

Supplementary Information

Genome Mining of Endophytic *Streptomyces wadayamensis* Reveals High Antibiotic Production Capability

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Table S1. Gene clusters type predicted by antiSMASH 3.0.5

BGC overview	Input name	Coordinates (nt location in the contig)	Gene cluster type
Cluster 1	LGO_A23_AS11_SC01	174778 - 225031	nrps-t1pks
Cluster 2	LGO_A23_AS11_SC01	258744 - 285332	terpene
Cluster 3	LGO_A23_AS11_SC01	365799 - 376053	bacteriocin
Cluster 4	LGO_A23_AS11_SC02	1 - 80422	t1pks
Cluster 5	LGO_A23_AS11_SC02	85376 - 126473	t3pks
Cluster 6	LGO_A23_AS11_SC02	208192 - 240719	terpene-bacteriocin
Cluster 7	LGO_A23_AS11_SC02	255844 - 300115	other
Cluster 8	LGO_A23_AS11_SC03	174427 - 195716	terpene
Cluster 9	LGO_A23_AS11_SC04	226420 - 263658	nrps
Cluster 10	LGO_A23_AS11_SC06	33172 - 55459	lassopeptide
Cluster 11	LGO_A23_AS11_SC06	214649 - 239475	nrps
Cluster 12	LGO_A23_AS11_SC08	175044 - 197626	terpene
Cluster 13	LGO_A23_AS11_SC08	191339 - 232541	nrps
Cluster 14	LGO_A23_AS11_SC12	2364 - 47328	nrps
Cluster 15	LGO_A23_AS11_SC13	174427 - 195716	ectoine
Cluster 16	LGO_A23_AS11_SC14	1 - 69344	t1pks
Cluster 17	LGO_A23_AS11_SC14	65097 - 139158	nrps-t1pks-lantipeptide
Cluster 18	LGO_A23_AS11_SC14	121771 - 149291	other
Cluster 19	LGO_A23_AS11_SC19	103751 - 123292	thiopeptide-lantipeptide
Cluster 20	LGO_A23_AS11_SC21	1 - 13059	lantipeptide
Cluster 21	LGO_A23_AS11_SC21	35751 - 96211	nrps
Cluster 22	LGO_A23_AS11_SC25	18428 - 30248	siderophore
Cluster 23	LGO_A23_AS11_SC35	39933 - 70892	nrps
Cluster 24	LGO_A23_AS11_SC38	37758 - 63241	nrps
Cluster 25	LGO_A23_AS11_SC42	6543 - 28843	terpene
Cluster 26	LGO_A23_AS11_SC44	14854 - 29885	siderophore
Cluster 27	LGO_A23_AS11_SC50	1 - 43271	nrps
Cluster 28	LGO_A23_AS11_SC52	8081 - 37721	nrps
Cluster 29	LGO_A23_AS11_SC57	12000 - 28910	bacteriocin
Cluster 30	LGO_A23_AS11_SC61	1 - 21760	t1pks
Cluster 31	LGO_A23_AS11_SC71	1 - 7760	t1pks
Cluster 32	LGO_A23_AS11_SC83	1 - 2205	nrps

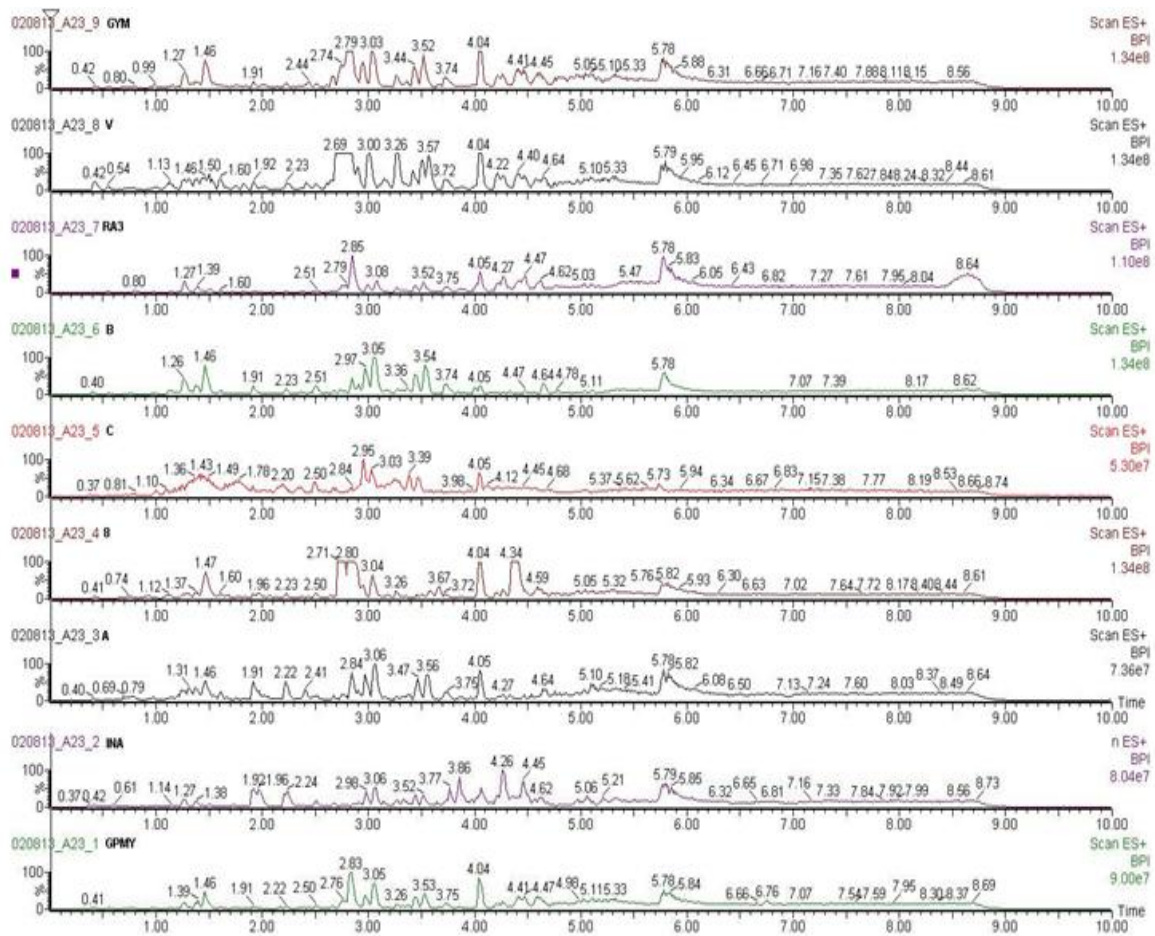
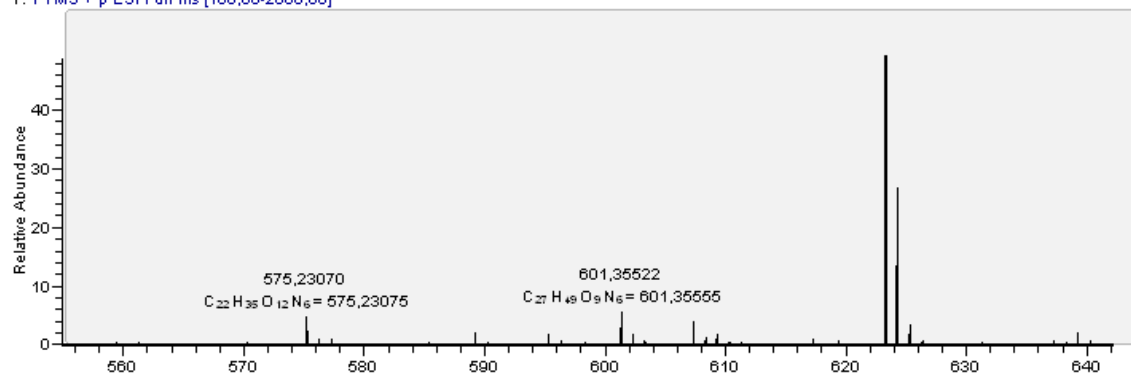


Figure S1. BPI chromatograms profile from ethyl acetate extracts of *S. wadayamensis* fermentation (GYM, V, RA3, B, C, 8, A, INA, GPMY) obtained by using UPLC-MS.

A_E POS #1 RT: 0,05 AV: 1 NL: 7,50E6
T: FTMS + p ESI Full ms [100,00-2000,00]



SCAN

MS MS 8 50 eV Fracao 9 9 (1.643) Cm (1:15)

1: Daughters of 601ES+
4.65e5

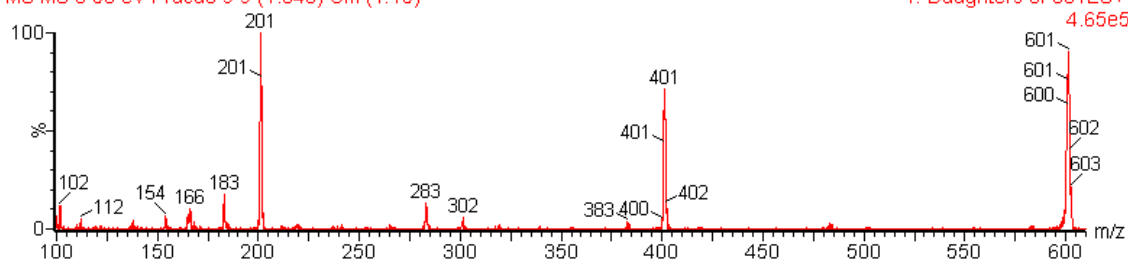


Figure S2. ESI(+) FT-ICR-MS of *Streptomyces* A23 crude extract (A medium) showing protonated Desferoxamine E (601.3552, $C_{27}H_{48}N_6O_9$); the fragmentation pattern of this class of compounds corresponds to neutral loss succinylcadaverine (neutral loss of 200 Da).

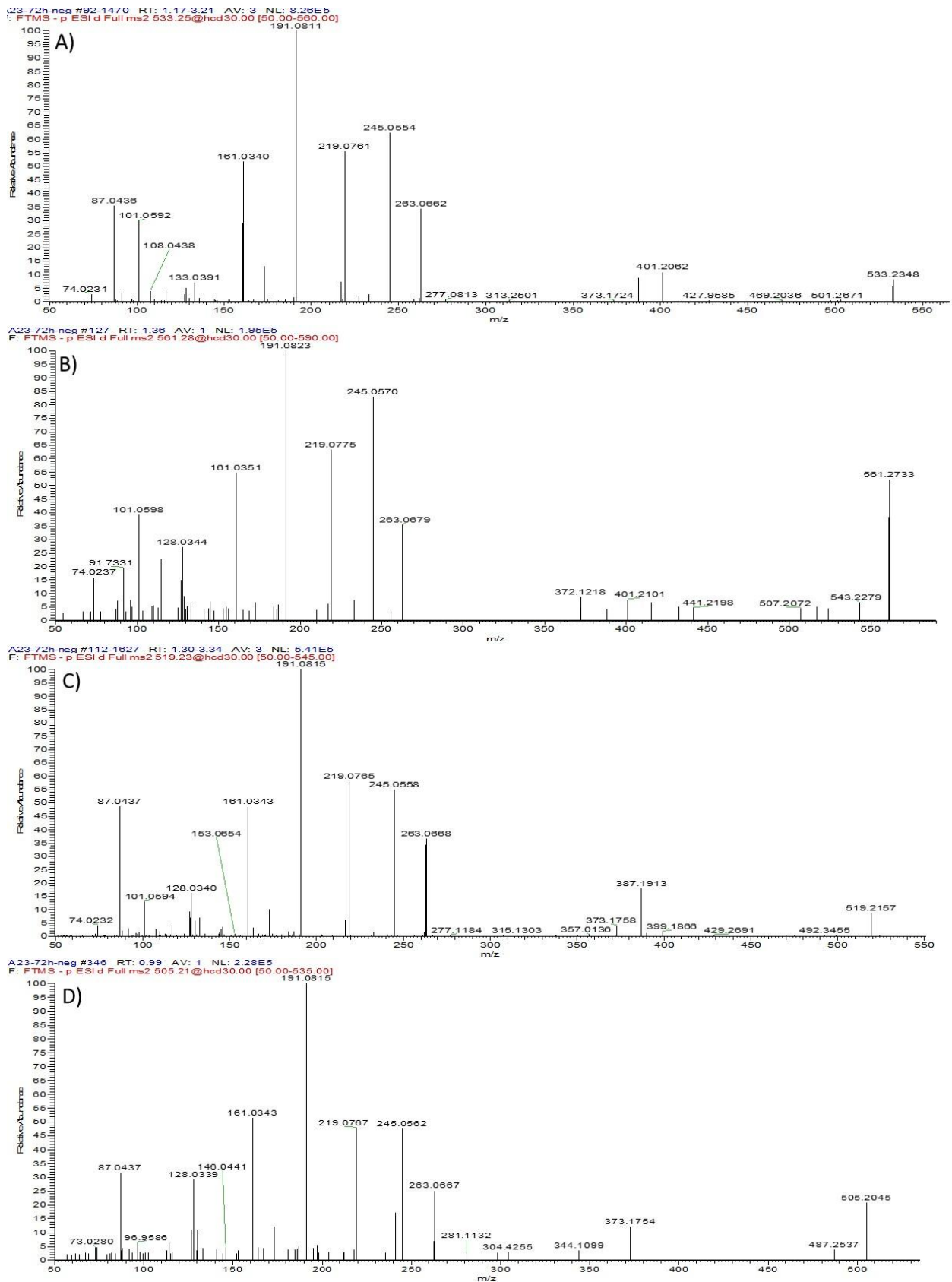


Figure S3. ESI(-) FT-ICR-MS/MS of *Streptomyces* A23 crude extract (AFMS medium) showing fragmentation of deprotonated antimycin analogues: (A) antimycins A2 and/or A8 of m/z 533.2348; (B) antimycin A10 and/or A15 of m/z of 561.2733; (C) antimycin A3 and/or A7 of m/z of 519.2157; and (D) antimycin A4 of m/z 505.2202.

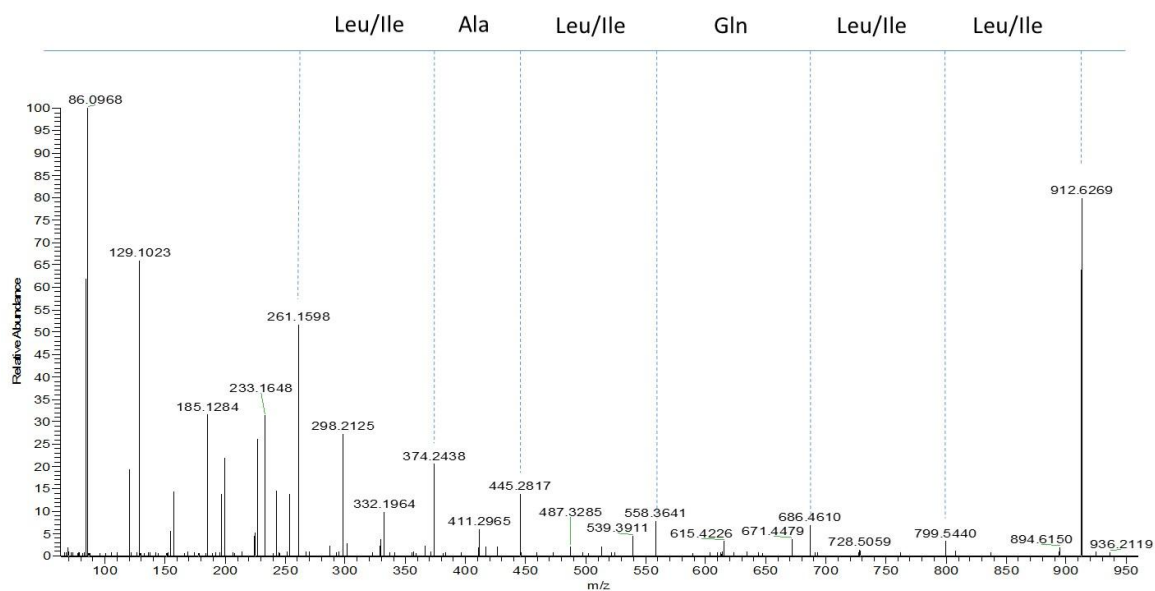


Figure S4. ESI(+)-FT-ICR-MS/MS of *Streptomyces* A23 crude extract (Anti 2 medium) showing fragmentation and annotation of the ion of m/z 912.6269 corresponding to a possible linear NRPS.