Generic and Specific Adaptive Responses of Streptococcus pneumoniae to Challenge with Three Distinct Antimicrobial Peptides, Bacitracin, LL-37, and Nisin

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SUPPLEMENTAL MATERIALS

Table S.1. Complete lists of differentially expressed genes of *S. pneumoniae* D39 exposure to bacitracin, nisin and LL-37 treatment. Genes with a fold change of ≤0.6 or ≥1.5 are indicated in bold.

A. List of genes up-regulated upon **15 min.** treatment with **bacitracin:**

Gene ID	Ratio	Bayes.p	NCBI annotation
SP0385	**2.1**	**2.40E-04**	**conserved hypothetical protein**
SP0386	**2.4**	**1.98E-05**	**putative sensor histidine kinase**
SP0387	**2.1**	**1.45E-04**	**DNA-binding response regulator**
SP0390	**2.1**	**1.77E-04**	**choline binding protein G**
SP0391	**2.0**	**2.76E-04**	**choline binding protein F**
SP0419	**1.8**	**5.79E-04**	**enoyl-(acyl-carrier-protein) reductase, *fabK***
SP0420	**1.9**	**4.07E-04**	**CoA-acyl carrier protein transacylase, *fabD***
SP0421	**2.0**	**1.25E-04**	**3-oxoacyl-[acyl-carrier protein] reductase, *fabG***
SP0422	**2.2**	**6.31E-05**	**3-oxoacyl-(acyl-carrier-protein) synthase II, *fabF***
SP0424	**2.2**	**4.39E-05**	**(3R)-hydroxymyristoyl-(acyl-carrier-protein) dehydratase, *fabZ***
SP0426	**2.1**	**2.19E-04**	**acetyl-CoA carboxylase, carboxyl transferase, beta subunit, *accD***
SP0427	**2.4**	**1.54E-04**	**acetyl-CoA carboxylase, carboxyl transferase, alpha subunit, *accA***
SP0430	**2.3**	**7.12E-05**	**conserved domain protein**
SP0785	**1.8**	**1.92E-04**	**conserved hypothetical protein**
SP0786	**2.0**	**1.82E-04**	**ABC transporter, ATP-binding protein**
SP0787	**1.8**	**3.65E-04**	**conserved hypothetical protein**
SP0861	**1.7**	**4.39E-04**	**hypothetical protein**
SP0910	**1.6**	**4.96E-04**	**conserved hypothetical protein**
SP0912	**8.2**	**8.26E-11**	**ABC transporter, ATP-binding protein**
SP0913	**12.4**	**3.07E-10**	**putative ABC transporter, permease protein**
SP1356	**1.7**	**6.21E-04**	**amidohydrolase family protein**
SP1480	**1.4**	**7.87E-04**	**hypothetical protein**
SP1714	**2.9**	**5.93E-06**	**transcriptional regulator, GntR family**
SP1715	**2.3**	**1.20E-04**	**ABC transporter, ATP-binding protein**

SP1925	1.8	6.85E-04	hypothetical protein
SP1926	1.8	7.32E-04	hypothetical protein
SP2086	1.9	9.20E-04	phosphate ABC transporter, permease protein, *pstA*

B. List of genes differentially expressed upon **30 min.** treatment with **bacitracin:**

up-regulated genes				down-regulated genes			
Gene ID	**Ratio**	**Bayes.p**	**NCBI annotation**	**Gene ID**	**Ratio**	**Bayes.p**	**NCBI annotation**
SP0069	1.8	3.87E-05	choline binding protein I, *cbpI*	*SP0005*	0.5	4.41E-06	peptidyl-tRNA hydrolase
SP0088	2.1	2.94E-05	hypothetical protein	*SP0095*	0.2	2.68E-09	conserved hypothetical protein
SP0101	2.1	4.98E-06	putative transporter	*SP0117*	0.5	3.06E-05	pneumococcal surface protein A, *pspA*
SP0107	2.4	2.14E-06	LysM domain protein	*SP0281*	0.5	3.47E-05	aminopeptidase C
SP0142	2.0	2.39E-05	hypothetical protein	*SP0285*	0.5	2.88E-06	alcohol dehydrogenase, zinc-containing
SP0157	2.0	5.73E-05	hypothetical protein	*SP0366*	0.6	6.66E-05	oligopeptide ABC transporter, oligopeptide-binding protein AliA
SP0189	2.0	8.66E-06	conserved hypothetical protein	*SP0400*	0.5	1.45E-05	trigger factor
SP0275	2.3	5.13E-06	conserved hypothetical protein	*SP0430*	0.5	3.79E-06	conserved domain protein
SP0276	1.9	8.91E-05	conserved hypothetical protein	*SP0435*	0.5	3.93E-05	translation elongation factor P, *efp*
SP0278	2.1	3.62E-06	hypothetical protein	*SP0453*	0.6	9.90E-05	amino acid ABC transporter, amino acid-binding protein/permease protein
SP0338	3.1	8.59E-09	putative ATP-dependent Clp protease, ATP-binding subunit	*SP0458*	0.5	1.68E-05	DNA-damage inducible protein P
SP0369	1.9	1.53E-05	penicillin-binding protein 1A	*SP0459*	0.4	2.98E-08	formate acetyltransferase
SP0370	1.8	4.70E-05	recombination protein U	*SP0516*	0.6	2.46E-05	heat shock protein GrpE
SP0371	2.0	3.35E-05	conserved hypothetical protein	*SP0565*	0.4	6.87E-07	conserved domain protein
SP0391	1.7	9.72E-05	choline binding protein F	*SP0566*	0.4	1.02E-06	acetyltransferase, GNAT family

SP0408	**2.6**	**2.29E-07**	**sodium:alanine symporter family protein**	***SP0568***	**0.5**	**1.87E-06**	**valyl-tRNA synthetase, *valS***
SP0487	**1.9**	**9.29E-05**	**hypothetical protein**	***SP0577***	**0.4**	**1.33E-06**	**PTS system, beta-glucosides-specific IIABC omponents**
SP0488	**1.9**	**2.19E-06**	**conserved hypothetical protein**	***SP0579***	**0.5**	**2.73E-05**	**phenylalanyl-tRNA synthetase, alpha subunit, *pheS***
SP0582	**2.5**	**2.41E-07**	**hypothetical protein**	***SP0580***	**0.6**	**5.64E-05**	**acetyltransferase, GNAT family**
SP0607	**2.3**	**4.15E-07**	**amino acid ABC transporter, permease protein**	***SP0581***	**0.5**	**1.43E-06**	**phenylalanyl-tRNA synthetase, beta subunit, pheT**
SP0608	**1.9**	**1.59E-05**	**amino acid ABC transporter, permease protein**	***SP0614***	**0.6**	**3.75E-05**	**tributyrin esterase, *estA***
SP0609	**1.9**	**1.34E-05**	**amino acid ABC transporter, amino acid-binding protein**	***SP0626***	**0.4**	**6.29E-07**	**branched-chain amino acid transport system II carrier protein brnQ**
SP0641	**3.0**	**1.26E-08**	**serine protease, subtilase family**	***SP0644***	**0.4**	**6.40E-06**	**hypothetical protein, truncation**
SP0709	**1.7**	**5.81E-05**	**amino acid ABC transporter, ATP-binding protein**	***SP0673***	**0.6**	**4.40E-05**	**hypothetical protein**
SP0785	**2.1**	**1.98E-06**	**conserved hypothetical protein**	***SP0731***	**0.5**	**1.48E-06**	**conserved domain protein**
SP0786	**2.3**	**3.40E-07**	**ABC transporter, ATP-binding protein**	***SP0736***	**0.6**	**7.06E-05**	**mannose-6-phosphate isomerase, *manA***
SP0787	**2.4**	**5.55E-07**	**conserved hypothetical protein**	***SP0742***	**0.4**	**1.23E-07**	**conserved hypothetical protein**
SP0790	**2.3**	**2.89E-06**	**conserved domain protein**	***SP0745***	**0.6**	**8.51E-05**	**uracil phosphoribosyltransferase**
SP0800	**1.9**	**3.76E-05**	**hypothetical protein**	***SP0770***	**0.6**	**4.67E-05**	**ABC transporter, ATP-binding protein**
SP0873	**2.0**	**6.25E-06**	**membrane protein**	***SP0775***	**0.5**	**2.09E-06**	**ribosomal protein S16, *rpsP***
SP0875	**2.1**	**2.56E-07**	**lactose phosphotransferase system repressor**	***SP0869***	**0.6**	**3.74E-05**	**aminotransferase, class-V**
SP0876	**2.2**	**2.30E-07**	**putative 1-phosphofructokinase**	***SP0870***	**0.5**	**5.24E-06**	**NifU family protein**
SP0877	**1.6**	**9.19E-05**	**PTS system, fructose specific IIABC components**	***SP0871***	**0.6**	**6.61E-05**	**conserved hypothetical protein**
SP0910	**2.1**	**4.07E-07**	**conserved hypothetical protein**	***SP0920***	**0.6**	**2.77E-05**	**carboxynorspermidine decarboxylase, nspC**
SP0912	**8.7**	**1.76E-12**	**ABC transporter, ATP-binding protein**	***SP0922***	**0.6**	**1.05E-05**	**carbon-nitrogen hydrolase family protein**
SP0913	**9.6**	**8.73E-11**	**putative ABC transporter, permease protein**	***SP1071***	**0.5**	**4.18E-05**	**ABC transporter, ATP-binding protein**
SP1025	**1.8**	**5.31E-05**	**hypothetical protein**	***SP1117***	**0.4**	**2.28E-06**	**DNA ligase, NAD-dependent, ligA**
SP1148	**1.9**	**7.03E-05**	**IS630-Spn1, transposase Orf2**	***SP1121***	**0.4**	**5.82E-06**	**hypothetical protein**
SP1343	**1.8**	**3.83E-06**	**prolyl oligopeptidase family protein**	***SP1122***	**0.5**	**9.90E-05**	**glucose-1-phosphate adenylyltransferase, glgC**

SP1344	1.9	5.84E-06	conserved hypothetical protein	*SP1175*	0.5	2.17E-05	conserved domain protein
SP1422	1.7	9.79E-05	hypothetical protein	*SP1383*	0.3	7.29E-08	alanyl-tRNA synthetase, alaS
SP1480	1.8	8.38E-05	hypothetical protein	*SP1384*	0.5	9.53E-07	conserved hypothetical protein
SP1588	2.2	7.12E-07	oxidoreductase, pyridine nucleotide-disulfide, class I	*SP1441*	0.5	8.21E-07	IS66 family element, Orf3, degenerate
SP1646	1.6	9.41E-05	metallo-beta-lactamase superfamily protein	*SP1468*	0.6	7.97E-05	pyridoxine biosynthesis protein
SP1648	2.5	3.13E-08	manganese ABC transporter, ATP-binding protein,psaB	*SP1474*	0.5	1.25E-06	glycyl-tRNA synthetase, beta subunit, glyS
SP1649	2.6	1.51E-06	putative manganese ABC transporter, permease, psaC	*SP1477*	0.5	2.22E-06	hypothetical protein
SP1674	1.9	3.60E-06	putative phosphosugar-binding transcriptional regulator	*SP1531*	0.5	2.29E-05	hypothetical protein
SP1683	2.9	1.00E-07	sugar ABC transporter, sugar-binding protein	*SP1533*	0.5	3.19E-05	conserved domain protein
SP1774	2.2	4.56E-07	putative transcriptional regulator	*SP1576*	0.4	1.45E-07	homoserine O-succinyltransferase, metA
SP1786	3.0	6.80E-08	conserved hypothetical protein	*SP1577*	0.5	3.45E-05	adenine phosphoribosyltransferase, apt
SP1787	2.3	1.48E-06	hypothetical protein	*SP1630*	0.3	1.39E-08	hypothetical protein
SP1854	2.0	8.24E-05	galactose operon repressor, *galR*	*SP1631*	0.4	5.92E-08	threonyl-tRNA synthetase, thrS
SP1885	2.0	2.18E-05	trehalose operon transcriptional repressor, *treR*	*SP1651*	0.4	4.36E-06	thiol peroxidase, psaD
SP2060	1.9	1.26E-05	pyrrolidone-carboxylate peptidase, pcp-2	*SP1659*	0.4	1.10E-06	isoleucyl-tRNA synthetase
SP2062	2.0	6.08E-05	transcriptional regulator, MarR family	*SP1661*	0.6	1.10E-05	cell division protein DivIVA
SP2063	7.4	1.65E-10	LysM domain protein	*SP1673*	0.6	8.38E-06	penicillin-binding protein 2B, *penA*
SP2084	2.5	1.78E-07	phosphate ABC transporter, phosphate-binding protein, *pstS*	*SP1695*	0.6	2.52E-05	putative acetyl xylan esterase
SP2086	1.9	8.29E-05	phosphate ABC transporter, permease protein, *pstA*	*SP1743*	0.6	1.41E-05	conserved hypothetical protein
SP2087	2.1	1.52E-06	phosphate ABC transporter, ATP-binding protein, *pstB*	*SP1906*	0.6	3.89E-05	chaperonin, 60 kDa
SP2088	1.8	3.84E-05	phosphate transport system regulatory protein PhoU	*SP2026*	0.4	3.78E-06	alcohol dehydrogenase, iron-containing
SP2136	3.6	2.70E-09	choline binding protein PcpA	*SP2055*	0.5	1.12E-06	alcohol dehydrogenase, zinc-containing
SP2197	1.8	1.44E-05	putative ABC transporter, substrate-binding protein	*SP2134*	0.6	2.65E-05	ribosomal protein L32, *rpmF*
SP2199	1.9	1.28E-05	conserved hypothetical protein	*SP2188*	0.6	3.03E-05	chaperonin, 33 kDa, hslO

				SP2189	**0.6**	**3.81E-05**	**putative TIM-barrel protein, NifR3 family**
				SP2239	**0.5**	**2.84E-05**	**serine protease**
				SP2240	**0.5**	**7.31E-05**	**spspoJ protein**

C. List of genes differentially expressed upon **15 min.** treatment with **nisin:**

up-regulated genes				down-regulated genes			
Gene ID	**Ratio**	**Bayes.p**	**NCBI annotation**	**Gene ID**	**Ratio**	**Bayes.p**	**NCBI annotation**
SP0185	1.3	7.81E-04	magnesium transporter, CorA family	*SP0229*	0.8	6.51E-04	ribosomal protein L15, *rplO*
SP0335	1.4	2.99E-05	cell division protein FtsL	*SP0230*	0.7	7.11E-05	preprotein translocase, SecY subunit, *secY*
SP0415	1.4	5.77E-05	enoyl-CoA hydratase/isomerase family protein	*SP0237*	0.7	2.26E-04	ribosomal protein L17, *rplQ*
SP0416	1.3	5.09E-04	transcriptional regulator, MarR family	*SP0285*	0.7	1.32E-04	alcohol dehydrogenase, zinc-containing
SP0641	1.3	2.33E-04	serine protease, subtilase family	*SP0366*	0.7	8.16E-05	oligopeptide ABC transporter, oligopeptide-binding protein AliA
SP0664	1.3	5.63E-04	zinc metalloprotease ZmpB	***SP0441***	**0.6**	**6.31E-06**	**ribosomal protein L28**
SP0851	**1.5**	**7.05E-05**	**conserved hypothetical protein**	***SP0501***	**0.5**	**3.15E-06**	**transcriptional regulator, MerR family**
SP0875	**1.6**	**1.01E-05**	**lactose phosphotransferase system repressor**	***SP0502***	**0.5**	**6.55E-05**	**glutamine synthetase, type I**
SP0876	**1.7**	**2.56E-06**	**putative 1-phosphofructokinase**	*SP0557*	0.7	3.17E-04	ribosome-binding factor A, *rbfA*
SP0912	**9.1**	**1.40E-12**	**ABC transporter, ATP-binding protein**	***SP0577***	**0.6**	**2.84E-06**	**PTS system, beta-glucosides-specific IIABC omponents**
SP0913	**13.3**	**5.84E-13**	**putative ABC transporter, permease protein**	***SP0578***	**0.6**	**3.17E-06**	**6-phospho-beta-glucosidase, *bglA*-2**
SP0914	**1.6**	**6.77E-05**	**nodulin-related protein, truncation**	***SP0645***	**0.6**	**1.06E-05**	**putative PTS system IIA component**
SP1178	**1.3**	**3.08E-04**	**NrdH-redoxin**	*SP0670*	0.7	1.46E-04	hypothetical protein
SP1343	1.3	5.41E-04	prolyl oligopeptidase family protein	*SP0731*	0.7	1.24E-04	conserved domain protein
SP1578	1.4	6.75E-04	putative methyltransferase	*SP0838*	0.7	1.87E-04	ribosomal protein S20, *rpsT*
SP1588	1.3	6.36E-04	oxidoreductase, pyridine nucleotide-disulfide, class I	*SP0922*	0.7	2.84E-04	carbon-nitrogen hydrolase family protein
SP1871	**1.6**	**5.99E-04**	**iron-compound ABC transporter, ATP-binding protein**	*SP0962*	0.8	5.53E-04	lactoylglutathione lyase, *gloA*

SP1872	**1.6**	**2.74E-04**	**iron-compound ABC transporter, iron-compound-binding protein**	*SP1080*	0.7	1.91E-04	hypothetical protein
SP2173	1.3	7.90E-04	dltD protein	*SP1187*	0.6	7.24E-06	transcription antiterminator LacT
SP2216	**1.5**	**5.33E-04**	**secreted 45 kd protein, *usp45***	*SP1220*	0.8	4.62E-04	L-lactate dehydrogenase
				SP1241	**0.5**	**6.49E-06**	**acid ABC transporter, amino acid-binding protein/permease protein**
				SP1242	**0.5**	**8.46E-07**	**amino acid ABC transporter, ATP-binding protein**
				SP1295	0.7	2.10E-04	crcB protein
				SP1297	**0.6**	**5.88E-05**	**flavodoxin**
				SP1306	**0.6**	**7.98E-06**	**NADP-specific glutamate dehydrogenase, *gdhA***
				SP1354	0.7	8.63E-05	ribosomal protein L7/L12, *rplL*
				SP1394	0.8	8.82E-04	amino acid ABC transporter, amino acid-binding protein
				SP1414	0.8	5.80E-04	ribosomal protein S21,*rpsU*
				SP1499	0.7	2.18E-04	bacterocin transport accessory protein
				SP1507	0.7	1.06E-04	ATP synthase F1, epsilon subunit, *atpC*
				SP1531	0.7	1.38E-04	hypothetical protein
				SP1648	0.7	3.46E-04	manganese ABC transporter, ATP-binding protein,psaB
				SP1649	0.8	2.98E-04	putative manganese ABC transporter, permease, psaC
				SP1864	0.7	3.17E-04	conserved hypothetical protein
				SP1959	0.7	2.25E-04	nucleoside diphosphate kinase
				SP1970	0.7	1.90E-04	aspartate--ammonia ligase, *asnA*
				SP1996	0.7	9.24E-05	universal stress protein family
				SP2055	0.7	5.72E-04	alcohol dehydrogenase, zinc-containing
				SP2108	0.7	6.14E-04	maltose/maltodextrin ABC transporter, maltose/maltodextrin-binding protein, *malX*
				SP2126	0.7	3.78E-04	dihydroxy-acid dehydratase, *ilvD*

D. List of genes differentially expressed upon **30 min.** treatment with **nisin:**

up-regulated genes	down-regulated genes

Gene ID	Ratio	Bayes.p	NCBI annotation	Gene ID	Ratio	Bayes.p	NCBI annotation
SP0148	**1.6**	**4.09E-04**	**ABC transporter, substrate-binding protein**	*SP0496*	0.7	4.22E-04	Na/Pi cotransporter II-related protein
SP0415	**2.0**	**6.16E-04**	**enoyl-CoA hydratase/isomerase family protein**	***SP0501***	**0.4**	**1.54E-06**	**transcriptional regulator, MerR family**
SP0419	**2.0**	**5.08E-04**	**enoyl-(acyl-carrier-protein) reductase**	***SP0502***	**0.5**	**5.47E-06**	**glutamine synthetase, type I**
SP0422	**2.2**	**1.62E-04**	**3-oxoacyl-(acyl-carrier-protein) synthase II, *fabF***	***SP1160***	**0.5**	**1.14E-04**	**putative lipoate-protein ligase**
SP0875	**1.5**	**8.49E-04**	**lactose phosphotransferase system repressor**	***SP1241***	**0.6**	**1.55E-04**	**acid ABC transporter, amino acid-binding protein/permease protein**
SP0876	**1.6**	**3.68E-05**	**putative 1-phosphofructokinase**	***SP1242***	**0.6**	**4.04E-05**	**amino acid ABC transporter, ATP-binding protein**
SP0912	**6.0**	**4.38E-09**	**ABC transporter, ATP-binding protein**	***SP1648***	**0.6**	**1.26E-05**	**manganese ABC transporter, ATP-binding protein,psaB**
SP0913	**11.9**	**4.14E-12**	**putative ABC transporter, permease protein**	***SP1649***	**0.6**	**2.09E-05**	**putative manganese ABC transporter, permease, psaC**
SP1588	**1.8**	**3.89E-06**	**oxidoreductase, pyridine nucleotide-disulfide, class I**	*SP1664*	0.7	7.90E-04	ylmF protein
SP1869	**1.7**	**3.36E-04**	**iron-compound ABC transporter, permease protein**	***SP2136***	**0.6**	**2.62E-05**	**choline binding protein PcpA**
SP1870	**2.5**	**7.42E-06**	**iron-compound ABC transporter, permease protein**				
SP1871	**1.9**	**3.85E-04**	**iron-compound ABC transporter, ATP-binding protein**				
SP1872	**1.8**	**5.11E-04**	**iron-compound ABC transporter, iron-compound-binding protein**				
SP2062	**1.6**	**7.32E-04**	**transcriptional regulator, MarR family**				
SP2063	**1.9**	**1.29E-04**	**LysM domain protein**				

E. List of genes differentially expressed upon **15 min.** treatment with **LL-37:**

up-regulated genes				down-regulated genes			
Gene ID	**Ratio**	**Bayes.p**	**NCBI annotation**	**Gene ID**	**Ratio**	**Bayes.p**	**NCBI annotation**

SP0001	1.4	5.73E-05	chromosomal replication initiator protein DnaA	*SP0004*	0.8	1.14E-04	GTP-binding protein
SP0055	1.3	3.16E-04	Hypothetical protein	*SP0008*	0.8	6.32E-04	Hypothetical protein
SP0056	1.3	9.36E-04	adenylosuccinate lyase	***SP0024***	**0.6**	**1.47E-07**	**conserved hypothetical protein**
SP0071	**1.5**	**6.03E-04**	**zinc metalloprotease ZmpC**	*SP0025*	0.8	3.97E-04	Hypothetical protein
SP0088	**1.5**	**3.08E-06**	**Hypothetical protein**	***SP0026***	**0.6**	**1.59E-06**	**Hypothetical protein**
SP0089	1.4	4.89E-04	Hypothetical protein	*SP0027*	0.8	2.71E-05	ribose-phosphate pyrophosphokinase
SP0157	**1.7**	**5.99E-08**	**Hypothetical protein**	*SP0032*	0.8	2.69E-04	DNA polymerase I
SP0185	1.3	1.99E-04	magnesium transporter, CorA family	*SP0034*	0.6	3.56E-06	membrane protein
SP0192	1.4	2.66E-05	conserved hypothetical protein	*SP0083*	0.8	2.37E-04	DNA-binding response regulator
SP0194	1.3	2.28E-04	conserved hypothetical protein	*SP0084*	0.7	1.55E-05	sensor histidine kinase
SP0197	1.5	2.94E-06	putative dihydrofolate synthetase	*SP0090*	0.7	9.96E-04	ABC transporter, permease protein
SP0200	1.3	2.98E-04	competence-induced protein Ccs4	*SP0107*	0.7	4.81E-04	LysM domain protein
SP0234	1.3	7.21E-04	ribosomal protein S13	***SP0117***	**0.5**	**4.76E-06**	**pneumococcal surface protein A**
SP0237	**1.7**	**5.03E-07**	**ribosomal protein L17**	*SP0202*	0.8	6.88E-04	anaerobic ribonucleoside-triphosphate reductase
SP0261	**1.5**	**8.59E-06**	**undecaprenyl diphosphate synthase**	***SP0238***	**0.6**	**6.26E-05**	**ACT domain protein**
SP0279	1.4	1.81E-04	conserved hypothetical protein	*SP0239*	0.7	1.24E-04	conserved hypothetical protein
SP0369	**1.8**	**2.06E-08**	**penicillin-binding protein 1A**	*SP0255*	0.7	2.13E-04	acetyltransferase, GNAT family
SP0370	**1.9**	**2.72E-07**	**recombination protein U**	*SP0268*	0.7	2.16E-04	putative alkaline amylopullulanase
SP0372	**1.5**	**3.00E-05**	**conserved hypothetical protein**	*SP0281*	0.7	7.96E-06	aminopeptidase C
SP0374	1.3	4.46E-04	hypothetical protein	***SP0282***	**0.3**	**1.84E-10**	**PTS system, mannose-specific IID component**
SP0385	**1.5**	**2.64E-06**	**conserved hypothetical protein**	***SP0283***	**0.2**	**9.42E-11**	**PTS system, mannose-specific IIC component**
SP0386	**1.5**	**1.55E-06**	**putative sensor histidine kinase**	***SP0284***	**0.2**	**1.37E-11**	**PTS system, mannose-specific IIAB components**
SP0402	1.4	1.40E-05	signal peptidase I	*SP0285*	0.7	2.08E-05	alcohol dehydrogenase, zinc-containing
SP0403	1.3	1.16E-04	ribonuclease HIII	***SP0287***	**0.5**	**1.94E-07**	**xanthine/uracil permease family protein**
SP0404	1.4	2.32E-05	hypothetical protein	*SP0289*	0.7	8.87E-04	dihydropteroate synthase
SP0405	**1.5**	**9.89E-06**	**conserved hypothetical protein**	*SP0290*	0.7	6.65E-06	dihydrofolate synthetase
SP0406	1.2	7.50E-04	MutS2 family protein	*SP0291*	0.7	6.09E-05	GTP cyclohydrolase I
SP0408	**1.9**	**1.20E-06**	**sodium:alanine symporter family protein**	*SP0292*	0.7	7.31E-04	bifunctional folate synthesis protein
SP0415	**1.5**	**1.30E-05**	**enoyl-CoA hydratase/isomerase family protein**	*SP0293*	0.7	7.63E-05	hypothetical protein
SP0416	1.3	3.65E-04	transcriptional regulator, MarR family	***SP0303***	**0.6**	**1.59E-04**	**6-phospho-beta-glucosidase**
SP0417	**1.5**	**6.68E-06**	**3-oxoacyl-(acyl-carrier-protein) synthase**	*SP0341*	0.8	9.71E-05	hypothetical protein

			III
SP0419	1.4	4.10E-05	enoyl-(acyl-carrier-protein) reductase
SP0424	1.3	2.28E-04	(3R)-hydroxymyristoyl-(acyl-carrier-protein) dehydratase, *fabZ*
SP0427	1.4	9.15E-06	acetyl-CoA carboxylase, carboxyl transferase, alpha subunit, accA
SP0457	1.3	2.79E-05	bacitracin resistance protein, *bacA*
SP0496	**1.5**	**2.39E-06**	**Na/Pi cotransporter II-related protein**
SP0499	1.4	8.94E-05	phosphoglycerate kinase
SP0501	**3.1**	**1.52E-10**	**transcriptional regulator, MerR family**
SP0502	**2.9**	**8.33E-11**	**glutamine synthetase, type I**
SP0503	**2.7**	**3.04E-07**	**hypothetical protein**
SP0504	**1.9**	**7.65E-07**	**hypothetical protein**
SP0524	**2.0**	**6.40E-07**	**BlpT protein, fusion**
SP0525	**1.6**	**6.11E-07**	**BlpS protein**
SP0526	1.4	6.28E-05	response regulator BlpR
SP0527	1.4	8.55E-05	putative sensor histidine kinase BlpH
SP0529	**1.7**	**8.10E-07**	**BlpB ABC transporter**
SP0530	**3.4**	**1.53E-09**	**BlpA ABC transporter**
SP0533	**1.5**	**3.41E-05**	**bacteriocin BlpK**
SP0545	**5.1**	**6.74E-12**	**immunity protein BlpY**
SP0546	**3.5**	**5.96E-09**	**BlpZ protein, fusion**
SP0547	**3.7**	**6.53E-10**	**conserved domain protein**
SP0552	1.3	9.69E-04	SP14.3 protein
SP0553	1.2	7.22E-04	N utilization substance protein A, *nusA*
SP0556	1.2	9.61E-04	translation initiation factor IF-2, *infB*
SP0557	**1.6**	**2.37E-05**	**ribosome-binding factor A, *rbfA***
SP0582	**1.6**	**3.96E-06**	**hypothetical protein**
SP0587	**1.6**	**4.17E-04**	**hypothetical protein**
SP0588	1.2	4.09E-04	polyribonucleotide nucleotidyltransferase
SP0589	1.3	1.19E-04	serine acetyltransferase, *cysE*
SP0590	1.3	1.03E-04	acetyltransferase, GNAT family

SP0366	**0.3**	**1.28E-11**	**oligopeptide ABC transporter AliA**
SP0413	0.7	1.03E-05	aspartate kinase
SP0445	0.7	1.73E-04	acetolactate synthase, large subunit, biosynthetic type,*ilvB*
SP0446	**0.6**	**1.08E-06**	**acetolactate synthase, small subunit, *ilvN***
SP0447	**0.6**	**4.01E-06**	**ketol-acid reductoisomerase, *ilvC***
SP0448	0.7	9.48E-05	hypothetical protein
SP0450	0.7	4.78E-05	threonine dehydratase, *ilvA*
SP0459	0.7	2.31E-06	formate acetyltransferase
SP0477	0.7	1.66E-04	6-phospho-beta-galactosidase, *lacG*-1
SP0479	0.8	0.000731	potassium uptake protein, Trk family
SP0516	**0.6**	**8.99E-07**	**heat shock protein GrpE**
SP0517	**0.6**	**8.46E-08**	**DnaK protein**
SP0518	0.7	1.69E-06	hypothetical protein
SP0519	0.8	5.08E-04	dnaJ protein
SP0565	0.7	5.87E-04	conserved domain protein
SP0566	0.7	1.25E-04	acetyltransferase, GNAT family
SP0568	0.7	2.55E-06	valyl-tRNA synthetase, *valS*
SP0577	**0.4**	**2.45E-06**	**PTS system, beta-glucosides-specific IIABC components**
SP0578	**0.3**	**1.38E-06**	**6-phospho-beta-glucosidase**
SP0579	0.7	8.16E-06	phenylalanyl-tRNA synthetase, alpha subunit, *pheS*
SP0581	0.8	3.65E-04	phenylalanyl-tRNA synthetase, beta subunit, *pheT*
SP0611	0.8	1.09E-04	single-stranded-DNA-specific exonuclease RecJ
SP0628	0.7	5.49E-05	HIT family protein
SP0637	0.8	3.79E-04	membrane protein
SP0638	0.8	1.06E-04	conserved hypothetical protein
SP0730	**0.5**	**7.37E-08**	**pyruvate oxidase**
SP0731	**0.5**	**8.12E-08**	**conserved domain protein**
SP0736	0.7	5.05E-04	mannose-6-phosphate isomerase, *manA*
SP0758	0.7	9.57E-05	PTS system, IIABC components

SP0591	1.3	3.64E-04	cysteinyl-tRNA synthetase
SP0592	1.4	3.76E-05	conserved hypothetical protein
SP0593	1.4	6.12E-06	leucine-rich protein
SP0617	**2.0**	**6.43E-08**	**conserved domain protein**
SP0742	**1.8**	**2.78E-07**	**conserved domain protein**
SP0748	1.3	4.73E-04	conserved hypothetical protein
SP0762	**1.7**	**2.06E-07**	**S-adenosylmethionine synthetase**
SP0783	**2.6**	**5.87E-09**	**conserved hypothetical protein**
SP0785	**4.1**	**6.34E-12**	**conserved hypothetical protein**
SP0786	**5.1**	**2.73E-12**	**ABC transporter, ATP-binding protein**
SP0787	**4.6**	**1.76E-11**	**conserved hypothetical protein**
SP0789	**1.6**	**8.25E-06**	**conserved hypothetical protein**
SP0790	**1.5**	**9.27E-06**	**conserved domain protein**
SP0798	**2.5**	**2.80E-10**	**DNA-binding response regulator CiaR**
SP0799	**2.4**	**4.81E-09**	**sensor histidine kinase CiaH**
SP0800	**1.5**	**1.41E-05**	**hypothetical protein**
SP0805	**1.5**	**2.10E-06**	**hydrolase, haloacid dehalogenase-like family**
SP0829	1.3	1.34E-04	Phosphopentomutase, *deoB*
SP0846	1.3	9.65E-04	sugar ABC transporter, ATP-binding protein
SP0851	1.4	3.10E-04	conserved hypothetical protein
SP0861	**1.6**	**1.60E-04**	**hypothetical protein**
SP0875	**1.7**	**3.98E-04**	**lactose phosphotransferase system repressor**
SP0876	**1.8**	**9.06E-04**	**putative 1-phosphofructokinase**
SP0877	**2.3**	**5.20E-06**	**SpoE family protein**
SP0878	**1.5**	**1.35E-06**	**hypothetical protein**
SP0895	1.3	2.86E-05	putative type I restriction-modification system, R subunit
SP0904	1.3	8.86E-05	conserved hypothetical protein
SP0770	0.7	1.67E-04	ABC transporter, ATP-binding protein
SP0775	0.7	7.38E-05	ribosomal protein S16
SP0845	**0.5**	**2.03E-07**	**lipoprotein**
SP0887	0.7	1.76E-05	putative type I restriction-modification system, S subunit
SP0916	**0.6**	**1.01E-04**	**lysine decarboxylase**
SP0918	**0.6**	**5.49E-06**	**spermidine synthase, *speE***
SP0919	**0.5**	**1.21E-07**	**conserved hypothetical protein**
SP0920	**0.5**	**9.91E-09**	**carboxynorspermidine decarboxylase**
SP0921	**0.5**	**1.98E-08**	**conserved hypothetical protein**
SP0922	**0.5**	**1.09E-05**	**carbon-nitrogen hydrolase family protein**
SP1013	0.7	4.82E-05	aspartate-semialdehyde dehydrogenase
SP1032	**0.5**	**8.37E-09**	**iron-compound ABC transporter, iron compound-binding protein**
SP1033	0.7	2.11E-04	iron-compound ABC transporter, permease protein
SP1034	**0.6**	**2.13E-07**	**iron-compound ABC transporter, permease protein**
SP1035	**0.5**	**7.59E-09**	**iron-compound ABC transporter, ATP-binding protein**
SP1036	**0.6**	**5.52E-04**	**hypothetical protein**
SP1037	0.8	2.89E-04	putative type II restriction endonuclease
SP1038	0.8	2.63E-04	hypothetical protein
SP1039	**0.6**	**5.65E-06**	**hypothetical protein**
SP1040	**0.6**	**1.23E-06**	**site-specific recombinase, resolvase family**
SP1041	**0.6**	**1.31E-05**	**hypothetical protein**
SP1069	0.7	9.57E-05	conserved hypothetical protein
SP1070	0.7	2.68E-04	conserved hypothetical protein
SP1114	0.8	6.85E-05	ABC transporter, ATP-binding protein
SP1119	**0.6**	**1.09E-05**	**glyceraldehyde-3-phosphate dehydrogenase, NADP-dependent, *gapN***
SP1127	0.7	3.88E-04	hypothetical protein
SP1128	0.7	7.45E-05	enolase

SP0905	1.3	2.95E-04	conserved hypothetical protein
SP0910	1.3	2.26E-04	conserved hypothetical protein
SP0913	**1.9**	**3.39E-05**	**putative ABC transporter, permease protein**
SP0925	**1.5**	**1.08E-04**	**conserved hypothetical protein**
SP0928	1.2	9.44E-04	signal peptidase II, *lspA*
SP0956	1.4	8.82E-04	hypothetical protein
SP0957	**1.9**	**3.00E-07**	**ABC transporter, ATP-binding protein**
SP0958	**2.0**	**3.52E-07**	**hypothetical protein**
SP0974	1.4	9.61E-04	putative preprotein translocase, SecG subunit
SP0975	**1.5**	**1.41E-05**	**exoribonuclease, VacB/Rnb family**
SP0976	**1.5**	**5.13E-06**	**SsrA-binding protein"**
SP0977	**1.6**	**4.65E-06**	**tellurite resistance protein TehB**
SP0981	1.3	1.88E-04	putative protease maturation protein
SP0987	1.3	2.31E-04	hypothetical protein
SP1023	1.3	5.22E-04	acetyltransferase, GNAT family
SP1024	1.2	8.22E-04	serine hydroxymethyltransferase, *glyA*
SP1027	**3.3**	**8.31E-11**	**conserved hypothetical protein**
SP1029	**1.7**	**9.81E-08**	**RNA methyltransferase, TrmA family**
SP1075	**1.7**	**2.37E-08**	**glycosyl transferase CpoA**
SP1076	1.4	1.44E-05	glycosyl transferase, group 1
SP1077	**1.6**	**1.07E-06**	**conserved domain protein**
SP1082	1.2	8.51E-04	acetyltransferase, GNAT family
SP1093	1.3	7.51E-04	hypothetical protein
SP1148	1.5	1.88E-05	IS630-Spn1, transposase Orf2
SP1149	1.4	2.97E-05	IS630-Spn1, transposase Orf1
SP1151	1.4	8.54E-05	exonuclease RexB
SP1170	0.7	4.48E-05	hypothetical protein
SP1171	0.7	4.22E-05	hydrolase, haloacid dehalogenase-like family
SP1175	0.7	2.83E-04	conserved domain protein
SP1185	**0.6**	**1.44E-05**	**PTS system, lactose-specific IIBC components, *lacE*-2**
SP1186	**0.5**	**1.85E-05**	**PTS system, lactose-specific IIA component, *lacF*-2**
SP1187	**0.5**	**2.75E-06**	**transcription antiterminator LacT**
SP1190	0.7	1.55E-04	tagatose 1,6-diphosphate aldolase, *lacD*
SP1191	0.7	7.79E-04	tagatose-6-phosphate kinase, *lacC*
SP1192	0.7	1.86E-05	galactose-6-phosphate isomerase, LacB subunit, *lacB*
SP1193	0.7	2.98E-04	galactose-6-phosphate isomerase, LacA subunit, *lacA*
SP1212	0.7	1.97E-05	tRNA pseudouridine synthase B, *truB*
SP1263	**0.6**	**7.02E-04**	**DNA topoisomerase I, *topA***
SP1298	**0.6**	**1.06E-08**	**DHH subfamily 1 protein**
SP1339	0.7	1.88E-04	hypothetical protein
SP1345	0.7	2.59E-04	hypothetical protein
SP1383	0.8	3.04E-04	alanyl-tRNA synthetase, *alaS*
SP1395	0.7	2.98E-05	putative phosphate transport system regulatory protein PhoU
SP1396	0.8	1.57E-04	putative phosphate ABC transporter, ATP-binding protein
SP1397	0.8	9.47E-04	putative phosphate ABC transporter, ATP-binding protein
SP1398	0.8	5.64E-04	putative phosphate ABC transporter, permease protein
SP1445	**0.6**	**1.94E-07**	**GMP synthase, *guaA***
SP1455	0.7	2.75E-04	hypothetical protein
SP1461	0.8	7.33E-04	amino acid ABC transporter, permease protein
SP1462	0.7	8.06E-06	conserved hypothetical protein
SP1463	**0.6**	**5.93E-07**	**methylated-DNA--protein-cysteine S-methyltransferase**
SP1464	**0.6**	**1.05E-06**	**acetyltransferase, GNAT family**

SP1161	1.4	9.15E-04	putative acetoin dehydrogenase complex, E3 component, dihydrolipoamide dehydrogenase	*SP1468*	0.7	9.65E-05	pyridoxine biosynthesis protein
SP1162	1.3	7.77E-04	putative acetoin dehydrogenase complex, E2 component, dihydrolipoamide acetyltransferase	*SP1469*	0.8	5.21E-04	NADH oxidase
SP1229	1.3	2.74E-04	formate--tetrahydrofolate ligase	*SP1491*	0.7	1.75E-05	putative glycerol uptake facilitator protein
SP1241	**2.4**	**2.27E-09**	**amino acid ABC transporter, amino acid-binding protein/permease protein**	*SP1500*	0.7	1.42E-04	amino acid ABC transporter, amino acid-binding protein
SP1242	**2.7**	**1.23E-09**	**amino acid ABC transporter, ATP-binding protein**	***SP1507***	**0.6**	**4.79E-06**	**ATP synthase F1, epsilon subunit, *atpC***
SP1243	**1.5**	**3.09E-06**	**glucose-6-phosphate 1-dehydrogenase, *zwf***	***SP1508***	**0.6**	**4.11E-07**	**ATP synthase F1, beta subunit, *atpD***
SP1260	1.3	3.36E-04	copper homeostasis protein CutC	***SP1509***	**0.6**	**2.36E-08**	**ATP synthase F1, gamma subunit, *atpG***
SP1261	1.3	7.39E-04	conserved hypothetical protein	***SP1510***	**0.6**	**3.47E-08**	**ATP synthase F1, alpha subunit, *atpA***
SP1283	**1.5**	**2.81E-06**	**heat shock protein HtpX**	***SP1511***	**0.6**	**1.31E-07**	**ATP synthase F1, delta subunit, *atpH***
SP1284	1.3	4.00E-04	lemA protein	***SP1512***	**0.6**	**5.14E-08**	**ATP synthase F0, B subunit, *atpF***
SP1299	1.3	8.50E-04	ribosomal protein L31, *rpmE*	***SP1513***	**0.6**	**1.44E-07**	**ATP synthase F0, A subunit, *atpB***
SP1305	**1.8**	**1.13E-04**	**hypothetical protein**	*SP1517*	0.8	5.46E-04	transcription elongation factor GreA
SP1306	**1.7**	**3.03E-07**	**NADP-specific glutamate dehydrogenase, *gdhA***	*SP1533*	0.8	7.19E-05	conserved domain protein
SP1315	1.3	1.20E-04	v-type sodium ATP synthase, subunit D	*SP1534*	0.8	5.84E-05	inorganic pyrophosphatase, manganese-dependent, ppaC
SP1378	1.3	7.95E-04	conserved hypothetical protein	*SP1540*	0.8	2.83E-04	single-strand binding protein
SP1380	1.3	2.64E-04	hypothetical protein	*SP1548*	0.7	2.81E-06	hypothetical protein
SP1381	**1.5**	**1.08E-04**	**ABC transporter, ATP-binding protein**	***SP1549***	**0.6**	**1.21E-05**	**polypeptide deformylase, *def*-2**
SP1405	1.4	2.67E-05	conserved hypothetical protein	*SP1574*	0.8	2.65E-04	triosephosphate isomerase
SP1422	1.4	5.19E-04	hypothetical protein	*SP1576*	0.8	6.73E-04	homoserine O-succinyltransferase, *metA*
SP1424	1.4	7.12E-04	hypothetical protein	***SP1578***	**0.6**	**3.23E-04**	**putative methyltransferase**
SP1479	1.3	1.71E-04	peptidoglycan N-acetylglucosamine deacetylase A, *pgdA*	***SP1580***	**0.4**	**8.68E-11**	**sugar ABC transporter, ATP-binding protein, *msmK***
SP1529	1.2	5.91E-04	putative polysaccharide biosynthesis protein	*SP1605*	0.7	3.44E-06	ferredoxin
SP1546	**1.7**	**3.42E-07**	**conserved domain protein**	*SP1607*	0.8	7.62E-04	UDP-glucose 4-epimerase, *galE*-1
SP1560	1.4	6.45E-05	conserved hypothetical protein	*SP1644*	0.7	3.68E-04	conserved hypothetical protein
SP1561	**1.5**	**3.64E-06**	**conserved hypothetical protein**	*SP1645*	0.7	2.36E-06	GTP pyrophosphokinase, *relA*
SP1562	1.3	4.88E-04	hypothetical protein	*SP1647*	0.7	6.36E-06	endopeptidase O, pepO
SP1623	1.3	3.01E-04	cation-transporting ATPase, E1-E2 family	*SP1659*	0.8	1.15E-04	isoleucyl-tRNA synthetase, *ileS*
SP1625	1.4	1.83E-04	putative cadmium resistance transporter	*SP1684*	0.7	1.64E-04	PTS system, IIBC components

SP1636	1.4	2.17E-05	Rrf2 family protein
SP1640	**1.6**	**3.03E-06**	**hypothetical protein**
SP1641	1.4	1.02E-04	conserved domain protein
SP1668	1.4	2.71E-05	hypothetical protein
SP1669	1.4	1.46E-05	MutT/nudix family protein
SP1670	1.4	1.85E-05	UDP-N-acetylmuramoylalanyl-D-glutamyl-2,6-diaminopimelate--D-alanyl-D-alanyl ligase, *murF*
SP1671	**1.5**	**4.46E-06**	**D-alanine--D-alanine ligase, *ddlA***
SP1674	1.3	5.73E-04	putative phosphosugar-binding transcriptional regulator
SP1695	**2.9**	**6.32E-10**	**putative acetyl xylan esterase**
SP1696	**2.8**	**2.01E-09**	**hypothetical protein**
SP1714	**7.2**	**1.63E-12**	**transcriptional regulator, GntR family**
SP1715	**11.4**	**3.27E-13**	**ABC transporter, ATP-binding protein**
SP1734	1.3	3.07E-04	rRNA methyltransferase RsmB
SP1750	1.3	1.31E-04	conserved hypothetical protein
SP1752	1.4	1.99E-05	putative mechanosensitive ion channel
SP1754	1.4	4.47E-05	conserved hypothetical protein
SP1774	1.4	1.92E-05	putative transcriptional regulator
SP1776	**1.5**	**3.63E-04**	**thioredoxin**
SP1786	**1.5**	**4.65E-06**	**conserved hypothetical protein**
SP1787	**1.5**	**6.31E-05**	**hypothetical protein**
SP1860	1.4	1.21E-04	choline transporter, *proWX*
SP1903	**1.5**	**1.01E-06**	**conserved hypothetical protein**
SP1923	1.4	1.29E-04	pneumolysin
SP1924	1.4	2.47E-04	hypothetical protein
SP1925	**1.5**	**2.63E-04**	**hypothetical protein**
SP1926	**1.7**	**2.41E-06**	**hypothetical protein**

SP1685	0.7	4.44E-05	conserved hypothetical protein
SP1709	**0.6**	**4.14E-08**	**phosphoglycerate dehydrogenase-related protein**
SP1710	0.7	4.85E-05	nitroreductase family protein
SP1711	0.7	2.38E-06	primosomal protein DnaI
SP1712	0.7	5.36E-06	hypothetical protein
SP1713	0.7	5.66E-05	conserved hypothetical protein
SP1716	0.7	5.18E-05	conserved hypothetical protein
SP1717	**0.5**	**5.03E-07**	**ABC transporter, ATP-binding protein**
SP1778	0.7	5.53E-06	aquaporin
SP1811	**0.4**	**4.06E-08**	**tryptophan synthase, alpha subunit, *trpA***
SP1812	**0.5**	**3.48E-06**	**tryptophan synthase, beta subunit, *trpB***
SP1813	**0.6**	**5.79E-06**	**N-(5'-phosphoribosyl)-anthranilate isomerase, *trpF***
SP1815	**0.6**	**3.52E-05**	**anthranilate phosphoribosyltransferase, *trpD***
SP1816	**0.5**	**2.01E-06**	**anthranilate synthase component II, *trpG***
SP1817	**0.5**	**4.71E-05**	**anthranilate synthase component I, *trpE***
SP1826	0.7	2.63E-04	ABC transporter, substrate-binding protein
SP1888	0.8	3.17E-04	oligopeptide ABC transporter, ATP-binding protein AmiE
SP1891	0.7	2.04E-06	oligopeptide ABC transporter, oligopeptide-binding protein AmiA
SP1906	0.7	2.53E-05	chaperonin, 60 kDa, *groEL*
SP1907	0.7	1.46E-04	chaperonin, 10 kDa, *groES*
SP1915	0.7	8.18E-04	hypothetical protein
SP1928	0.8	1.94E-04	IS1381, transposase OrfB
SP1942	0.8	1.45E-04	putative transcriptional regulator
SP1943	0.8	1.06E-04	acetyltransferase, GNAT family
SP1960	0.8	7.84E-05	DNA-directed RNA polymerase, beta' subunit
SP1961	0.7	2.45E-05	DNA-directed RNA polymerase, beta subunit, *rpoB*

			membrane protein
SP1972	1.3	6.41E-05	
SP2013	**1.5**	**6.47E-06**	**conserved hypothetical protein**
SP2016	**1.9**	**3.96E-06**	**nicotinate-nucleotide pyrophosphorylase, nadC**
SP2020	1.3	8.61E-04	transcriptional regulator, GntR family
SP2106	**3.2**	**6.99E-12**	**glycogen phosphorylase family protein**
SP2107	**3.4**	**1.76E-12**	**4-alpha-glucanotransferase**
SP2151	1.3	4.04E-04	carbamate kinase, *arcC*
SP2152	**1.6**	**1.70E-05**	**conserved hypothetical protein**
SP2173	**1.6**	**8.93E-07**	**dltD protein**
SP2174	**1.6**	**3.60E-05**	**D-alanyl carrier protein, *dltC***
SP2175	**1.6**	**9.92E-08**	**dltB protein**
SP2176	**1.8**	**1.62E-08**	**D-alanine-activating enzyme, *dltA***
SP2204	1.3	8.76E-04	ribosomal protein L9, *rplI*
SP2205	**1.5**	**5.99E-07**	**DHH subfamily 1 protein**
SP2225	1.2	9.61E-04	conserved hypothetical protein
SP2238	**1.9**	**6.58E-06**	**conserved hypothetical protein**
SP2239	**3.0**	**6.94E-09**	**serine protease**
SP2240	**3.5**	**1.35E-11**	**spspoJ protein**

SP1968	0.8	4.68E-05	phosphopantetheine adenylyltransferase, *coaD*
SP1970	**0.3**	**2.32E-11**	**aspartate--ammonia ligase, *asnA***
SP1994	0.8	4.05E-05	aminotransferase, class I
SP1997	0.7	9.73E-06	Cof family protein
SP2026	**0.6**	**1.71E-04**	**alcohol dehydrogenase, iron-containing**
SP2030	0.7	7.97E-05	transketolase
SP2040	0.7	3.72E-05	putative jag protein
SP2041	0.7	5.44E-05	SpoIIIJ family protein
SP2042	0.8	4.32E-04	ribonuclease P protein component, *rnpA*
SP2044	0.7	8.25E-07	acetate kinase, *ackA*
SP2054	0.7	1.41E-04	conserved hypothetical protein
SP2055	0.7	9.15E-06	alcohol dehydrogenase, zinc-containing
SP2058	**0.6**	**7.13E-05**	**queuine tRNA-ribosyltransferase**
SP2065	0.8	1.98E-04	MATE efflux family protein
SP2069	0.7	1.39E-05	glutamyl-tRNA synthetase, *gltX*
SP2078	**0.6**	**5.79E-08**	**arginyl-tRNA synthetase, *argS***
SP2081	0.8	4.71E-05	conserved hypothetical protein
SP2108	**0.6**	**4.15E-07**	**maltose/maltodextrin ABC transporter, *malX***
SP2109	**0.6**	**7.41E-06**	**maltodextrin ABC transporter, permease protein, *malC***
SP2134	**0.6**	**2.53E-07**	**ribosomal protein L32, *rpmF***
SP2135	**0.6**	**3.62E-05**	**ribosomal protein L33, *rpmG*-3**
SP2144	0.7	8.16E-04	conserved hypothetical protein
SP2185	**0.6**	**2.51E-05**	**hypothetical protein**
SP2186	**0.5**	**1.45E-06**	**glycerol kinase**
SP2187	0.8	7.59E-04	conserved domain protein
SP2188	0.7	3.32E-07	chaperonin, 33 kDa, *hslO*
SP2189	0.7	4.26E-05	putative TIM-barrel protein, NifR3 family
SP2214	0.7	1.83E-05	translation elongation factor Ts
SP2215	0.7	1.91E-05	ribosomal protein S2, *rpsB*
SP2216	0.7	2.12E-04	secreted 45 kd protein, *usp45*
SP2218	0.8	8.03E-05	rod shape-determining protein MreC
SP2230	0.7	7.99E-05	ABC transporter, ATP-binding protein
SP2233	**0.3**	**1.52E-06**	**hypothetical protein**

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F. List of genes differentially expressed upon **30 min.** treatment with **LL-37**:

up-regulated genes				down-regulated genes			
Gene ID	**Ratio**	**Bayes.p**	**NCBI annotation**	**Gene ID**	**Ratio**	**Bayes.p**	**NCBI annotation**
SP0057	1.4	4.35E-04	beta-N-acetylhexosaminidase	***SP0024***	**0.5**	**3.10E-06**	**Conserved hypothetical protein**
SP0071	**2.2**	**6.27E-05**	**zinc metalloprotease ZmpC**	***SP0025***	**0.6**	**4.78E-05**	**Hypothetical protein**
SP0088	**1.8**	**5.71E-07**	**hypothetical protein**	***SP0026***	**0.5**	**6.92E-05**	**Hypothetical protein**
SP0141	**1.7**	**1.28E-05**	**transcriptional regulator**	***SP0034***	**0.5**	**1.37E-06**	**membrane protein**
SP0143	**1.5**	**3.87E-05**	**conserved domain protein**	***SP0117***	**0.6**	**3.55E-04**	**pneumococcal surface protein A**
SP0144	**1.7**	**1.28E-05**	**hypothetical protein**	*SP0239*	0.7	9.64E-04	conserved hypothetical protein
SP0145	**1.5**	**2.10E-05**	**conserved hypothetical protein**	***SP0281***	**0.5**	**2.60E-06**	**aminopeptidase C, *pepC***
SP0151	1.4	2.06E-04	ABC transporter, ATP-binding protein	***SP0282***	**0.3**	**4.30E-07**	**PTS system, mannose-specific IID component**
SP0157	**2.0**	**1.09E-07**	**hypothetical protein**	***SP0283***	**0.3**	**1.52E-07**	**PTS system, mannose-specific IIC component, *manM***
SP0178	**1.5**	**5.20E-05**	**riboflavin biosynthesis protein RibD**	***SP0284***	**0.2**	**2.54E-08**	**PTS system, mannose-specific IIAB components, *manL***
SP0184	**1.5**	**5.74E-06**	**hypothetical protein**	***SP0285***	**0.6**	**3.24E-05**	**alcohol dehydrogenase, zinc-containing**
SP0185	**1.7**	**2.55E-05**	**magnesium transporter, CorA family**	*SP0286*	0.7	3.40E-04	Cof family protein
SP0189	**1.7**	**1.95E-06**	**conserved hypothetical protein**	***SP0287***	**0.6**	**4.48E-04**	**xanthine/uracil permease family protein**
SP0190	1.4	9.20E-04	hypothetical protein	*SP0289*	0.7	1.69E-04	dihydropteroate synthase
SP0191	1.4	3.22E-04	hypothetical protein	*SP0290*	0.7	2.68E-04	dihydrofolate synthetase, *folC*
SP0196	**1.5**	**5.50E-04**	**hypothetical protein**	*SP0291*	0.7	5.74E-04	GTP cyclohydrolase I, *folE*
SP0197	**1.5**	**6.42E-05**	**putative dihydrofolate synthetase**	*SP0292*	0.7	2.05E-04	bifunctional folate synthesis protein, *sulD*
SP0198	1.3	9.14E-04	hypothetical protein	***SP0293***	**0.6**	**1.28E-05**	**hypothetical protein**
SP0199	**1.5**	**2.01E-04**	**cardiolipin synthetase**	***SP0366***	**0.3**	**1.13E-09**	**oligopeptide ABC transporter oligopeptide-binding protein AliA**
SP0200	**1.6**	**3.40E-06**	**competence-induced protein Ccs4**	***SP0368***	**0.6**	**9.29E-04**	**cell wall surface anchor family protein**
SP0233	**1.5**	**1.27E-04**	**ribosomal protein L36**	***SP0411***	**0.6**	**3.65E-06**	**seryl-tRNA synthetase, *serS***
SP0234	**1.6**	**2.53E-06**	**ribosomal protein S13**	*SP0413*	0.7	1.30E-04	aspartate kinase
SP0235	**1.5**	**1.91E-05**	**ribosomal protein S11**	*SP0435*	0.7	6.22E-04	translation elongation factor P
SP0236	**1.5**	**3.63E-05**	**DNA-directed RNA polymerase, alpha subunit, *rpoA***	***SP0445***	**0.6**	**1.35E-04**	**acetolactate synthase, large subunit, biosynthetic type, i*lvB***
SP0237	**2.9**	**2.30E-07**	**ribosomal protein L17**	***SP0446***	**0.5**	**3.24E-08**	**acetolactate synthase, small subunit, ilvN**
SP0261	**1.7**	**4.50E-06**	**undecaprenyl diphosphate synthase, *uupS***	***SP0447***	**0.5**	**8.68E-08**	**ketol-acid reductoisomerase, *ilvC***

SP0262	**1.7**	**1.25E-06**	**phosphatidate cytidylyltransferase**
SP0263	1.4	5.45E-04	eep protein
SP0264	1.4	2.97E-04	prolyl-tRNA synthetase, *proS*
SP0275	**1.6**	**1.63E-05**	**conserved hypothetical protein**
SP0276	**1.5**	**3.23E-05**	**conserved hypothetical protein**
SP0277	**1.5**	**1.06E-04**	**hypothetical protein**
SP0278	1.4	7.66E-04	aminopeptidase PepS
SP0331	**1.9**	**3.81E-05**	**hypothetical protein; this gene contains a frame shift**
SP0333	**1.7**	**1.39E-05**	**putative transcriptional regulator**
SP0346	**1.5**	**5.64E-05**	**capsular polysaccharide biosynthesis protein Cps4A**
SP0347	**1.7**	**2.49E-05**	**capsular polysaccharide biosynthesis protein Cps4B**
SP0369	**2.2**	**2.47E-06**	**penicillin-binding protein 1A, *pbp1A***
SP0370	**2.2**	**4.25E-06**	**recombination protein U, *recU***
SP0371	1.4	5.28E-04	conserved hypothetical protein
SP0372	**1.5**	**1.56E-05**	**conserved hypothetical protein**
SP0385	**1.6**	**2.34E-04**	**conserved hypothetical protein**
SP0386	**1.7**	**1.06E-04**	**putative sensor histidine kinase**
SP0387	**1.5**	**3.08E-04**	**DNA-binding response regulator**
SP0402	**1.5**	**1.30E-04**	**signal peptidase I**
SP0403	**1.5**	**2.85E-05**	**ribonuclease HIII, *rnhC***
SP0404	**1.6**	**1.74E-04**	**hypothetical protein**
SP0405	**1.6**	**1.26E-04**	**conserved hypothetical protein**
SP0408	**2.1**	**2.38E-05**	**sodium:alanine symporter family protein**
SP0409	**1.5**	**3.01E-04**	**conserved hypothetical protein**
SP0415	**1.9**	**1.27E-06**	**enoyl-CoA hydratase/isomerase family protein**
SP0416	**1.6**	**2.11E-06**	**transcriptional regulator, MarR family**
SP0417	**1.8**	**6.64E-07**	**3-oxoacyl-(acyl-carrier-protein) synthase III, *fabH***
SP0419	**1.8**	**9.50E-07**	**enoyl-(acyl-carrier-protein) reductase,**
SP0448	**0.5**	**2.03E-06**	**hypothetical protein**
SP0449	**0.6**	**3.22E-04**	**hypothetical protein**
SP0450	0.7	5.78E-04	threonine dehydratase
SP0453	0.7	7.31E-04	amino acid ABC transporter, amino acid-binding protein/permease protein
SP0479	**0.6**	**1.71E-05**	**potassium uptake protein, Trk family**
SP0480	0.7	2.77E-04	potassium uptake protein, Trk family
SP0516	**0.6**	**3.04E-04**	**heat shock protein GrpE**
SP0517	**0.5**	**6.00E-07**	**DnaK protein**
SP0518	**0.6**	**9.03E-06**	**hypothetical protein**
SP0519	**0.6**	**2.86E-05**	**dnaJ protein**
SP0565	**0.6**	**2.38E-05**	**conserved domain protein**
SP0566	**0.6**	**1.57E-04**	**acetyltransferase, GNAT family**
SP0568	**0.6**	**9.92E-06**	**valyl-tRNA synthetase, *valS***
SP0577	**0.2**	**1.43E-11**	**PTS system, beta-glucosides-specific IIABC**
SP0578	**0.2**	**1.12E-11**	**6-phospho-beta-glucosidase, *bglA*-2**
SP0579	**0.5**	**1.22E-07**	**phenylalanyl-tRNA synthetase, alpha subunit, *pheS***
SP0580	**0.5**	**1.91E-06**	**acetyltransferase, GNAT family**
SP0581	**0.5**	**9.45E-07**	**phenylalanyl-tRNA synthetase, beta subunit**
SP0605	**0.6**	**1.76E-04**	**fructose-bisphosphate aldolase**
SP0615	0.7	1.59E-04	beta-lactam resistance factor, *fibA*
SP0616	0.7	1.35E-04	beta-lactam resistance factor, *fibB*
SP0730	**0.5**	**3.64E-06**	**pyruvate oxidase, *spxB***
SP0731	**0.6**	**2.07E-06**	**conserved domain protein**
SP0770	0.7	6.53E-04	ABC transporter, ATP-binding protein
SP0771	**0.6**	**2.78E-05**	**peptidyl-prolyl cis-trans isomerase, cyclophilin-type**
SP0775	**0.6**	**5.04E-05**	**ribosomal protein S16, *rpsP***
SP0845	**0.4**	**4.40E-06**	**lipoprotein**
SP0856	0.7	1.12E-04	branched-chain amino acid

			fabK				aminotransferase, *ilvE*
SP0420	**1.6**	**1.30E-05**	**malonyl CoA-acyl carrier protein transacylase, *fabD***	***SP0857***	**0.6**	**7.10E-04**	**putative membrane protein**
SP0421	**1.6**	**3.38E-05**	**3-oxoacyl-[acyl-carrier protein] reductase, *fabG***	***SP0858***	**0.6**	**2.95E-04**	**membrane protein**
SP0422	1.4	1.12E-04	3-oxoacyl-(acyl-carrier-protein) synthase II, *fabF*	*SP0862*	0.7	5.33E-04	ribosomal protein S1, *rpsA*
SP0423	**1.5**	**5.41E-05**	**acetyl-CoA carboxylase, bitoin carboxyl carrier protein, *accB***	***SP0887***	**0.6**	**1.29E-05**	**putative type I restriction-modification system, S subunit**
SP0424	**1.6**	**1.45E-05**	**(3R)-hydroxymyristoyl-(acyl-carrier-protein) dehydratase, *fabZ***	***SP1004***	**0.6**	**1.24E-04**	**conserved hypothetical protein**
SP0425	**1.6**	**1.07E-05**	**acetyl-CoA carboxylase, biotin carboxylase. *accC***	***SP1008***	**0.6**	**9.34E-06**	**peptidase t, *pepT***
SP0426	**1.6**	**1.69E-05**	**acetyl-CoA carboxylase, carboxyl transferase, beta subunit, *accD***	*SP1013*	0.7	1.24E-04	aspartate-semialdehyde dehydrogenase
SP0427	**2.1**	**8.26E-07**	**acetyl-CoA carboxylase, carboxyl transferase, alpha subunit, *accA***	***SP1032***	**0.6**	**3.24E-05**	**iron-compound ABC transporter, iron compound-binding protein**
SP0429	**1.7**	**1.36E-04**	**hypothetical protein**	*SP1034*	0.7	4.24E-04	iron-compound ABC transporter, permease protein
SP0430	**1.9**	**3.87E-05**	**hypothetical protein**	***SP1035***	**0.6**	**7.60E-04**	**iron-compound ABC transporter, ATP-binding protein**
SP0431	**1.6**	**2.66E-04**	**conserved domain protein**	***SP1069***	**0.6**	**1.68E-04**	**conserved hypothetical protein**
SP0484	1.4	1.15E-04	cobalt transport protein	***SP1070***	**0.6**	**4.65E-05**	**conserved hypothetical protein**
SP0489	**1.5**	**6.77E-05**	**PAP2 family protein**	***SP1089***	**0.6**	**2.59E-06**	**glutamine amidotransferase, class I**
SP0490	**1.5**	**2.02E-04**	**hypothetical protein**	***SP1090***	**0.6**	**1.47E-06**	**conserved hypothetical protein**
SP0491	**1.5**	**7.54E-04**	**hypothetical protein**	*SP1114*	0.7	2.72E-04	ABC transporter, ATP-binding protein
SP0492	**1.6**	**4.95E-05**	**conserved domain protein**	***SP1119***	**0.5**	**1.76E-05**	**glyceraldehyde-3-phosphate dehydrogenase, NADP-dependent**
SP0496	**1.6**	**8.35E-05**	**Na/Pi cotransporter II-related protein**	***SP1128***	**0.6**	**3.75E-04**	**enolase**
SP0501	**2.1**	**1.77E-05**	**transcriptional regulator, MerR family**	*SP1167*	0.7	8.55E-04	dihydroorotase, multifunctional complex type, *pyrC*
SP0502	**2.1**	**4.40E-06**	**glutamine synthetase, type I**	***SP1170***	**0.5**	**6.74E-06**	**hypothetical protein**
SP0503	**1.7**	**9.69E-04**	**hypothetical protein**	***SP1171***	**0.5**	**1.20E-06**	**hydrolase, haloacid dehalogenase-like family**
SP0504	**2.0**	**2.41E-06**	**hypothetical protein**	***SP1175***	**0.5**	**2.17E-07**	**conserved domain protein**
SP0524	**1.8**	**1.33E-05**	**BlpT protein, fusion**	*SP1182*	0.7	6.59E-06	lactose phosphotransferase system repressor, *lacR*-2
SP0525	**1.8**	**2.25E-06**	**BlpS protein**	***SP1185***	**0.6**	**1.87E-05**	**PTS system, lactose-specific IIBC**

SP0526	**1.6**	**2.50E-06**	**response regulator BlpR**
SP0527	**1.8**	**2.47E-05**	**putative sensor histidine kinase BlpH**
SP0528	**1.8**	**2.75E-04**	**peptide pheromone BlpC**
SP0529	**2.2**	**5.50E-09**	**BlpB ABC transporter**
SP0530	**3.6**	**2.25E-09**	**BlpA ABC transporter**
SP0533	**1.5**	**1.50E-05**	**bacteriocin BlpK**
SP0545	**5.9**	**2.80E-11**	**immunity protein BlpY**
SP0546	**3.8**	**4.27E-10**	**BlpZ protein, fusion**
SP0547	**4.0**	**1.87E-08**	**conserved domain protein**
SP0557	**1.8**	**5.88E-05**	**ribosome-binding factor A, *rbfA***
SP0582	**2.2**	**6.33E-06**	**hypothetical protein**
SP0589	1.3	8.94E-04	serine acetyltransferase, *cysE*
SP0592	**1.5**	**1.80E-05**	**conserved hypothetical protein**
SP0593	**1.6**	**7.21E-06**	**leucine-rich protein**
SP0617	**1.5**	**1.40E-04**	**conserved domain protein**
SP0641	**1.5**	**7.95E-04**	**serine protease, subtilase family**
SP0655	1.3	4.70E-04	transporter, monovalent cation:proton antiporter-2 (CPA2) family
SP0656	1.3	2.36E-04	putative ribonuclease BN
SP0657	1.4	4.65E-05	cytochrome c-type biogenesis protein CcdA
SP0742	**1.8**	**5.88E-05**	**conserved hypothetical protein**
SP0748	1.4	3.92E-04	conserved hypothetical protein
SP0762	**1.7**	**3.31E-06**	**S-adenosylmethionine synthetase**
SP0783	**2.3**	**8.25E-07**	**conserved hypothetical protein**
SP0785	**5.5**	**3.64E-12**	**conserved hypothetical protein**
SP0786	**5.0**	**1.34E-07**	**ABC transporter, ATP-binding protein**
SP0787	**6.1**	**1.14E-09**	**conserved hypothetical protein**
SP0789	**1.6**	**1.94E-05**	**conserved hypothetical protein**
SP0790	**1.5**	**1.25E-05**	**conserved hypothetical protein**
SP0798	**2.1**	**2.78E-04**	**DNA-binding response regulator CiaR**
			components, *lacE*-2
SP1187	**0.5**	**2.70E-06**	**transcription antiterminator LacT**
SP1190	0.7	4.65E-04	tagatose 1,6-diphosphate aldolase, *lacD*
SP1191	0.7	7.67E-04	tagatose-6-phosphate kinase, *lacC*
SP1193	0.7	6.94E-04	galactose-6-phosphate isomerase, LacA subunit, *lacA*
SP1212	**0.6**	**1.02E-04**	**tRNA pseudouridine synthase B, *truB***
SP1294	**0.6**	**8.02E-04**	**crcB protein, *crcB*-1**
SP1295	**0.6**	**1.29E-05**	**crcB protein, *crcB*-2**
SP1298	**0.5**	**2.36E-08**	**DHH subfamily 1 protein**
SP1383	0.7	1.41E-04	alanyl-tRNA synthetase, *alaS*
SP1384	0.7	6.11E-04	conserved hypothetical protein
SP1441	0.7	9.41E-04	This gene is interrupted by an RUP element
SP1445	**0.3**	**5.03E-10**	**GMP synthase, *guaA***
SP1462	**0.6**	**1.28E-05**	**conserved hypothetical protein**
SP1463	**0.5**	**1.08E-06**	**methylated-DNA--protein-cysteine S-methyltransferase**
SP1464	**0.6**	**1.40E-06**	**acetyltransferase, GNAT family**
SP1469	0.7	5.52E-04	NADH oxidase
SP1474	0.7	2.15E-04	glycyl-tRNA synthetase, beta subunit, *glyS*
SP1491	0.7	3.12E-04	putative glycerol uptake facilitator protein
SP1500	**0.5**	**6.35E-06**	**amino acid ABC transporter, amino acid-binding protein**
SP1501	0.7	1.25E-05	amino acid ABC transporter, ATP-binding protein
SP1502	0.7	6.27E-05	amino acid ABC transporter, permease protein
SP1505	0.7	5.63E-04	membrane protein
SP1508	0.7	3.00E-04	ATP synthase F1, beta subunit, *atpD*
SP1509	**0.6**	**7.45E-07**	**ATP synthase F1, gamma subunit, *atpG***
SP1510	**0.6**	**2.31E-06**	**ATP synthase F1, alpha subunit, *atpA***
SP1511	**0.6**	**1.74E-04**	**ATP synthase F1, delta subunit, *atpH***
SP1512	**0.6**	**2.83E-05**	**ATP synthase F0, B subunit, *atpF***
SP1513	**0.6**	**5.47E-06**	**ATP synthase F0, A subunit, *atpB***
SP1533	0.7	1.99E-04	conserved domain protein

SP0800	**2.1**	**8.88E-06**	**sensor histidine kinase CiaH**
SP0805	1.3	3.75E-04	hydrolase, haloacid dehalogenase-like family
SP0827	1.3	4.52E-04	conserved hypothetical protein, authentic point mutation
SP0829	**1.5**	**6.63E-05**	**Phosphopentomutase, *deoB***
SP0838	**1.5**	**1.25E-04**	**ribosomal protein S20, *rpsT***
SP0851	1.4	7.64E-04	conserved hypothetical protein
SP0875	**2.2**	**6.03E-07**	**lactose phosphotransferase system repressor**
SP0876	**2.2**	**8.37E-07**	**putative 1-phosphofructokinase**
SP0877	**2.3**	**4.79E-07**	**PTS system, fructose specific IIABC components**
SP0878	**1.6**	**8.50E-05**	**SpoE family protein**
SP0880	**1.6**	**1.90E-06**	**aminotransferase, class-V**
SP0881	**1.7**	**2.87E-06**	**thiazole biosynthesis protein ThiI**
SP0895	**1.5**	**3.44E-05**	**DNA polymerase III, alpha subunit, dnaE**
SP0904	1.3	5.93E-04	conserved hypothetical protein
SP0913	**1.8**	**3.15E-04**	**putative ABC transporter, permease protein**
SP0925	1.4	9.27E-04	conserved hypothetical protein
SP0931	**1.6**	**3.87E-06**	**glutamate 5-kinase, *proB***
SP0932	1.3	4.32E-04	gamma-glutamyl phosphate reductase
SP0956	**1.7**	**3.30E-05**	**hypothetical protein**
SP0957	**2.2**	**2.63E-07**	**ABC transporter, ATP-binding protein**
SP0958	**2.2**	**2.47E-08**	**hypothetical protein**
SP0974	1.4	7.44E-04	putative preprotein translocase, SecG subunit
SP0975	**1.7**	**5.41E-07**	**exoribonuclease, VacB/Rnb family**
SP0976	**1.7**	**7.57E-06**	**SsrA-binding protein**
SP0977	**1.7**	**2.67E-06**	**tellurite resistance protein TehB**
SP1027	**2.7**	**2.18E-06**	**conserved hypothetical protein**
SP1548	**0.6**	**6.34E-06**	**hypothetical protein**
SP1549	**0.6**	**1.32E-04**	**polypeptide deformylase, *def*-2**
SP1573	**0.6**	**2.78E-05**	**Lysozyme, *lytC***
SP1574	0.7	4.02E-04	triosephosphate isomerase
SP1580	**0.5**	**1.18E-07**	**sugar ABC transporter, ATP-binding protein, *msmK***
SP1604	0.7	3.23E-04	hypothetical protein
SP1605	**0.6**	**2.95E-06**	**ferredoxin**
SP1606	**0.6**	**1.47E-06**	**glycosyl transferase, family 2**
SP1607	**0.6**	**1.14E-05**	**UDP-glucose 4-epimerase, *galE*-1**
SP1630	0.7	2.24E-04	hypothetical protein
SP1631	**0.6**	**1.22E-05**	**threonyl-tRNA synthetase**
SP1645	0.7	6.61E-04	GTP pyrophosphokinase
SP1647	**0.5**	**4.45E-08**	**endopeptidase O, *pepO***
SP1651	**0.5**	**6.17E-07**	**thiol peroxidase, *psaD***
SP1659	**0.6**	**1.93E-05**	**isoleucyl-tRNA synthetase, *ileS***
SP1709	**0.5**	**1.27E-06**	**phosphoglycerate dehydrogenase-related protein**
SP1710	0.7	9.46E-04	nitroreductase family protein
SP1711	0.7	4.47E-04	primosomal protein DnaI
SP1712	0.7	4.64E-04	hypothetical protein
SP1717	**0.6**	**8.93E-05**	**ABC transporter, ATP-binding protein**
SP1811	**0.4**	**6.87E-04**	**tryptophan synthase, alpha subunit, *trpA***
SP1812	**0.5**	**6.23E-04**	**tryptophan synthase, beta subunit, *trpB***
SP1813	**0.5**	**3.11E-05**	**N-(5'-phosphoribosyl)-anthranilate isomerase, *trpF***
SP1815	**0.4**	**1.15E-06**	**anthranilate phosphoribosyltransferase, *trpD***
SP1816	**0.4**	**5.54E-06**	**anthranilate synthase component II, *trpG***
SP1817	**0.5**	**3.77E-04**	**anthranilate synthase component I, *trpE***

SP1044	**1.9**	**2.31E-06**	**putative hydrolase**
SP1072	1.3	4.27E-04	DNA primase, *dnaG*
SP1075	**1.7**	**2.77E-05**	**glycosyl transferase CpoA**
SP1076	**1.6**	**3.59E-05**	**glycosyl transferase, group 1**
SP1077	**1.5**	**9.44E-06**	**conserved domain protein**
SP1093	1.4	2.00E-04	hypothetical protein
SP1147	**1.5**	**4.36E-04**	**integrase/recombinase, phage integrase family, truncation**
SP1148	**1.8**	**2.40E-07**	**IS630-Spn1, transposase Orf2**
SP1149	**1.8**	**2.48E-06**	**IS630-Spn1, transposase Orf1**
SP1151	**1.6**	**4.87E-05**	**exonuclease RexB**
SP1152	1.4	4.55E-04	exonuclease RexA
SP1153	1.4	4.41E-04	hypothetical protein
SP1162	**1.5**	**2.79E-04**	**putative acetoin dehydrogenase complex, E2 component, dihydrolipoamide acetyltransferase**
SP1207	1.4	7.39E-05	exodeoxyribonuclease VII, large subunit, xseA
SP1208	1.4	1.92E-04	uridine kinase
SP1233	**1.5**	**9.59E-05**	**hypothetical protein**
SP1234	**1.7**	**3.31E-05**	**transcriptional regulator, biotin repressor family**
SP1240	**1.7**	**9.20E-06**	**conserved hypothetical protein**
SP1241	**1.6**	**8.32E-05**	**amino acid ABC transporter, amino acid-binding protein/permease protein**
SP1242	**1.8**	**5.22E-06**	**amino acid ABC transporter, ATP-binding protein**
SP1275	**2.1**	**7.36E-06**	**carbamoyl-phosphate synthase, large subunit *carB***
SP1276	**1.9**	**1.06E-05**	**carbamoyl-phosphate synthase, small subunit, *carA***
SP1277	**1.7**	**1.76E-04**	**aspartate carbamoyltransferase, *pyrB***
SP1315	**1.5**	**4.95E-05**	**v-type sodium ATP synthase, subunit D, *ntpD***
SP1888	0.7	2.08E-04	oligopeptide ABC transporter, ATP-binding protein AmiE
SP1889	0.7	3.30E-04	oligopeptide ABC transporter, permease protein AmiD
SP1891	**0.6**	**3.50E-05**	**oligopeptide ABC transporter, oligopeptide-binding protein AmiA**
SP1906	**0.6**	**1.82E-04**	**chaperonin, 60 kDa, *groEL***
SP1907	**0.6**	**8.24E-05**	**chaperonin, 10 kDa, *groES***
SP1968	0.7	8.07E-04	phosphopantetheine adenylyltransferase, *coaD*
SP1970	**0.4**	**2.49E-07**	**aspartate--ammonia ligase, *asnA***
SP1994	**0.6**	**2.13E-04**	**aminotransferase, class I**
SP1997	**0.6**	**2.44E-04**	**Cof family protein**
SP2026	**0.4**	**9.86E-08**	**alcohol dehydrogenase, iron-containing**
SP2027	**0.6**	**1.29E-04**	**conserved hypothetical protein**
SP2028	0.7	4.73E-04	phosphotyrosine protein phosphatase
SP2030	**0.5**	**1.84E-04**	**transketolase**
SP2044	**0.6**	**2.78E-04**	**acetate kinase**
SP2058	0.7	6.27E-04	queuine tRNA-ribosyltransferase
SP2069	**0.6**	**7.74E-05**	**glutamyl-tRNA synthetase, *gltX***
SP2078	**0.6**	**1.22E-05**	**arginyl-tRNA synthetase, *argS***
SP2081	0.7	8.95E-04	conserved hypothetical protein
SP2109	0.7	9.53E-04	maltodextrin ABC transporter, permease protein, *malC*
SP2134	0.7	7.36E-04	ribosomal protein L32, *rpmF*
SP2188	**0.6**	**4.64E-05**	**chaperonin, 33 kDa, *hslO***
SP2189	**0.6**	**8.60E-05**	**putative TIM-barrel protein, NifR3 family**
SP2230	**0.6**	**1.08E-04**	**ABC transporter, ATP-binding protein**
SP2231	**0.5**	**2.04E-06**	**putative ABC transporter, permease protein**

SP1380	**1.6**	**2.61E-05**	**hypothetical protein**
SP1381	**1.6**	**7.21E-05**	**ABC transporter, ATP-binding protein**
SP1388	1.3	6.66E-04	spermidine/putrescine ABC transporter, permease protein
SP1390	1.3	4.62E-04	UDP-N-acetylenolpyruvoylglucosamine reductase, *murB*
SP1392	1.3	8.55E-04	alpha-acetolactate decarboxylase, *aldB*
SP1405	**1.5**	**1.24E-05**	**conserved hypothetical protein**
SP1426	1.4	3.94E-04	ABC transporter, ATP-binding protein
SP1479	1.4	9.25E-04	peptidoglycan N-acetylglucosamine deacetylase A, *pgdA*
SP1521	**1.5**	**7.17E-04**	**UDP-N-acetylmuramate--alanine ligase, murC**
SP1522	1.4	4.23E-04	conserved domain protein
SP1523	1.4	7.00E-04	Snf2 family protein
SP1546	**1.7**	**1.71E-05**	**conserved domain protein**
SP1560	**1.5**	**1.62E-05**	**conserved hypothetical protein**
SP1561	**1.6**	**6.49E-06**	**conserved hypothetical protein**
SP1562	**1.6**	**4.26E-06**	**hypothetical protein**
SP1600	**1.7**	**8.74E-06**	**putative membrane protein**
SP1602	**1.4**	**4.80E-04**	**phnA protein**
SP1623	**1.7**	**4.43E-06**	**cation-transporting ATPase, E1-E2 family**
SP1625	1.4	9.69E-04	putative cadmium resistance transporter
SP1636	1.4	2.71E-04	Rrf2 family protein
SP1640	**1.6**	**2.09E-06**	**hypothetical protein**
SP1641	**1.6**	**2.22E-05**	**Conserved hypothetical protein**
SP1668	**1.6**	**4.06E-05**	**hypothetical protein**
SP1669	1.3	3.04E-04	MutT/nudix family protein
SP1670	1.3	8.29E-04	UDP-N-acetylmuramoylalanyl-D-glutamyl-2, 6-diaminopimelate--D-alanyl-D-alanyl ligase, *murF*
SP1671	1.4	3.06E-04	D-alanine--D-alanine ligase, *ddlA*
SP1674	**1.6**	**2.42E-06**	**putative phosphosugar-binding transcriptional regulator**
SP1695	**2.3**	**6.74E-05**	**putative acetyl xylan esterase**
SP1696	**2.5**	**3.28E-05**	**hypothetical protein**

SP2232	**0.4**	**6.15E-05**	**nserved hypothetical protein, authentic frame shift**
SP2233	**0.3**	**1.47E-06**	**hypothetical protein**
SP2234	**0.5**	**3.09E-05**	**transcriptional regulator, TetR family**
SP2235	0.7	7.63E-04	response regulator ComE

SP1714	**9.1**	**9.49E-14**	**transcriptional regulator, GntR family**				
SP1715	**13.0**	**2.33E-15**	**ABC transporter, ATP-binding protein**				
SP1720	1.3	9.91E-04	conserved hypothetical protein				
SP1752	1.4	3.56E-04	putative mechanosensitive ion channel				
SP1774	**1.6**	**1.44E-06**	**putative transcriptional regulator**				
SP1776	**1.5**	**3.55E-05**	**thioredoxin**				
SP1786	**1.9**	**7.55E-07**	**conserved hypothetical protein**				
SP1787	**1.8**	**3.07E-07**	**hypothetical protein**				
SP1860	**1.8**	**2.85E-07**	**choline transporter, *proWX***				
SP1861	**1.7**	**1.96E-06**	**choline transporter, *proV***				
SP1862	**1.5**	**1.02E-04**	**hypothetical protein**				
SP1863	**1.5**	**1.18E-05**	**transcriptional regulator, MarR family**				
SP1903	**1.6**	**3.27E-05**	**conserved hypothetical protein**				
SP1926	**1.5**	**3.74E-05**	**hypothetical protein**				
SP1938	**1.6**	**4.12E-04**	**hypothetical protein**				
SP1939	**1.5**	**5.01E-05**	**MATE efflux family protein DinF**				
SP1972	1.4	5.69E-04	membrane protein				
SP2007	**1.5**	**5.76E-04**	**transcription antitermination protein NusG**				
SP2009	**1.5**	**6.82E-05**	**ribosomal protein L33, *rpmG*-2**				
SP2013	**1.9**	**4.11E-08**	**conserved hypothetical protein**				
SP2016	**2.0**	**3.92E-07**	**nicotinate-nucleotide pyrophosphorylase, *nadC***				
SP2062	**1.5**	**4.84E-04**	**transcriptional regulator, MarR family**				
SP2106	**2.6**	**4.50E-06**	**glycogen phosphorylase family protein**				
SP2107	**2.9**	**5.56E-06**	**4-alpha-glucanotransferase, *malQ***				
SP2148	**1.5**	**4.07E-06**	**arginine deiminase, *arcA***				
SP2150	1.4	9.24E-05	ornithine carbamoyltransferase, *argF*				
SP2151	**1.6**	**2.33E-06**	**carbamate kinase, *arcC***				
SP2152	**1.9**	**2.88E-07**	**conserved hypothetical protein**				
SP2153	**1.5**	**1.51E-04**	**peptidase, M20/M25/M40 family**				
SP2202	**1.6**	**7.03E-05**	**conserved hypothetical protein**				
SP2205	**1.5**	**2.67E-05**	**DHH subfamily 1 protein**				
SP2226	1.3	8.27E-04	conserved hypothetical protein				
SP2239	**2.3**	**8.74E-05**	**serine protease**				
SP2240	**2.2**	**7.51E-04**	**spspoJ protein**				

Table S.2. List of genes commonly up- and down-regulated upon **15 and 30** min.

A : treatment with each AMP:

Bacitracin	**Nisin**	**LL-37**					
SP0430	*SP0415*	*SP0071*	*SP0447*	*SP0787*	*SP1193*	*SP1695*	*SP2188*
SP0785	*SP0501*	*SP0024*	*SP0448*	*SP0789*	*SP1212*	*SP1696*	*SP2189*
SP0786	*SP0502*	*SP0025*	*SP0450*	*SP0790*	*SP1241*	*SP1709*	*SP2205*
SP0787	*SP0876*	*SP0026*	*SP0479*	*SP0798*	*SP1242*	*SP1710*	*SP2230*
SP0910	*SP0875*	*SP0034*	*SP0496*	*SP0800*	*SP1380*	*SP1711*	*SP2233*
SP0912	*SP0912*	*SP0088*	*SP0501*	*SP0805*	*SP1381*	*SP1712*	*SP2239*
SP0913	*SP0913*	*SP0117*	*SP0502*	*SP0829*	*SP1383*	*SP1714*	*SP2240*
SP1480	*SP1241*	*SP0157*	*SP0503*	*SP0845*	*SP1405*	*SP1715*	
SP2086	*SP1242*	*SP0185*	*SP0504*	*SP0851*	*SP1445*	*SP1717*	
	SP1588	*SP0197*	*SP0516*	*SP0875*	*SP1462*	*SP1752*	
	SP1648	*SP0200*	*SP0517*	*SP0876*	*SP1463*	*SP1774*	
	SP1649	*SP0234*	*SP0518*	*SP0877*	*SP1464*	*SP1776*	
	SP1871	*SP0237*	*SP0519*	*SP0878*	*SP1469*	*SP1786*	
	SP1872	*SP0239*	*SP0524*	*SP0887*	*SP1479*	*SP1787*	
		SP0261	*SP0525*	*SP0895*	*SP1491*	*SP1811*	
		SP0281	*SP0526*	*SP0904*	*SP1500*	*SP1812*	
		SP0282	*SP0527*	*SP0913*	*SP1508*	*SP1813*	
		SP0283	*SP0529*	*SP0925*	*SP1509*	*SP1815*	
		SP0284	*SP0530*	*SP0956*	*SP1510*	*SP1816*	
		SP0285	*SP0533*	*SP0957*	*SP1511*	*SP1817*	
		SP0287	*SP0545*	*SP0958*	*SP1512*	*SP1860*	
		SP0289	*SP0546*	*SP0974*	*SP1513*	*SP1888*	

		SP0290 *SP0291* *SP0292* *SP0293* *SP0366* *SP0369* *SP0370* *SP0372* *SP0385* *SP0386* *SP0402* *SP0403* *SP0404* *SP0405* *SP0408* *SP0413* *SP0415* *SP0416* *SP0417* *SP0419* *SP0424* *SP0427* *SP0445* *SP0446* *SP0547* *SP0557* *SP0565* *SP0566* *SP0568* *SP0577* *SP0578* *SP0579* *SP0581* *SP0582* *SP0589* *SP0592* *SP0593* *SP0617* *SP0730* *SP0731* *SP0742* *SP0748* *SP0762* *SP0770* *SP0775* *SP0783* *SP0785* *SP0786* *SP0975* *SP0976* *SP0977* *SP1013* *SP1027* *SP1032* *SP1034* *SP1035* *SP1069* *SP1070* *SP1075* *SP1076* *SP1077* *SP1093* *SP1148* *SP1149* *SP1151* *SP1162* *SP1171* *SP1175* *SP1185* *SP1187* *SP1190* *SP1191* *SP1533* *SP1546* *SP1548* *SP1549* *SP1560* *SP1561* *SP1562* *SP1574* *SP1580* *SP1605* *SP1607* *SP1623* *SP1625* *SP1636* *SP1640* *SP1641* *SP1645* *SP1647* *SP1659* *SP1668* *SP1669* *SP1670* *SP1671* *SP1674* *SP1891* *SP1903* *SP1906* *SP1907* *SP1926* *SP1968* *SP1970* *SP1972* *SP1997* *SP2013* *SP2016* *SP2026* *SP2030* *SP2044* *SP2058* *SP2069* *SP2078* *SP2081* *SP2106* *SP2107* *SP2109* *SP2134* *SP2151* *SP2152*

B List of genes commonly regulated upon **15 and 30** min. treatment with:

Nisin and LL-37	**Bacitracin and LL-37**	**Bacitracin and nisin**	**Bacitracin, nisin and LL-37**
SP0415	*SP0785*	*SP0912*	*SP0913*

SP0875	*SP0786*		
SP0876	*SP0787*		
SP0501			
SP0502			
SP1241			
SP1242			

Table S.3. List of genes whose expression changed significantly in more than 1 stress and depicted in FIG. 1.

A. List of genes commonly **down-regulated** after 15 or 30 min. upon treatment with:

nisin and LL-37	**bacitracin and LL-37**
SP0285	*SP0117*
SP0366	*SP0281*
SP0578	*SP0285*
SP0577	*SP0366*
SP0731	*SP0435*
SP0922	*SP0453*
SP1187	*SP0516*
SP1507	*SP0565*
SP1970	*SP0566*
SP2055	*SP0568*
SP2108	*SP0577*
	SP0579
	SP0580
	SP0581
	SP0731
	SP0770
	SP0775
	SP1175

	SP1383 *SP1384* *SP1441* *SP1474* *SP1533* *SP1630* *SP1631* *SP1651* *SP1659* *SP1906* *SP2026* *SP2134* *SP2188* *SP2189*

B. List of genes commonly **up-regulated** upon 15 min. treatment with:

bacitracin and LL-37	**nisin and LL-37**	**nisin and bacitracin**	**bacitracin, nisin and LL-37**
SP0385	*SP0185*	*SP0912*	*SP0913*
SP0386	*SP0415*		
SP0419	*SP0416*		
SP0424	*SP0851*		
SP0427	*SP0875*		
SP0785	*SP0876*		
SP0786	*SP2173*		
SP0787			
SP0861			
SP0910			
SP1714			
SP1715			
SP1925			

SP1926			

C. List of genes commonly **up-regulated** upon 30 min. treatment with:

bacitracin and LL-37	nisin and LL-37	bacitracin and nisin	bacitracin, nisin and LL-37
SP0088	*SP0415*	*SP0912*	*SP0875*
SP0157	*SP0419*	*SP0913*	*SP0876*
SP0189	*SP0422*		*SP0913*
SP0275			*SP2062*
SP0276			
SP0278			
SP0369			
SP0370			
SP0371			
SP0408			
SP0582			
SP0641			
SP0785			
SP0786			
SP0787			
SP0790			
SP0800			
SP0877			
SP1148			
SP1674			
SP1774			
SP1786			
SP1787			

Table S.4. List of genes differentially regulated by more than one AMP at either time point

A. List of genes induced upon **15 or 30** min. treatment with:

Bacitracin, nisin and LL-37	Bacitracin and LL-37	Bacitracin and nisin	Nisin and LL-37
SP0419	*SP0088*	*SP0912*	*SP0185*
SP0422	*SP0157*	*SP1343*	*SP0415*
SP0641	*SP0189*	*SP1588*	*SP0416*
SP0875	*SP0275*	*SP2063*	*SP0851*
SP0876	*SP0276*		*SP2173*
SP0913	*SP0278*		
SP2062	*SP0369*		
	SP0370		
	SP0371		
	SP0385		
	SP0386		
	SP0387		
	SP0408		
	SP0420		
	SP0421		
	SP0424		
	SP0426		
	SP0427		
	SP0430		
	SP0582		
	SP0785		
	SP0786		
	SP0787		

	SP0790		
	SP0800		
	SP0861		
	SP0877		
	SP0910		
	SP1148		
	SP1674		
	SP1714		
	SP1715		
	SP1774		
	SP1786		
	SP1787		
	SP1925		
	SP1926		

B. List of genes commonly down-regulated upon **15 or 30** min. treatment with:

Bacitracin, nisin and LL-37	**Nisin and LL-37**	**Bacitracin and LL-37**
SP0285	*SP0578*	*SP0117*
SP0366	*SP1187*	*SP0281*
SP0731	*SP1295*	*SP0435*
SP0922	*SP1507*	*SP0453*
SP2055	*SP1970*	*SP0459*
	SP2108	*SP0516*
		SP0565
		SP0566
		SP0568
		SP0577
		SP0579
		SP0580
		SP0581
		SP0736

		SP0770 *SP0775* *SP0920* *SP1175* *SP1383* *SP1384* *SP1441* *SP1468* *SP1474* *SP1533* *SP1576* *SP1630* *SP1631* *SP1651* *SP1659* *SP1906* *SP2026* *SP2134* *SP2188* *SP2189*