

1 Supplementary files

2 Table S1: Genes assigned for stress response system in *S. thermophilus* SMQ-301

Encoded proteins	Assigned genes
General stress regulator	SMQ301_RS08365
Universal stress protein UspA	SMQ301_RS07845
Acid resistance	
<i>F0F1-ATPase system</i>	
F0F1-ATPase synthase gene cluster	SMQ301_RS02525 SMQ301_RS02530 SMQ301_RS02535 SMQ301_RS02540 SMQ301_RS02545 SMQ301_RS02550 SMQ301_RS02555 SMQ301_RS02560
<i>Urease</i>	
Urease gene cluster	SMQ301_RS01350 SMQ301_RS09900 SMQ301_RS08175 SMQ301_RS01590 SMQ301_RS01595 SMQ301_RS01600 SMQ301_RS01605 SMQ301_RS01610 SMQ301_RS01615 SMQ301_RS01620 SMQ301_RS02605
Ammonia permease	
Cold and heat response	
Heat shock protein GrpE (conserved chaperone complexes: GrpE-DnaK-DnaJ)	SMQ301_RS00785 SMQ301_RS00790 SMQ301_RS00795
Heat shock protein Hsp33 Molecular chaperone GroES-GroEL	SMQ301_RS01135 SMQ301_RS01240 SMQ301_RS01245
Heat shock protein HtpX Molecular chaperone GroES CtsR family transcriptional regulator of class III stress genes (heat shock response)	SMQ301_RS03715 SMQ301_RS04675
ATP-dependent Clp protease ATP-binding subunit	SMQ301_RS00545 SMQ301_RS00050 SMQ301_RS03050 SMQ301_RS03175 SMQ301_RS07740 SMQ301_RS01940
ATP-dependent Clp protease proteolytic subunit Cold-shock protein	SMQ301_RS04365 SMQ301_RS04370
Salt resistance	
Sodium transporter	SMQ301_RS06655
Cation transporter	SMQ301_RS04495 SMQ301_RS04665 SMQ301_RS05145
Oxidative stress response	
Glutamate-cysteine ligase	SMQ301_RS06775
Glutathione reductase	SMQ301_RS02205
Thioredoxin	SMQ301_RS00025 SMQ301_RS08680

	<i>SMQ301_RS08905</i>
	<i>SMQ301_RS07910</i>
Thioredoxin reductase	<i>SMQ301_RS06220</i>
NADH oxidase	<i>SMQ301_RS08995</i>
Superoxide dismutase	<i>SMQ301_RS06495</i>
Peptide methionine sulfoxide reductase Msr B	<i>SMQ301_RS07820</i>
Methionine sulfoxide reductase A	<i>SMQ301_RS05030</i>
Peroxidase	

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35 Table S2: Gene table for bacteriocin area of interest for *S. thermophilus* SMQ-301

Name	Function
LanK	Sensor histidine kinase spaK Methylenetetrahydrofolate--tRNA-(uracil-5-)-methyltransferase TrmFO OS=Streptococcus thermophilus (strain ATCC BAA-491 / LMD-9) OX=322159 GN=trmFO PE=3 SV=1
orf00002	Uncharacterized protein YxjG OS=Bacillus subtilis (strain 168) OX=224308 GN=yxjG PE=4 SV=3
orf00004	Uncharacterized protein YxjH OS=Bacillus subtilis (strain 168) OX=224308 GN=yxjH PE=4 SV=4
orf00007	Nucleoside diphosphate kinase OS=Streptococcus thermophilus (strain CNRZ 1066) OX=299768 GN=ndk PE=3 SV=2
orf00010	Sulfurtransferase Alvin_2599 OS=Allochromatium vinosum (strain ATCC 17899 / DSM 180 / NBRC 103801 / NCIMB 10441 / D) OX=572477 GN=rhd_2599 PE=1 SV=1
orf00011	Diacetyl reductase [(S)-acetoin forming] OS=Staphylococcus aureus (strain COL) OX=93062 GN=butA PE=3 SV=1
orf00014	Diacetyl reductase [(S)-acetoin forming] OS=Klebsiella pneumoniae OX=573 GN=budC PE=1 SV=2
orf00017	Elongation factor 4 OS=Streptococcus thermophilus (strain ATCC BAA-491 / LMD-9) OX=322159 GN=lepA PE=3 SV=1
orf00020	HTH-type transcriptional regulator rgg OS=Streptococcus gordonii (strain Challis / ATCC 35105 / BCRC 15272 / CH1 / DL1 / V288) OX=467705 GN=rgg PE=4 SV=1
orf00022	Putative mycofactocin radical SAM maturase MftC OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) OX=83331 GN=mftC PE=3 SV=1
BmbF	Uncharacterized 32.2 kDa protein in hmfB 3'region OS=Methanothermus fervidus OX=2180 PE=3 SV=1
orf00030	Acetolactate synthase OS=Bacillus subtilis (strain 168) OX=224308 GN=alsS PE=2 SV=3
orf00032	Alpha-acetolactate decarboxylase OS=Streptococcus thermophilus OX=1308 GN=aldC PE=1 SV=1
orf00034	ATP-dependent protease OS=Lactococcus lactis subsp. lactis OX=1360 PE=4 SV=1
orf00037	Macrolide export ATP-binding/permease protein MacB OS=Bdellovibrio bacteriovorus (strain ATCC 15356 / DSM 50701 / NCIB 9529 / HD100) OX=264462 GN=macB PE=3 SV=1
ABC	Probable oxidoreductase OS=Streptomyces lividans OX=1916 PE=3 SV=1
orf00047	Uncharacterized HTH-type transcriptional regulator YxbF OS=Bacillus subtilis (strain 168) OX=224308 GN=yxbF PE=4 SV=1
orf00050	

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