



Supporting Information

for

Discovery of unguisin J, a new cyclic peptide from *Aspergillus heteromorphus* CBS 117.55, and phylogeny-based bioinformatic analysis of UngA NRPS domains

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Spectroscopic and spectrometric data of 1 and 2. Bioinformatic data of the biosynthetic gene clusters

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Table S1: DNA and protein sequences of ung” BGC mined from *A. heteromorphus* CBS 117.55.

Gene	Putative DNA sequence	Predicted protein sequence
ungA”	<p>ATGCCGACAGAGAATGGGGAGGTCCAGCACCGGATCGACGGCCTTCAGGATCAGGATACTGTGGAGATATTGCTGGTTACCTTGAATC ATGGGCCCTGCAGGCTGTGGAGGAGTTCAAAGCCAGCAAGGGCATGCTCGAGATAGGCAGCGTGAGCGACAGATCGAACGATGCCCC TAAGGTGAAGATTGAGCTAGATGGGGAACTGAGAATATATTGGCGCAATTGCGAGGGGAATGGGTGCGCCAGCTGGTGCACCAGCAC CACGAAGCAGCCAGTAATTTTGGCGCTCCATAATTTGGATGGCAGCCAGAGAGGCTGCTGGTCTTGGGTTATGGAAAGGAGGG AAGCCTGGGTGTCGGAGGAGGCGCCTAAGAGCTGGTCCAGGAAAGGAGGTGTGCACCCTTCTAGAGATGCATTGCCAGGCTCGCC CAGAAGAGCTGCAATTCATATCGTCTCGCCTCCTCTGTTGCGGCGCAAGCATTGTGCAGCACCTGGATTTGCGGATCCGACAGTCCA TTTCCAATCGCAGTCTCGCAGACGTGCCGGTAGAGACTGTGCCCTGCCGCTCGGACAGCGAGCTCAGGGCCATCTGGGGCTGGAATGG CACGCTTCTGAGGGAGTGCAGAGATGCGTTACAGATATCATCGCCAGCAGGCGGACTGCGGCGCACACGCGCCAGCAGTCTCGCCT GGGACGCGAGCTGGACTATCAGCAACTGGATCGGATCTCCACTCGATTGGCCATTACTGGTGCGAGCTGGGTGCTGCGCCAGATGAT ATCATCCCCCTGCTTCGAGAAGTCCAAGTGGATGATGGTGGCCATTCTGGCCGTGATGAAGTCAGGGGCTGTATCGCTGCCCTGGAC CCGACACAGCCGAGGATCGCCTGCGAAGCATTGTGAAGCAGCTGCAGCCAGCTGGATTCTGACATCGCCGCCAGATCGAAGTGG CCGACGCTCGAGATCAGCAATGTCATCGTCTCGACGAAGCGCCCTACGGCAACTGCCAGACTCGAAGGAAGACATCTCCATGC GTTGATCCCTCCGTAACCTGTACATTGTTTTACGTGCGGCAGCACTGGAACGCCAAGGGAGTTCATGATCAATCACACCAACTTTAGC AGCGCCATCGCCTACCAGCATGAGGCATTGGGGATGGATAACCCGCGGAGTGTTCGACTTCGCTTCATACGCCTTTGATCTGGCCTGG GGGAACATCATCCATACCTCGCGGCGGGGGGTGCTATGCATCCCAAGTGAAGTGAGCGCCGTGGAACATCGCCGAGGCAATCC GCAGACTTGGGGTGAACCATCTCCAGCTGACCCCCAGTGTGCTCGCCTCATCGATCCGCGAGATATCCCCGAGTGCATGGATCCTCC TGATCGGAGAGCCAATGACCCAGGCGGATGTTGCTCAATGGAGCCATACTGCAAATGATCAATTCCTACGGCCAGCGGAATGCACG GTGGCGGTGACCTCCAGACAATCCCCACGGCCGACCTTGGGACTCGAGTATGGGAAAGGCGTGCAGTGCAGTACCTGGATCGTTG ACGAGGAGCATGGGGAGACACTGGTCCCCCTTGGCCACACAGCGGAGTGTGGCTGGAAGGACCGCTGGTGGCCAGGGATATCTAG GAGACTGGAGAAGAGCGCGGAGTTTCATCGATAGCCCTGCCTGGCTGACCCGGGAATACCAGGGGTGCTCCCGCGCCGCGAG GCCGACTATATAAAACTAGAGATCTGGTGCCTACAACCCGACGGCTCGCTGGTTTACGTGGCTCGCAAGGATACGCAGATCAAGATCC GGGGCCAGCGGTGGAACCTGGGCGATGTGAATATCACTGAAGCTTGCAGTCCCGACAAGATTCATCTGTTGCAGCCGAGGCCAT CACCCCGCGGGGTAGCAGCAGCACCATCCTCGTCGATACCTGGCCCTCGGCGAAGAAGCAACTGGCGCCGCGGAGAGCACCCGGGA GAGTCTAGCCAGTTGCCTGCATGGGGTGAAGAGTACCTGGCCGACCGACTGCTCGCTACATGGTGCCAGCTGTATCTTGCAGTCC CCGAGATCCCATGACTGCCACCGCAAGACAGACCGGCTACGCTGCGTGAGATCGGGTCTTCTTAACCTGGATCAGCTGGCAGCC TTGCAGCCTCGCGAGCAGTGGAGATCAAGGCTCCCGAGACCGAGATGGAGCACCGCTTCAACAGCTCTGGGCGGCAACATTGAATA TCAGCCGAGCAGCATAGGGACAGGCGACAGTTTCTCCGAATCGGCGGAGAATCGATGGCAGCCATCCGCTGGTGCAGCTCGCCG GAAAGAGGGCATAATCCTGACAGTGGCCGATATTTCAACCACCGCGCCTCGGCGATATGGCGCAAGAAGCCAAACGAGAACGGGCC CAGGACGTGACGACCATCCCTCCCTTCTCCCTGCTGCGTAGGGGCCACGACGTAAGAGATGCCTGCGCGTGGCTGCAGCCGAATGCCG CGTTTCGGCAAACCTCCATCGCCGACCTCTGCCCTGCACCCGCTGCAGGAAGGGCTGTTGGCCCTGACTGTCAAGCAGGCGGGGAA TATGTCGCGAGATGATCAGAGCTTCCAGTGGATGTGGATCTGGCGCGCTTCCGCGCTGACTGGCCCAAGTGTATCATGAAGCGGC GATTTTTCGCAACCGGATTTGAGCTGCCAACGCGGCTCCTGCAGGTGATGCGAGTCCAGCCAGCCGAATGGCCACGCGGGAG CGATCTCGGTATTTCTGGAGTCAGAGAAAGGAAAGCCATGGGACTGGGGACGTCGTTGGCGGGTTGGTCTGGTGTGCGATCAA GCGCAAGGCAAGGTGCTTTCTGCTGGACCATCCACCAGCCTTGATGATGGCTGGTGCCTGCGGCGATGCTGGAACGGGTGGAAG CCATTTATGCGGGTGGCAGCTGCGATATGCTCCCTCGTTTGGGGGTTTGTGAAATATCTGGCGGATGGTACAGTGGAAAGATGCGCAG GGTACTGGCAATCCAGTTCAATGGGATCCAGGCCGAGTCTTCCAGCCTTGCCTCCCAAGACTACCAGCCAAAGTGTGAGGATCTG CTCCAATACCAGTCTCGGAGTGTCTTGGCCCGGGAATGATATCAGGCCCTCACTGCAGTGCGAACAGCATGGGCAATTGTGCGAAG CCGTTATACCAGTCTCGGATGTGATCTTGGGGCCACAGTGTCCGGGCGACAGGCACCGTCCCGTTCGTTGAACGCATGCGCGGT CAACCATGCGACTGTTCCAGTCCGCGTGAATGTGCAGGGGGATGCCACGGTGGCCAGTTTGTGATGCGAGCGTTTCAGACACAGGCCGT</p>	<p>MPTENGEVQHRIDGLQDQDQDVEILLVTLSE WALQAVEEFKASKGMLEIGSVSDRSNDARK VKIELDGGTENILAQLRGEWVRLVHQHHE AASNFAASIILDGSPERLLVLRFMERREAWVS EEAPKSWCQERRCAPFLEMHCQARPEELQF HIVSPPVAAQAFVQHLDLRIRQISNRSLAD VPVETVPAASDELRAIWGWNGTLPQGVQR CVHDIIAQARLRPHAPAVSAWDGELDYQQ LDRISTRLAHYLVQLGAGPDDIIPLCFEKSKW MMVAILAVMKSQAVIAALDPTQPEDRLRSIV KQLQPRWILTSPAQIEVAARLEISNVIALDEGR LRQLPDSEGRHLPCVDPSRNLYIVFTSGSTGT PKGVMINHTNFSSAIAYQHEALGMDNTRAV FDASYAFDLAWGNIIHTLAAGGCLCIPSESE RRGNIAEAIIRLGNVHNLQTLPSVARLIDPRDIP AVRWILLIGEPMTQADVAQWTPYCKLINSYQ PAECTVAVTFQTIHPHRPWSSMGKGVACS TWIVDEEHGETLVPLGHTGELWLEGPLVQ GYLDLEKSAASFIDSPAWLTRGIPVVPGRR GRLYKTRDLVRYNPDGSLVYVARKDQIKIRG QRVELGDVEYHLKALPDKIPVAAEAITPRG SSSTILVAYLALGEEATGAAESTRESLASCLHG VEEYLADRLPRYMPVPSLYLAVPEIPMTATGKT DRLRLREIGSSSLTDQLAALQPSRAVEIKAPET EMEHLRQLLWAATLNIPSSIGTGSFLRIGG ESMAAIRLVQLARKEIILTVADIFNHPRLDG MAQEAQRERAQDVTTIPFSLRRRHGDVVD ACALAAAEVRVSANSIADLLPCTPLQEGLLAL TVKQAGEYVRQMVSELVVDVDFRFRAAW AQVIHEAAILRTRIVDLNAGLLQVVVADQPE WATGSDLGHFLESEKGMPLGLTSLARFGLV SDQAQKGLFVWTHHPLYDVGWLSLPAMLER VEAIYAGGSCDMLPSFAGFVKYLADGTVEDA QGYWQSQFNGIQAAVFPALPSPDYQPKCQD LLQYHVASVSWPGNDITASTAVRTAWAIVAS RYTQSPDVFIFGATVSGRQAPVFPVERMAGPT IATVPRVNVQGDATVASLMQSVQTQAVA MIPYEQTGLNQIRRNISDADQATQFQSLVQ QPPSSKTSRRPDECLFRVDLADGDEFRSINTY</p>

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GTCGCTGCTGCTGGACGAGGTCAGCAAGGCCTACCACGGGACCGCGAGCGACGGCCTGTCTCCTTCAAGACAATGATCAAGTATGTG

DAISIRVLKRELCAAYDDALPADPGPRYSYIS
HLQSLPTTEAKEYWQTLQAGAQCIFPTLNE
PIAEPKDAAAVTSPLISPETDQALRQFCRSHA
LTPANVFLAWMLVLRYSSESVCYGYLISGR
DVPIHQVDRVGPFINMVMVNHVEIDSNRLL
AMLQEVQAGYLGSLKYNQYPLAEILHDLSTE
GQPFNTVLSVQSGGRADSAQPPDPTITLE
NETWHDPNEDIAASVLLDDNPRITLNSR
HLLSERQASAVGATFVEALANIVRHPDRNLC
DLETTISPQDLATIWDWNAKVATLSSSPEL
FSRWVKQPDQAQVCAWDGDLTYRQLDEG
SSRLAHHLLARGVPRQJILPLCFEKSRRVPA
MLGVLKAGCAVVTMDPEQPVERLQLVQKT
QGILTSPACQGLASQLRPEAVVDGRSLER
MPQDPPLSLPTIHPTDRLFLVSSGTTGTPKG
SVMISHQNACSAVHHQARLGLPPAARMID
CLSYAFDAPWFNLFHFSSGGCLCVPSDQQR
KDNLAGCIESLKANYALLTPSIARVLDPAVPG
LETLAFGGEAIRAEDISRWHEVKLMGYGYS
ECTVSTIHQFESKTEPRMLGYSSGLTAWVV
DPLQGRRLAPLGLATGELCEVGLVQGYIDE
PQKTAASFVEDPSWLLRGGGPDFGRRGRV
YKTGDLVFRFPDGSLLVGRKDTQVKIRGQR
VELGEVEHHRQTLPAVDVPPVVELVHPHA
SANPVLVAFPLVPGKEAAGSSEMRVLDRYT
HGVEDRLMARLPSYMPRMYIPVPAIFTTT
GKTDRRSLQRVASSYTLQLAALQPSRDTRR
APTAMERRLQGMWATILDI DAVTIAATDSF
LRIGGDSIGAIRLVRLAAEQDILLTVAIFKSPIL
CDMAQVATLGSTSGPHDIPPFLLKQDQVDS
QARLQVAAWCELSPSAVEDILPCTPLQEGLLS
LTVKNQGAYVNRQVLRLREVDLGRFQTAW
NQVAMATSILRTRIVDLPQGQLVQVVTSEVP
RWNHGRSLDALVQDDLQRPVTLGTLATFG
LVDAGDVGGDRQRVFLTLHHALYDGSLSL
LLEDESKAYHGTASDGLVSFKMIIKYVTELGA
EADSYWQGSGLDGLVAEPFALPSPMYQPRA
QDILEHNVGLRLWLNHHITPATTLRAAWAI
LTHTYQSADVLFGSTVTRQAPIHRVGLVEG
PTIATVPVRIAIQEKATLAGLLDQVQEYSVDM
IPYEQVGLQRIRLSADTERACQFQTLVVQP
APEPSATDGPALFHAEDDLSQAALSSFSNY

<p>ACAGAGCTGGGTGCCGAGGCGGACTCCTACTGGCAAGGCAGCCTGGATGGTCTGGTGGCCGAGCCATTCCCTGCCCTGCCCTCTCCAT GTACCAGCCACGCGCAAGACATCCTGGAGCACAACTATTAGGGCTACGGTGGTTGCAAAACCACCATCACACCGGCAACCCTC TTCGCGCGCTGGGCCATTCTACAACCCACTACACCAATCTGCGGATGTCCTTTTTGGATCGACCGTGACTGGACGCGAGGCTCCCA TTCACCCGCTGGGACTGGTGAAGGGCCGACAATTGCAACTGTGCCGGTCCGCATTGCCATCCAGGAAAAGGCTACCCTGGCAGGCT ACTCGACCAGGTCCAAGAGCAGTCTGTGCATATGATCCCTACGAACAGGTGCGGGTTCGAGCGAATCCGGAGGCTCAGCGCCGACACC GAGCGAGCTTGTCACTTCAGACGCTCCTGGTGGTGCAGCCAGCCCCGGAACCGAGCGCCACAGATGGACCTCTGCACTGTTCCATG CAGAAGATGACACTCTCAGCCAGGCGGCTCTCAGCAGCTTCAATTACACGCTCTCTTGTGCAATGCCAGCTGACGGCCACGGGGTG TCCATGCAGATGAGCTACGACTCGCATGTCATGGCACAACCGCAGGTGCAACGGCTGGCCCCGCGAGTTCGAGCATCTAGTACGACTCCT TTGCGATGAGTCTCAGCACTCATCCTCTGTTGCTCACATAGATGCGGTCTGCGAGGATGATCTGCGAAGGATCTGGGCGCTGAACCTCCC GCCCCGGCCAGAGTGGACGCTCATGCAGACTTGATACCGAGCAGGCCACGCGCGGAGTCTCACAGCCGTCGCTGCATG GGATGGAGAGCTCAGCTATCGCGAGCTGGACGAGCTCTCCACCCAGTTGGCATATGGCCTCGTCAACTTGGGGTGGCCCCCATGCG GTGGTGCCTCTGTCTTTGAGAAATCAATGTGGATGCCCGTGGCAATGCTGGAGTCAAGAAAGCCGCGGTGCATCGGTGGCCATGGA TATCACGCGCCAGAGGACCGCTTCGACGGTAGTGCAGCAGGTACAGCCTCCTCTGGTCTGAGCTCCCTGGAGGCAGAGGACCTG GCACGGCTCTGAGCGATAGGCCGTCACGTTGCTCTCAAGACAGACTGCAGACGACGTCGCTGGGCGAGCGCCAGGGCGGCCAA TTGCCCCAGTTGAGCCGACAGACAGGCTGTATATTGCCTTACCTCAGGTAGTACGGGGTCCCGAAAGGCGCGGTATGTCCACCA GAACTTACCAGTGCCGTGCACCACCAACCCTCGAGTTTACTGCGTCCGCCAGGGTGTGTTGACTTTTCTGCTCCTACGCGTTCGATG TTGCTGGTGAACCTTCTCCATACGATGGCGGGGTGCTGTCTGTCATCCCCTCCGAAGAGGAGCGCAAGAGCGACATCACTGGCT GCATGCGCCGCTGGCCGTGACTTATGCGAACTCACGCCATCCACCGCAGTCTGATCGATCCGACGTCCGTCGCCAGCCTCCAGACCC TCGTTCTGGTCCGAGAGCCGGTGGCACAGCAGGACATCACTCAGTGGAAAGCCACGTCAGCTGAAGAACGGTTATGGCCCTGCGG AATGCAGCGCCATCTCCACCAGTTCGATCTCGGGCAAAGTGACCACGACCCGGCAACCATGGCGCGGAGAGGAATGGTGACCTG GGTGGTTGAGCCGACCGAAAGCCGACATTTGTCGCCGTACGGGGCTGTGGCGAGCTGTGGGTGGAAGTCTCTGTTGGATTAGG GTATCTCGGCCGTCGGATCTCAGTGCTGCAAGCTTCGTCGACAACCCCCATGGCTGCTGCGCGGGGACCCAGGGGTTCCAGGTC GACATGGCCGCTTACCACCGGCTGACCTGGTGGGTATAATCTGGACGGCACCCTGGTCTGTATTGGCCGAAAGATGCCAGGTC AAGATCCGCGGACAGCGGTGGAGCTGGCCGAGGTCGAGCATCATCTGCACCAGGCTTACCTTCCGCCGCGTGGACGTCTCTGTGG CAGTCGAGGTCATACCCTGCAGGGCAGTGCCAATCCACTGCTAGTCGCTTTGTGGCGATGGGGGAGCGGCCCTGGGCCGCGG AGACTGTCCGAGCAAAGCTGGCTCTTACAGCCAGGGGGCCAGGGAGCGCATGGCAGACCAGTGCCTCTACATGGTGCCAGTCT GCTTCTCCGGCGTTGAAATTCCACGAGGCCACGGGCAAAAGAGATCGACGCGGGTGCCTGAGATGTGGGCTCCAAGTCCCTG GAGGAACTGGCCGAGCTGCAGCCGACCAAGGGCAACCACCAAGCACCGACGACAGACGTCGAACGGCGGATTCTGCAACTGTGGG CGAGTGCTGAATATCAGCGCATCGAAGATCAGCATTACGATAGCTTCTTCGCCCTTGGCGGGGACTCAATCCTCCGCCATGCAGCTCT GGCAAAGGGCCGCTCCATCGACTCCAGATGACTGTAGGGGACATTTTCAAGTACAAGACAATCGCTCGACTGGCTCTCAGCATCTCC CAGCAGTGAATCGGCCGTGTACATGCCCCAGAGGGCCAGGGTGCCTCTTTGCCCTGTCTCTATCCAGCAGATGTTCCGTCGATGC AGCAGGGGGTTAGCAACCATTTCAACCAAGCTTTTTCTGTCAGGTACGTCGACCGTCCAGCTCAGATCCAGGCGGCTGTGGAT GCCCTGGTCGCCATCATGGCATGTTGCGCGCGCTTTCAAGTGCAGCAGGGAGAATATCGAGCGAGTGGATTCTGCCCCGGGGA CCACAGGAAGTATCGCGTTTGCAGCATGAGGTTGCGGGTCTTACGGCAGCCTCGCGGTGATCAATCACAGCCAGGAGTCGCTAGA CATCCAGAACGGTCCGCTCATGGCGTGCATCTGATCAATGCAGACGAGGGCCAATACCTTTTCTGGTGGTCCACCACATGGTCTGCA CCTGGTGTCTTGGAGAATCATCTGGCTGATCTGGAAGAGCACTTGACCACCGCATCCCTCTCCGGTTCACCTCGATGTCCTTCCAGAC CTGGTGCCAGTTGACGGCTGACCACCACGCGAGAGCCCCCTTTCGAGCTGGAGGCTGTCTGCCAAAACGGGGCTCCGCTCCGCTGCTG CCACAGTACTACTGGGTGAGGTCAGGTCGCGAGCTTAAACACATTGATAACATGATCAAGGATGGCGTGGTCTCGGCAGGCAGGACAC AGAGACCTTGTAGGGCTGGAATGGGCATTGACACAAAATGGTGGAGCTCCTCATCGGCCATCCTACATTCCTTTGCCAATGT CTTCCAGACCGGGCACCTCCGACGGTATTACGCGAAGGCCATGGTGGGAGCCCTGGAGGTCTGCAATCGATATTTACGCACGGTGC GGTGGTTTACCAGATGTTCCCTGTGGTCCGCACAGCCAAGAAGGGAGATAGTATTGCCAGCATTGTGCGCCATGCAAGGACCGTCA CGCCAGATACCCGATAATGGCCGGCCATACTTTGCAAGCCGCTTCTACTCCGGTGGCAAGCGGGCTTCCAGGTCAATGGCCCTGTC</p>	<p>ALLQCQLTATGVSQMMSYDSHVMAQPQV QLRLARQFEHLVRLLCDESEQHSSVAHIDAVCE DDLRRRIWALNSPPPARVDACMHDLITEQAQ RRPVSQVAVAWDGELTYRELDLSTQLAYGL VNLGVGPHAVVALCFEKSMWMPVAMLGV MKAGGASVAMDITQPEDRLRTVVQQVQPP LVLSLEAEDLARRLSDRPVHVVSQDRLQTT LGGGQGGQLPPVQPTDRLYIAFTSGTGPVK GAVMSHQNFSAVHHQTALEFTASARVDF SSYAFDACWLNFLHTMAAGACLPISEERK SDITGCMRRLAVTYANLTPSTARLIDPTSVPSL QTLVLVGEVPAQQDITQWKAHVQLKNGYGP AECSAISTTFFDLQSDHDPATIGAGRMV WVVEPTESRHSPYGAUGELWVEGPLVGLGY LGRPDLAASFVDNPPWLLRGGPQGFGRH GRLYRTGDLVRYNLDGTLVLCIGRKAQVKIRG QRVELAEVEHHLHQALPSAAVDVSVAVEVIT LQGSANPLLVAFVAMGEAALGPRETVRAKLA LYSQGARERMADQLPVYMPVSLLLPAVEIPT TATGKRDRRLREMWASKLEELAELOPTKG NHQAPTTDVERRILQWAECLNISASKSIHD SFFALGGDSISAMQLSAKGRSIDLQMTVGDIF KYKTIARLALSIPAVESAVLHAPEQGASFAL SPIQQMFADMQQGVSNNHFNQSFVQVRRP VTLPQIQAADVLAHVHGMRLRARFKSRENI WSQWILPPGTTGSYRVCQHEVAGLQAASAV INHSEQSLDIQNGRLMAVDLINADEGQYFL VVHMMVVDLVSWRILADLEEHLTTASLSGFT SMSFQTWCQLQADHHAESPFLEAVLPNGA PPPLLPQLDYWGQVRSNLTFDNMIKDGVL GRQDTELLGPANAADFQTMVELLHAILHS FANVFHDRAPPTVFSEGHGREPVSAIDISR TVGWFTTMFPVATAKKGDSIASIVRVKDR RRQIPDNRPYFASRFLTPAGKRAFQVNGPV EVIFNYLGLYQLERSDALFHMREMPDGDV DMADISGSLFRFALVDISASVTDGLHVD YNRHMQHQASIRAWIKECRQSLHAAQELP LIQPSYTLCSFPLLRMTDPALAILQRLTELDL AYGQVEDIYPCSPQLDGLMSQIKNPDLRTR IRWMAQSAQGSTAVDTNRLKHAWQVVD RHPALRTIFVDSISGRGLKQVVRNLRADV HIVQSADEASIEDMSPTKGTSSVLTSTNS</p>
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<p>GAGGTGATTTTCAACTACCTCGGGCTGTACCAGCAACTCGAGCGGTGGACGCCCTTCCACATGCGCGAGATGCCGGACGGGGTGG ATGACATGGCTGATATCTCGGGGAGCCTGTTCCGATTGCTCTGGTGGATATCTCGGCATCGGTGACGGATGGCTGTTTCATGTTGACTT CATGTACAATCGGCACATGCAACACCAGGCTCCATCCGCGGTGGATCAAGGAATGCAGGCAGTCCCTCCACGCCGAGCGCAGGAG CTTCTCTGATACAGCCAAGTTATACCCTCTGCAGCTTCCGCTGCTGCGCATGACAGACCCGGCATTGGCAATCTGCAGCAGAGGCTG ACGGAGCTGGACCTCGCATACGGGCAGGTGAAGATATCTACCCTGCTCGCGCTCCAGGATGGAATCCTCATGAGCCAGATCAAGAA CCCAGACCTCTACAGGACACGCATCCGGTGGATGGCACAGTCTGCACAGGGATCAACAGCAGTTGATACCAACGGGCTCAAGCACGGC TGGCAGCAGGTGGTAGACCGCATCCAGCCCTGCGCACCATCTTGTGACAGCATCTCGGGCAGGGGACTGAAGGATCAAGTGGTGG TGAGGAATCTCCGGGACAGACTCCACATCGTCCAGTCCGCGGACGAAGCAAGTATCGAGGACATGCCCCAACAAAAGGCAAAACCAG CTCAGTGTCACTCTGTGACGACGAACCTCGGGCTCTGTGCGAGCTATCGATCAGCCATCGGCTCATCGACGCCCTTACCTTGGGAAT CCTCAAGCAGGAGCTGTGTGCGCATATACTGGCCTCTTCTCTTCCCTGGACCCCTGTATAGCGACTACATCCACTTTCATCCAGTCCC TGCCCGCTGGGTACGCCGCGGCATACTGGCAGGAGCATCTCCAGGAGGTCAAGCCCTGTCTATTTCATCCTTGGGCGGTCTAAATACG GAAGGCCGGCGGTGCAAGCTCACATCCCTATTACCTTCGAGCGAGAGCTACACCTGGCATTGCGCATCTTTGTCATGGAGCATGGACT GACGGTGTCTAATATCTTCATGTCGCTTGGGCCCTGGTCTGCGGGCTTATACTGGTTGGATACTGTCTGCTTTGGCTATCTCACATCAG GCCGAGATATTCTCTGCAAGGGGCTGACGGAAACCGTTGGTCCATTATCAATATGCTTCCAGCCGCGTGGACTGGGCAGTAAGGAC TCGCTGATGACCCCTGGTACAGAGGGACAGGAGCAGTATCTCAACAGTTTGGAGTTTCAGCATTACCCGCTGGCCAAGATCTCCACTT GATTGATACGCCGAGAAGGGGCTTTCAACACCGCATGTCAGTCCAAGCTAGTACTGCTGCCAAGGACTGCCAATCGGCTATATC GCTTGTAGATGAAGGAGGAGATGATCCACCGAGGTAAGAAAAGATAAGAAAGACTTTTTCTTTGTGTGACTGCGCTAATGCGAGACTCA GTATGATATCATGATAAACATTGGCGTCCGAGACGAGGACACCGGATGCAACTTTACCTTTAACGAATCGGTGATATGACCCGCTATGCA AAGAGTGCCATCGACTGTTCTTGACGCCGTCTCACATATTGTTACAGCAGCGGACCAGACGGCCAGGAAGCCAATTTATCATGACAA GCAAGACCTGCAATCGATCTGGCAGTGAATGCCGCCGTAGCAACGCCTCTGGACTGGTGTTCATGAATTTATCATAGAGCAGGCAG AGAAACAACCGCGCGGTGCCATCTGCGCGTGGATGGTAATCTACGTATAAGCAACTCAACGATCTGTCCACGCAGCTGGCAGTGC CACATCCGACAACCTGGGTGTTGGGCCAGGGGTTAATGTCCCGTTGCTCTTTGAGAAGTCGCGGTGGATGTCGGTTGCCAGTCTGGCGGT CATGAAGGCTGGTGAACCATGGTGGGCTTGGATCCTGGTCCAGCTGCGAGGAGACTACGAAGTATCATCGATCAAGTCCAGCCTTGTCT TCATTTTACTTTCGGCCGAAATAGCAACAGCGCGGACGCTTTTGCATCCTGCCATGTTGTCCGGGTGGATGACGCCAGTTTGGCCAG CTGGCCACGCCGTGCAATGCTCTGTTACCCCGGTTGACCTGCCAGCAGCTATACTGGTATTACCTCTGGGAGTACAGGCGTGCCA AAGGGTGTGGCCATCAGCCATTGCAACCTCAGCACCAGGATTACTACCAAAAGCGCATCTTGAACCTTCTGTGCGCTGAGGGTACTT GAATTGCTTTCATGATTCGATGTCCTCGGGTACAATCCTTACACCTTGCAGGCTGGTGGCTGCTGCTGCGTGAAGAGTTCG GAACGCCGCGGAGATATCAGTCCGCAATGCGTCCGATGGAGGTAAGTACGCGCATCTTACTCCATCTGTTGCGCGTCTTCTGAACCT TCCAATGTGCCGCTCTCCAAACCTCGTCTTGTAGTGGAGAAGCCGTATCGCGAGCGGATGGAGCAGTGGAGCCGGCACGTCATCT GATCAACCGGTACGGCCCTGCTGAGGCCGCGTATGGGTGATATCGCACACCTCGACTCAGCATTGTCCATGCCCTCCATCGGAAAGGG GGGTGGCTGACCACGTGGATTGTTGACCCTAGTGCACCCGACCAATTAGCCCCAGTGGGCTGCGGGGTGAGCTCTGGCTGGAAGGT CCACTAGTGGGAGTGGCTATCTCACGACCCGAAACGAGCAGCGGCTTATCGAGAACCAGGATGTTGCTCCAAAGGAGCAG GAGGGCCCATGGCCCTGGCCGACAGGACGGCTTTATCGGACTGGAGACTTGGCCCGGTATACACCCGAGGGTTCGATTGTTTATATT GGGAGAAAGGATAAACCAGATCAAGATCCACGGTCAAAGGGTGGAGTTGGAAGAGGTAGAGAAATATTGAGCAAGCCATGCTAAACA GCGCCGACGACACGAGTCCCTGTGGTAGCAGCGGTGTCACCCCTCAAGGAAGCAAGAGGCAATTCTGGCAGCTTATCTGGCTCT GGGTGAGCCGGCCACGGGCTCTGTGAAATTTGCGCAAATCTCTCAGCAGGTACTGTTGGATCATCAACCCGGCCTTGGAAAGAGAGC CTGCCGACCTATATGAGCCGAGCATCTACATCCCGTGGCGGAGATCCCACGACTACCAATGGAAGGCTGACCGCAGCAAACCTCGC AACCATGGCATCAGTGCAGTCTGGCTGAATGGGCTGGCCTTCAACCTCTGAGGGCAAATGGCGCCTGTATGCTCCGGGGGAGC TGGGCTGACAGAGACTGTTGCTGAAGTGTGAATATGGACCAGAGCCTAGTAGGCATGGACGACAGCTTCTTCTGCTCGGCGGTGAT TCCATTACCGGATGACGCTGTGCGCAAGTCCCAATCCAGCCTTCTTATATACGGTGGGCGATATATCAAGCACAAAGACCGTGCAC AACTGGCAAGCAATGCAAGGCAGACAGCGACACCTCCGTGCAGCTCCCGGAAGTCCCAACAGCTGTTCCGAGCTGTCGCCGATCCA GCAGCTATTCTTTCCTCGCAGGACAAGGGCAAGAACCTGTTAACAGTCTTCTGGTCCGCGTTCGCCGCTCCCTGAATCCCAACGA</p>	<p>GVLCELSISHALIDAFTLILKQELCAAYTGLLS SSLAPLYSDYIHFIOQLPAGSAAAYWQEHLQE VKPCLFPSLGLNTEGRRSQAHIPITFERELHL ALRIFCMEHGLTVSNIFHVAWALVLRAYTGLD TVCFGYLTSGRDIPLQADGTVGPFINMLAS RVDLGSKDSLMTLVQRDQEYQNSLEFQHYH LAKIFHLIDTPEKGLFNAMSVQASDSGPKDC QSAISLVDEGGDDPTEYDIMINIGVGEDDTG CNFTFNESVIDRYAKSAIDLFLHAVSHIVQHA DQTAQEANFISKQDLQSIWQWNAAVATPLD WCVHELIIQAEKQPAAAAICAWDGNLTYKQ LNDLSTQLACHIRQLGVGPGVNVPLLEKSR WMSVASLAVMKAGGTMVGLDPGQPAGRL RSIIDQVQPLIITLTSAGNSNSAAAFASCHVVR VDDASLAQLATPCNALLPPVPASSLYLVFTS GSTGVPGVAISHNSLSTAITHQKRILKLSVAS RVLEFASYAFDVSWGTILHTLAAGGCVCVPEE SERRGDISAAMRRMEVNYAHLTPSVARLLNP SNVPLLQTLVLSGEAVSRADMEQWSRVHHLI NAYGPAEAAVWVIFAHLDSLMPISIGLVRG CTTWIVDPSPRDQLAPVGTGALVLEGLV GRGYLHDPERTAAAFIENPRWLLQAGAGAH GPGRQGRLYRTGDLARYTPDGSIYIGRKN QIKIHQRVELEEVKEYIEQAMLNSAAAPAV PVVAAVVTPQGSKKAILAAYLALGEPATGSVEI VRKLSRYTGIIINPALEESLPTMYRPSIYIPVAEI PTTTNGKADRSLATMASSRTLAEWAGLQT SEGKWRPVSSPGLGLQRLFAEVLNMDQSL VGMDDSFSLGGDSITAMQLSAKSQSLLYIT VGDIFKHKTVAQLASNARQTASTSVQLPEVP NSLFELSPIQLFFASQDKGNLNFQSRFLRV SRSLNPNELQKAIQVLAARHSMLRARFVQSA DGWVWQKIVNDSAGCYTFRSHHITLQDME PLLHSSQELLDIVQGPILAVELIDSSHGQYLF MTAHLVVDLVSWRILLGDLEEFIRSGTITGF PPFSFQSWSQLQANYARDHLPPKIALPFKVS PPRHEYWGLVPHGDANTLSDSGRSFTMN KRLTDILMGTANSFDTQPVEILHAALLYAFA QTFQDREAPPLFTEGHGREAWDSGIDLSTRT GWFTTIFPVAASITQNHSLPEVVRVVKDTRR QTPRNGWSYFTSRYLNTDGRQAFQIKGPVEI IFNYMGLYQQLERPDSLQCDIAVTAPPA</p>
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<p>GCTCCAGAAGCGATTGGAGTTTTGGCAGCACGCCATTCATGCTCCGGGCTCGGTTCTGTCAAAGCGCGGACGGCGTCTGGCAGCAG AAGATTGTAACGATTGAGTGGCTGCTATACATTCGCGAGCCACCACATCACCAGCTGCAAGATATGGAGCCCCTCCTCATAGCAGCC AGGAGTTGCTGGATATTGCCAGGGTCCCATCCTGGCCGTGGAAGTATTGATTCGAGCCACGATGGGCAGTATCTTTCATGACAGCCC ATCATCTCGTGGTGGACCTTGTCTCATGGAGAATTCTGCTGGGCGATCTGGAGGAGTTCATCCGCTCGGGCACAATCACCAGGATCCCTC CATTCTCATTCCAATCATGGAGTCAACTGCAGGCGAACTATGCGCGAGACCATTGCTCCAAAGATCGCGCTGCCTTTAAGGTCAGTCC GCCCCGGCATGAGTACTGGGGACTGGTCCCTGGGCACGATGCAAACACCCTGAGCGATTCCGGTTCGAGGCAGCTTCACGATGAACAAG CGCTGACCGACATTCTCATGGGCACGGCCAACCGCCCTTGATACGCGAGCCGGTTGAGATCCTCCACGAGCCCTGCTGTATGCGTTT GCACAGACATTCCAGGACCGCAAGCACCGCCTCTTCCACCGAGGGGCTGGTTCGAGAAGCCTGGGACTCGGGCATTGACCTGTCCA GAACTGTTGGCTGGTTTACCACCATCTTCCCTGTGGCAGCTTCGATTACGCAAACCACAGTCTCCAGAGGTTGGTCCGCGGTGTAAG GATACACGCGGCGAGACACCAGCAACCGGTGGTCTATTTCACCTCGCGTACTGAATACTGAGCAGGCGAGGCTCCAGATCAA GGGCCCTGTGGAGATTATTTTAAATTACATGGGCTTATATCAGCAGCTGGAGCGGCCGATTCCCTGTTCCAGCAGTGTGATATTGCGGT ACAGCGCCCCCTGCTGCTGCGGCGACTCTCTCGCGGTTTGCCTGATCGAGCTCGCAGCATCTGTTGTGAGGGTTCAGTGAAGTTCGA GTTCTTATACAACAGGGAGATGAAAGGACAAGACAGGATACTTGAATGGATCAGCAAGACAGAATCCTCACTCAAAGCGGCAGCGGAA GAACTTCTGTTGCAGAGCCCAAGCTATACCATCTGCGACTTCCCTGCTCTCTCACCGACCAGGGTCTCGACGAGCTTCTCAATAGG GTCTCCCGGCTGTGGGTCTTCTACGCGCCAGATCGAAGACATCTACCCCTGTGCGCCGATTGAGGAGGCGCATCATGAGCCAGGCC AAGAGCCCTGAGCTCTATTGACTCGAGTGGTGGAGCGGTGAGTCAACAGGCACGTCGCCAGTGCATCTCGATCGGTTGAGGCGGG CCTGGCAGATGGTGTGAACCGTCACTCGATTTTACGCACGATATTTATGACGGTATCGGATCCGGCCAGGTGAAGGACCAGGTGGTCC TCAAGGACTTTCCGGTGGACGTCGAGGTCCCTCATGCCGAGCTGCATCAGCTCGCAGAGCCAGTCACTGGGCGTCAATGGCACACCGAT CTGTGAGCAGAAGAGACACCCCGCAGCATTCCCTGGTGTGACGCAAACAGCGTCTGGAGTCGTGTTCTGCGACTTGGAGCTCAACC ATGCGATGGTTCGATCGTATTCTTAGCCCTTTGAGGCAGGAGATCTGTGCGGCATATACTGGCTCACTGCCACACCCGCGCGG CCTACCAAGCGTATATTGAGCAGCTGCAGGGGCTGCCCTTGTGAAGGACAACGCTTCTGGCAGACATATCTTGACAACGCTCAGCCCT GTCACTTTCCGGCCCTCGGCCAGCGGATGTACAGACGGCTCGAACGCCCGCGGGGCTATCCATCTCGTTGGACGCGGCCACTCAT CAAGCCCTGCGTGTCTTCTGCCAGCAGCAGCAGTTACACCCTCGAACGTGTTCTACTGGCTTGGGGGCTTCTTCTCGCGCTACT GGCTTAGACACAGTGTGTTTCGGCTACTTACGTCGGGCGCGATGTCCTGTCCAGGGGTCGATAGGATTGTTGGTCCGCTCATTAA ATGCTTGTCTGTGTTCTGGAATTCAGGACTGGGGCATCGGTGCGATCGGCCATGCAGAAGTCCAGGAAGACTATCTCGCCGCCCTGCA GTATCAATCTACGCCTCTCAGCAAGATCTGCAGCTTCTGGGACGTCGGTTCGGGCGCTATCAATACCGGCATATCGGTCAGGGCGG TGCTACTTCCGCGAACCAGCAGCAGATGATATCATAGTACGCGATCAGACAGGCTGGATTGCGCAGAGGATGTGTTTTGTTCTTCT GTCGTGGTACGATTCCCTTTGCTCTCCATAGCTGACCCGGTCCACAGTACGACATTGCCGTTGCTATCTCCACGATGAGGAGGAGA CGGAGATTGCATTCGACTACATGGCCGTACCTTGTCGACCAAGGGGGTCAAAGCCTTGCAAGTCTTTTTGTTCAAGTTGTGCTGAT GTCATACGTGCTCCGGATCAAACGGTCCAGGCTGTCAATGTGATCAGCAAGGAAGACCTCCAGAGTCTGTGGACCTGGAATCGAACGT CCCGGAAACCGTACAGGCGTGTTCATGATATGATTGGACAAAAGCCTGTGATAGCCCTGATCCCGGCAATCCATGCATGGGATGG CGCGCTTACATATCAAGAGTTGGACCTTCTGTCCACCCGACTGCCCGGTTATATAGACTAGGGGTCGGCAGAATACAGCTCACCCT CTATGTTTCCAGAAAGTCCATGTGGATGCCGTTAGCTGCACTGGCAGTGTGATGAAGACAGGCGCTGATGCGTGGCCATGGATATGACCCA GCCAGAGAAGCGCTGCAGGCGATTGTGGACCTGGTGCAGCCGATCTTCTCGTGCATCCGTCGCAAATCGAAGACCGTCCAGCAA CTGGCAGACACGAAGGCCGTGTTGGCGATTGACCAGGCATTCTTTCCAAATCGCACCTCCACGTCGCTGCTGCGACAGTCTCC CCATCAAGTCTCTCTATACCGTCTTTACATCTGGCAGTACCGGCACACCAAGGGAGCAGTCACTAGCCATGCCAACTTTGCCAGTGCCA TTGTGCATCAAACGGACCTGCTCGCACTGGACCCGATTGCGCGCTTTGACTTTGTCTCGTATGCCCTTGTGTTTCTGTTGCGAACCT ACTCCACAGCTGCGCGCTGGGGCATGTTTGTGCATCCCCTCCGAAGCATGCGCCGGGACAACCTGTGAGGCCATGACAGGCGATG AAAGTGACCATGCCAATTTACCCCGTGCATGGCCGTACAGTGGACCCGGATCAATGCAAGACGCTCAAGGCCTTGATCTGGGCGG CGAGGCCATGTCCAGCACGACATCGCTGTCTGGGACCTTGGGTTGACCTTCTGTTGCGTATGGTCCGCGGAGTGTACGGTTGCCG CCGTCATGGACACAGTCCCTGAGCAGTCCGGACATCGGACTTCCGGAAGATAGGGCGGGGCTTGGTTGGAACACCTGGATTGTCAG CGTATCGGATGGAGAGCGCCTGGCCCGGTGGGCACTGTGGGAGAGCTGTGGCTGGAAGGGCCCTGGTGGGCTGGGCTATCTTGA</p>	<p>AATLSRFALIDVAASVVQGLKFEFLYNREMK GQDRILEWISKTESSLKAEEELLQSPSYTIC DFPLSLTDQGLDELLNRVLPVGLSYGQIEDI YPCAPIQEGIHMSQAKSPELYWTRVRWTVQS TGTSPVDLRLRRWQMVVNRHSILRTIFID GIGSGQVKDQVVLKDFPVDVEVLHAEHLQL AEPVTGRQWHTDLSRRDTPQHSLVLTQTAS GVVFCDELNHAMVDAYSLLLRQEICAAYT GSLPATPAPAYQAYIEHLQGLSLVEGQRFWQT YLDNAQPCHPALGQPDVTDGSNARRALSIS LDAATHQALRVFCQHAVTPSNVFLAWGL LLRAYTGLDTCVFGYLTSGRDVPVPGVDRIVG PLINMLVCVLEFRTGASVRSAMQKVQEDYLA ALQYQSTPLSKILQSGTSGRGLFNTGISVQG GATSGEPDEHDIIVTDQTGLDSPEYDIAVAISH DEEETEIAFDYMAVTLSDQGGQSLAGLQVQV VADVIRAPDQTVQAVNVISKEDLQSLWTWN RTVPETVQACVHDMIGQKACDPSDPAIHA WDGALTYQELDLLSTRLARYLIDLGRQNTAI PLCFEKSMWMPVAALAVMKTGAACVAMD MTQPEKRLQAIVDLVQPDLLVTSVANRKTQV QLADTKAVLAIDQAFSQAIPPTSSCLPTVSPS SPLYTVFTSGTGTGPKGAVISHANFASAIHQ DLLALDPSRVDFVSYAFDVSWSNLLHTLA AGACLCIPSEAMRRDNPVEAMQAMKVTHA QFTPSMARTVDPDQCKTLKALILGGEAMSQ HDIADVWAPVWDLRVAYGPAECTVAAVMDT VPEQSGHRDFGKIGRGLSNTWIVSVSDGE RLAPVGTGELWLEGLVGLGYLDQDEKTA SFIDNPAWLLRGGPGVPRGRRLYRTGDLVR YCFDGSILFLGRKDNQVVRGQRLVQEV HLQAHLSGTTGVVADVVKPQSSNAMLVAY LAVGETIHSPLDSVHAALRPLTQGLTDSLARI PQYMVPSMYLPVAEIPVTTTGKIDRKLHEL GSSLTMEQLAQIQPPQEGEQAPQTDLEKLL QQLWAELS AKLRSAGFRIAPVDFIKLTISR PSAASVQGRMKTTWETREDEFELAPVQ MFVNVVRRKCNHFNQSFLLRITRQVRAEDV RRALDLIVTQHPMLRRAFASDQGGHWTQHI KPYTPGCRYCEHVESLAEASPLLDASQVAL DLESGPVFSGDLLQIRDSGDQYLYLVAHHLAV DLVSWRIILADMEDHLTAKASSFTPMFPQA</p>
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ungD''	<p>ATGGCCATGCTGGTTCGAGGACAATGACAAGTACCCCGGAGTGCATGACTACGCGCTGAATGAGTTGATCCGCGAGGACTTCTGTTCT GGACAACCATTGGACGACGGCAAACGTACCATTTAGGATATCTGTCCATCGGACCGGAATGCCGGCCATAACTTCTCGCTGGAG CTGTGTATGCTGACAAGCAGGCCACTGTTCAAGATGTGGTGTAGGAGCTTGTGCTTCTCCCGTCTACCGCACCCACGACGACTACC AGTACAATAACGCCATGTATATCGTGGCGTGCATCTTATCCAACAGTGCATGGCGATGACCTCGGCTCTATCTTTCAAAGCACATCTGG GACCCTCTCGGGATGAGCAGCAGTATTTCCGCTGGATGATGACTTGGCAGTCAAAGCCCTTGGCAAAGGGCTATGCTTCCGCGA GGCAAGTATGAAGCGGTGGAGTGAAGAAGCAGGCCGAAATCTCCGGCGCGGTGCCATTATCAGCACTGTGGAAGACTACGCGAA ATGGATCTACGCACTACTGAATCAGAGCGGGTGCCTCTTCTCGGAGGGCTACGGAACACTCTGGACCAGGAGACTCATTCCAA ATTCCGAGCCGTTTTTGGCCCCGATGGCGTATGCCCTTGGATGGGACCGTTACATCTACAGGGAGTGGAGATCATCACTCAGATGGGG GGATAGAGGGATTCCGAGCCGAGATTGTGATGATCCCGCGCTAAATTTGGGGTTCATACCATTGGCTAACTCGACTTATCTCCA ATGGGGGAACATGCCTGGCGTATGAGCTTATCGATTGCAAGCTGGGCATCGTGTGGGGGACAGATTGACTGGAAACAAAAGTGTGT</p>	<p>MAMLVEDNDKYPGVQWTTVPNELIREDFVL DNHWTTANVTIEDILSHRTGMPGHNFSLGA VYADKQATVQDVVRSRFLRFPSTAPPRTTYQY NNAMYIVASHLIQTVMGDDLGSIFQKHIWD PLGMSSTYFRLDDALASQKPLAKGYAFAEGK YEAWEWKNRPEISGAGAIISTVEDYAKWIYAL LNQSGPLSSEGYTLWTARALIPNSEPFLAP MAYALGWDRYIYQVVEIITHDGGIEGFGEIV MIPALKFGVITMANSTYSSNYGGTCLAYELID SKLGIAGDRFDWKQKYVDIVDQMDAYNA</p>

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Figure S1: A domain sequence alignment comparing UngA, UngA', and UngA". The table displays pairwise sequence identity percentages for various regions (A1-A7) across the three protein variants. The diagonal represents self-alignments, while the off-diagonal cells show the percentage of identity between different regions of different variants.

Figure S1: A domain sequence alignment comparing UngA, UngA', and UngA".

Figure S2: C domain sequence alignment comparing UngA, UngA', and UngA". The table displays pairwise sequence identity percentages for various regions (C1-C7) across the three protein variants. The diagonal represents self-alignments, while the off-diagonal cells show the percentage of identity between different regions of different variants.

Figure S2: C domain sequence alignment comparing UngA, UngA', and UngA".



Figure S3: A domain AMP binding motif identified in extracted A domains.



Figure S4: C domain active site identified in extracted C domains.

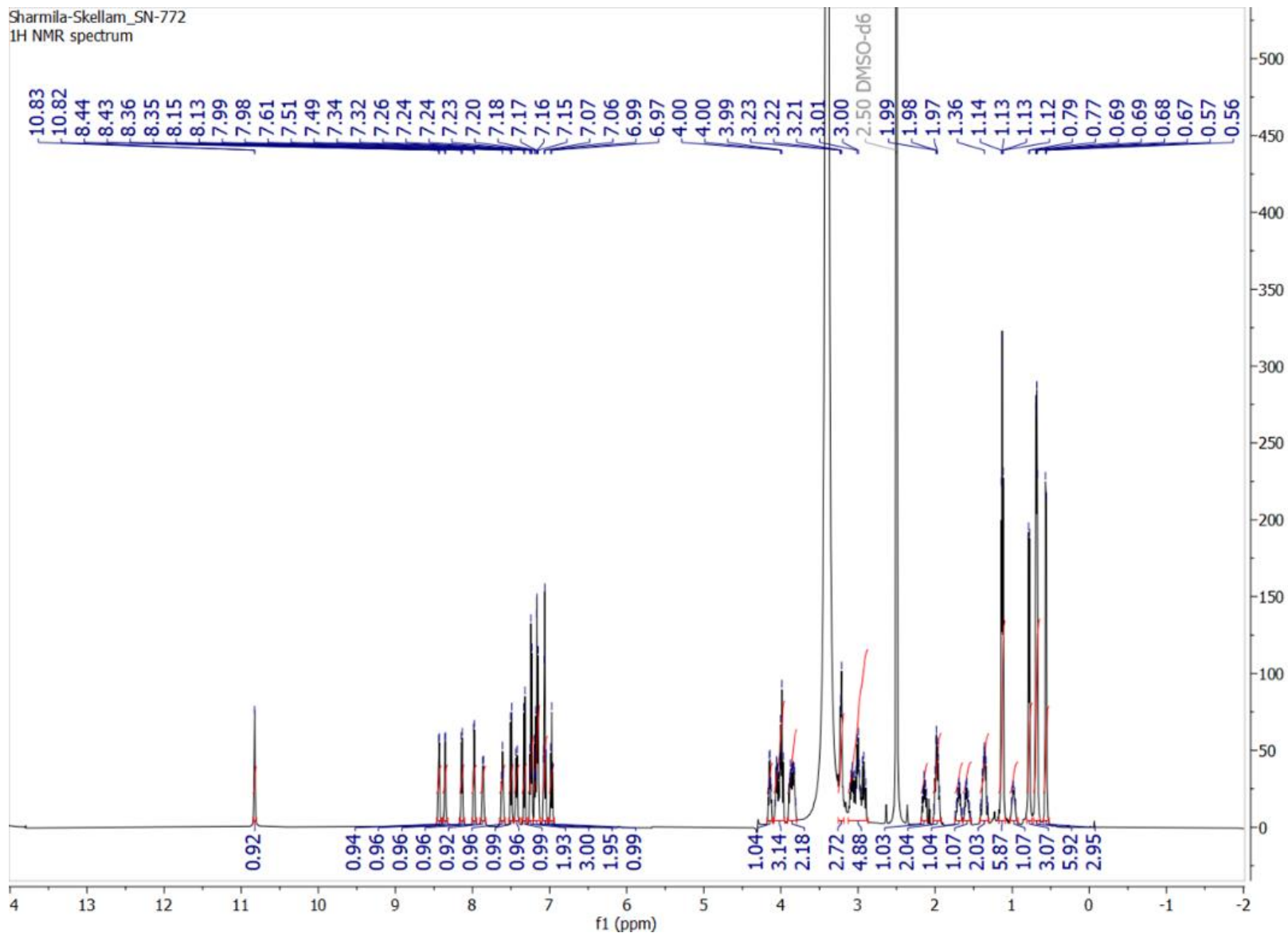


Figure S5: ¹H NMR spectrum of **1** (500 MHz, DMSO-*d*₆).

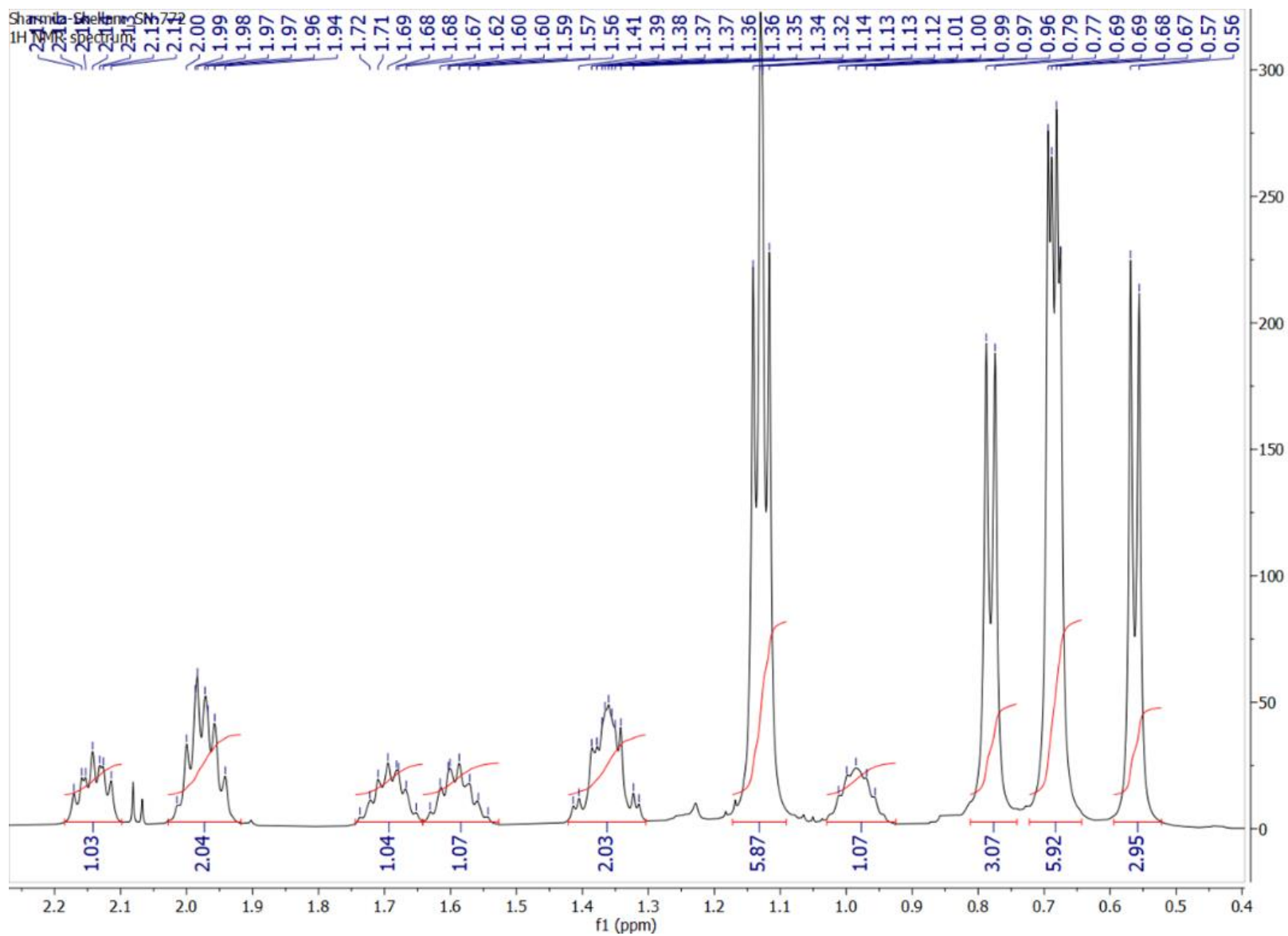


Figure S6: Expansion of the ^1H NMR spectrum of **1** (500 MHz, $\text{DMSO-}d_6$).

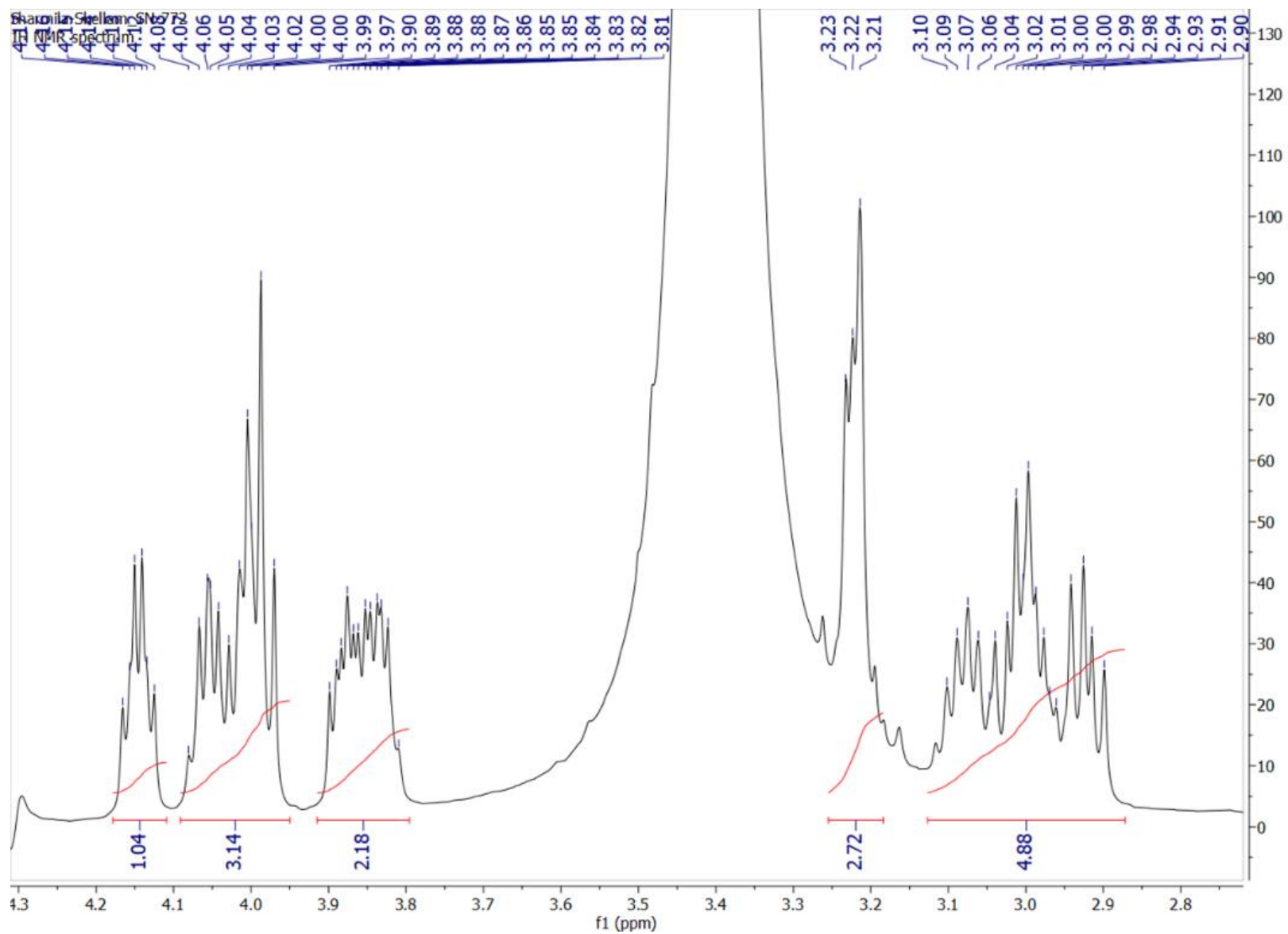


Figure S7: Expansion of the ^1H NMR spectrum of **1** (500 MHz, $\text{DMSO-}d_6$).

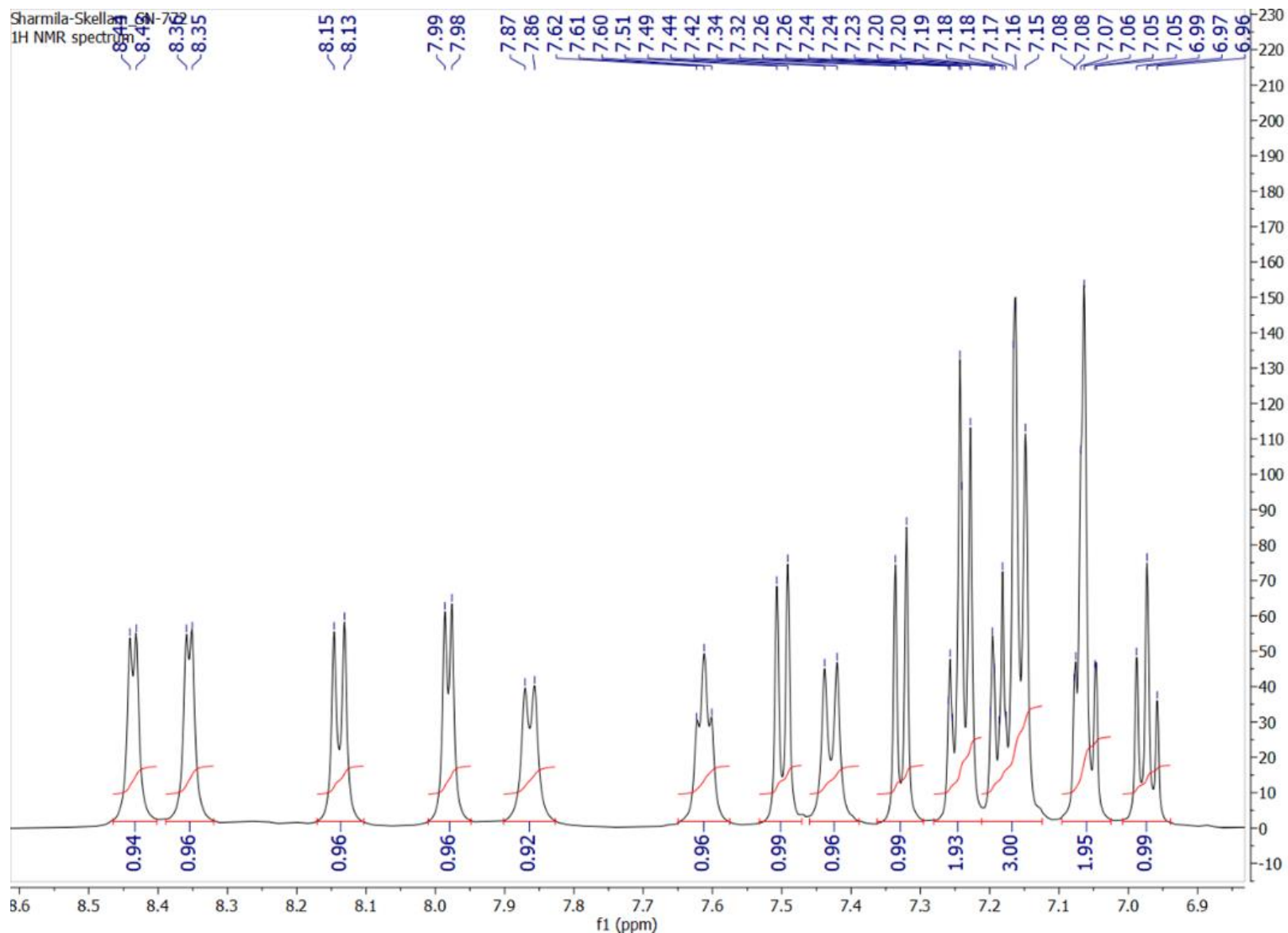


Figure S8: Expansion of the ¹H NMR spectrum of **1** (500 MHz, DMSO-*d*₆).

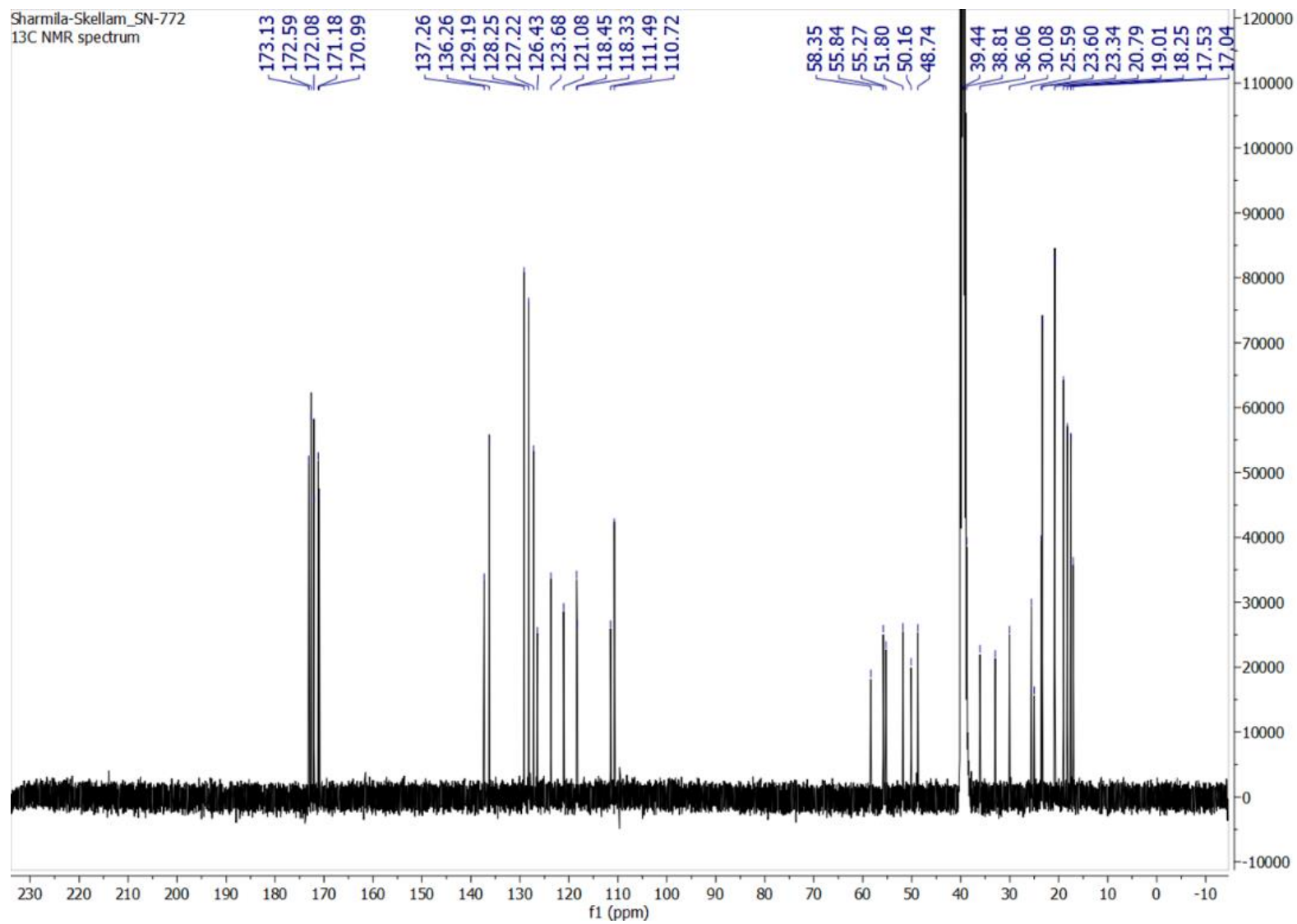


Figure S9: ^{13}C NMR spectrum of **1** (125 MHz, $\text{DMSO-}d_6$).

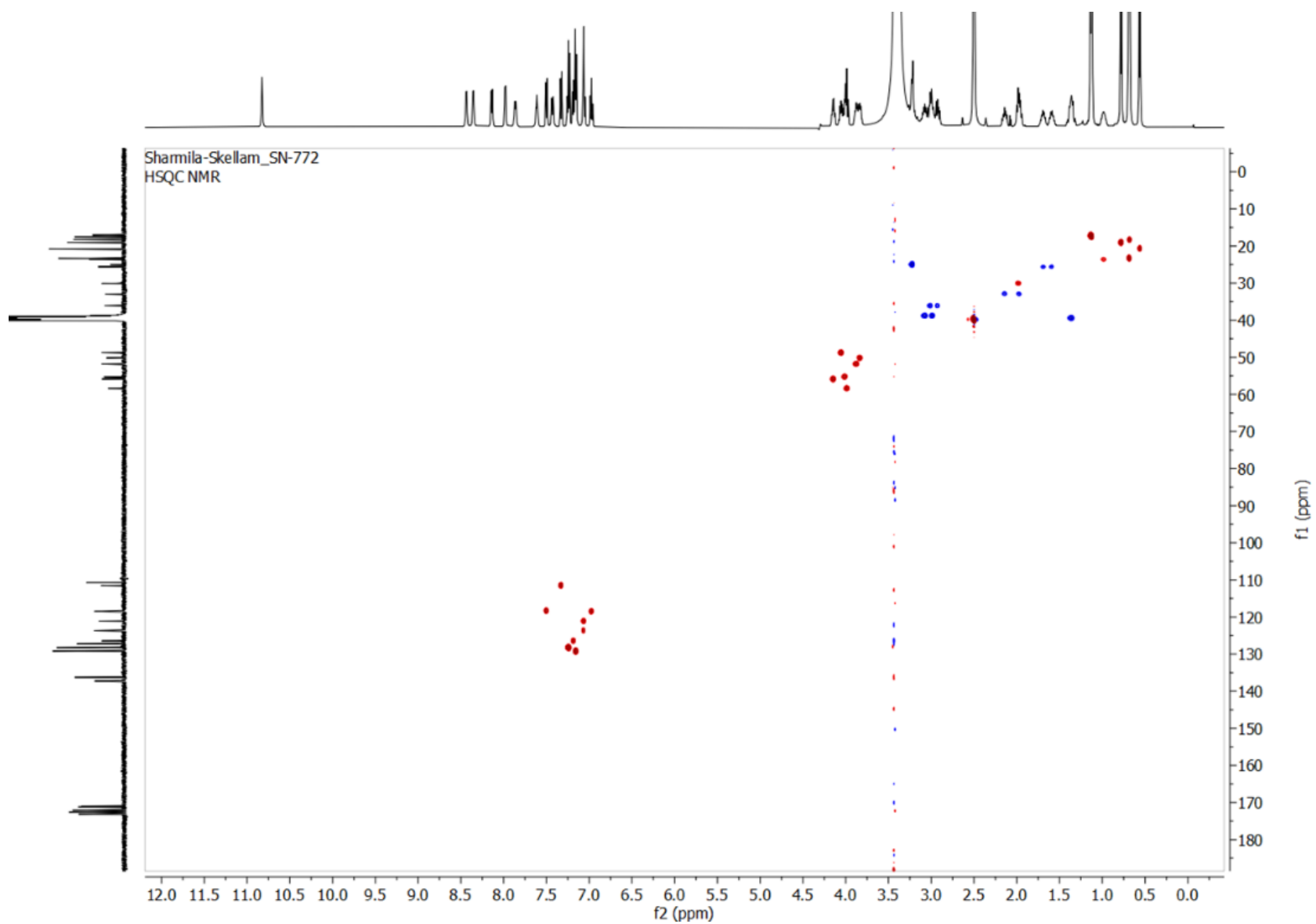


Figure S10: gHSQC spectrum of **1** (^1H :500 MHz; ^{13}C :125 MHz, $\text{DMSO-}d_6$).

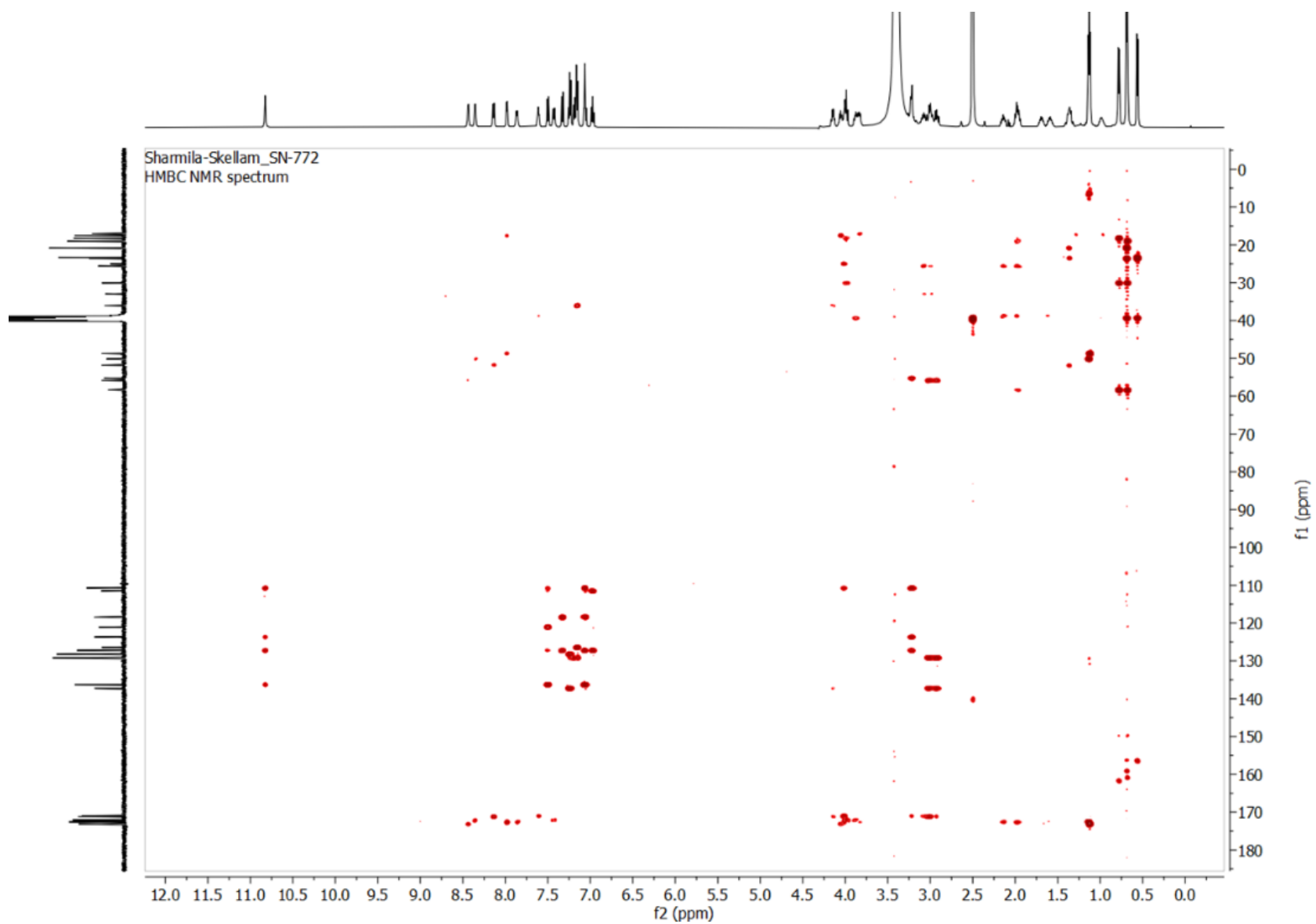


Figure S11: gHMBC spectrum of **1** (^1H :500 MHz; ^{13}C :125 MHz, $\text{DMSO}-d_6$).

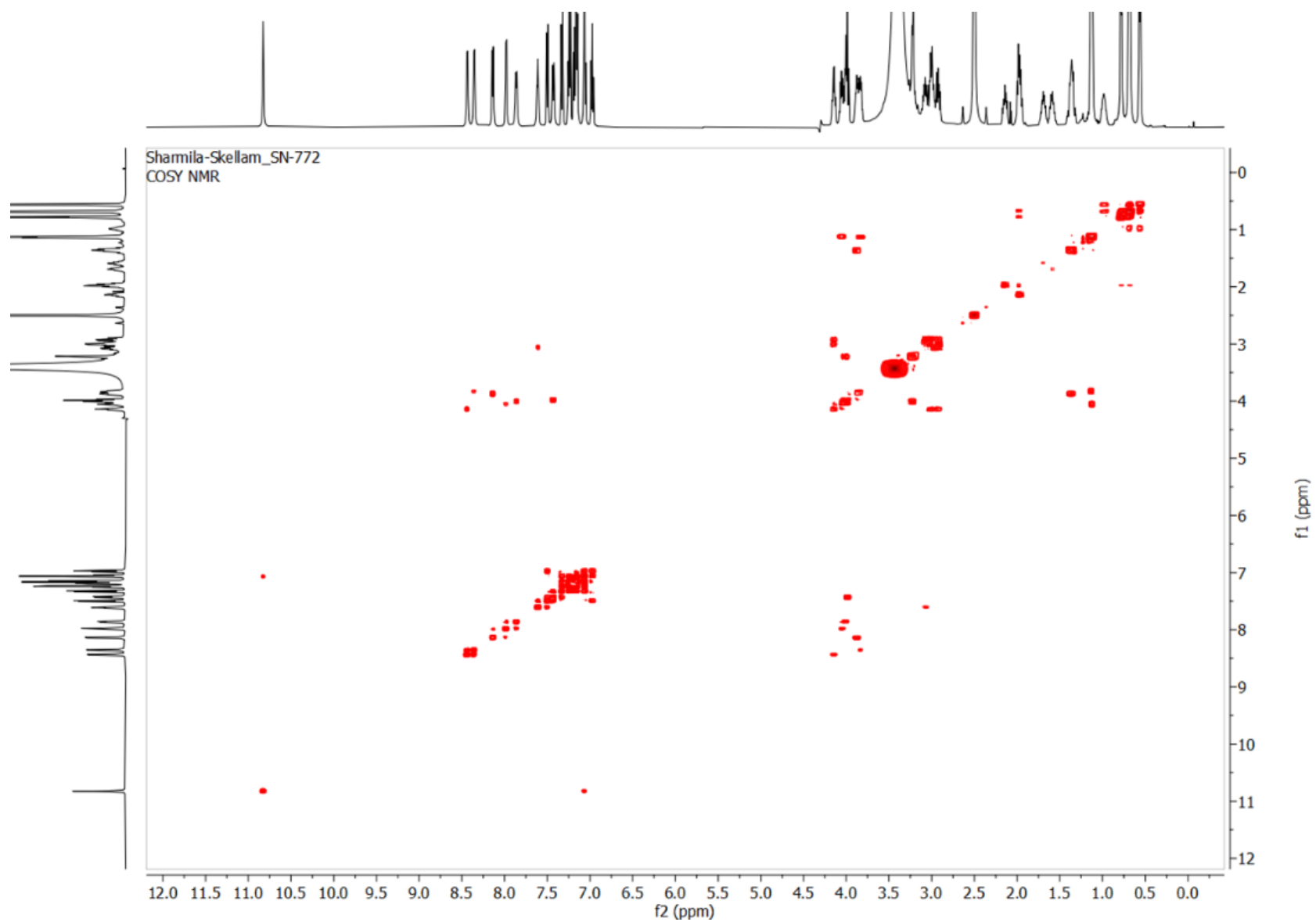


Figure S12: gCOSY spectrum of **1** (500 MHz, DMSO- d_6).

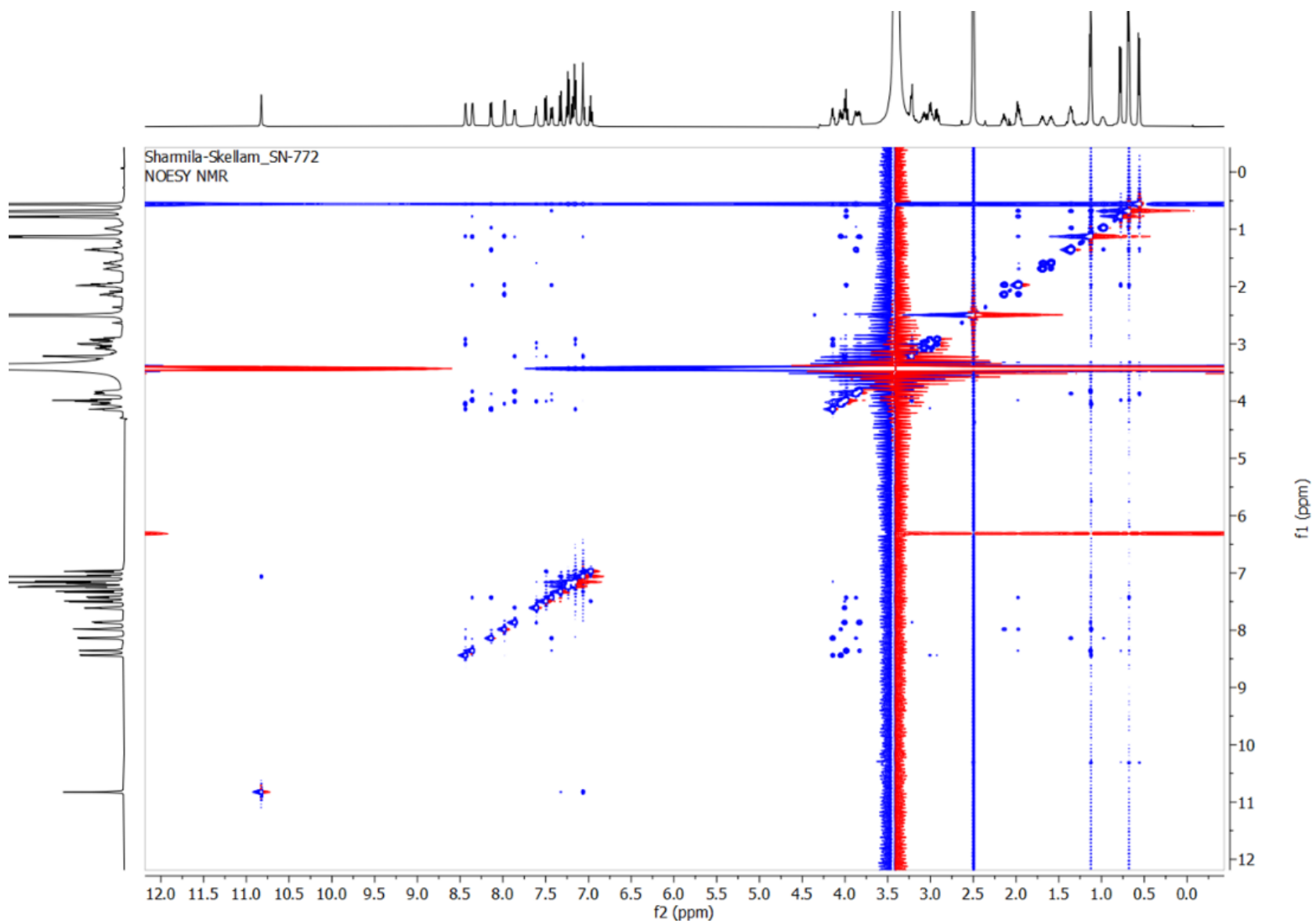


Figure S13: 2D-NOESY spectrum of **1** (500 MHz, DMSO-*d*₆).

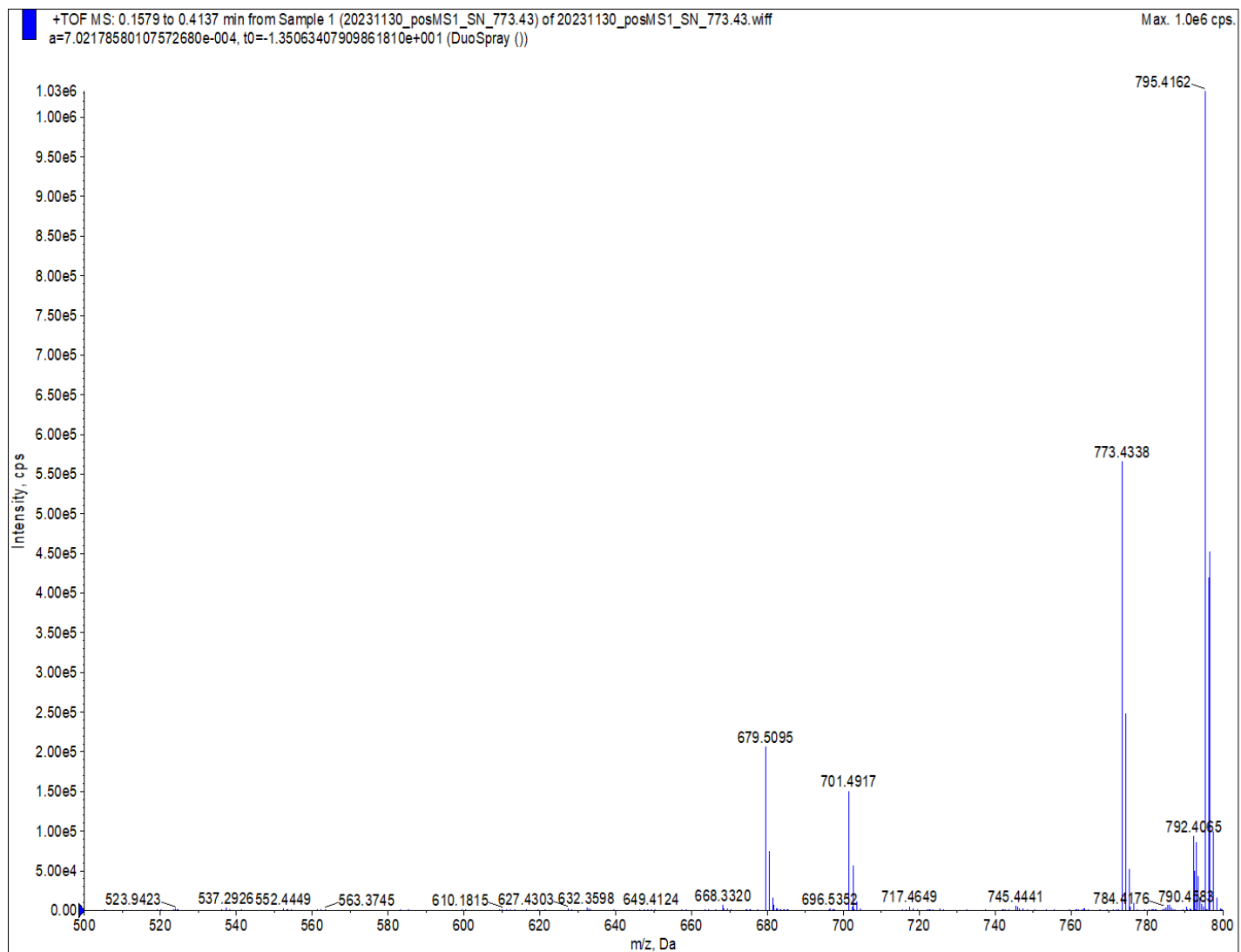


Figure S14: HRESIMS spectrum of **1** in positive ionization mode.

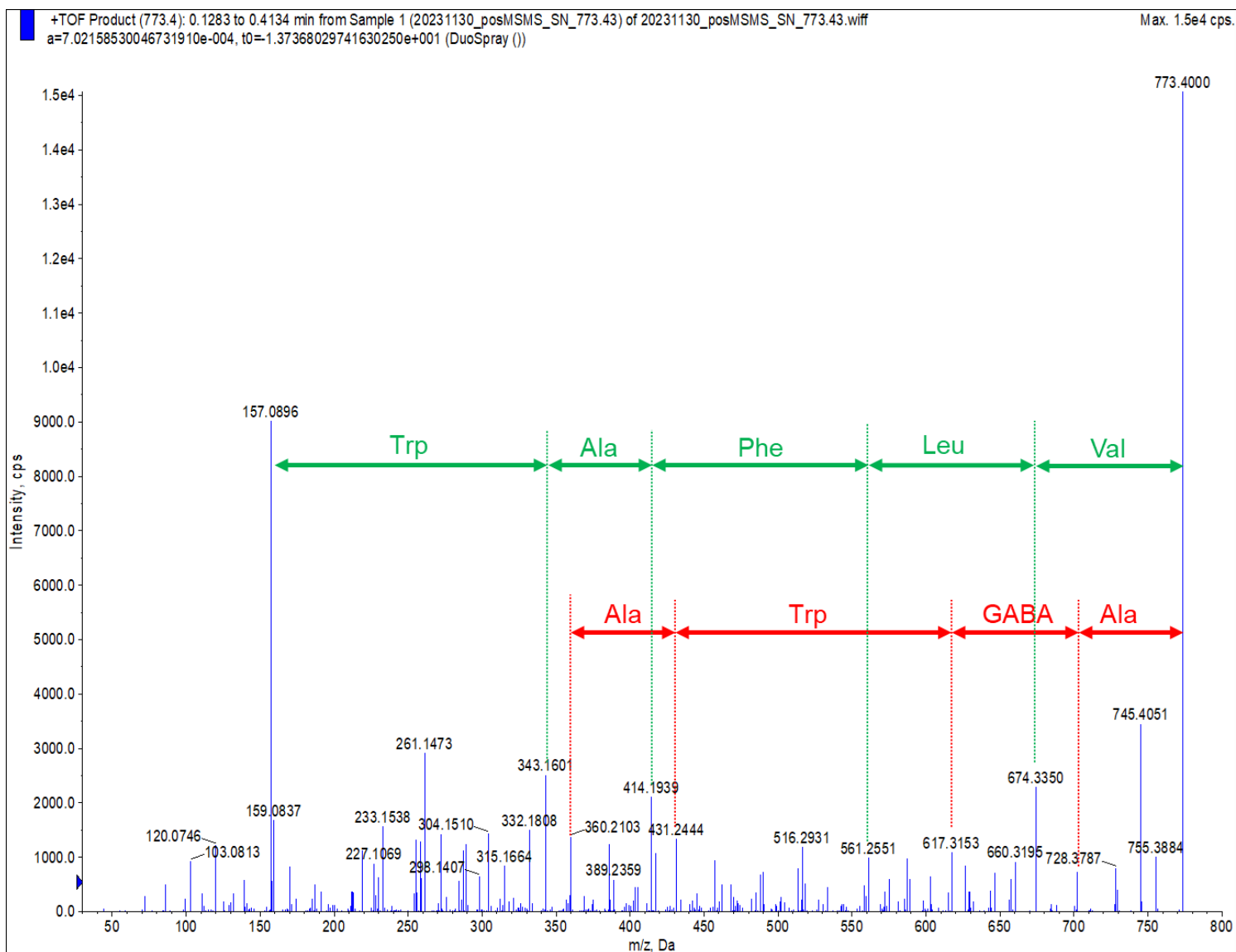


Figure S15: HRESIMS/MS spectra of **1** and fragmentation patterns in positive ionization mode.

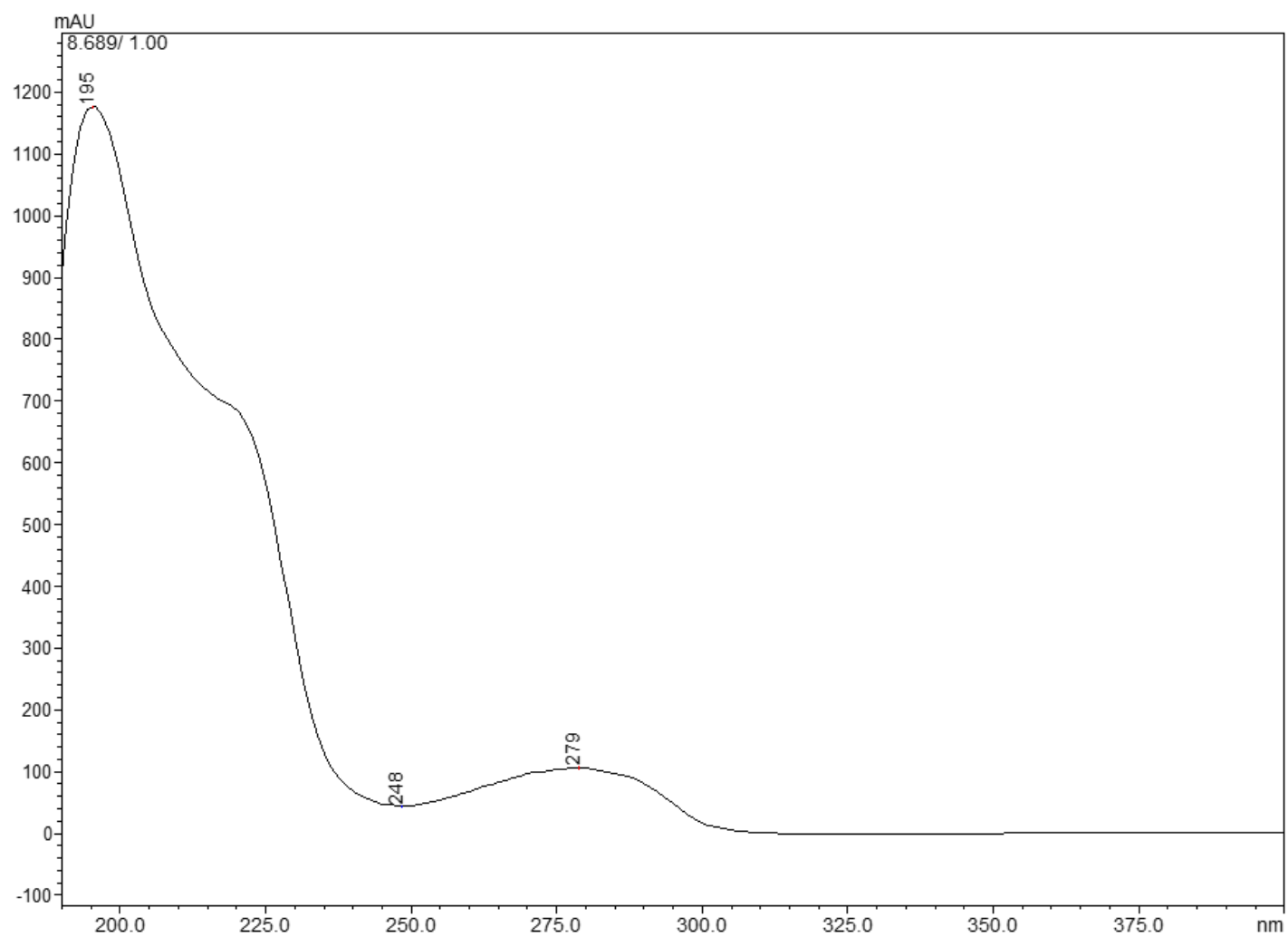


Figure S16: UV spectrum (photodiode array, H₂O:MeCN) of **1**.

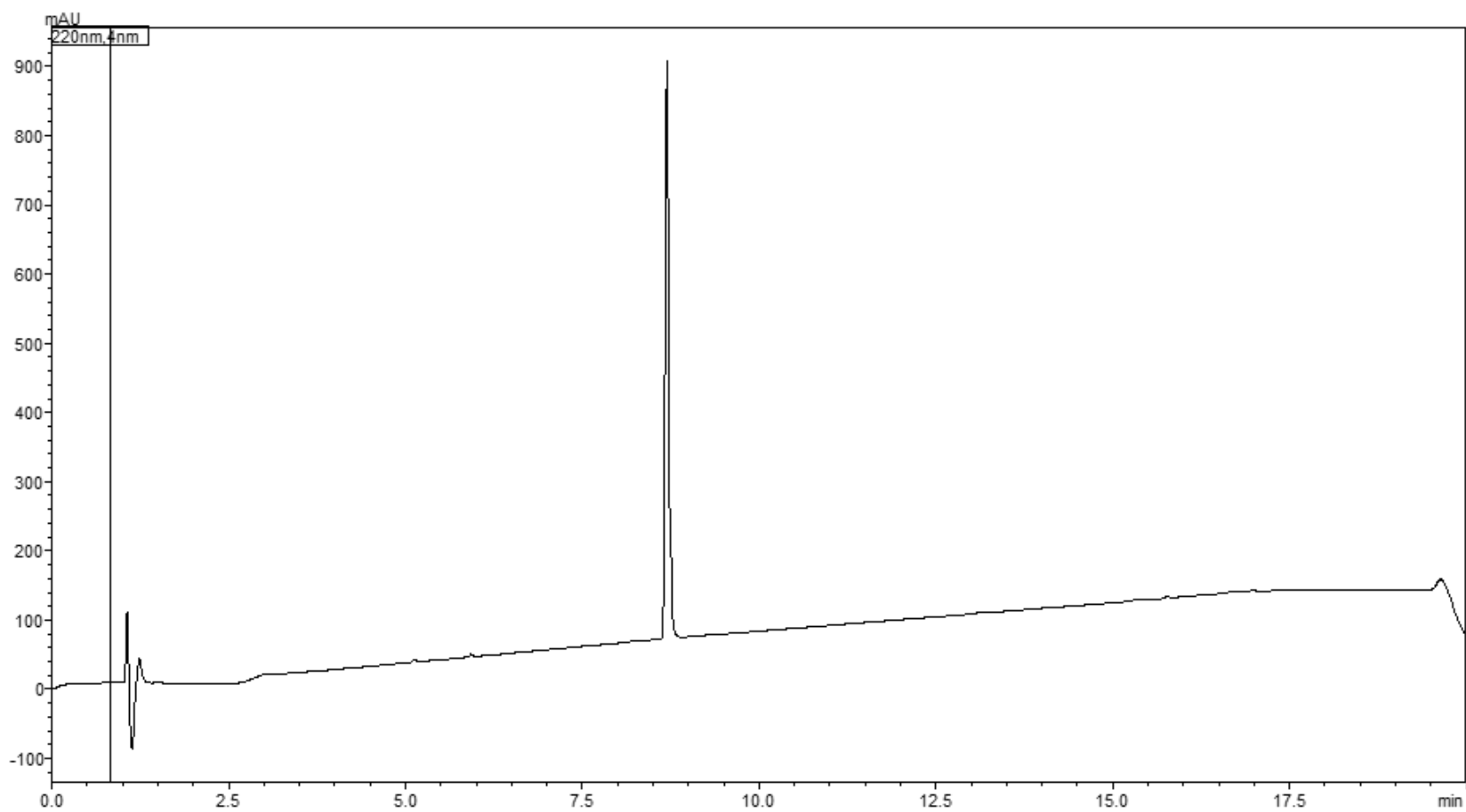


Figure S17: HPLC-PDA chromatogram of unguisin J (1).

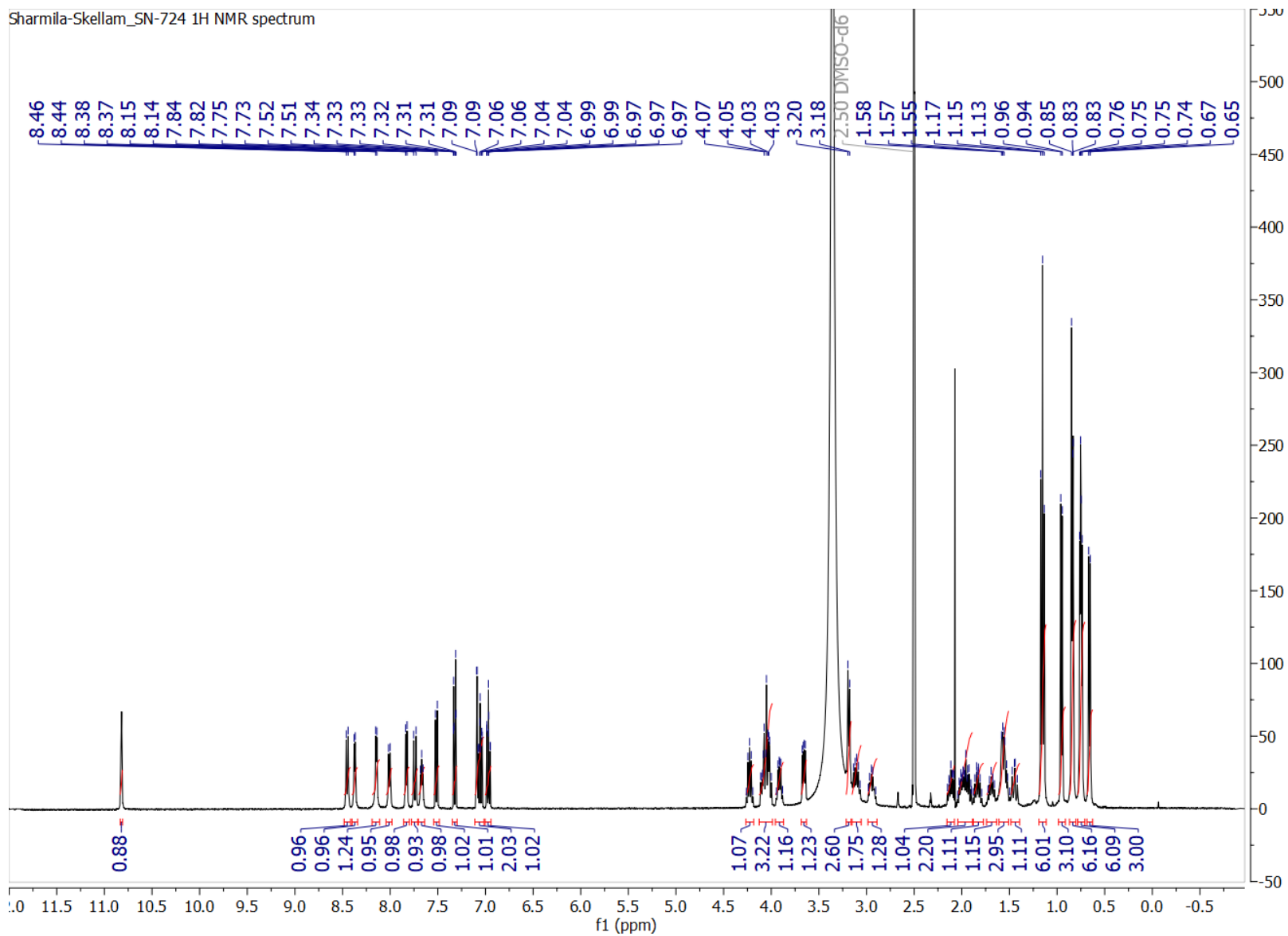


Figure S18: ¹H NMR spectrum of **2** (500 MHz, DMSO-*d*₆).

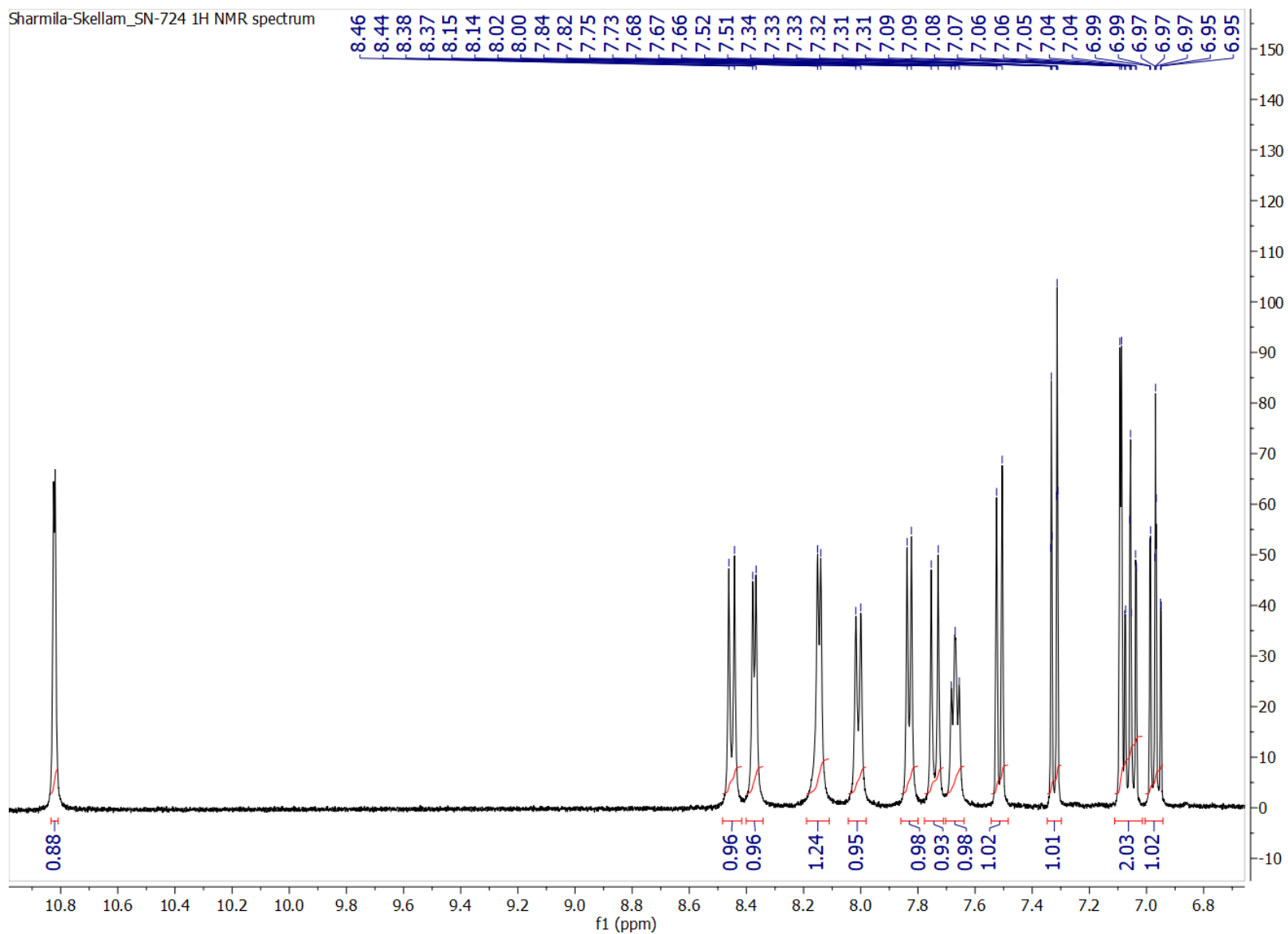


Figure S19: Expansion of the ^1H NMR spectrum of **2** (500 MHz, $\text{DMSO-}d_6$).

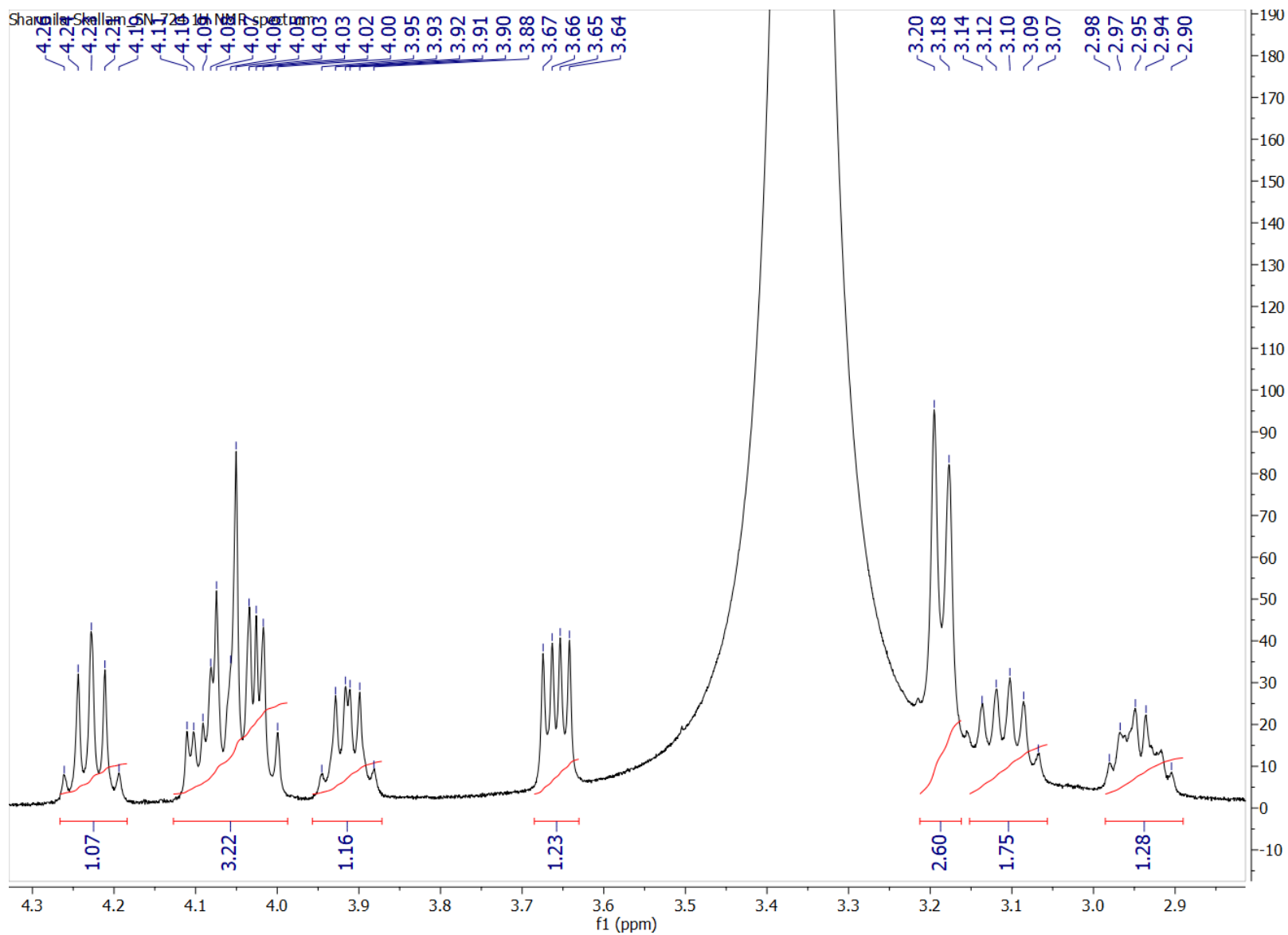


Figure S20: Expansion of the ^1H NMR spectrum of **2** (500 MHz, $\text{DMSO-}d_6$).

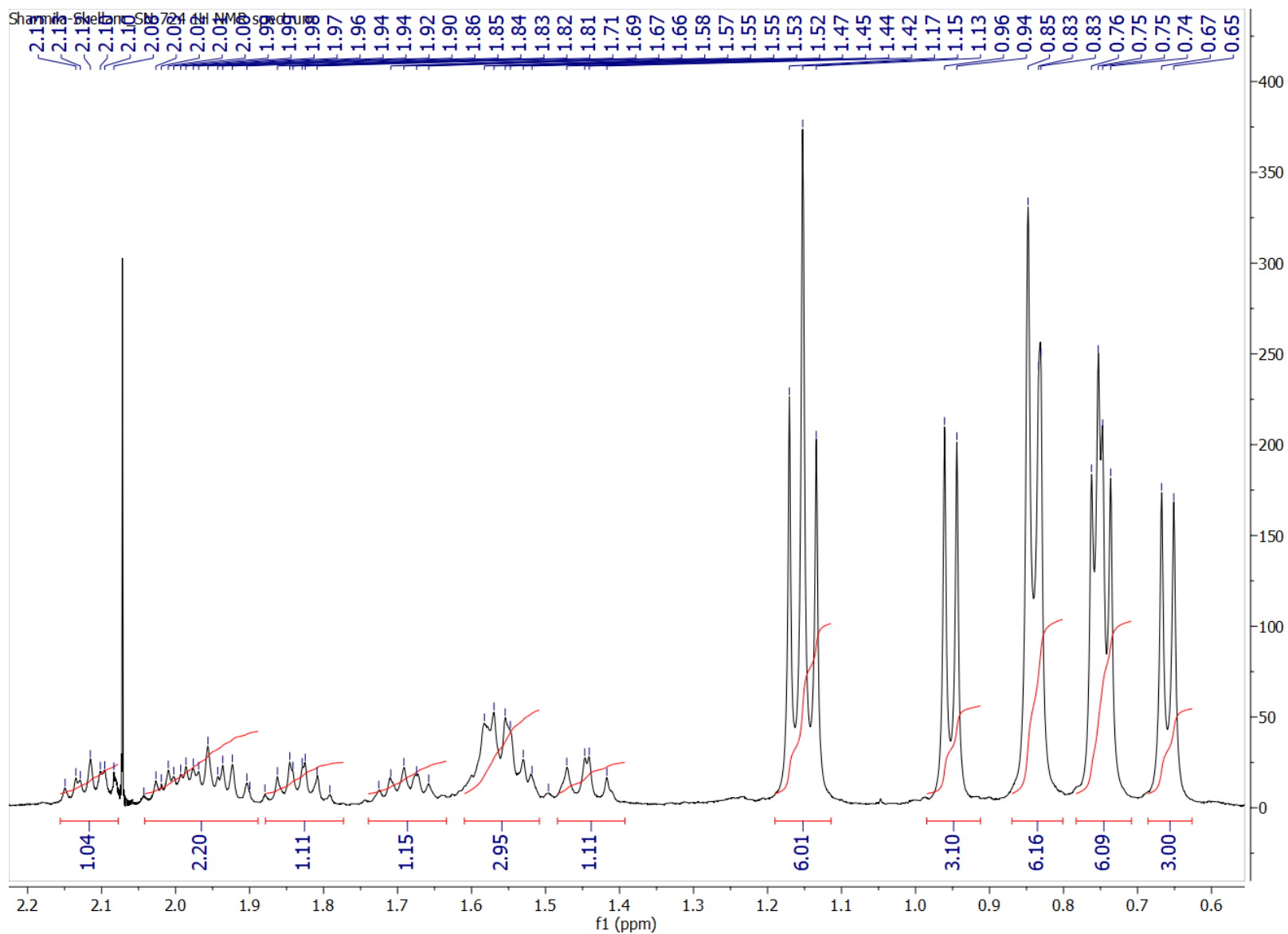


Figure S21: Expansion of the ^1H NMR spectrum of **2** (500 MHz, $\text{DMSO-}d_6$).

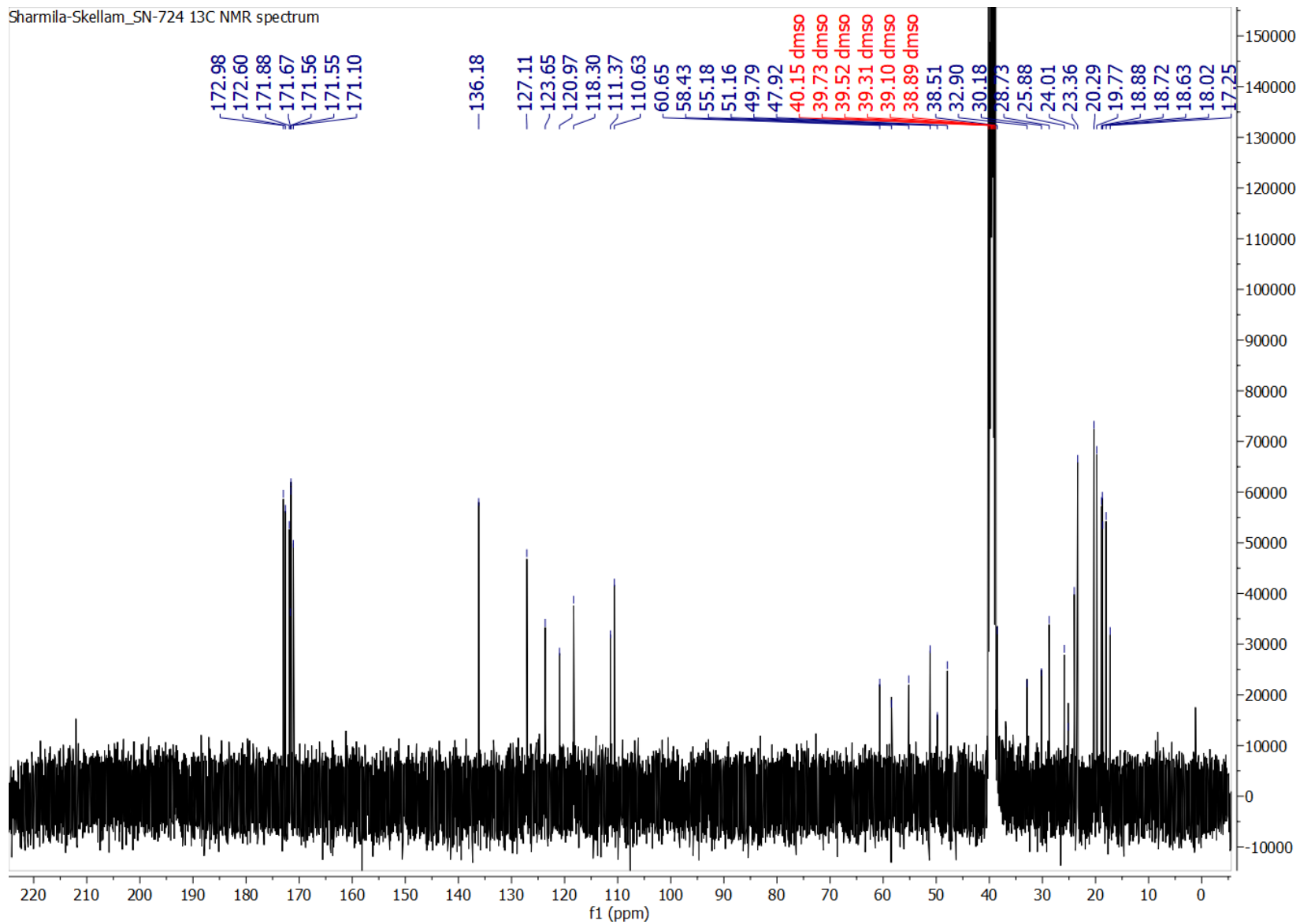


Figure S22: ^{13}C NMR spectrum of **2** (125 MHz, $\text{DMSO-}d_6$).

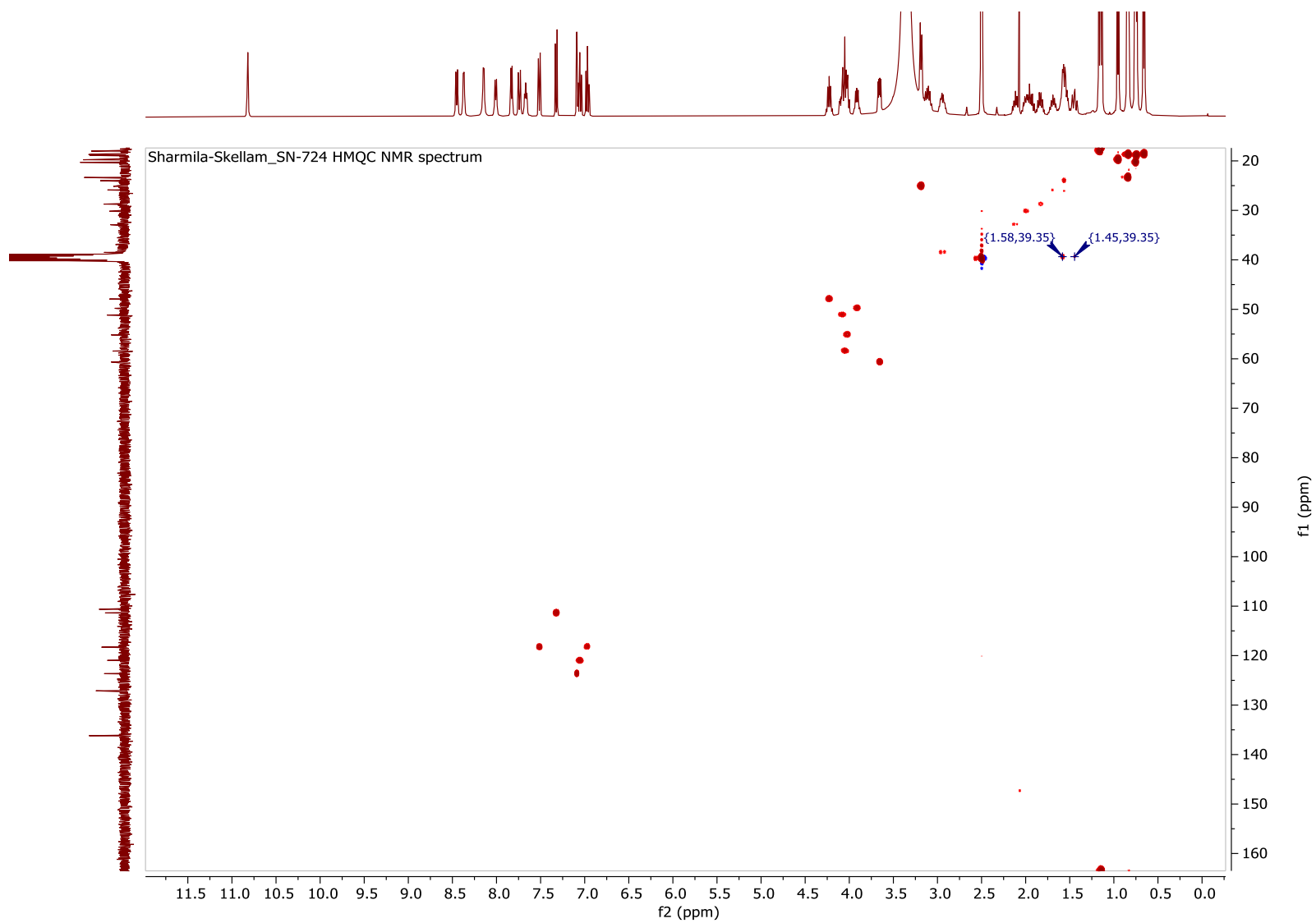


Figure S23: gHSQC NMR spectrum of **2** (^1H :500 MHz; ^{13}C :125 MHz, $\text{DMSO-}d_6$).

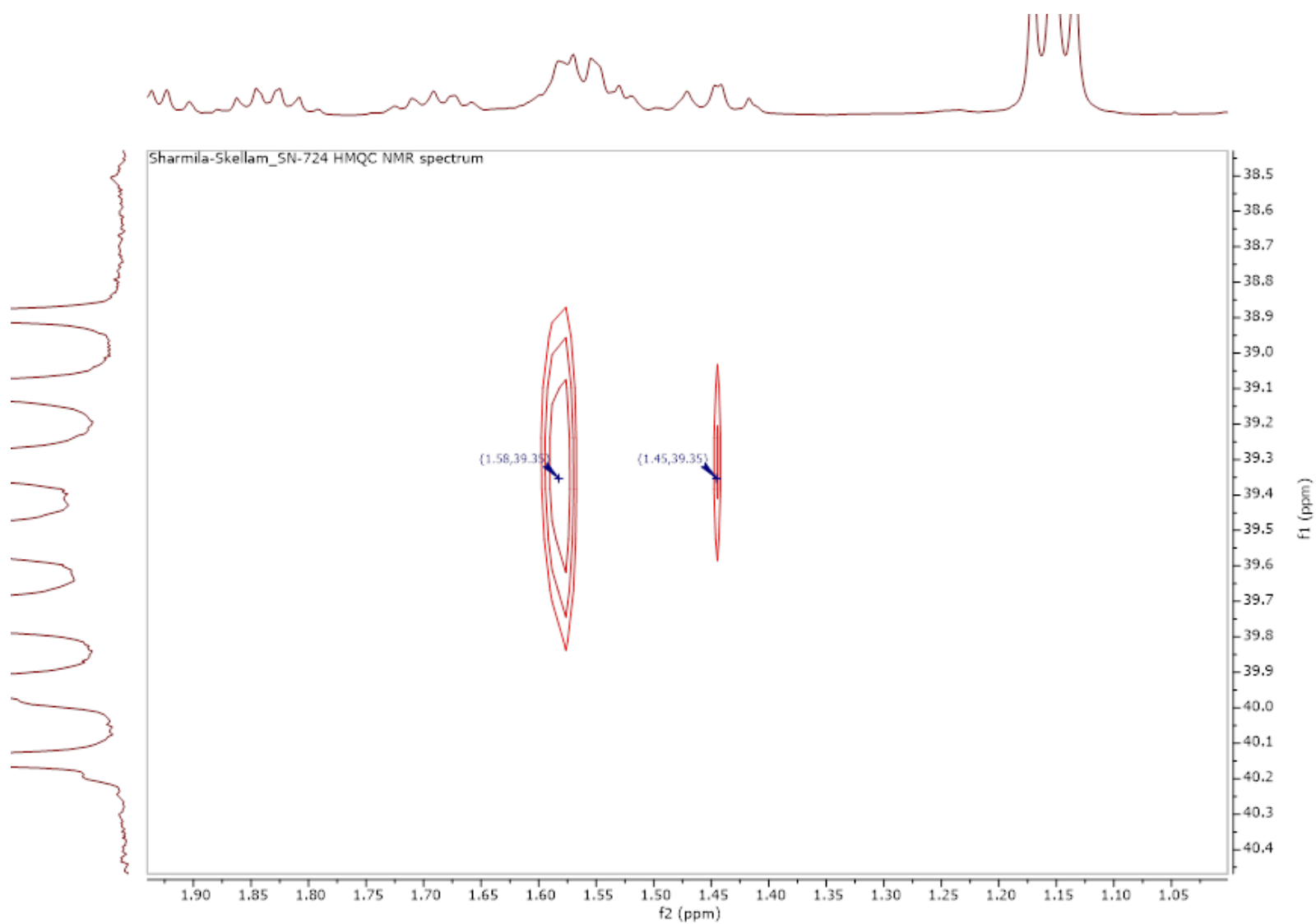


Figure S24: Expansion of the gHSQC NMR spectrum of **2** (^1H :500 MHz; ^{13}C :125 MHz, $\text{DMSO-}d_6$).

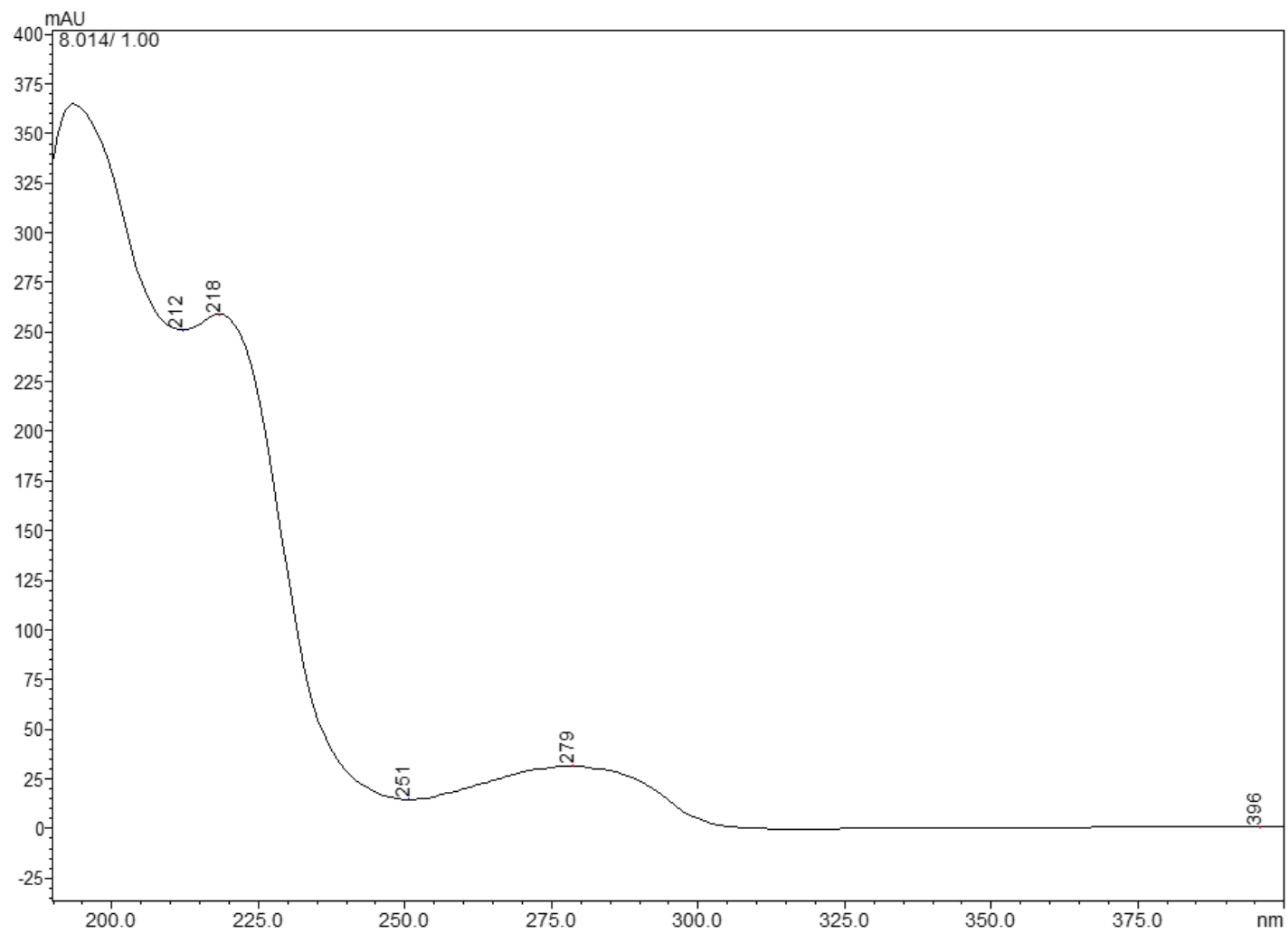


Figure S25: UV spectrum (photodiode array, H₂O:MeCN) of **2**.

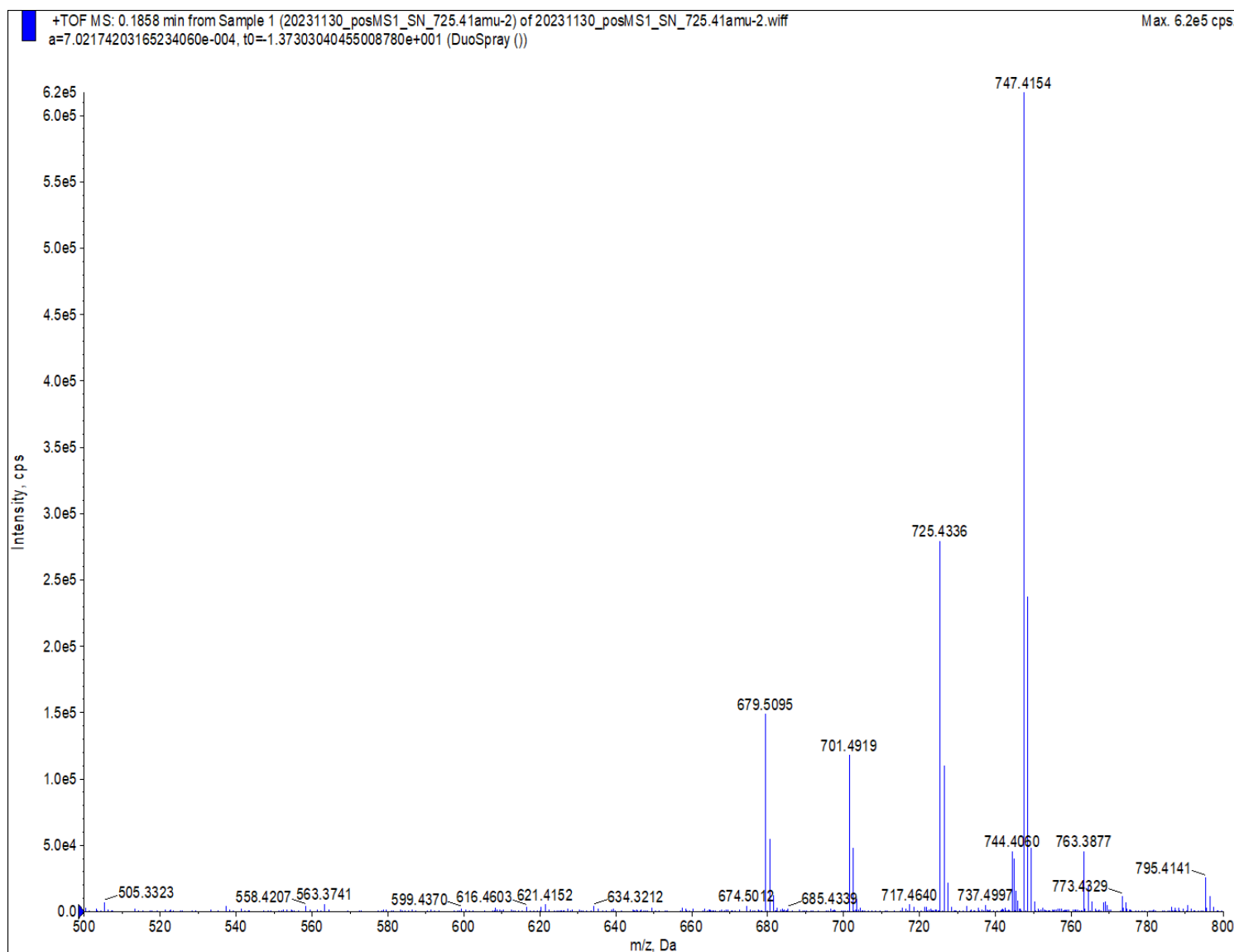


Figure S26: HRESIMS spectrum of **2** in positive ionization mode.

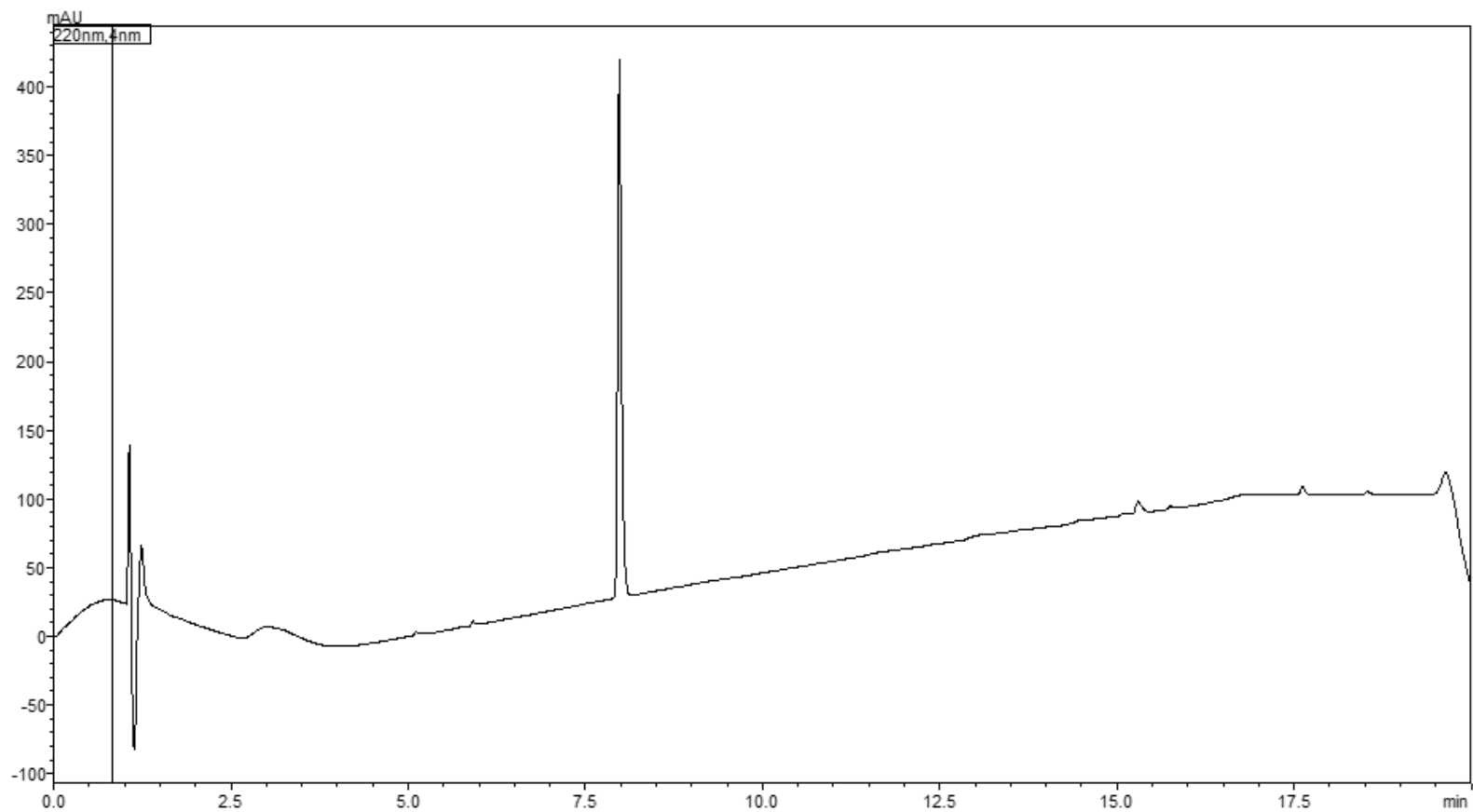


Figure S27: HPLC-PDA chromatogram of unguisin B (2).

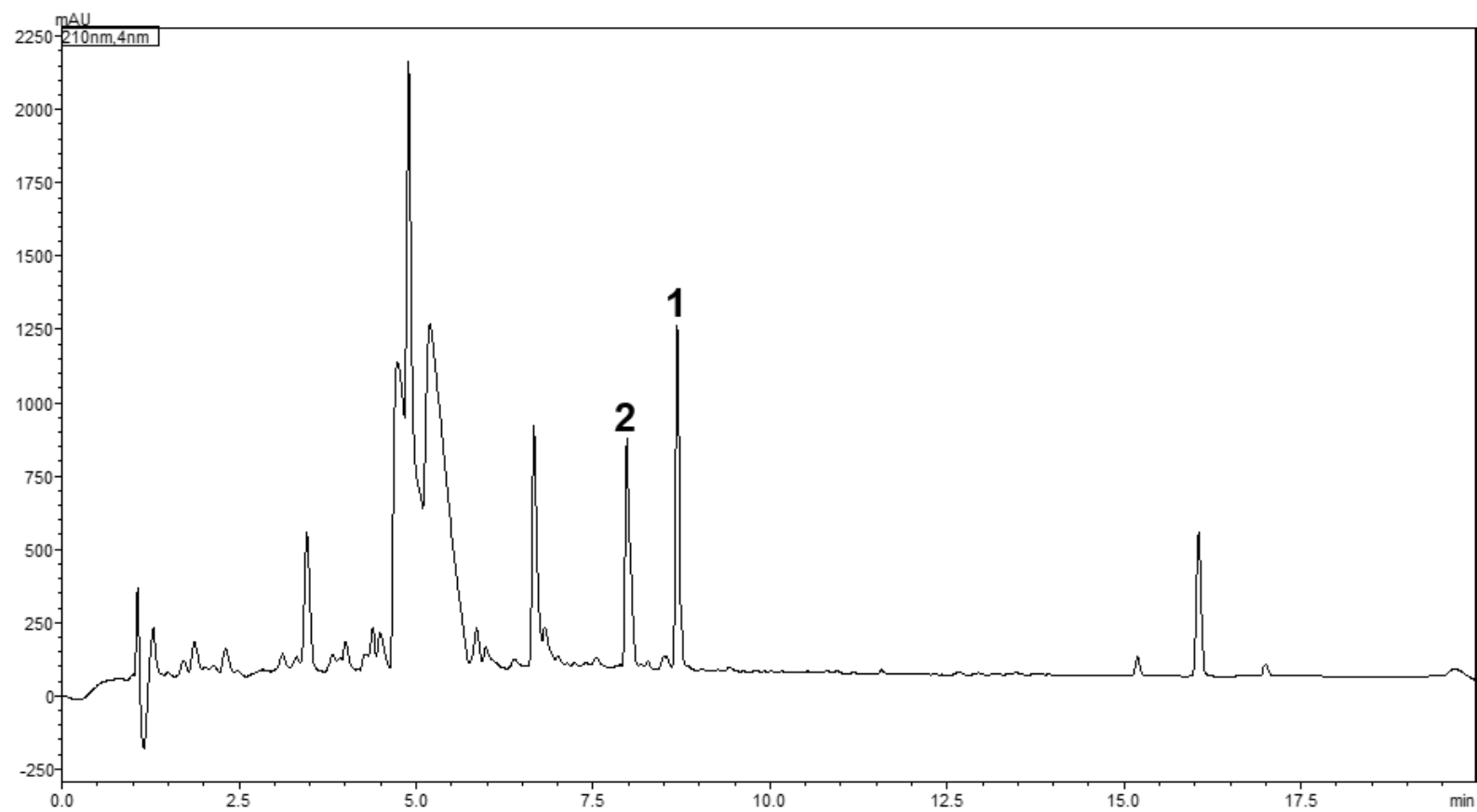


Figure S28: HPLC-PDA chromatogram of soluble-organic extract from rice culture of *A. heteromorphus*. Peak labels represent Unguisin J (1) and Unguisin B (2).

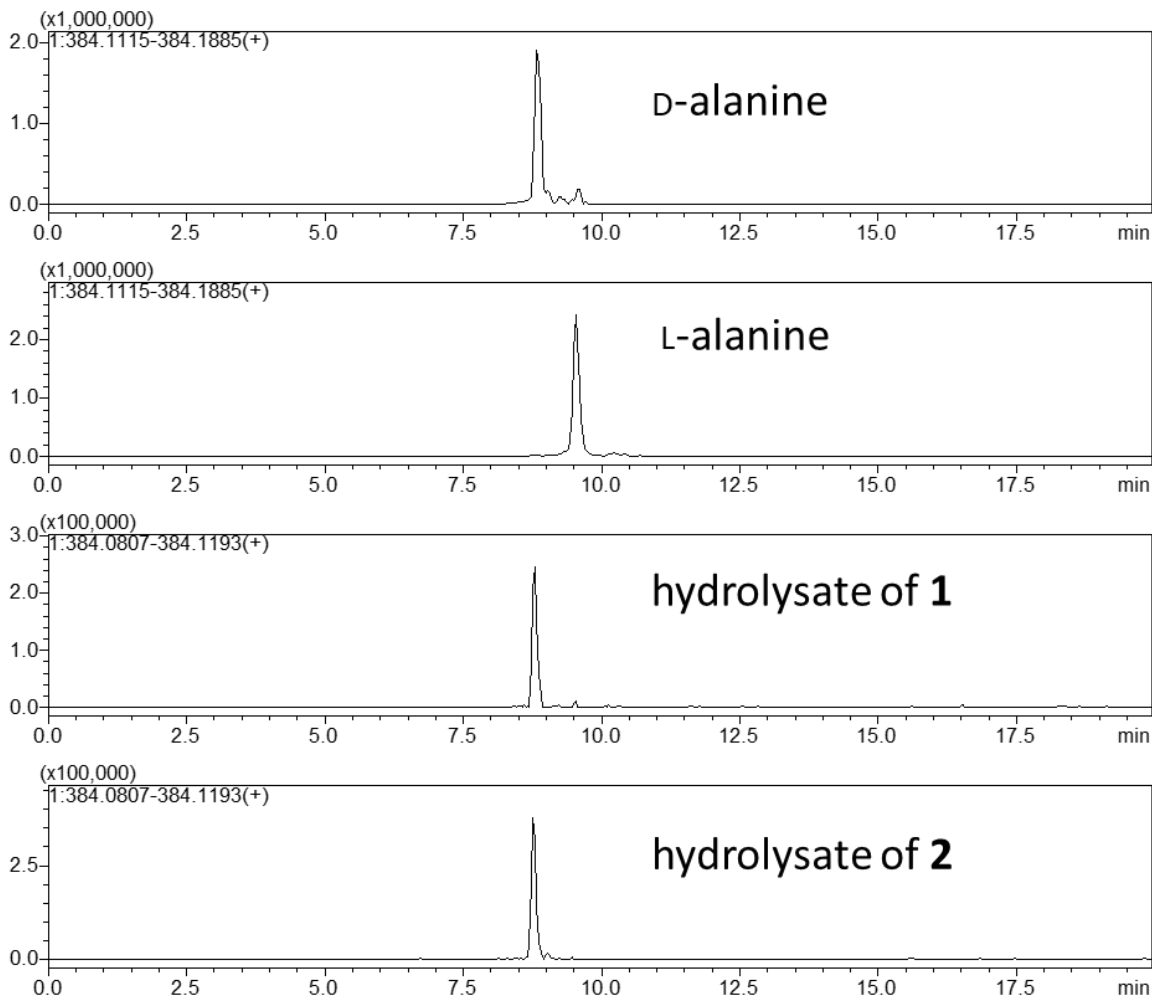


Figure S29: LC-MS analysis of N^{α} -(5-fluoro-2,4-dinitrophenyl)-D-leucinamide derivatives of the hydrolysates of **1** and **2** as well as the alanine amino acid standards.

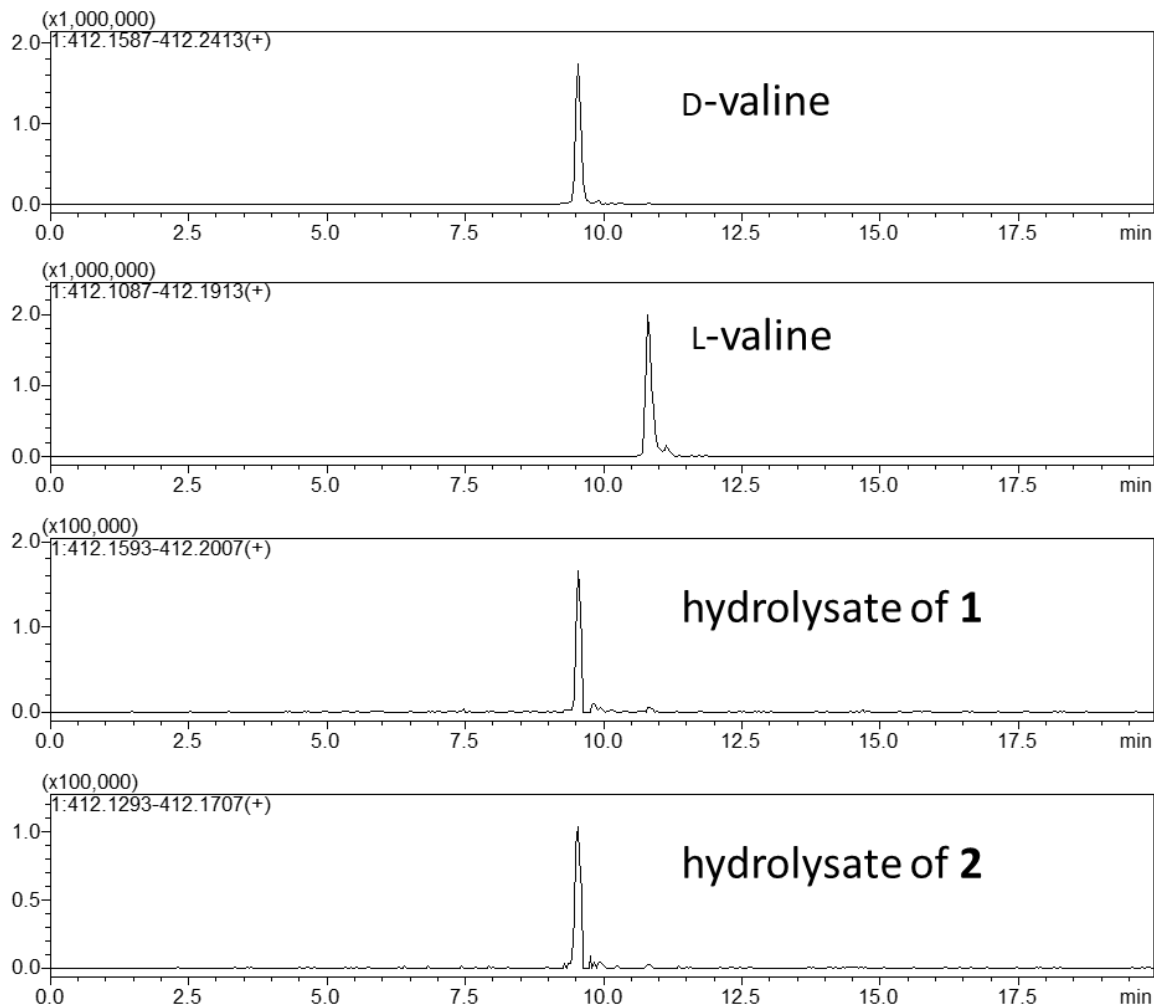


Figure S30: LC-MS analysis of N^α -(5-fluoro-2,4-dinitrophenyl)-D-leucinamide derivatives of the hydrolysates of **1** and **2** as well as the valine amino acid standards.

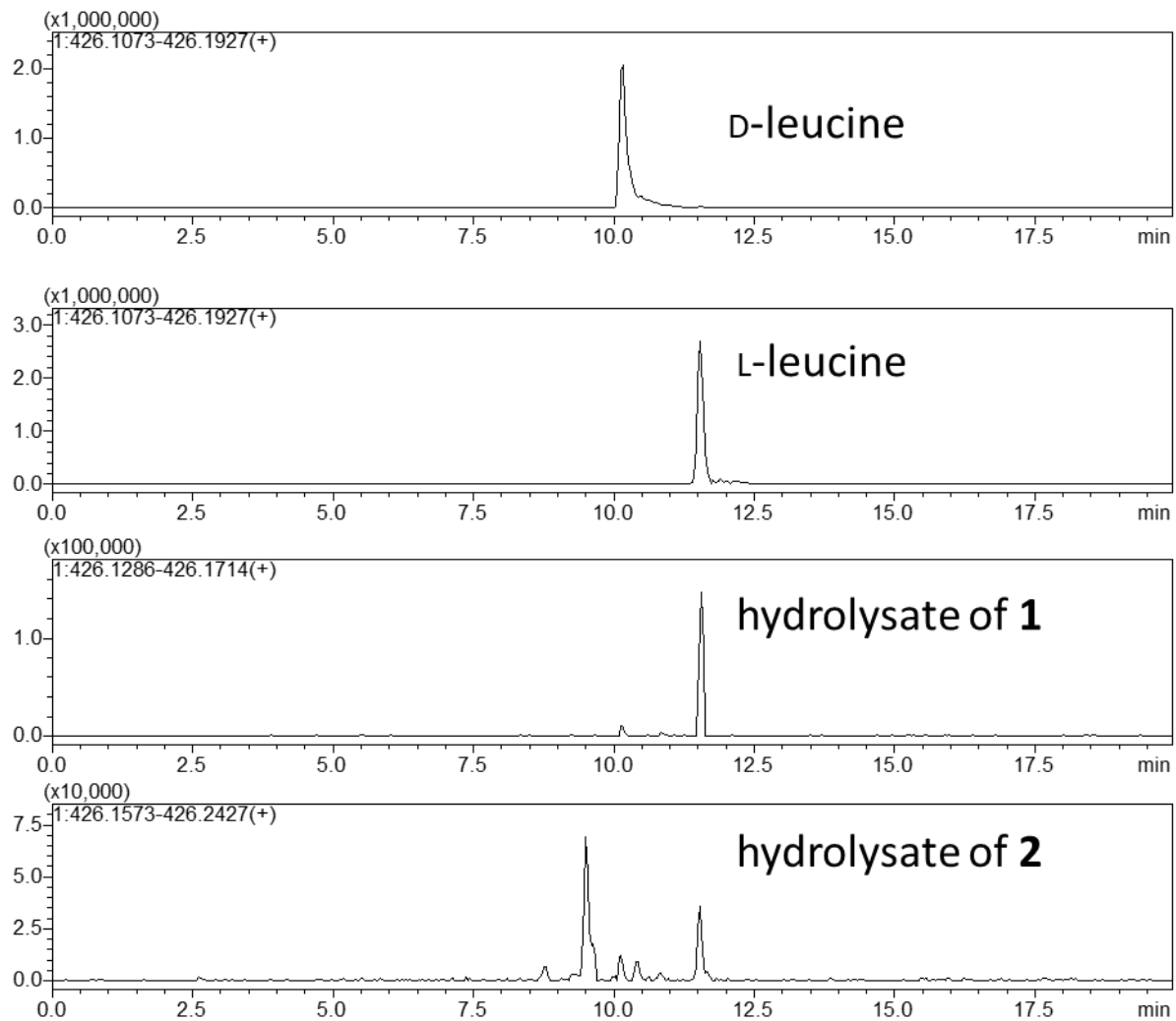


Figure S31: LC-MS analysis of N^α -(5-fluoro-2,4-dinitrophenyl)-D-leucinamide derivatives of the hydrolysates of **1** and **2** as well as the leucine amino acid standards.

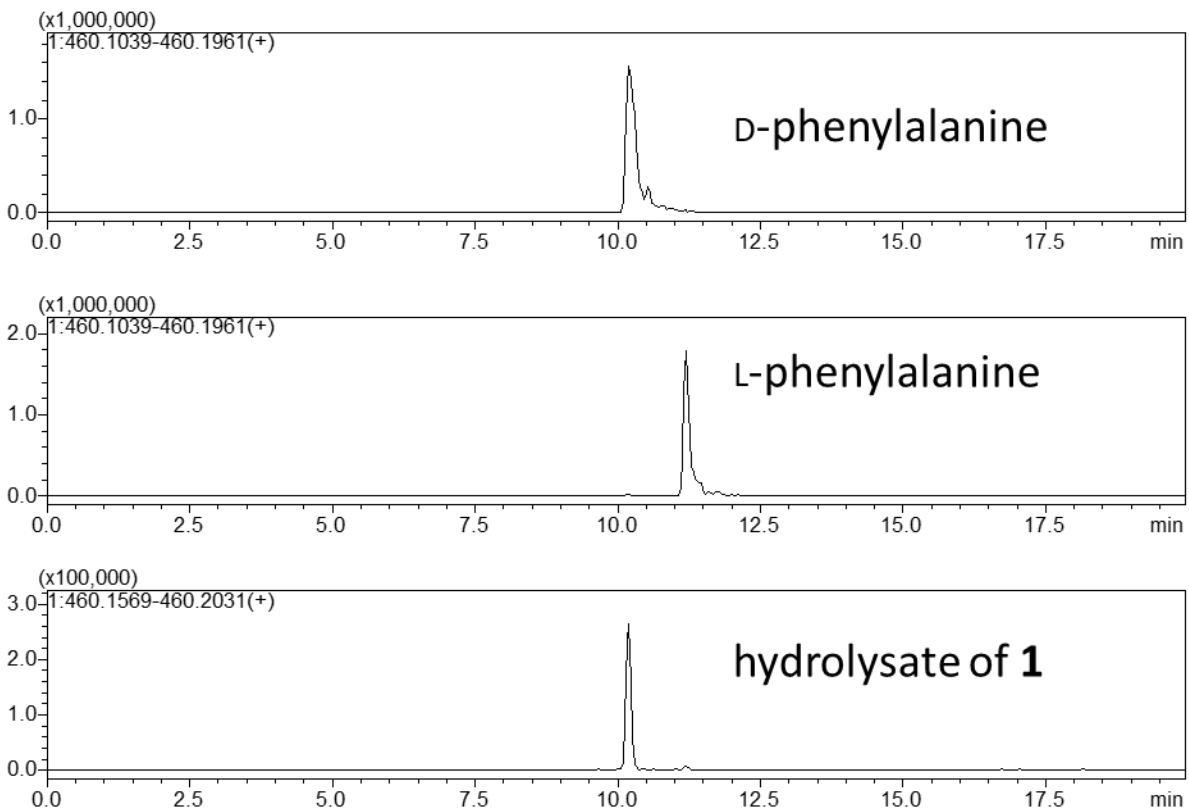


Figure S32: LC-MS analysis of N^{α} -(5-fluoro-2,4-dinitrophenyl)-D-leucinamide derivative of the hydrolysate of **1** as well as the phenylalanine amino acid standards.

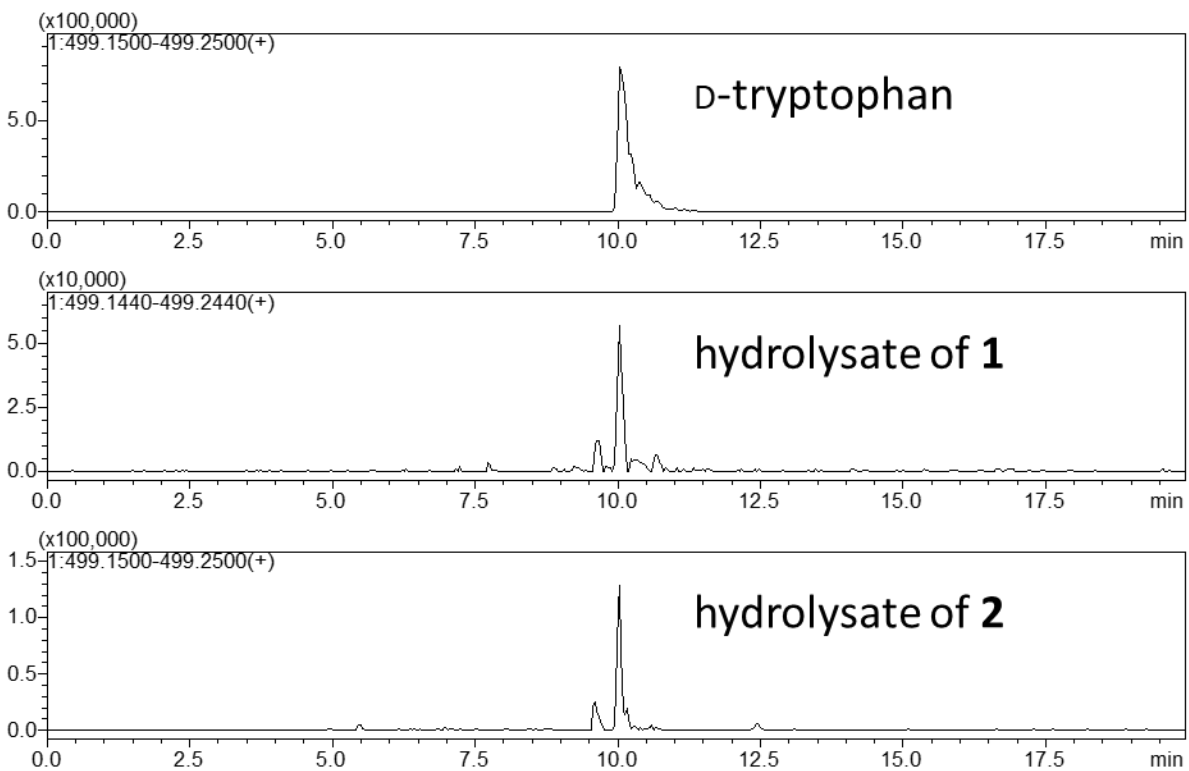


Figure S33: LC-MS analysis of N^α -(5-fluoro-2,4-dinitrophenyl)-D-leucinamide derivatives of the hydrolysates of **1** and **2** as well as the D-tryptophan standard.

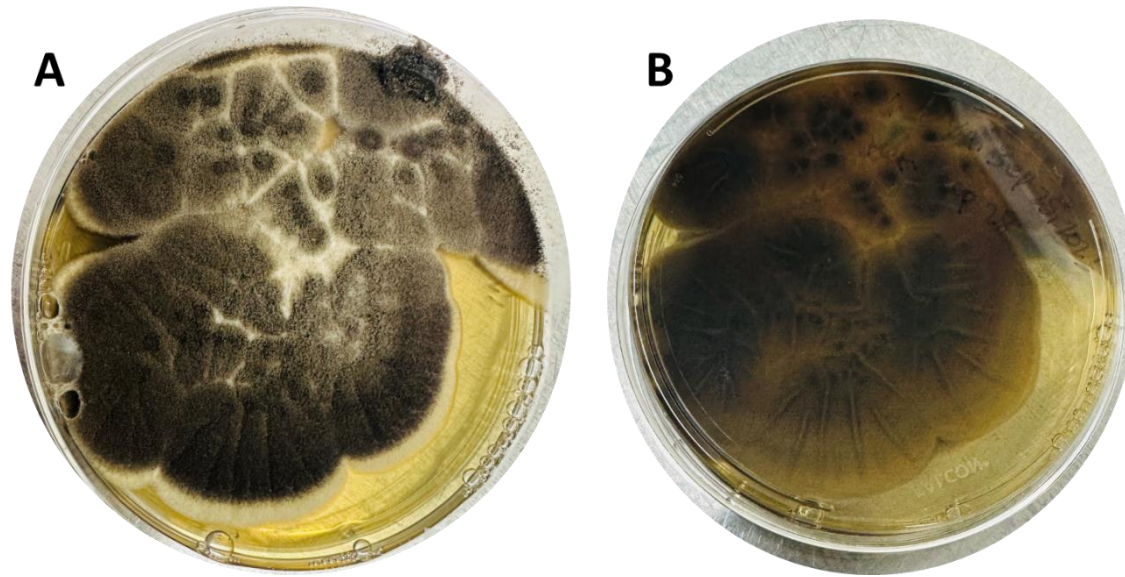


Figure S34: Colonies of *Aspergillus heteromorphous* CBS 117.55 with 7 days of growth at 25 °C. Colonies on DPY agar plate verse (A) and obverse (B).



Figure S35: Colonies of *Aspergillus heteromorphous* CBS 117.55 with 21 days of growth at 25 °C on solid rice in Erlenmeyer flasks.

Table S2: ¹H and ¹³C NMR data for **2** (¹H: 500MHz, ¹³C:125MHz; DMSO-*d*₆).

		2		Unguisin B (Malmstron, 1999)	
residue/position		δ_C	δ_H (mult., J in Hz)	δ_C	δ_H (mult., J in Hz)
Alanine	NH	-	8.37 (d, 4.9)	-	8.36 (d, 4.6)
	Cα	49.8	3.91 (m)	49.8	3.92 (m)
	Cβ	17.3	1.14 (d, 7.1)	17.3	1.16
Alanine	NH	-	7.83 (d, 6.2)	-	7.82 (d, 6.1)
	Cα	47.9	4.22 m	48.0	4.23 (m)
	Cβ	18.0	1.16 (d, 7.1)	18.1	1.16
Valine	NH	-	8.14 (d, 4.5)	-	8.13 (d, 4.4)
	Cα	60.6	3.66 (dd, 8.4, 4.4)	60.6	3.67 (dd, 4.6, 8.2)
	Cβ	28.7	1.83 (m)	28.8	1.82 (m)
	Cγ	19.8	0.95 (d, 6.7)	19.7	0.95 (d, 6.6)
	Cγ	18.7	0.84 (d, 6.4)	18.8	0.84 (d, 6.4)
Valine	NH	-	7.74 (d, 9.8)	-	7.73 (d, 9.7)
	Cα	58.4	4.05 (m)	58.5	4.07 (m)
	Cβ	30.2	2.00 (m)	30.2	2.00 (m)
	Cγ	18.6	0.66 (d, 6.6)	18.6	0.66 (d, 6.6)
	Cγ	18.9	0.74 (d, 6.6)	18.9	0.74
GABA	NH	-	7.67 (t, 5.5)	-	7.65 (t, 5.3)
	Cα	38.5	3.11 (m), 2.94 (m)	38.5	3.11 (m), 2.95 (m)
	Cβ	25.9	1.69 (m), 1.55 (m)	25.9	1.65 (m), 1.58 (m)
	Cγ	32.9	2.11 (m), 1.95 (m)	32.9	2.11 (m), 1.94 (m)
Tryptophan	NH	-	8.0 (d, 7.1)	-	7.98 (d, 6.8)
	Cα	55.2	4.02 (m)	55.2	4.05 (m)
	Cβ	25.2	3.18 (d, 7.2)	25.2	3.20 (d, 8.5)
	NH	-	10.82 (d, 2.4)	-	10.81 (d, 2.0)
	C-2	123.7	7.08 (d, 2.3)	123.6	7.11 (d, 2.2)
	C-3	110.6	-	110.6	-
	C3a	127.1	-	127.1	-
	C-4	118.3	7.51 (d, 7.9)	118.3	7.54 (d, 7.9)
	C-5	121.0	7.06 (ddd, 7.9, 7.1, 1.1)	121.0	7.08 (t, 6.9)
	C-6	118.3	6.97 (ddd, 8.1, 7.1, 1.1)	118.3	6.97 (t, 7.2)
	C-7	111.4	7.32 (dt, 8.1, 0.8)	111.4	7.35 (d 8.1)
	C-7a	136.2	-	136.2	-
	Leucine	NH	-	8.45 (d, 7.9)	-
Cα		51.2	4.07 (m)	51.2	4.09 (m)
Cβ		39.4 ^a	1.58 (m), 1.45 (m)	38.7	1.58 (m)
Cγ		24.0	1.57 (m)	24.1	1.58 (m)
Cδ		23.4	0.84 (d, 6.4)	23.4	0.84 (d, 6.4)
Cδ		20.3	0.75 (d, 6.0)	20.4	0.74

^aConfirmed by HSQC. Carbons signals at δ_C 171.1, 171.6, 171.6, 171.7, 171.9, 172.6 and 173.0 ppm.

Table S3: Summary of additional NRPS identified in the genome of *A. heteromorphus* CBS 117.55. Abbreviations as in main text; R = reductase.

fungiSMASH contig ID	NCBI GeneID	Putative NRPS size (aa)	Putative domain arrangement
2.2	37069286	4028	C _T -A-PCP-C-A-MT-PCP-C-A-PCP-TE
35.2	37070309	5593	A-PCP-C-A-E-PCP-C-A-E-PCP-A-C-PCP-C-PCP
57.3	37069398	1436	C-A-PCP-R
119.1	37067680	5115	A-PCP-A-PCP-C-A-PCP-C-A-PCP-C-A-PCP
139.1	37063074	2302	A-PCP-C-A-PCP-R
143.1	37069176	2452	A-PCP-C-A-PCP-C _T
150.1	37069727	9562	A-PCP-C-A-PCP-E-C-A-PCP-C-A-PCP-E-C-A-PCP-E-C-A-PCP-E-C-A-PCP-C _T
161.1	37069763	2775	A-PCP-C-A-PCP-E (truncated; close to scaffold edge)
172.1	37061517	671	A-PCP (truncated; close to scaffold edge)
172.2	37067500	4765	A-PCP-C-A-PCP-C-A-PCP-E-A-PCP-C (truncated; close to scaffold edge)
172.5	37069805	1931	A-PCP-C-A-PCP (truncated; close to scaffold edge)