Supplementary Figure

Fig. S1 Quantification of violacein inhibition and measurement of growth by cell free lysate of *E. ludwigii* (PUFSTb09) and *B. cereus* (MTCC 1272)

Fig. S2 Phylogenetic tree of *E. ludwigii* derived by neighbor joining method with closest BLAST hits.

Fig. S3 HP-TLC chromatograms showing the degradation profile of AHLs. Lane 1: N-hexanoyl-homoserine lactone (HHL) standard; Lane 2: AHL extracted from culture broth of *Y. enterocolitica* (KT266804); Lane 3: Degradation of AHL by cell free lysate of *E. ludwigii* (PUFSTb09), and Lane 4: Degradation of AHL by cell free lysate of *B. cereus* (MTCC 1272).

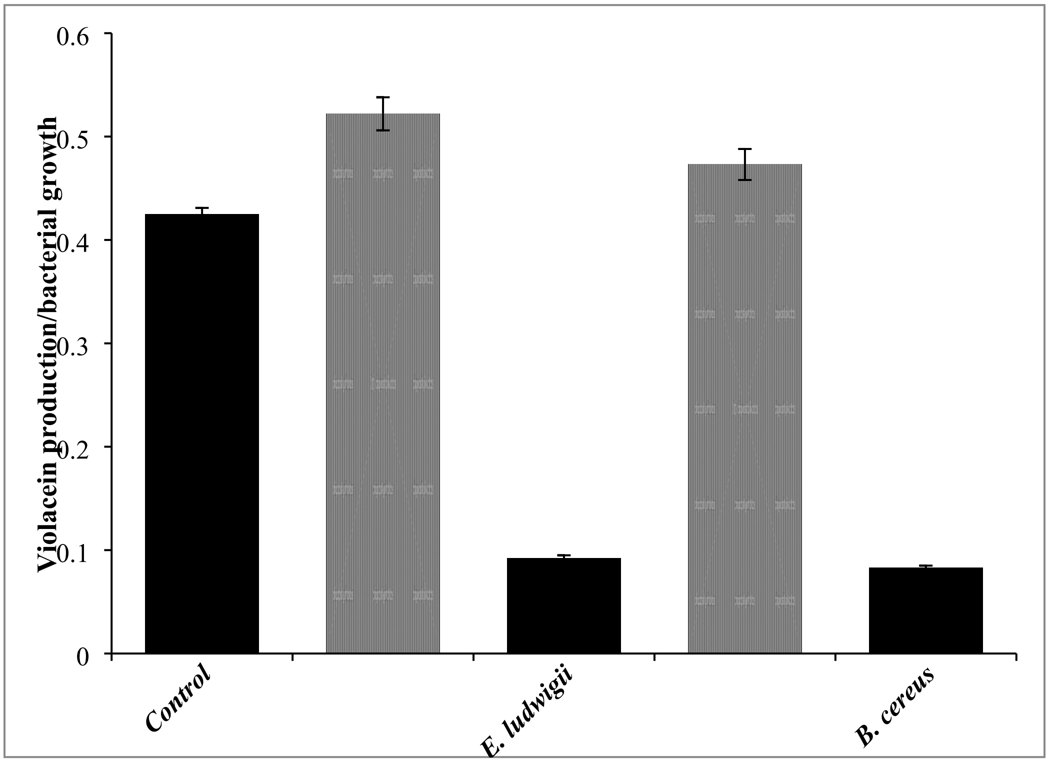
Fig. S4 Effect of cell free lysate on quorum regulated phenotypes. (A) Inhibition of biofilm formation and cell measurement of *Y. enterocolitica*. (B) Reduction in EPS production and cell measurement of *Y. enterocolitica.*

Fig. S5 Microscopic analysis of biofilm formation by *Y. enterocolitica* (KT266804). Confocal laser microscopic images of untreated slide (A), treated slides with cell free lysate of *E. ludwigii* and *B. cereus* (B & C). Scanning electron microscopic images of untreated slide (D), treated slides with cell free lysate of *E. ludwigii* and *B. cereus* (E & F).

Fig. S6 Multiple alignment of AHL-lactonase amino acid sequence from *E. ludwigii* (PUFSTb09) with other known sequences. AHL lactonase of KU53012 was aligned with *Enterobacter ludwigii* (AiiA, accession number: AHE80976.1) and *Enterobacter aerogenes* (AiiA, accession number: AHE80975.1). ClustalW was used for alignment of sequences. Motifs were boxed based on the metal ligands according to Thomas et al.[40]

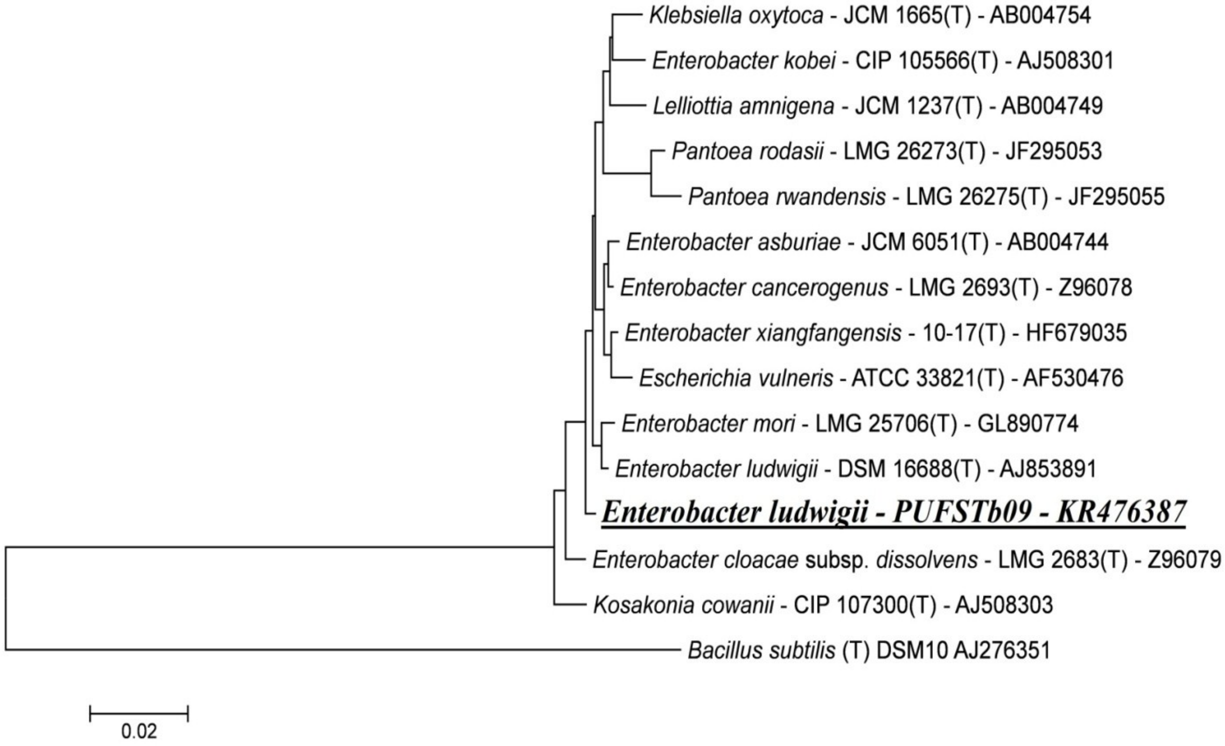
Fig. S7 RMSD profile of AHL in complex with LasR and Lactonase. The Red colored graph represents LasR-AHL complex and black colored graphs represents AHL-Lactonase complex.

Fig. S1



Violacein production/bacterial growth
0.6
0.5
0.4
0.3
0.2
0.1
0
Control
E. ludwigii
B. cereus

Fig. S2


Klebsiella oxytoca - JCM 1665(T) - AB004754
Enterobacter kobei - CIP 105566(T) - AJ508301
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Pantoea rodasii - LMG 26273(T) - JF295053
Pantoea rwandensis - LMG 26275(T) - JF295055
Enterobacter asburiae - JCM 6051(T) - AB004744
Enterobacter cancerogenus - LMG 2693(T) - Z96078
Enterobacter xiangfangensis - 10-17(T) - HF679035
Escherichia vulneris - ATCC 33821(T) - AF530476
Enterobacter mori - LMG 25706(T) - GL890774
Enterobacter ludwigii - DSM 16688(T) - AJ853891
Enterobacter ludwigii - PUFSTb09 - KR476387
Enterobacter cloacae subsp. dissolvens - LMG 2683(T) - Z96079
Kosakonia cowanii - CIP 107300(T) - AJ508303
Bacillus subtilis (T) DSM10 AJ276351
0.02

Fig. S3

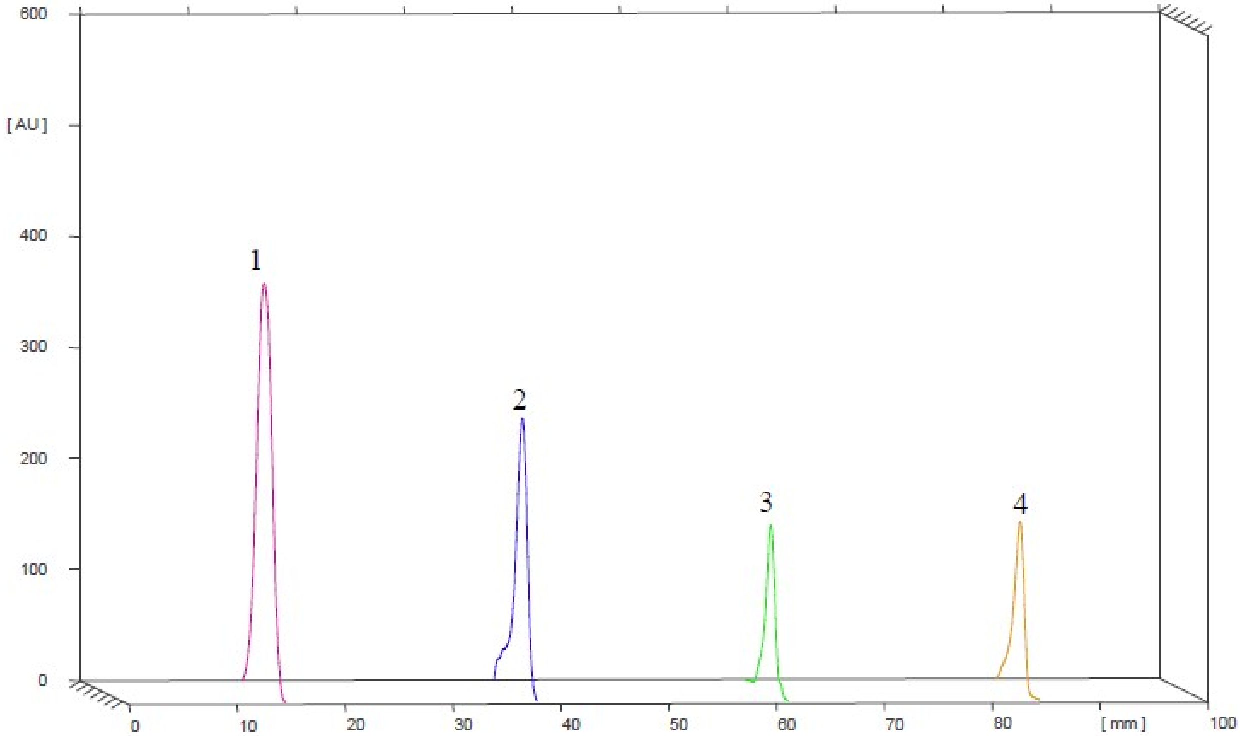


Fig. S4

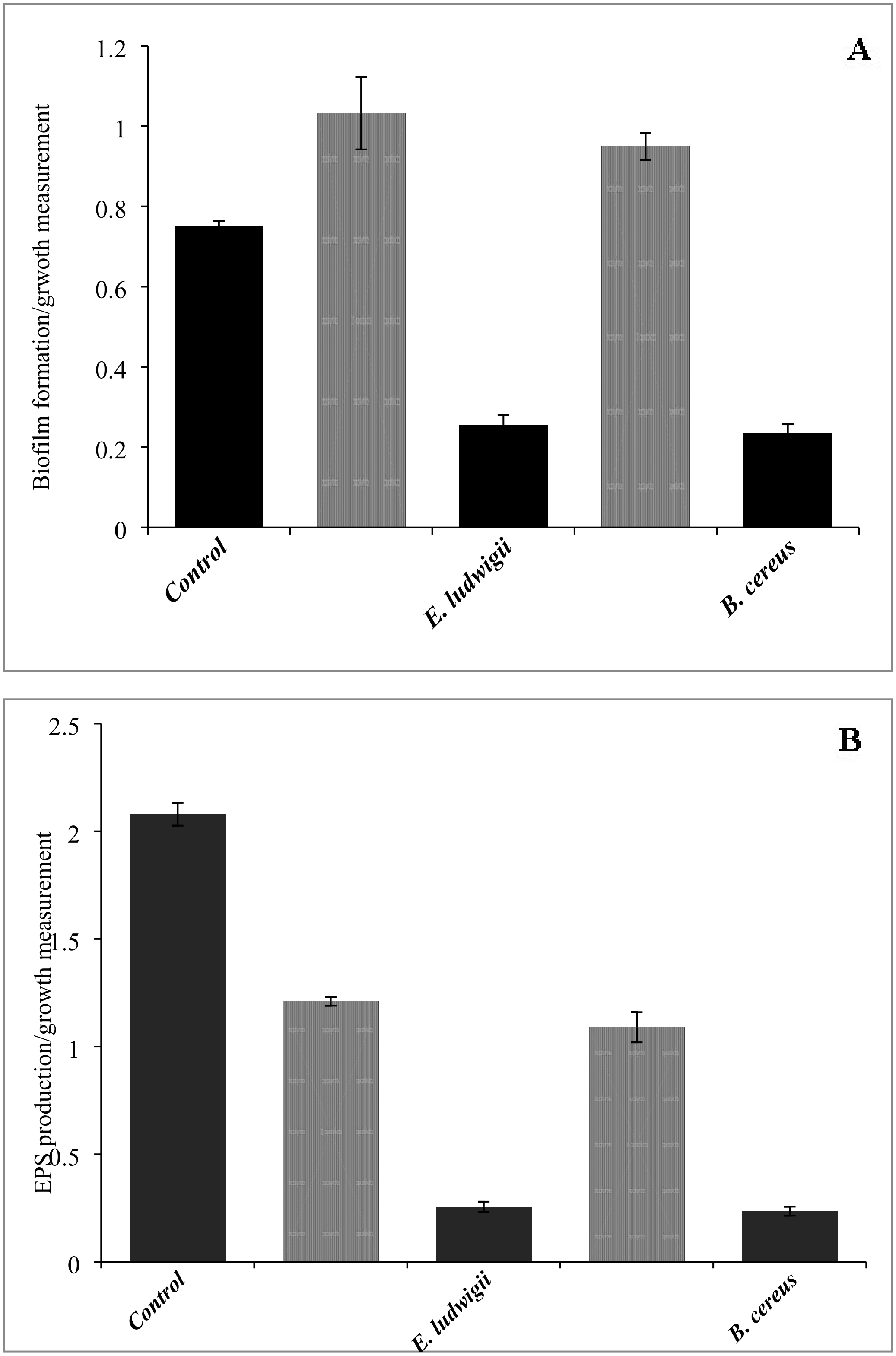

A
Biofilm formation/grwoth measurement
1.2
1
0.8
0.6
0.4
0.2
0
Control
E. ludwigii
B. cereus
B
EPS production/growth measurement
2.5
2
1.5
1
0.5
0
Control
E. ludwigii
B. cereus

Fig. S5

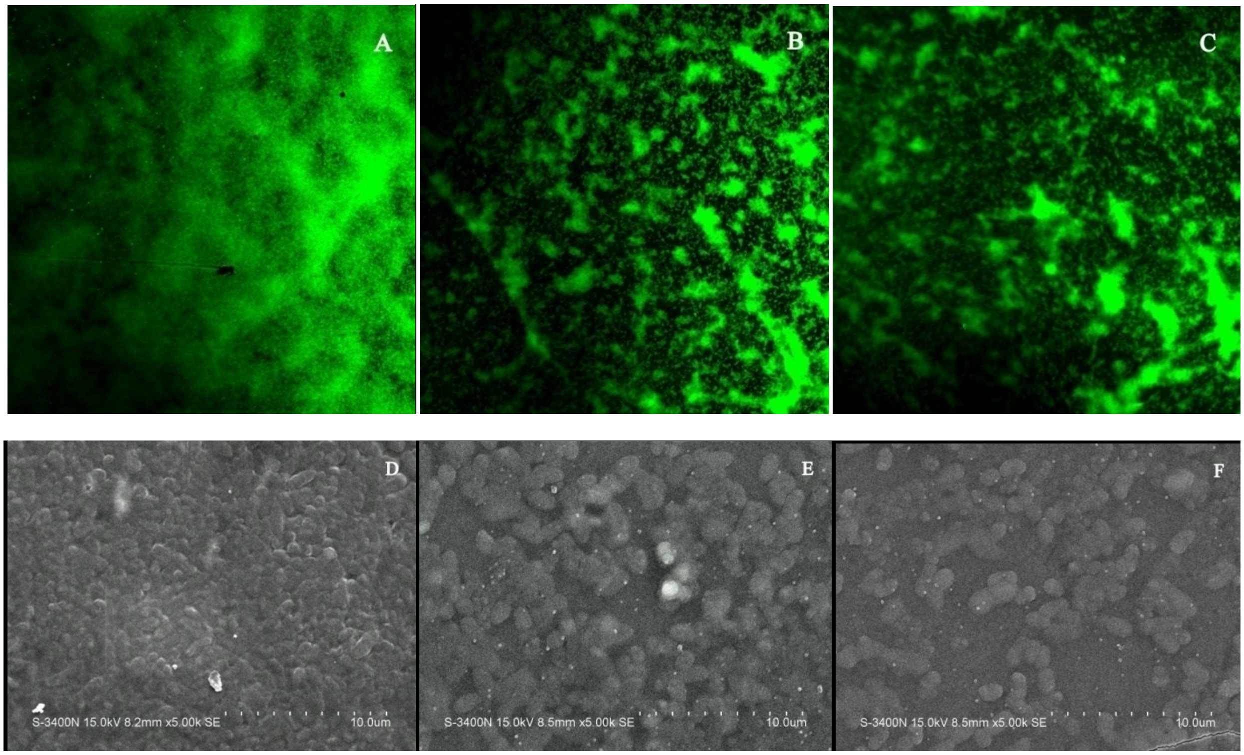
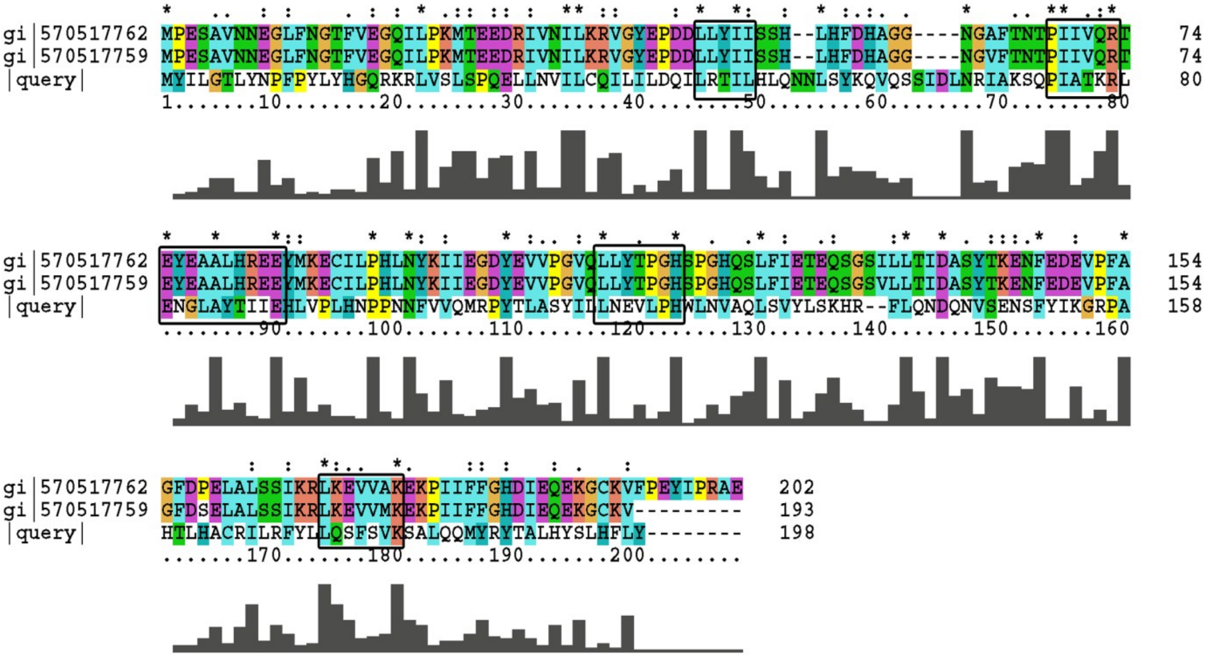

A
B
C
D
E
F
S-3400N 15.0kV 8.2mm x5.00k SE
10.0um
S-3400N 15.0kV 8.5mm x5.00k SE
10.0um
S-3400N 15.0kV 8.5mm x5.00k SE
10.0um

Fig. S6



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gi|570517759  MPESAVNNEGLFNGTFVEGQILPKMTEEDRIVNILKRVGYEPDDLLYIISSH--LHFDHAGG----NGVFTNTPIIVQRT    74
|query|       MYILGTLYNPFPYLYHGQRKRLVSLSPQELLNVILCQILILDQILRTILHLQNNLSYKQVQSSIDLNRIAKSQPIATKRL    80
              1.......10........20........30........40........50........60........70........80

              *   *    *::     *  *: :    * :.. : *  .  *  .  .* :  .:    :*  * . :::.*  :   *
gi|570517762  EYEAALHREEYMKECILPHLNYKIIEGDYEVVPGVQLLYTPGHSPGHQSLFIETEQSGSILLTIDASYTKENFEDEVPFA    154
gi|570517759  EYEAALHREEYMKECILPHLNYKIIEGDYEVVPGVQLLYTPGHSPGHQSLFIETEQSGSVLLTIDASYTKENFEDEVPFA    154
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              ........90.......100.......110.......120.......130.......140.......150.......160

                     :  :  *:..  *.    :: :   : .   :
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gi|570517759  GFDSELALSSIKRLKEVVMKEKPIIFFGHDIEQEKGCKV---------    193
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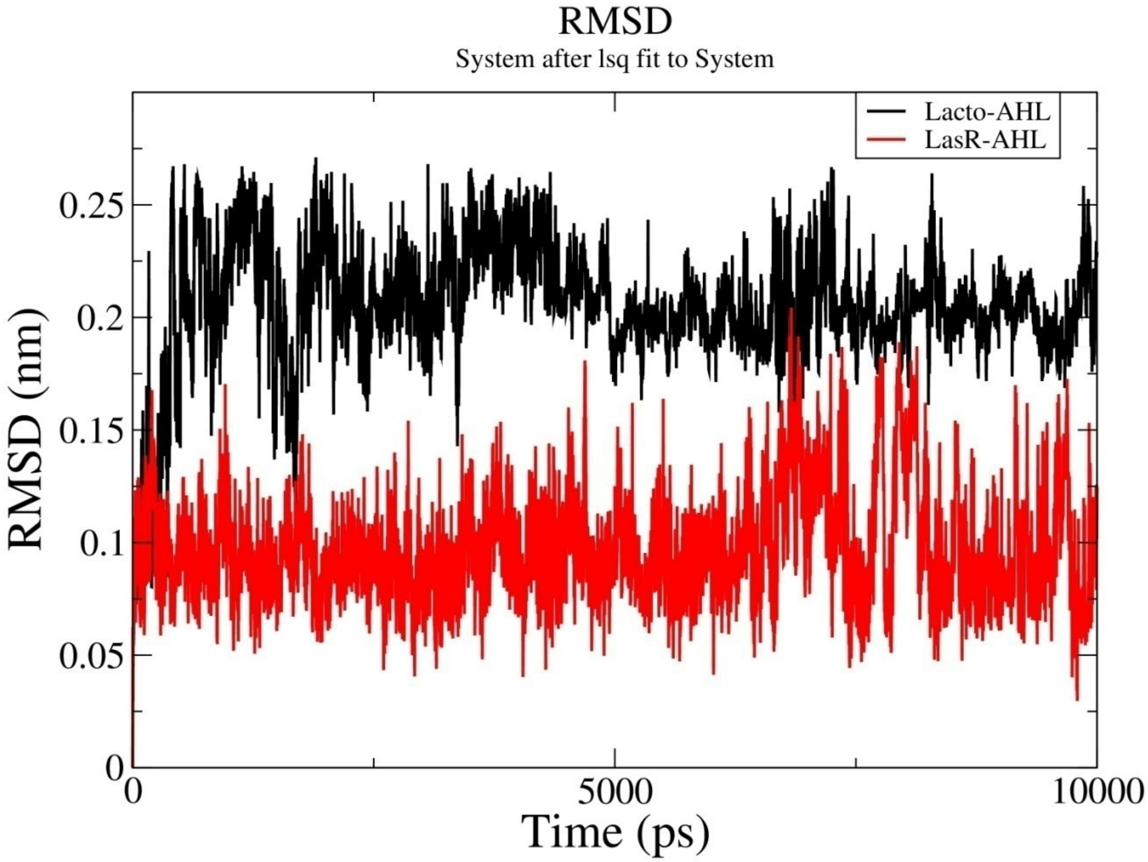
Fig. S7



RMSD
System after lsq fit to System
Lacto-AHL
LasR-AHL
RMSD (nm)
0
0.05
0.1
0.15
0.2
0.25
Time (ps)
0
5000
10000