

Supplementary Information for

Studies on Argentine *Phylacia* species (*Hypoxylaceae*) using a polythetic taxonomic approach

Christopher Lambert^{1,2,3}, Rahel Schiefelbein^{1,2}, Marc Stadler^{1,2,*}, Esteban B. Sir^{4,*}

1. Department- Microbial Drugs, Helmholtz-Centre for Infection Research GmbH, Inhoffenstraße 7, 38124 Braunschweig, Germany
2. Institute of Microbiology, Technische Universität Braunschweig, Spielmannstraße 7, 38106 Braunschweig
3. Department for Cell Biology, Helmholtz-Centre for Infection Research GmbH, Inhoffenstraße 7, 38124 Braunschweig, Germany.
4. Instituto de Bioprospección y Fisiología Vegetal-INBIOFIV (CONICETUNT), San Lorenzo 1469, San Miguel de Tucumán, Tucumán, 4000, Argentina

*Corresponding author, e-mail: marc.stadler@helmholtz-hzi.de, phone: +49 531 6181-4240,

Table S1: Flanking positions of MAFFT alignments using gblocks for automatic minimization of alignment errors.

Locus	Flanking positions	Proportion of the original positions
ITS	[61-78], [104-121], [130-141], [473-483], [497-510], [1056-1177], [1179-1222], [1229-1252], [1254-1268], [1297-1331], [1337-1356], [1367-1381], [1420-1438], [1459-1512]	421/2842 (14%)
LSU	[636-668], [670-888], [890-975], [977-1013], [1021-1105], [1107-1152], [1157-1285], [1289-1467], [1563-1577], [2132-2177], [2179-2428], [2814-2911], [2913-2953], [2955-2969]	1279/2994 (42%)
<i>rpb2</i>	[1424-1540], [1561-2023], [2036-2278], [2282-2294], [2301-2421]	957/3942 (24%)
<i>tub2</i>	[83-103], [163-172], [196-206], [279-288], [324-336], [399-437], [459-470], [507-519], [522-531], [544-571], [641-688], [776-854], [956-1129], [1131-1141], [1143-1766], [1819-1828], [1840-1869]	1143/1943 (58%)

Table S2: Characteristics of the final multigene alignment used for phylogenetic inference for IQTree2 and Mrbayes 3.2.7a.

Locus	Sequences	Total Sites	Unquie	Informative	Invariable	Constant
ITS	60	421	240	141	213	213
LSU	52	1279	305	126	1058	1058
<i>rpb2</i>	54	957	556	451	464	464
<i>tub2</i>	55	1143	519	385	634	634

Table S3: Tested best-fit models as determined by Modelfinder according to Bayesian Information Criterion (BIC) for molecular phylogenetic inference using IQTree2.

Locus	Model	Speed	Parameters
ITS	TPM2+G4	1.1792	TPM2{1.5923,3.81635}+FQ+G4{0.273641}
LSU	TNe+I+I+R2	0.2201	TNe{3.48625,5.20213}+FQ+I{0.74663} +R2{0.209687,1.699,0.0436828,14.7367}
<i>rpb2</i>	TIM3+F+I+I+R3	1.9017	TIM3{1.55529,6.05054,11.3752}+F{0.256367,0.258211,0.268041,0.217381} +I{0.424203}+R3{0.180734,0.213836,0.238549,1.52606,0.156513,3.81636}
<i>tub2</i>	TIM2+F+I+I+R3	1.0517	TIM2{1.38405,5.09981,8.71024}+F{0.197536,0.316228,0.244878,0.241358} +I{0.424668}+R3{0.281354,0.271365,0.183531,1.9981,0.110447,5.04259}

Table S4: Tested best-fit models as determined by PartitionFinder2 as implemented in Phylosuite according to Bayesian Information Criterion (BIC) for molecular phylogenetic inference using MrBayes 3.2.7a.

Locus	Best Model
ITS, LSU	K80+I+G
<i>Rpb2</i> , <i>tub2</i>	GTR+I+G

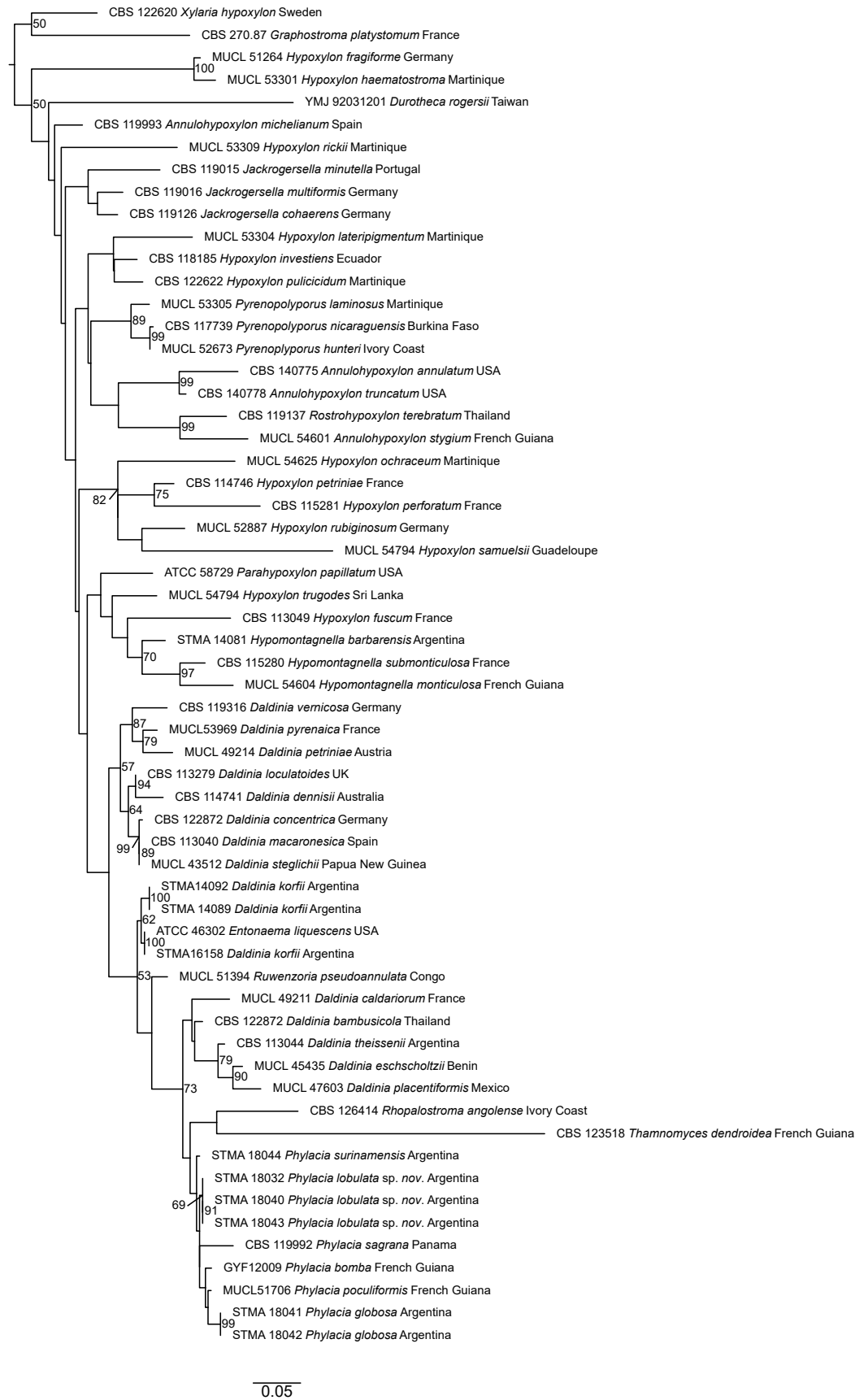


Figure S1: Maximum-Likelihood (MLn=-4780.8136) tree inferred from ITS sequences of selected *Hypoxylaceae* and species of related families as outgroup. Bootstrap support values (BS) $\geq 50\%$ are included at the respective branches.

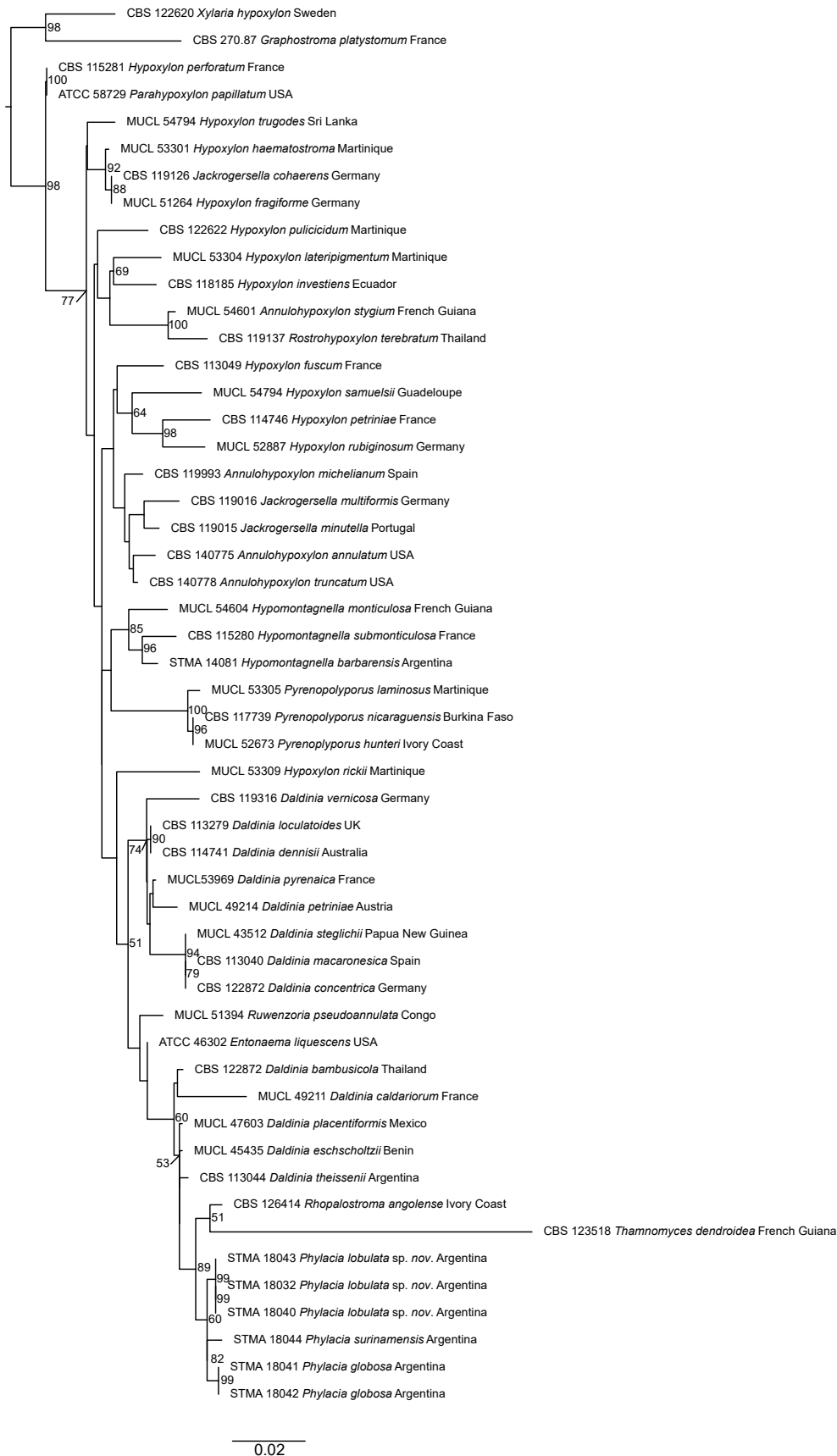


Figure S2: Maximum-Likelihood (ILn=-4988.2755) tree inferred from LSU sequences of selected *Hypoxylaceae* and species of related families as outgroup. Bootstrap support values (BS) $\geq 50\%$ are included at the respective branches.

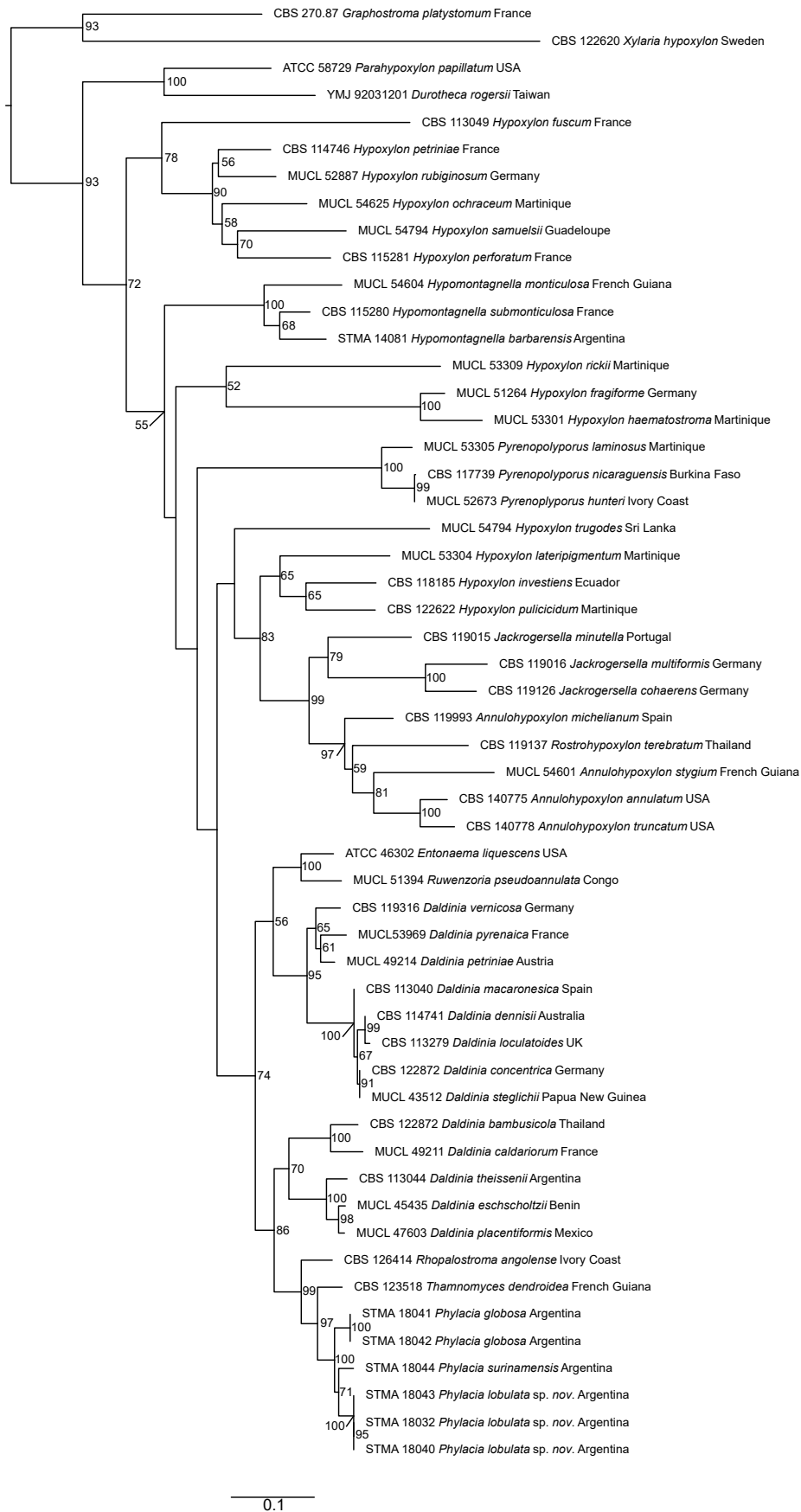


Figure S3: Maximum-Likelihood (ILn=-14780.8391) tree inferred from *RPB2* sequences of selected *Hypoxylaceae* and species of related families as outgroup. Bootstrap support values (BS) $\geq 50\%$ are included at the respective branches.

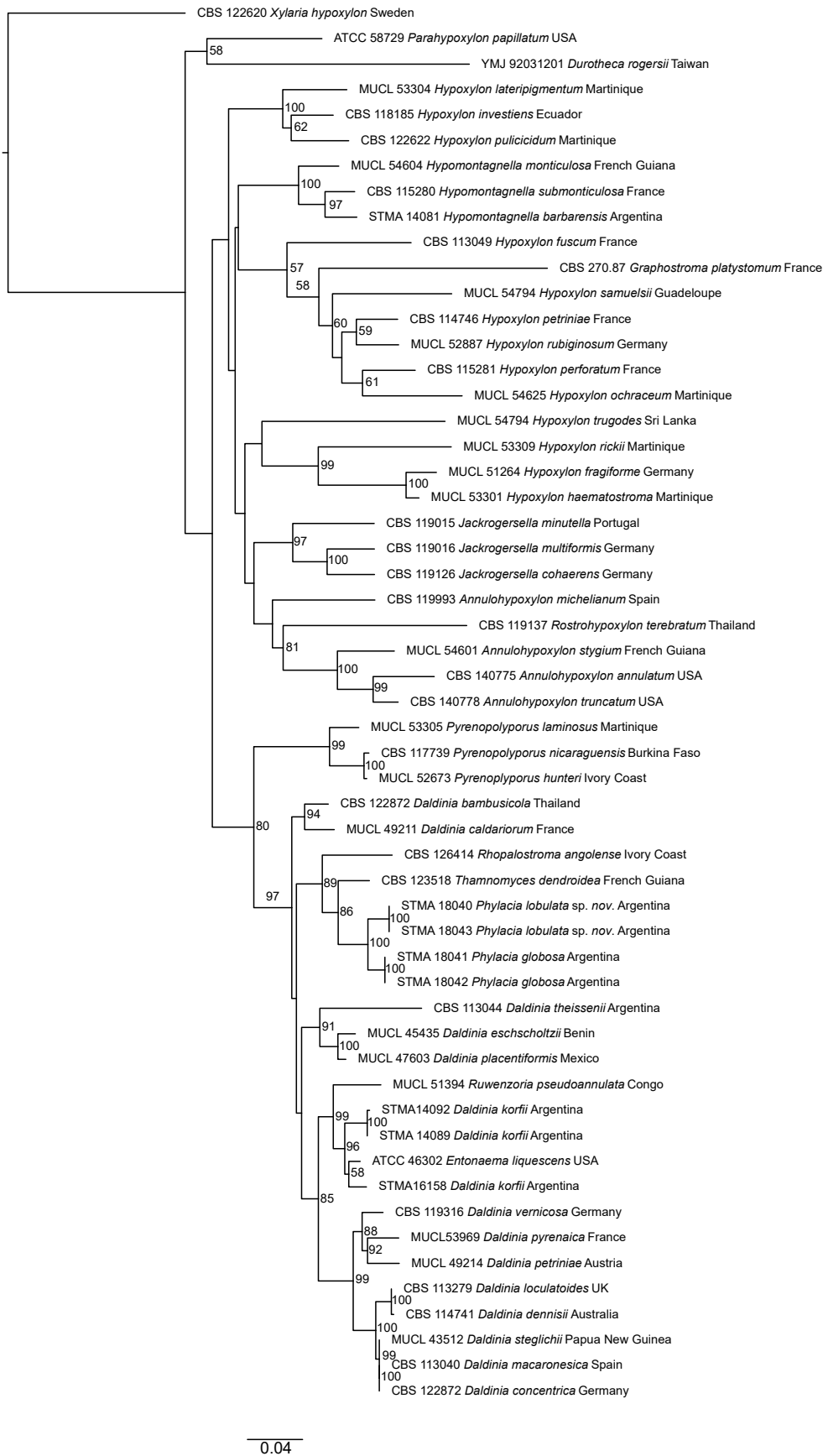


Figure S4: Maximum-Likelihood (ILn=-12655.2327) tree inferred from *TUB2* sequences of selected *Hypoxylaceae* and species of related families as outgroup. Bootstrap support values (BS) $\geq 50\%$ are included at the respective branches.

Figure S5: UV and MS chromatogram of compound **1** (RT = 4.6 - 4.8 min).

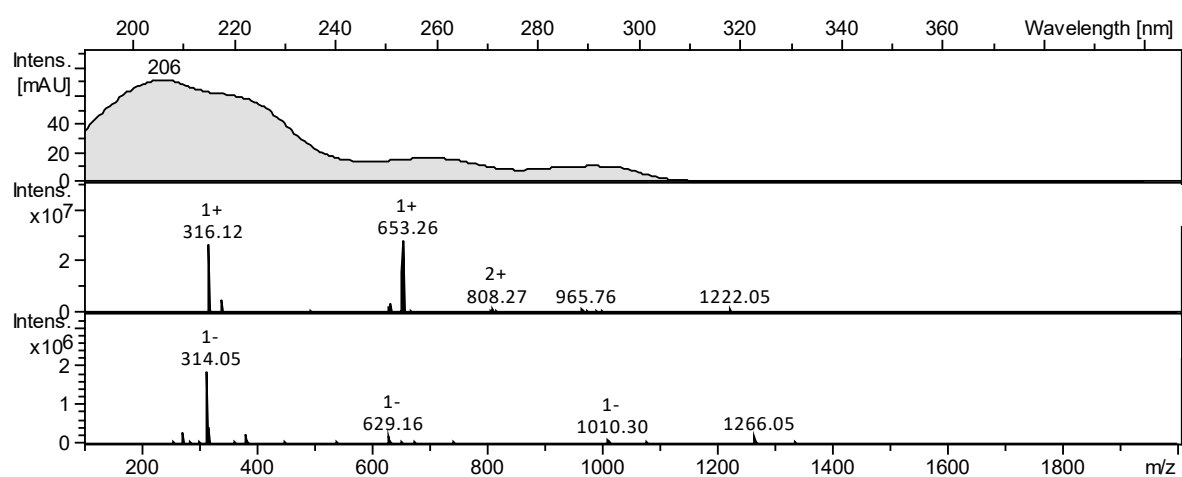


Figure S6: UV and MS chromatogram of compound **2** (RT = 6.9 - 7.0 min).

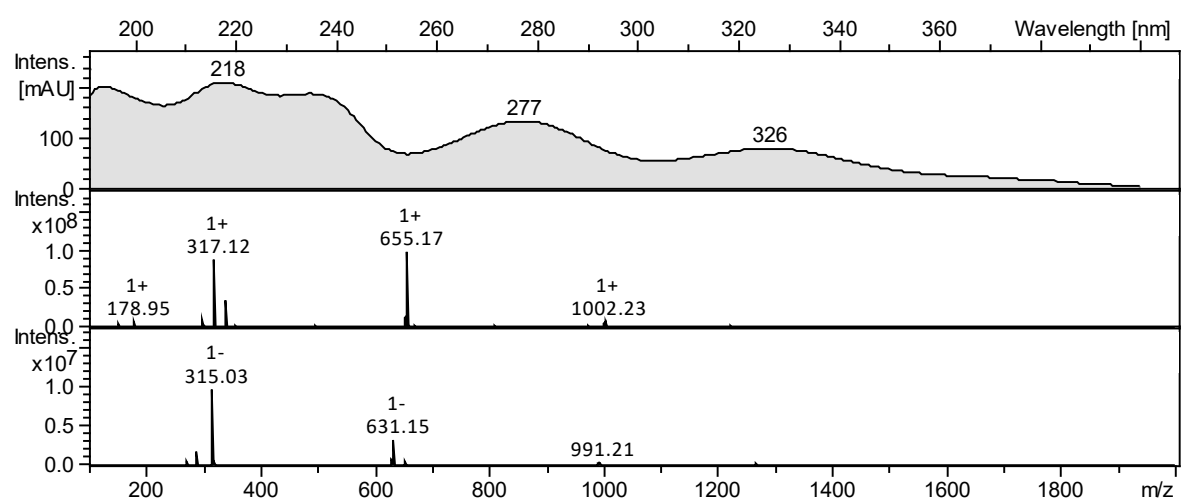


Figure S7: UV and MS chromatogram of compound **3** (RT = 7.1 - 7.3 min).

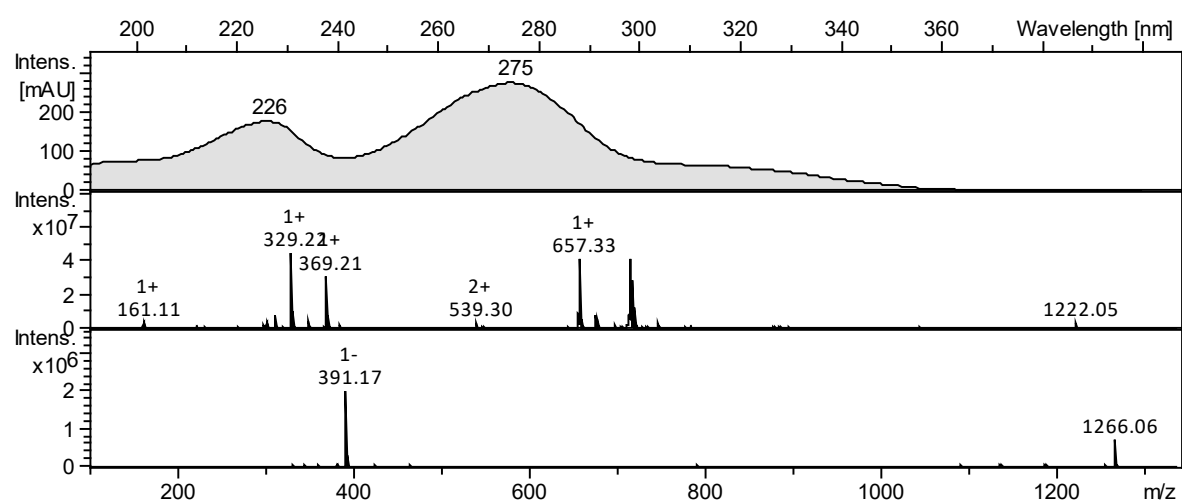


Figure S8: UV and MS chromatogram of compound **4** (RT = 7.6 - 7.8 min).

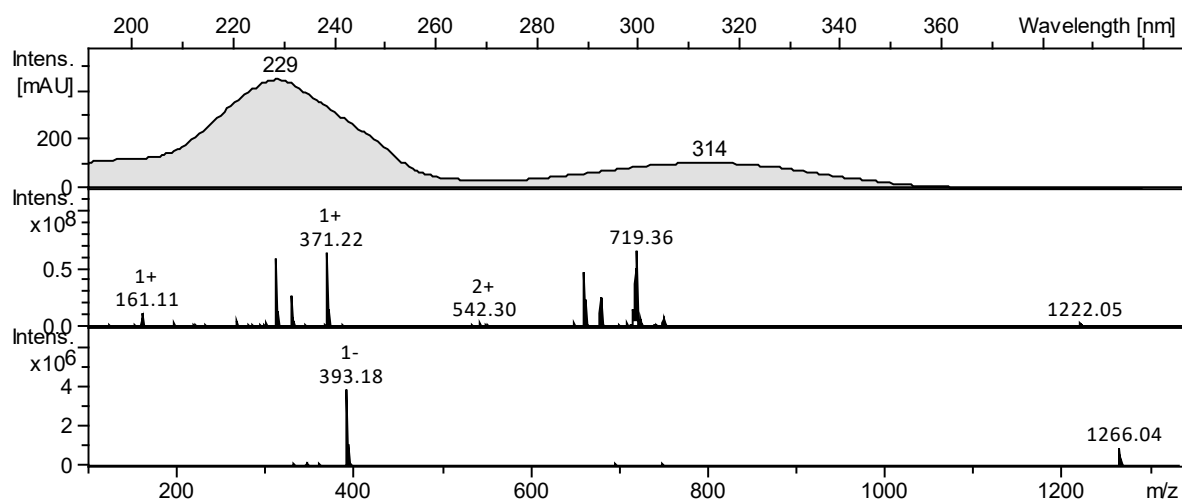


Figure S9: UV and MS chromatogram of compound **5** (RT = 8.0 - 8.1 min).

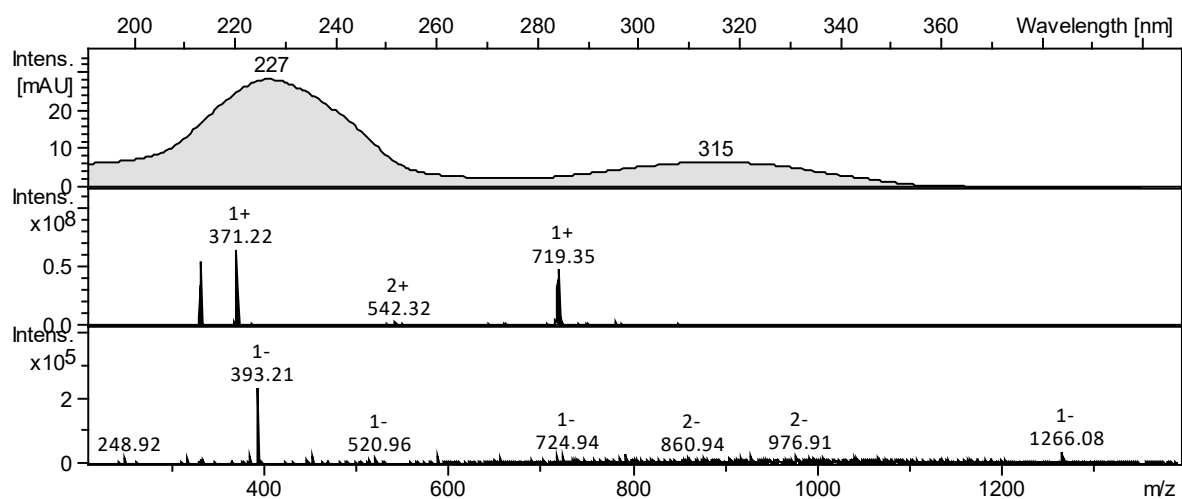


Figure S10: UV and MS chromatogram of compound **6** (RT = 8.3 - 8.6 min).

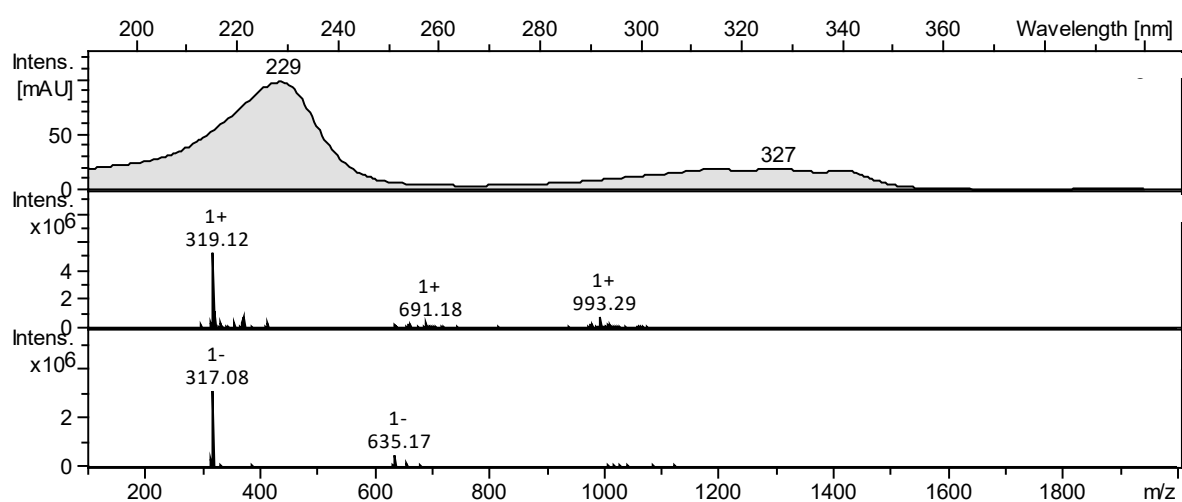


Figure S11: UV and MS chromatogram of compound **7** (RT = 10.1 - 10.3 min).

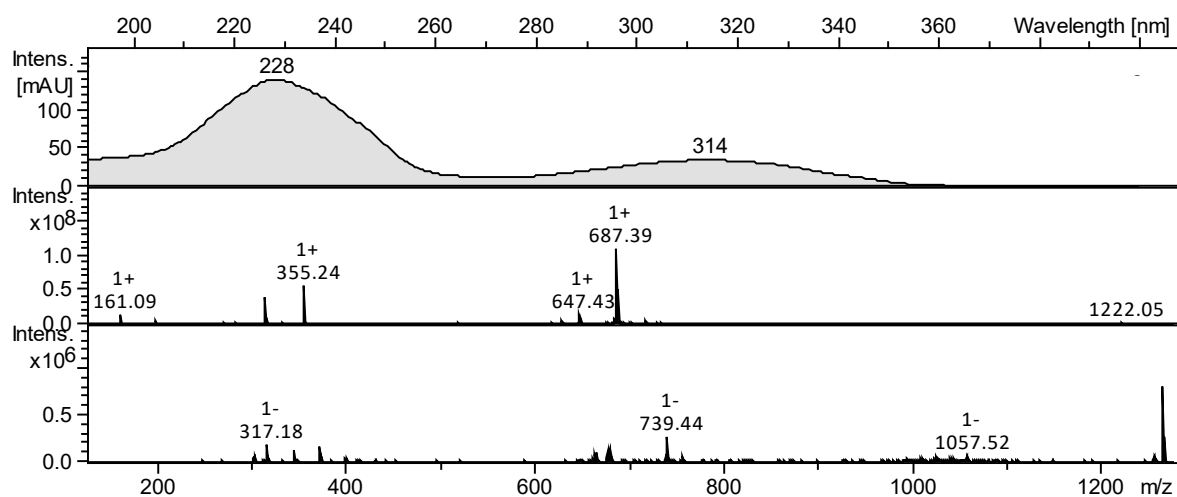


Figure S12: UV and MS chromatogram of compound **8** (RT = 10.1 – 10.3 min).

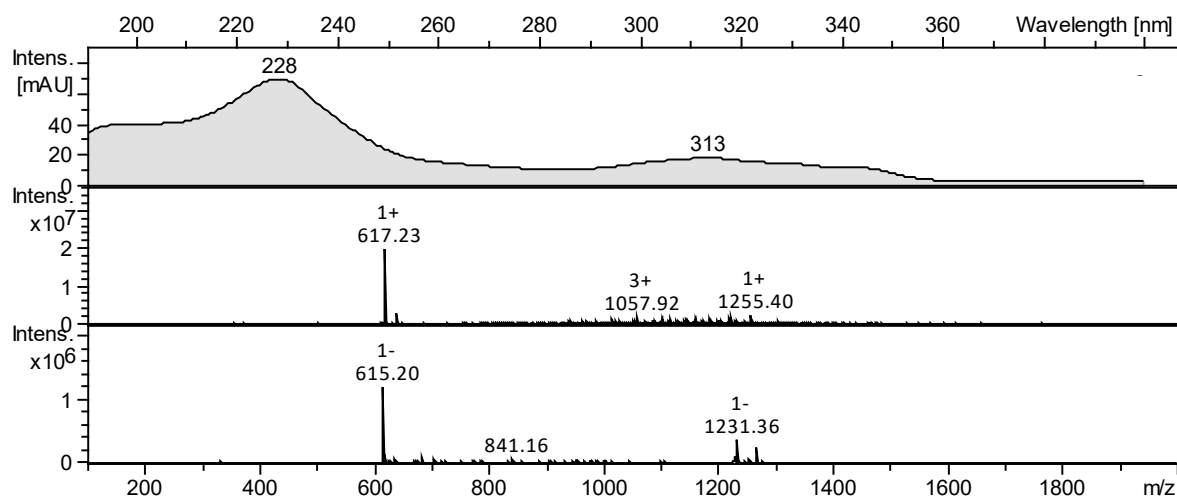


Figure S13: UV and MS chromatogram of compound **9** (RT = 10.5 – 10.7 min).

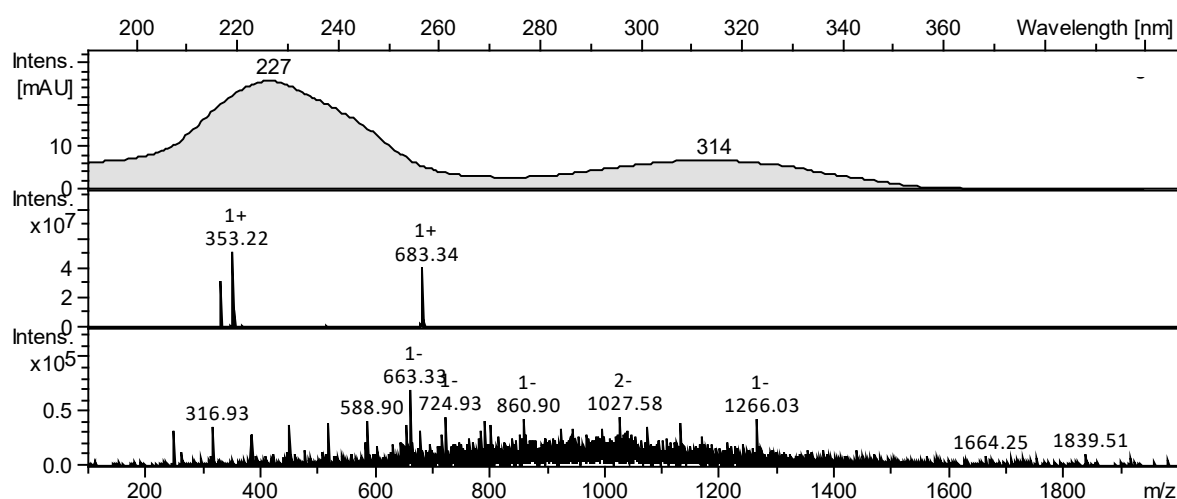


Figure S14: UV and MS chromatogram of compound **10** (RT = 11.5 – 11.7 min).

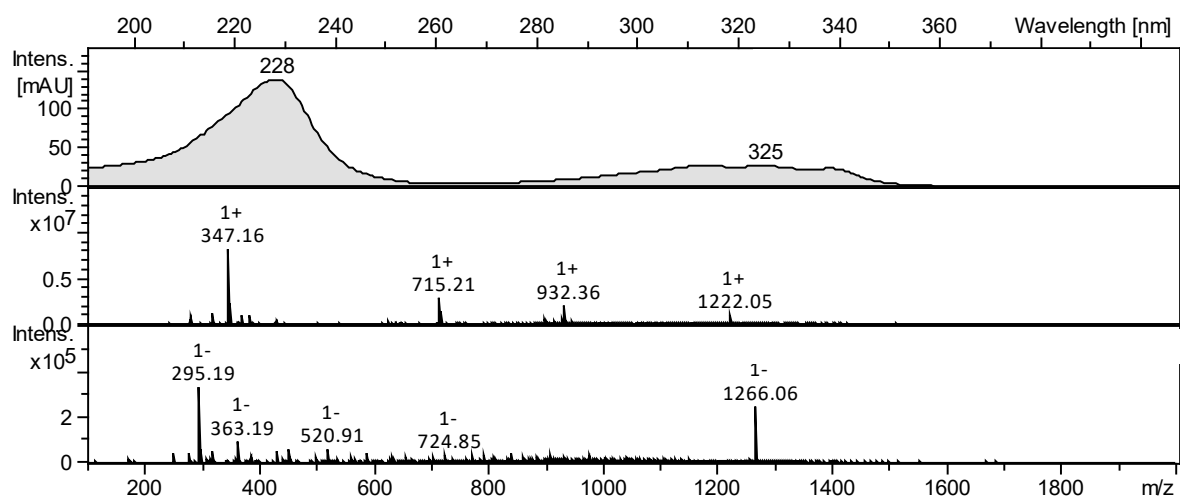


Figure S15: UV and MS chromatogram of compound **11** (RT = 14.0 – 14.2 min).

