

Isolation of Talarodioxadione & Talarooxime from *Talaromyces stipitatus*

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Supplementary Information

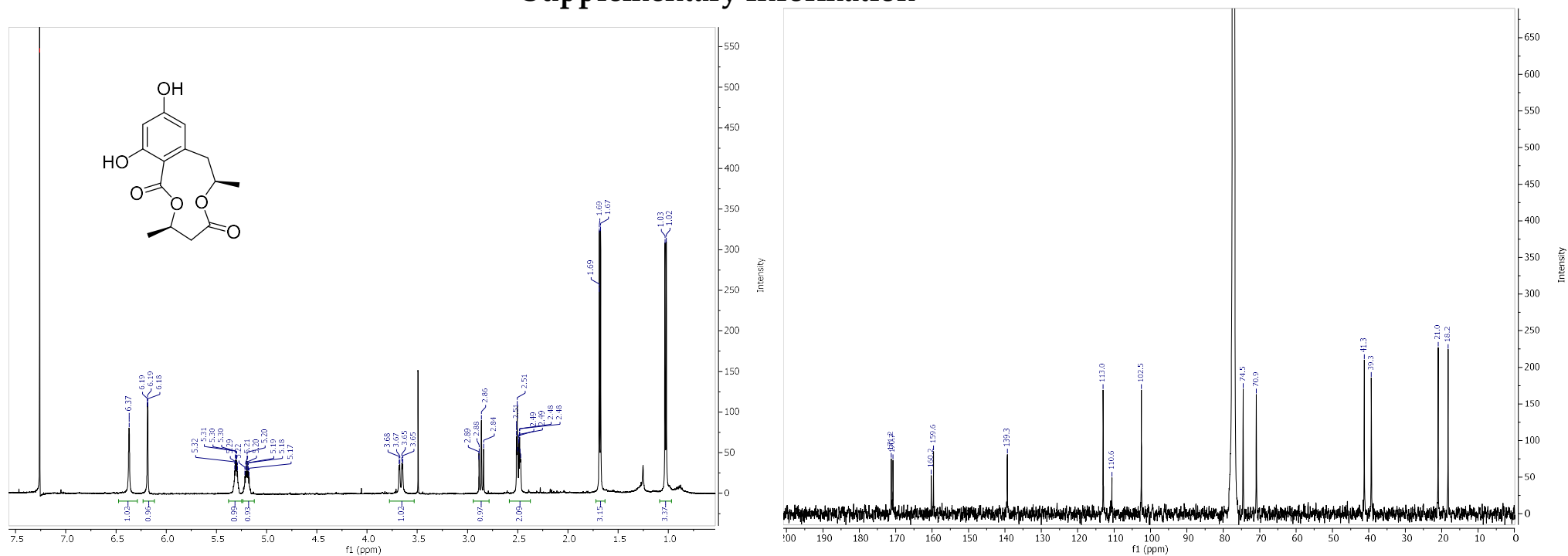


Figure S1. ^1H -NMR and ^{13}C -NMR spectra of Talarodioxadione **1** (CDCl_3 , 600 and 150 MHz).

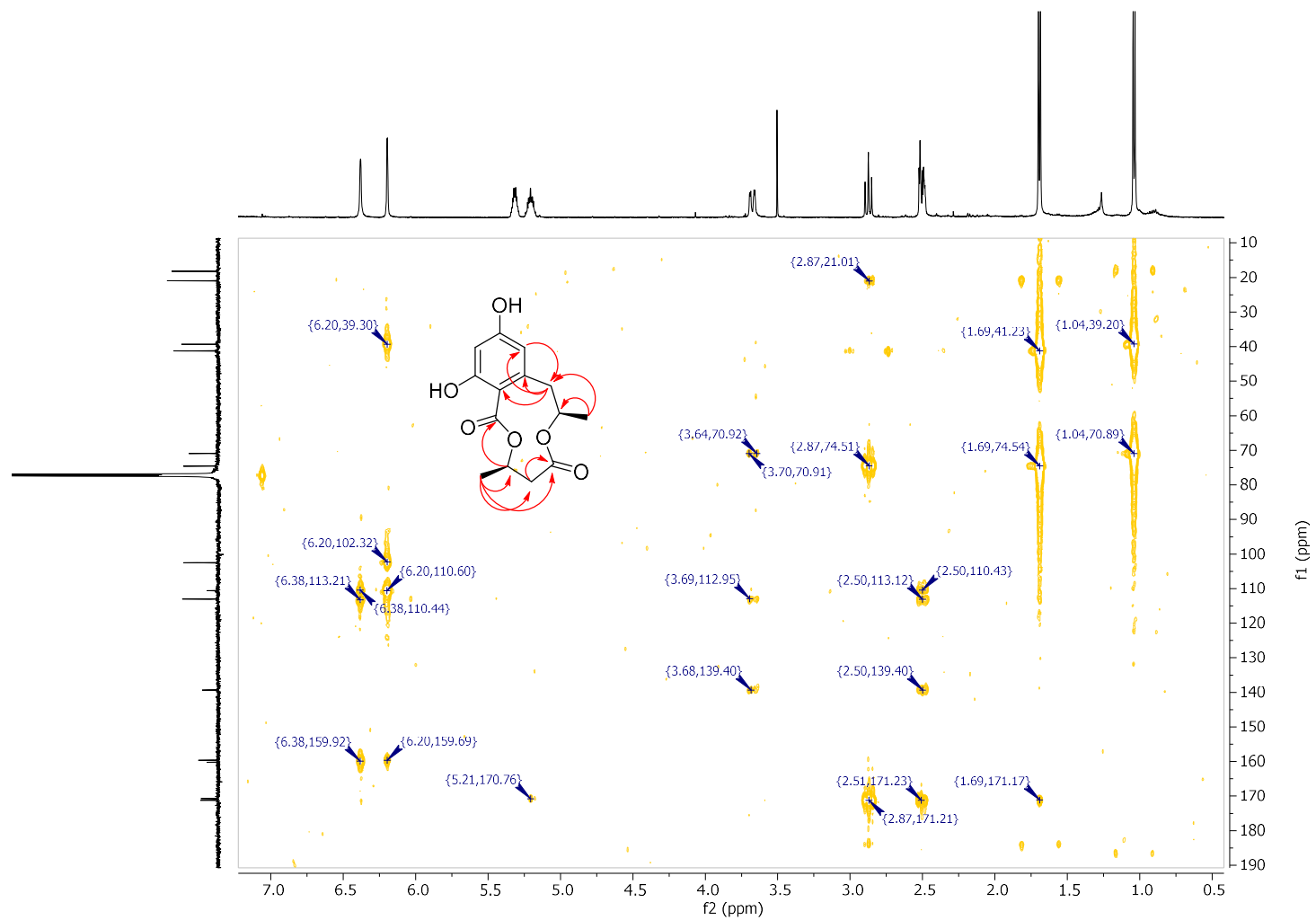


Figure S2. HMBC spectrum of Talarodioxadione **1** (CDCl₃, 600 MHz).

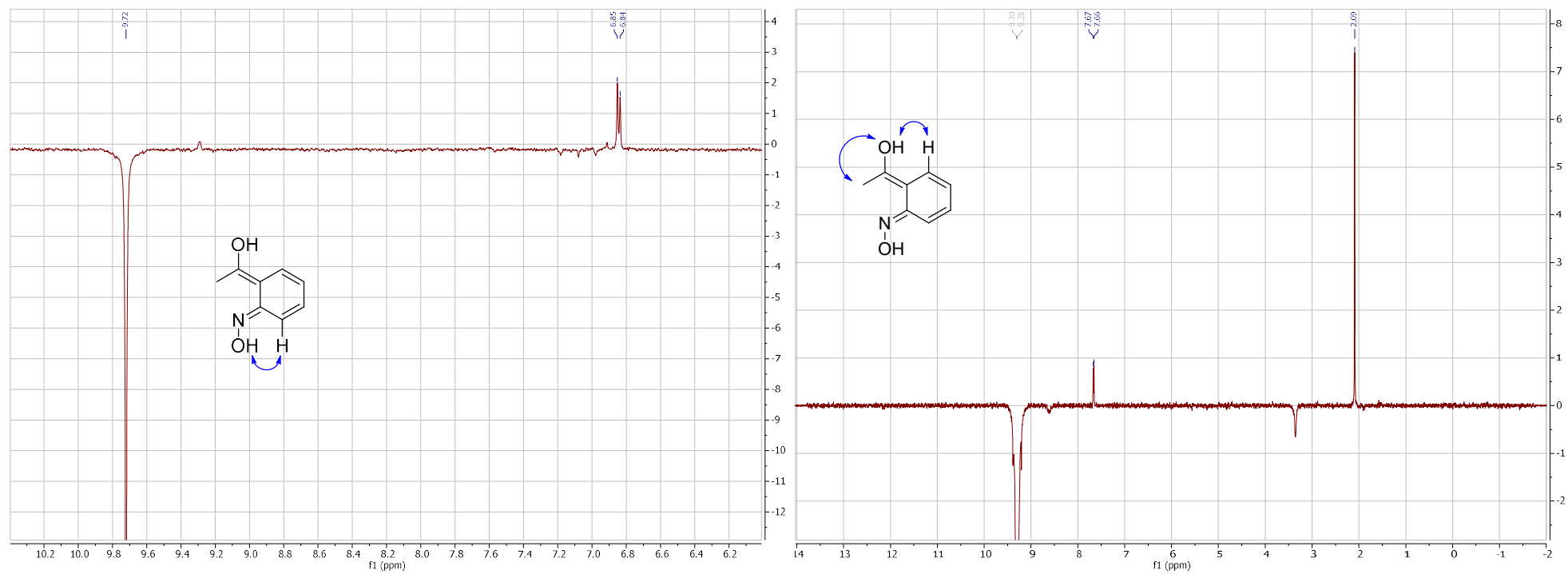


Figure S3. 1D-NOESY spectrum of Talarooxime 5 (DMSO- d_6 , 600 MHz).

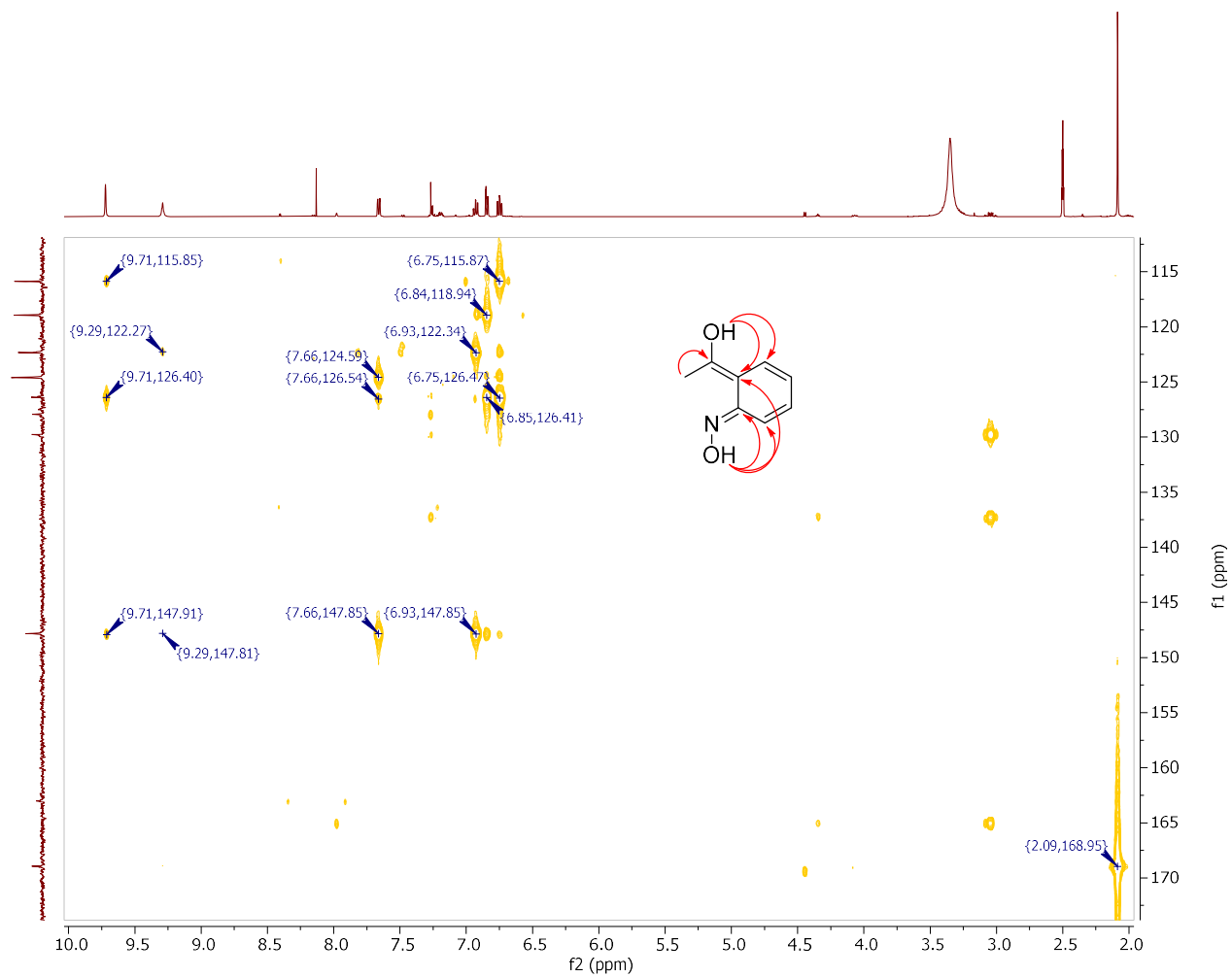


Figure S4. HMBC spectrum of Talarooxime 6 (DMSO- d_6 , 600 MHz).

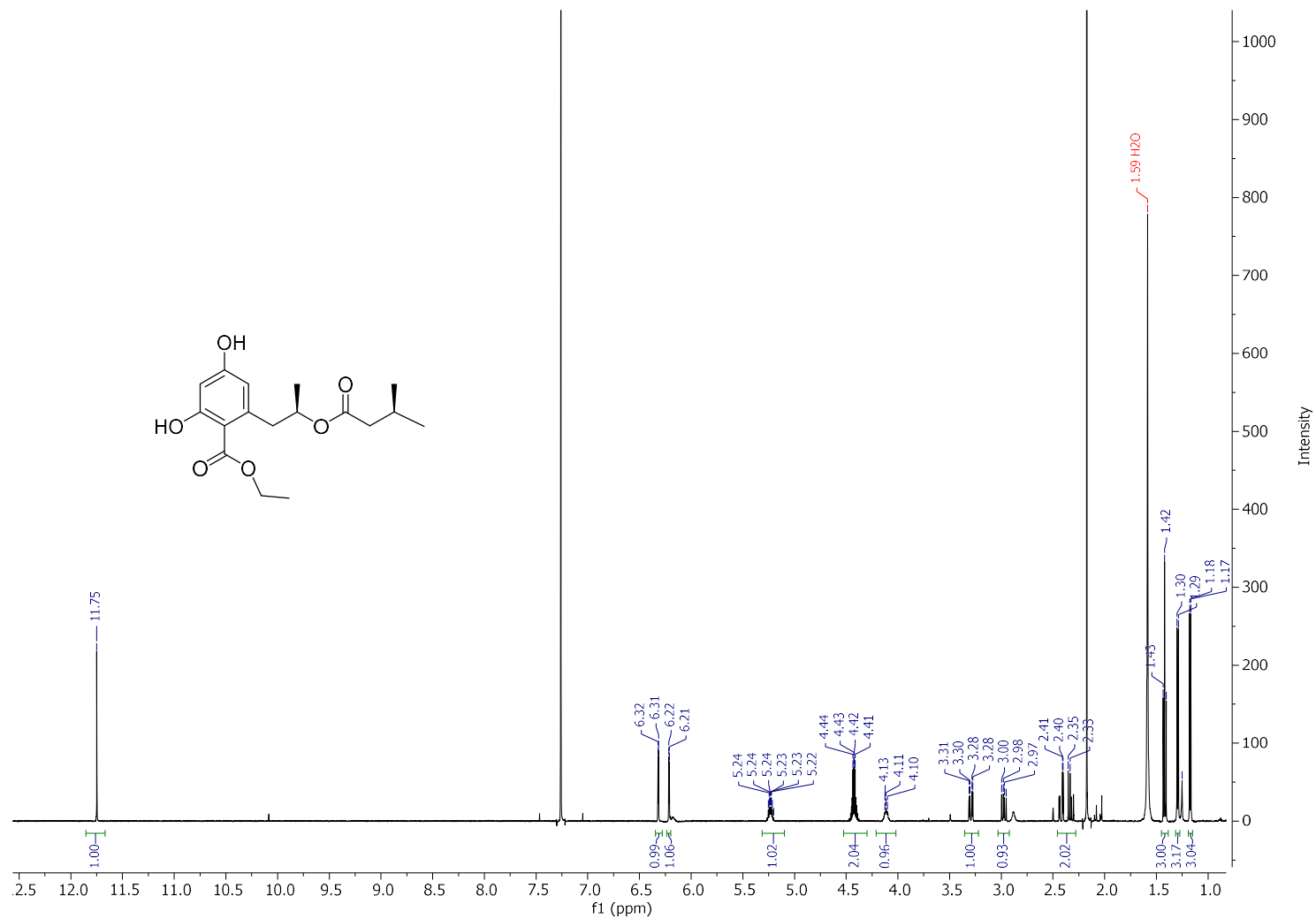


Figure S5. ¹H-NMR spectrum of Talapolyester G 2 (CDCl₃, 600 MHz).

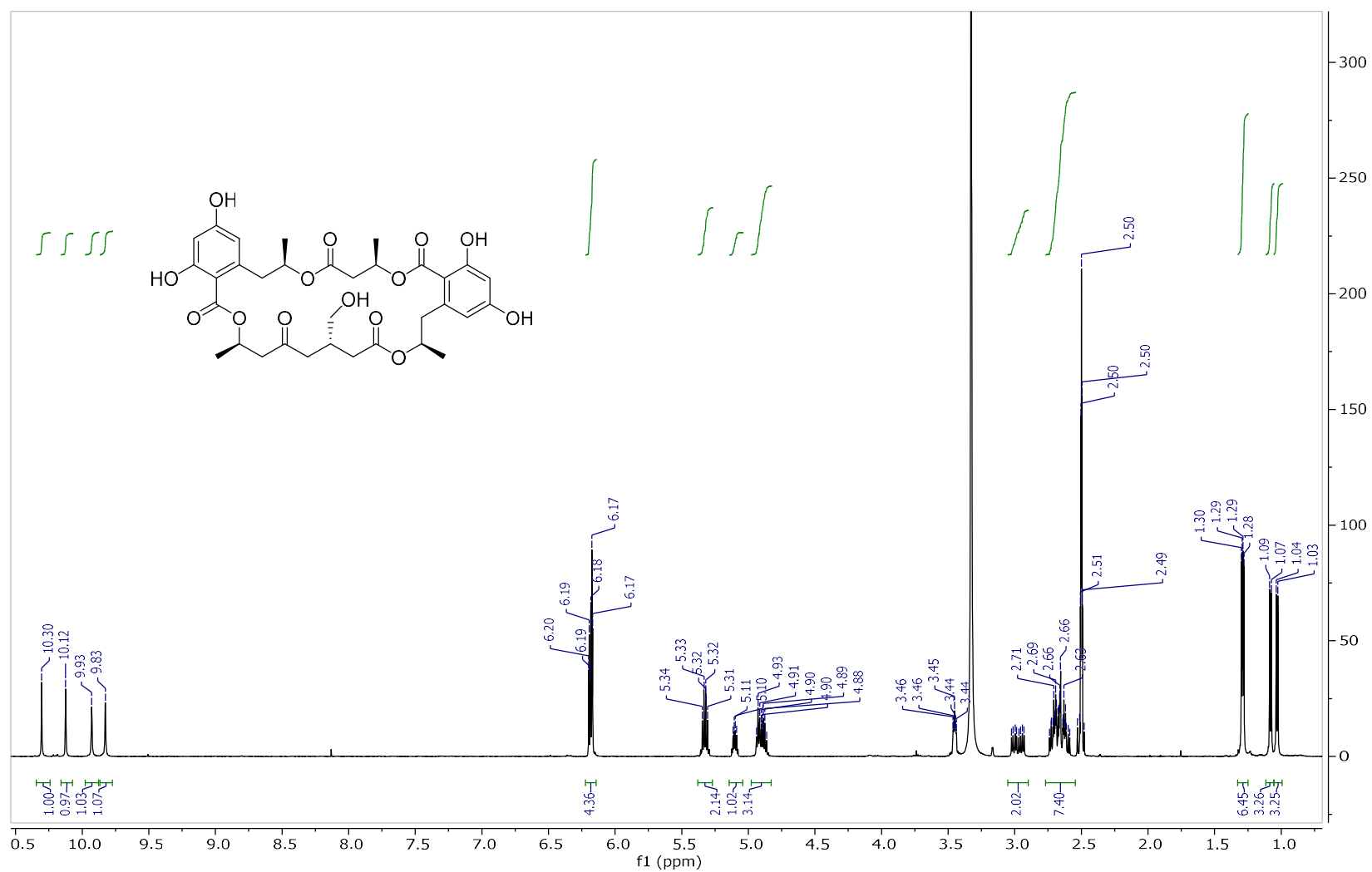


Figure S6. ^1H -NMR spectrum of 15G256 α 3 ($\text{DMSO}-d_6$, 600 MHz).

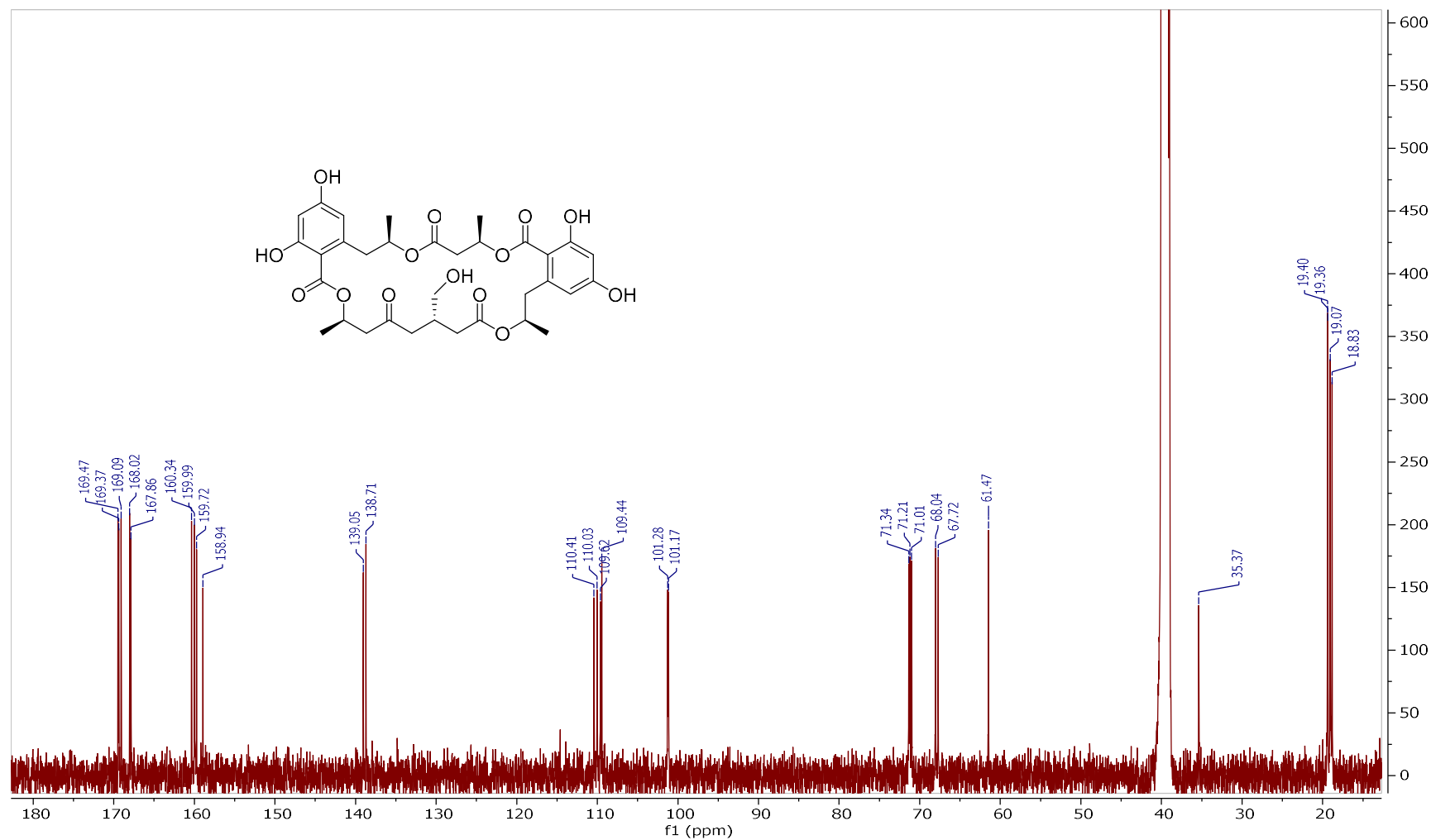


Figure S7. ^{13}C -NMR spectrum of 15G256 α 3 ($\text{DMSO}-d_6$, 150 MHz).

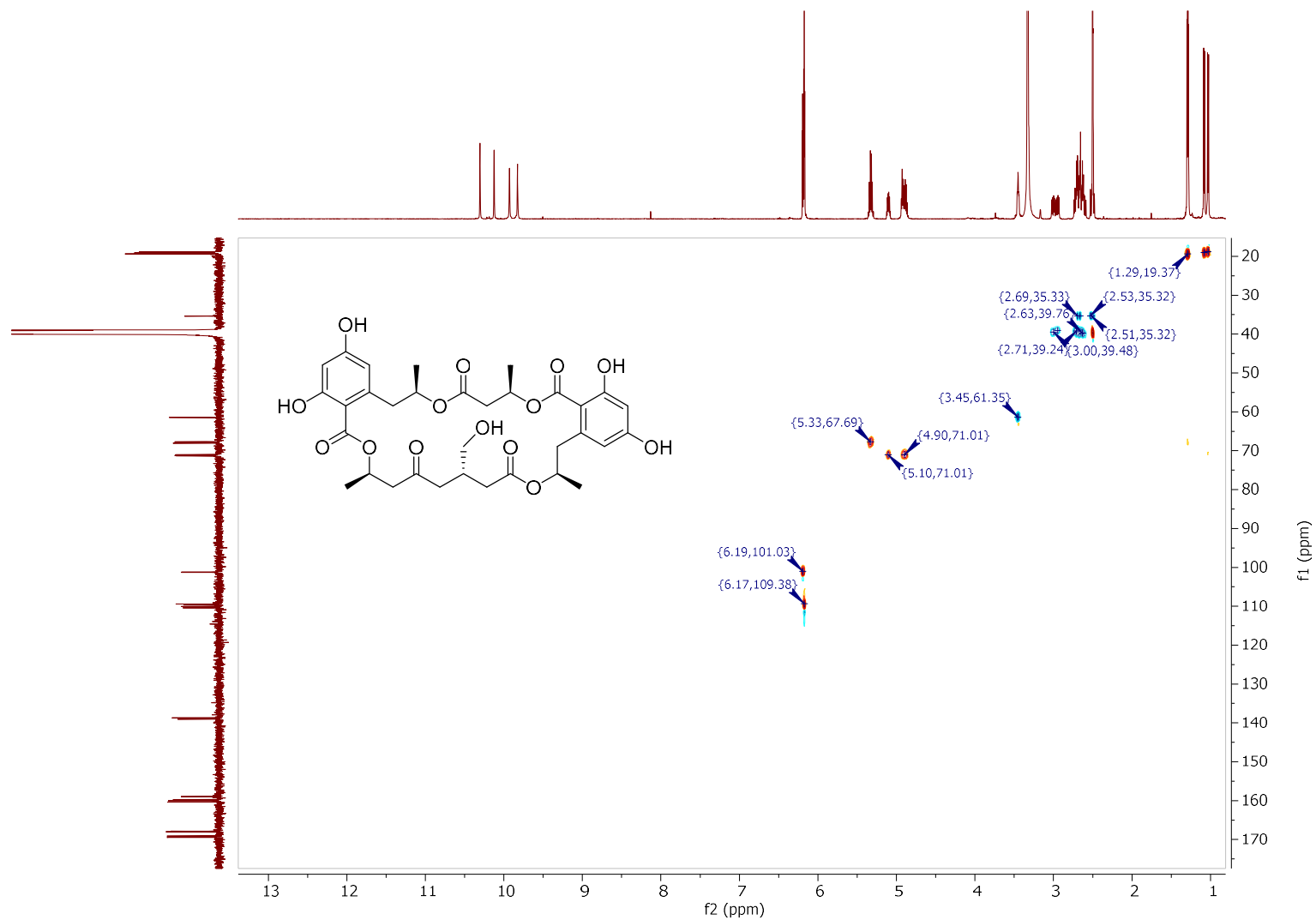


Figure S8. HSQC spectrum of 15G256 α 3 (DMSO- d_6 , 600 MHz).

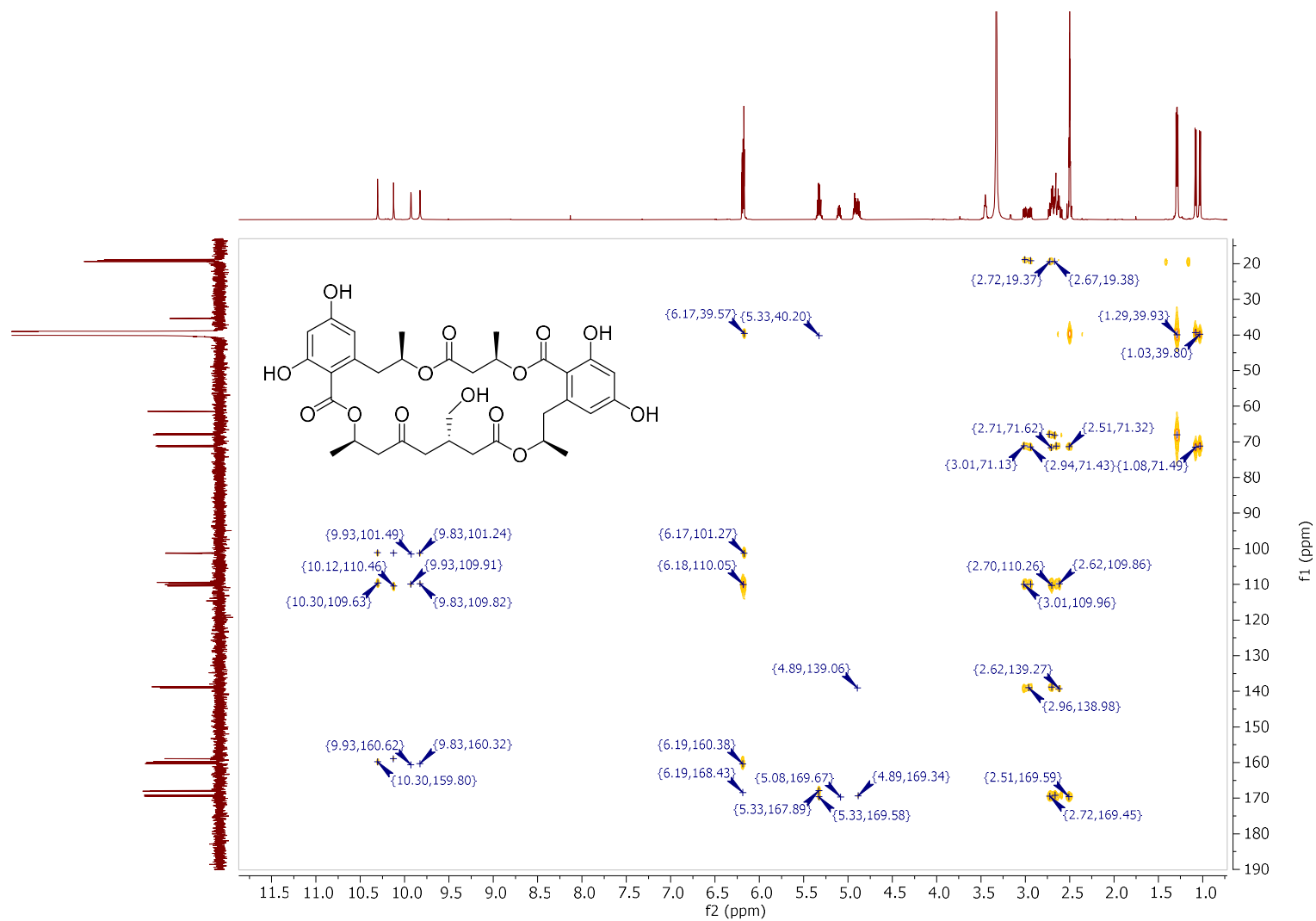


Figure S9. HMBC spectrum of 15G256α 3 (DMSO- d_6 , 600 MHz).

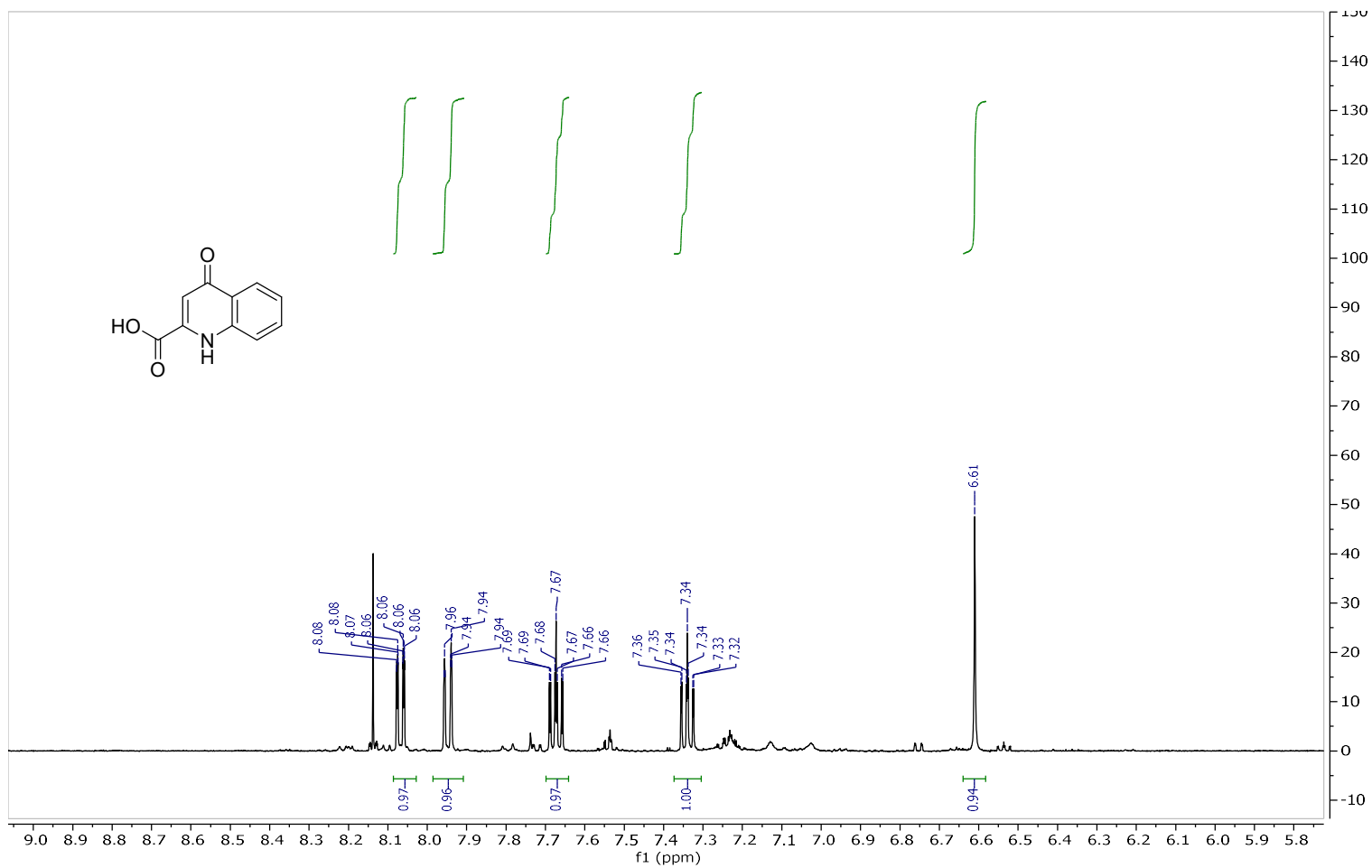


Figure S10. ¹H-NMR spectrum of **4** (DMSO-*d*₆, 600 MHz).

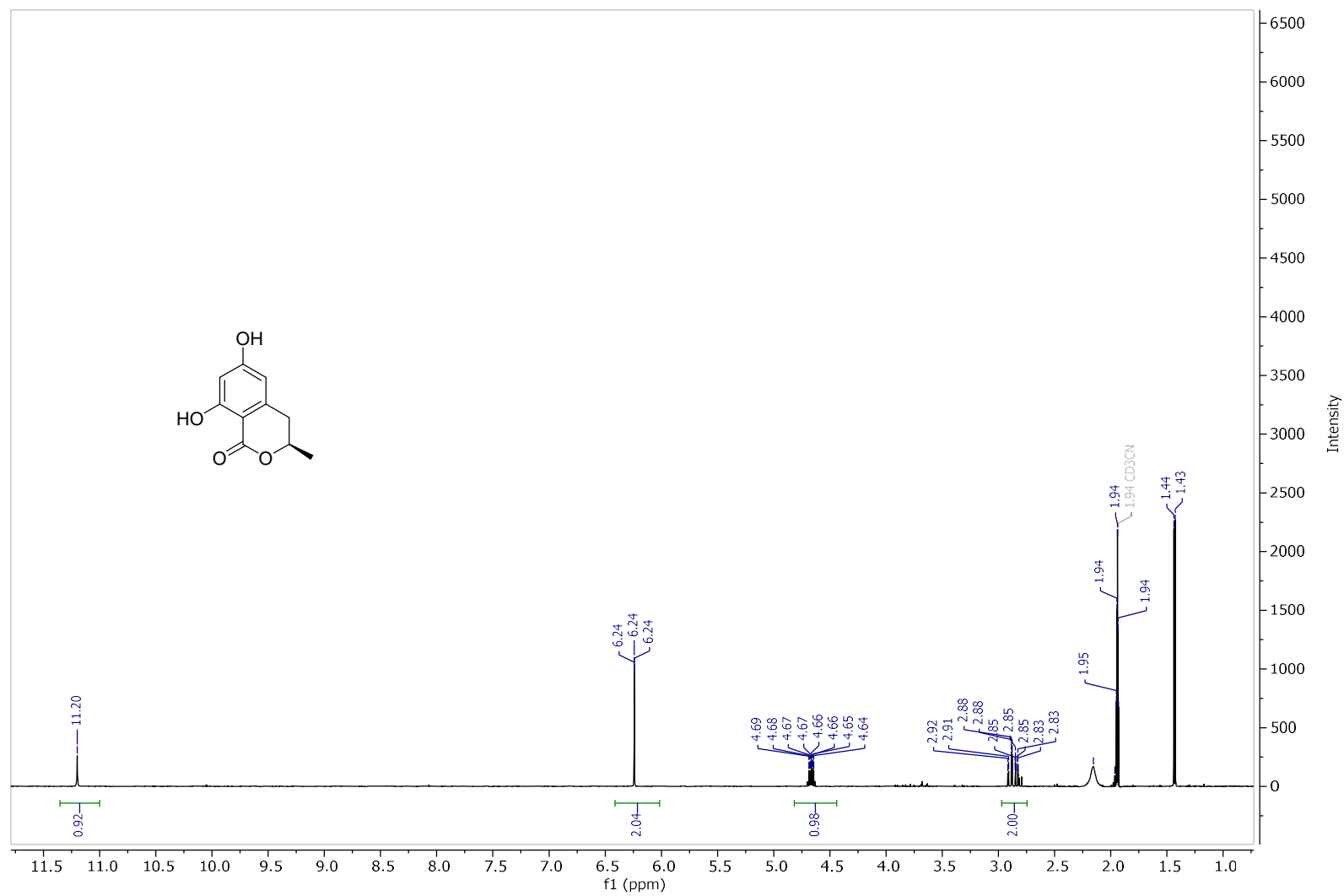


Figure S11. ^1H -NMR spectrum of **6** (CD_3CN , 600 MHz).

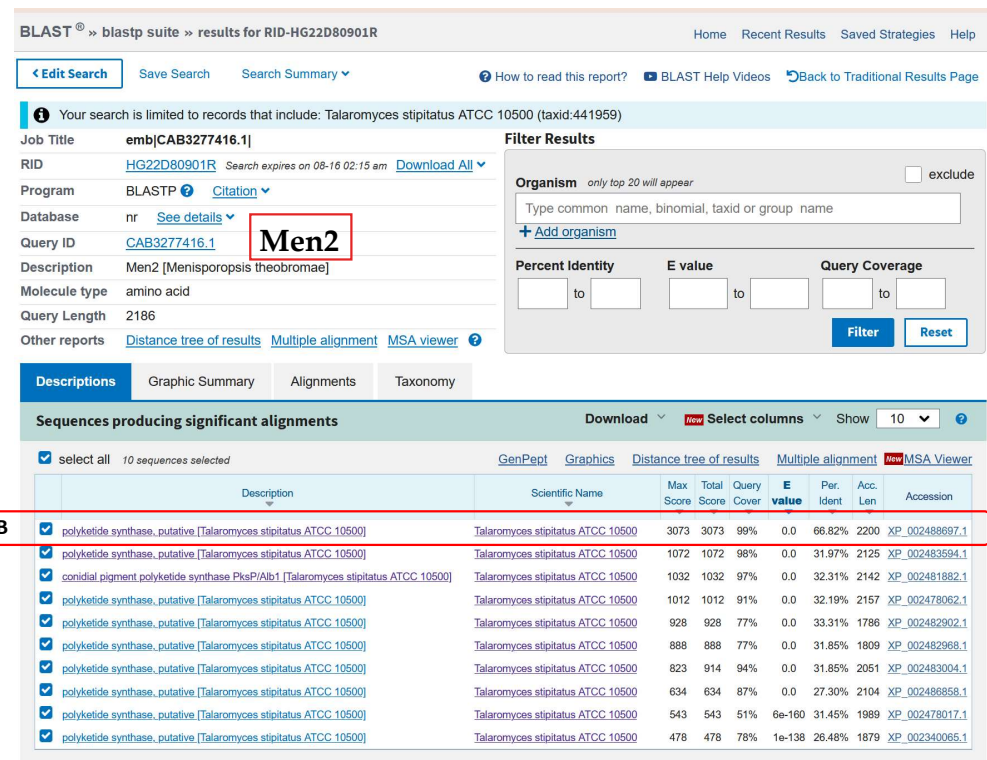
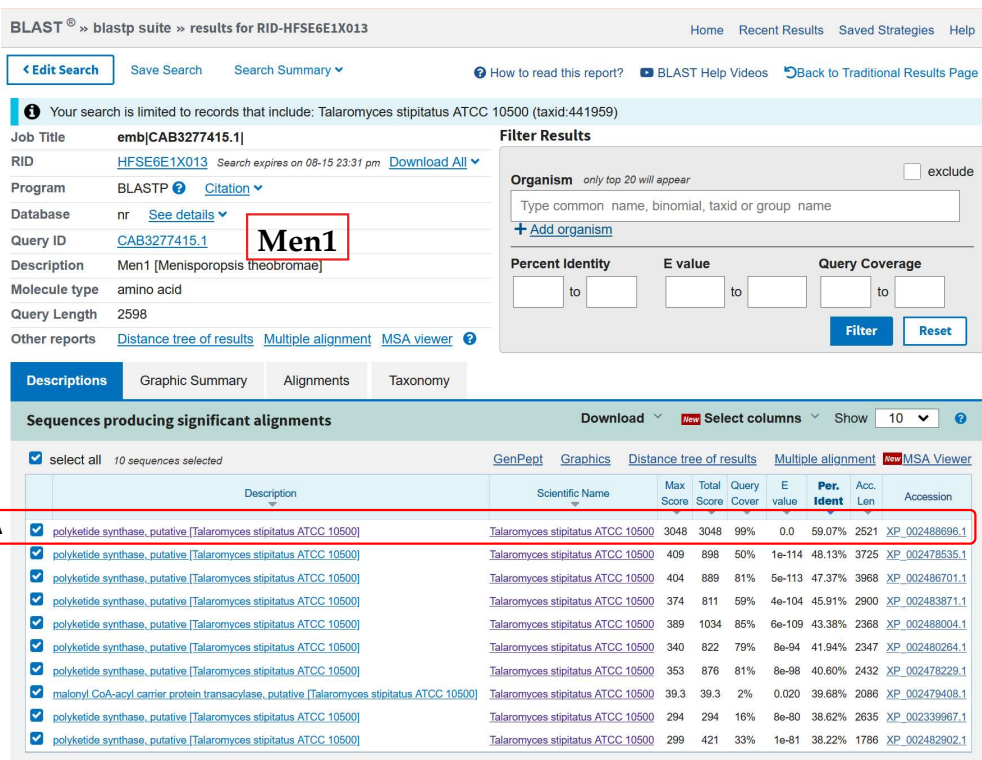


Figure S12. The result of protein Blast searches of Men1 (left) and Men2 (right) amino acid sequences against *Talaromyces stipitatus* protein database.



MENSYDDQSI~~AVIGLS~~CRFGDADNVERFWNLLREGQSAISTVPGNRWNSRRFQDDKNHSQNTSRTNRAHFLKEDVS~~AFDANFFSISKSEAVSMDPQQRLMLEVSYEAFENAGLAVES~~
~~LAQSQMGCWSSFSQDWREMQFSDLQSVPKYAMSGMQPEMLANRVSYFFDLHGPSMALETACSGSLVGLHVACQSLRSGECDAALVGGANFLNPNMFLALSNQNFLAPDGLSKA~~
~~FDASANGYGRGEGFAAVILKPVEKAIRDGDPIRAVIRATGTNQDGRTKGLTMPNGDAQETLIRSTYRSAGLELKD~~TAYFEAHGTGTQVGDFEELSAIARTVADARKREGLEELWVGS~~AKTNI~~
~~GHLEATAGLAGVLKAILVLENGVIPPNLHFKNPNPRIPFQEYHIRVPTQEV~~TWNPDTIRRVSVNSFGFGGSNAHAIIDNGKQYLHQR~~RSKATLVNGTHAADDKELKPEVPQIFVINSSDQEG~~
~~LGRQRSALRHYLANFGKEGRANS~~GWFRDLAFTLGKKRCRLPWRSFCTASTVLELSEALEATDFPKIRSGTAALRLAY~~VTGQGAQWAQMGLELFQFPTFKQSVVAADSHLKKLGCPWSV~~
~~VEELQRSGAESNIHVS~~WYSQTLCTVLQVALVELLQSWGITPRSVVGHSSGEMAAFAIGALAREDAWKIAYWRGKLSELTERAPDLSGAMMAVGASHEQAQKWVEGLTRGKCVVACI
~~N~~SPSSVTVSGDDAGLDELAAMLKEKEVFARKLKVTAYHSHHMKVVAEAYHDVLKDVEVRNVPTDGPQMFTSVSETLVNPSDLASHWVANLVSPVLSNTVAELARAKTPKDQATGS
~~AVDLMLEIGPHAALRGPVTQILQAKGLRNVEYQSL~~SRGNAIQTTLAAVADLICRGVTADIDAVNNAHTPQGAGHKTMPANTLTTLPPYAWNHSRTFWTESRMLREAKAVNDSP~~SSFI~~
~~GLPMPSFVANEHIWRGFLRLEHVPWVRHHKM~~QSAVLFPAGGFLAMAIEGASQFQ~~GKDNSRVAKGYKL~~R~~DV~~RIDSAVILTEESNIEHILQLRPHDTARSQQTDSYDGWWFEKISTSAGSD
~~ESLKCNCYGLVTVEFEQLIHP~~SHASKASSTTVQQAFAFYERLESVGLYGP~~SFQA~~IKTILHSSGGQTEGEIEMDIDVNSTTPGGS~~DGRPYV~~VHPTTLEALFQMAYAAFDNQSDGVKKALLVT
~~DIEELLLDASISHTPGARLQTSARSSRLGFREMLADVT~~VSPTASNAGGISVRGLT~~CVEMPSTAGVNSDVGITGREGYDSMLS~~KFVWKPALNLLSATEREHLIAATKVTD~~AETE~~ILAREAAD
~~FQNVKSALQASQRGKTGSLKLRNALKWISQELPDAKVF~~GKALENVSQDGGGAGPTGP~~IVD~~VLSTPDPVLLSGYGSTEF~~LAALPGVKVSLQKMYQLVS~~IMAHENPD~~LA~~VLEIGSGSSG
~~EEDTSIFSTTDIPTTIKYTRAVATPEILRN~~LQEFSPAGPIPRFTVLDLEQDLADQGIDLASFDIIIGNNVLSNSRNVENVLRRTKSLLRDEGNMCFVELTKPSSRAVPVLGVVCDWWKRGDDG
~~LRRPLSSDSIKDILTEQGFTLDFLSPDFV~~DPAIQQSSLVFASSSAENLPTASATDDADDEEIYILISPELKSPDAVVQNVASSFQHSQIVTWGAGVDFKGYIISLLELYDPFINHLTEEDFDILKKLV
~~TQASSLLWVTGIPEPHASTILGFARVVRFEIPSLDFRVL~~TLDPATIEDAKKNSIHISQVQRSKSPDKEYKELDSIVHIPRVTVDASLNHQISNLCSEAIESKPLGSLERPQKLCIRNP~~GMLNTLCF~~
~~QADNVSENELQDDEVEVRVMASGLNSKDV~~MVALGHITDTHLGLEASGV~~VL~~RVGASVTHLQLGDKV~~VML~~ANGAHR~~TT~~LRGKA~~AVCQ~~KIPQDMTYEEAAGFPFAYCTAYY~~TLLH~~VLRAQ
~~SGQSVLIHAAAGAVGQALVRLAQHLGLEV~~TTAESADDRA~~FVQELLGLFPDRIYHPQDKGLVQHV~~MRITGDVGVD~~FIVNPLSVEE~~IADSLNCLADFGTFVEMGMENDSRHSTLNTRLFRR
~~DTTFVAVNLQRVLELRPKLIGELQKALGLFQDGQVKS~~VSPSNVYPVSEAEAAIQMFQDN~~RHHGKITLSYSS~~EDFVSVLQNPKDSLKSPDNTYLIAGGLGGIGRSLATLLVDCGARHIAMVS
~~RSGVTSVEQQQLIDNLSERGAKIGVYKCSIGDANALGRALTQCASEMPPIKGI~~HS~~AVVFRDAVLHN~~MTYKQWDEL~~LDGKL~~RGSWN~~LHAL~~TTSYNLDFFLCIGSFMAIIGGISQSNYAAGSA
~~FQDGLAHLRQSQGLPAVTIDLGIVKGF~~GAVEEQGAVGHTLEWREPFVSEPEVHALIKGALLGQRGNWALD~~VPAQ~~MINSIPTGGMVRSSGVSQPYFDDPRFSIMAKIGMDSENSDTQ
~~ASVSLKELLADAESSDDAVLFVTGAVISKVAKLMQVA~~EEEEIDTGKSLHAYGV~~DSLVAVEYVSWAKKEVSADITVFDVMASKPIMS~~FARDLVGKGKWGAAPACKS

Figure S13. The amino acid sequence and domains of TpeA which were identified using SMART as follows: KS (green), AT (pink), DH (yellow), ER (cyan), KR (orange) and ACP (red).



MGSLSAARESAQRITFFGDQTVDTLLCIKDLANRSHQLPILRRYLREAADKLQLLLSQIELGDYECYRNFETIVELAEIYSKQDGTYEPIGCALWTISQFADYLSRSETDPSILTLS
 DSAAQPTYVVGVCGLLLGAAAATARDINELLDIGRKLVDVSFNLGVAQWKRAMDIEGKPGRWAVAIVNVPPKQIRNIITAFNEDMAIPKHRQFYISFLAKGWAAISGPPS
 IFPELWEYSSTLSSASKMDLPLGTPAHAAHLRSLNIEELIGSGSVLDLPVRQDRLVISTSTCKPFESQTFGSLSSSLHDITGETLHIAGVNDYVASCLSRETLVQVSSFGPTSQIG
 SFKKALEDGLKVDLDLSPESKTPNLLKNPDARDGSGNMIAIVGQSVRLPGSDDVKTFFWENLKAGQTFESEIPSRFDLQNYDDTTGAKKSSVTRFGHFDRPGLFDCRLF
 NVSPREAKQMDPIQRLLLMCSYEALQTAGYSPDSSLSTNMRVATYFGQSGDDWRQGRASQDVDIYIPGTIRSFAPGKLNHYHKWGGGNYSDSACAASTTSVIMAC
 NALLGRECDMALAGGGQLHLEPENYAGLSRAGFLSKTTGGCKTFREDADGYCRGEGIGVVLRLEDALADNDNVLAVVRGADRNYSWDASSITHPSANAQATVIQRV
 LRNTGVEPADIGFVEMHGTGTAGDSVEMKTVTTVFGSRPKDNPLYIGAVKANFGHGEAAAGITSLKAVQMLGQKTIPIRQPGFPGPKDPTFDHLDAMNIRIPDSSFPFP
 TPTRPFSQDGMRLVNNFDASGGNNCVLLEEAPDKNVSIQIDPRQYYTVAISARTTKSLQKNMERLSDYLVKHPDTPVADVAYTSTARRIHEDLKRSYTVDESTESLVGLLQ
 ADLKKDLTGIRPATPRSVVFAFTGQGSQYSGMTKQLFETCTPFRESVQSLHDLAVWQDFPSFLNLTDDVTDEISAPIQTQLAIVVLEMSLANLWKSXWVEPDLVIGYSLG
 EYVALYVSGVLSAHDVFLVGNRAQLMDERCEIGSYSMLAVQASPEDLEEPLKAYPTSNVACRGAPRSTTVSGPSEDIKLAHELKEKSISGTLNVPYGFHCAQVDPILED
 RDLLDRVPFSKPRIPVASSLDGVIIVTDDVFSYSMVVRQTRPVAFVSALKAIETSHLVDNTSLWVEIGPKRVLSFIKATLAVDHRLLHSVDEKASNWRTIATAITACWQG
 GVSIKWQNFHRQFTKHLRLVDLPTYAFDLKDYWIEPAAPIVQQRSAAEPLRQVAVPAVPGFPTASLQRVREERIQQDAAVTFESTLSHPDLMGLIRGHQVNGVDLFPAS
 GWWDMAYTAAKYIHHRIQPSRGAAPGLSMLDCSITHPLMPSASEDQQKLVIIVAKKQAGSSVVEVSFKSQEKSVEQDHGCKIRFESKADWEAERSAHFIKAANKNV
 VTNATRPDGNHKLKPKVVYTLFSNFVNYSGDFKGIQQVYLNADFQREVADVLPAGMYNFNLNPNYWSDALIHACGFMHSDPDLPTQDCFLNGFEELRFLMDDL
 PGVPYTSYVFMHDTNSQEVPAKRTNRVTGDIYIFQGEKIVGTQGVVFQRLTKRILTTILGKSQDHHNSNEVRNGNATTTHTNPPAHATTQSFAPPGIKPAVAFSSAPATV
 GEETAEAVIAKILTKGANRASLESTTLGEIGLDSLEWIELVGVFRSALDIEVPASFFFEYPKVLRLRQAI AELPLEGEKEESGSSSPDSPYGMILPATGRFTPITASRSTHNSDG
 PANYANIVLDIVLSQTGFDDKDDVLPSTRFDDMGLDSLCTMEVVSLSVREQTGLDLPASFFHHHPTVADVRKNLGPNTEDKSKDSVKASASIAVSEPATELVVVHHPGNPAP
 ESLPIIDEDLKDYHCDFFLMQGSDDSAEIPMFLLPDGTGYPAVLLKLPPVFKGDNPLFTCKSPLLHRAEGREVACTIEGLALSIAEAIARRTRPHGPYLLAGYSLGAAYAYEVAKIL
 ADAGEIVQGLLFVDFNMAASVGLHRERKPVPTNLNVGVMEQVGWMNGIHNDKFNHIPPAPPKIKFHALSVFKSLTRYFPKPMTPSQRPNTYALWAGAGMEDLLG
 PSNAGFLPEFGIIDWQMGSRRENNGPAGWENFIGGPVRCATVPCDHLSIMMSTDWVGTTANIIKDLEDALESNPGTP

Figure S14. The amino acid sequence and domains of TpeB which were identified using SMART as follows: SAT (yellow), KS (green), AT (pink), PT (cyan), ACP1 (red), ACP2 (red) and TE (orange).

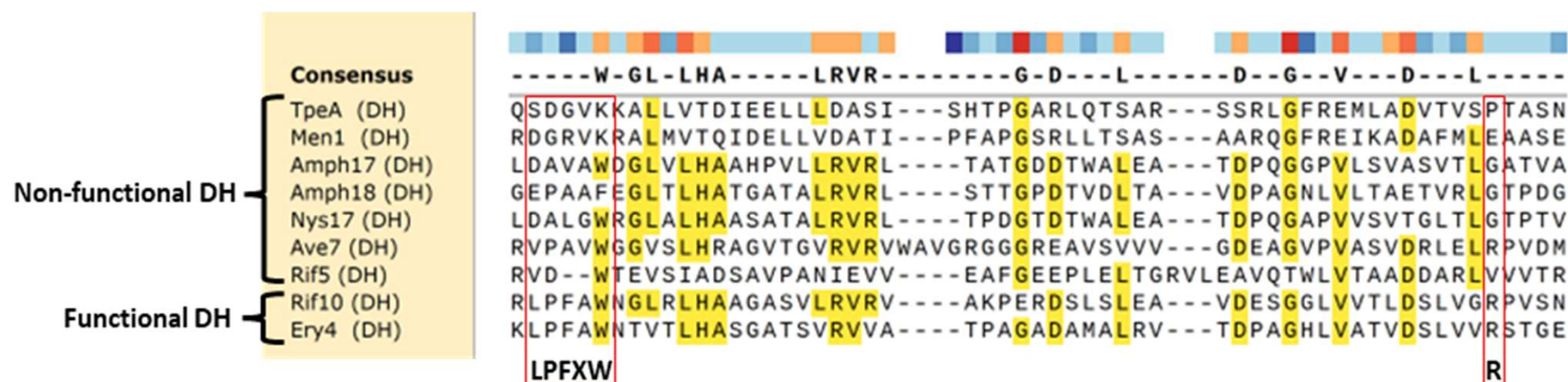


Figure S15 : Protein sequence alignment of the predicted site in DH domains for ACP interaction of TpeA and other functional and nonfunctional DH domains including Men1 and modular HR-PKs such as Amph17 (AJE44526) and Amph18 (AJE39059) from *Streptomyces nodosus*, Nys17 (AAF71767) from *Streptomyces noursei* ATCC 11455, Ave7 (BAA84478) from *Streptomyces avermitilis*, Rif5 (AAC01711) and Rif10 (AEK39124) from *Amycolatopsis mediterranei* S699 and finally Ery4 (CAM00064) from *Saccharopolyspora erythraea* NRRL 2338.

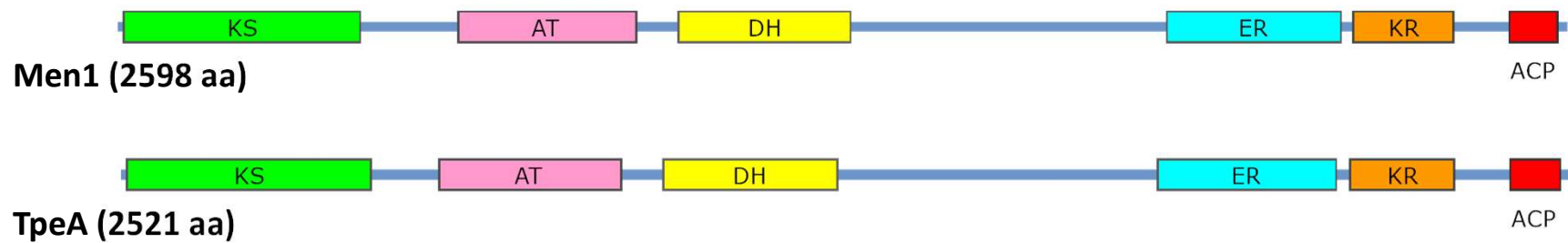


Table S1. The similarity of TpeA domains to their counterparts in Men1.

Domains	Size (aa)	Similarity to Men1 domains	E-value
KS	428	79.72%	0.0
AT	318	76.49%	5e-170
DH	302	50.00%	2e-89
ER	313	42.54%	2e-85
KR	181	77.90%	2e-93
ACP	85	70.59%	7e-32

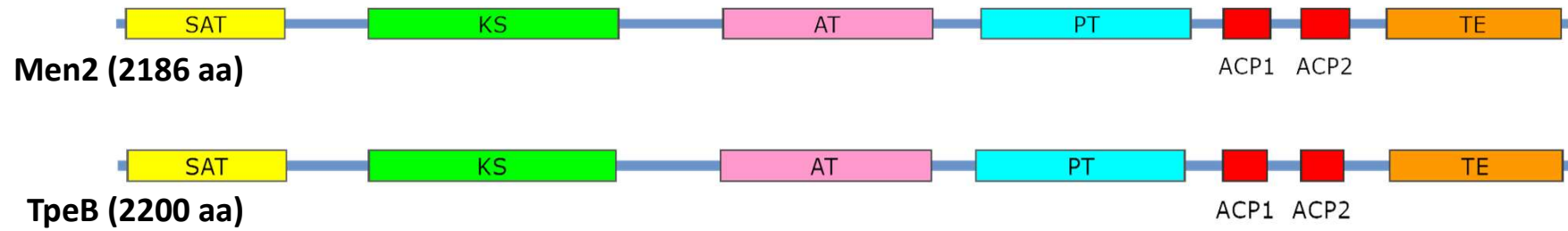


Table S2. The similarity of TpeB domains to their counterparts in Men2.

Domains	Size (aa)	Similarity to Men2 domains	E-value
SAT	241	73.75%	7e-113
KS	376	79.79%	0.0
AT	320	68.75%	4e-159
PT	318	58.62%	5e-134
ACP1	67	64.18%	3e-27
ACP2	65	83.08%	8e-36
TE	262	78.16%	4e-132