Putative Biosynthesis of Talarodioxadione & Talarooxime from *Talaromyces stipitatus*

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Supplementary Information
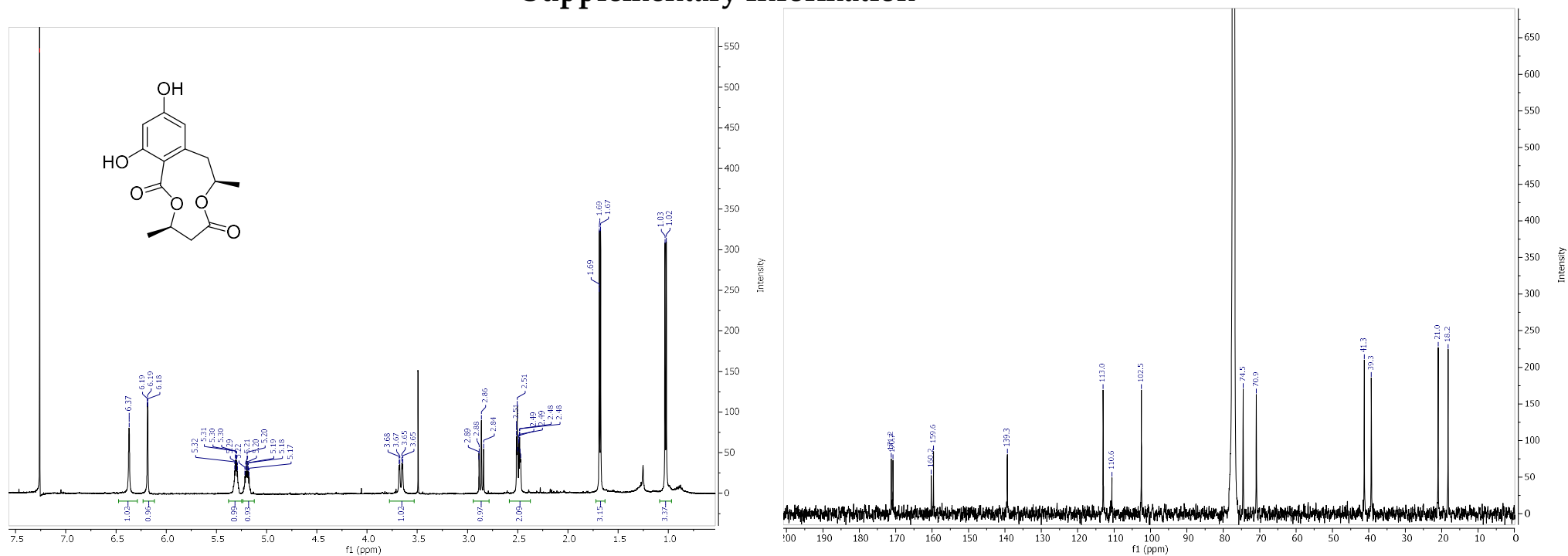

Figure S1. ^{1}H-NMR and ^{13}C-NMR spectra of Talarodioxadione **1** (CDCl$_3$, 600 and 150 MHz).
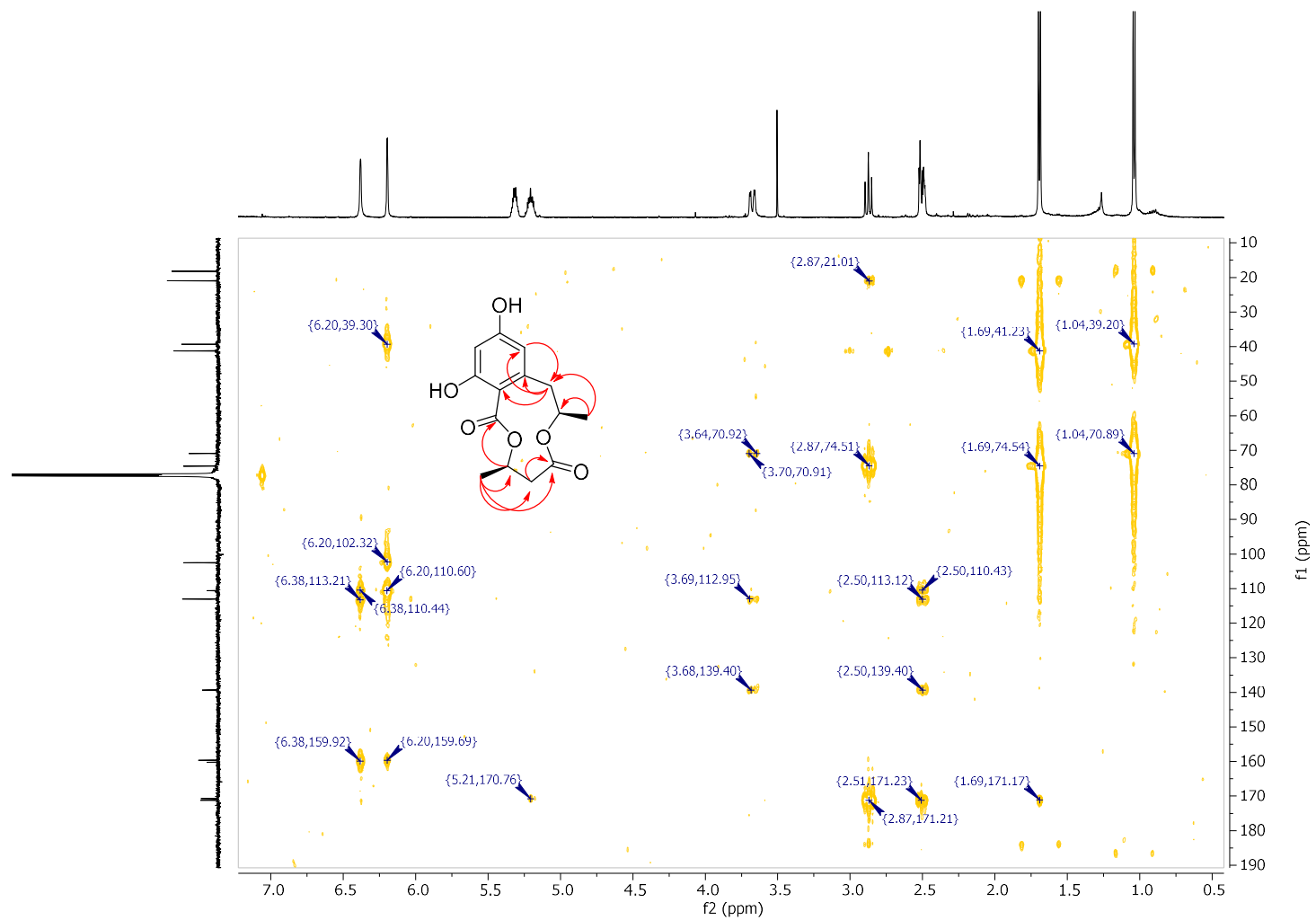
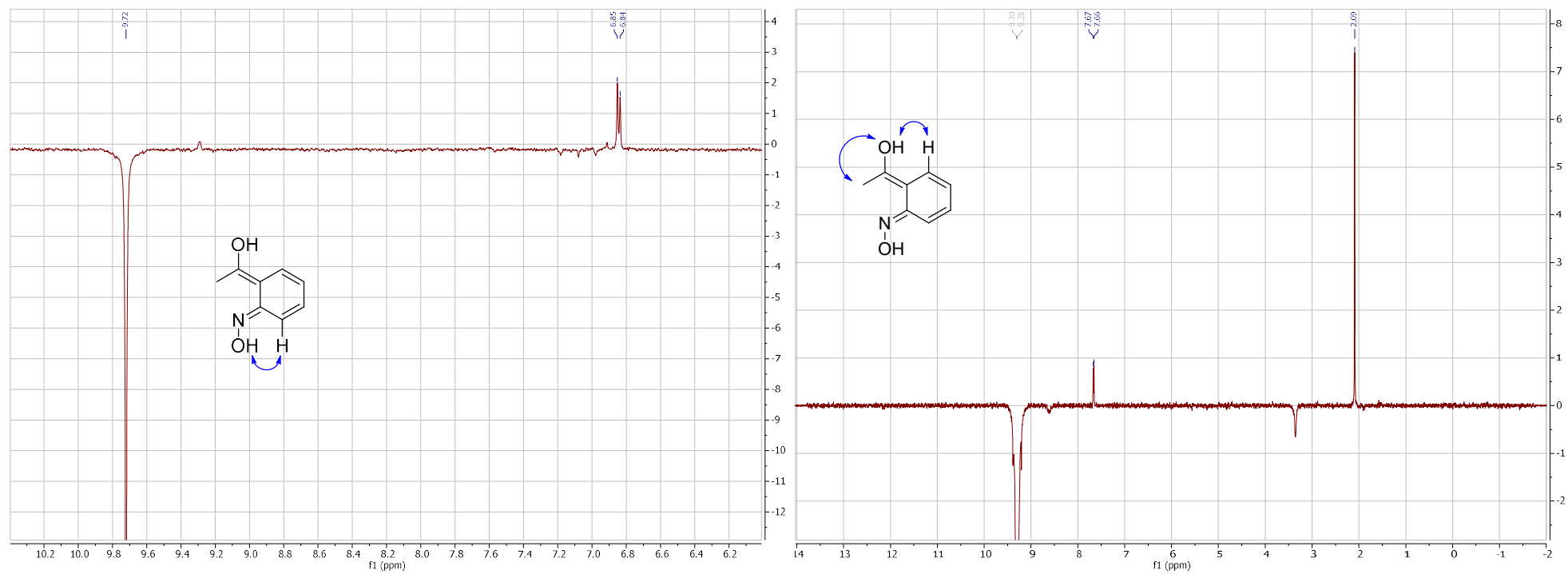**Figure S2.** HMBC spectrum of Talarodioxadione **1** (CDCl$_3$, 600 MHz).

Figure S3. 1D-NOESY spectrum of Talarooxime **5** (DMSO-d_6, 600 MHz).
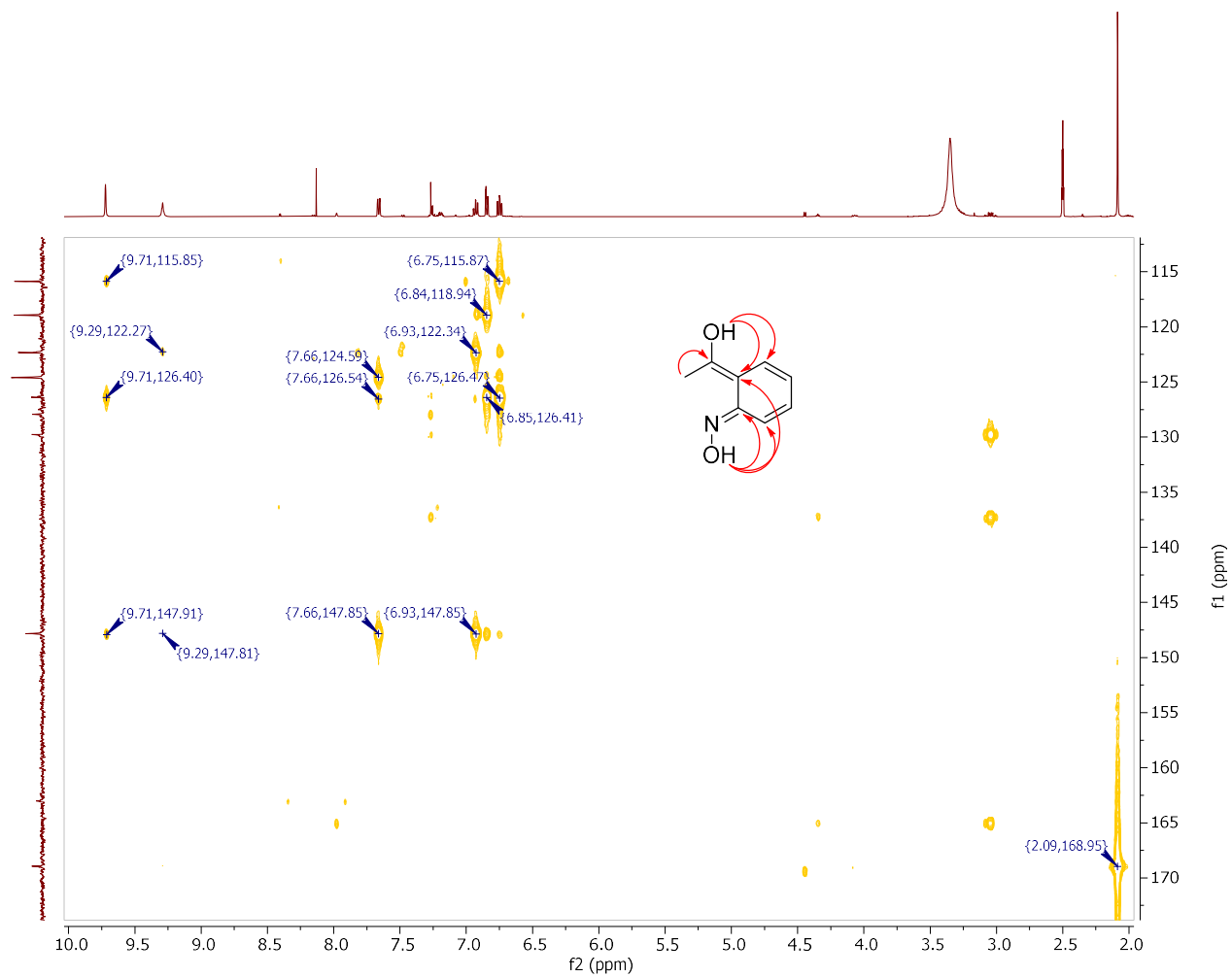
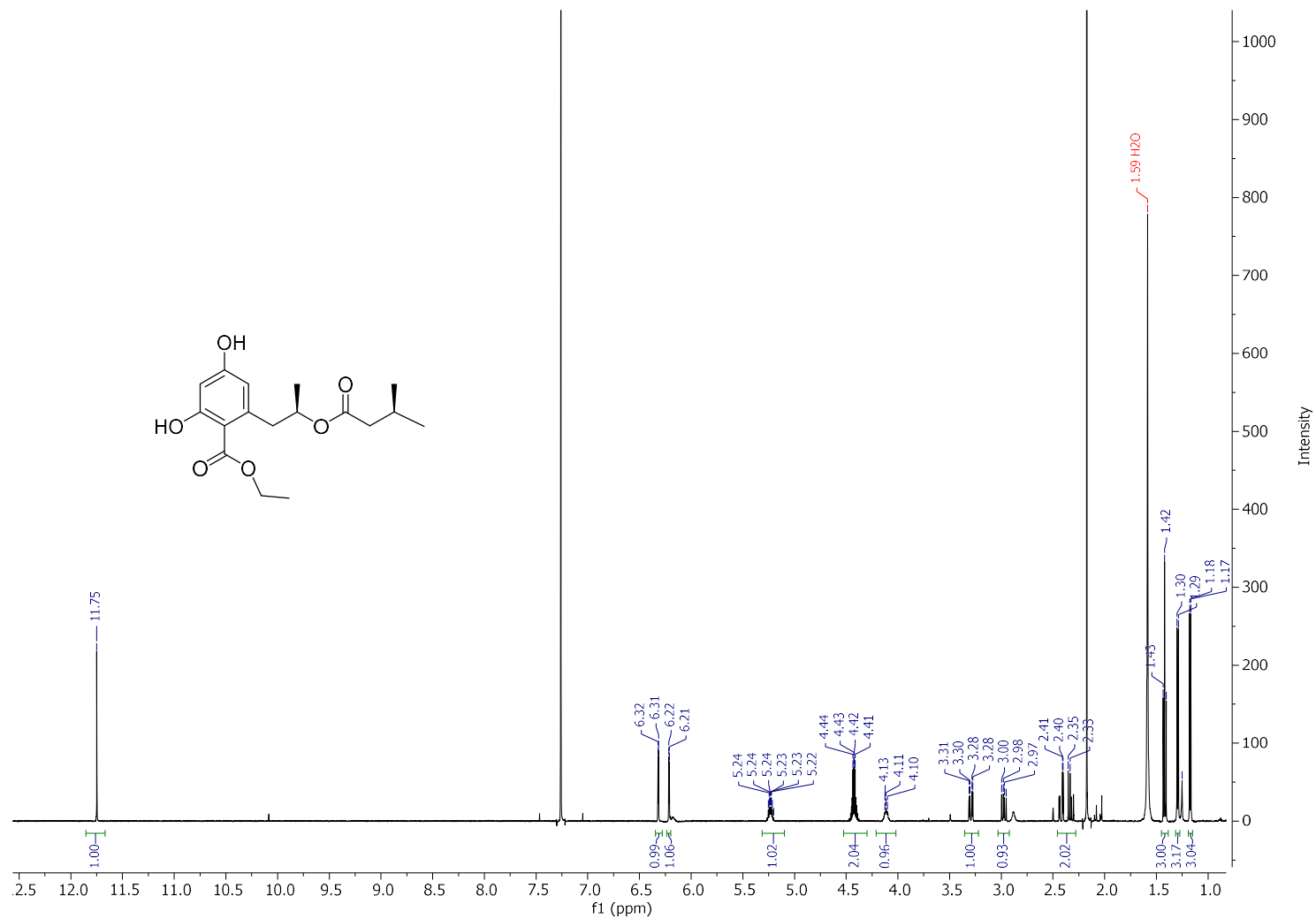**Figure S4.** HMBC spectrum of Talarooxime **6** (DMSO-d_6, 600 MHz).

Figure S5. ^{1}H-NMR spectrum of Talapolyester G **2** (CDCl$_3$, 600 MHz).
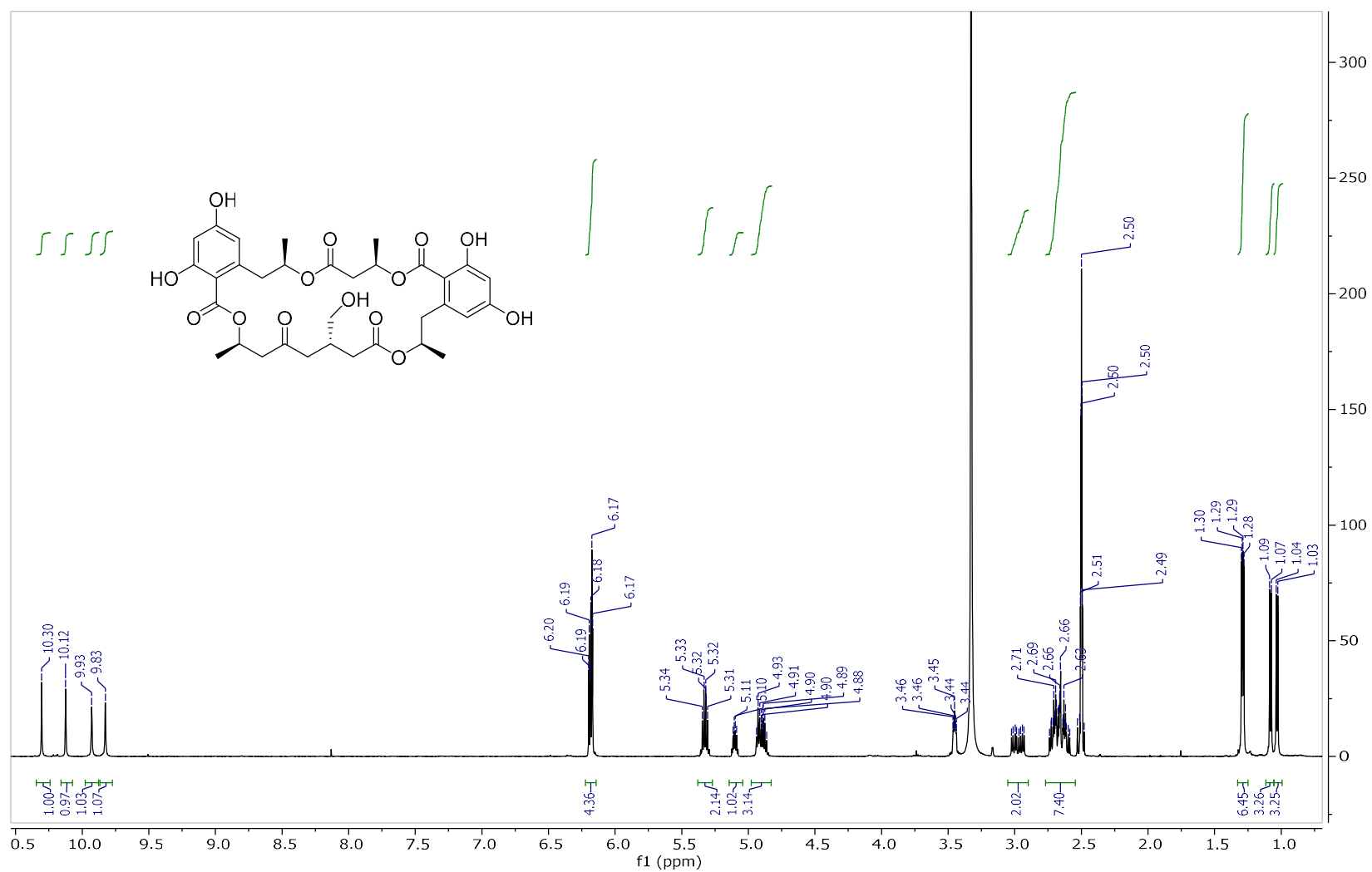
Figure S6. ^{1}H-NMR spectrum of 15G256α **3** (DMSO-d_6, 600 MHz).
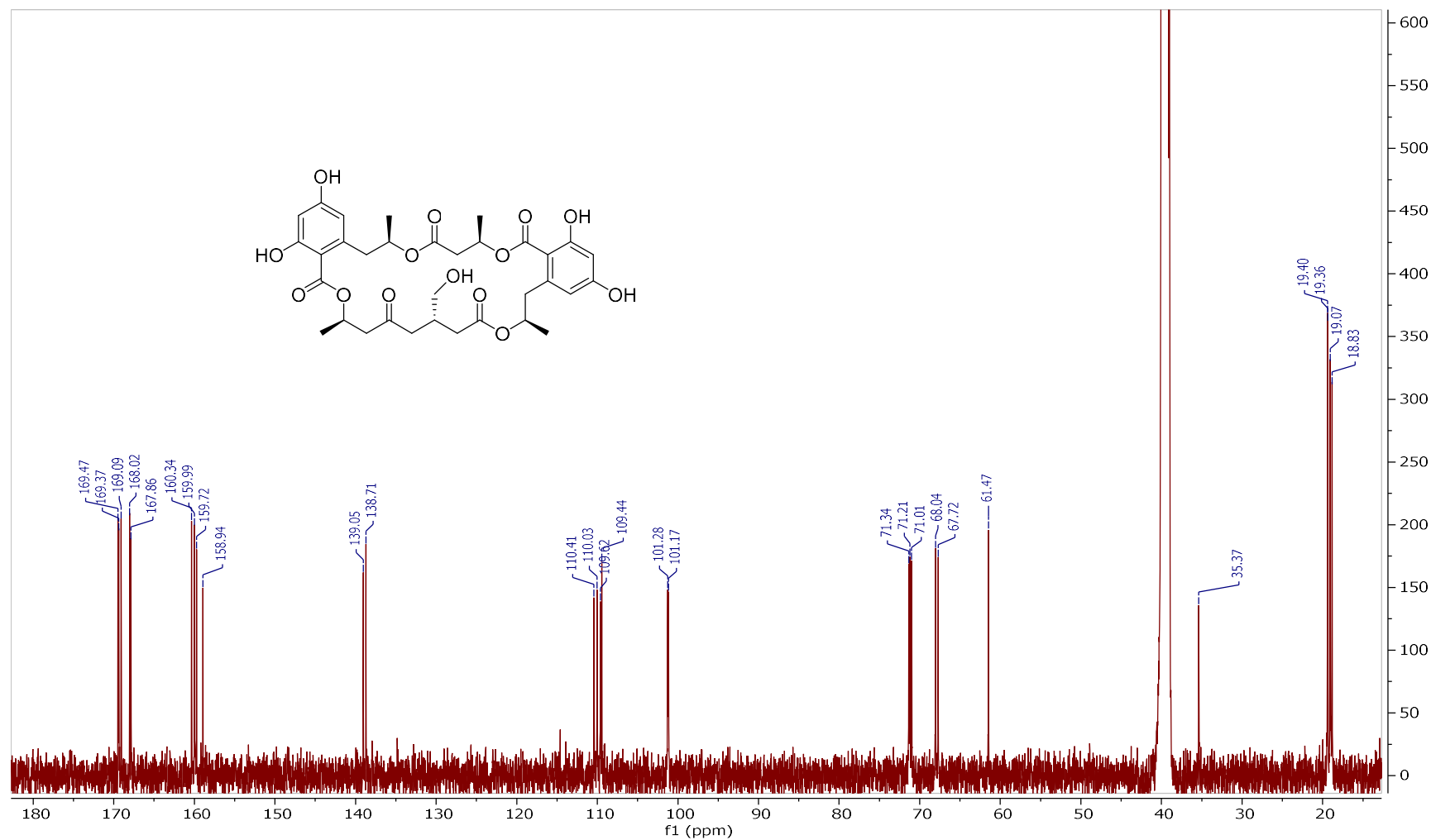
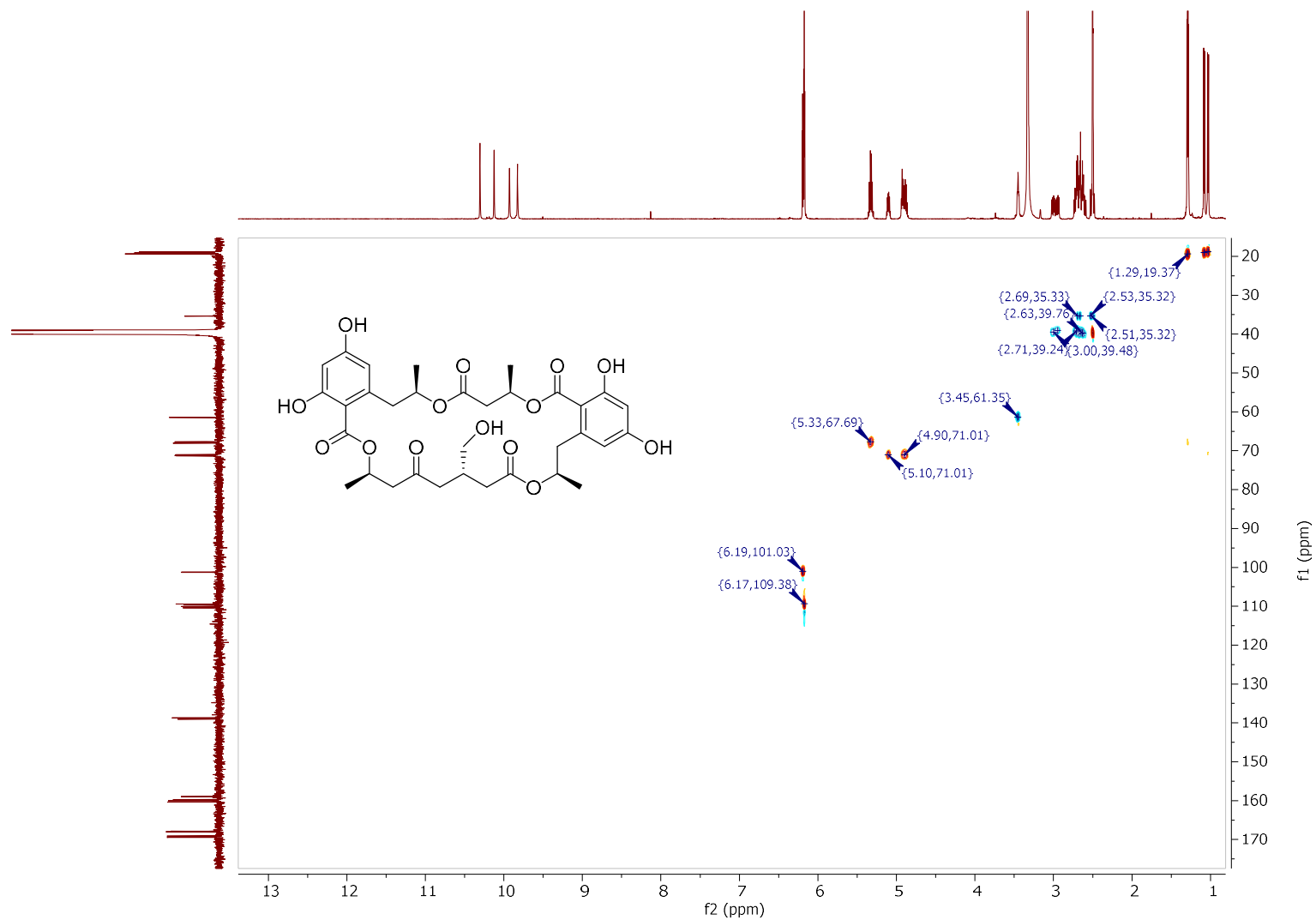**Figure S7.** ^{13}C-NMR spectrum of 15G256α **3** (DMSO-d_6, 150 MHz).

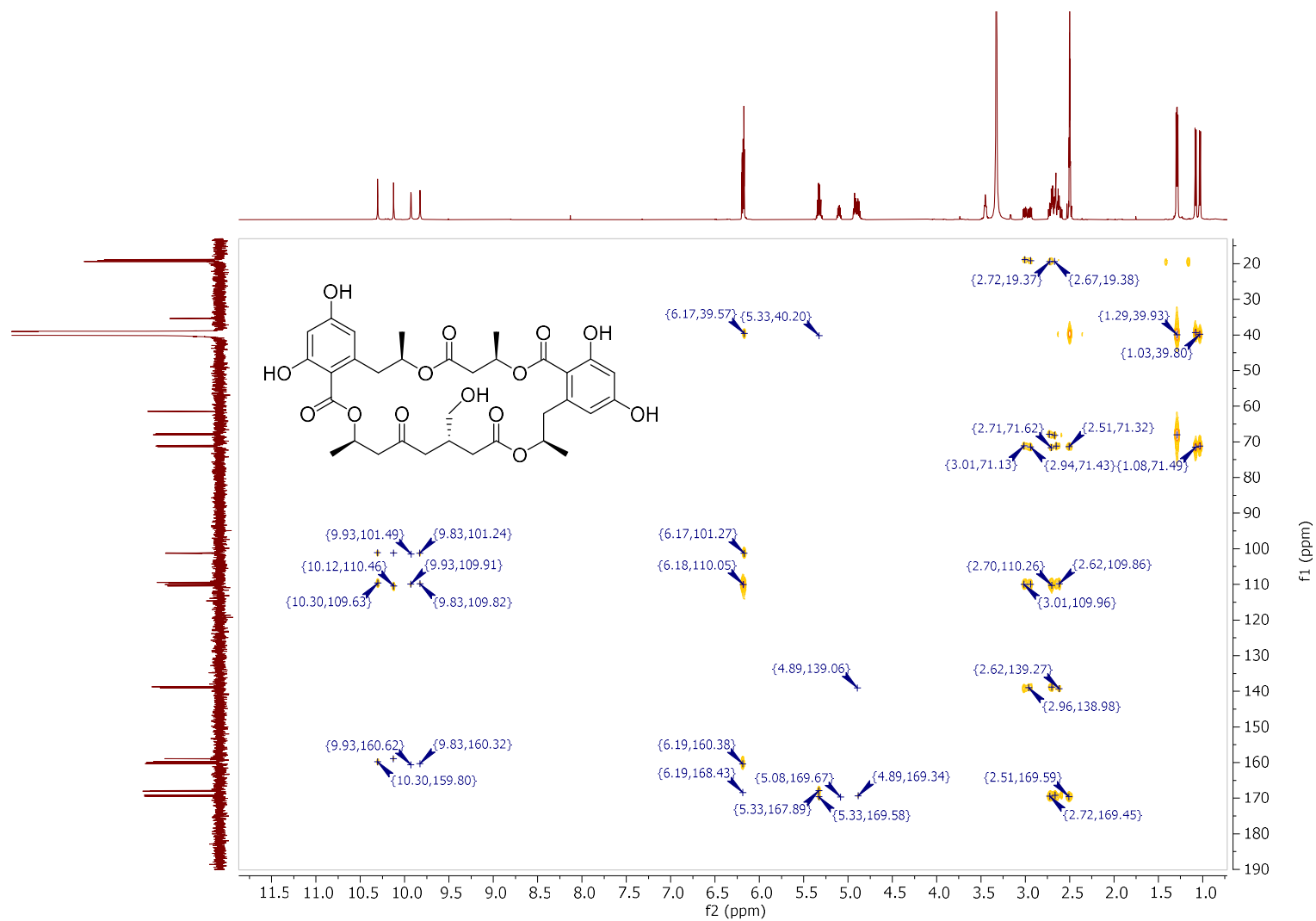**Figure S8.** HSQC spectrum of 15G256α **3** (DMSO-d_6, 600 MHz).

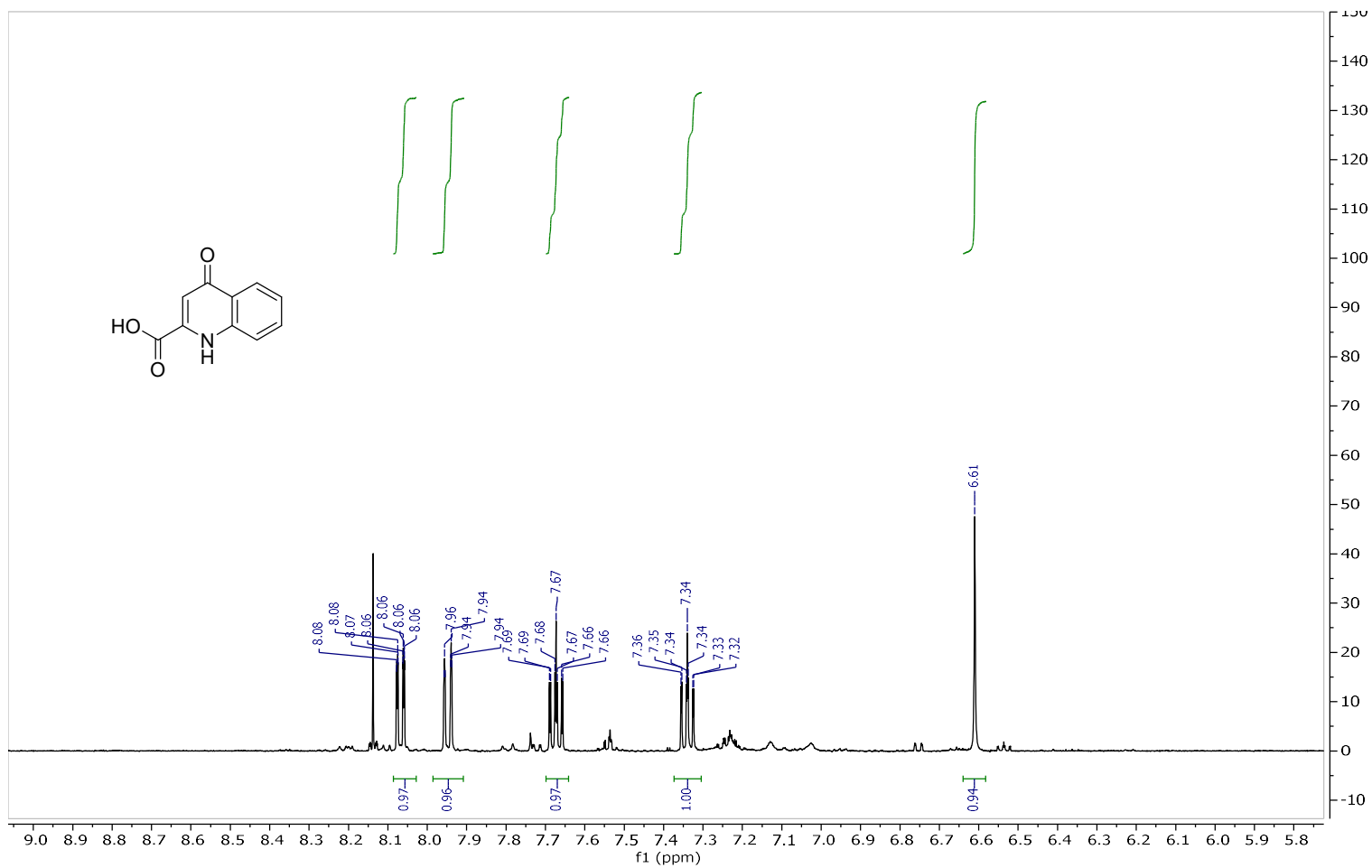**Figure S9.** HMBC spectrum of 15G256α **3** (DMSO-d_6, 600 MHz).

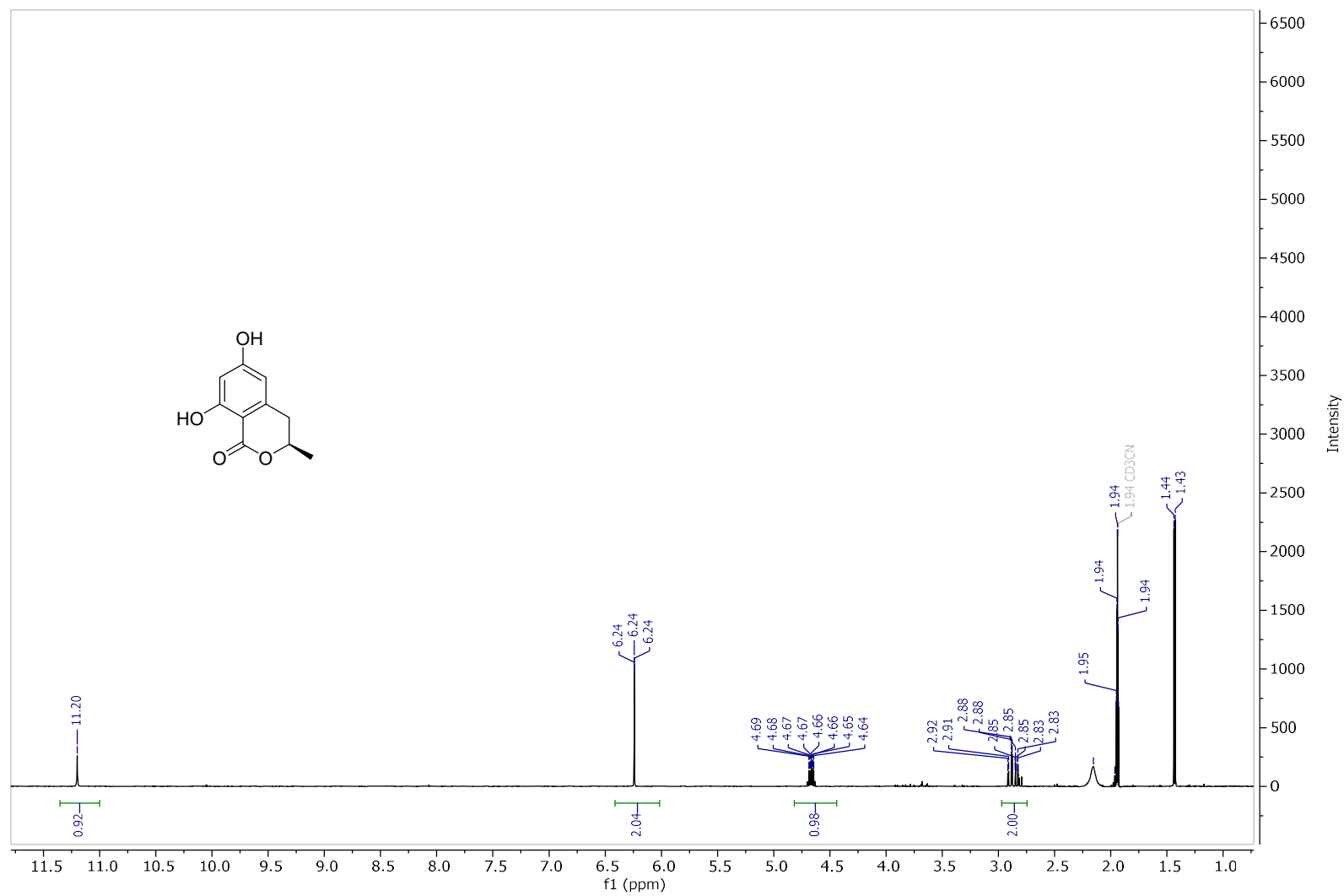**Figure S10.** ^{1}H-NMR spectrum of **4** (DMSO-d_6, 600 MHz).

Figure S11. ^{1}H-NMR spectrum of **6** (CD$_3$CN , 600 MHz).
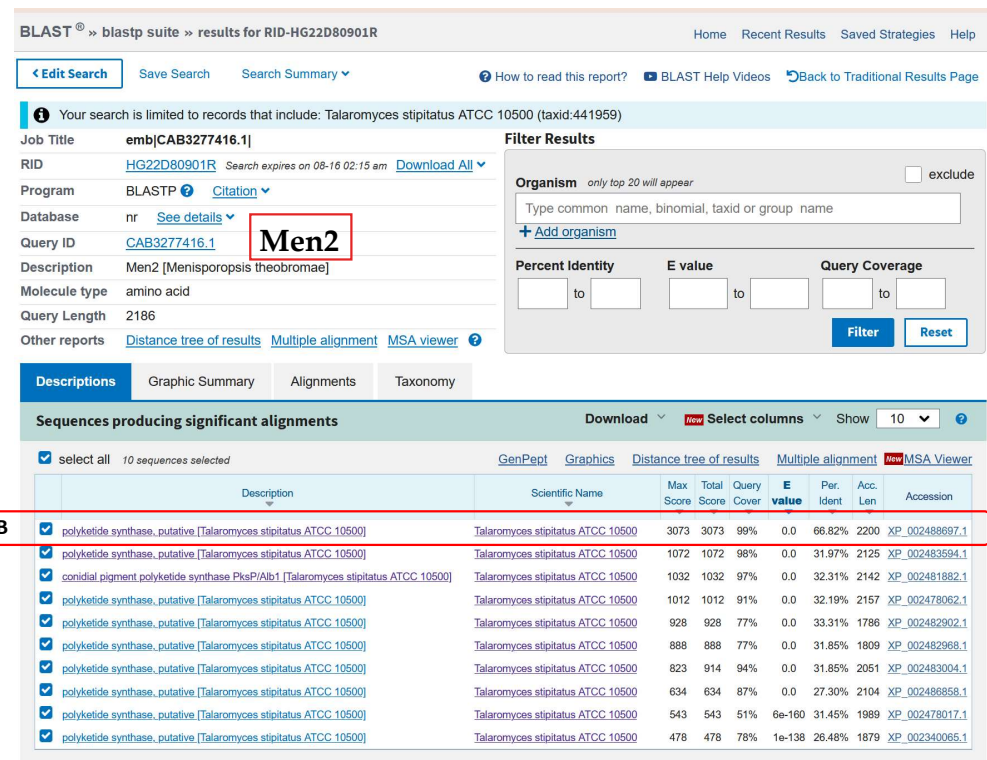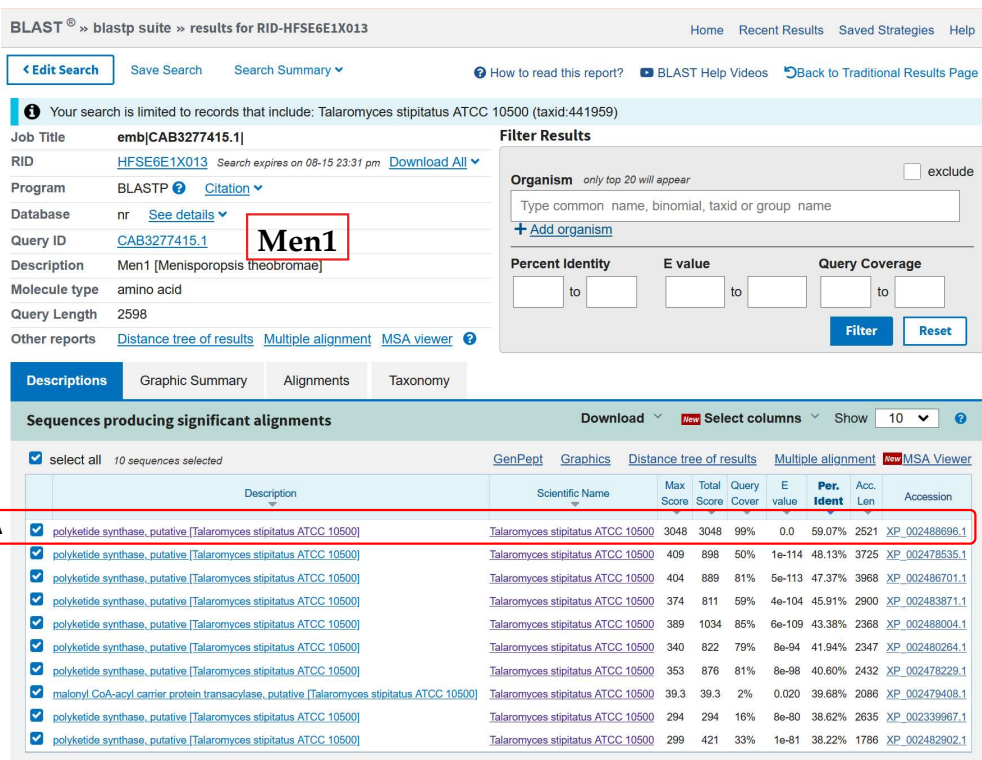
Figure S12. The result of protein Blast searches of Men1 (left) and Men2 (right) amino acid sequences against *Talaromyces stipitatus* protein database.

TpeA (2521 aa)

MENSYDDQSIAVIGLSCRFPGDADNVERFWNLLREGQSAISTVPGNRWNSRRFQDDKNHSQNTSRTNRAHFLKEDVSAFDANFFSISKSEAVSMDPQQRLMLEVSYEAFENAGLAVES
LAQSQMGCWVSSFSQDWREMQFSDLQSVPKYAMSGMQPEMLANRVSYFFDLHGPSMALETACSGSLVGLHVACQSLRSGECDAALVGGANLFLNPNMFLALSNQNFLAPDGLSKA
FDASANGYGRGEGFAAVILKPVEKAIRDGDPIRAVIRATGTNQDGRTKGLTMPNGDAQETLIRSTYRSAGLELKDTAYFEAHGTGTQVGDFEELSAIARTVADARKREGLEELWVGSAKTNI
GHLEATAGLAGVLKAILVLENGVIPPNLHFKNPNPRIPFQEYHIRVPTQEVTWNPDTIRRVSVNSFGFGGSNAHAIIDNGKQYLHQRRSKATLVNGTHAADDKELKPEVPQIFVINSSDQEG
LGRQRSALRHYLANFGKEGRANSGWFRDLAFTLGKKRCRLPWRSFCTASTVLELSEALEATDFPKIRSGTAALRLAYVFTGQGAQWAQMGLELFQFPTFKQSVVAADSHLKKLGCPWSV
VEELQRSGAESNIHVSWYSQTLCTVLQVALVELLQSWGITPRSVVGHSSGEMAAAFAIGALAREDAWKIAYWRGKLSSELTERAPDLSGAMMAVGASHEQAQKWVEGLTRGKCVVACI
NSPSSVTVSGDDAGLDELAAMLKEKEVFARKLKVTTAYHSHHMKVVAEAYHDVLKDVEVRNVPTDGPQMFTSVSETLVNPSDLDASHWVANLVSPVLFSNTVAELARAKTPKDQATGS
AVDLMLEIGPHAALRGPVTQILQAKGLRNVEYQSLLSRGCNAIQTTLAAVADLICRGVTADIDAVNNAHTPQGAGHKTMPANTLTTLPPYAWNHSRTFWTESRMLREAKAVNDSPSSFI
GLPMPSFVANEHIWRGFLRLEHVPWVRHHKMQSAVLFPAGGFLAMAIEGASQFQGKDNSRVAKGYKLRDVRIDSAVILTEESNIEHILQLRPHDTARSQQTDSYDGWWEFKISTSAGSD
ESLKCNCYGLVTVEFEQLIHPSHASKASSTTVQQAEAFYERLESVGLEYGPSFQAIKTILHSSGGQTEGEIEIMDIDVNSTTPGGSDGRPYVVHPTTLEALFQMAYAAFDNQSDGVKKALLVT
DIEELLLDASISHTPGARLQTSARSSRLGFREMLADVTVSPTASNAGGISVRGLTCVEMPSTAGVNSDVGITGREGYDSMLSKFVWKPALNLLSATEREHLLIAATKVTDAETEAILAREAAD
FQNVKSALQASQRGKTGSLKLRNALKWISQELPDAKVFGKALENVSQDGQGAGPTGPIVDVLSGTSTPDVLLSGYGSTEKFLAALPGVKVSLQKMYQLVSIMAHENPDLAVLEIGSGSSG
EEDTSIFSTTDIPTTIKYTRAVATPEILRNLQEFSPPAGPIPRFTVLDLEQDLADQGIDLASFDIIIGNNVLSNSRNVENVLRRTKSLLRDEGNMCFVELTKPSSRAVPVLGVVCDWWKRGDDG
LRRPLSSDSIKDILTEQGFTLDFLSPDFVDPAIQQSSLVFASSSAENLPTASATDDADDEEIYILISPELKSPDAVVQNVASSFQHSQIVTWGAGVDFKGKYIISLLELYDPFINHLTEEDFDILKKLV
TQASSLLWVTGIPEPHASTILGFARVVRFEIPSLDFRVLTLDPATIEDAKKNSIHISQVQRSKSPDKEYKELDSIVHIPRVTVDASLNHQISNLCLSEAIESKPLGSLERPQKLCIRNPGMLNTLCF
QADNVSENELQDDEVEVRVMASGLNSKDVMVALGHITDTHLGLEASGVVLRVGASVTHLQLGDKVVMLANGAHRTTLRGKAAVCQKIPQDMTYEEAAGFPFAYCTAYYTLLHVLRAQ
SGQSVLIHAAAGAVGQALVRLAQHLGLEVFTTAESADDRAFVQELLGLFPDRIYHPQDKGLVQHVMRITGDVGVDFIVNPLSVEEIADSLNCLADFGTFVEMGMENDSRHSTLNTRLFRR
DTTFVAVNLQRVLELRPKLIGEILQKALGLFQDGQVKSVSPSNVYPVSEAEAAIQMFQDNRHHGKITLSYSSEDFVSVLQNPKDSLKLSPDNTYLIAGGLGGIGRSLATLLVDCGARHIAMVS
RSGVTSVEQQQLIDNLSERGAKIGVYKCSIGDANALGRALTQCASEMPPIKGIIHSAVVFRDAVLHNMTYKQWDELLDGKLRGSWNLHALTTSYNLDFFLCIGSFMAIIGGISQSNYAAGSA
FQDGLAHLRQSQGLPAVTIDLGIVKGFGAVEEQGAVGHTLEWREPFGVSEPEVHALIKGALLGQRGNWALDVPAQMINSIPTGGMVRSSGVSQPYYFDDPRFSIMAKIGMDSENSDTQ
ASVSLKELLADAESSDDAVLFVTGAVISKVAKLMQVAEEEIDTGKSLHAYGVDSLVAVEYVSWAKKEVSADITVFDVMASKPIMSFARDLVGKGKWGAAIPACKS

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).

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).
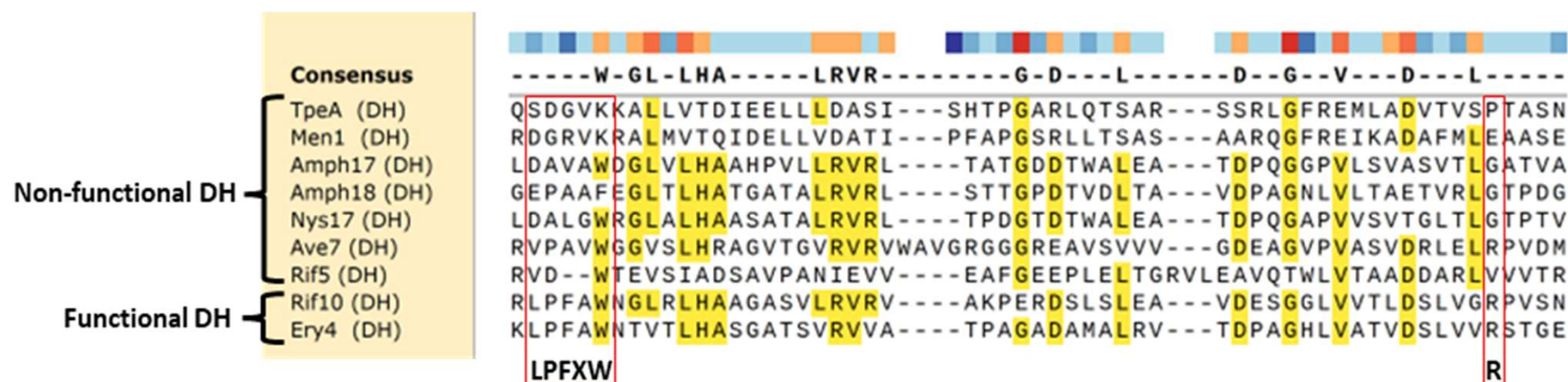
Figure S15 : Protein sequence alignment of the predicted site in DH domains for ACP interaction of TpeA and other functional and nonfunctional DH domains including Men1 and modular HR-PKSs such as Amph17 (AJE44526) and Amph18 (AJE39059) from *Streptomyces nodosus*, Nys17 (AAF71767) from *Streptomyces noursei* ATCC 11455, Ave7 (BAA84478) from *Streptomyces avermitilis*, Rif5 (AAC01711) and Rif10 (AEK39124) from *Amycolatopsis mediterranei* S699 and finaly Ery4 (CAM00064) from *Saccharopolyspora erythraea* NRRL 2338.
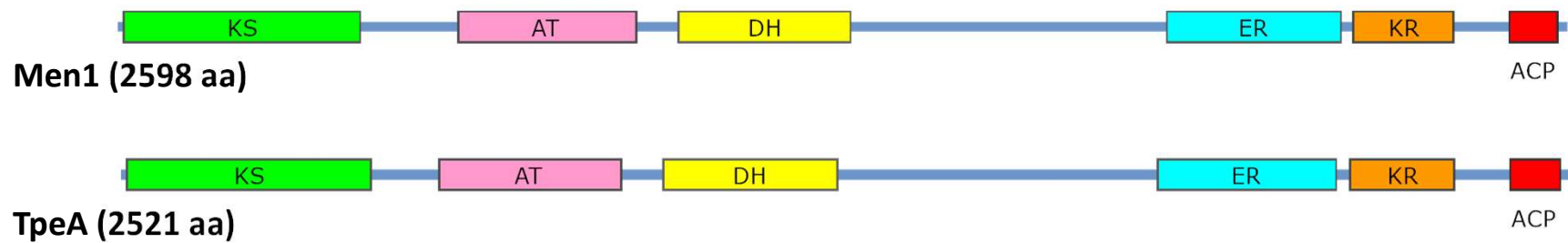
Men1 (2598 aa)

TpeA (2521 aa)

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

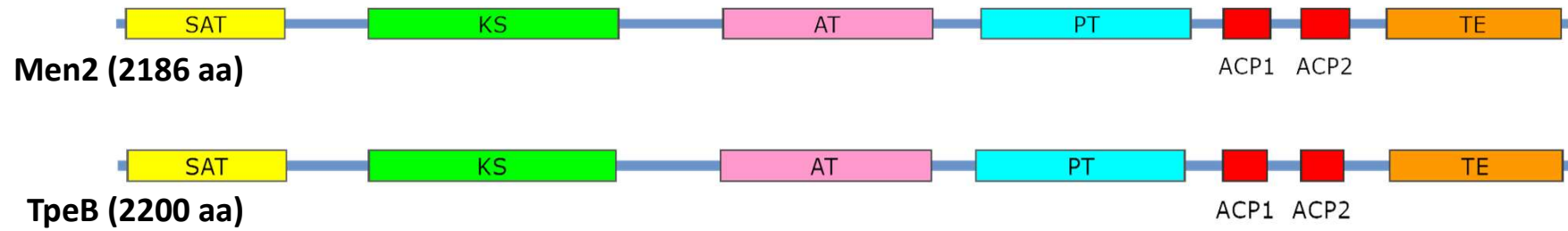| Domains	Size (aa)	Similarity to Men1 domains	E-value
KS	428	79.72%	0.0
AT	318	76.49%	5e-170
DH	302	50.00%	2e-89
ER	313	42.54%	2e-85
KR	181	77.90%	2e-93
ACP	85	70.59%	7e-32

Men2 (2186 aa)

TpeB (2200 aa)

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