

Genome Mining of α -pyrone Natural Products from the Ascidian-Derived Fungus *Amphichorda felina* SYSU-MS7908

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Contents

Table S1 Primers used in this study	3
Table S2 Plasmids constructed in this study	4
Table S3 <i>A. oryzae</i> transformants constructed in this study	5
Table S4 ¹ H NMR and ¹³ C NMR data of udagawanone A (3)	5
Figure S1 The antiSMASH (fungal version) result of <i>Amphichordafelina</i> SYSU-MS7908	5
Figure S2 Amino acid sequence alignment of AmpB with Sol1	6
Figure S3 Amino acid sequence alignment of AmpC with Sol2	6
Figure S4 HRESIMS spectrum of Amphichopyrone A (1)	7
Figure S5 The IR spectrum of Amphichopyrone A (1)	7
Figure S6 The UV spectrum of Amphichopyrone A (1)	8
Figure S7 HRESIMS spectrum for Amphichopyrone B (2)	8
Figure S8 The IR spectrum of Amphichopyrone B (2)	9
Figure S9 The UV spectrum of Amphichopyrone B (2)	9
Figure S10 PCR analysis for the AO- <i>ampABCDEFGHIJ</i> construct	9
NMR spectra	10

Table S1. Primers used in this study

Primer	Sequence (5' to 3')
pUSA_A-F	CTCCGAATTCGAGCTC GGTACC CTGAGTAAAGCATCTCCAGCTC
pUSA_A-R	CTACTACAGATCCCCG GGTACC GGTATATTTTCTCTCTGGCATGC
pTAex3_B-F	AGCTCCGAATTCGAGCTC GGTACC ATCGTCAGTCGTCAAAGCGAAG
pTAex3_B-R	CACGAGCTACTACAGATC CCCGGG CAATCATCGAAAGCTTTTTGGCTCA
pUSA_C-F	CAAGCTGAATTCGAGCTC GGTACC TACTGCCTCAAGATTCGCTGGT
pUSA_C-R	CACGAGCTACTACAGATC CCCGGG CTGCGAGCCGATGTGACCCC
pUSA_D-F	CTCCGAATTCGAGCTC GGTACC ACTCGCCAATCTGCCAAATATTCAT
pUSA_D-R	CACGAGCTACTACAGATC CCCGGG CTCACAAGCACTGCTGCG
pTAex3_E-F	AGCTCCGAATTCGAGCTC GGTACC GCTGACCATTGCTTCAACACC
pTAex3_E-R	CACGAGCTACTACAGATC CCCGGG ATGCGAGACTCCCAAATAGTGAG
pTAex3_F-F	AGCTCCGAATTCGAGCTC GGTACC GCAGCTAAGCCGTGTCCAG
pTAex3_F-R	CACGAGCTACTACAGATC CCCGGG TACAGGTTCTCAAACAGCCAAGGCA
pTAex3_G-F	AGCTCCGAATTCGAGCTC GGTACC ACGATGTACTAAGATCCGGCCG
pTAex3_G-R	CACGAGCTACTACAGATC CCCGGG CATACGTGATATCTGTCTCGGTGG
pTAex3_H-F	CTCCGAATTCGAGCTC GGTACC TTAGCCTTATCCCTGGGTGC
pTAex3_H-R	CTACTACAGATCCCCG GGTACC ATGAATGTGGGGATTGAGGTT
pTAex3_I-F	CTCCGAATTCGAGCTC GGTACC ATTACAAGCAAAACAGGCAACCT
pTAex3_I-R	CTACTACAGATCCCCG GGTACC GCACCCAGGGATAAGGCTGA
pTAex3_J-F	CAAGCTGAATTCGAGCTC GGTACC GCTGAGCAGGCTGAGCAGGG
pTAex3_J-R	CACGAGCTACTACAGATC CCCGGG CGACTCTAGGAGTTCCTGTTTAGGT
Infu_pAdeA_SpeI_F	TAGAGGATCT ACTAGT CAAGAGCAGAATGTGAACG
Infu_pAdeA_SpeI_R	AATCCATATG ACTAGT GATACATGAGCTTCGGTG
Infu-pBARI-HindIII-F	TGACCATGATTACGCC AAGCTT CAAGAGCAGAATGTGAACG
Infu-pBARI-HindIII-R	CGACCTGCAGGCATGC AAGCTT GTAAGATACATGAGCTTCGG
Infu-pPTRI-HindIII-F	TGACCATGATTACGCC AAGCTT CGACTCCAATCTTCAAGAGC
Infu-pPTRI-HindIII-R	GCAGGCATGC AAGCTT GTAAGATACATGAGCTTCGG
Infu-linker-F1	GCTCGCGAGCGCGTTCCACTGCATCATCAGTCTAG
Infu-linker-R1	AACGCGCTCGCGAGCAAGTACCATACAGTACCGCG
Infu-linker-F2	TCGCGTGCGCGTTTACCCATCATGGTGTTTTGATC
Infu-linker-R2	TAAACGCGCACGCGACATTAATCCGGATCCTTTCC
Infu-linker-pUSA-F	GCTCGCGAGCGCGTTTCGATATCATGGTGTTTTGATC
Infu-linker-pUSA-R	AACGCGCTCGCGAGCCTTTTCCTATAATAGACTAGCGTG
iNOS_F	GGCAGCCTGTGAGACCTTTG
iNOS_R	GCATTGGAAGTGAAGCGTTTC
TNF- α F	TTCTGTCTACTGAACTTCGGGGTGATCGGTCC
TNF- α R	GTATGAGATAGCAAATCGGCTGACGGTGTGGG
IL-6F	TCCAGTTGCCTTCTTGGA
IL-6R	GTGTAATTAAGCCTCCGACTTG
COX-2F	TGAGTACCGCAAACGCTTCTC

COX-2R	TGGACGAGGTTTTTCCACCAG
IL-1 β F	GAAAGACGGCACACCCACCCT
IL-1 β R	GCTCTGCTTGTGAGGTGCTGATGTA
GAPDH-F	CATGACCACAGTCCATGCCATCAC
GAPDH-R	TGAGGTCCACCACCCTGTTGCTGT

Table S2. Plasmids constructed in this study

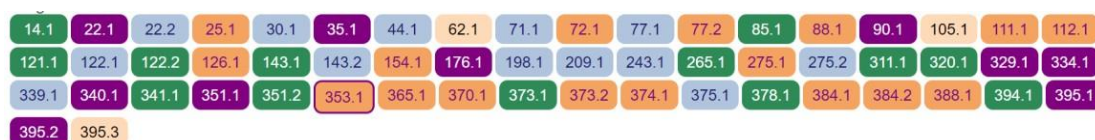
Plasmid	Inserts	Primer 1	Primer 2	PCR Template	Vector
pUSA- <i>ampA</i>	<i>ampA</i>	pUSA_A-F	pUSA_A-R	gDNA	pUSA digested with KpnI and SmaI
pTAex3- <i>ampB</i>	<i>ampB</i>	pTAex3_B-F	pTAex3_B-R	gDNA	pTAex3 digested with KpnI and SmaI
pUSA- <i>ampC</i>	<i>ampC</i>	pUSA_C-F	pUSA_C-R	gDNA	pUSA digested with KpnI and SmaI
pUSA- <i>ampD</i>	<i>ampD</i>	pUSA_D-F	pUSA_D-R	gDNA	
pTAex3- <i>ampE</i>	<i>ampE</i>	pTAex3_E-F	pTAex3_E-R	gDNA	pTAex3 digested with KpnI and SmaI
pTAex3- <i>ampF</i>	<i>ampF</i>	pTAex3_F-F	pTAex3_F-R	gDNA	
pTAex3- <i>ampG</i>	<i>ampG</i>	pTAex3_G-F	pTAex3_G-R	gDNA	
pTAex3- <i>ampH</i>	<i>ampH</i>	pTAex3_H-F	pTAex3_H-R	gDNA	
pTAex3- <i>ampI</i>	<i>ampI</i>	pTAex3_I-F	pTAex3_I-R	gDNA	
pTAex3- <i>ampJ</i>	<i>ampJ</i>	pTAex3_J-F	pTAex3_J-R	gDNA	
pUSA- <i>ampA</i> +C	<i>ampA</i> -TamyB	pUSA_A-F	Infu-linker- pUSA-R	pUSA- <i>ampA</i>	pUSA digested with KpnI and SmaI
	PamyB- <i>ampC</i>	Infu-linker- pUSA-F	pUSA_C-R	pUSA- <i>ampC</i>	
pAdeA- <i>ampE</i> +F	PamyB- <i>ampE</i> -TamyB	Infu_pAdeA_SpeI_F	Infu-linker-R1	pTAex3- <i>ampE</i>	pAdeA digested with SpeI
	PamyB- <i>ampF</i> -TamyB	Infu-linker-F1	Infu_pAdeA_SpeI_R	pTAex3- <i>ampF</i>	
pPTRI- <i>ampD</i> +G	PamyB- <i>ampD</i> -TamyB	Infu-pPTRI-HindIII-F	Infu-linker-R1	pUSA- <i>ampD</i>	pPTRI digested with HindIII
	PamyB- <i>ampG</i> -TamyB	Infu-linker-F1	Infu-pPTRI-HindIII-R	pTAex3- <i>ampG</i>	
pBARI- <i>ampH</i> +I+J	PamyB- <i>ampH</i> -TamyB	Infu-pBARI-HindIII-F	Infu-linker-R1	pTAex3- <i>ampH</i>	pBARI digested with HindIII
	PamyB- <i>ampI</i> -TamyB	Infu-linker-F1	Infu-linker-R2	pTAex3- <i>ampI</i>	
	PamyB- <i>ampJ</i> -TamyB	Infu-linker-F2	Infu-pBARI-HindIII-R	pTAex3- <i>ampJ</i>	

Table S3. *A. oryzae* transformants constructed in this study

Strains	Host strain	Plasmids used for transformation
<i>AmpB</i>	<i>A. oryzae</i> NSAR1	pTAex3- <i>ampB</i>
<i>AmpBC</i>	<i>A. oryzae</i> NSAR1	pTAex3- <i>ampB</i> , pUSA- <i>ampC</i>
<i>AmpABCDEFG</i>	<i>AmpABC</i>	pAdeA- <i>ampE</i> + <i>F</i> , pPTRI- <i>ampD</i> + <i>G</i>
<i>AmpABCDEFGHIJ</i>	<i>AmpABCDEFG</i>	pBARI- <i>ampH</i> + <i>I</i> + <i>J</i>

Table S4. ¹H NMR and ¹³C NMR data of udagawanone A (**3**) (400 and 100 MHz) (in CD₃OD-*d*₄, δ in ppm, *J* in Hz)

No	δ _H (<i>J</i> in Hz)	δ _C type
2		166.9, C
3		111.5, C
4		172.2, C
5		110.5, C
6		155.6, C
7	6.45, dd (15.3, 1.4)	121.4, CH
8	6.67, dq (15.4, 6.9)	135.9, CH
9	1.95, dd (6.9, 1.2)	18.7, CH ₃
10	4.53, s	55.2, CH ₂
11	1.99, s	9.6, CH ₃
12	4.08, s	62.4, CH ₃

**Figure S1.** The antiSMASH (fungal version) result of *Amphichorda felina* SYSU-MS7908

Sol1 MTSQYGTNGASADPEFIAIVGMGCRWPGGVRDASLWELKKNRSQYREFGDRHFRKGFHHFHNSEHFGTVATEGFLLAEDPRLFDHAFQIGSLEVEIMDPSQRKL 108
 AmpBMTSTORDPHERVAIVGMGCRWPGGVRDSSHFWEFLDRDVGWKEFDDPRFSTRGFHHFNADRPQSVAMKGAFLAHEDARYFDHAFQGMTGLEVEIMDPSQRKL 103
 Sol1 LEVYYEAFENSGEPWDSYSGSTTGTVGVGNFSNDHLITGGRTDHPRPYASVGTSTISLRNVNIFNLRGSPVITDACSMMYALHLAISAIRNGDCDPSAIVASNT 216
 AmpB LEVAYEAIENAGETWDSYSGSRTGVGVGNFCLDHWMIQSRDWDNRPYPATGAGTBIANRISYIFNLQGPSLTVDTACSMMYALHLAVNAIRAGDCDPSAIVASNA 211
 Sol1 IIDPSTXLMMTKGLVLSPTSTSHTFDSSADYARGEGFSALYLKRMSTAVGDGYPIRALVRGSALNANGRTGGITHPREGQEAIVIRKAYENAGNLPMDKDTTFECHO 324
 AmpB VADRGVQVIALDKGALSASSRCHTFDARAEYARGEGYGAIYLKRPSLAIADLSPIRAMIRGTAVNSNGRTGGITRPSAKGQEVVIREAYRSAGDLPFSDTSYEECHO 319
 Sol1 TGTVPDGPDIETIAIGNVFGSATTEPKFLVGSIKTNIGHTEPASAIAGIMKVVLALENGLIPPSIGIKKLNPKLDLKGGRINILTENTPWPDGRVRRASVNSFGYGG 432
 AmpB TGTTVVGGDPIEVALAGLRVFAERSADDPMIGSVKSNVGHGEGASALASVMKVVLSLEKGAIPRVFNLETRNNIDFDGAKVQPVTEVTPWPEFGLORASINSFGYGG 427
 Sol1 NGHCIIIDVRLTPDYKKRTANTSIGHINGHTNGHTNGHTN.....GHTNG.....HTNGHTNGHTNGAH....ASDG..HNGHHQNMNGNSASHMSEK 516
 AmpB NAHCIIIDHMKNVLPDYVAPGVYQSLHERNGTTNGHANGTNGHKNGANHKNGTNGHIPASNGYANGFNGHTNGHANGTNGHPNGTNGHTNGHHNGGNGNPQTQ..... 530
 Sol1 ADKVHYFYSKYPTLVKDFNAKPRRRVLIPFSAHNEASLDNITAISEAIKRENADVAYTLAAKRSRFMQRTFIVDSESPANGFAVKEVLASGDTOTARLGDFVFTG 624
 AmpBHNHIIINSLOLAPSPNAATQQLVLLHSAHNENSLLENLNLASRVDKFPLABIAYTLASRRSFADRSSESIDKDNVTQSLTLATKVARAPLQTPNIGFIFTG 634
 Sol1 GAQWHAMGADLFYAVFRTSLEYLDSIASLFTPSANKIEDI LARNDDPNIDHKPEVSQTVCTAVGIBLVDLLTYNNVRPSAAVHSSGIEAITYAAGRITAAQAIJA 732
 AmpB GAQWHMGADLFYAVFRFTIQQLHVLGTLKAPSWTLQDILSGDQDAGIQTAEISGAVCTAVGVQLVDLLASWVRPSQVAGHSSGIEAAYASGRITAAQAIJS 742
 Sol1 AYFRGQAVSNKSKGLMLAVGLGDKAEAFISLDSSVRIAAINSFSDYTLSSQESTIKDVAANKNEBKVFNRKLTGQAYHSHHMLALDEFNSTUSEGLDYVKSL 840
 AmpB AYLRGQAVSRNKRKRAMLAVGLGSEEDVKLEQREAKVAAVNSPQSVTLSEPTAIDEISAMTADGVFNRLKLTGQAYHSHHMLAIGVEWAEILEEGIHHRDS 850
 Sol1 GQAEPSQLATRPWMSYSPYSKSTENPPVSPSYWRANLESPPRFSEALNNMNLDPDPIDVLEIGPHPAKGPVGQISRSVDKSLPFPFTLNRTGNGISLLQLAGS 947
 AmpB GQAEPSQLATRPWMSYSPYSKSTADFKAPASYWRANLESPPVSLFQAVARLVNDNEVPIHSLVEIGPHPAKGPVLDQILKAGGKTVAAYASTLVAGNGQSRQLQLAG 958
 Sol1 LFSLNAEVDLTAVNAVDSANOLKLVHGTITATNLPPYQYAYGVPIYHESRFSKEFRGDIRVRHDLGSKLPQNAKLRPQWRNIRLKLDPWLNDHKLPLYPVFPAG 1055
 AmpB LFSLNATIDLAAYNAVVDVST..RLEHGCTCTELPPYKVTYGGLYNHESRASKERYRVSRLRHDLGSKVVGNAKLRPQWRNIRLKMKVLPWLGDHRLVPAVFPAG 1064
 Sol1 VIATVIEAASRIYNEQSEPLDITGYKLRNVFTSSAMRLPDDDFLEIITSLELADAANPKAPTWTATFISSSVAREAGTWTEHCSRVRVIAGTSAV..NEKMSTEMDA 1161
 AmpB VIATVIEAASRIYNEQSEPLDITGYKLRNVFTSSAMRLPDDDFLEIITSLELADAANPKAPTWTATFISSSVAREAGTWTEHCSRVRVIAGTSAV..NEKMSTEMDA 1172
 Sol1 RLTDLKAWYKFAEIGLGYGTFQPLSNIRADPSKGLAVQLALHTTROTVEGGESNYPLHPASLDGAVDLSLVASHGGQIDRVCAAFVPHIDQLVVRNGVSDSAV 1269
 AmpB RSVDAWYKFAELDGLGYGTFQPLSNIRADPSKGLAVQLALHTTROTVEGGESNYPLHPASLDGAVDLSLVASHGGQIDRVCAAFVPHIDQLVVRNGVSDSAV 1277
 Sol1 AIALGSMKRLSAHAKLQVLQDKSEQVLDVGNLRCVITYTEVLPSTGADKEAFISPLRLSWKPDIRAMDEQVQRFPFPPTENVEKAYLFDKLERGLTYLVAEIHERY 1377
 AmpB IIVARGERRGISAYLDLQMLKPGNGVLASDGLRCVFSSEAK....DORTFASPLRLSWKPDIRATLSNRDARHMFPPKANVERSLWGVNTVAEAAPEADVEKHLQVAPHA 1382
 Sol1 AGQQQFSAPAHIDNLSVWRMRMKDKNKW..AEANSLTSSQGLIKELFAEVOGHISDVKIANKVFNNMEDILNERKTGLEVVIPDNLLHGMVEDSLMTGAVPOLV 1484
 AmpB GKLEDDPKPSDDVGHFEFWIKRGGQNSHPLMEAREFVNGGELLEIDELVSGQAPVMEVKIAKLLHDNAADILYQRRTGMVILISEGLLTPLYESGLMTGIVPOLV 1490
 Sol1 RFFDLGYANPNMRILEIGAGTGGATRIKILKTLIDPHIDIKRYODYTFDIDVSGLAQAREAFADFODMKYSVLDIQENFLEHGYEAVYQVVVAGECHLATPSIVKTL 1592
 AmpB HVLGKIAHNSPNRLVLEIGAGTGGATRIAMNAFNPNIDIKARYDYTFDIDVSGLAQAREAFADFODMKYSVLDIQENFLEHGYEAVYQVVVAGECHLATPSIVKTL 1598
 Sol1 NCRKLVKPGQRLVVENTRAVIGHLLVLGHLGSHYWDGIPDGRVESPFLLLEGWNASLNOTFAGAEVLDDYFARYTTARTIVSAYVEPAKVQGSQPNGTVHLVHGDN 1700
 AmpB NCRKLVKPGQRLVVENTRAVIGHLLVLGHLGSHYWDGIPDGRVESPFLLLEGWNASLNOTFAGAEVLDDYFARYTTARTIVSAYVEPAKVQGSQPNGTVHLVHGDN 1705
 Sol1 RPELLSRTEHELTERTGTEFKVISIGDVETHLPDNRSTVAFADSKSLVLNASENDLKSFKALIRKSNLVWVTFGGIWHGHDPASITTGLLRTLTSTENPASQFLSID 1807
 AmpB PAPPLAQIISKELEKRGVVARVGTFFESSLESFTPESTRIVALFDCKHLLANAKEODLKTVOHLARNSTSLVALTSCGVVKGRNADGALISOLLRLVQENPASHYVSD 1813
 Sol1 VSPDSD...FQEIERTITLDOELASD....RIAGESRDEYFVWGEDCLWVSRVLPDVALQDKLELSESPRAEMLPLDSGGVQAAETPGLLTSLYFKPYE 1906
 AmpB MDADHFEVSNDDQDLARCLVDFEFELVGGTPVDGNEGNPNDOEFSWGGCLWVSRHVPDAGFHSQHGLDARSMPKELLPLGRGQPVRAETEPGQVNSCETTYNE 1920
 Sol1 TWKSLPDDWQVKAAGVGLNWKDLTLAGRFDMNTFSSEYSGVAVGVGLNVTNVAAGDRVYVYGRGHFGNYVRAPANFAYRMLPGEDFKMATIPLVGMTAIYSFEC 2014
 AmpB LLQPLQPGFVDVKAAGVGLNWKDLTLAGRFDMNTFSSEYSGVAVGVGLNVTNVAAGDRVYVYGRGHFGNYVRAPANFAYRMLPGEDFKMATIPLVGMTAIYSFEC 2028
 Sol1 TQLKQGERLLIQSATGGLGSLAQAKAKAGAEIFATAGTOEKRRYLDIVVGISPASHVSSRDPADFAKLMEATDGKGFNVILSTSSBELLYSIKMLAPMGRIDVGR 2122
 AmpB AHLKEQGSVLDQSGATDLGLIASCFAKAKAGADVATVQTPQEGASFVADDELGPASHVLIQAPSLADLRRAAQTTRAKAHEVISTATGELLSSFLKVLARLHGLIDVGG 2136
 Sol1 IDVNSTSLALELFRKNATFTSPDLAVADADRALGPALMKAVNKRVAAGMGFLSSITTYDVSQDQALMAFSKGTHVSKLVVTFQNDPDLVKMVPAPFAHQAARNA 2230
 AmpB ADPESLRQTILELPTNATYSVDPFIILSSDPVVGTELMKAIIDAYYRGLGIGIPKIIITAPDVSQSSALGDPS..SMIGKLVNSESFENESLVMITIPAAFTVKGDPDS 2242
 Sol1 NYLITGGLGGLRSIVNFMARAGHFTVLSRSRKINS..EGBMLIDKLTSGTVVCEVSDSDSKDVARAVDDAAVVRPIKGIIVHAAVSODLSFDBKAIIEQWTSAL 2337
 AmpB CVVVTAGLGLGGLIRWMGDRGARHMAVLSREISSVQAGELVESLASRDHLSHVCDVSDKQDQIRVIGKISATRPKGVVHAAVSYDLTFDQSTSRWNGDL 2350
 Sol1 AAKVQGTKNLHEATKTHALDFFLMTTITIEFVALATQASAYTAANNFQDFYARWRQOGLPASTVSFQIRDVQHLSTNSTLALMARNKVMIDSEYNFRLLEPAFLN 2445
 AmpB SAKVQGTKNLHEATKTHALDFFLMTTITIEFVALATQASAYTAANNFQDFYARWRQOGLPASTVSFQIRDVQHLSTNSTLALMARNKVMIDSEYNFRLLEPAFLN 2458
 Sol1 NESALDPAASKPEYTRAVDDPLSVTVNVTGCDPATMATRKREAAENNGNTGNSPRWYTDARVSLIRAFDDAERYQASAGGGGDOGNERNAGVASRSEFGAEVK 2553
 AmpB NKTAGE..TSPQWLQEEEDPLSVTVNVTGCDPATMATRKREAAENNGNTGNSPRWYTDARVSLIRAFDDAERYQASAGGGGDOGNERNAGVASRSEFGAEVK 2560
 Sol1 ACPAERSRTVALVTDIVKTVQAQMLFVDSAGVDASRTVADYGVDSLSIAELRNWFFNVAFGADVSMLEMLDTATSMKILANKIVDGAAL 2642
 AmpB EGADARASTVGLVGGAIKTAFAEMLFVDVESIDPAKSVADLGVDSLIAELRNWFFLQGLATNISMULDLPSTI..... 2634

Figure S2. Amino acid sequence alignment of AmpB with Sol1. The sequences are aligned using the program Clustal Omega and Jalview.

AmpC MTIQTNNGNSNGTMA SQPNKGHLNGTSTIQNNGGIQGESTSILSLAQNILDLTQDMTKYFQANNLAAPTALQSQDPPDT 80
 Sol2MALKSTNGTHAGPTASAASLASLANISEKAASLSTYLESQGHQAPSFPLPGCADPPET 58
 AmpC PEYRRIHANLKTSLSDLSRLIDGPRKWLRAFCTGTGYDLGALQVALDFEFFQLVPAHGEIKLEDLAEKAGLDADRTGRVVR 160
 Sol2 EEYLAHLTSLTSSLEDLQVLVDGPRRLSRPCTIGNDLALALQVAFDFGFFQLIRPEGSMDVETLAHKVGIADRTGRVVR 138
 AmpC QLMTYRIFEEELRPRFISHSSTS LAMQQDDQLRCSVVHYSLDEMLKAAADCNVSLKANPYEAHQNNQNPFTVRHGVGIFEFYK 240
 Sol2 QMLATHRIFVEPKPGFFAHTAASAVFHDDEELRCAGHYMLDECFAKATACSDCIKASPNDSDTHSPFNTYFGVPMFSYK 218
 AmpC KDPEKARRFAKAMAGLRKMDRHLDYLLKDGFDWSAIQGTVVDCGGGNGHISKTLAELYFNLDVVEDSNADMLAESKESL 320
 Sol2 QNPQFAARFAKAMAVDRQIA.....ELRDCFPWGDIKGTVVDCGGGSGHISMA LARNFKLDFIVQDDSEKMLAQRARN 293
 AmpC PKDLDRGVKYLQHSFFDPQPVKDAAFILRQCTHNWADNDVVTIFKSFVPGLEGSGPDTPLLINDIIPPEPTWRHQR 400
 Sol2 LSDIEGRISFMKHSFFHPQPIGGGAGAFFIRQCTHNWCDRDVVKILKSFVPGLENSAPGTPLLINDTLPVPGSKPLHEER 373
 AmpC VVRQVDMVMLVNCQAKQRTKAEFEALLKEADSRYEIRNVFDNGPLSLLEVYLNRY* 456
 Sol2 ALRQMDMLMFVVLGAKQRTAKEFEALLKEADARYEIRRVHADGSMGLVEVHLNI* 428

Figure S3. Amino acid sequence alignment of AmpC with Sol2. The sequences are aligned using the program Clustal Omega and Jalview.

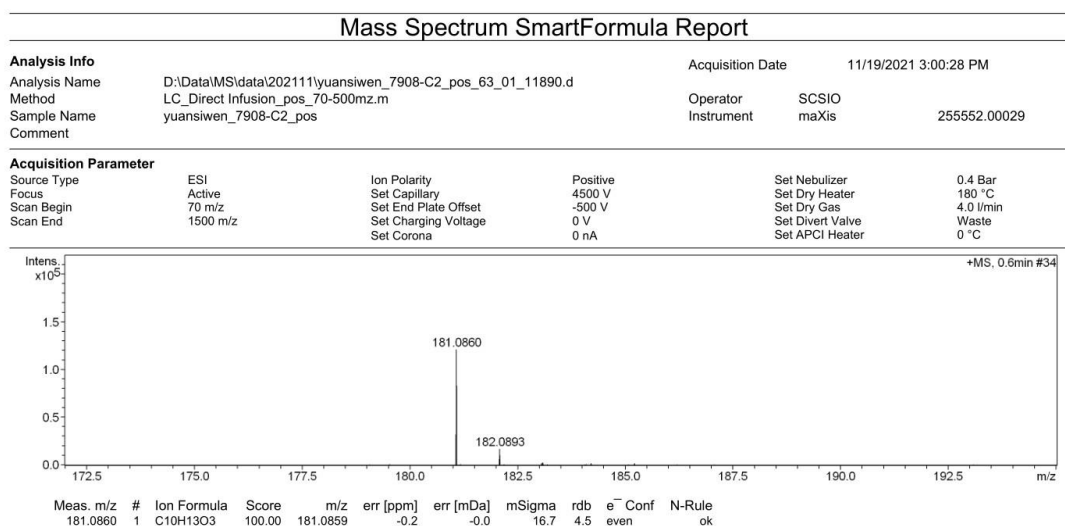


Figure S4. HRESIMS spectrum for amphichopyrone A (1)

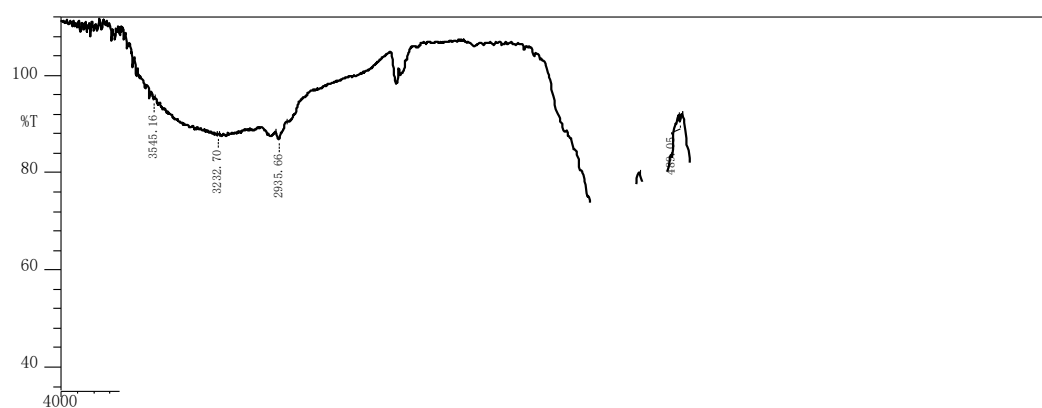


Figure S5. The IR spectrum of Amphichopyrone A (1)

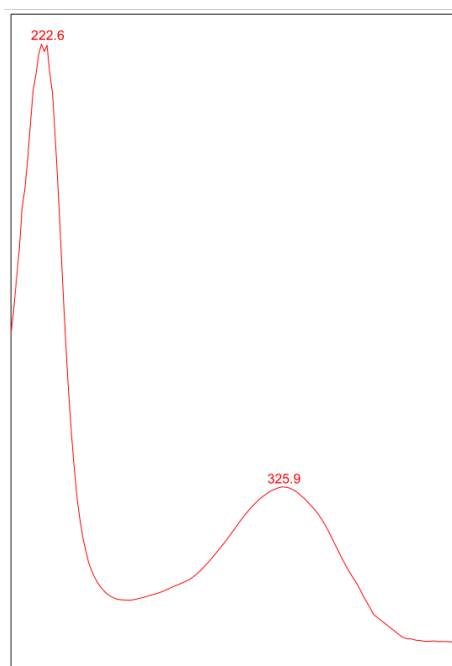


Figure S6. The UV spectrum of Amphichopyrone A (1)

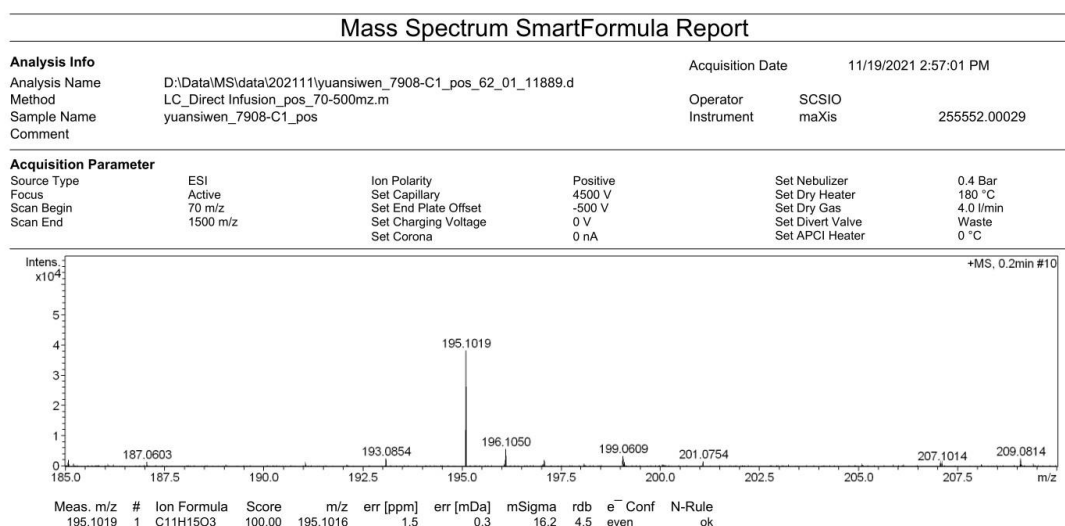


Figure S7. HRESIMS spectrum for amphichopyrone B (2)

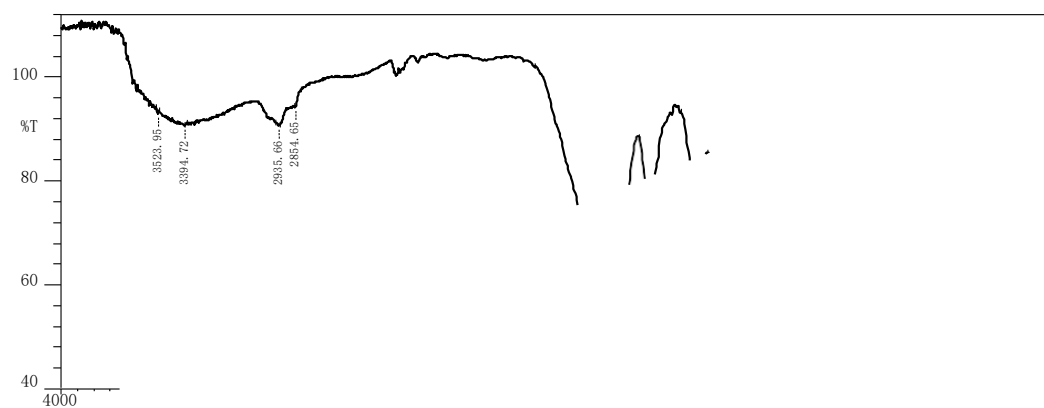


Figure S8. The IR spectrum of Amphichopyrone B (2)

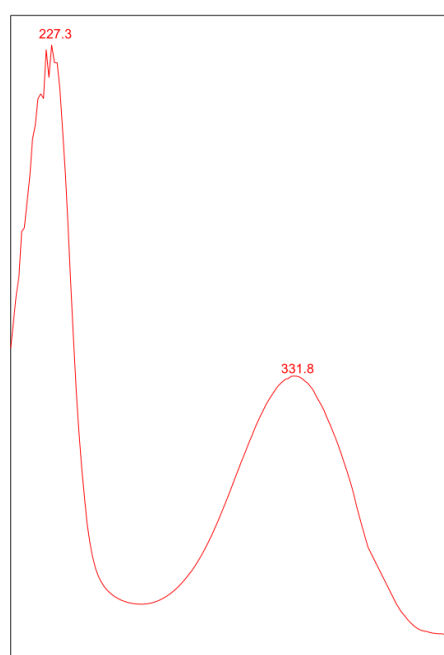


Figure S9. The UV spectrum of Amphichopyrone B (2)

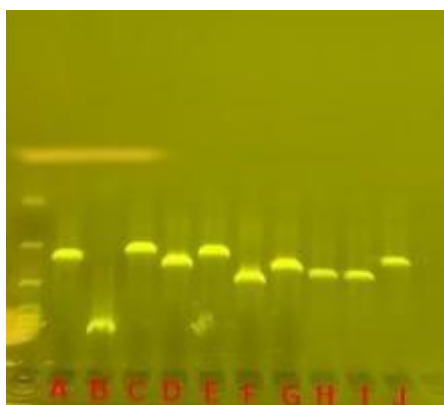


Figure S10. PCR analysis for the AO-*amp*ABCDEFGHII construct.

