

Supplementary information

Gut bacteria of *Rattus rattus* (rat) produce broad-spectrum antibacterial lipopeptides

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Figure S1:

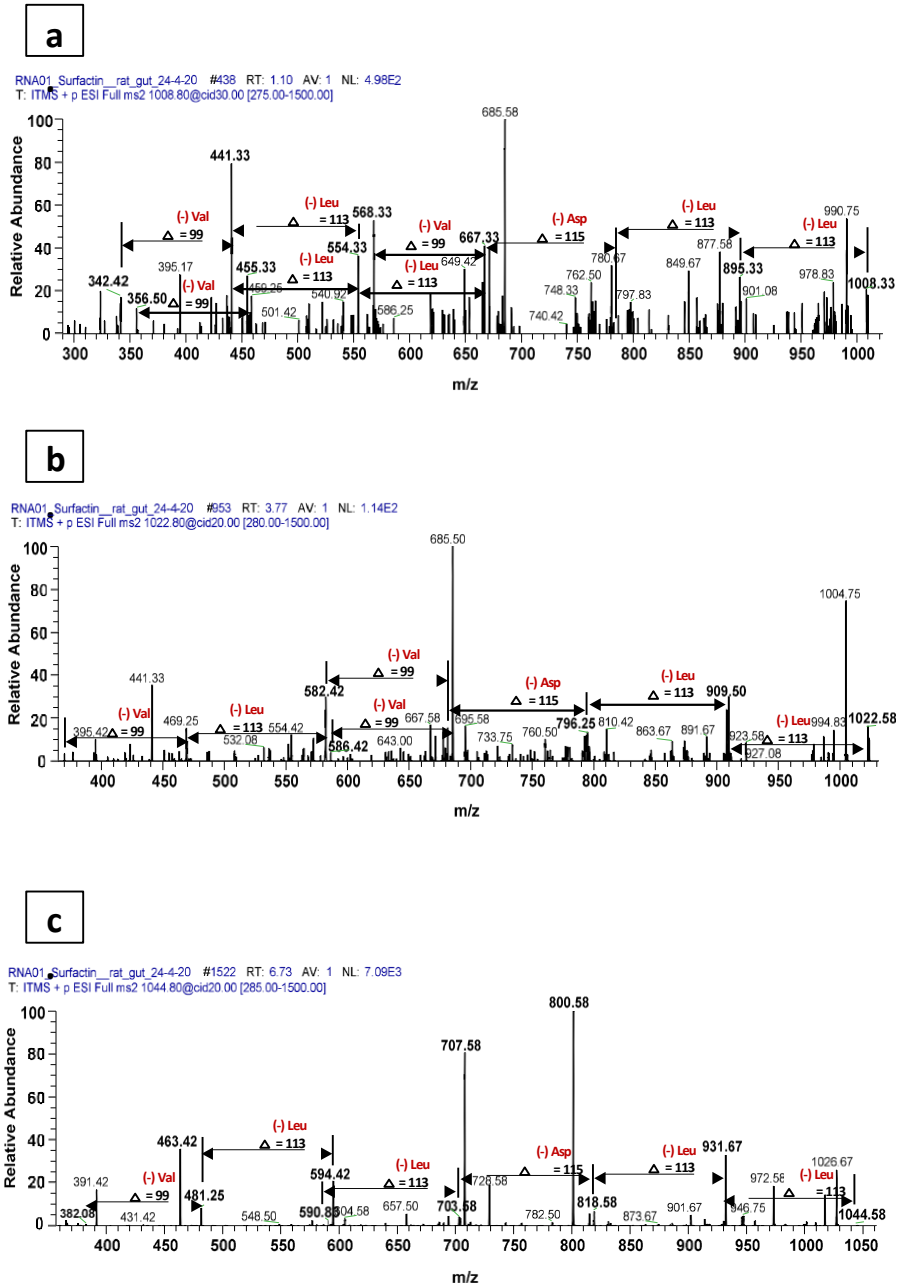


Figure S1:

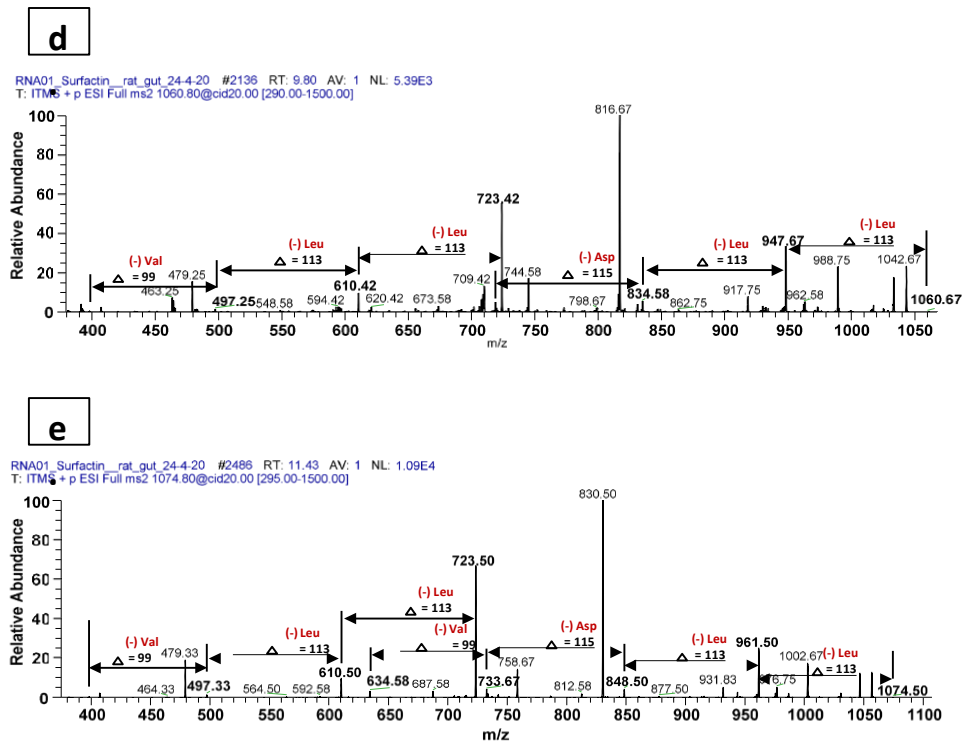
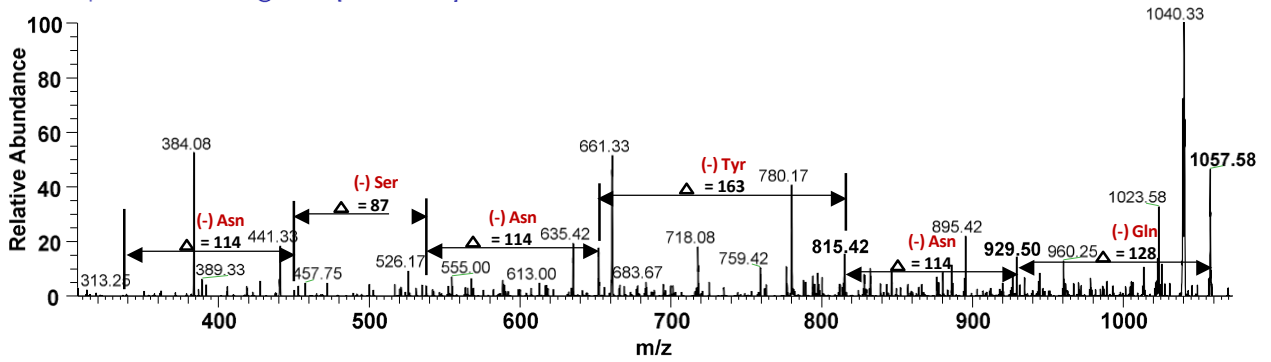


Figure S1. ESI/MS spectrum of *B. subtilis* CM2 extract demonstrated the presence of surfactin analogues analyzed at positive ion mode. **a)** Profiling of the fragmentation data generated through the ESI-MS/MS of m/z 1008.33 $[M+H]^+$ by CID (energy 30.0) at positive ion mode. **b)** Presumed structures of the all fragments ion generated through CID of the m/z 1022.58 $[M+H]^+$. **c)** Putative structures of fragments ions of m/z 1044.58, **d)** Profiling of fragmentation data of 1060.67 and **e)** Profiling of the fragmentation data of 1074.50 $[MMH]^+$.

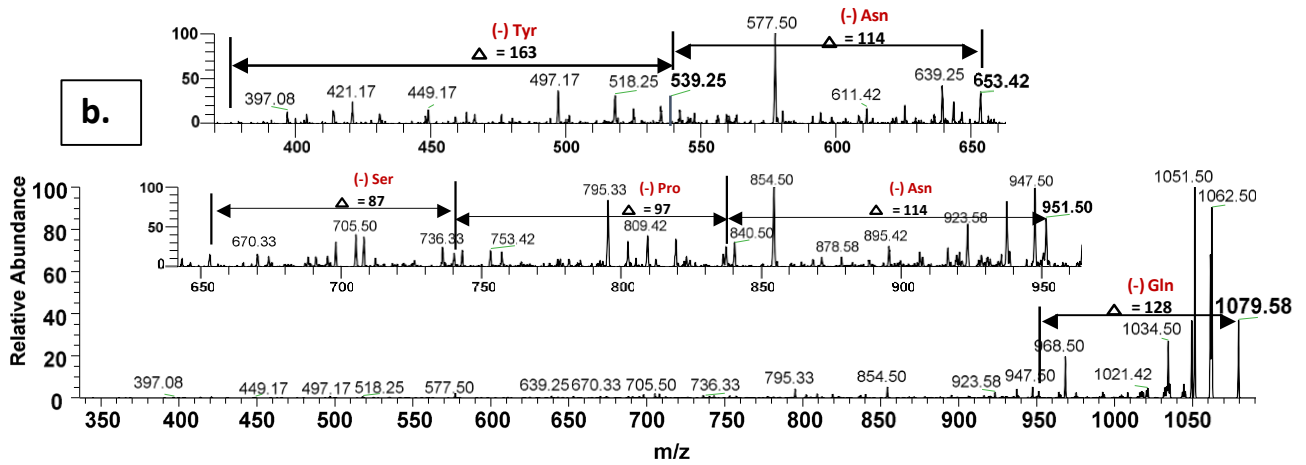
Figure S2:

a.

RNA01_IiturinA_rat_gut #454 RT: 2.73 AV: 1 NL: 5.00E2
T: ITMS + p ESI Full ms2 1057.58@cid10.00 [290.00-1300.00]



b.



c.

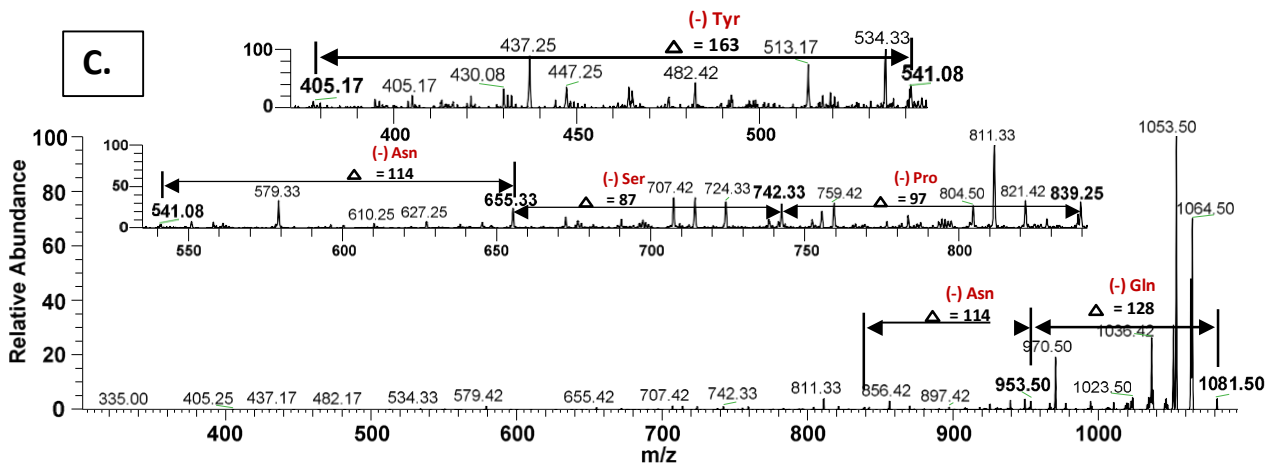
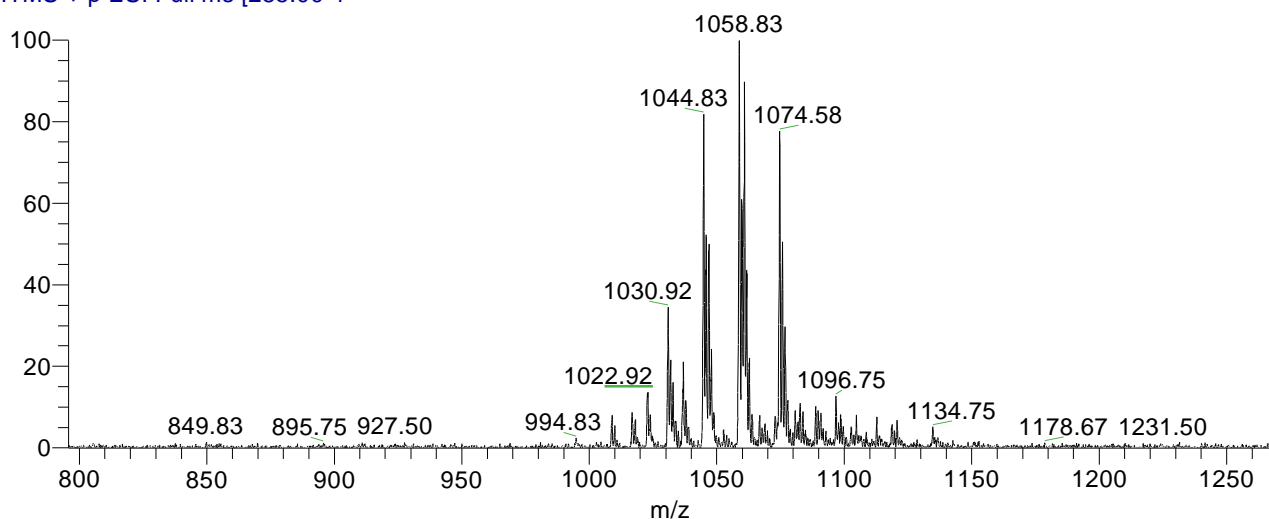


Figure S2. Putative structures of the fragment ion generated through CID of the a) m/z at 1057.58, b) 1079.58 and c) 1081.50 $[M+H]^+$ respectively.

Figure S3:

a.

Surfactin_standard_20-10-20 #1681 RT: 7.48 AV: 1 NL: 6.16E4
T: ITMS + p ESI Full ms [285.00-1



b.

Surfactin_standard_20-10-20 #1170 RT: 4.76 AV: 1 NL: 1.92E3
T: ITMS + p ESI Full ms2 1030.80

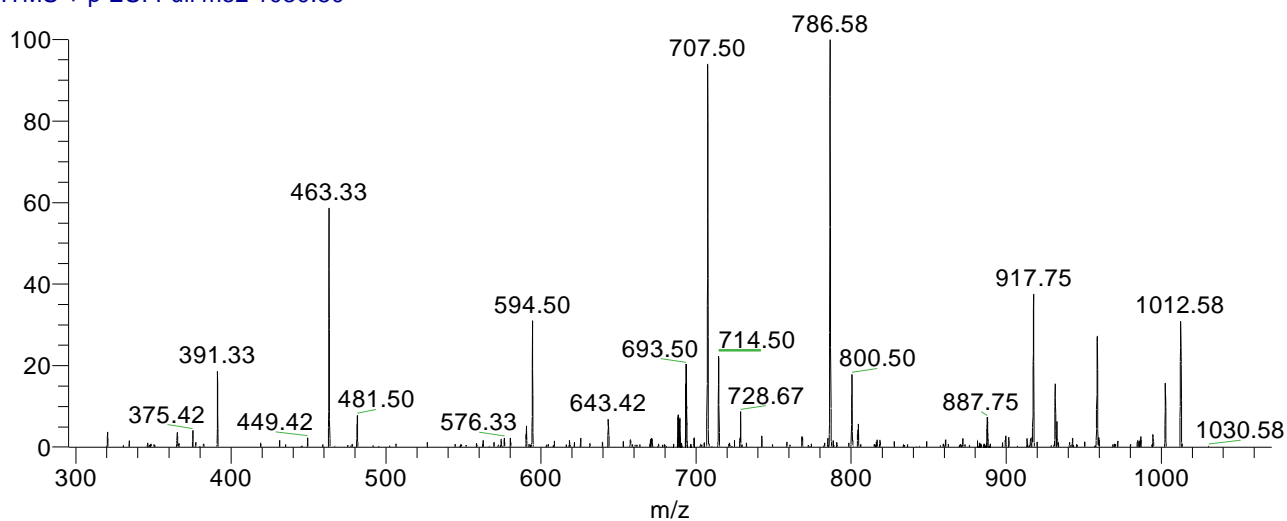
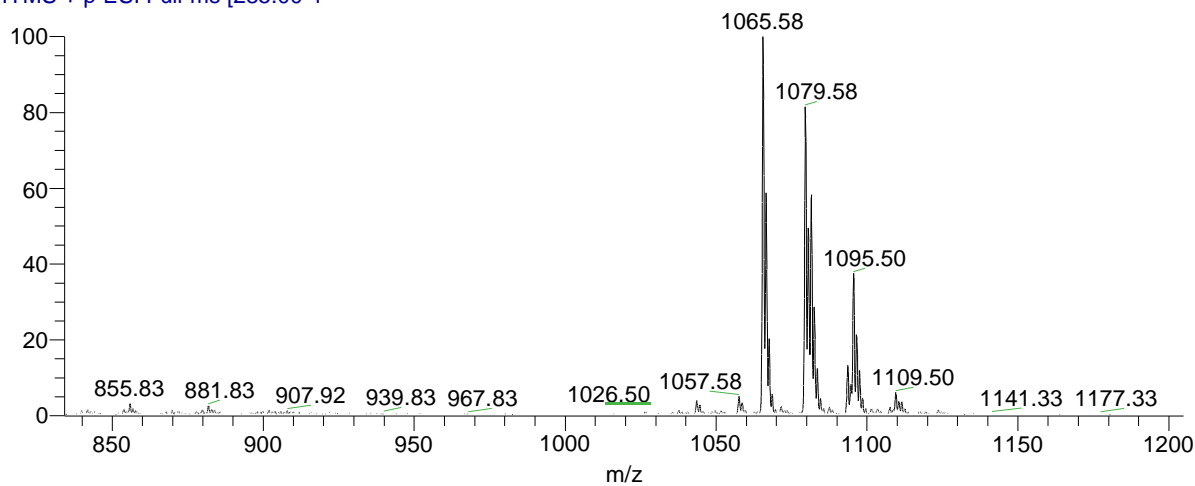


Figure S3. ESI-MS spectrum of surfactin standard. **a)** Full scan spectrum of surfactin molecules and **b)** MS/MS of m/z at 1030.58 $[M+H]^+$.

Figure S4:

a.

Standard Iturin A Sigma #323 RT: 2.00 AV: 1 NL: 2.98E3
T: ITMS + p ESI Full ms [285.00-1



b.

Standard Iturin A Sigma #451 RT: 2.72 AV: 1 NL: 4.12
T: ITMS + p ESI Full ms2 1057.58

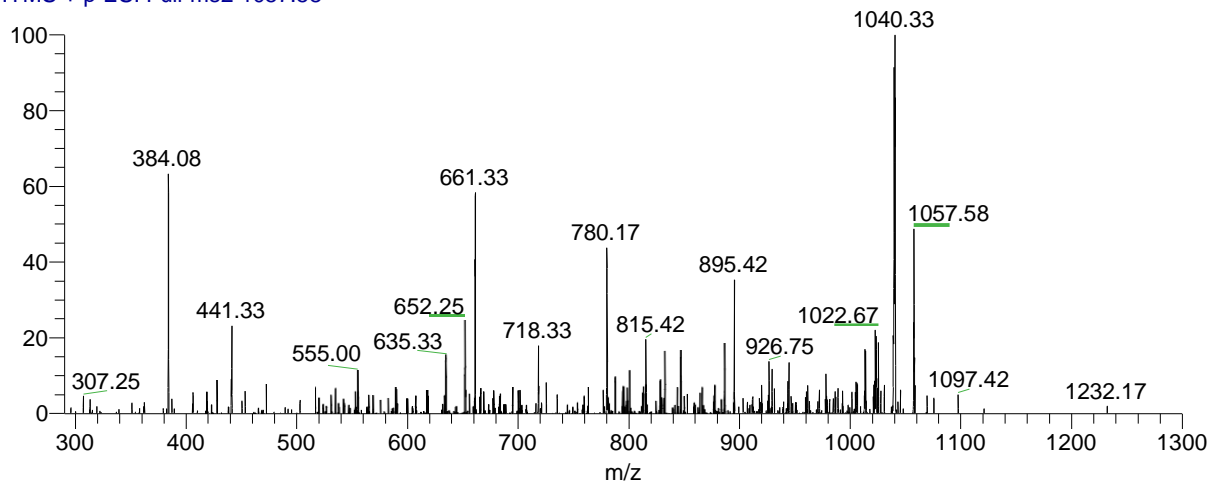


Figure S4. ESI-MS spectrum of Iturin A standard. **a)** Represents the full scan spectrum of Iturin A molecules and **b)** m/z at 1057.58 $[M+H]^+$.