**Genome mining reveal secondary metabolites of antarctic bacterium *Streptomyces albidoflavus* ANT\_B131 related to antimicrobial and antiproliferative activities.**

Paula de França1,2,\*, Jonas Henrique Costa3, Taícia Pacheco Fill3, Marcelo Lancelotti4, Ana Lucia Tasca Gois Ruiz4, Fabiana Fantinatti-Garboggini1,\*.

1 Division of Microbial Resources, Pluridisciplinary Center for Chemical, Biological and Agricultural Research, University of Campinas, Paulínia, SP, Brazil

2Graduate Program in Genetics and Molecular Biology, Institute of Biology, University of Campinas, Campinas, SP, Brazil

3Institute of Chemistry, University of Campinas, CP 6154, 13083-970, Campinas, SP, Brazil.

4 Faculty of Pharmaceutical Sciences, University of Campinas, Campinas, SP, Brazil.

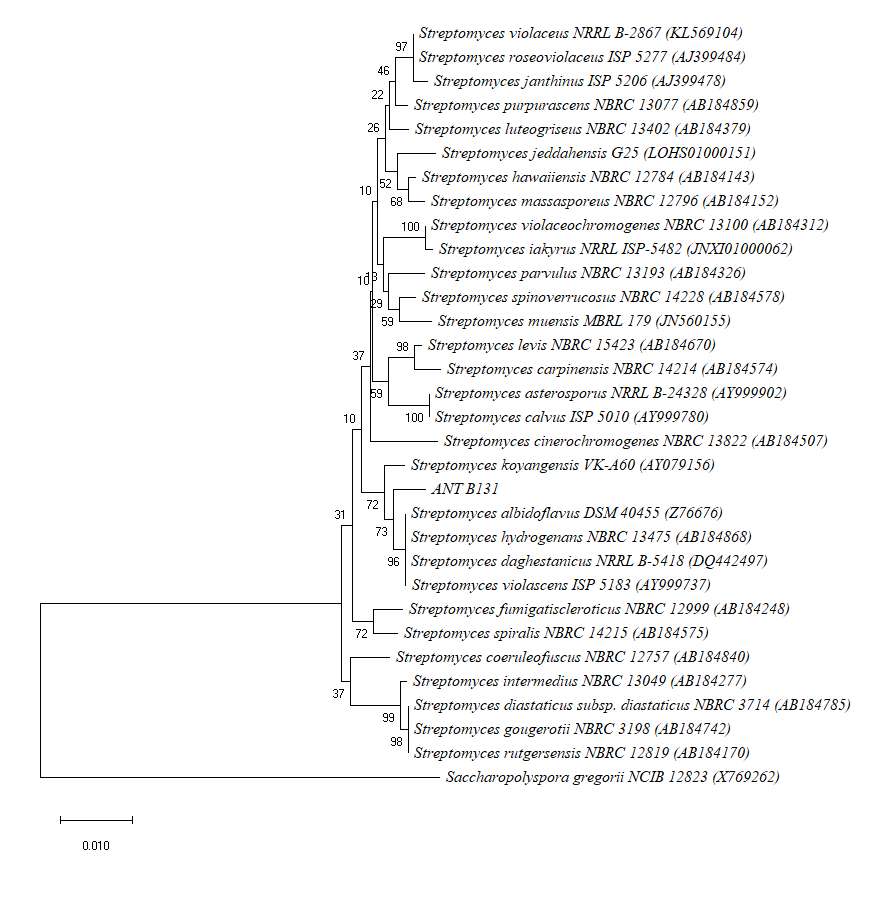
**\*Correspondence:**

Paula de França

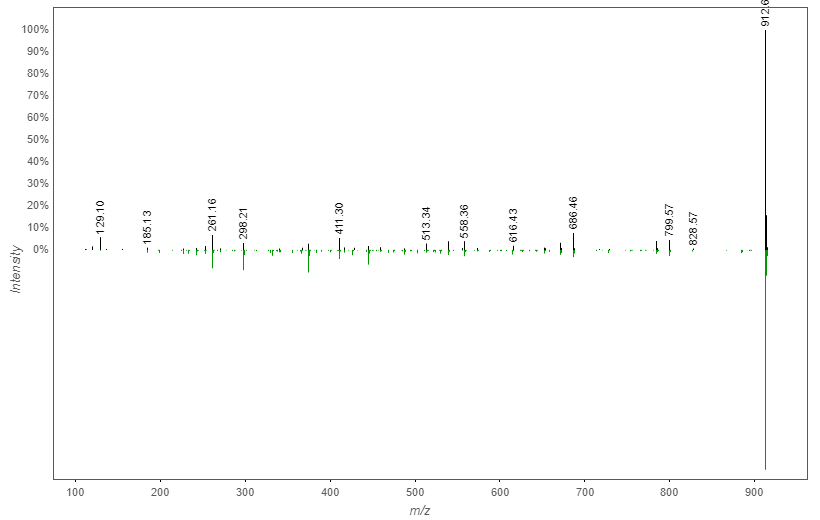
pauladfranca@gmail.com

Dr. Fabiana Fantinatti-Garboggini  
fabianaf@cpqba.unicamp.br

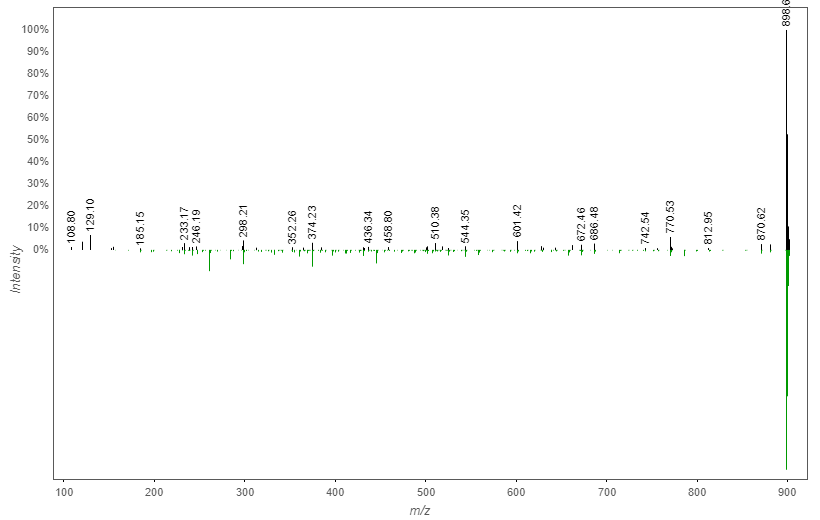
**SUPPORT INFORMATION**



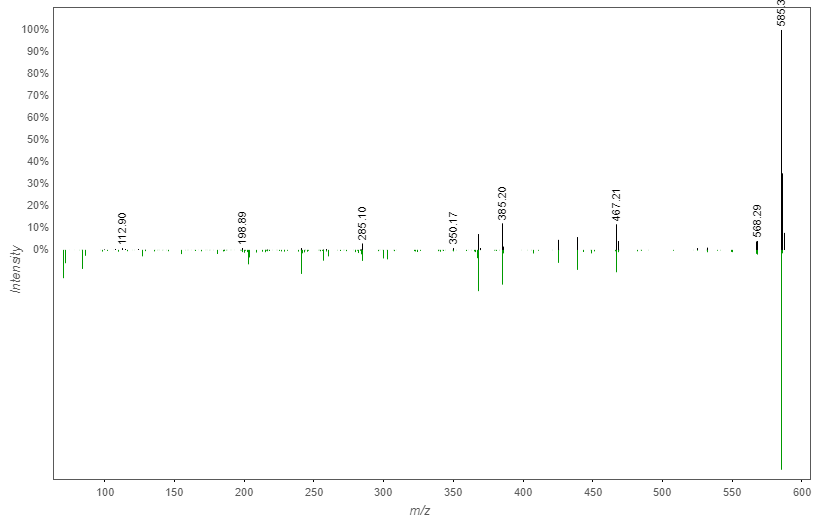
Supplementary Figure. 1. Phylogenetic tree based on the phylogenetic analysis of the 16S ribosomal RNA gene sequence of the ANT\_B131 bacteria isolated from Antarctic and related microorganisms. Bootstrap values (1000 repetitions, showed as %) are listed. Scale bar represents 1 nucleotide substitution per 100 nucleotides position. *Saccharopolyspora gregorii* NCIB 12823 was used as outgroup.



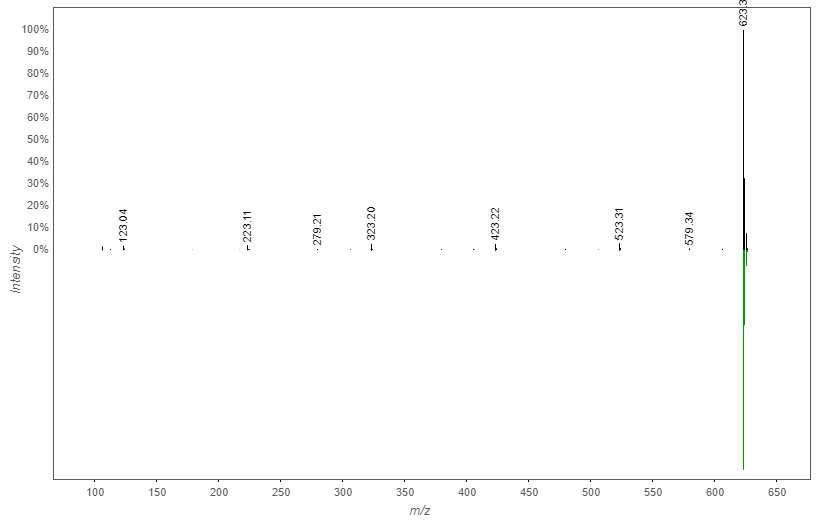
Supplementary Figure 2. MS/MS match for surugamide A between GNPS database (green) and *S. albidoflavus* ANT\_B131 extracts (black).



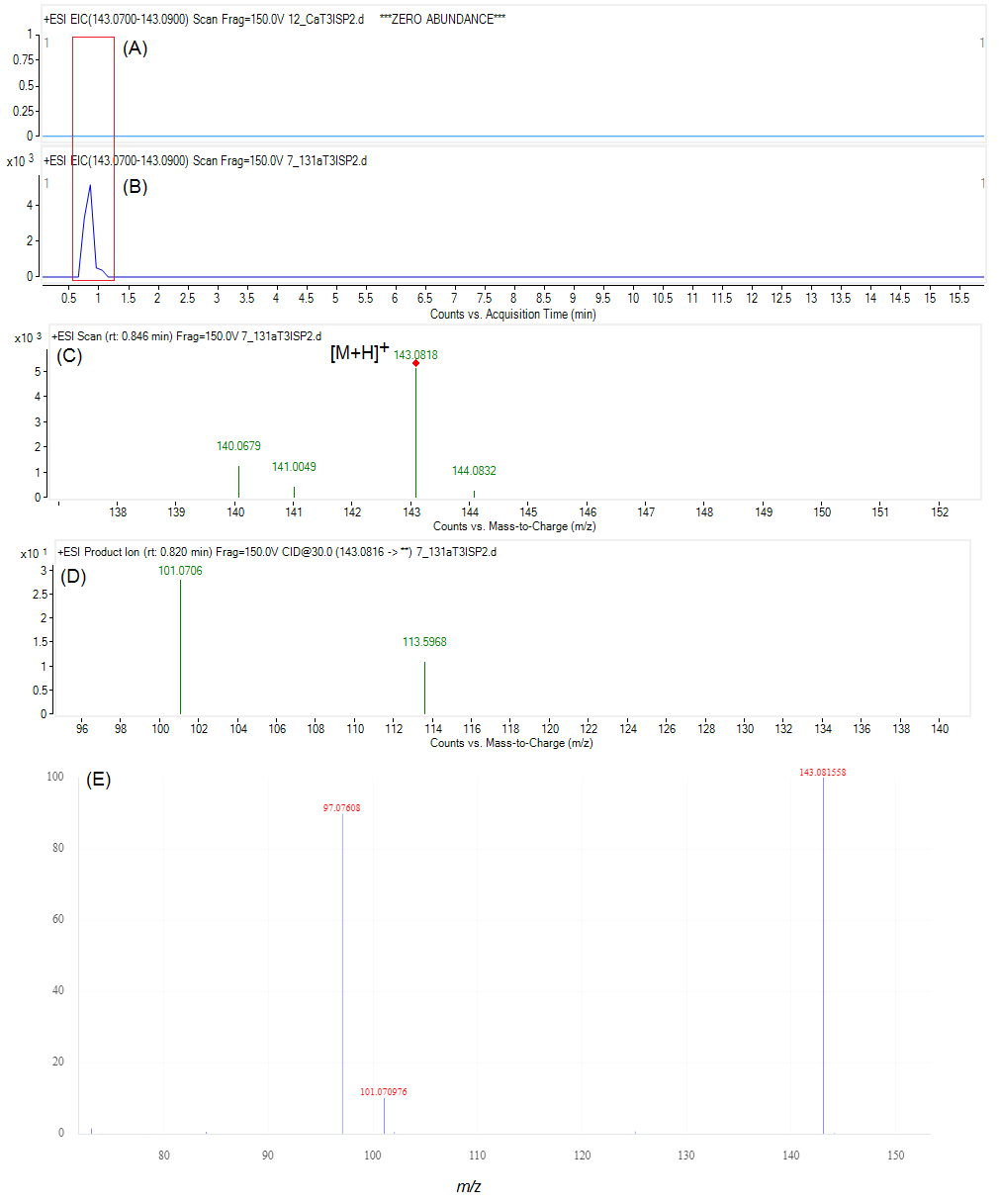
Supplementary Figure 3. MS/MS match for surugamide D between GNPS database (green) and *S. albidoflavus* ANT\_B131 extracts (black).



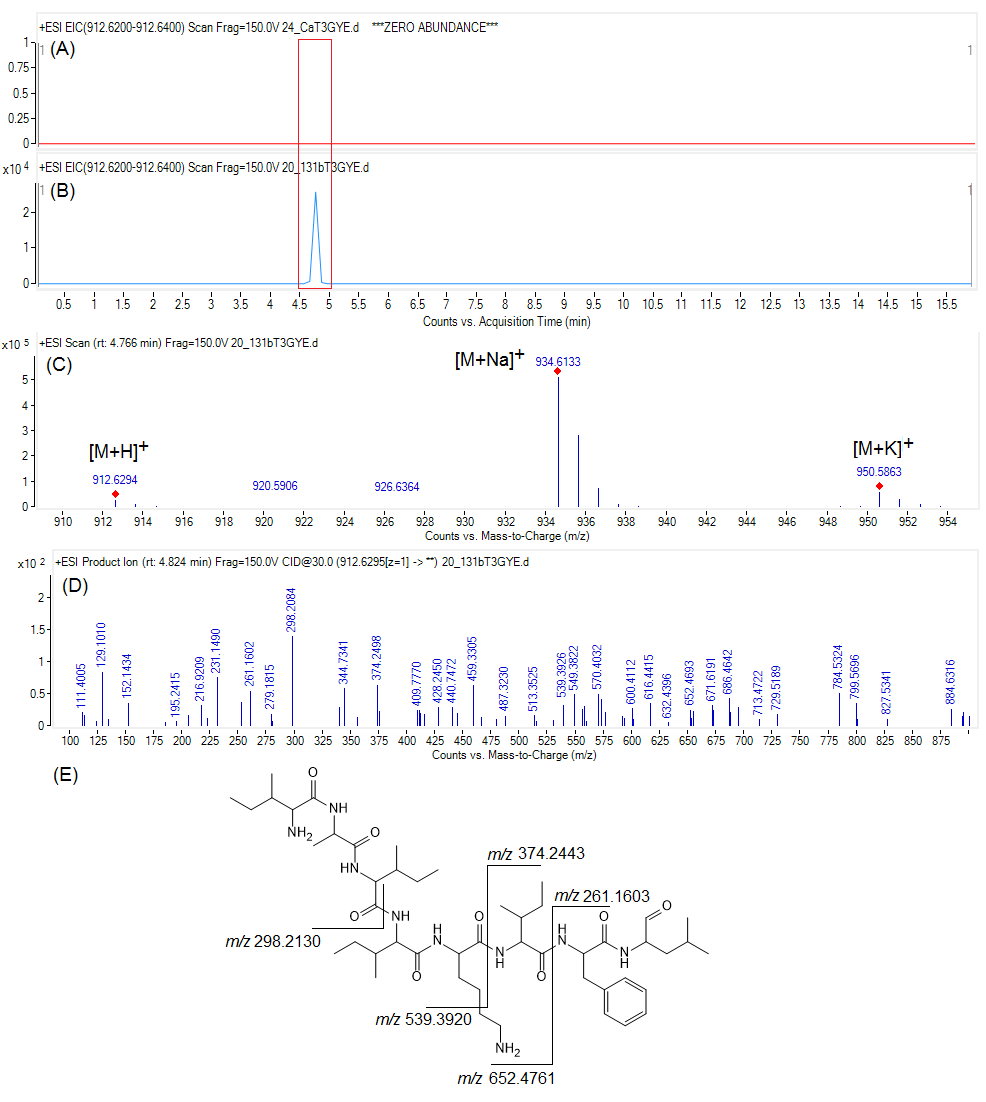
Supplementary Figure 4. MS/MS match for desferrioxamine B between GNPS database (green) and *S. albidoflavus* ANT\_B131 extracts (black).



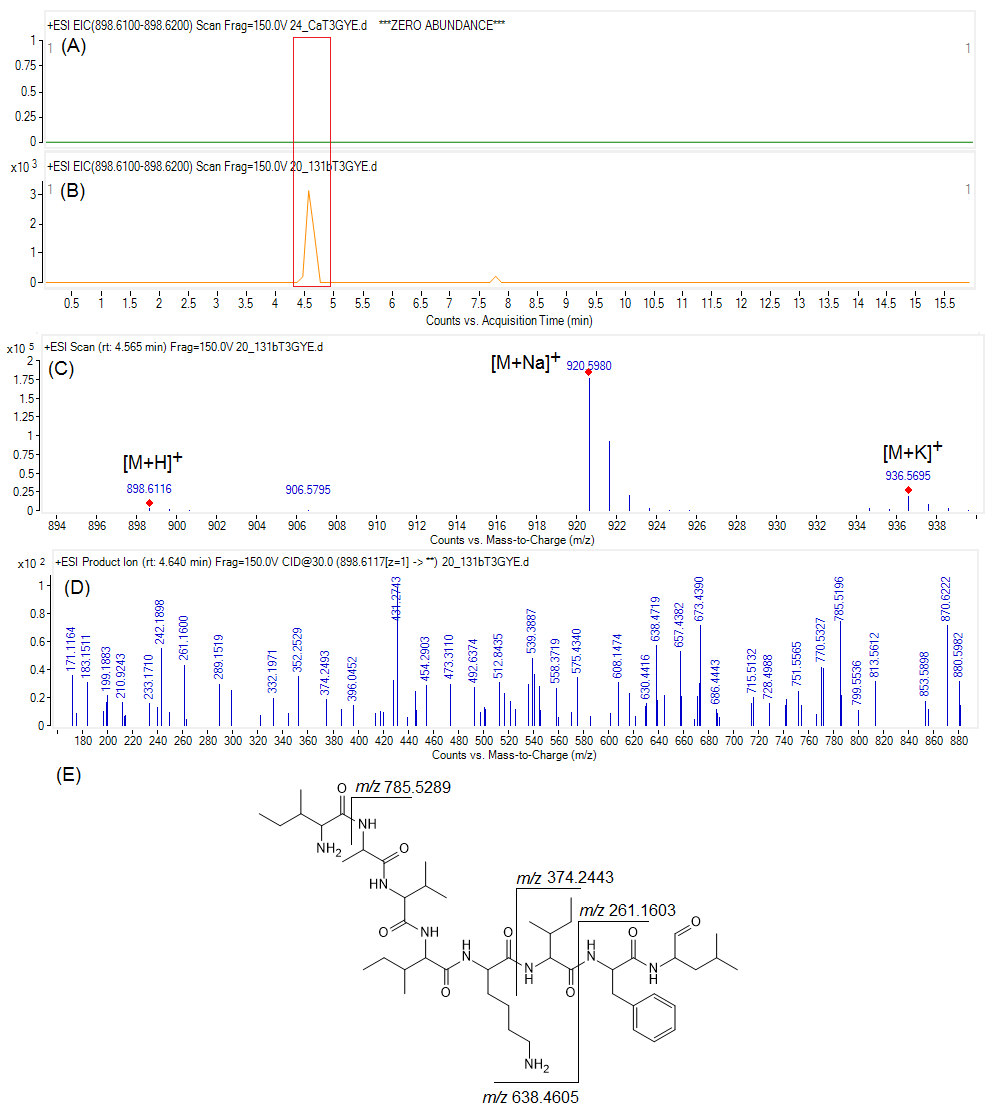
Supplementary Figure 5. MS/MS match for desferrioxamine E between GNPS database (green) and *S. albidoflavus* ANT\_B131 extracts (black).

****

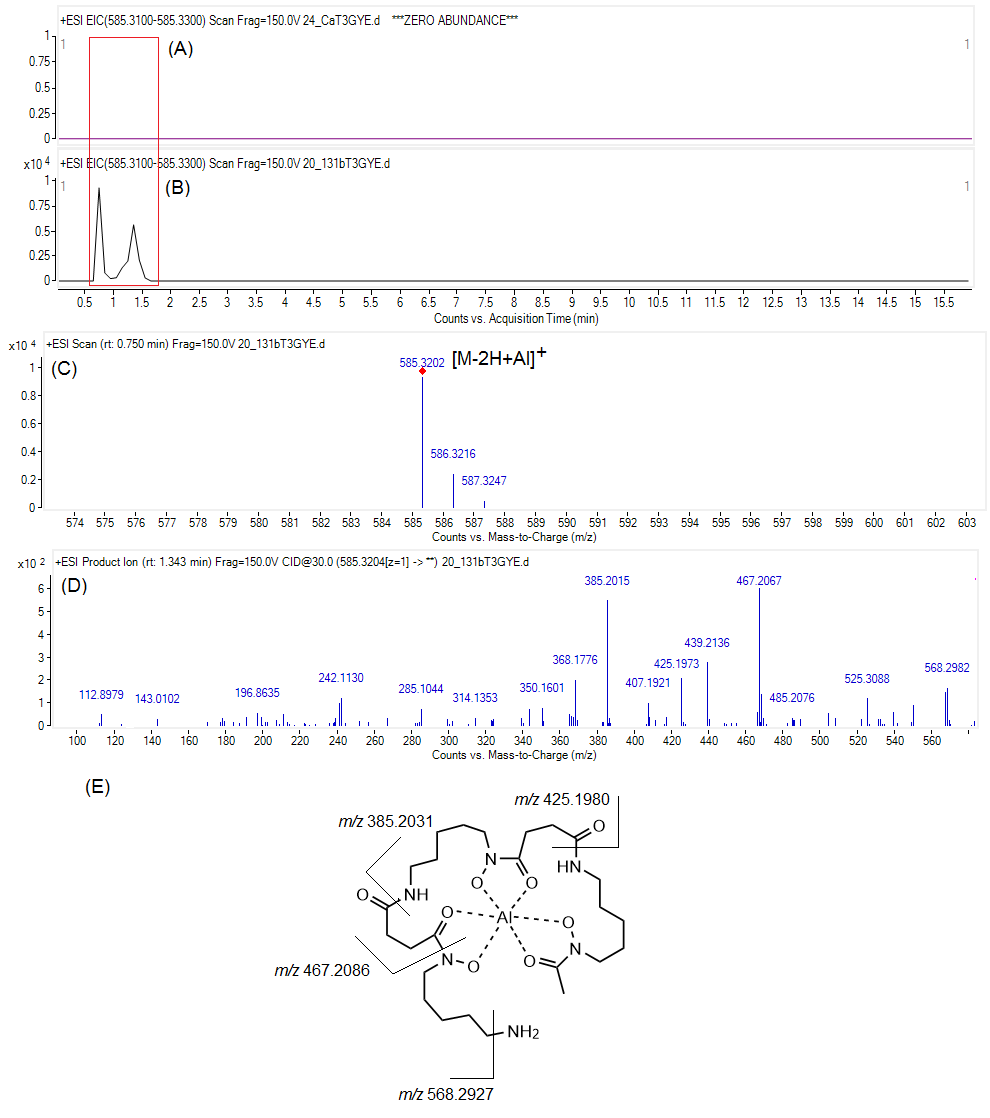
Supplementary Figure 6. Extracted ion chromatograms of *m/z* 143.08 for extracts of (A) culture media (control) and (B) *S. albidoflavus* ANT\_B131. (C) Mass spectrum obtained for ectoine. (D) MS/MS spectrum of ion [M+H]+ *m/z* 143.0816. (E) MS/MS spectrum of ectoine in Mass MassBank of North America database (adapted from https://mona.fiehnlab.ucdavis.edu/spectra/display/CCMSLIB00005435933 - acessed 18th September of 2020).



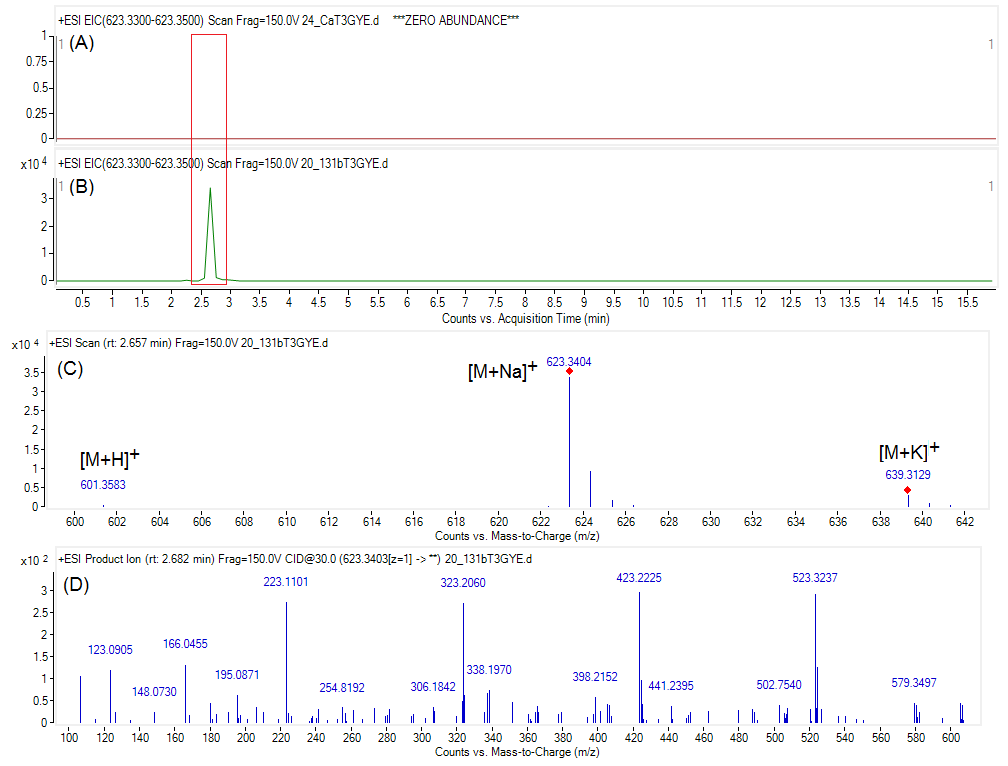
Supplementary Figure 7. Extracted ion chromatograms of *m/z* 912.62 for (A) culture media (control) and (B) *S. albidoflavus* ANT\_B131. (C) Mass spectrum obtained for surugamide A.(D) MS/MS spectrum of ion [M+H]+ *m/z* 912.6295. (E) Typical mass fragments of surugamide A.



Supplementary Figure 8. Extracted ion chromatograms of *m/z* 898.61 for (A) culture media (control) and (B) *S. albidoflavus* ANT\_B131. (C) Mass spectrum obtained for surugamide D.(D) MS/MS spectrum of ion [M+H]+ *m/z* 898.6117. (E) Typical mass fragments of surugamide D.



Supplementary Figure 9. Extracted ion chromatograms of *m/z* 585.32 for (A) culture media (control) and (B) *S. albidoflavus* ANT\_B131. (C) Mass spectrum obtained for desferrioxamine B.(D) MS/MS spectrum of ion [M-2H+Al]+ *m/z* 585.3204. (E) Typical mass fragments of desferrioxamine B + Al.



Supplementary Figure 10. Extracted ion chromatograms of *m/z* 623.34 for (A) culture media (control) and (B) *S. albidoflavus* ANT\_B131. (C) Mass spectrum obtained for desferrioxamine E.(D) MS/MS spectrum of ion [M+Na]+ *m/z* 623.3403.

Supplementary Table 1. Sequence accession number of genes used in Multilocus Sequence Analysis

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| **Name** | **Strain** | **Accession number GenBank** | | | | |
| **atpD** | **gyrB** | **recA** | **rpoB** | **trpB** |
| *Streptomyces daghestanicus* | NRRL B-5418 | KJ137021 | KJ137038 | KJ137055 | KJ137072 | KJ137089 |
| *Streptomyces albidoflavus* | NRRL B-1271 | KT384451 | KT384800 | KT385148 | KT388770 | KT389120 |
| *Streptomyces violascens* | NRRL B-2700 | KT384752 | KT385100 | KT385454 | KT389072 | KT389421 |
| *Streptomyces violaceochromogenes* | NRRL B-5427 | KT384748 | KT385096 | KT385450 | KT389068 | KT389417 |
| *Streptomyces purpurascens* | NRRL B-12230 | KT384696 | KT385046 | KT385397 | KT389017 | KT389365 |
| *Streptomyces luteogriseus* | NRRL B-12422 | KT384632 | KT384981 | KT385332 | KT388952 | KT389301 |
| *Streptomyces hawaiiensis* | NRRL B-1988 | KT384592 | KT384941 | KT385290 | KT388912 | KT389261 |
| *Streptomyces levis* | NRRL B-16370 | KT384621 | KT384970 | KT385320 | KT388941 | KT389290 |
| *Streptomyces violaceus* | JCM 4533 | LC381981 | LC381982 | LC381983 | LC381984 |  |
| *Streptomyces iakyrus* | NRRL B-3317 | KT384600 | KT384949 | KT385298 | KT388920 | KT389269 |
| *Streptomyces massasporeus* | NRRL B-3300 | KT384636 | KT384985 | KT385336 | KT388956 | KT389305 |
| *Streptomyces roseoviolaceus* | NRRL B-12177 | KT384710 | KT385060 | KT385411 | KT389031 | KT389379 |
| *Streptomyces janthinus* | NRRL B-3365 | KT384604 | KT384953 | KT385303 | KT388924 | KT389273 |
| *Streptomyces carpinensis* | NRRL B-16921 | KT384503 | KT384852 | KT385200 | KT388822 | KT389172 |
| *Streptomyces cinerochromogenes* | NRRL B-16928 | KT384514 | KT384863 | KT385211 | KT388833 | KT389183 |
| *Streptomyces parvulus* | NRRL B-1628 | KJ196367 | KJ196369 | KJ196371 | KJ196373 | KJ196375 |
| *Streptomyces muensis* | JCM 17576 | KX784758 |  | KX784760 | KX784762 | KX784764 |
| *Streptomyces asterosporus* | NRRL B-24328 | KT384471 | KT384820 | KT385168 | KT388790 | KT389140 |

Supplementary Table 2. Pairwise correlation between whole genome of *S. albidoflavus* ANT\_B131 and phylogenetic closest strains *S. albidoflavus* SM254 and *S. albidoflavus* J1074.

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| Pairwise correlation between strains | ANIb (%) | ANIm (%) | TETRA | isDDH | Difference in %G+C |
| ANT\_B131 x SM254 | 97.41 | 97.78 | 0.99961 | 79.50 | 0.17 |
| ANTB\_131 x J1074 | 97.02 | 97.80 | 0.99952 | 79.60 | 0.15 |