Natural products from Actinobacteria associated with fungus-growing termites

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Table S1. Information of colonies of *Macrotermes natalensis* (Mn) used for isolation of actinobacteria for metatranscriptome data (including one *Odontotermes* colony [Od]), along with their geographic locations and year of collection.

colony ID	geographic location	GPS location	year	use
Mn101	ARC	S25 43 41.9 E28 14 06.1	2010	Bacteria isolation
Mn102	ARC	S25 43 45.2 E28 14 05.8	2010	Bacteria isolation
Mn103	ARC	S25 43 45.9 E28 14 08.9	2010	Bacteria isolation
Mn104	ARC	S25 43 44.8 E28 14 20.6	2010	Bacteria isolation
Mn105	Mookgophong	S24 40 30.5 E28 47 50.4	2010	Bacteria isolation
Mn106	Mookgophong	S24 40 30.5 E28 47 50.4	2010	Bacteria isolation
Mn107	Mookgophong	S24 40 30.5 E28 47 50.4	2010	Bacteria isolation
Mn110	ARC	S25 43 53.2 E28 14 12.0	2010	Bacteria isolation
Mn156	Experimental farm	S25 44.623 E28 15.655	2016	metatranscriptomic
Mn160	Experimental farm	S25 44 34.7 E28 15 38.7	2015	Bacteria isolation
Mn162	Mookgophong	S24 40 30.5 E28 47 50.4	2015	Bacteria isolation
Mn163	ARC	S25 43.761 E28 14.167	2015	Bacteria isolation
Od127	Experimental farm	S25 44.562 E28 15.391	2016	metatranscriptomic

Table S2. Strains isolated from fungus-growing termites, including the medium they were initially isolated on, their ID and the ID of the chemical extract.

Colony	**Termite species**	**Colony part**	**Bacteria genus**	**Isolation media**	**Bacteria ID**	**Extract ID**
Mn101	*Macrotermes natalensis*	abdomen	*Streptomyces*	chitin	RB90	E77
Mn101	*Macrotermes natalensis*	abdomen	*Streptomyces*	chitin	RB91	E49
Mn101	*Macrotermes natalensis*	abdomen	*Streptomyces*	chitin	RB92	E144
Mn101	*Macrotermes natalensis*	abdomen	*Streptomyces*	chitin	RB93	E148
Mn101	*Macrotermes natalensis*	abdomen	*Streptomyces*	MC	RB94	E61
Mn102	*Macrotermes natalensis*	comb	*Streptomyces*	chitin	RB102	E143
Mn103	*Macrotermes natalensis*	comb	*Streptomyces*	MC	RB3	E47
Mn103	*Macrotermes natalensis*	comb	*Streptomyces*	chitin	RB108	E45
Mn103	*Macrotermes natalensis*	comb	*Streptomyces*	MC	RB111	E154
Mn104	*Macrotermes natalensis*	abdomen	*Streptomyces*	MC	RB2	E58
Mn104	*Macrotermes natalensis*	abdomen	*Streptomyces*	chitin	RB95	E149
Mn104	*Macrotermes natalensis*	abdomen	*Streptomyces*	chitin	RB96	E150
Mn104	*Macrotermes natalensis*	abdomen	*Streptomyces*	chitin	RB97	E151
Mn104	*Macrotermes natalensis*	comb	*Streptomyces*	chitin	RB103	E153
Mn105	*Macrotermes natalensis*	abdomen	*Streptomyces*	MC	RB98	E57
Mn105	*Macrotermes natalensis*	abdomen	*Actinomadura*	chitin	RB99	E60
Mn105	*Macrotermes natalensis*	abdomen	*Streptomyces*	chitin	RB100	E48
Mn105	*Macrotermes natalensis*	abdomen	*Streptomyces*	chitin	RB101	E152
Mn105	*Macrotermes natalensis*	comb	*Streptomyces*	chitin	RB104	E59
Mn105	*Macrotermes natalensis*	comb	*Streptomyces*	chitin	RB109	E147
Mn106	*Macrotermes natalensis*	comb	*Streptomyces*	chitin	RB105	E145
Mn106	*Macrotermes natalensis*	comb	*Streptomyces*	chitin	RB110	RB142
Mn106	*Macrotermes natalensis*	abdomen	*Arthrobacter*	chitin	RB112	E155
Mn107	*Macrotermes natalensis*	comb	*Streptomyces*	chitin	RB106	E146
Mn110	*Macrotermes natalensis*	comb	*Streptomyces*	chitin	RB107	E46
Mn160	*Macrotermes natalensis*	gut	*Streptomyces*	chitin	RB4	E74
Mn160	*Macrotermes natalensis*	gut	*Streptomyces*	chitin	RB5	E1
Mn160	*Macrotermes natalensis*	gut	*Micromonospora*	chitin	RB6	E4
Mn160	*Macrotermes natalensis*	gut	*Streptomyces*	chitin	RB7	E3
Mn160	*Macrotermes natalensis*	gut	*Micromonospora*	chitin	RB8	E5
Mn160	*Macrotermes natalensis*	gut	*Streptomyces*	chitin	RB9	E103
Mn160	*Macrotermes natalensis*	gut	*Streptomyces*	chitin	RB10	E8
Mn160	*Macrotermes natalensis*	gut	*Streptomyces*	chitin	RB11	E9
Mn160	*Macrotermes natalensis*	gut	*Streptomyces*	chitin	RB13	E11
Mn160	*Macrotermes natalensis*	gut	*Streptomyces*	chitin	RB14	E12/E13
Mn160	*Macrotermes natalensis*	gut	*Streptomyces*	chitin	RB15	E65
Mn160	*Macrotermes natalensis*	gut	*Streptomyces*	chitin	RB16	E66
Mn160	*Macrotermes natalensis*	gut	*Streptomyces*	chitin	RB17	E38
Mn160	*Macrotermes natalensis*	gut	*Cellulosimicrobium*	chitin	RB18	E68
Mn160	*Macrotermes natalensis*	gut	*Nocardia*	chitin	RB20	E16
Mn160	*Macrotermes natalensis*	gut	*Nocardia*	chitin	RB21	E17

Mn160	*Macrotermes natalensis*	gut	*Luteimicrobium*	chitin	RB22	E18/E19
Mn160	*Macrotermes natalensis*	gut	*Micromonospora*	chitin	RB23	E50
Mn160	*Macrotermes natalensis*	gut	*Mycobacterium*	chitin	RB24	E20/E21
Mn160	*Macrotermes natalensis*	gut	*Streptomyces*	chitin	RB25	E135
Mn160	*Macrotermes natalensis*	gut	*Streptomyces*	chitin	RB26	E22/E23
Mn160	*Macrotermes natalensis*	gut	*Streptomyces*	chitin	RB27	E26/E27
Mn160	*Macrotermes natalensis*	gut	*Streptomyces*	chitin	RB28	E67
Mn160	*Macrotermes natalensis*	gut	*Actinomadura*	chitin	RB29	E62
Mn160	*Macrotermes natalensis*	gut	*Streptomyces*	chitin	RB30	E40
Mn160	*Macrotermes natalensis*	gut	*Streptomyces*	chitin	RB31	E42
Mn160	*Macrotermes natalensis*	gut	*Mycobacterium*	chitin	RB32	E43
Mn160	*Macrotermes natalensis*	gut	*Mycobacterium*	chitin	RB33	E44
Mn160	*Macrotermes natalensis*	gut	*Streptomyces*	chitin	RB34	E80
Mn160	*Macrotermes natalensis*	gut	*Streptomyces*	chitin	RB36	E63
Mn160	*Macrotermes natalensis*	gut	*Streptomyces*	chitin	RB38	E54
Mn160	*Macrotermes natalensis*	gut	*Streptomyces*	chitin	RB40	E56
Mn160	*Macrotermes natalensis*	gut	*Sphaerisporangium*	chitin	RB41	E113
Mn160	*Macrotermes natalensis*	gut	*Streptomyces*	chitin	RB42	E70
Mn160	*Macrotermes natalensis*	gut	*Streptomyces*	chitin	RB44	E75
Mn160	*Macrotermes natalensis*	gut	*Streptomyces*	chitin	RB45	E86
Mn160	*Macrotermes natalensis*	gut	*Streptomyces*	chitin	RB47	E136
Mn160	*Macrotermes natalensis*	gut	*Streptomyces*	chitin	RB48	E76
Mn160	*Macrotermes natalensis*	gut	*Streptomyces*	chitin	RB50	E88
Mn160	*Macrotermes natalensis*	gut	*Streptomyces*	chitin	RB52	E91
Mn160	*Macrotermes natalensis*	gut	*Streptomyces*	chitin	RB53	E93
Mn160	*Macrotermes natalensis*	gut	*Streptomyces*	chitin	RB54	E94
Mn160	*Macrotermes natalensis*	gut	*Streptomyces*	chitin	RB55	E95
Mn160	*Macrotermes natalensis*	gut	*Nocardia*	chitin	RB56	E104
Mn160	*Macrotermes natalensis*	gut	*Streptomyces*	chitin	RB60	E105
Mn160	*Macrotermes natalensis*	gut	*Streptomyces*	chitin	RB62	E109
Mn160	*Macrotermes natalensis*	gut	*Streptomyces*	chitin	RB63	E96
Mn160	*Macrotermes natalensis*	gut	*Microbispora*	chitin	RB64	E97
Mn160	*Macrotermes natalensis*	gut	*Actinomadura*	chitin	RB66	E98
Mn160	*Macrotermes natalensis*	gut	*Actinomadura*	chitin	RB68	E99
Mn160	*Macrotermes natalensis*	gut	*Streptomyces*	chitin	RB72	E100
Mn160	*Macrotermes natalensis*	gut	*Streptomyces*	MC	RB78	E119
Mn160	*Macrotermes natalensis*	gut	*Streptomyces*	MC	RB79	E120
Mn160	*Macrotermes natalensis*	gut	*Streptomyces*	MC	RB80	E121
Mn160	*Macrotermes natalensis*	gut	*Actinomadura*	MC	RB81	E122
Mn160	*Macrotermes natalensis*	gut	*Curtobacterium*	chitin	RB129	E41
Mn162	*Macrotermes natalensis*	gut	*Leifsonia*	ISP2	RB71	E110
Mn162	*Macrotermes natalensis*	gut	*Streptomyces*	MC	RB74	E102
Mn162	*Macrotermes natalensis*	gut	*Streptomyces*	chitin	RB76	E112/E113
Mn162	*Macrotermes natalensis*	gut	*Aeromicrobium*	chitin	RB77	E118
Mn162	*Macrotermes natalensis*	gut	*Streptomyces*	chitin	RB82	E123
Mn162	*Macrotermes natalensis*	gut	*Streptomyces*	chitin	RB83	E124

Mn162	*Macrotermes natalensis*	gut	*Leifsonia*	chitin	RB84	E125
Mn162	*Macrotermes natalensis*	gut	*Streptomyces*	chitin	RB85	E126
Mn162	*Macrotermes natalensis*	gut	*Streptomyces*	chitin	RB86	E127
Mn162	*Macrotermes natalensis*	gut	*Streptomyces*	chitin	RB87	E128
Mn162	*Macrotermes natalensis*	gut	*Streptomyces*	chitin	RB88	E129
Mn162	*Macrotermes natalensis*	gut	*Leifsonia*	chitin	RB89	E130
Mn163	*Macrotermes natalensis*	abdomen	*Streptomyces*	chitin	RB113	E35
Mn163	*Macrotermes natalensis*	abdomen	*Streptomyces*	chitin	RB114	E78
Mn163	*Macrotermes natalensis*	comb	*Streptomyces*	chitin	RB115	E36
Mn163	*Macrotermes natalensis*	comb	*Streptomyces*	chitin	RB116	E37

Table S3. Identities of isolated actinobacterial strains, including the top three hits resulting from BLASTn searches against the NCBI database (https://blast.ncbi.nlm.nih.gov/Blast.cgi, last visit 26.07.2018, 00:58 AM).

Strain ID	Accession number	length [nt]	Hit	Max Score	Similarity[a]	Accession Number
RB2	KX344916	1374	*Streptomyces mirabilis* NBRC 13450	2519	100%	NR_041137.1
			Streptomyces mirabilis CSSP107	2518	100%	NR_115357.1
			Streptomyces mirabilis ATCC 27447	2495	99.93%	NR_114494.1
RB3	KX344917	1363	*Streptomyces puniciscabiei* S77	2462	99.56%	NR_025156.1
			Streptomyces durhamensis NBRC 13441	2451	99.34%	NR_112399.1
			Streptomyces durhamensis CSSP538	2451	99.34%	NR_043352.1
RB4	KX344918	1365	*Streptomyces yanglinensis* 1307	2427	99.04%	NR_043244.1
			Streptomyces paucisporeus 1413	2383	99.19%	NR_043247.1
			Streptomyces polygonati NEAU-G9	2355	98.02%	NR_148782.1
RB5	KY558696	1374	*Streptomyces aureoverticillatus* NBRC 12742	2390	98.54%	NR_112580.1
			Streptomyces aureoverticillatus CSSP526	2390	98.54%	NR_043346.1
			Streptomyces variegatus NBRC 15462	2381	98.32%	NR_112473.1
RB6	KY558697	1351	*Micromonospora tulbaghiae* TVU1	2490	100%	NR_116241.1
			Micromonospora echinospora ATCC	2447	99.63%	NR_118843.1
			Micromonospora chalcea ATCC 12452	2431	99.26%	NR_118842.1
RB7	KY558698	1368	*Streptomyces cacaoi* NBRC 12748	2505	99. 85%	NR_041061.1
			Streptomyces violaceoruber CSSP679	2473	99.63%	NR_115407.1
			Streptomyces smyrnaeus SM3501	2381	98.68%	NR_134201.1
RB8	KY312017	1362	*Micromonospora yasonensis* DS3186	2459	99.34%	NR_149817.1
			Micromonospora olivasterospora MK-70	2420	98.825%	NR_036966.1
			Micromonospora viridifaciens DSM 43909	2410	98.751%	NR_044889.1
RB9	MH044507	863	*Streptomyces hoynatensis* S1412	1500	98.49%	NR_133871.1
			Streptomyces specialis GW41-1564	1474	97.91%	NR_042689.1
			Streptomyces hainanensis YIM 47672	1474	97.56.%	NR_042561.1
RB10	KY558699	1367	*Streptomyces yanglinensis* 1307	2433	99.05	NR_043244.1
			Streptomyces paucisporeus 1413	2394	99.26%	NR_043247.1
			Streptomyces polygonati NEAU-G9	2361	98.09%	NR_148782.1

RB11	KY558700	1370	*Streptomyces yanglinensis* 1307	2425	98.90%	NR_043244.1
			Streptomyces paucisporeus 1413	2381	99.04%	NR_043247.1
			Streptomyces polygonati NEAU-G9	2359	98.02%	NR_148782.1
RB13	KY558735	1366	*Streptomyces violaceolatus* NBRC 13101	2507	99.85%	NR_112370.1
			Streptomyces humiferus NBRC 12244	2507	99.85%	NR_112243.1
			Streptomyces violaceolatus DSM 40438	2507	99.85%	NR_027223.1
RB14	KY558701	1361	*Streptomyces flavidovirens* NBRC 13039	2420	99.34%	NR_041099.1
			Streptomyces longisporus NBRC 12885	2420	99.34%	NR_112319.1
			Streptomyces longisporus ISP 5166	2420	99.34%	NR_025492.1
RB15	KY558702	1366	*Streptomyces rameus* NBRC 3782	2468	99.27%	NR_112497.1
			Streptomyces coacervatus IFM 11055	2440	98.90%	NR_112916.1
			Streptomyces galbus DSM 40089	2427	99.12%	NR_026178.1
RB16	KY558703	1359	*Streptomyces rameus* NBRC 3782	2449	99.19%	NR_112497.1
			Streptomyces coacervatus IFM 11055	2416	98.75%	NR_112916.1
			Streptomyces galbus DSM 40089	2409	99.04%	NR_026178.1
RB17	KY558704	1373	*Streptomyces lanatus* NBRC 12787	2409	99.12%	NR_041220.1
			Streptomyces echinatus NBRC 12763	2409	99.12%	NR_112264.1
			Streptomyces lanatus ISP 5090	2409	99.12%	NR_114826.1
RB18	KY558705	1371	*Cellulosimicrobium funkei* W6122	2507	99.78%	NR_042937.1
			Cellulosimicrobium aquatile 3bp	2497	99.78%	NR_146008.1
			Cellulosimicrobium cellulans DSM 43879	2488	99.49%	NR_119095.1
RB20	KY558706	1352	*Nocardia miyunensis*	2318	98.44%	NR_117333.1
			Nocardia miyunensis 117	2318	98.44%	NR_043059.1
			Nocardia niigatensis W8186	2313	97.63%	NR_117402.1
RB21	KY558707	1362	*Nocardia miyunensis*	2394	98.82%	NR_117333.1
			Nocardia miyunensis 117	2394	98.82%	NR_043059.1
			Nocardia niigatensis W8186	2388	98.31%	NR_117402.1
RB22	KY558708	1369	*Luteimicrobium album* RI148-Li105	2460	99.41%	NR_108122.1
			Luteimicrobium xylanilyticum W-15	2385	98.54%	NR_126237.1
			Luteimicrobium subarcticum R19-04	2333	97.88%	NR_112891.1
RB23	KY558709	1362	*Micromonospora chokoriensis* 2-19	2508	100%	NR_041349.1
			Micromonospora violae NEAU-P5	2492	99.85%	NR_134089.1
			Micromonospora saelicesensis Lupac 09	2475	99.71%	NR_042312.1

RB24	KY312018	1369	*Mycobacterium parafortuitum* DSM 43528	2459	99.27%	NR_026285.1
			Mycobacterium psychrotolerans WA101	2438	99.12%	NR_028998.1
			Mycobacterium sphagni Sph 38	2436	99.27%	NR_104774.1
RB25	KY558710	1364	*Streptomyces rameus* NBRC 3782	2470	99.41 %	NR_112497.1
			Streptomyces coacervatus IFM 11055	2436	98.97%	NR_112916.1
			Streptomyces galbus DSM 40089	2431	99.27%	NR_026178.1
RB26	KY558711	1374	*Streptomyces humidus* NBRC 12877	2447	98.83%	NR_112316.1
			Streptomyces resistomycificus NBRC 12814	2442	98.91%	NR_112287.1
			Streptomyces caniferus NRRL B-16358	2440	98.83%	NR_116095.1
RB27	KY558712	1375	*Streptomyces lanatus* NBRC 12787	2420	99.12%	NR_041220.1
			Streptomyces shenzhenensis 172115	2418	98.69%	NR_118018.1
			Streptomyces lanatus ISP 5090	2418	99.12%	NR_114826.1
RB28	KY558713	1357	*Streptomyces durhamensis* NBRC 13441	2431	99.264%	NR_112399.1
			Streptomyces durhamensis CSSP538	2431	99.26%	NR_043352.1
			Streptomyces yaanensis Z4	2414	98.89%	NR_132305.1
RB29	KY312019	1355	*Parvopolyspora pallida* IFO 14788	2409	99.63%	NR_112013.1
			Actinomadura rayongensis RY35-68	2379	99.19%	NR_134688.1
			Actinomadura atramentaria DSM 43919	2368	98.52%	NR_114850.1
RB30	KY558714	1375	*Streptomyces regensis* NBRC 13448	2519	100%	NR_112402.1
			Streptomyces regensis NRRL B-11479	2514	99.93%	NR_043495.1
			Streptomyces rameus NBRC 3782	2447	99.05%	NR_112497.1
RB31	KY558715	1369	*Streptomyces chattanoogensis* NBRC 12754	2468	99.20%	NR_112260.1
			Streptomyces sioyaensis NRRL B-5408	2462	99.12%	NR_043498.1
			Streptomyces sioyaensis NBRC 12820	2462	99.12%	NR_112289.1
RB32	KY558716	1352	*Mycobacterium obuense* 47001	2433	99.48%	NR_029218.1
			Mycobacterium chubuense ATCC 27278	2425	99.04%	NR_041902.1
			Mycobacterium houstonense ATCC 49403	2423	99.33%	NR_042913.1
RB33	KY558717	1357	*Mycobacterium madagascariense* P2	2370	98.60%	NR_104690.1
			Mycobacterium barrassiae CIP 108545	2361	98.60%	NR_115330.1
			Mycobacterium smegmatis ATCC 19420	2355	98.67%	NR_115233.1
RB34	KY312020	1367	*Streptomyces echinatus* NBRC 12763	2484	99.56%	NR_112264.1
			Streptomyces echinatus ISP 5013	2475	99.49%	NR_114823.1
			Streptomyces durhamensis NBRC 13441	2418	99.56%	NR_112399.1

RB36	KY558718	1349	*Streptomyces coeruleorubidus* ISP 5145	2322	98.64%	NR_114791.1
			Streptomyces bellus NBRC 12844	2320	98.14%	NR_041222.1
			Streptomyces coerulescens CSSP046	2320	98.35%	NR_043337.1
RB38	KY558719	1365	*Streptomyces misionensis* NBRC 13063	2503	99.85%	NR_112355.1
			Streptomyces misionensis JCM 4497	2499	99.85%	NR_044138.1
			Streptomyces phaeoluteichromatogenes NRRL B-5799	2486	99.56%	NR_042096.1
RB40	KY558720	1365	*Streptomyces thermocarboxydus* NBRC 16323	2516	100%	NR_112585.1
			Streptomyces thermocarboxydus AT37	2510	99.93%	NR_026072.1
			Streptomyces lusitanus NBRC 13464	2486	99.63%	NR_041143.1
RB41	KY558721	1341	*Sphaerisporangium corydalis* NEAU-YHS15	2302	98.05	NR_148314.1
			Sphaerisporangium cinnabarinum DSM 44094	2290	98.05%	NR_044874.1
			Sphaerisporangium rufum R10-82	2261	98.05%	NR_125470.1
RB42	KY312021	1355	*Streptomyces phaeochromogenes* NRRL B-1248	2492	99.85%	NR_116382.1
			Streptomyces phaeochromogenes ATCC 3338	2492	99.85%	NR_116381.1
			Streptomyces phaeochromogenes NBRC 3180	2492	99.85%	NR_041200.1
RB44	KY558722	1364	*Streptomyces misionensis* NBRC 13063	2512	100%	NR_112355.1
			Streptomyces misionensis JCM 4497	2508	100%	NR_044138.1
			Streptomyces phaeoluteichromatogenes NRRL B-5799	2495	99.78%	NR_042096.1
RB45	KY558723	1371	*Streptomyces misionensis* NBRC 13063	2532	100%	NR_112355.1
			Streptomyces misionensis JCM 4497	2527	100%	NR_044138.1
			Streptomyces phaeoluteichromatogenes NRRL B-5799	2516	99.78%	NR_042096.1
RB47	KY558724	1371	*Streptomyces atriruber* NRRL B-24165	2427	99.12%	NR_116447.1
			Streptomyces chartreusis ISP 5085	2405	98.83%	NR_114825.1
			Streptomyces bobili NBRC 16166	2405	98.69%	NR_112584.1
RB48	KY558725	1365	*Streptomyces costaricanus* NBRC 100773	2514	100%	NR_041414.1
			Streptomyces murinus NBRC 14802	2514	100%	NR_112445.1
			Streptomyces murinus NBRC 12799	2514	100%	NR_041072.1
RB50	KY558726	1372	*Streptomyces thermocarboxydus* NBRC 16323	2534	100%	NR_112585.1
			Streptomyces thermocarboxydus AT37	2529	99.93%	NR_026072.1
			Streptomyces lusitanus NBRC 13464	2501	99.56%	NR_041143.1
RB52	KY558727	1372	*Streptomyces shenzhenensis* 172115	2499	99.64%	NR_118018.1
			Streptomyces graminisoli JR-19	2494	99.56%	NR_125577.1
			Streptomyces jiujiangensis JXJ 0074	2466	99.20%	NR_125706.1

RB53	KY558728	1365	*Streptomyces yanglinensis* 1307	2442	99.05%	NR_043244.1
			Streptomyces paucisporeus 1413	2398	99.19%	NR_043247.1
			Streptomyces polygonati NEAU-G9	2375	98.17%	NR_148782.1
RB54	MH044508	953	*Streptomyces paucisporeus* 1413	1709	99.26%	NR_043247.1
			Streptomyces yanglinensis 1307	1692	98.95%	NR_043244.1
			Streptomyces yogyakartensis DSM 41766	1688	98.74%	NR_117958.1
RB55	KY558729	1369	*Streptomyces shenzhenensis* 172115	2501	99.63%	NR_118018.1
			Streptomyces graminisoli JR-19	2495	99.56%	NR_125577.1
			Streptomyces jiujiangensis JXJ 0074	2468	99.20%	NR_125706.1
RB56	KY558730	1362	*Nocardia pseudobrasiliensis* ATCC 51512	2368	98.16%	NR_117336.1
			Nocardia pseudobrasiliensis DSM 44290	2368	98.16%	NR_041864.1
			Nocardia rayongensis RY45-3	2362	98.05%	NR_149226.1
RB60	KY558731	1368	*Streptomyces purpurascens* NBRC 13077	2464	99.41%	NR_112521.1
			Streptomyces purpurascens JCM 4509	2464	99.41%	NR_104281.1
			Streptomyces spinoverrucosus NBRC 14228	2451	99.27%	NR_041159.1
RB62	KY312022	1358	*Streptomyces rubrogriseus* NBRC 15455	2479	99.71%	NR_041188.1
			Streptomyces rubrogriseus DSM 41477	2473	99.63%	NR_114667.1
			Streptomyces albogriseolus DSM 40003	2473	99.63%	NR_042760.1
RB63	KY558732	1365	*Streptomyces rubrogriseus* NBRC 15455	2512	100%	NR_041188.1
			Streptomyces rubrogriseus DSM 41477	2507	99.93%	NR_114667.1
			Streptomyces albogriseolus DSM 40003	2507	99.93%	NR_042760.1
RB64	KY558733	1369	*Microbispora corallina* DF-32	2494	99.71%	NR_028605.1
			Microbispora hainanensis 211020	2442	99.71%	NR_116600.1
			Microbispora bryophytorum NEAU-TX2-2	2377	99.04%	NR_134769.1
RB66	MH044509	1366	*Actinomadura nitritigenes* NBRC 15918	2507	99.93%	NR_112736.1
			Actinomadura nitritigenes L 46	2495	99.78%	NR_025652.1
			Actinomadura montaniterrae	2449	99.71%	NR_151939.1
RB68	MH044510	1356	*Actinomadura hibisca* DSM 44148	2338	98.30%	NR_114849.1
			Actinomadura nitritigenes NBRC 15918	2327	97.79%	NR_112736.1
			Actinomadura hibisca IMSNU 22185	2326	97.08%	NR_042031.1
RB71	KY558734	1374	*Leifsonia shinshuensis* DB 102	2468	99.27%	NR_043663.1
			Leifsonia xyli subsp. *cynodontis* JCM 9733	2440	99.34%	NR_125442.1
			Leifsonia lichenia 2Sb	2418	98.61%	NR_112644.1

RB72	MH044511	1366	*Streptomyces alni* D65	2453	99.34%	NR_043866.1
			Streptomyces abietis A191	2392	98.39%	NR_114347.1
			Streptomyces cocklensis BK168	2364	98.02%	NR_108501.1
RB74	MH044512	975	*Streptomyces flaveolus* NRRL B-1334	1751	99.28%	NR_116094.1
			Streptomyces glaucescens NRRL B-2706	1751	99.28%	NR_115773.1
			Streptomyces viridochromogenes NBRC 13347	1751	99.28%	NR_112526.1
RB76	KY558736	1376	*Streptomyces griseoaurantiacus* NBRC 15440	2510	99.78%	NR_041186.1
			Streptomyces griseoaurantiacus DSM 40430	2510	99.78%	NR_115231.1
			Streptomyces jietaisiensis FXJ46	2479	99.56%	NR_042836.1
RB77	KY558737	1363	*Aeromicrobium massiliense* JC14	2495	99.71%	NR_125588.1
			Aeromicrobium erythreum NRRL B-3381	2254	96.99%	NR_024846.1
			Aeromicrobium alkaliterrae KSL-107	2248	96.70%	NR_043207.1
RB78	KY558738	1365	*Streptomyces rameus* NBRC 3782	2460	99.49%	NR_112497.1
			Streptomyces coacervatus IFM 11055	2433	98.67%	NR_112916.1
			Streptomyces galbus DSM 40089	2420	99.34%	NR_026178.1
RB79	KY558739	1364	*Streptomyces cocklensis* BK168	2422	99.34%	NR_108501.1
			Streptomyces bryophytorum NEAU-HZ10	2425	99.12%	NR_146707.1
			Streptomyces yanglinensis 1307	2401	98.53%	NR_043244.1
RB80	MH044513	1365	*Streptomyces cocklensis* BK168	2444	99.34%	NR_108501.1
			Streptomyces bryophytorum NEAU-HZ10	2427	99.12%	NR_146707.1
			Streptomyces yanglinensis 1307	2403	98.53%	NR_043244.1
RB81	MH044514	1356	*Actinomadura nitritigenes* NBRC 15918	2488	99.85%	NR_112736.1
			Actinomadura nitritigenes L 46	2477	99.70%	NR_025652.1
			Actinomadura montaniterrae	2449	99.63%	NR_151939.1
RB82	KY558740	1376	*Streptomyces gilvifuscus* T113	2447	99.49%	NR_137389.1
			Streptomyces sasae JR-39	2440	98.98%	NR_137361.1
			Streptomyces panaciradicis 1MR-8	2425	98.76%	NR_134200.1
RB83	KY558742	1370	*Streptomyces actinomycinicus* RCU-197	2438	98.98%	NR_147753.1
			Streptomyces sasae JR-39	2436	99.27%	NR_137361.1
			Streptomyces neopeptinius KNF 2047	2427	99.20%	NR_116261.1
RB84	KY558743	1365	*Leifsonia xyli* subsp. *cynodontis* JCM 9733	2494	99.71%	NR_125442.1
			Leifsonia shinshuensis DB 102	2494	99.19%	NR_043663.1
			Leifsonia naganoensis DB103	2455	99.19%	NR_043662.1

RB85	MH044515	962	*Streptomyces nogalater* NBRC 13445	1744	99.48%	NR_112401.1
			Streptomyces lavendulígriseus NBRC 13405	1744	99.48%	NR_112391.1
			Streptomyces nogalater JCM 4799	1744	99.48%	NR_112122.1
RB86	KY558741	1360	*Streptomyces filipinensis* NBRC 12860	2453	99.19%	NR_041083.1
			Streptomyces durhamensis NBRC 13441	2447	99.12%	NR_112399.1
			Streptomyces durhamensis CSSP538	2447	99.12%	NR_043352.1
RB87	KY558744	1366	*Streptomyces glaucescens* NRRL B-2706	2440	98.97%	NR_115773.1
			Streptomyces glaucescens NBRC 12774	2440	98.97%	NR_041219.1
			Streptomyces minutiscleroticus NBRC 13361	2407	98.53%	NR_112379.1
RB88	KY558745	1375	*Streptomyces sasae* JR-39	2501	99.71%	NR_137361.1
			Streptomyces panaciradicis 1MR-8	2497	99.64%	NR_134200.1
			Streptomyces capoamus NBRC 13411	2460	99.20%	NR_112394.1
RB89	KY558746	1365	*Leifsonia xyli* subsp. *cynodontis* JCM 9733	2492	99.71%	NR_125442.1
			Leifsonia shinshuensis DB 102	2453	99.19%	NR_043663.1
			Leifsonia naganoensis DB103	2442	99.19%	NR_043662.1
RB90	KY558671	1365	*Streptomyces californicus* NBRC 12750	2514	100%	NR_112257.1
			Streptomyces californicus NBRC 3386	2514	100%	NR_112486.1
			Streptomyces californicus CSSP711	2514	100%	NR_115432.1
RB91	KY558672	1359	*Streptomyces rameus* NBRC 3782	2416	98.75%	NR_112497.1
			Streptomyces coacervatus IFM 11055	2383	98.31%	NR_112916.1
			Streptomyces levis NRRL B-16370	2375	98.31%	NR_115778.1
RB92	KY558669	1366	*Streptomyces pratensis* ch24	2516	100%	NR_125616.1
			Streptomyces pratensis ch24	2516	100%	NR_125619.1
			Streptomyces anulatus NBRC 13369	2516	100%	NR_112527.1
RB93	KY558670	1364	*Streptomyces griseus* NBRC 15744	2510	100%	NR_112475.1
			Streptomyces erumpens NBRC 15403	2510	100%	NR_112455.1
			Streptomyces griseus NBRC 12875	2510	100%	NR_112314.1
RB94	KY558673	1361	*Streptomyces regensis* NBRC 13448	2481	99.56%	NR_112402.1
			Streptomyces regensis NRRL B-11479	2475	99.49%	NR_043495.1
			Streptomyces rameus NBRC 3782	2409	98.60%	NR_112497.1
RB95	KY558678	1377	*Streptomyces bungoensis* NBRC 15711	2436	99.12%	NR_041191.1
			Streptomyces galbus NBRC 12864	2422	99.05%	NR_026178.1
			Streptomyces longwoodensis NBRC 14251	2425	98.98%	NR_041161.1

RB96	KY558680	1370	*Streptomyces virginiae* NBRC 3729	2518	100%	NR_112496.1
			Streptomyces cinnamonensis NBRC 15873	2518	100%	NR_041194.1
			Streptomyces virginiae NBRC 12827	2518	100%	NR_041078.1
RB97	KY558679	1372	*Streptomyces humidus* NBRC 12877	2435	98.83%	NR_112316.1
			Streptomyces resistomycificus NBRC 12814	2429	98.91%	NR_112287.1
			Streptomyces caniferus NRRL B-16358	2427	98.83%	NR_116095.1
RB98	KY558683	1370	*Streptomyces achromogenes* subsp. *rubradiris* NBRC 14000	2473	99.42%	NR_112428.1
			Streptomyces achromogenes subsp. *rubradiris* CSSP713	2499	99.42%	NR_043365.1
			Streptomyces nodosus NBRC 12895	2455	99.27%	NR_112324.1
RB99	KY558684	1368	*Actinomadura nitritigenes* NBRC 15918	2512	99.93%	NR_112736.1
			Actinomadura nitritigenes L 46	2501	99.78%	NR_025652.1
			Actinomadura montaniterrae	2473	99.71%	NR_151939.1
RB100	KY558685	1376	*Streptomyces collinus* NBRC 12759	2420	98.83%	NR_041063.1
			Streptomyces collinus DSM 40129	2420	98.83%	NR_114792.1
			Streptomyces viridochromogenes NBRC 13347	2416	99.20%	NR_112526.1
RB101	KY558686	1373	*Streptomyces collinus* NBRC 12759	2423	98.91%	NR_041063.1
			Streptomyces collinus DSM 40129	2423	98.91%	NR_114792.1
			Streptomyces viridochromogenes NBRC 13347	2420	99.27%	NR_112526.1
RB102	KY558674	1375	*Streptomyces coelicolor* DSM 40233	2525	100%	NR_116633.1
			Streptomyces sampsonii NBRC 13083	2525	99.93%	NR_112362.1
			Streptomyces coelicolor NBRC 12854	2525	99.93%	NR_112305.1
RB103	KY558677	1367	*Streptomyces jiujiangensis* JXJ 0074	2457	99.27%	NR_125706.1
			Streptomyces graminisoli JR-19	2446	99.41%	NR_125577.1
			Streptomyces hyaluromycini MB-PO13	2429	98.90%	NR_146364.1
RB104	KY558682	1366	*Streptomyces graminisoli* JR-19	2460	99.27%	NR_125577.1
			Streptomyces actinomycinicus RCU-197	2435	99.56%	NR_147753.1
			Streptomyces shenzhenensis 172115	2433	98.90%	NR_118018.1
RB105	KY558689	1365	*Streptomyces pseudogriseolus* NRRL B	2510	100%	NR_043835.1
			Streptomyces pseudogriseolus NBRC 12902	2510	100%	NR_112329.1
			Streptomyces gancidicus NBRC 15412	2507	100%	NR_041179.1
RB106	KY558690	1360	*Streptomyces thermocarboxydovorans* AT52	2398	98.75%	NR_026071.1
			Streptomyces glomeratus NBRC 15898	2390	99.04%	NR_041409.1
			Streptomyces somaliensis CSSP138	2388	98.60%	NR_115358.1

RB107	KY558691	1373	*Streptomyces seoulensis* NBRC 16668	2512	99.75%	NR_041432.1
			Streptomyces recifensis NBRC 12813	2510	99.93%	NR_041074.1
			Streptomyces griseoluteus CSSP409	2501	99.71%	NR_043341.1
RB108	KY558675	1365	*Streptomyces pulveraceus* NBRC 3855	2501	99.85%	NR_041213.1
			Streptomyces atratus NRRL B-16927	2479	99.56%	NR_043490.1
			Streptomyces gelaticus NRRL B-2928	2479	99.56%	NR_043488.1
RB109	KY558681	1372	*Streptomyces cocklensis* BK168	2436	99.63%	NR_108501.1
			Streptomyces bryophytorum NEAU-HZ10	2420	99.12%	NR_146707.1
			Streptomyces yanglinensis 1307	2407	98.69%	NR_043244.1
RB110	KY558688	1374	*Streptomyces californicus* NBRC 12750	2523	100%	NR_112257.1
			Streptomyces californicus NBRC 3386	2523	100%	NR_112486.1
			Streptomyces californicus CSSP711	2523	100%	NR_115432.1
RB111	KY558676	1362	*Streptomyces costaricanus* NBRC 100773	2451	99.27%	NR_041414.1
			Streptomyces murinus NBRC 14802	2451	99.27%	NR_112445.1
			Streptomyces murinus NBRC 12799	2451	99.27%	NR_041072.1
RB112	KY558678	1368	*Arthrobacter luteolus* CF-25	2481	99.49%	NR_025362.1
			Arthrobacter koreensis CA15-8	2466	99.34%	NR_025665.1
			Arthrobacter gandavensis R 5812	2444	99.12%	NR_025475.1
RB113	KY558692	1371	*Streptomyces ramulosus* NRRL B-2714	2521	100%	NR_043503.1
			Streptomyces ramulosus NBRC 15798	2521	100%	NR_112476.1
			Streptomyces ramulosus NBRC 12812	2521	100%	NR_112286.1
RB114	KY558695	1374	*Streptomyces lannensis* TA4-8	2521	100%	NR_113181.1
			Streptomyces chiangmaiensis TA4-1	2429	98.83%	NR_113180.1
			Streptomyces glomeratus NBRC 15898	2390	98.40%	NR_041409.1
RB115	KY558694	1360	*Streptomyces lincolnensis* NRRL 2936	2374	98.82%	NR_119101.1
			Streptomyces cyaneus NBRC 13346	2368	98.45%	NR_112525.1
			Streptomyces lincolnensis NBRC 13054	2368	98.82%	NR_041104.1
RB116	KY558693	1373	*Streptomyces chattanoogensis* NBRC 12754	2466	99.20%	NR_112260.1
			Streptomyces sioyaensis NRRL B-5408	2460	99.13%	NR_043498.1
			Streptomyces sioyaensis NBRC 12820	2460	99.13%	NR_112289.1
RB129	MH044516	993	*Curtobacterium oceanosedimentum* ATCC 31317	1790	99.80%	NR_116064.1
			Curtobacterium oceanosedimentum ATCC 31317	1790	99.80%	NR_104839.1
			Curtobacterium luteum DSM 20542	1783	99.80%	NR_026157.1

[a] Sequence similarities were calculated using method recommended by Meier-Koltfoff [1].

Table S4. Ecologically relevant fungal s used as targets in the bioactivity tests.

Strain #	Strain affiliation; and strain number including GenBank accession number of 18S rRNA gene of the closest relative from BLASTn search	GenBank	Growth on PDA[a]	Inoculation
#1	*Cladosporium* sp.; *C .perangustum* CPC18229(JF499836	KJ817314	Slow	method B
#2	*Cladosporium* sp.; *C. perangustum* CPC18229 (JF499836)	KJ817319	slow	method B
#4	*Pleosporales* sp.; *P.* sp. LH222 (HQ832821)	KJ817321	slow	method B
#5	*Fusarium sp.;* *Fusarium lateritium strain BBA 63665* (AF310982.1)	KJ817322	medium	method B
#7	*Coriolopsis* sp.; *C.* sp. aff17 (EU863193)	KJ817324	medium	method B
#8	*Coriolopsis* sp.; *C.* sp. aff17 (EU863193)	KJ817325	slow	method B
#10	*Fusarium* sp.; *F.equiseti* ATT040 (HQ607811)	KJ817326	slow	method B
#12	*Cunninghamella* sp.; *C. echinulata* var. *nodosa* (AF346407)	KJ817330	Fast (aerial hyphae)	method A
#13	*Cladosporium* sp.; *C.* sp. CLJ-2 (LC373145)	KJ817329	slow	method B
#14	*Umbelopsis* sp.; *Umbelopsis isabellina* UI1 (JF303862)	KJ817309	Fast (aerial hyphae)	method A
#15	*Alternaria* sp.; *A. alternata* ATCC MYA-4642 (HQ263343)	KJ817328	medium	method B
#17	*Trichoderma* sp.; *T.* sp. ATT151 (HQ607860)	KJ817310	medium	method B
#22	*Trichoderma* sp.; *T.* sp. TPK IMEA5 (JF831494)	KJ817316	fast	method A
#24	*Hypocrea* sp.; *H. virens* (anamorph of *Trichoderma virens*) TR039 (HQ608079)	KJ817318	fast	method A
T112	*Termitomyces* sp. from *Odontototermes* cf. *badius* colony Od112	KX250316	slow	method B
T115	*Termitomyces* sp. from *Macrotermes natalensis* colony Mn115	N/A	slow	method B
T153	*Termitomyces* sp. from *Macrotermes natalensis* colony Mn153	KX097054	slow	method B
P5	*Termitomyces* sp. from *Macrotermes natalensis* colony Mn105	JDCH00000000	slow	method B
BB	*Beauveria bassiana* ST 17960 (JMRC)	N/A	slow	method B
MA	*Metarhizium anisopliae* ATCC 24942 (JMRC)	N/A	fast	method B

[a] slow: fungus requires > 7 days to overgrow agar plate; medium: fungus requires 3-7 days to overgrow agar plate; fast: fungus requires 1-3 days to overgrow agar plate.

Table S5. Antimicrobial assay results of extracts of isolated bacteria against eight medically relevant bacteria and fungi (average zone of inhibition given in mm).

Strain ID	**Extract ID**	**cultivation medium**	***Bacillus subtilis* ATCC 6633**	***Staphylococcus aureus* IMET 10760**	***Escherichia coli* SG 458**	***Pseudomonas aeruginosa* K799/61**	***Mycobacterium vaccae* IMET 10670**	***Sporobolomyces salmonicolor* SBUG-549**	***Candida albicans* BMSY 212**	***Penicillium notatum* JP36**
RB2	E58	ISP2	0	0	0	0	0	0	0	0
RB3	E47	ISP2	15	17	0	0	13	0	0	0
RB4	E74	ISP2	0	0	0	0	0	0	0	0
RB5	E1	ISP2	10	0	0	10	0	0	0	0
RB6	E4	ISP2	0	0	0	0	0	0	0	0
RB7	E3	ISP2	14	13	14	0	12	22	22	18
RB8	E5	ISP2	0	0	0	0	0	0	0	0
RB9	E103	ISP2	10	11	0	10	20	0	0	0
RB10	E8	ISP2	0	0	0	0	0	0	0	0
RB11	E9	ISP2	0	0	0	0	0	15	0	0
RB13	E11	ISP2	12	12	0	0	0	21	22.5	20
RB14	E12	ISP2	11	0	0	0	16	0	0	0
RB14	E13	PDB	12	14	19	0	19	17.5	0	19
RB15	E65	ISP2	0	0	0	0	14	12	15	13
RB16	E66	ISP2	0	0	0	0	12	0	0	12
RB17	E38	ISP2	19	18.5	14	12	21	13	0	16.5
RB18	E68	ISP2	0	0	0	0	0	0	0	0
RB19	E69	ISP2	0	0	0	0	0	0	0	0
RB20	E16	ISP2	0	0	0	0	0	0	0	0
RB21	E17	ISP2	0	0	0	0	0	0	0	0
RB22	E18	ISP2	0	0	0	0	0	0	0	0
RB22	E19	PDB	0	0	0	0	0	0	0	0
RB23	E50	ISP2	12	15	0	0	13	0	0	0
RB24	E20	ISP2	0	0	0	0	0	0	0	0
RB24	E21	PDB	0	0	0	0	0	0	0	0
RB25	E135	ISP2	10	0	0	0	12	11	0	0
RB26	E22	ISP2	10	0	0	0	0	0	0	0
RB26	E23	PDB	10	0	0	0	0	0	0	0

RB27	E26	ISP2	14	13	13	0	13	12	0	14.5
RB27	E27	PDB	13	13.5	16	0	21	19	0	15.5
RB28	E67	ISP2	0	0	0	0	13	0	0	0
RB29	E62	ISP2	14	0	0	0	0	0	0	0
RB30	E40	ISP2	20	22	15	14	27	14	0	16
RB31	E42	ISP2	0	0	0	0	0	31	28	30
RB32	E43	ISP2	0	0	0	0	0	0	0	0
RB33	E44	ISP2	0	0	0	0	0	0	0	0
RB34	E80	ISP2	0	0	0	0	0	0	0	0
RB36	E63	ISP2	0	0	0	0	0	0	0	0
RB38	E54	ISP2	11	0	0	0	25	0	0	0
RB39	E55	ISP2	0	0	0	0	0	0	0	0
RB40	E56	ISP2	13	11	0	0	19	0	0	0
RB41	E113	ISP2	19	17.5	14	0	14	0	0	0
RB42	E70	ISP2	0	0	0	0	0	0	0	0
RB43	E72	ISP2	10	0	0	0	0	0	0	0
RB44	E75	ISP2	10	0	21	0	18	21	0	0
RB45	E86	ISP2	10	0	13	0	13	18	0	0
RB47	E136	ISP2	12	12	0	0	0	0	0	0
RB48	E76	ISP2	11	15	0	0	30	24	18	21
RB50	E88	ISP2	17	17.5	13	0	28	15	0	0
RB51	E106	ISP2	0	0	0	11	0	0	0	0
RB52	E91	ISP2	0	0	0	0	12	0	0	0
RB53	E93	ISP2	0	0	0	0	0	0	0	0
RB54	E94	ISP2	0	0	0	0	0	0	0	0
RB55	E95	ISP2	24	22	14	11	36	15	12	0
RB56	E104	ISP2	12	13	0	10	28	0	0	0
RB58	E114	ISP2	0	0	0	0	0	0	0	0
RB59	E107	ISP2	0	0	0	0	0	0	0	0
RB60	E105	ISP2	0	0	0	0	0	0	0	0
RB62	E109	ISP2	0	0	0	0	0	0	0	0
RB63	E96	ISP2	0	0	0	0	0	0	0	0
RB64	E97	ISP2	0	0	0	0	0	0	0	0

RB66	E98	ISP2	16	27	0	11	20	25	15	21.5
RB68	E99	ISP2	16	17	0	0	25.5	0	0	0
RB71	E110	ISP2	0	0	0	0	0	0	0	0
RB72	E100	ISP2	22	21	0	11	23	48	48	37
RB74	E102	ISP2	11	16	0	10	32	0	0	0
RB76	E112	ISP2	15.5	16	0	0	16	14	0	0
RB77	E118	ISP2	0	0	0	0	0	0	0	0
RB78	E119	ISP2	12	12	0	0	0	0	0	0
RB79	E120	ISP2	12	13	0	0	0	0	0	0
RB80	E121	ISP2	13	13	0	0	0	0	0	0
RB81	E122	ISP2	13	11	0	0	12	0	0	0
RB82	E123	ISP2	11	11	0	0	24	0	0	0
RB83	E124	ISP2	11	10	0	0	12	0	0	0
RB85	E126	ISP2	12	11	10	0	13	0	0	0
RB86	E127	ISP2	11	10	15	0	17	17	0	0
RB87	E128	ISP2	11	11	0	0	14	0	0	0
RB88	E129	ISP2	10	0	0	0	0	13	0	0
RB89	E130	ISP2	10	0	0	0	0	0	0	0
RB90	E77	ISP2	20	20	12	0	20	13	12	15
RB91	E49	ISP2	12	11	0	0	32	21	0	0
RB92	E144	ISP2	11	11	0	0	0	13	0	12
RB93	E148	ISP2	14.5	13.5	0	16	20	0	0	0
RB94	E61	ISP2	33.5	32	13	21	40	15	15	13
RB95	E149	ISP2	11	11	0	0	18	0	0	0
RB96	E150	ISP2	11	0	0	10	21	0	0	0
RB97	E151	ISP2	10	0	0	0	0	0	0	0
RB98	E57	ISP2	12	12.5	0	10	24	16	0	11
RB99	E60	ISP2	11	11	0	10	13	23	0	0
RB100	E48	ISP2	19	20	23	10	22	24	13	12
RB101	E152	ISP2	12	13.5	0	10	18	12	0	0
RB102	E143	ISP2	20	19	0	0	20	19	24	17.5
RB103	E153	ISP2	11	12	0	0	28	0	0	0
RB104	E59	ISP2	11	11	0	10	18	20	0	12

RB105	E145	ISP2	18	15	0	0	33	0	0	11
RB106	146	ISP2	12	11.5	0	0	33	0	0	11
RB107	E46	ISP2	11	12	0	10	19	0	0	0
RB108	E45	ISP2	0	0	0	0	11	19	19	19
RB109	E147	ISP2	15	15	0	0	26.5	0	0	20
RB110	E142	ISP2	18	16	0	21	17	15	14	14.5
RB111	E154	ISP2	10	13	0	0	11	0	0	0
RB112	E155	ISP2	0	0	0	0	0	0	0	0
RB113	E35	ISP2	12	15	13	10	21.5	0	0	0
RB114	E78	ISP2	10	11	0	0	0	0	0	0
RB115	E36	ISP2	0	0	0	0	0	0	0	0
RB116	E37	ISP2	0	0	15	0	17	24	18	23.5
RB129	E41	ISP2	0	0	0	0	15	0	0	0

Table S6. Antifungal assay results of extracts of isolated bacteria against ecologically-relevant fungi # 1 - #24 (T115: *Termitomyces* sp. from *Macrotermes natalensis* (Mn) colony Mn115, T112: *Termitomyces* sp. from *Odontototermes badius* colony Od112, T153: *Termitomyces* sp. from Mn colony Mn153, P5: *Termitomyces* sp. from Mn colony Mn105, MA - *Metarhizium anisopliae* ATCC 24942, BB *Beauveria bassiana* ST 17960- (I= very weak inhibition, without measurable zone of inhibition SI= strong inhibition, inhibition zone not measurable; average in mm given).

Extract ID	#1	#2	#4	#5	#8	#10	#12	#13	#15	#17	#22	#24	**T115**	**T112**	**T153**	**P5**	**MA**	**BB**
E3	0	0	8	9	0	0	0	0	5	0	0	0	5	23	23	16	13	9
E9	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
E11	6	0	9	10	0	0	0	0	5	0	0	0	13	2	2	17	12	10
E12	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
E13	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
E26	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
E27	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
E37	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
E38	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
E40	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
E42	6	0	15	13	0	13	0	10	9	0	0	0	15	15	12	12	12	13
E45	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
E48	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
E49	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
E57	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
E59	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
E60	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
E61	0	0	0	0	0	0	0	0	I	0	0	0	0	0	0	0	0	0
E65	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
E66	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
E75	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
E76	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
E77	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
E86	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
E88	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
E95	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
E98	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

E100	18	0	31	8	0	0	0	0	10	5	0	0	0	23	10	I	I	I
E127	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
E129	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
E131	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
E135	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
E136	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
E142	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
E143	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
E144	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
E145	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
E146	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
E147	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Amp.B 1	SI	0	SI	10	0	0	I	0	11	13	0	I	I	I	I	I	10	11
Amp.B 2	SI	0	SI	16	0	0	I	0	11	10	0	I	I	I	I	I	9	8
Cyclo. 1	SI	0	SI	33	0	23	I	28	24	17	0	I	I	I	I	I	15	15
Cyclo. 2	SI	0	SI	32	0	0	I	31	25	20	0	I	I	I	I	I	15	18

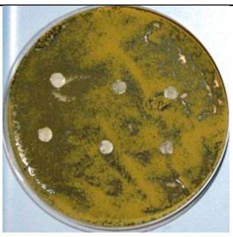
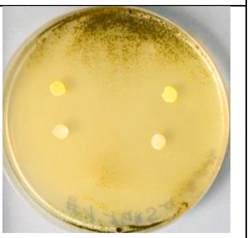
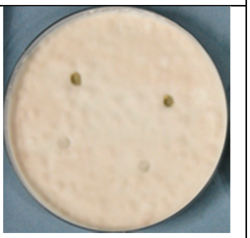
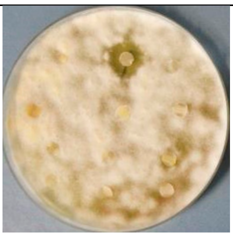
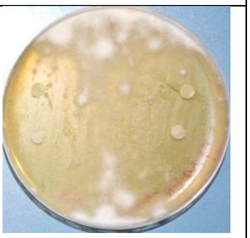
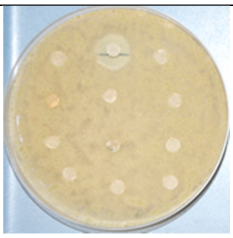
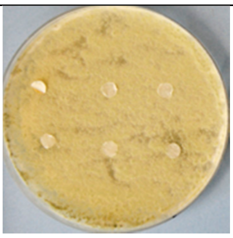
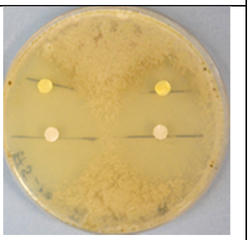
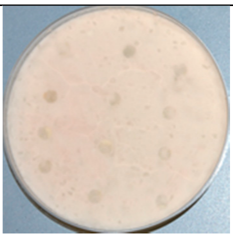
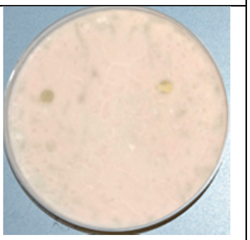
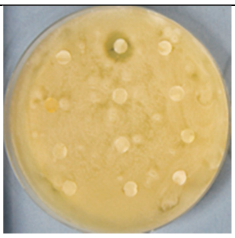
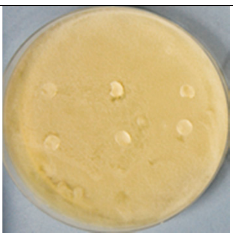
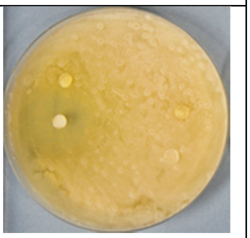
Amp.: amphotericin B; Cyclo.: cycloheximide

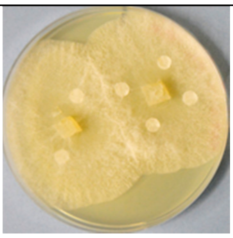
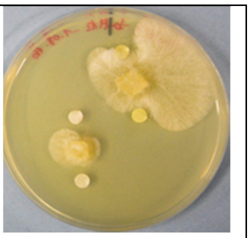
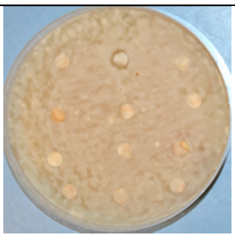
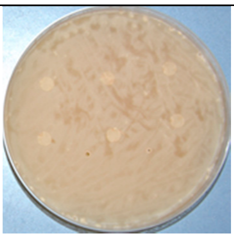
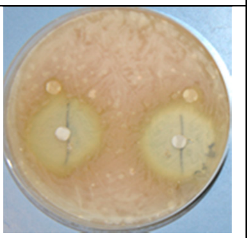
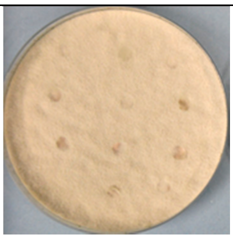
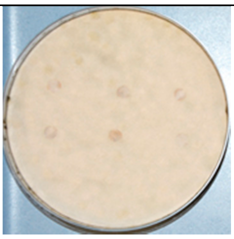
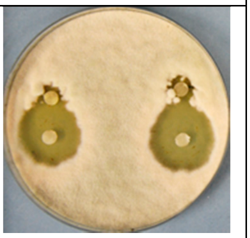
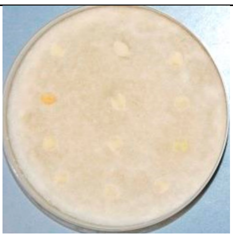
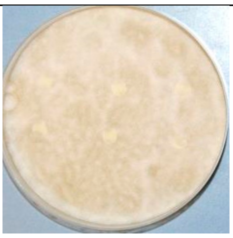
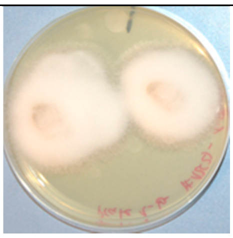
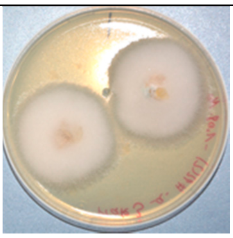
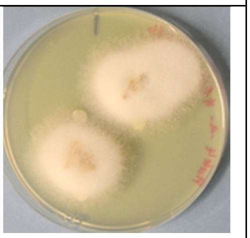
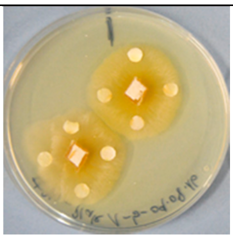
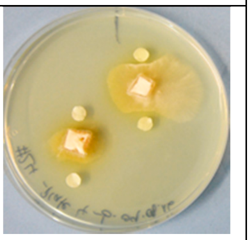
Table S7. Antimicrobial activity of *cyclo*(*N*Me-L-3,5-dichlorotyrosine-Dhb) (**11**, 0.1 mg/mL in MeOH), ciprofloxacin (cip.) and amphotericin B (amp.) towards Gram (+) and Gram (–) bacteria and fungi.[a]

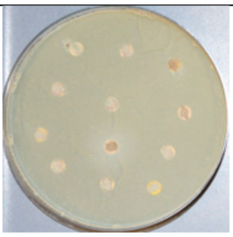
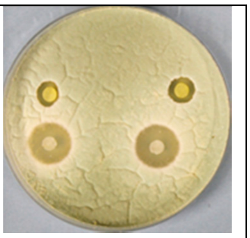
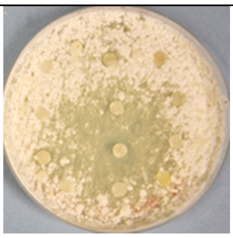
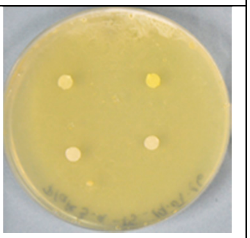
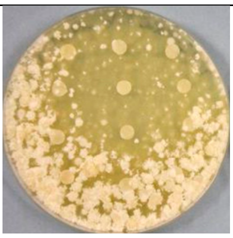
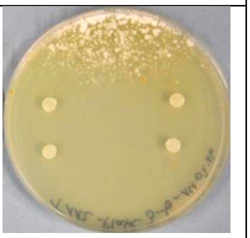
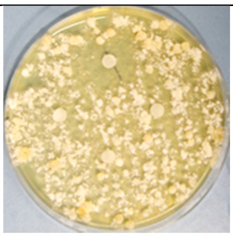
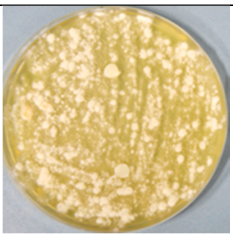
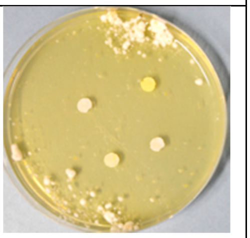
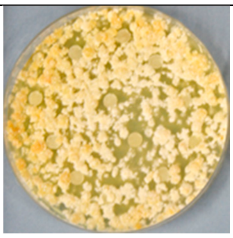
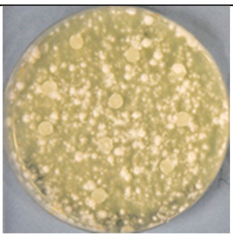
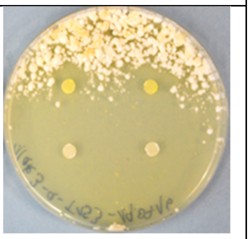
compd.	***B.subtilis*** **ATCC 6633**	***S. aureus*** **IMET 10760**	***E.coli*** **SG 458**	***P. aeruginosa*** **SG137**	***P. aeruginosa*** **K799/61**	**MRSA** ***S.sureus*** **134/93**	**VRSA** ***E. faecalis*** **1528**	***M.vaccae*** **IMET 10670**	***S. salmonic.*** **SBUG 549**	***C.albicans*** **SBSY 212**	***P. notatum*** **JP36**
11	10	0	0	0	10	0	10	10	0	0	0
cip.	29	19	24/32p	26	26/34p	0	17F	21p			
amp.									18p	21p	19p

[a]: The value indicated the diameter of inhibition zone (in mm).

Table S8. Representative images of antifungal paper disc assay against co-isolated fungi, the fungal cultivar and insectpathogenic fungi.

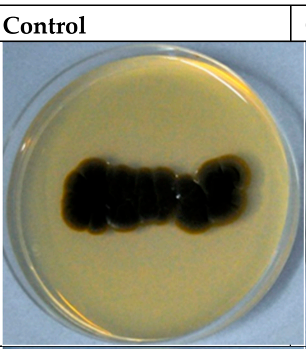
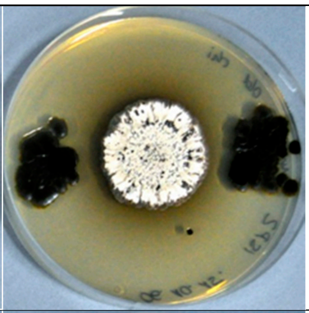
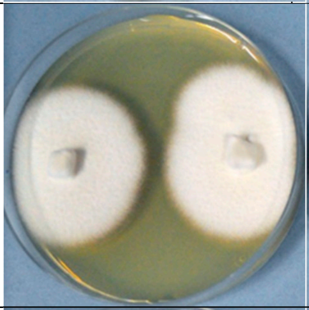
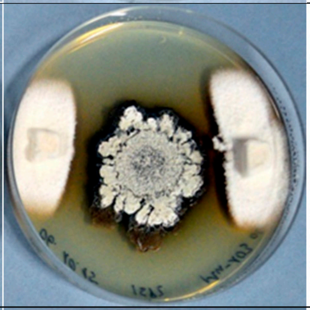
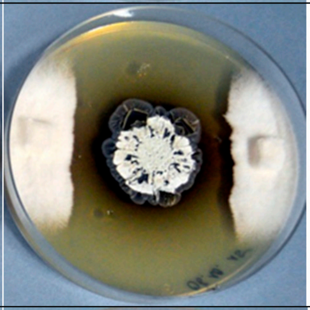
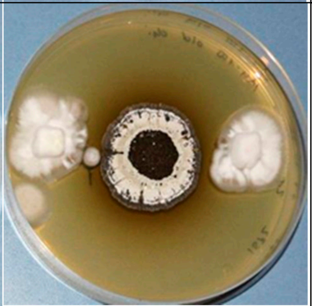
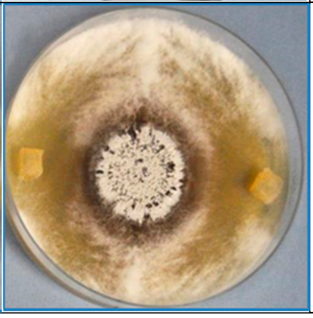
Fungus	**Extracts E3 – E38**	**Negative control**[a]	**Positive control**[b]
#1 *Cladosporium sp.* (KJ817314)			
#2 *Cladosporium* sp.(KJ817319)			
#4 *Pleosporales* sp. (KJ817321)			
#5 *Fusarium* sp. (KJ817322)			
#8 *Coriolopsis* sp. (KJ817325)			
#10 *Fusarium* sp. (KJ817326)			

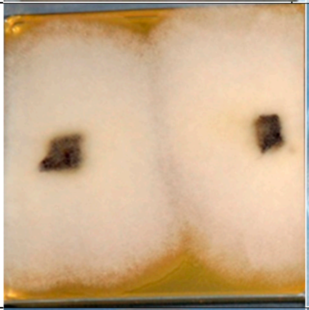
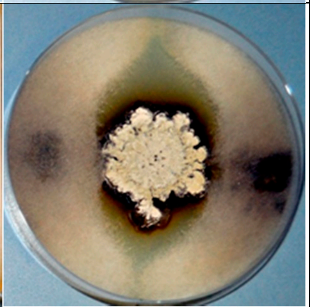
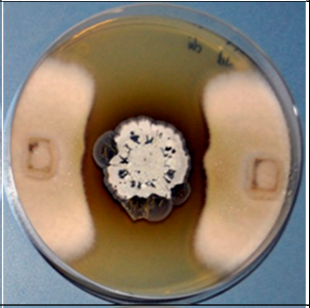
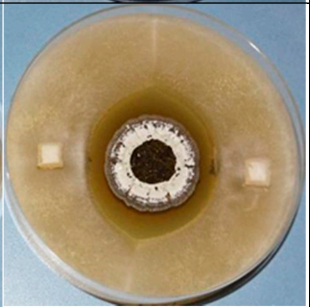
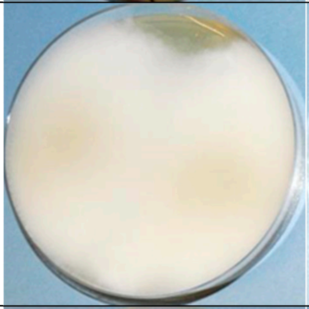
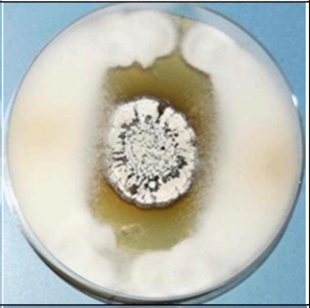
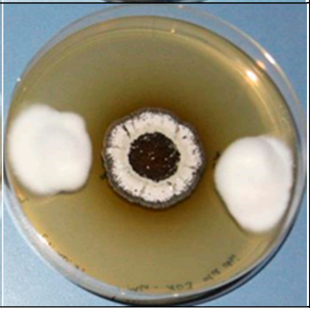
#12 *Cunninghamella* sp. (KJ817330)			
#13 *Cladosporium* sp. CLJ-2 (KJ817329)			
#15 *Alternaria* sp. (KJ817328)			
#17 *Trichoderma* sp. (KJ817310)			
#22 *Trichoderma* sp. (KJ817316)			
#24 *Hypocrea* sp. (KJ817318)			
BB *Beauveria bassiana* ST 17960			

MA *Metarhizium anisopliae* ATCC 24942			
P5 *Termitomyces* sp. from *Macrotermes natalensis* colony Mn105			
T112 *Termitomyces* sp. from *Odontototermes* cf. *badius* colony Od112			
T115 *Termitomyces* sp. from *Macrotermes natalensis* colony Mn115			
T153 *Termitomyces* sp. from *Macrotermes natalensis* colony Mn153			

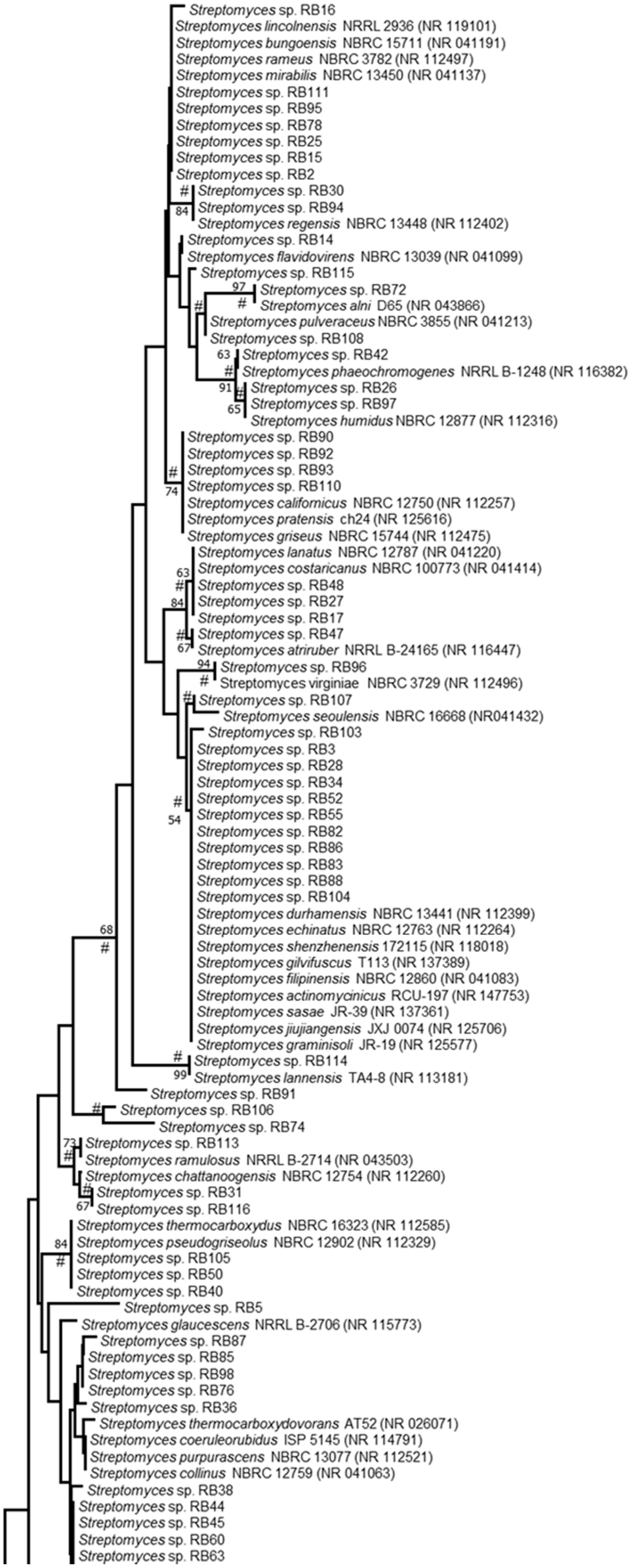
[a)] Negative control (paper discs + MeOH); [b)] positive control (Amphotericin B (upper row) and cycloheximide (lower row).

Table S9. Representative co-cultivation of *Streptomyces* sp. RB108 against co-isolated fungi.

Strain	Inhibition	Control	Co-culture	Method	Time
#1 *Cladosporium sp.* (KJ817314)	moderate			B	7-day
#4 *Pleosporales sp.* (KJ817321)	moderate			B	7-day
#7 *Coriolopsis sp.* (KJ817324)	moderate			B	7-day
#8 *Coriolopsis sp.* (KJ817325)	weak			B	7-day
#12 *Cunninghamella* sp. (KJ817330)	no			B	7-day

#13 *Cladosporium sp.* CLJ-2 (KJ817329)	moderate			B	7-day
#14 *Umbelopsis* sp. (KJ817309)	weak			B	7-day
#15 *Alternaria* sp. (KJ817328)	moderate			B	7-day
#17 *Trichoderma* sp. (KJ817310)	moderate			B	7-day
#22 *Trichoderma sp.* (KJ817316)	weak			B	7-day
BB *Beauvaria bassiana* ST 17960	no			B	7-day

MA *Metarhizium anisopliae* ATCC 24942	weak		B	7-days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Streptomyces bungoensis NBRC 15711 (NR 041191)
Streptomyces rameus NBRC 3782 (NR 112497)
Streptomyces mirabilis NBRC 13450 (NR 041137)
Streptomyces sp. RB111
Streptomyces sp. RB95
Streptomyces sp. RB78
Streptomyces sp. RB25
Streptomyces sp. RB15
Streptomyces sp. RB2
#
84
Streptomyces sp. RB30
Streptomyces sp. RB94
Streptomyces regensis NBRC 13448 (NR 112402)
Streptomyces sp. RB14
Streptomyces flavidovirens NBRC 13039 (NR 041099)
Streptomyces sp. RB115
97
#
Streptomyces sp. RB72
Streptomyces alni D65 (NR 043866)
#
Streptomyces pulveraceus NBRC 3855 (NR 041213)
Streptomyces sp. RB108
63
#
Streptomyces sp. RB42
Streptomyces phaeochromogenes NRRL B-1248 (NR 116382)
91
#
65
Streptomyces sp. RB26
Streptomyces sp. RB97
Streptomyces humidus NBRC 12877 (NR 112316)
Streptomyces sp. RB90
Streptomyces sp. RB92
#
74
Streptomyces sp. RB93
Streptomyces sp. RB110
Streptomyces californicus NBRC 12750 (NR 112257)
Streptomyces pratensis ch24 (NR 125616)
Streptomyces griseus NBRC 15744 (NR 112475)
Streptomyces lanatus NBRC 12787 (NR 041220)
63
#
84
Streptomyces costaricanus NBRC 100773 (NR 041414)
Streptomyces sp. RB48
Streptomyces sp. RB27
Streptomyces sp. RB17
#
67
Streptomyces sp. RB47
Streptomyces atriruber NRRL B-24165 (NR 116447)
94
#
Streptomyces sp. RB96
Streptomyces virginiae NBRC 3729 (NR 112496)
#
Streptomyces sp. RB107
Streptomyces seoulensis NBRC 16668 (NR041432)
Streptomyces sp. RB103
Streptomyces sp. RB3
Streptomyces sp. RB28
Streptomyces sp. RB34
#
54
Streptomyces sp. RB52
Streptomyces sp. RB55
Streptomyces sp. RB82
Streptomyces sp. RB86
Streptomyces sp. RB83
Streptomyces sp. RB88
Streptomyces sp. RB104
Streptomyces durhamensis NBRC 13441 (NR 112399)
68
#
Streptomyces echinatus NBRC 12763 (NR 112264)
Streptomyces shenzhenensis 172115 (NR 118018)
Streptomyces gilvifuscus T113 (NR 137389)
Streptomyces filipinensis NBRC 12860 (NR 041083)
Streptomyces actinomycinicus RCU-197 (NR 147753)
Streptomyces sasae JR-39 (NR 137361)
Streptomyces jiujiangensis JXJ 0074 (NR 125706)
Streptomyces graminisoli JR-19 (NR 125577)
#
99
Streptomyces sp. RB114
Streptomyces lannensis TA4-8 (NR 113181)
Streptomyces sp. RB91
#
Streptomyces sp. RB106
Streptomyces sp. RB74
73
#
Streptomyces sp. RB113
Streptomyces ramulosus NRRL B-2714 (NR 043503)
Streptomyces chattanoogensis NBRC 12754 (NR 112260)
#
67
Streptomyces sp. RB31
Streptomyces sp. RB116
Streptomyces thermocarboxydus NBRC 16323 (NR 112585)
84
#
Streptomyces pseudogriseolus NBRC 12902 (NR 112329)
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Streptomyces sp. RB50
Streptomyces sp. RB40
Streptomyces sp. RB5
Streptomyces glaucescens NRRL B-2706 (NR 115773)
Streptomyces sp. RB87
Streptomyces sp. RB85
Streptomyces sp. RB98
Streptomyces sp. RB76
Streptomyces sp. RB36
Streptomyces thermocarboxydovorans AT52 (NR 026071)
Streptomyces coeruleorubidus ISP 5145 (NR 114791)
Streptomyces purpurascens NBRC 13077 (NR 112521)
Streptomyces collinus NBRC 12759 (NR 041063)
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Streptomyces sp. RB60
Streptomyces sp. RB63

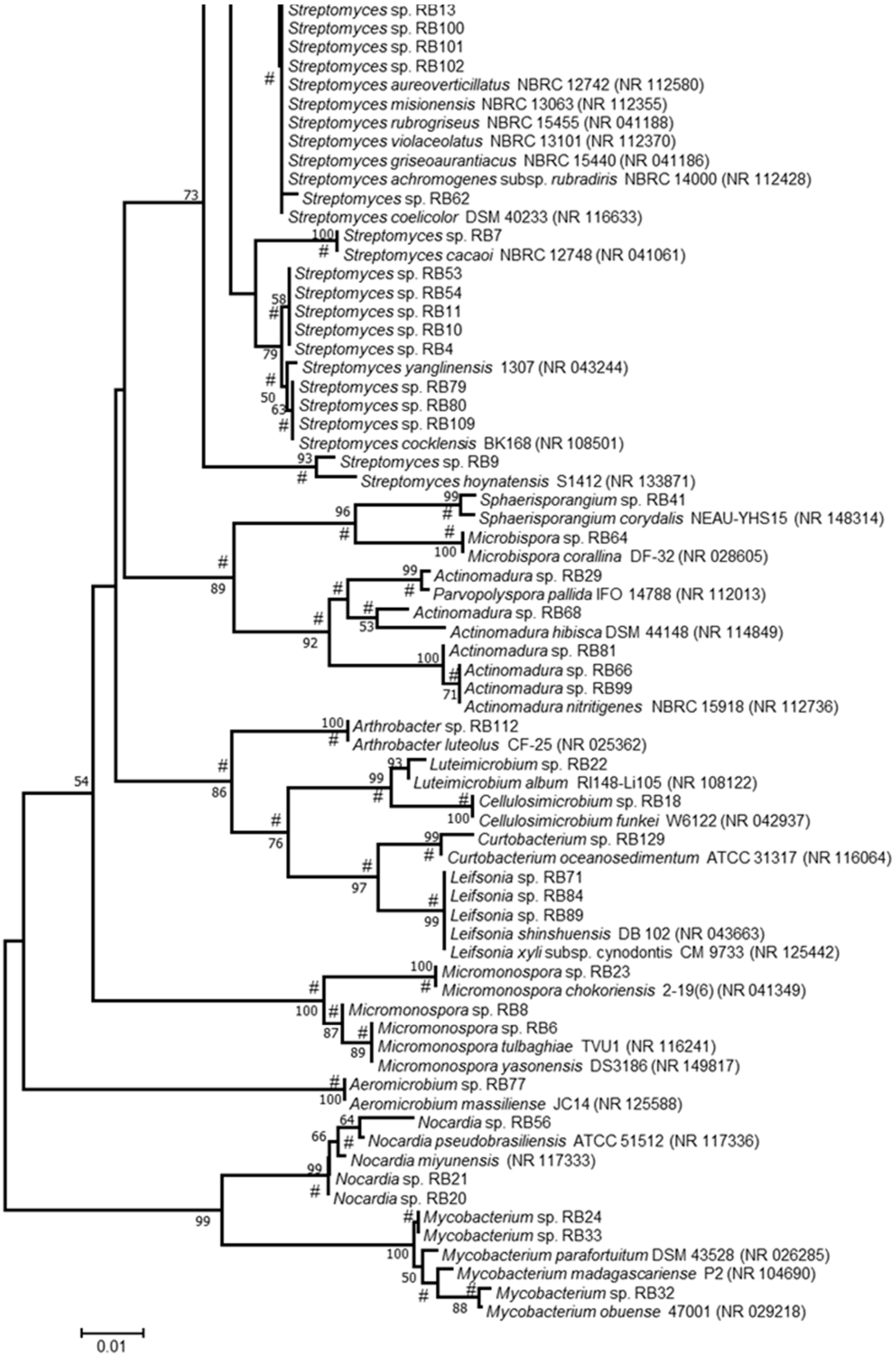


Figure S1. Unrooted Neighbour-joining tree based on near-complete 16S rRNA gene sequences showing relationships between isolated Actinobacteria and closest relatives. Hashtags indicate branches that were also recovered in the maximum-likelihood tree. Only bootstrap values above 50% (based on 1000 pseudoreplicates) are shown. The scale bar indicates 0.01 substitutions per nucleotide position.

Table S10. Presence/absence of transcripts identified in gut microbiome metatranscriptome data from major old worker guts of *M. natalensis* Mn156 and *Odontotermes* sp. Od127.[a]

Gene	Function	Mn156	Od127
alaS	Alanyl-tRNA synthetase	+	+
aspS	Aspartyl-tRNA synthetase	+	-
dnaX	DNA polymerase III gamma-tau subunits	+	-
topA	DNA topoisomerase I	+	-
rpoB	DNA-directed RNA polymerase beta chain	-	-
fus	Elongation factor G	-	-
tufA	Elongation factor Tu	+	+
infB	Initiation factor 2	+	+
glnS	Glutamyl-tRNA synthetase	+	+
metS	Methionyl-tRNA synthetase	+	+
rpl2	Ribosomal protein L2	+	+
rpsE	Ribosomal protein S5	+	+
rpsH	Ribosomal protein S8	+	+
rpsK	Ribosomal protein S11	+	+
zhrS	Threonyl-tRNA synthetase	+	+

a) Transcriptomic analysis: Due to the high isolation rate of Actinobacteria from the gut fluid of termite workers, a mostly microaerophilic or anaerobic gut environment, we analyzed the transcript levels of fifteen Actinobacteria-specific house-keeping genes in our gut microbiome metatranscriptome data from the termite species *Macrotermes natalensis* and *Odontotermes* sp. Gut microbiome transcripts were collected from old major worker gut metatranscriptome data of *M. natalensis* colony Mn156 and *Odontotermes* sp. colony Od127. Transcripts were aligned to the Pfam database (v30.0) by HMMER (v3.1b2) [2] with e-value < 1e-6 and the best matched domain were taken, followed the extraction of transcripts matched to protein domain of the bacterial housekeeping gene Alanyl-tRNA synthetase (PF00152), Aspartyl-tRNA synthetase (PF11734), Glutamyl-tRNA synthetase (PF00749), Methionyl-tRNA synthetase (PF09334), Threonyl-tRNA synthetase (PF00587), Initiation factor 2 (PF11987), Elongation factor G (PF07299), Elongation factor Tu (PF03144), Ribosomal protein L2 (PF00181, PF03947), Ribosomal protein S5 (PF03719, PF00333), Ribosomal protein S8 (PF00410), Ribosomal protein S11 (PF00411), DNA-directed RNA polymerase beta chain (PF03431), DNA polymerase III gamma-tau subunits (PF12169) and DNA topoisomerase I (PF01131). Extracted transcripts were aligned to Nucleotide collection database (nt) of NCBI by BLASTn (e-value < 1e-5) and taken as transcripts of housekeeping gene coded by Actinobacteria if the best matched sequence was from the phylum Actinobacteria. The absence/presence of Actinobacteria housekeeping genes domain were then counted.

Overall, thirteen of the fifteen analyzed house-keeping genes were identified in the *M. natalensis* transcriptome and ten identified in *Odontotermes* sp. transcriptome data. However transcript levels were particularly low indicating towards very only low metabolic activity within the gut.

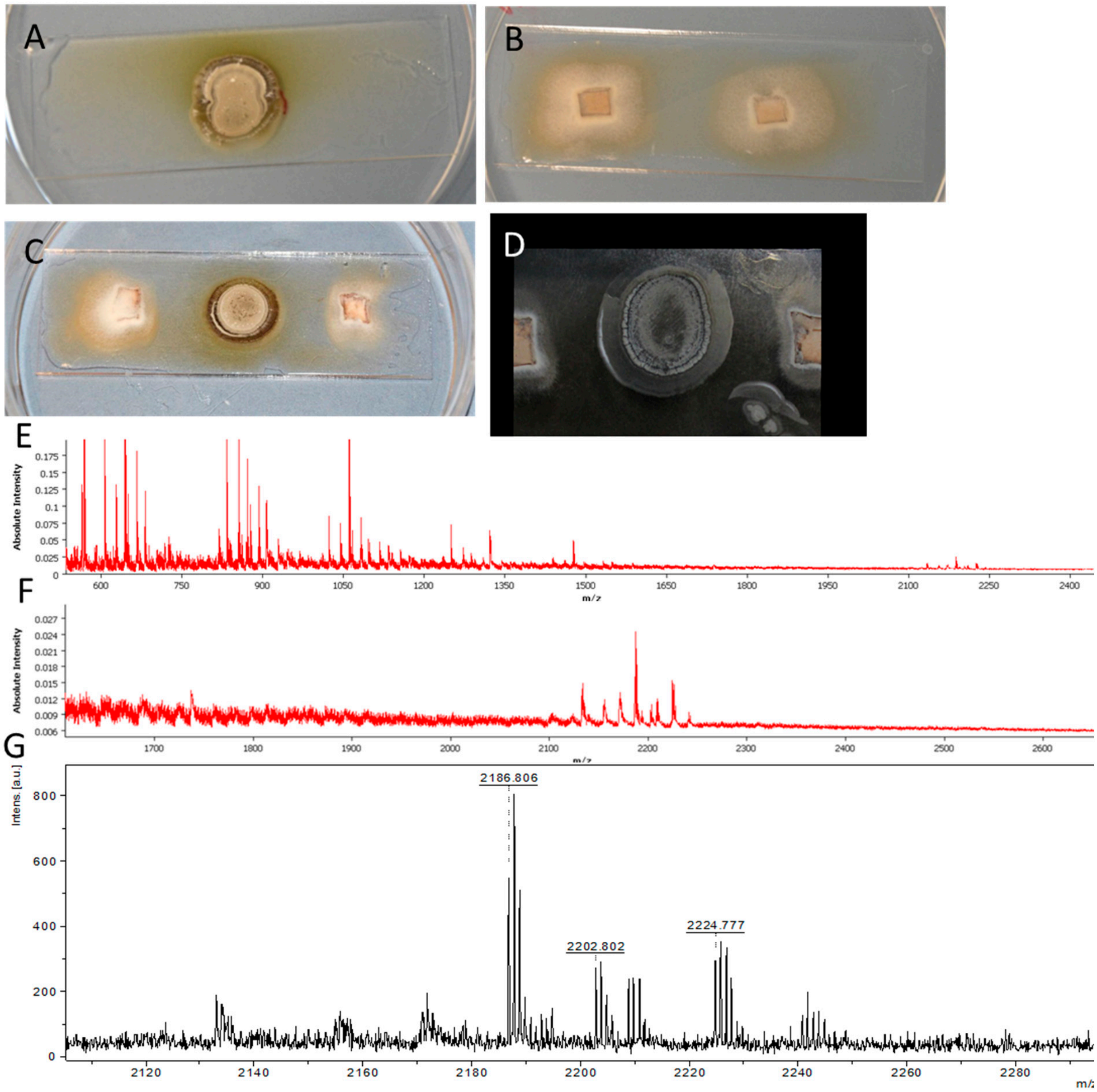


Figure S2. Indium tin oxide (ITO) coated glass slide with 1 ml of ISP2 medium and inoculated with A) *Streptomyces* sp. RB108 (after 7 days); B) *Pleosporales* sp. #4; C). co-culture of *Streptomyces* sp. RB108 and *Pleosporales* sp. #4 ; D) optical picture of the challenge assay between *Streptomyces* sp. RB108 and *Pleosporales* sp. #4 after drying. E) Average MS spectra of the MALDI Imaging MS analysis (TIC normalization). F) Zoom in the region of the average MS spectra between *m*/*z* 1700-2500 showing the up-regulated RiPPs. G) Zoom in the region of the average MS spectra between *m*/*z* 2100-2300 showing the up-regulated RiPPs.

Table S11. Rubromidin biosynthetic protein annotations based on sequence homology.

locus tag	Protein	size (aa)	short name	proposed function	closest homolog(s)[a]	identity (%) / alignment length	accession number
RS25505	WP_103565560	234		TetR/AcrR family transcriptional regulator	TetR/AcrR family transcriptional regulator	70/78	WP019631302
RS25510	WP_103565561	277		TIGR02452 family protein	TIGR02452 family protein	71/99	WP_075898259
RS25515	WP_103565562	381		DUF3152 domain-containing protein	DUF3152 domain-containing protein	64/95	WP_051107817
RS25520	WP_103565563	455		3' terminal RNA ribose 2'-O-methyltransferase Hen1	3' terminal RNA ribose 2'-O-methyltransferase Hen1	76/100	WP_026400644
RS25525	WP_103565564	846		polynucleotide kinase-phosphatase	polynucleotide kinase-phosphatase	85/100	WP_019631305
RS25530	WP_103565565	87		hypothetical protein			
RS25535-50	WP_103565566	613		ATP-binding cassette domain-containing protein	daunorubicin resistance protein DrrA family ABC transporter ATP-binding protein	68/52	WP_030367886
RS25555	WP_103565567	295	RumX	Nif11 family protein	G339_RS0112020[c] CinX	66/98 50/98	WP_019631330 CAD60522
RS25560	WP_103565568	1066	RumM	type 2 lantipeptide synthetase	G339_RS0112025[c] CinM	76/99 58/99	WP_019631331 CAD60521
RS25565	WP_103565569	80	RumA	cinnamycin family lantibiotic	G339_RS0112030 CinA[c]	80/98 51(98	WP_019631332 CAD60520
RS25570	WP_103565570	123	RumN	hypothetical protein	G339_RS0112035[c] Cinorf7 DivN	74/99 49/97 37/86	WP_019631333 CAD60519 ARD09209
RS25575	WP_103565571	113		hypothetical protein			
RS25580	WP_103565572	274		carbohydrate ABC transporter permease	carbohydrate ABC transporter permease	68/97	WP_026313950
RS25585	WP_103565891	295		sugar ABC transporter permease	cellobiose transport system permease protein	66/99	SNR90611
RS25590	WP_103565573	414		carbohydrate ABC transporter substrate-binding protein	Maltose-binding periplasmic proteins/domains	60/94	CND69635
RS25595	WP_103565574	528		DUF3459 domain-containing protein	alpha-amylase	73/98	PKK14679
RS25600	WP_103565575	221		nucleotidyltransferase	hypothetical protein SAMN05443665_1007127	72/96	SNS66748
RS25605	WP_103565893	253		putative nucleotidyltransferase	Predicted nucleotidyltransferase	68/98	SPT49826
RS25610		102		hypothetical protein			
RS25615	WP_103565576	384		hypothetical protein			
RS25620	WP_103565577	213		hypothetical protein			

[a] For RS25555–70, only homologs from biosynthetic gene clusters encoding for characterized compounds were considered. Origin of gene clusters: Cin= *Streptomyces cinnamoneous*; Div= *Prochloron didemni*, cinnamycin B cluster from *Actinomadura atramentaria* DSM43919

[b] Percent alignment and identify were determined using BLASTp, following default parameters. Percent alignment is the proportion of the Rum query sequence that aligns to each homolog. [c] Locus taq of cinnamycin B cluster from *Actinomadura atramentaria* DSM43919 as already described [3].

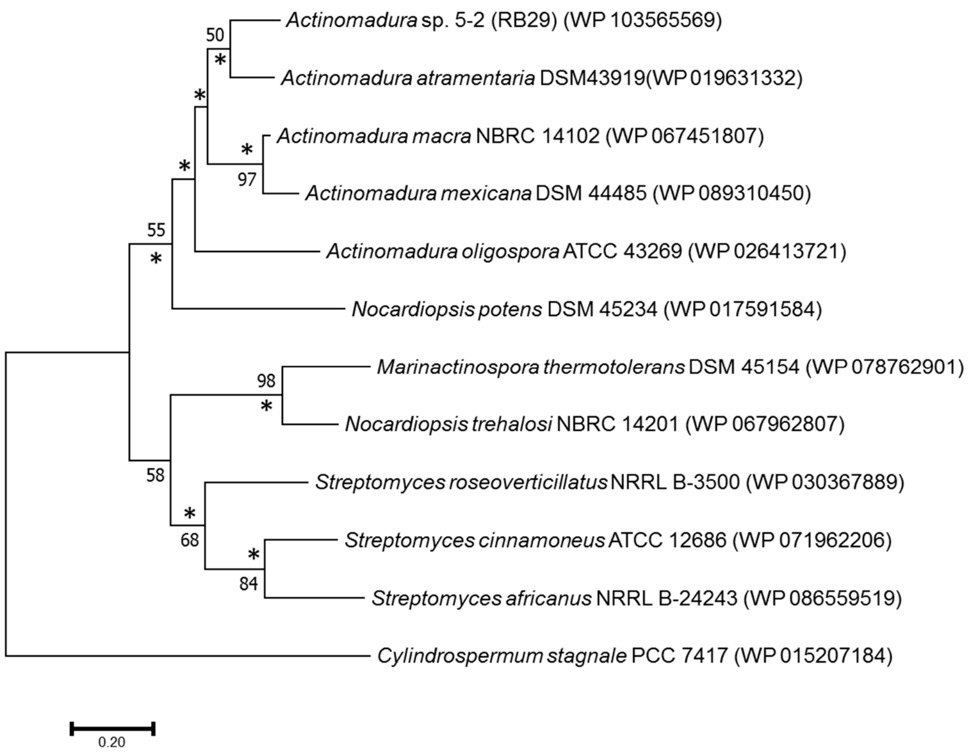


Figure S3. Neighbour-joining tree based on peptide sequence of precursor peptide sequence (RumA, WP 103565569).Star indicate branches that were also recovered in the maximum-likelihood tree. Only bootstrap values above 50% (based on 1000 pseudoreplicates) are shown. The scale bar indicates 0.2 substitutions per amino acid position.

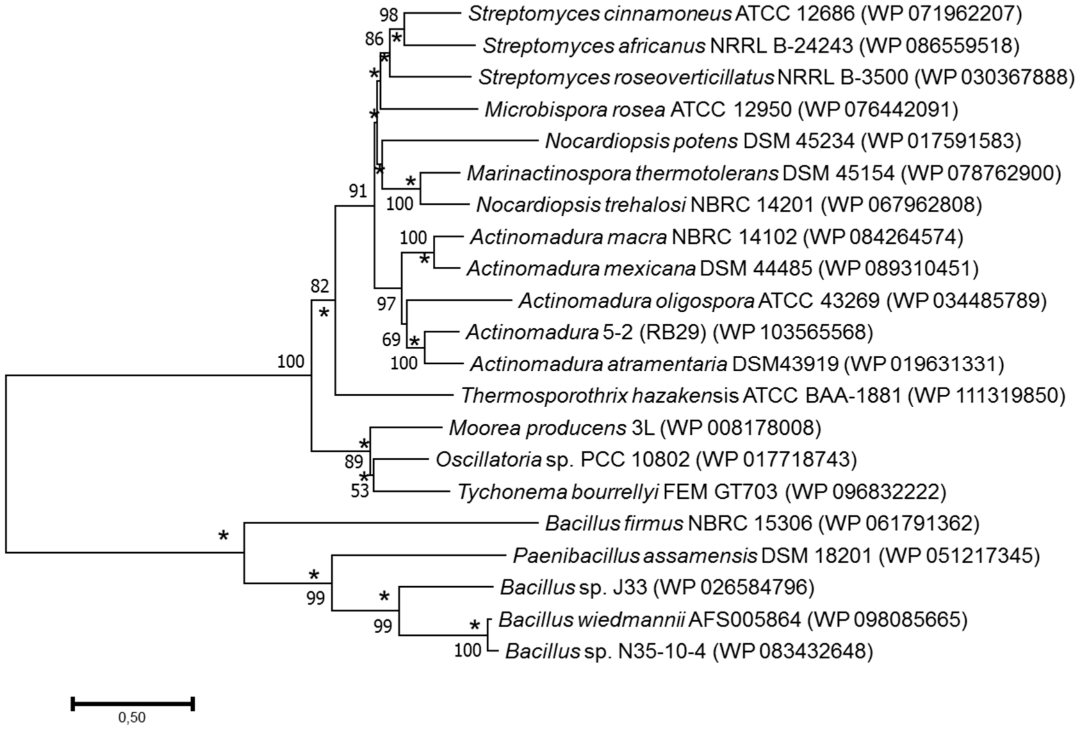
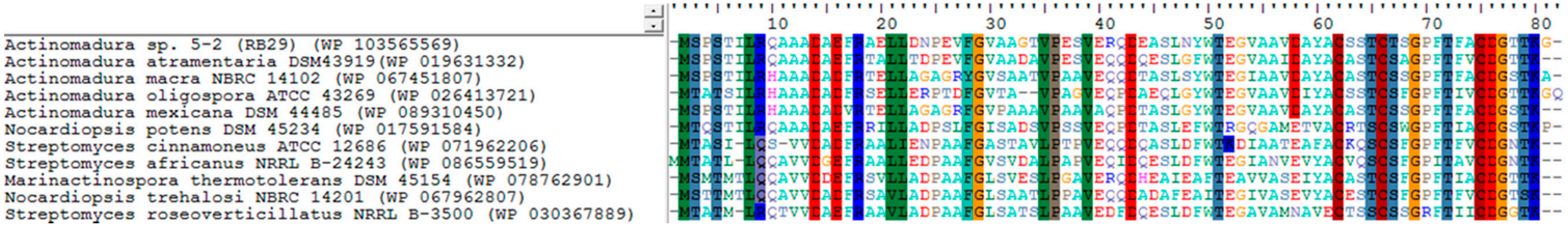


Figure S4. Neighbour-joining tree based on type 2 lantipeptide synthetase sequence RumM. Star indicates branches that were also recovered in the maximum-likelihood tree. Only bootstrap values above 50% (based on 1000 pseudoreplicates) are shown. The scale bar indicates 0.5 substitutions per amino acid position.



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Actinomadura sp. 5-2 (RB29) (WP 103565569)              -MSPSTILRQAAADAEFRAELLDNPEVFGVAAGTVPESVERQDEASLNYWTEGVAAVDAYACSSTCTSGPFTFACDGTTKG-
Actinomadura atramentaria DSM43919(WP 019631332)        -MSPSTILRQAAADAEFRTALLTDPEVFGVAADAVPESVEQQDQESLGFWTEGVAAIDAYACASTCSAGPFTFVCDGTTK--
Actinomadura macra NBRC 14102 (WP 067451807)            -MSPSTILRHAAADADFRTELLAGAGRYGVSAATVPAAVEQQDTASLSYWTEGIAAVDAYACASTCSSGPFTFACDGSTKA-
Actinomadura oligospora ATCC 43269 (WP 026413721)       -MTATSILRHAAADADFRSELLERPTDFGVTA--VPAGVEQPDAEQLGYWTEGVAAVDIYACSSTCSFGPFTIVCDGTTKGQ
Actinomadura mexicana DSM 44485 (WP 089310450)          -MSPSTILRHAAADADVRTELLAGAGRFGVPAAAVPAAVAQPDTASLGYWTEGVAAVDAYACASTCSSGPFTFACDGSTK--
Nocardiopsis potens DSM 45234 (WP 017591584)            -MTQSTILRQAAADAEFRRILLADPSLFGISADSVPSSVEQPDTASLEFWTRGQGAMETVACRTSCSWGPFTIACDGSTKP-
Streptomyces cinnamoneus ATCC 12686 (WP 071962206)      -MTASI-LQS-VVDADFRAALIENPAAFGASTAVLPTPVEQQDQASLDFWTKDIAATEAFACKQSCSFGPFTFVCDGNTK--
Streptomyces africanus NRRL B-24243 (WP 086559519)      MMTATL-LQQAVVDGEFRAALLEDPAAFGVSVDALPAPVEQIDQESLDFWTEGIANVEVYACVQSCSFGPITAVCDGNTK--
Marinactinospora thermotolerans DSM 45154 (WP 078762901) -MSMTMTLQQAVVDDEFRSVLLADPAAFGLSVESLPGAVERQDHEAIEAFTEAVVASEIYACASTCSFGPFTIACDGTTK--
Nocardiopsis trehalosi NBRC 14201 (WP 067962807)        -MSTTMTLQQAVVDADFRSAVLADPAAFGLSAATLPPAVEQQDADAFEAITEGIVASEVYACESTCSFGPFTFVCDGTSK--
Streptomyces roseoverticillatus NRRL B-3500 (WP 030367889) -MTATM-LRQTVVDAEFRAAVLADPAAFGLSATSLPAAVEDFDQESLDFWTEGAVAMNAVECTSSCSSGRFTIICDGGTK--
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Figure S5. Comparative sequence alignment of precursor peptide sequence (RumA, WP_103565569).

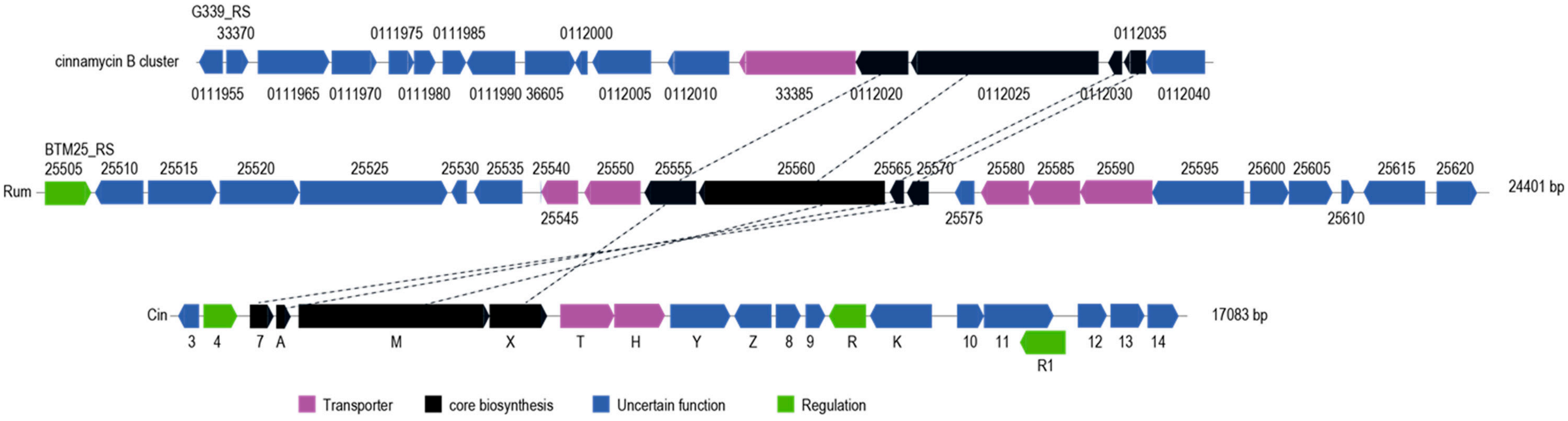


Figure S6. Comparative gene maps of *rum* and *cin* biosynthetic clusters and proposed cinnamycin B biosynthetic cluster..

Table S12. NMR Data (500 MHz, DMSO-d_6, at 300 K) for barceloneic acid A (**7**).

	barceloneic acid A (**7**)			
positio	δ$_C$, mult.[a]	δ$_H$, mult. (*J* in Hz)	COSY	HMBC
1	171.7, qC			
2	n.d.			
3	157.4, qC			
4	107.9, CH	5.95, br s		1, 3, 5, 6, 8
5	140.6, qC			
6	110.9, CH	6.26, br s		1, 3, 4, 7, 8
7	161.0, qC			
8	21.2, CH_3	2.07, s		4, 5, 6
9	136.2, qC			
10	151.6, qC			
11	101.1, CH	6.23, d (2.7)		9, 10, 12, 13
12	156.1, qC			
13	102.0, CH	6.44, d (2.7)		12, 14, 15
14	136.4, qC			
15	58.3, CH_2	4.51, br s		9, 10, 12, 13, 14
16	54.9, CH_3	3.68, s		12
		7.00, br s		

[a]:^{13}C chemical shifts were extracted from HSQC and HMBC spectra.

Table S13. NMR Data comparison with reported and isolated barceloneic acid A (**7**).

Position	barceloneic acid A[a]		barceloneic acid A[b]	
	δ$_H$, mult. (J in Hz)	δ$_C$, mult.	δ$_H$, mult. (J in Hz)	δ$_C$, mult.
1		171.86, qC		171.7, qC
2		100.91, qC		n.d.
3		159.14, qC		157.4, qC
4	6.03, br s	105.31, CH	5.95, br s	107.9, CH
5		147.85, qC		140.6, qC
6	6.50, br s	112.64, CH	6.26, br s	110.9, CH
7		164.40, qC		161.0, qC
8	2.18, s	22.00, CH_3	2.07, s	21,2, CH_3
9		132.36, qC		136.2, qC
10		151.03, qC		151.6, qC
11	6.54, d (3.0)	102.41, CH	6.23, d (2.7)	101.1, CH
12		159.25, qC		156.1, qC
13	6.68, d (3.0)	105.51, CH	6.44, d (2.7)	102.0, CH
14		137.38, qC		136.4, qC
15	4.53, br s	60.31, CH_2	4.51, br s	58.3, CH_2
16	3.80, s	55.74, CH_3	3.68, s	54.9, CH_3

[a] NMR data (acetone-d_6) from literature reported in ref. 4.

[b] NMR data (DMSO-d_6) of isolate

Table S14. NMR Data comparison with reported and isolated banegasine (**10**).

Position	banegasine[a]		banegasine[b]
	δ_H, mult. (J in Hz)	δ_C, mult.	δ_H, mult. (J in Hz)
1			
2	3.84, dd (9.3, 3.9)	56.8, CH	3.48, dd (8.6, 3.9)
3	3.13, dd (15.3, 9.6)	28.5, CH_2	2.99, dd (15.1, 8.9)
	3.50, dd (15.3, 3.9)		3.31, dd (15.1, 3.7)
4		109.7, qC	
5	7.18, s	125.1, CH	7.22, d (1.2)
6		174.5, qC	
1′		128.5, qC	
2′		138.4, qC	
3′	7.35, d (8.1)[c]	112.4, CH	7.35, d (8.1)
4′	7.11, td (8.4, 1.5)[c]	122.7, CH	7.06, t (7.8)
5′	7.03, td (7.8, 1.2)[c]	120.1, CH	6.97, t (7.2)
6′	7.68, d (8.1)[c]	119.3, CH	7.56, d (7.9)
			10.97, br s

[a] NMR data (MeOD-*d*$_4$) from literature reported in ref. 5.

[b] NMR data (600 MHz, DMSO-*d*$_6$, 300 K) of isolate.

Table S15. NMR Data (DMSO-*d*$_6$, at 300 K) for *cyclo*(*N*Me-L-3,5-dichlorotyrosine-Dhb) **(11).**[a]

position	*cyclo*(*N*Me-L-3,5-dichlorotyrosine-Dhb) (**11**)				
	δ_C, mult.[b]	δ_H, mult. (*J* in Hz)	COSY	HMBC	NOESY
1	165.5, qC				
2	62.5, CH	4.29, dd (5.0, 3.4)	3a, 3b	1, 3, 4, 8, 9	8
3	35.2, CH_2	3.03, dd (14.0, 5.0)	2	1, 2, 4, 5	2, 3b, 5
		2.92, dd (14.0, 3.4)	2	1, 2, 4, 5	2, 3a, 5
4	127.2, qC				
5	129.7, 2 CH	6.94, s, 2H		2, 3, 6, 7	3a, 3b, 8
6	121.9, 2 qC				
7	148.8, qC				
8	32.1, CH_3	2.94, s, 3H		2, 9	2, 5
9	159.0, qC				
10	126.9, qC				
11	112.0, CH	5.41, q, 7.5	12	9, 12	12
12	10.7, CH_3	1.46, d, 7.5	11	9, 10, 11	11, *N*H
*N*H		9.92, br s		1, 2, 9, 10	12

[a] 600 MHz for ^{1}H NMR and 150 MHz for ^{13}C NMR

[b] numbers of attached protons were determined by analysis of 2D spectra.

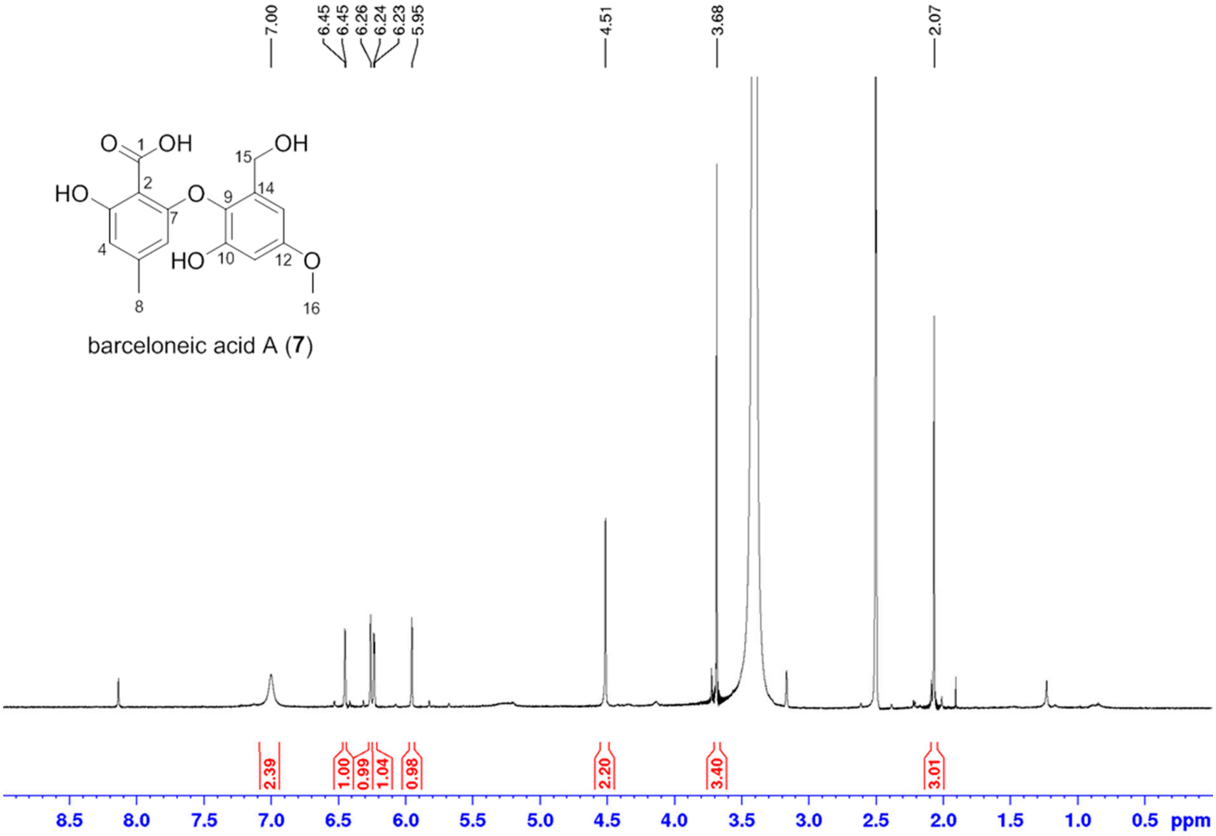


Figure S7. ^{1}H NMR spectrum of barceloneic acid A (**7**) (DMSO-d_6, 300K, 500 MHz).

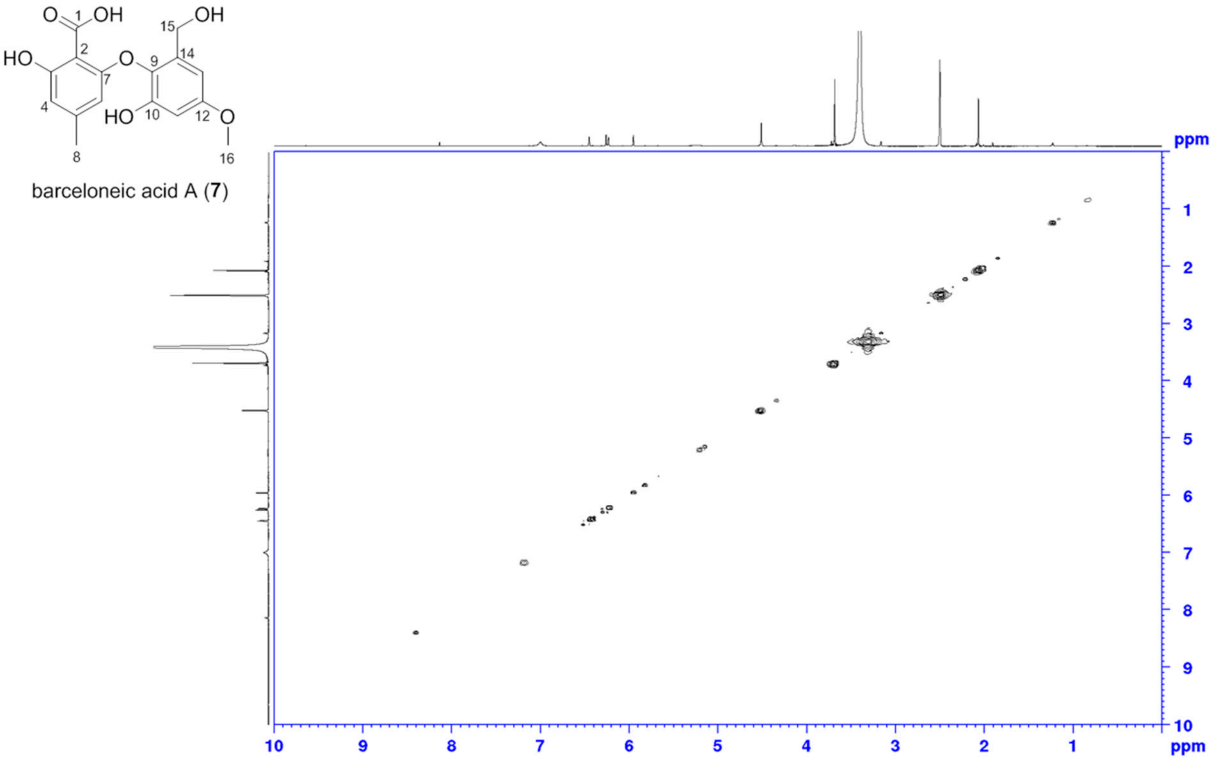


Figure S8. COSY spectrum of barceloneic acid A (**7**) (DMSO-d_6, 300K, 500 MHz).

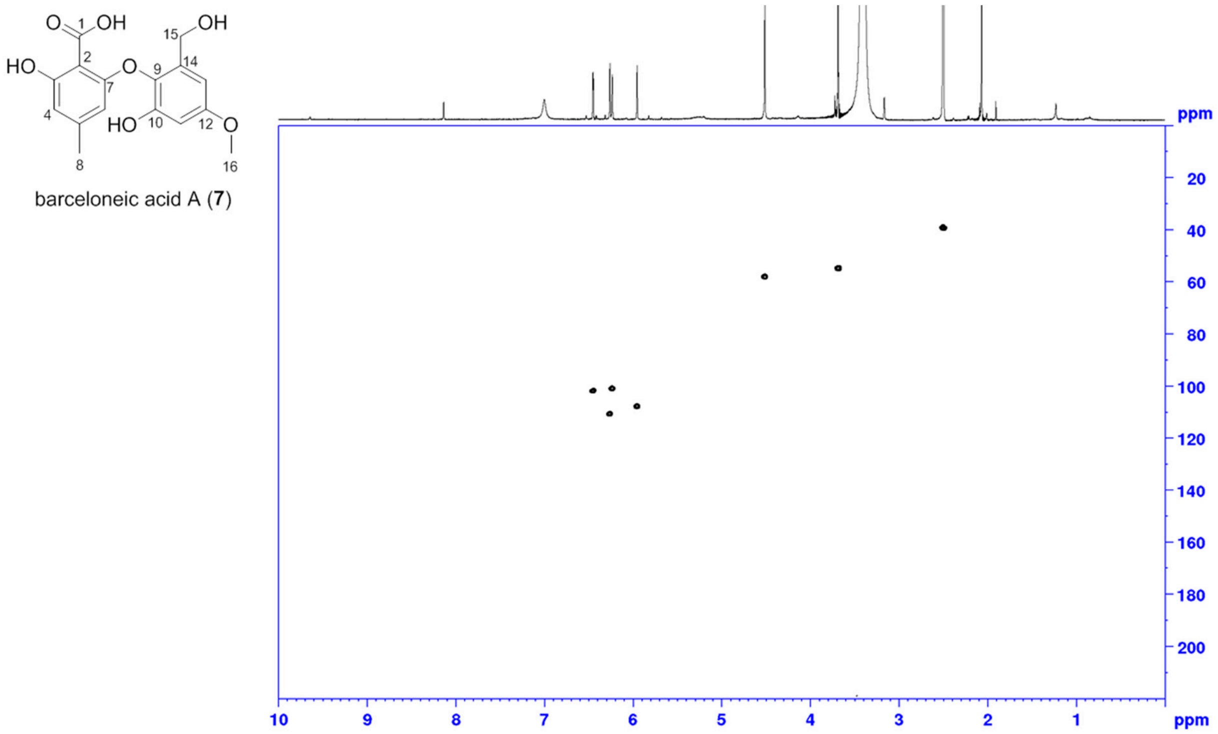


Figure S9. HSQC NMR spectrum of barceloneic acid A (**7**) (DMSO-d_6, 300K, 500 MHz).

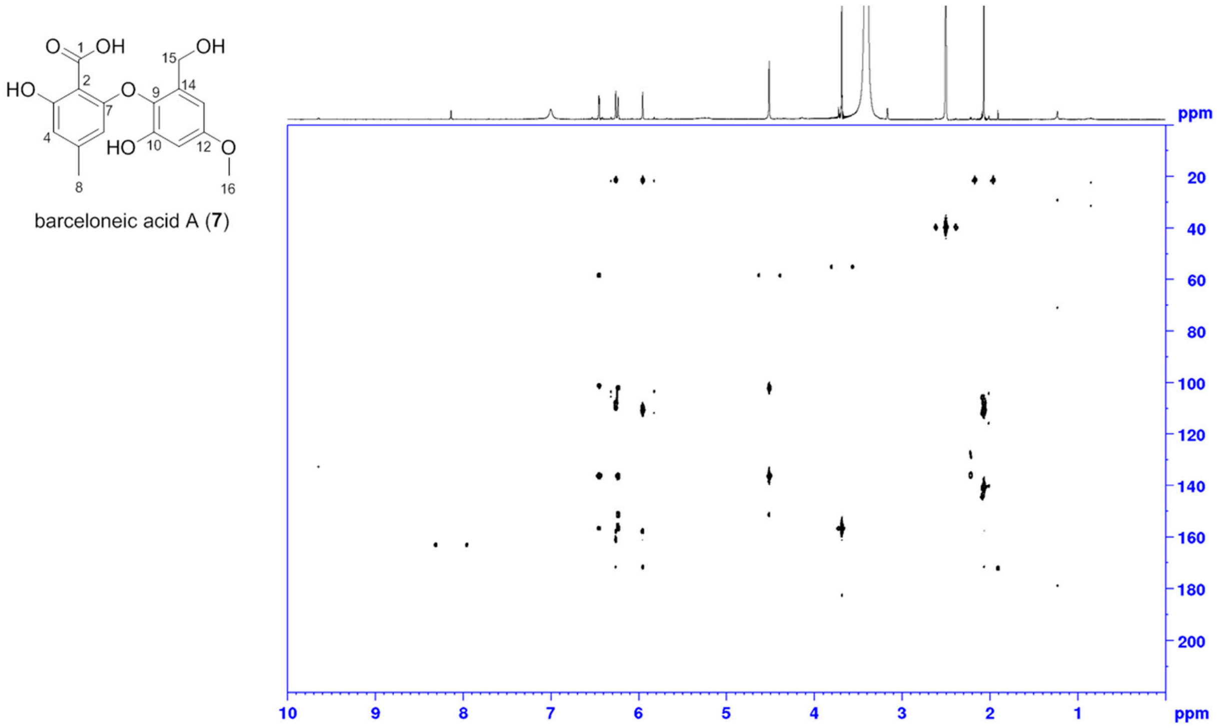


Figure S10. HMBC NMR spectrum of barceloneic acid A (**7**) (DMSO-d_6, 300K, 500 MHz).

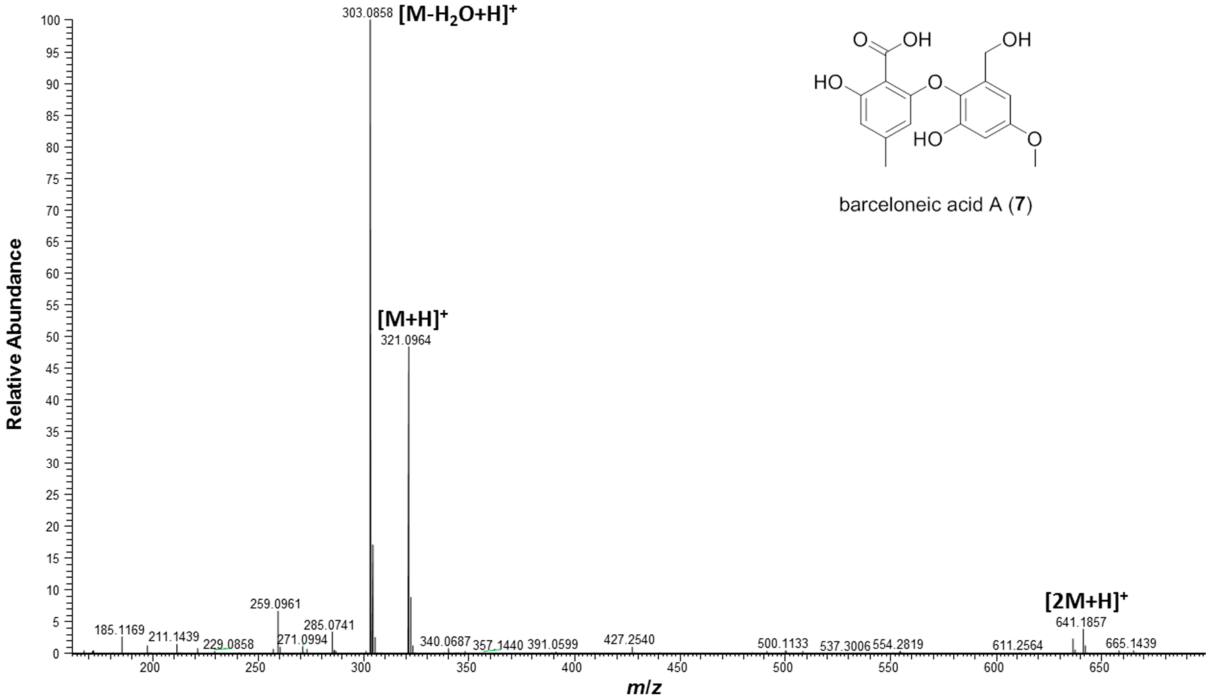


Figure S11. ESI-HRMS spectrum of barceloneic acid A (**7**) under the positive mode.

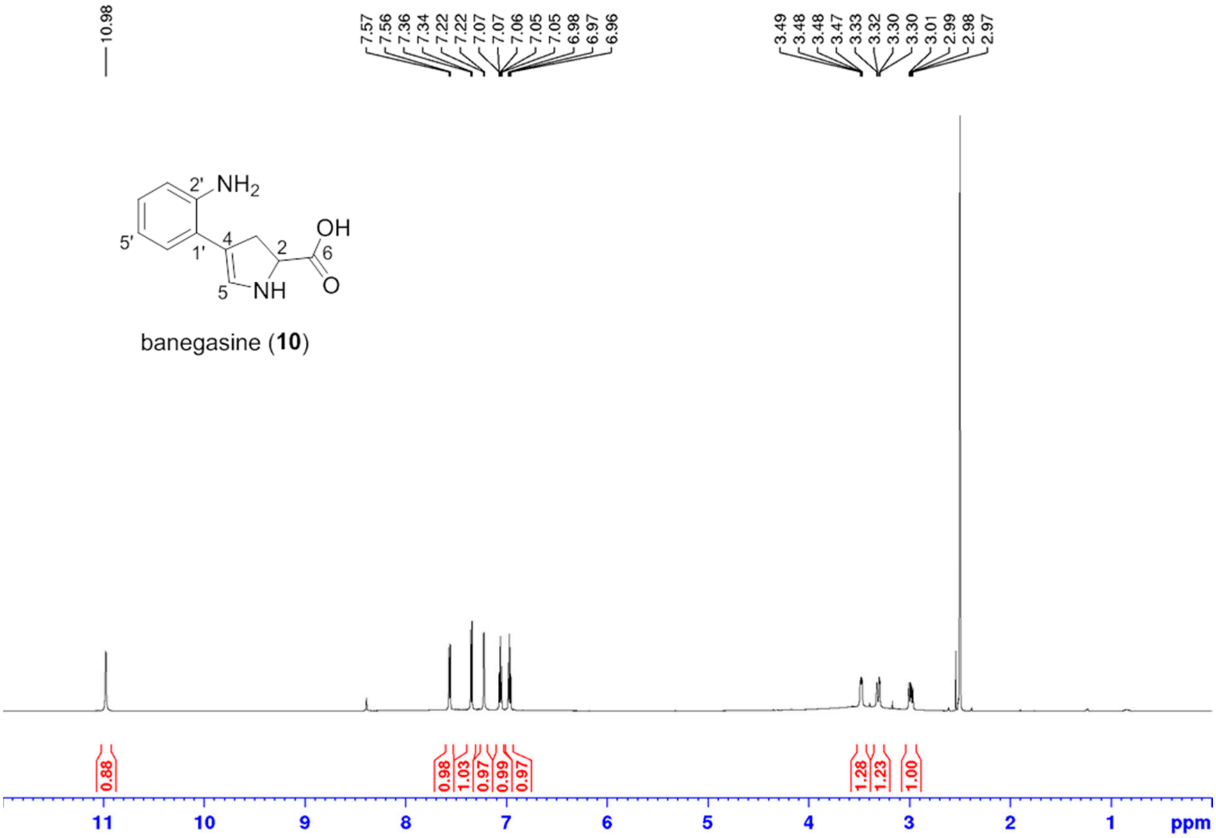


Figure S12. ^{1}H NMR spectrum of banegasine (**10**) (DMSO-d_6, 300K, 600 MHz).

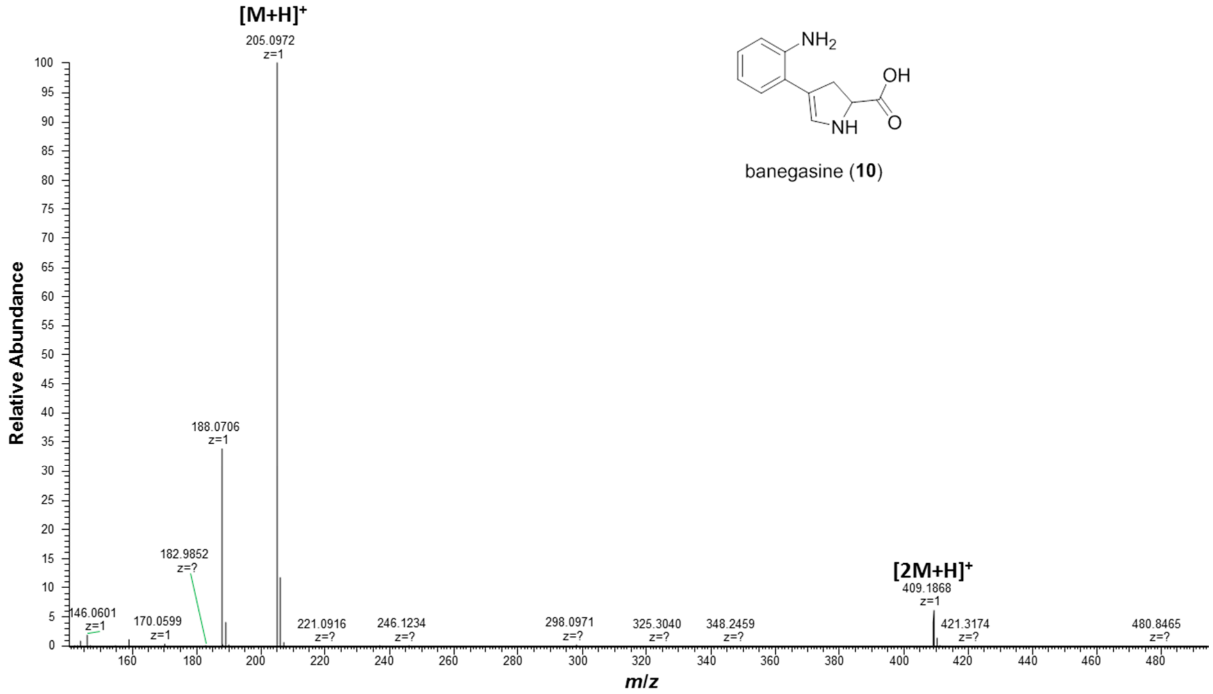


Figure S13. ESI-HRMS spectrum of banegasine (**10**) under the positive mode.

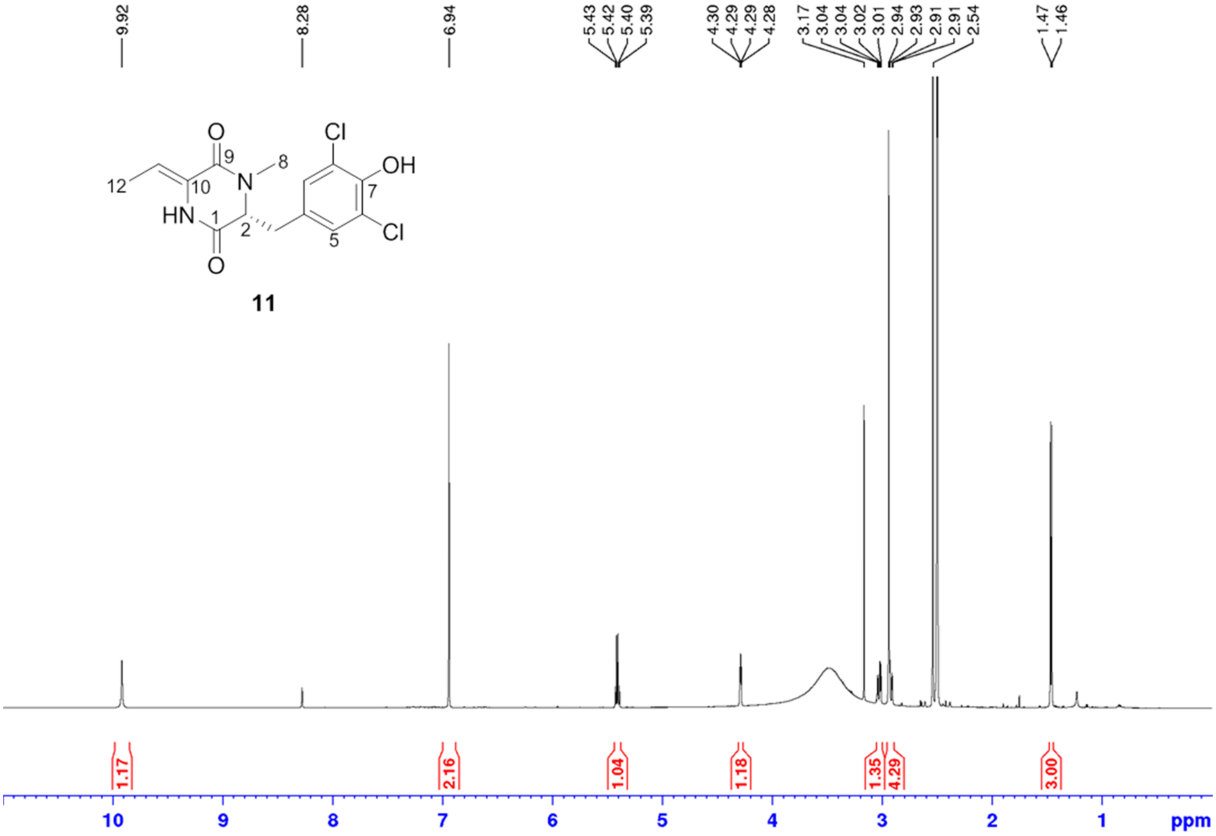


Figure S14. ^{1}H NMR spectrum of *cyclo*(*N*Me-L-3,5-dichlorotyrosin-Dhb) (**11**) (600 MHz, DMSO-*d*$_6$, 300 K).

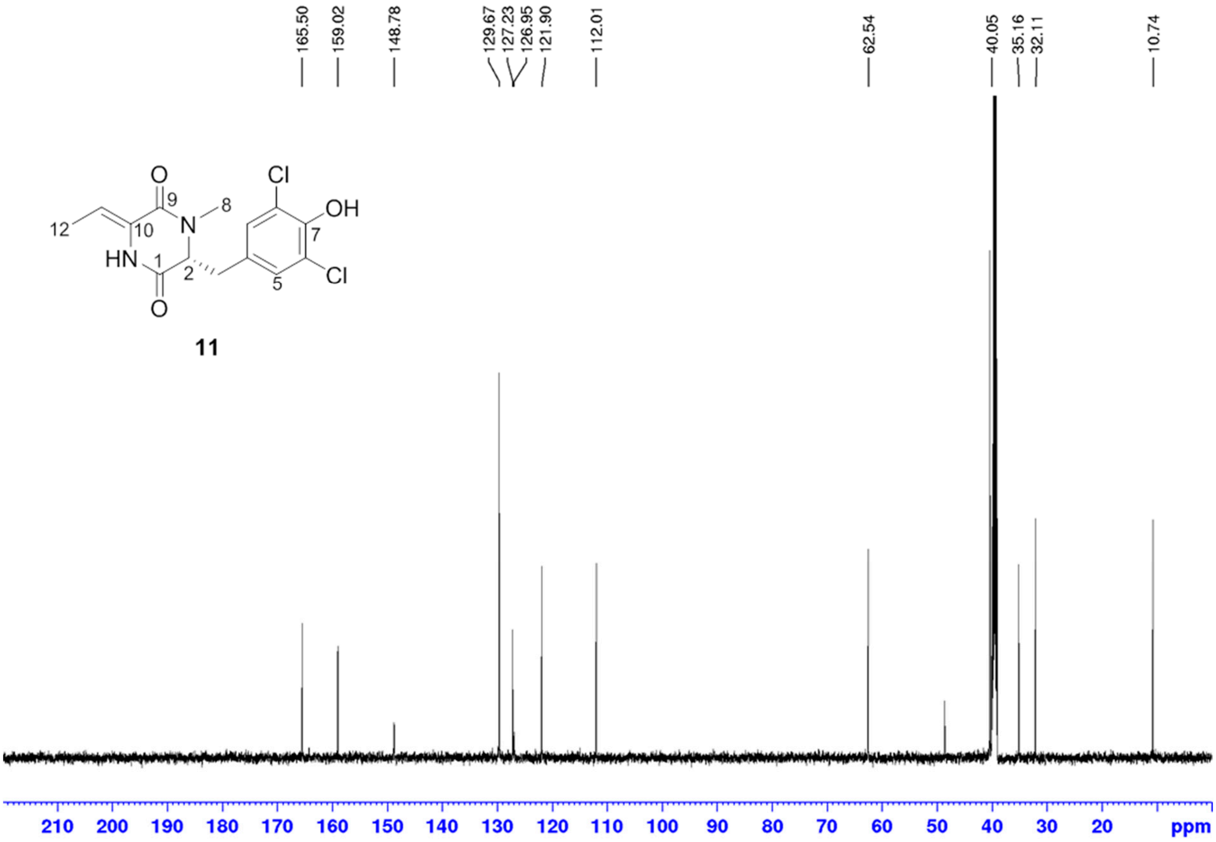


Figure S15. ^{13}C NMR spectrum of *cyclo*(*N*Me-L-3,5-dichlorotyrosin-Dhb) (**11**) (150 MHz, DMSO-d_6, 300 K).

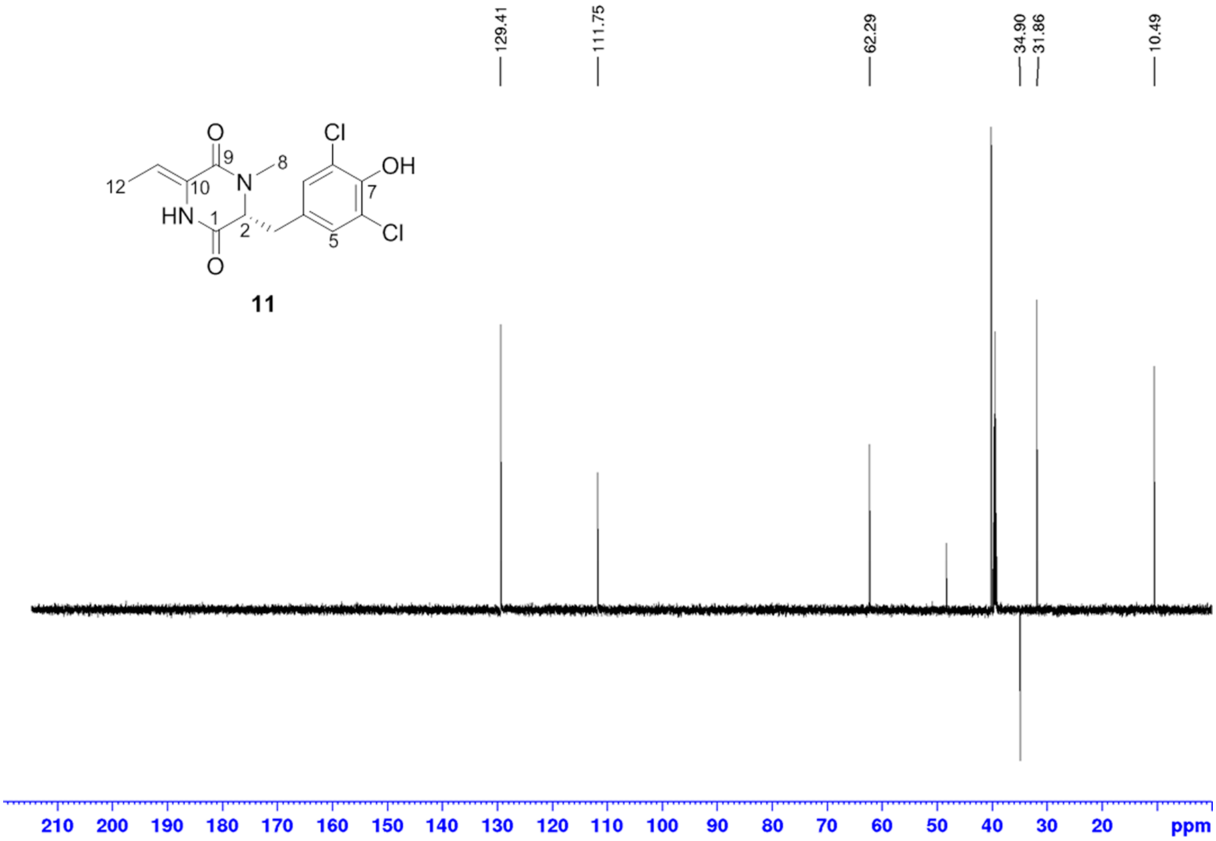


Figure S16. DEPT135 spectrum of *cyclo*(*N*Me-L-3,5-dichlorotyrosin-Dhb) (**11**) (600 MHz, DMSO-d_6, 300 K).

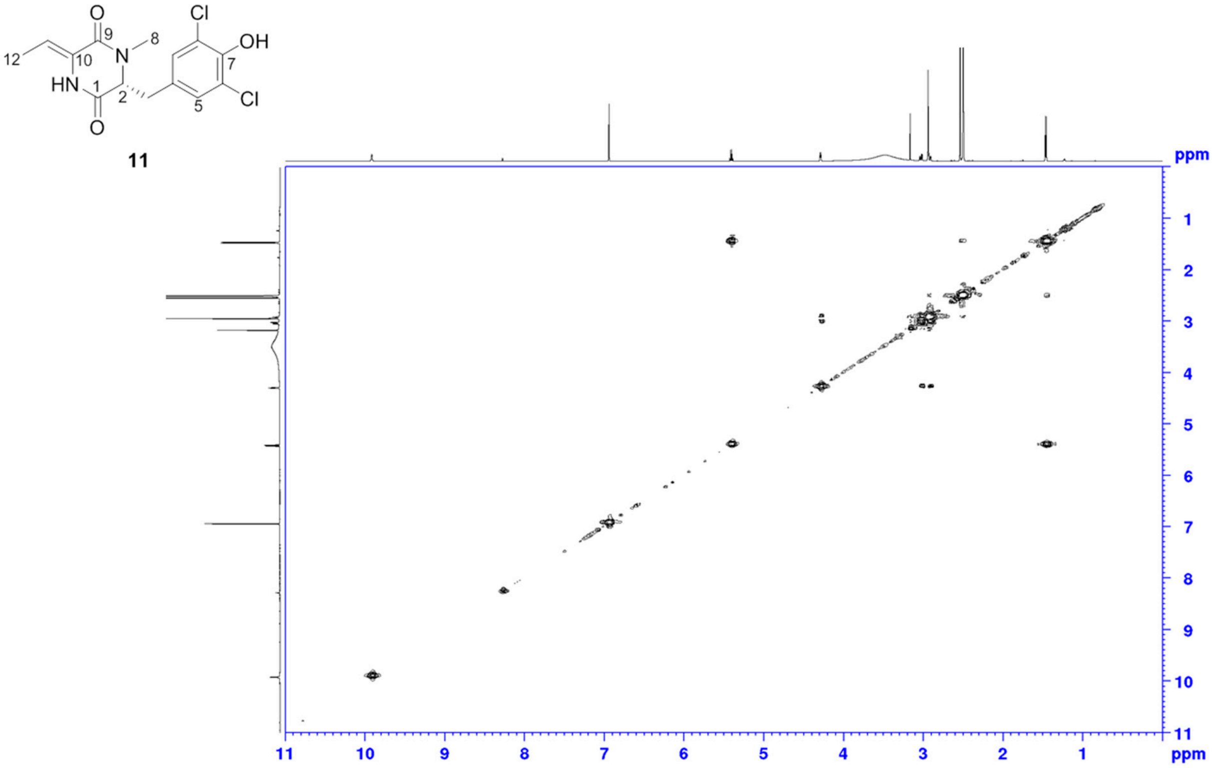


Figure S17. COSY spectrum of *cyclo*(*N*Me-L-3,5-dichlorotyrosin-Dhb) (**11**) (600 MHz, DMSO-d_6, 300 K).

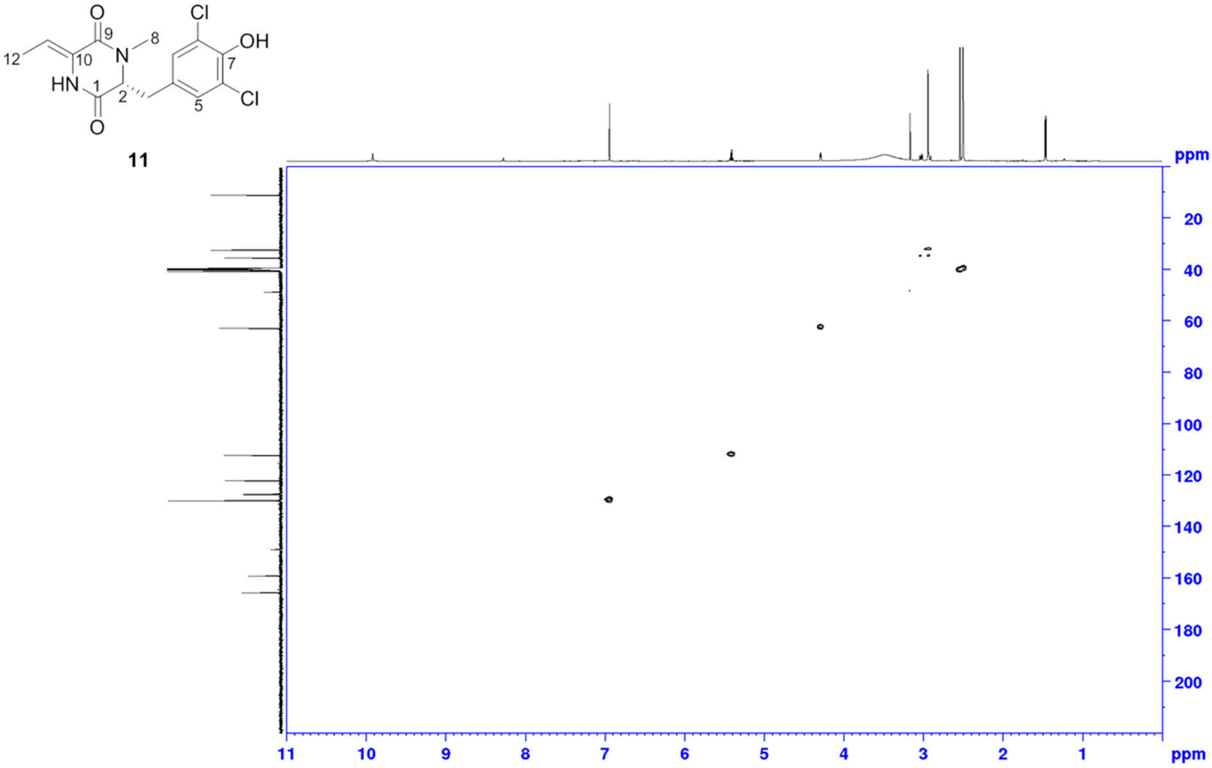


Figure S18. HSQC spectrum of *cyclo*(*N*Me-L-3,5-dichlorotyrosin-Dhb) (**11**) (600 MHz, DMSO-d_6, 300 K).

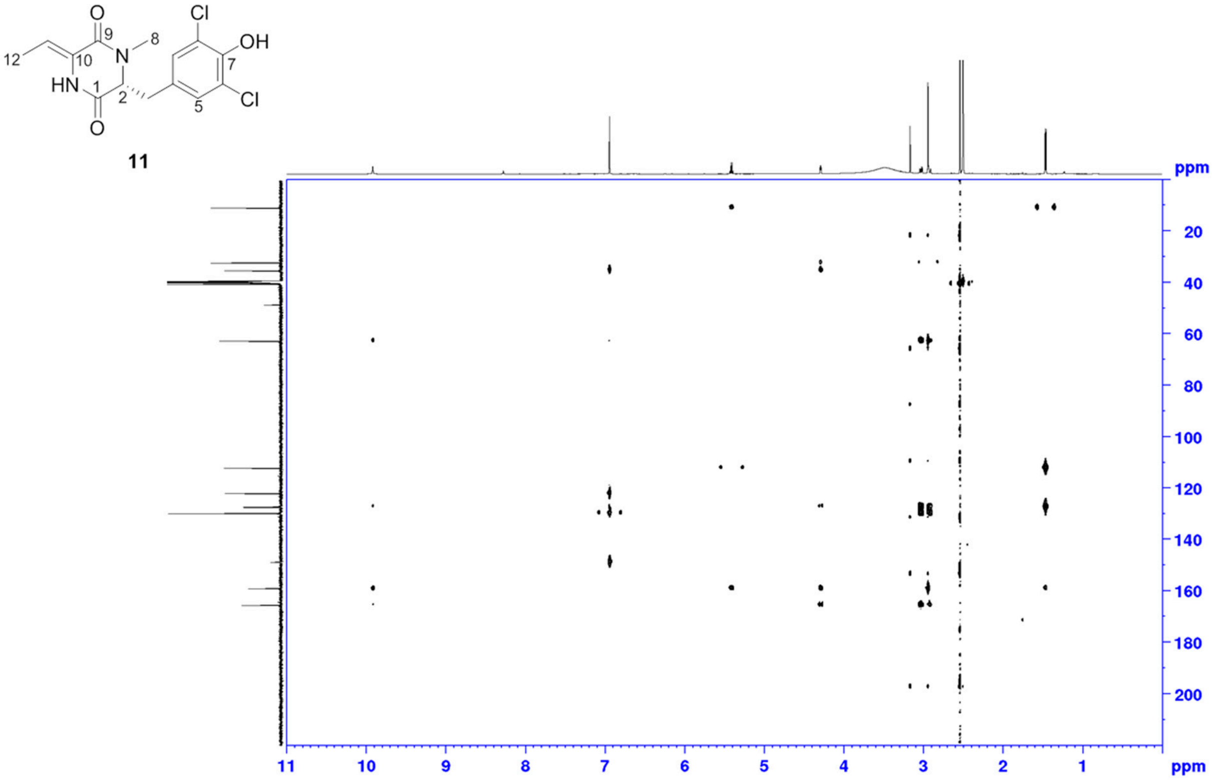


Figure S19. HMBC spectrum of *cyclo*(*N*Me-L-3,5-dichlorotyrosin-Dhb) (**11**) (600 MHz, DMSO-d_6, 300 K).

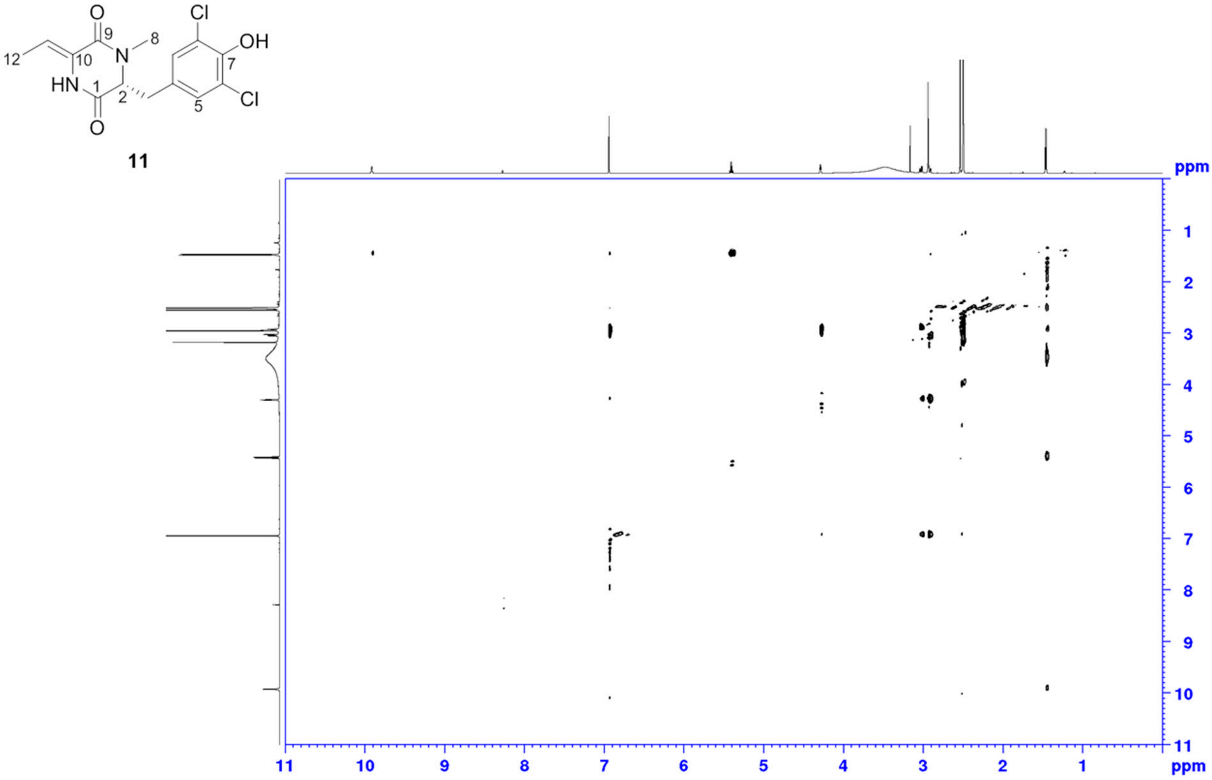


Figure S20. NOESY spectrum of *cyclo*(*N*Me-L-3,5-dichlorotyrosin-Dhb) (**11**) (600 MHz, DMSO-d_6, 300 K).

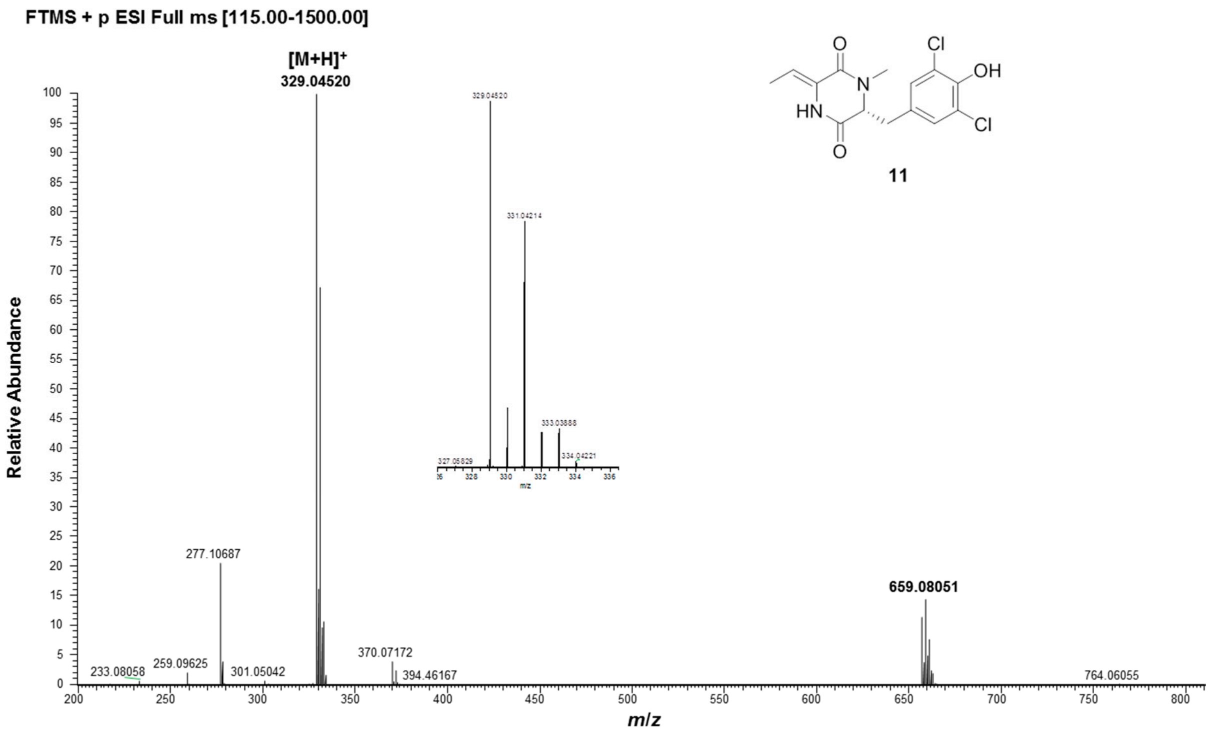


Figure S21. ESI-HRMS spectrum of *cyclo*(*N*Me-L-3,5-dichlorotyrosin-Dhb) (**11**).

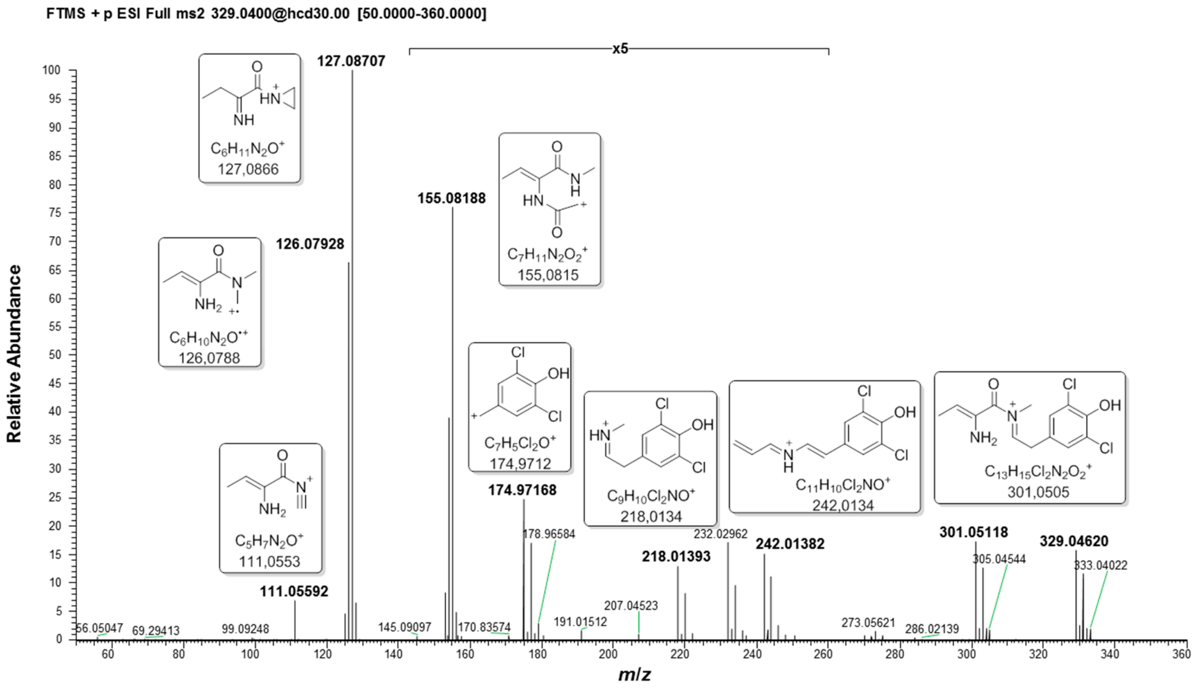


Figure S22. ESI-HRMS^2 spectrum of *cyclo*(*N*Me-L-3,5-dichlorotyrosin-Dhb) (**11**).

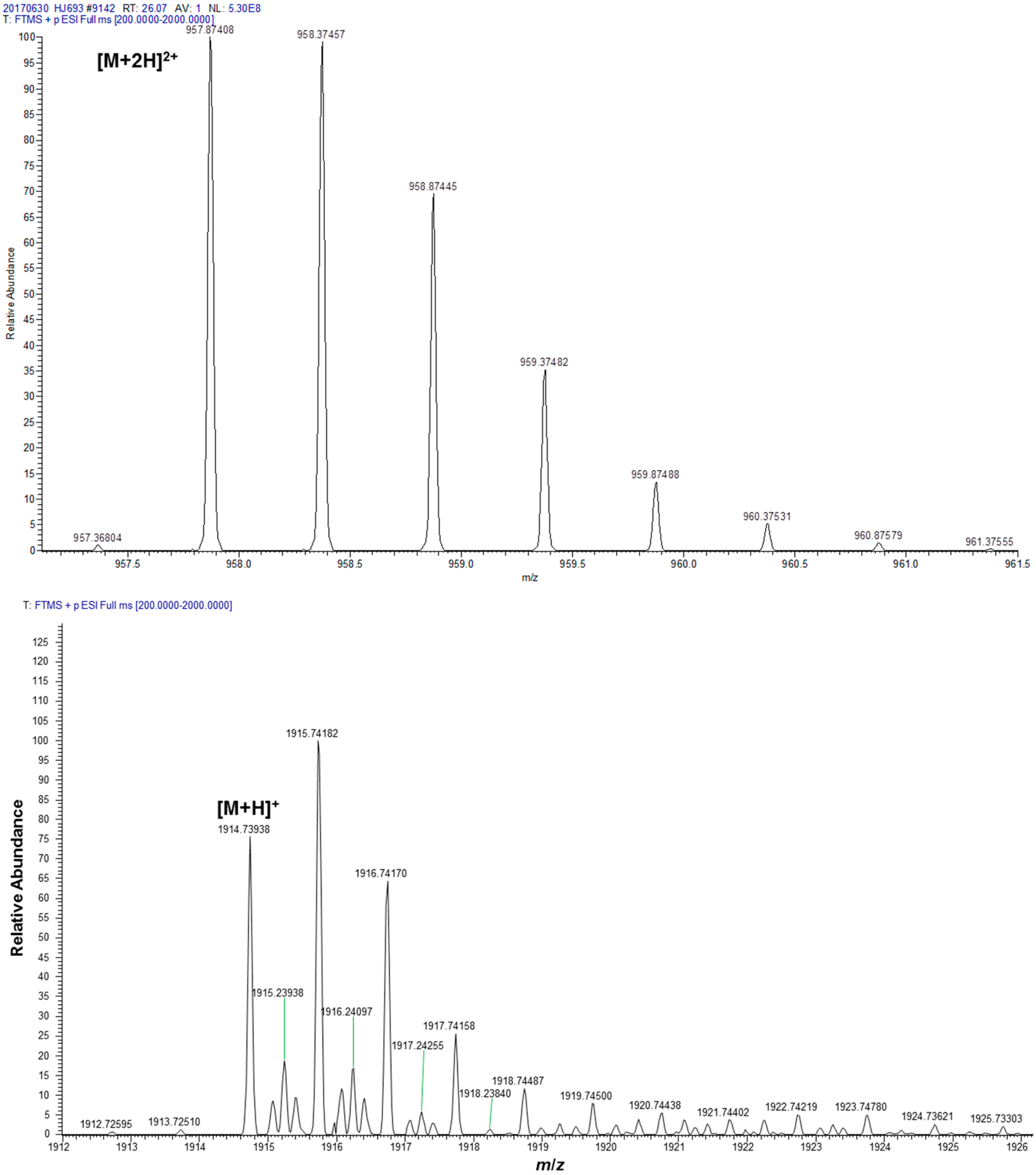


Figure S23. ESI-HRMS spectrum of rubrominin A (**12**).

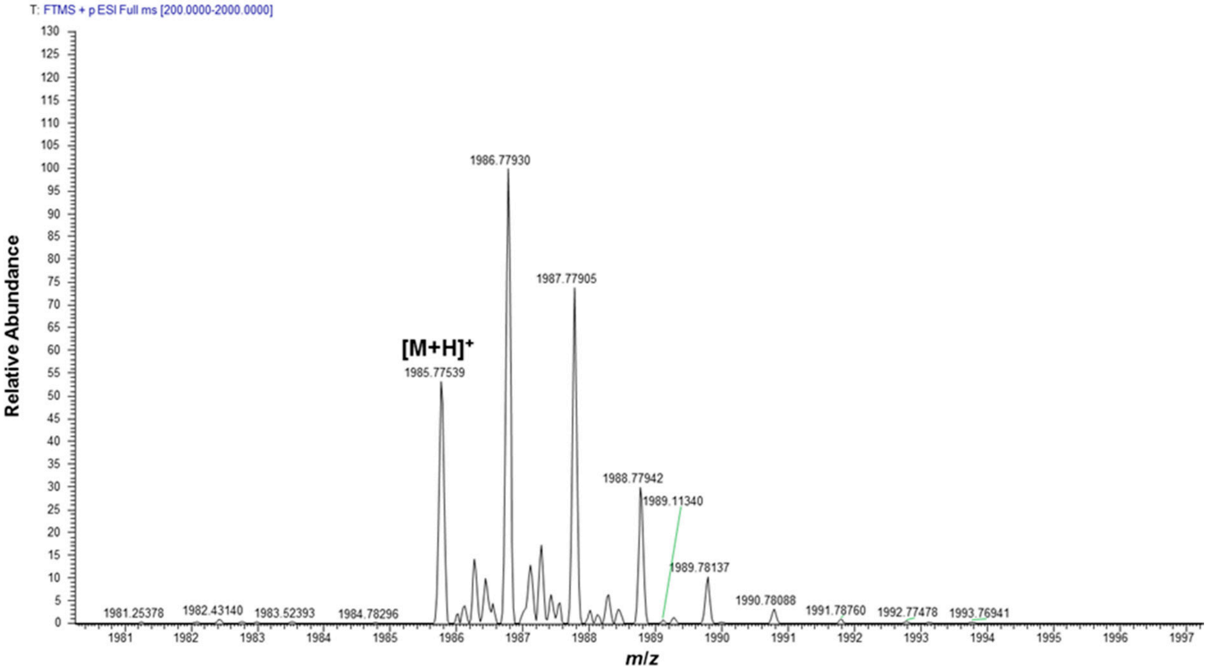


Figure S24. ESI-HRMS spectrum of rubrominin B (**13**).

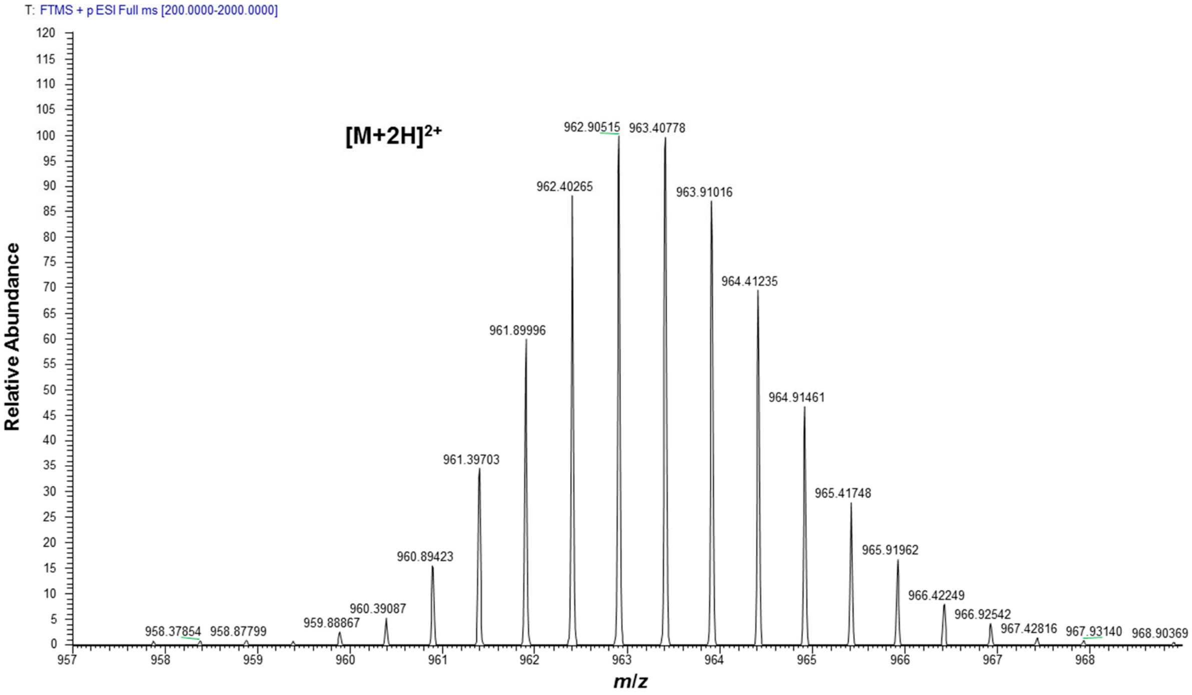


Figure S25. ESI-HRMS spectrum of rubrominin A (**12**) labled with L-Serine-2,3,3-d3.

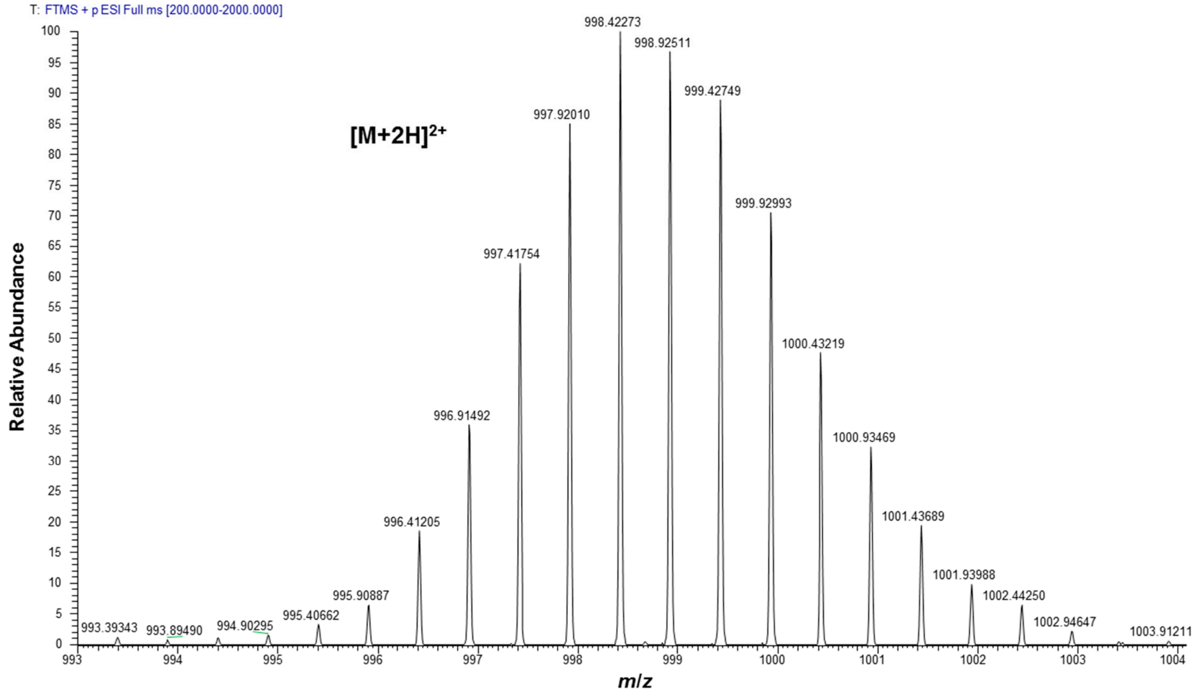


Figure S26. ESI-HRMS spectrum of rubrominin B (**13**) labled with L-serine-2,3,3-D3.

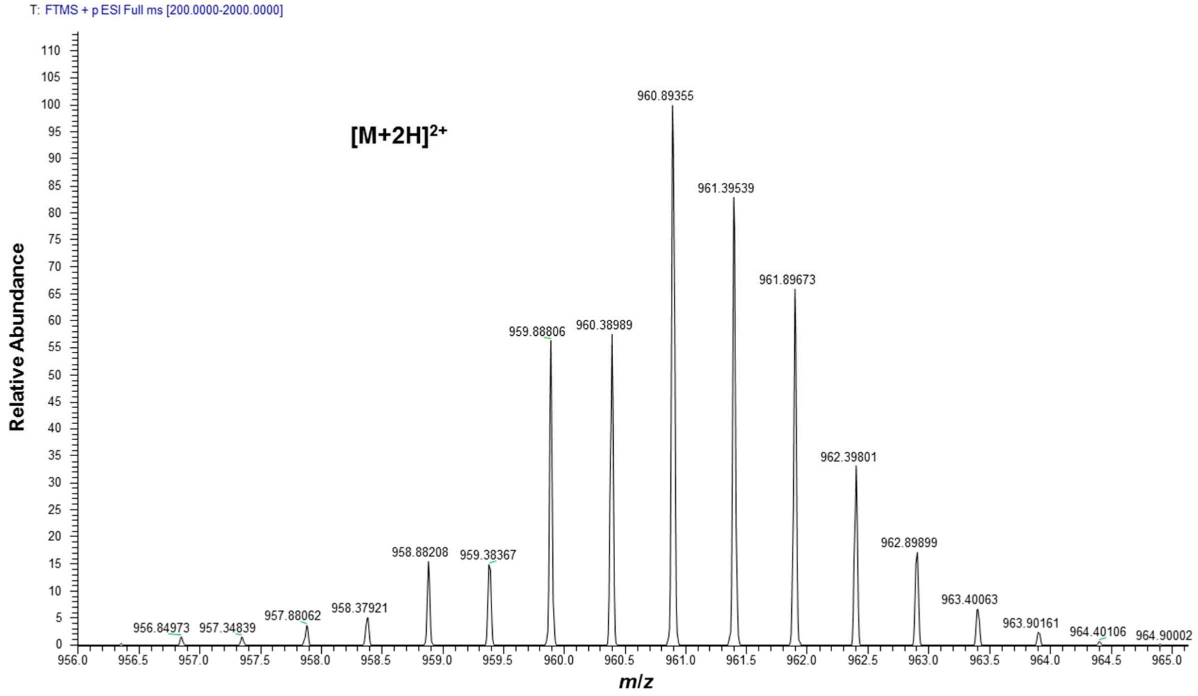


Figure S27. ESI-HRMS spectrum of rubrominin A (**12**) labled with DL-cystein-3,3-D2.

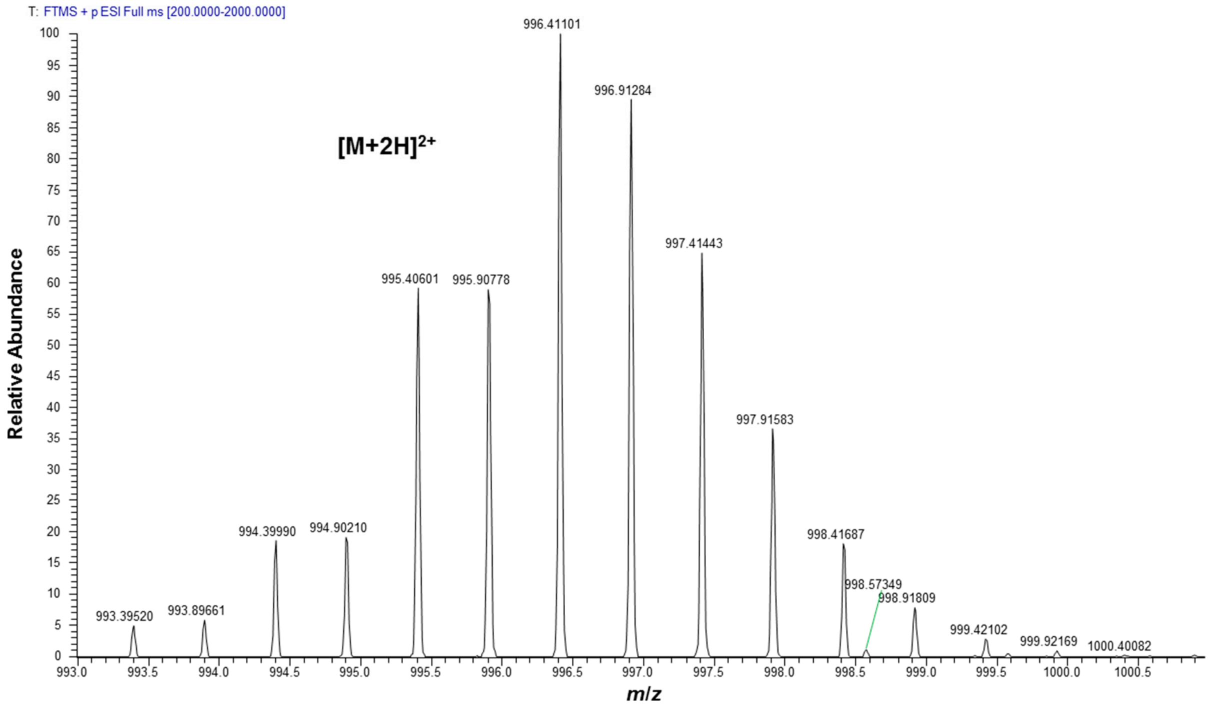
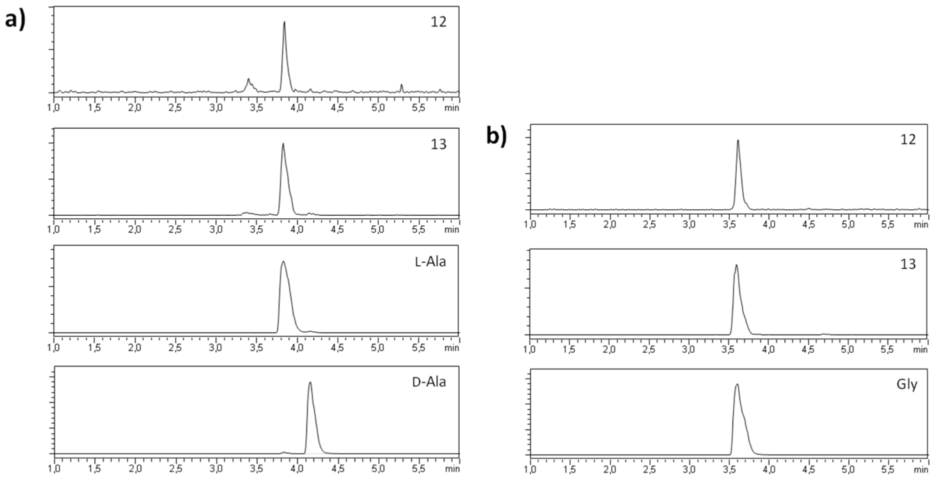


Figure S28. ESI-HRMS spectrum of rubrominin B (**13**) labled with DL-cystein-3,3-D2.



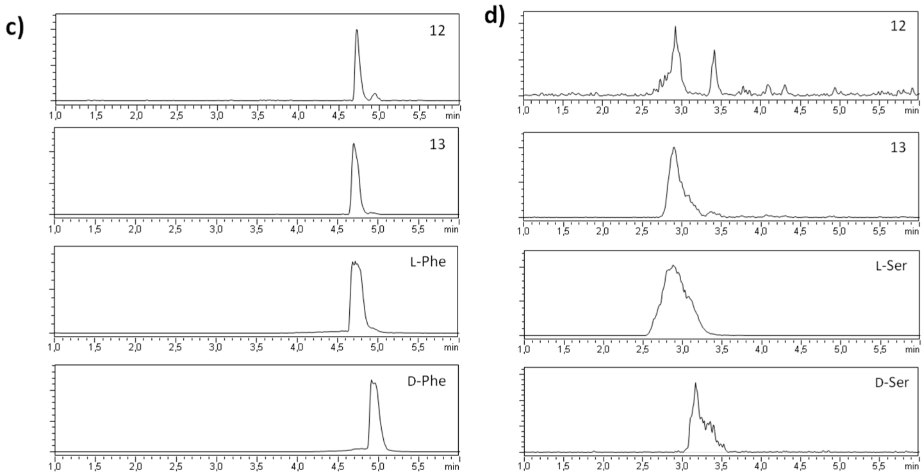


Figure S29. UHPLC-MS chromatogram of Marfey's reaction (1): a) extracted ion chromatograms of Marfey's derivative of standard L-alanine (m/z 342.00, tR = 3.83 min), D-alanine (m/z 342.00, tR = 4.17 min); b) extracted ion chromatograms of Marfey's derivative of standard glycine (m/z 328.00, tR = 3.60 min); c) extracted ion chromatograms of Marfey's derivative of standard L-phenylalanine (m/z 418.00, tR = 4.73 min), D-phenylalanine (m/z 418.00, tR = 4.93 min); d) extracted ion chromatograms of Marfey's derivative of standard L-serine (m/z 358.00, tR = 2.94 min), D-serine (m/z 358.00, tR = 3.15 min).

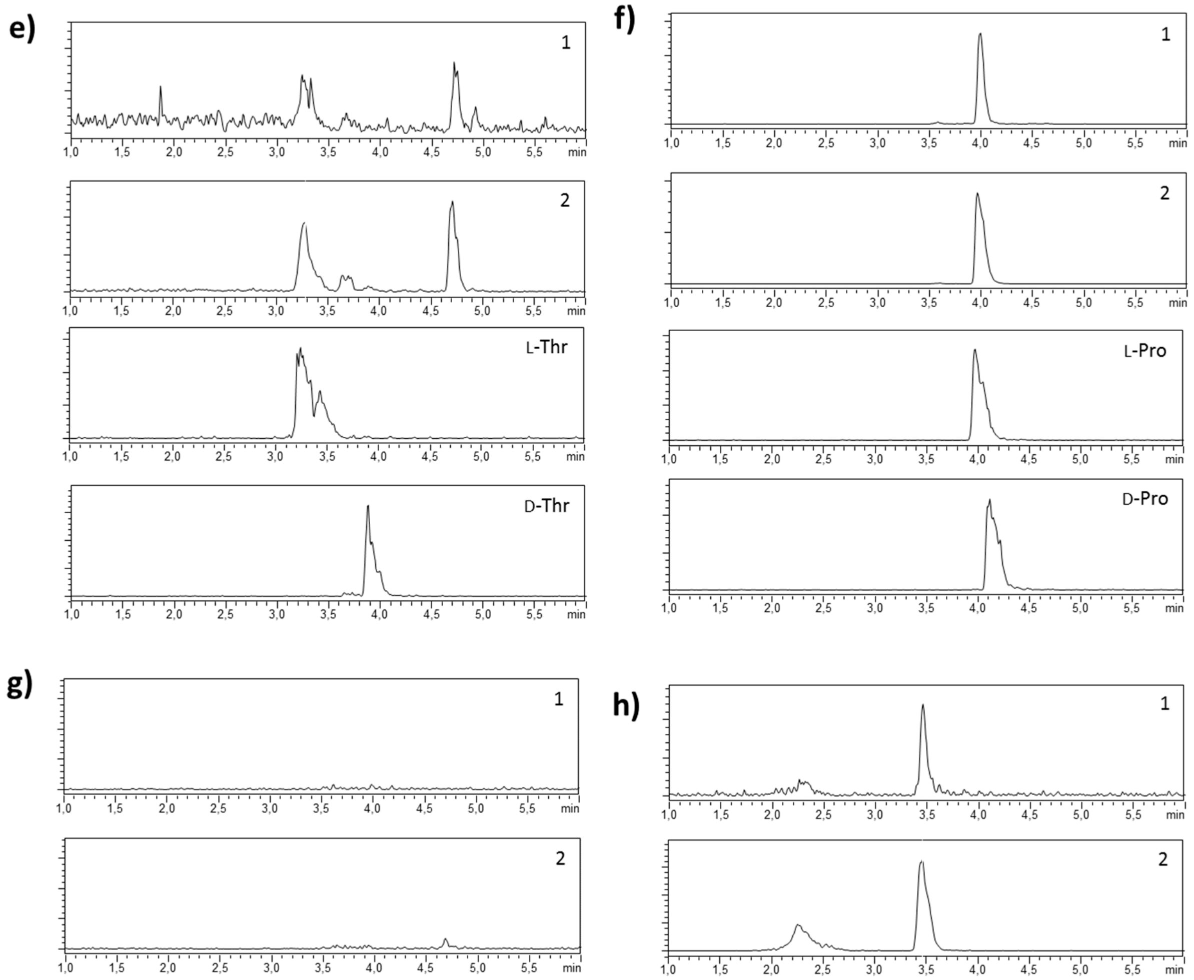


Figure S30. UHPLC-MS chromatogram of Marfey's reaction (2): e) extracted ion chromatograms of Marfey's derivative of standard L-theorine (m/z 372.00, tR = 3.26 min), D-theorine (m/z 372.00, tR = 3.87 min); f) extracted ion chromatograms of Marfey's derivative of standard L-proline (m/z 368.00, tR = 3.98 min), D-proline (m/z 368.00, tR = 4.12 min); g) extracted ion chromatograms of proposed Marfey's derivative of lanthionine (m/z 461.0); h) extracted ion chromatograms of proposed Marfey's derivative of methyllanthionine (m/z 475.0) .

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