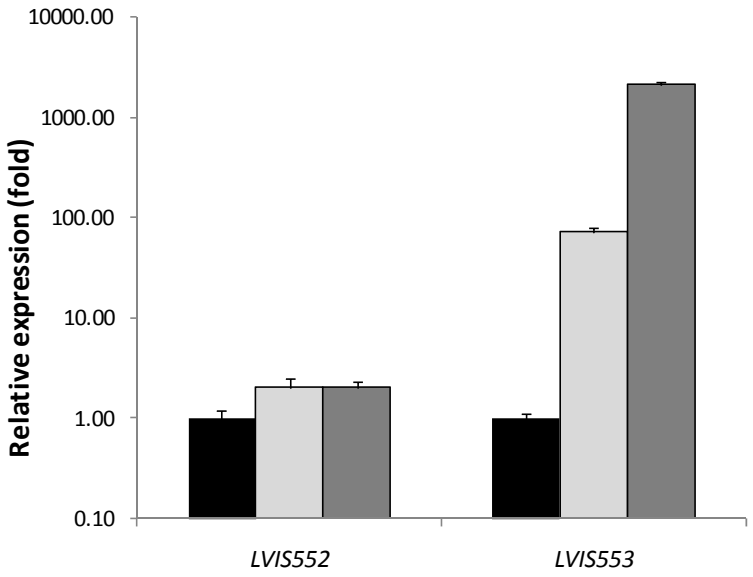
Supplementary Data

Figure S1. Effect of novobiocin on the expression of *LVIS553* measured by quantitative real-time PCR. *L. brevis* ATCC367 was grown in MRS broth with increasing concentrations of novobiocin (A) or coumermycin A1 (B). Novobiocin was added at a concentration of 1 μM (light grey bars) or 5 μM (dark grey bars) while coumermycin A1 was at 0.1 μM (light grey bars), or 0.5 μM (dark grey bars) concentrations. RNA extractions and qRT-PCR was performed as described under "Experimental Procedures". The amplification values obtained were corrected with those obtained using *rpoD* as internal control. The values shown are relative to those observed for the same gene in cells grown in absence of novobiocin or coumermycin A1 (black bar).

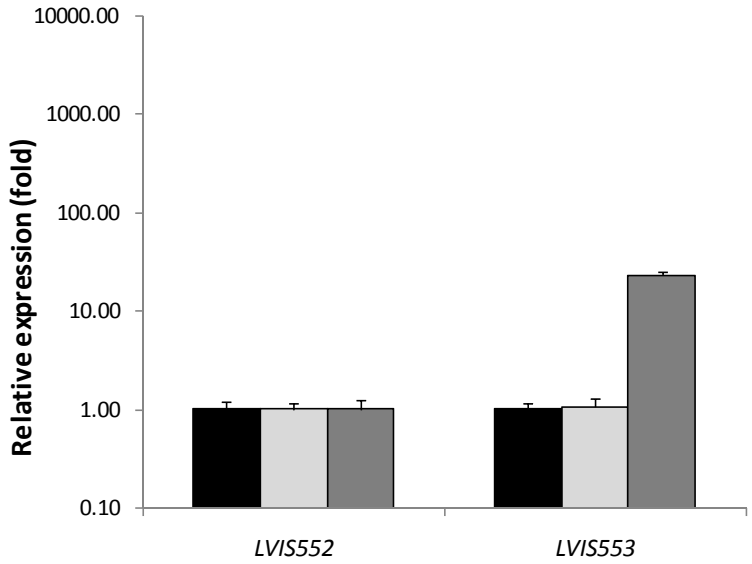
Figure S2. Comparison of *LVIS553* with the closest sequence and structural homologs. (A) Model of LVIS553 structure (in green) constructed using MTH313 (in blue) as template. In red is shown salicylate from MTH313. Residues within 4 Å of SAL1 are shown as sticks. (B) Sequence based alignment was performed using ClustalW (43) with the top two sequence homologs (Lpa, *L. plantarum*, gi|28378594; Cme, *Clostridium methylpentosum*, gi|225017503), the structural homolog MTH313 (*Methanothermobacter thermautotrophicus*, gi|15678341, pdb #3BPX) and MarR (*E. coli*, gi|89108371, pdb # 1JGS). The secondary structure of MTH313 is displayed on top of the alignment, α helices as rectangles and β barres as arrows. Similarly to MTH313, LVIS553 binding site contains a high proportion of charged and polar residues.

Figure S1.

A


10000.00
1000.00
100.00
10.00
1.00
0.10
Relative expression (fold)
LVIS552
LVIS553

B


10000.00
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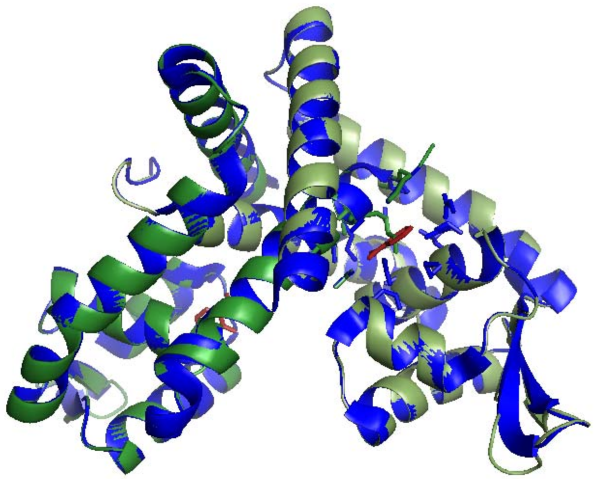
100.00
10.00
1.00
0.10
Relative expression (fold)
LVIS552
LVIS553

Figure S2

A



B

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                                α1                         α2
LVIS553   ------------MTQPITFNKYIASIYRQSKHDFNEQIAALDLRATTGDLLLFVADHPGL 48
Lpa       MDLSTIYKKGVLTIEYFSLTKYIAGIYRESKNSINTQLQALNIRATESDLLLVVYDHPAQ 60
Cme       -------------MSMRIFGKWISIISRFSGIYYSEHMESLGLSSGQYIFFLCICDHPGL 47
3BPX      ------------MDRDIPLKGLLSIILRSHRVFIGRELGHLNLTDAQVACLLRIHREPGI 48
1JGS      -----MKSTSDLFNEIIPLGRLIHMVNQKKDRLLNEYLSPLDITAAQFKVLCSIRCAACI 55
                            :   :  : :      .  :  *.:       :  :   .
              α3            α4          β1    W1    β2           α5
LVIS553   TQREIAHQMVLDPSLVARDLRALTTKQLVERTPDPQDGRAQRITLTPTGYQQADQIRQVM 108
Lpa       TQKDLAASLMLDPSLLARTVRQLEQRQLVIRFRDPADQRSLRISLTPAGEQIAIAIKKTL 120
Cme       TQDELAAELAFNKSTVARVVASLEKNGFVERRVNPQDKRAVNLYPTQRAEEISPRVREIL 107
3BPX      KQDELATFFHVDKGTIARTLRRLEESGFIEREQDPENRRRYILEVTRRGEEIIPLILKVE 108
1JGS      TPVELKKVLSVDLGALTRMLDRLVCKGWVERLPNPNDKRGVLVKLTTGGAAICEQCHQLV 115
          .  ::   : .: .::* :  *     : *  :* : *   :  *  .        :
              α5                 α6
LVIS553   -GAWWQALFAATPQANAQVTGQQLAAIYQTLQQRQERN------ 145
Lpa       -IDWWHDFFAAHPEVNEQVFTNQLQQVYLALQEKRD-------- 155
Cme       -DEWNLRITDGFTSEESDVFEALLIRASENARRHAKLAKEKNKL 150
3BPX      -ERWEDLLFRDFTEDERKLFRKMCRRLAEEAVRMRGEWR----- 146
1JGS      GQDLHQELTKNLTADEVATLEYLLKKVLP--------------- 144
                 :    .  :
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