyanine biosynthetic process
<u>Q9HU21</u>	dTDP-4-dehydrorhamnose 3,5-epimerase	rmlC PA5164	Lipopolysaccharide biosynthesis, extracellular polysaccharide biosynthesis, dTDP-L-rhamnose biosynthesis
<u>Q9I299</u>	Methylcrotonyl-CoA carboxylase, alpha-subunit (Biotin-containing)	liuD PA2012	isoprenoid catabolic process, leucine catabolic process, terpene catabolic process
<u>Q9I5T1</u>	Ribulose-phosphate 3-epimerase	rpe PA0607	Carbohydrate metabolic process, pentose catabolic process
<u>Q9I406</u>	Glutathione hydrolase proenzyme	ggt PA1338	Glutathione catabolic process, glutathione biosynthetic process
<u>Q9HVL5</u>	Octaprenyl-diphosphate synthase	ispB PA4569	Isoprenoid biosynthetic process
<u>Q9I282</u>	Uncharacterized protein	PA2033	Iron assimilation

<u>Q3XD20</u>	Periplasmic serine endoprotease DegP-like	mucD PA0766	Endopeptidase, signal transduction
<u>Q69753</u>	Phenazine biosynthesis protein PhzB1	phzB1 PA4211	Phenazine biosynthetic process
<u>Q9HWV5</u>	Probable aldehyde dehydrogenase	PA4073	Phenylacetaldehyde dehydrogenase activity
<u>Q04633</u>	Adenine phosphoribosyltransferase	apt PA1543	Adenine salvage, AMP salvage, purine ribonucleoside salvage
<u>Q51508</u>	Salicylate biosynthesis isochorismate synthase	pchA PA4231	pyochelin biosynthetic process, salicylic acid biosynthetic process
<u>Q9HWG3</u>	Pyochelin biosynthesis protein PchD	pchD PA4228	Catalytic activity
<u>Q9HUM3</u>	Protein HflC	hflC PA4941	Peptidase activity
<u>Q9HVI3</u>	Uncharacterized protein	PA4606	Cellular response to nutrient levels, Starvation response
<u>Q9I6K7</u>	Sulfate-binding protein	sbp PA0283	Sulfate transmembrane transporter activity
<u>Q9I765</u>	Oligopeptidase A	prlC PA0067	Metal ion binding, signal peptide processing
<u>Q9HUG9</u>	Bifunctional protein HldE	hldE rfaE, PA4996	ADP-L-glycero-beta-D-manno-heptose biosynthesis, Carbohydrate phosphorylation, LPS core biosynthesis
<u>Q9HUA7</u>	Probable binding protein component of ABC transporter	PA5076	Ionotropic glutamate receptor
<u>Q9HU18</u>	C4-dicarboxylate-binding periplasmic protein DctP	dctP PA5167	C-4 dicarboxylate transport, transmembrane transport
<u>Q9I3L9</u>	Sulfate-binding protein of ABC transporter	cysP PA1493	Sulfate transmembrane transporter activity
<u>Q9I1R3</u>	Probable binding protein component of ABC transporter	PA2204	ionotropic glutamate receptor activity
<u>Q9I6L0</u>	Sulfate/thiosulfate import ATP-binding protein CysA	cysA PA0280	Sulfate transmembrane transporter activity
<u>Q9HX28</u>	Uncharacterized protein	PA3992	Metal ion binding
<u>Q9HVF9</u>	Uncharacterized protein	PA4632	Metallopeptidase activity
<u>Q9HZ48</u>	Probable binding protein component of ABC sugar transporter	PA3190	Carbohydrate transport
<u>Q9HY13</u>	Uncharacterized protein	PA3613	Carbohydrate metabolic process
<u>Q9I427</u>	Cytochrome bo(3) ubiquinol oxidase subunit 2	cyoA PA1317	ATP synthesis coupled electron transport, copper ion binding
<u>Q9HVZ0</u>	Phosphoheptose isomerase	gmhA PA4425	Carbohydrate biosynthesis, Lipopolysaccharide core region biosynthesis
<u>Q9HU53</u>	2,3-bisphosphoglycerate-independent phosphoglycerate mutase	gpmI pgm, PA5131	Glycolysis
<u>Q9I3G1</u>	Cytochrome c oxidase, cbb3-type, CcoO subunit	ccoO2 PA1556	Aerobic respiration, respiratory electron transport chain
<u>Q9I3D5</u>	Succinate dehydrogenase flavoprotein subunit	sdhA PA1583	Anaerobic respiration, Tricarboxylic acid cycle
<u>Q9HTQ4</u>	Cytochrome c5	cycB PA5300	Electron transfer activity, heme binding, iron ion binding

<u>P00106</u>	Cytochrome c4	cc4 PA5490	Electron transfer activity, heme binding, iron ion binding
<u>Q9HTD7</u>	Aspartate ammonia-lyase	aspA PA5429	Aspartate metabolic process, tricarboxylic acid cycle
<u>Q7DC81</u>	Phenazine biosynthesis protein PhzE	phzE1 phzE2, PA1903, PA4214	Glutamine metabolic process, tryptophan biosynthetic process, phenazine biosynthetic process
<u>Q51342</u>	Amidophosphoribosyltransferase	purF PA3108	IMP biosynthetic process, Purine nucleobase biosynthetic process, Nucleoside metabolic process, Glutamine metabolic process,
<u>Q9HXQ3</u>	Uncharacterized protein	PA3741	acyl-CoA metabolic process, fatty acid metabolic process
<u>P42512</u>	Fe(3+)-pyochelin receptor	fptA PA4221	Iron transport, iron ion homeostasis, siderophore transport
<u>Q9I6B4</u>	Thiazole synthase	thiG PA0381	Transferase activity, thiamine diphosphate biosynthesis
<u>Q9HVV3</u>	Nucleotide-binding protein PA4465	PA4465	ATP binding, GTP binding
<u>Q51551</u>	Dihydroorotase-like protein	pyrC' pyrX, PA0401	Purine nucleobase catabolic process, Pyrimidine nucleotide biosynthetic process
<u>Q59654</u>	Orotidine 5'-phosphate decarboxylase	pyrF PA2876	Pyrimidine biosynthetic process
<u>Q9HUV8</u>	Phosphoribosylamine--glycine ligase	purD PA4855	Purine nucleobase biosynthetic process, IMP biosynthetic process
<u>Q9I671</u>	Glutaryl-CoA dehydrogenase	gcdH PA0447	Acyl-CoA dehydrogenase activity, flavin adenine dinucleotide binding
<u>Q9I1Z9</u>	Putative hydro-lyase PA2116	PA2116	Lyase activity
<u>Q9HVB9</u>	Carbonic anhydrase	PA4676	Carbon utilization
<u>Q9I030</u>	Probable glutathione S-transferase	PA2813	Transferase activity
<u>Q9I5Y8</u>	Transketolase	tktA PA0548	Transketolase activity
<u>Q9HZA8</u>	Folypolyglutamate synthetase	folC PA3111	Dihydrofolate synthase activity, tetrahydrofolypolyglutamate synthase activity
<u>Q9HTD0</u>	Probable biotin carboxylase subunit of a transcarboxylase	PA5436	Ligase activity
<u>Q9HT95</u>	Acetyltransferase PA5475	PA5475	Transferase activity
<u>Q9HYR8</u>	Probable non-ribosomal peptide synthetase	PA3327	Biosynthetic process
<u>Q9HY07</u>	Ferredoxin 1	fdxA PA3621	electron transfer activity, metal ion binding
<u>G3XCV2</u>	Dihydroaeruginosic acid synthetase	pchE PA4226	Metabolic process
<u>Q9I179</u>	Probable non-ribosomal peptidesynthetase	PA2402	Metabolic process
<u>Q9I3P2</u>	Probable short-chain dehydrogenase	PA1470	Dehydrogenase activity

<u>Q9HYR5</u>	Probable short chain dehydrogenase	PA3330	Dehydrogenase activity
<u>Q9HV16</u>	Uncharacterized protein	PA4792	Lipid metabolic process
<u>G3XD40</u>	Probable acyl-CoA thiolase	PA3925	Fatty acid beta oxidation
<u>Q9HYR2</u>	3-oxoacyl-[acyl-carrier-protein] synthase 3	fabH PA3333	Fatty acid biosynthesis
<u>P15713</u>	Non-hemolytic phospholipase C	plcN PA3319	Lipid catabolic process, phosphatidylcholine phospholipase C activity
<u>O54439</u>	Acyl carrier protein 1	acpP1 acpP, PA2966	Lipid A Biosynthetic process
<u>G3XCV6</u>	Conserved cytoplasmic membraneprotein, CmpX protein	cmpX PA1775	Transmembrane transport

Table S12. The newly detected metabolism-related proteins after 3-HPAA exposure

<u>Protein ID</u>	<u>Protein Name</u>	<u>Gene Name</u>	<u>Function</u>
<u>Q9HX03</u>	Ethanolamine ammonia-lyase large subunit	eutB PA4024	Amino acid metabolic process
<u>G3XD76</u>	2,3,4,5-tetrahydropyridine-2,6-dicarboxylate N-succinyltransferase	dapD PA3666	Lysine biosynthetic process
<u>Q59653</u>	Aspartate carbamoyltransferase	pyrB PA0402	Amino acid metabolic process
<u>P38103</u>	4-hydroxy-tetrahydrodipicolinate reductase	dapB PA4759	Lysine biosynthetic process
<u>Q91235</u>	Kynureninase	kynU PA2080	Alanine biosynthetic process
<u>Q9HVV9</u>	Histidinol dehydrogenase	hisD PA4448	Histidine biosynthetic process
<u>Q912Z5</u>	Probable amidotransferase	PA1742	Glutamine metabolic process
<u>Q9HZ66</u>	Phosphoserine aminotransferase	serC PA3167	Serine biosynthetic process
<u>Q9HTE9</u>	Serine hydroxymethyltransferase 1	glyA1 PA5415	Glycine biosynthetic process
<u>Q91452</u>	Probable 3-mercaptopyruvate sulfurtransferase	sseA PA1292	Cysteine metabolic process
<u>Q91352</u>	Bacteriohemerythrin	PA1673	Oxygen carrier activity
<u>Q9HTV9</u>	Probable ATP-binding/permease fusion ABC transporter	PA5231	ATPase activity
<u>Q9HXR4</u>	Uncharacterized protein	PA3728	ATPase activity
<u>Q9HVS5</u>	Probable binding protein component of ABC transporter	PA4496	Transmembrane transport
<u>Q91672</u>	Uncharacterized protein	PA0446	Catalytic activity
<u>Q9HTZ7</u>	Phosphoenolpyruvate carboxykinase (ATP)	pckA PA5192	Gluconeogenesis
<u>Q915Y1</u>	Fructose-bisphosphate aldolase	fbpA, PA0555	Glycolysis
<u>Q913G5</u>	Cbb3-type cytochrome c oxidase subunit	ccoP1 PA1552	Oxidative phosphorylation
<u>Q915E3</u>	Citrate synthase	prpC PA0795	Tricarboxylic acid cycle
<u>Q910J8</u>	NADH-quinone oxidoreductase subunit E	nuoE PA2640	Respiratory electron transport chain
<u>Q916H4</u>	Uncharacterized protein	PA0317	Respiratory electron transport chain, lactate oxidation

<u>Q9HVF1</u>	Probable malate:quinone oxidoreductase 2	mqo2 mqoB, PA4640	Tricarboxylic acid cycle
<u>Q9I139</u>	L-serine dehydratase	sdaA PA2443	Gluconeogenesis
<u>Q9HTJ5</u>	Phosphate transport system permease protein PstA	pstA PA5367	Phosphate ion transmembrane transport
<u>Q9HWA8</u>	Phosphate transporter	PA4292	Phosphate ion transmembrane transport
<u>P40695</u>	Phospholipase C accessory protein PlcR	plcR PA0843	Regulation of synthesis of phospholipase C (possible)
<u>Q9HW15</u>	Probable short-chain dehydrogenase	speA PA4389	Fatty acid elongation
<u>Q9HZP8</u>	Enoyl-[acyl-carrier-protein] reductase [NADH]	fabV PA2950	Fatty acid biosynthesis
<u>P37799</u>	Biotin carboxyl carrier protein of acetyl-CoA carboxylase	accB fabE, PA4847	Fatty acid biosynthesis
<u>G3XD52</u>	Uncharacterized protein	PA3302	Fatty acid synthase activity, Fatty acid biosynthesis
<u>Q9I2A8</u>	Acetyl-CoA acetyltransferase	atoB PA2001	Fatty acid beta oxidation
<u>Q9HX44</u>	Probable acyl-CoA dehydrogenase	PA3972	Flavin adenine dinucleotide binding
<u>Q9I558</u>	Acetyl-coenzyme A synthetase 1	acsA1 PA0887	Acetyl-Co A Biosynthetic process
<u>Q9HYA2</u>	Probable short-chain dehydrogenase	PA3507	Nucleotide binding
<u>Q9HWX5</u>	6,7-dimethyl-8-ribityllumazine synthase	ribH ribE, PA4053	Riboflavin biosynthesis
<u>Q9HXM6</u>	GMP synthase[glutamine-hydrolyzing]	guaA PA3769	GMP biosynthesis in purine metabolism
<u>Q9HUT1</u>	Uncharacterized protein	PA4882	Nitrate assimilation
<u>P43898</u>	Oxygen-dependent coproporphyrinogen-III oxidase	hemF PA0024	Protoporphyrin-IX biosynthesis
<u>Q51548</u>	L-ornithine N(5)-monooxygenase	pvdA pvd-1, PA2386	Pyoverdinin biosynthesis, siderophore biosynthesis
<u>Q9I0W4</u>	Toluene 1,2-dioxygenase alpha subunit	xytX PA2518	Dioxygenase activity

Table S13. The undetected virulence-related proteins after 3-HPAA exposure

Protein ID	Protein Name	Gene Name	Function
<u>P26276</u>	Phosphomannomutase/ phosphoglucomutase protein	algC PA5322	Alginate biosynthetic process, GDP-alpha-D-mannose biosynthetic process, lipopolysaccharide core region biosynthetic process, O antigen biosynthetic process and pathogenicity.
<u>P55222</u>	Cyclic AMP receptor-like protein	vfr PA0652	Pathogenesis
<u>Q9HYR3</u>	Uncharacterized PhzA/B-like protein PA3332	PA3332	Antibiotic biosynthesis

Table S14. The newly detected virulence-related proteins after 3-HPAA exposure

Protein ID	Protein Name	Gene Name	Function
<u>Q9I3D8</u>	Uncharacterized protein PA1579	PA1579	It might have a role in interaction of the bacterium with animal cells
<u>Q9HVG7</u>	Uncharacterized protein	PA4624	Single-species biofilm formation

Table S15. The undetected uncharacterized proteins after 3-HPAA exposure

Protein ID	Protein Name	Gene Name	Function	Protein Blast Results
<u>Q9HW11</u>	UPF0234 protein PA4395	PA4395	Uncharacterized	YajQ family cyclic di-GMP-binding protein
<u>Q9HTF0</u>	Uncharacterized protein	PA5414	Uncharacterized	Hypothetical protein
<u>Q9HZC7</u>	Uncharacterized protein	PA3081	Uncharacterized	DUF1329 domain-containing protein
<u>Q9I748</u>	Uncharacterized protein	PA0084	Uncharacterized	Type VI secretion system contractile sheath large subunit
<u>Q9HTQ1</u>	Uncharacterized protein	PA5303	Uncharacterized	RidA Family protein
<u>Q9I5H1</u>	Uncharacterized protein	PA0758	Uncharacterized	HDOD domain-containing protein
<u>Q9I456</u>	Probable outer membrane protein	PA1288	Uncharacterized	Hypothetical protein, Long-chain fatty acid transport protein
<u>Q9HXI3</u>	Uncharacterized protein	PA3819	Uncharacterized	Glycine zipper 2TM domain-containing protein
<u>Q9I079</u>	Uncharacterized protein	PA2764	Uncharacterized	Alpha/beta hydrolase
<u>Q9I746</u>	Uncharacterized protein	PA0086	Uncharacterized	Tetratricopeptide repeat protein
<u>Q9I2X1</u>	Uncharacterized protein	PA1768	Uncharacterized	ATP-dependent zinc protease
<u>Q9I6H6</u>	Uncharacterized protein	PA0315	Uncharacterized	DUF4399 domain-containing protein
<u>Q9HVV9</u>	Uncharacterized protein	PA4611	Uncharacterized	DUF465 domain-containing protein
<u>Q9HW30</u>	Uncharacterized protein	PA4372	Uncharacterized	Imelysin
<u>Q9HVS6</u>	Uncharacterized protein	PA4495	Uncharacterized	DUF541 domain-containing protein
<u>Q9I5Z9</u>	Uncharacterized protein	PA0537	Uncharacterized	LemA family protein
<u>Q9HXJ6</u>	Uncharacterized protein	PA3801	Uncharacterized	Tetratricopeptide repeat protein
<u>Q9HYI6</u>	UPF0162 protein PA3419	PA3419	Uncharacterized	Transglut_core2 superfamily hypothetical protein
<u>Q9HU46</u>	Uncharacterized protein	PA5138	Uncharacterized	ABC transporter substrate-binding protein
<u>Q9HYJ2</u>	Uncharacterized protein	PA3413	Uncharacterized	YebG superfamily hypothetical protein
<u>Q9HXR1</u>	Uncharacterized protein	PA3731	Uncharacterized	PspA/IM30 family protein
<u>Q9HU31</u>	Amino acid (Lysine/arginine/ornithine/histidine/octopine) ABC transporter periplasmic binding protein	PA5153	Uncharacterized	Amino acid ABC transporter substrate-binding protein
<u>G3XD27</u>	Uncharacterized protein	PA5055	Uncharacterized	DUF971 domain-containing protein
<u>Q9HV96</u>	Uncharacterized protein	PA4701	Uncharacterized	COG2187 and AA_33 superfamilies hypothetical protein
<u>Q9HTR9</u>	Uncharacterized protein	PA5285	Uncharacterized	Hypothetical protein
<u>Q9I020</u>	Uncharacterized protein	PA2823	Uncharacterized	ATP-binding protein
<u>Q9HTY0</u>	Probable secretion pathway ATPase	PA5210	Uncharacterized	Type II/IV secretion system protein
<u>Q9I585</u>	Uncharacterized protein	PA0856	Uncharacterized	DUF2059 domain-containing protein
<u>Q9I749</u>	Uncharacterized protein	PA0083	Uncharacterized	Type VI secretion system contractile sheath small subunit

<u>Q9HZ94</u>	Uncharacterized protein	PA3130	Uncharacterized	Acyl-CoA thioesterase
<u>Q9I2R6</u>	Uncharacterized protein	PA1829	Uncharacterized	Phosphotransferase family protein
<u>Q9HXF7</u>	Nucleoid-associated protein PA3849	PA3849	Uncharacterized	Nucleoid-associated protein YejK
<u>Q9HZ96</u>	Probable short-chain dehydrogenase	PA3128	Uncharacterized	SDR family oxidoreductase

Table S16. The newly detected uncharacterized proteins after 3-HPAA exposure

Protein ID	Protein Name	Gene Name	Function	Protein Blast Results
<u>Q9HTL9</u>	Uncharacterized protein	PA5339	Uncharacterized	RidA Family protein
<u>Q9I622</u>	Uncharacterized protein	PA0496	Uncharacterized	Biotin-dependent carboxyltransferase family protein
<u>Q9HXG8</u>	Uncharacterized protein	PA3836	Uncharacterized	ABC transporter substrate binding protein
<u>Q9HTQ5</u>	Uncharacterized protein	PA5299	Uncharacterized	Acetyl-CoA hydrolase, putative
<u>Q9I3B5</u>	Uncharacterized protein	PA1606	Uncharacterized	DUF3859 Domain containing protein, protein of unknown function
<u>Q9HTC5</u>	Uncharacterized protein	PA5441	Uncharacterized	Hypothetical protein, Outer membrane assembly lipoprotein YfiO
<u>Q9I2Z1</u>	Uncharacterized protein	PA1746	Uncharacterized	Hypothetical protein, Appr-1-p processing protein

Table S17. Protein ID and Gene Name Lists of Mutually Unchanged Proteins

(Search the ID in “uniprot.org” for the detailed information about the protein of interest)

Protein IDs	Gene Names
P48372	gyrA PA3168
P28811	mmsB PA3569
Q9HWC6	rplA PA4273
Q9I500	PA0959
O52760	rpoA PA4238
Q9HWF0	rplF PA4248
Q9HUC3	phaF PA5060
P13982	arcC PA5173
Q9HVC5	prs PA4670
Q9HZP5	PA2953

Q9I2R5	PA1830
Q59637	aceE aceA, PA5015
Q9I2W7	PA1772
Q9HY22	erdR PA3604
Q9HTD1	PA5435
Q9HVV3	rpsI PA4432
Q9HW32	icmP PA4370
Q9I576	hpd PA0865
Q9HYX8	PA3262
Q9HZH7	moaB2 PA3029
Q9HWE3	rpmC PA4255
Q9I659	PA0459
Q9I5E2	prpB PA0796
Q9HYZ6	minD PA3244
P50987	argH PA5263
Q9I0A0	infC PA2743
Q9HT80	polA PA5493
Q9I0L2	mnmA trmU, PA2626
Q9HWD8	rplB PA4260
Q9I2V5	acnB PA1787
O50175	astB aruB, PA0899
Q9HWD6	rplD PA4262
Q9HWD0	rpsL PA4268
P72173	aspC PA3139
Q9HXN2	purL PA3763
Q9HWE2	rplP PA4256
Q9I1M0	bkdB PA2249
Q9I0K4	PA2634
Q9I4W9	nadA PA1004
Q9I6M4	davT PA0266
Q9HVV2	rplM PA4433
P47205	lpxC envA, PA4406
Q9HTM1	rpoZ PA5337

Q9I0R1	PA2575
Q9I0M6	serS PA2612
Q9I6J1	spuD PA0300
Q9HZJ5	topA PA3011
Q9I3D3	sucA PA1585
Q9HX05	PA4022
Q59636	ndk PA3807
Q9I4X2	pqsB PA0997
Q9I747	hcp1 PA0085
Q9HTR6	glnK PA5288
Q9I5Y4	pgk PA0552
Q9I636	glcB PA0482
Q9HW68	PA4333
Q9HXL0	PA3785
Q9HZK4	PA3001
Q9HYZ0	PA3250
Q9HWC7	rplJ PA4272
P13794	oprF PA1777
Q9HWD9	rpsS PA4259
Q9HWF8	rpsK PA4240
Q9I6Z3	ahpC PA0139
Q9I5U9	PA0588
Q9HWE4	rpsQ PA4254
Q9HWD1	rpsG PA4267
Q51404	fumC2 PA4470
Q9HVA8	hitA PA4687
Q9HVN5	clpB PA4542
Q9HUY5	mgtA PA4825
P34002	aroB PA5038
Q9I047	tal PA2796
Q9I2W9	ppsA PA1770
Q9HTP2	PA5312
Q9HZA4	leuD PA3120

Q9HVT7	gatB PA4484
Q9I344	aroC PA1681
Q9HXJ4	ispG PA3803
Q9HW04	argJ PA4402
P57112	sthA sth, PA2991
Q9HV55	infB PA4744
Q9I4W0	purC PA1013
Q9HXP9	rpsP PA3745
Q9I5I4	PA0745
Q9HZ98	ibpA PA3126
Q9HT17	atpH PA5557
Q9I5Z0	metK PA0546
Q9HZE0	gdhB PA3068
Q9I5E4	PA0794
P08308	arcB PA5172
Q9HWD2	fusA fusA1, PA4266
Q9HUD3	PA5046
Q9HT21	atpC PA5553
Q9HZIP7	etfA PA2951
Q9HZJ2	fadB PA3014
Q9I4I2	nrdB PA1155
P05384	hupB PA1804
Q9HV43	dnaK PA4761
Q9HZF5	PA3053
Q9I3D2	sucB PA1586
P53641	sodB PA4366
Q9I5F6	putA PA0782
Q9HWW7	PA4061
Q9HT16	atpF PA5558
Q9HV51	tpiA PA4748
Q51567	sucD PA1589
Q9I2U0	clpX PA1802
Q9I4Z4	pal oprL, PA0973

Q51344	asd PA3117
P57668	tpx PA2532
Q59638	aceF aceB, PA5016
Q9HX76	PA3940
Q9HV54	nusA PA4745
Q9HTN4	coaC PA5320
Q9HXV4	adk PA3686
Q9HW45	xenB PA4356
Q9I0J6	nuoG PA2642
Q9HVC4	rplY etc, PA4671
Q9X2T1	trxA trx, PA5240
O30508	aruC argD, astC, PA0895
Q9I338	PA1689
P28810	mmsA PA3570
Q9HU24	rmlB PA5161
P52002	mexB PA0426
Q9HU11	PA5178
Q9I6H5	serA PA0316
Q9HVY4	PA4431
Q9HTD9	adhA PA5427
Q9I0D5	PA2707
Q9I0A3	pheS PA2740
Q9HVL6	rplU PA4568
Q9HWF7	rpsM PA4241
Q9I4I1	nrdA PA1156
Q9HV46	greA PA4755
Q9HUC5	hslU PA5054
Q9HVD1	pagL PA4661
P37798	accC fabG, PA4848
P20580	trpE PA0609
P43335	phhB PA0871
Q9I3B2	fabB PA1609
Q9I3G2	ccoP2 PA1555

Q9HTM3	PA5335
Q9I078	PA2765
Q9I4X1	pqsC PA0998
Q9I5U3	surA PA0594
Q9HWF1	rplR PA4247
Q9I2Y7	PA1750
O69077	lysC PA0904
Q9H XK2	PA3795
Q9HW86	mvaT PA4315
P30718	groL groEL, mopA, PA4385
Q9HX01	PA4026
Q9I7A8	def PA0019
Q9HWE1	rpsC PA4257
Q9HUM9	rpsF PA4935
Q51384	PA3808
Q9HVW4	PA4453
Q9HWC8	rplL PA4271
P08280	recA PA3617
Q9I0T1	PA2553
P43501	pilH PA0409
Q9I3D4	sdhB PA1584
Q9I407	ansB PA1337
P00282	azu PA4922
P13981	arcA PA5171
Q9I3F5	acnA PA1562
Q9I184	pvdF PA2396
Q9HXQ2	rplS PA3742
Q9I6M5	davD PA0265
Q9I0A2	rplT PA2741
O82852	pyrH PA3654
Q9HV69	panC PA4730
Q9HVA2	ilvC PA4694
P15276	algP algR3, PA5253

Q9I1L9	lpdV PA2250
Q9I137	gcvP1 PA2445
Q51422	aspS PA0963
Q9I6G0	ilvA1 ilvA, PA0331
Q9HYU4	fadD1 PA3299
Q9HVT8	gatA PA4483
Q9I140	gcvT2 PA2442
P30720	groS groES, mopB, PA4386
Q9HZN4	rpmF PA2970
Q9HUN2	rplI PA4932
Q9I0D3	cysK PA2709
Q9HTN8	rpmB PA5316
P38100	carB PA4756
Q9HW49	PA4352
Q9HYY3	prc PA3257
Q9HX91	PA3922
Q9I2U2	tig PA1800
Q9HXZ5	eno PA3635
Q9I7C2	gyrB PA0004
Q51561	rpoB PA4270
Q9I5H0	PA0759
Q9HY77	PA3533
Q9HWC9	rpoC PA4269
Q9I5Q9	argC PA0662
Q9HZJ3	fadA PA3013
Q9HT20	atpD PA5554
Q9I3C5	htpG PA1596
P43903	qor PA0023
Q9HX33	leuS PA3987
Q9HZ71	rpsA PA3162
P14165	gltA PA1580
Q9HTU9	PA5245
Q9HUC8	argS PA5051

P77915	hemN PA1546
Q9HWD4	rpsJ PA4264
Q9HV59	pnp PA4740
P11221	oprI PA2853
Q9I083	PA2760
Q9HYL8	PA3383
Q9HU65	glnA PA5119
Q9I690	PA0423
Q9I687	metF PA0430
P09591	tufA PA4265
P09591	tufB PA4277
Q9HWE6	rplX PA4252
O52759	rpsD PA4239
Q9I296	liuA PA2015
Q9HX20	proA PA4007
Q9I0K9	purB PA2629
Q9I138	glyA2 PA2444
P72157	purE PA5426
Q9I402	PA1342
Q9HTV1	rho PA5239
Q59643	hemB PA5243
Q9HWE7	rplE PA4251
Q9HXZ4	pyrG PA3637
Q9HWX4	ribB PA4054
Q9I5V8	rpsU PA0579
Q9HZZ2	efp PA2851
G3XD47	aotJ PA0888
Q9HWF4	rplO PA4244
Q9HVV6	trpS PA4439
Q9HVV5	PA4463
Q9HVM8	rne PA2976
O82853	frt PA3653
Q9I502	proS PA0956

Q9I7B8	glyS PA0008
Q9HYT5	PA3309
Q9HWC5	rplK PA4274
Q9HWD5	rplC PA4263
O52762	katA PA4236
Q9HWF3	rpmD PA4245
Q9HWE8	rpsN PA4250
Q9I1F7	PA2318
Q9HV42	grpE PA4762
P21175	braC PA1074
Q9I2U9	ppiB PA1793
Q9HXM5	guaB PA3770
Q9HT25	glmS PA5549
Q9HVV6	PA4429
Q9I1N7	pslB PA2232
Q9HVJ1	PA4595
P53593	sucC PA1588
Q9I0L5	icd PA2623
Q9I297	liuB PA2014
Q9HY81	PA3529
Q9HVI7	glyA2 PA4602
P0DP44	ppk PA5242
Q9I658	PA0460
Q9I7B7	glyQ PA0009
O87125	cheB1 PA1459
Q9I3D1	lpdG PA1587
Q9HY84	argG PA3525
Q9I0L4	idh PA2624
Q9HV50	glmM PA4749
O82851	tsf PA3655
Q9HX12	PA4015
Q9HVQ3	speC PA4519
Q9HWC4	nusG PA4275

Q9I5G8	lepA le, PA0767
Q9HXJ9	PA3798
O52761	rplQ PA4237
Q9HWF2	rpsE PA4246
Q9I685	ahcY sahH, PA0432
O54438	fabG PA2967
Q9I553	alaS PA0903
Q9I6J2	spuC PA0299
Q9I6E0	ilvD PA0353
P38098	carA PA4758
P24559	pilT PA0395
Q9HW72	pykA PA4329
Q9I0Y8	mexF PA2494
Q9I185	pvdO PA2395
Q9HWW1	oprG PA4067
Q9HWE9	rpsH PA4249
Q9HYZ3	apeB PA3247
Q9I171	PA2410
P43336	phhC PA0870
P26275	algR PA5261
O82850	rpsB PA3656
Q9HT18	atpA PA5556
Q9HVS8	roxR PA4493
Q9HUM6	purA PA4938
Q9I015	PA2828
Q9HYG6	PA3440
Q9I4Z7	PA0962
Q9I0H1	PA2667
Q9I662	PA0456
Q9HYK7	fpr PA3397
P20577	trpC PA0651
G3XDA8	pstS PA5369
Q9HXZ2	accA PA3639

Q9HVF2	PA4639
Q9HTQ0	dadA1 dadA, PA5304
Q9I4W2	PA1011
Q9HXU0	lysS PA3700
Q9HZP6	etfB PA2952

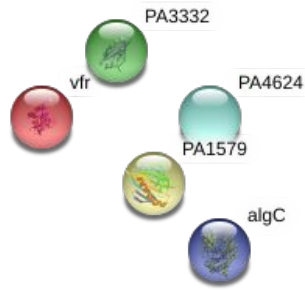


Figure S2. Interaction network of virulence-related undetected and newly detected proteins after 3-HPAA exposure by STRING. Proteins are represented as nodes.

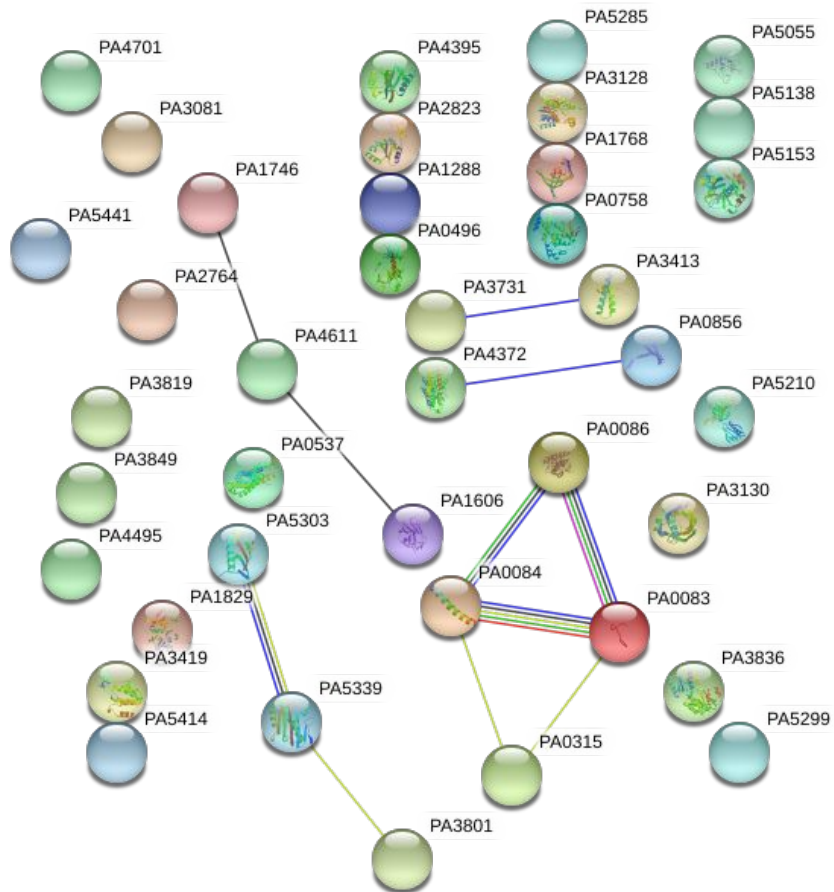


Figure S3. Interaction network of uncharacterized-functioned undetected and newly detected proteins after 3-HPAA exposure by STRING. Proteins are represented as nodes.

Supporting Information 3

Validation of Undetection of 30S Ribosomal Protein S15 after 3-HPAA exposure by RT-qPCR

Bacterial cultures were prepared by the same protocol of protein isolation prior to total RNA isolation. The isolation of the total RNA from control 3-HPAA treated *P. aeruginosa* was performed by GeneJET RNA purification kit (#K0732 Thermo Scientific) according to the manufacturer's instructions (numbers of the washing steps were modified as two times with buffer 1 and three times for buffer 2). Total RNA samples were isolated from the 18 hour cultures of *P. aeruginosa* for being comparable to protein data. The samples were kept at -80°C until cDNA preparation. The cDNA preparation was performed according to the manufacturer's instructions of the kit (# K1622 Thermo RevertAid First Strand cDNA Synthesis Kit). The primers of RT-qPCR were designed for the genes of 30S ribosomal protein S15 (*rpsO*) and S12 (*rpsL*) by Primer BLAST programme in Refseq database among Pseudomonadales with maximum target size of 200 (Table S18). The housekeeping gene was determined as *rpsL* depending on the studies of Dumas et al. and Llanes et al. (Dumas et al., 2006; Llanes et al., 2004; see reference list). The PCR mixture was obtained by using the protocol of SYBR green kit (LightCycler 480 SYBR Green I Master Mix, Roche) with half of the recommended volume. The PCR was carried out in the following conditions: 5 minutes at 25°C; 60 minutes at 42°C and 5 minutes at 70°C. The cDNA concentration was 250 ng, melting temperature was 50°C and the annealing cycles were 40 during the PCR process. The produced cDNA samples were kept at -20°C until usage.

Table S18. The primers used in RT-qPCR.

Genes	F Primer	R Primer
rpsL	CGTACATCGGTGGTGAAGGT	CGACCCTGCTTACGGTCTTT
rpsO	TACAAGCAAGCTGAAGGCGA	CCATACGGATCAGACCACGG

The relative fold change calculation of three biological samples and three technical repeats were performed with delta Ct method. The average fold change in Ct value of mRNA expression of *rpsO* gene was 0.8 (± 0.04) after 3-HPAA exposure. The normalization was done based on the mRNA expression of housekeeping gene and untreated group (as 1.0 in fold change). These results showed that expression of *rpsO* gene decreased 1.3 fold. It is consistent

with the protein data, thus, 3-HPAA treatment resulted in a reduction in the 30S ribosomal protein S15 in *P. aeruginosa* (Figure S4).

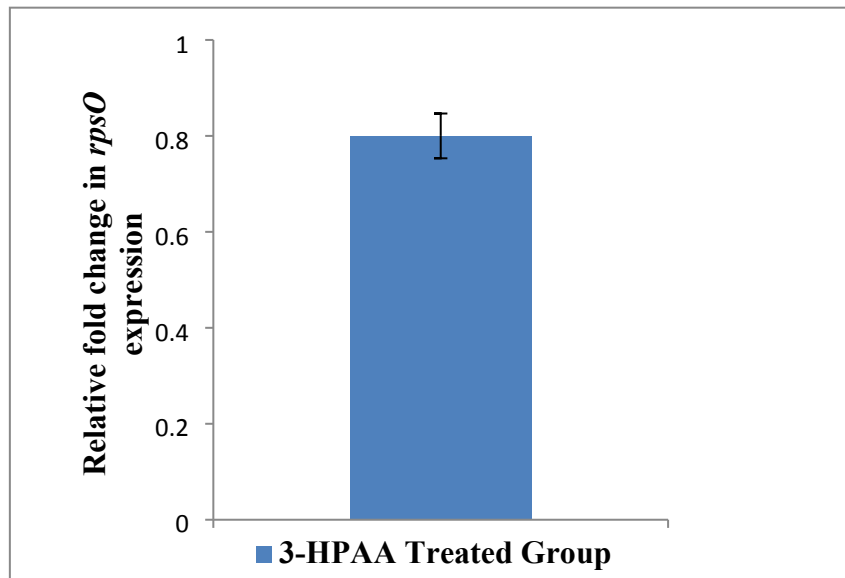


Figure S4. Relative fold change in the expression of *rpsO* gene. Delta Ct method was applied for three biological and three technical repeats. Normalization was performed based on *rpsL* gene expression and untreated group ($p < 0.05$).

Supporting Information 4

The IDs of the Genes in the Categories of KEGG Pathway Enrichment Analysis

Table S19. Entrez gene IDs used in the KEGG pathway analysis via DAVID

Detection State of the Protein	Category	Entrez Gene ID
Undetected	Biosynthesis of siderophore group nonribosomal peptides	880048, 881821, 880566, 881846
Undetected	Metabolic Pathways	877749, 882904, 878291, 882585, 878748, 879406, 878259, 878603, 880534, 880477, 882952, 879172, 882699, 879231, 881680, 878523, 883049, 877840, 881821, 877877, 882812, 882498, 882262, 880316, 878596, 878162, 879802, 882212, 880890, 881513, 879394, 879012, 878446, 883103, 879350, 881934, 879918, 881182, 879056, 879865, 881166, 878828, 878134, 878236, 878275, 878687, 880940, 880542, 881423, 881196, 879525, 879047, 882484
Undetected	Biosynthesis of antibiotics	878523, 881821, 877749, 882904, 878291, 879406, 881846, 881934, 881182, 881423, 880534, 880477, 879991 878162 879525, 879047, 882699, 878236, 878134, 879805

Undetected	Glutathione Metabolism	882952, 879865, 878570, 882262, 880278
Newly Detected		878956, 879732, 880792, 881338, 880066, 882903, 880992, 880552, 879312, 880413, 882347, 883043, 883061, 881249, 879594, 882647, 879557, 879002, 882700, 879081, 882930, 882931, 879244, 878267, 880901, 881495, 880490, 879046, 881759, 877856, 880584
	Metabolic Pathways	
Newly Detected		880792, 879732, 879557, 880066, 882700, 879312, 879046, 882930, 881249, 882931
	Carbon metabolism	
Newly Detected		879732, 879557, 879312, 879046, 880413, 881249
	Pyruvate metabolism	
Newly Detected		880792, 879732, 880066, 882700
	Methane metabolism	
Newly Detected		880792, 879732, 879557, 880066, 882700, 882903, 881495, 879312, 879046, 881759, 880413, 880584, 881249
	Microbial metabolism in diverse environments	