

Supporting Information

Enzymatic Assembly of Diverse Lactone Structures: An Intramolecular C–H Functionalization Strategy

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1. General Procedures

Unless otherwise noted, all chemicals and reagents were obtained from commercial suppliers (Sigma-Aldrich, VWR, TCI America, Fischer Scientific, Alfa Aesar, Acros, and Combi Blocks) and used without further purification. Silica gel chromatography was carried out using AMD Silica Gel 60, 230–400 mesh. ^1H and ^{13}C NMR spectra were recorded on a Bruker Prodigy 400 MHz instrument (400 MHz for ^1H and 101 MHz for ^{13}C NMR) or a Varian 300 MHz Spectrometer (300 MHz for ^1H NMR). Chemical shifts (δ) are reported in ppm downfield from tetramethylsilane, using the solvent resonance as the internal standard (^1H NMR: $\delta = 7.26$, ^{13}C NMR: $\delta = 77.16$ for CDCl_3). Data for ^1H NMR are reported as follows: chemical shift (δ ppm), multiplicity (s = singlet, d = doublet, t = triplet, q = quartet, p = pentet, sext = sextet, m = multiplet, dd = doublet of doublets, dt = doublet of triplets, ddd = doublet of doublet of doublets), coupling constant (Hz), integration. Sonication was performed using a Qsonica Q500 sonicator. High-resolution mass spectra were obtained at the California Institute of Technology Mass Spectral Facility. Samples were analyzed by field ionization (FI) using a JEOL AccuTOF GC-Alpha (JMS-T2000GC) mass spectrometer interfaced with an Agilent 8890 GC system. Ions detected by FI are radical cations.

Escherichia coli cells were grown using Luria-Bertani medium or HyperBroth (AthenaES) with 100 $\mu\text{g/mL}$ ampicillin (LB_{amp} or HB_{amp}). Primer sequences are available upon request. T5 exonuclease, Phusion polymerase, and *Taq* ligase were purchased from New England Biolabs (NEB, Ipswich, MA). M9-N minimal media (abbreviated as M9-N buffer, pH = 7.4) were used as buffering systems for whole cells, unless otherwise specified. M9-N buffer was used without a carbon source, it contains 47.7 mM Na_2HPO_4 , 22.0 mM KH_2PO_4 , 8.6 mM NaCl, 2.0 mM MgSO_4 , and 0.1 mM CaCl_2 .

1.1 Chromatography

Chemical reactions were monitored using thin layer chromatography (Merck 60 silica gel plates) and a UV lamp for visualization. Analytical reverse-phase high-performance liquid chromatography (HPLC) was carried out using an Agilent 1200 series instrument and a Kromasil 100 C18 column (4.6 mm \times 50 mm, 3 μm) or an Agilent C18 column (InfinityLab Poroshell 120 EC-C18, 4.6 x 50 mm, 2.7 μm ; Part Number: 699975-902T) with water and acetonitrile, both

containing 0.1% acetic acid, as the mobile phase. Analytical chiral normal-phase HPLC was conducted using either an Agilent 1200 series instrument with *n*-hexane and isopropanol as the mobile phase or JASCO SF-2000 integrated analytical supercritical fluid chromatography (SFC) system with supercritical CO₂ and isopropanol as the mobile phase. Enantiomers were separated using one of the following chiral columns: Chiralpak IA, Chiralpak IB, Chiralpak IC, Chiralpak AD-H, and Daicel CHIRALCEL OJ-H (all 4.6 mm × 250 mm, 5 μm).

1.2 Cloning and Site-Saturation Mutagenesis

The genes encoding all enzymes described in this study were cloned using Gibson assembly¹ into vector pET22b(+) (Novagen) between restriction sites *Nde*I and *Xho*I in frame with a C-terminal 6×His-tag. Site-saturation mutagenesis was performed using the “22c-trick”² or “NNK” as degenerative codons. The PCR products were digested with *Dpn*I, gel purified, and ligated using Gibson MixTM.¹ Without further purification after the Gibson step, 1 μL of the Gibson product was used to transform 50 μL of electrocompetent *E. coli* BL21 *E. cloni*[®] (Lucigen) cells.

1.3 Expression of P411 Variants in 96-Well Plates

Single colonies from LB_{amp} agar plates were picked using sterile toothpicks and cultured in deep-well 96-well plates containing LB_{amp} (300 μL/well) at 37 °C, 80% humidity, and 220 rpm shaking overnight. Subsequently, HB_{amp} (1000 μL/well) in a deep-well plate was inoculated with an aliquot (50 μL/well) of these overnight cultures and allowed to shake for 2.5 hours at 37 °C, 80% humidity, and 220 rpm. The plates were then cooled on ice for 30 minutes, and the cultures were induced with 0.5 mM isopropyl β-D-1-thiogalactopyranoside (IPTG) (final concentration). The expression was supplemented with 1.0 mM 5-aminolevulinic acid (ALA) (final concentration). Expression was then conducted at 20 °C, 220 rpm for 20–22 hours.

1.4 Plate Reaction Screening in Whole-Cell Format

E. coli cells harboring P411 variants in deep-well 96-well plates were pelleted (3,500 g, 5 min, 4 °C) and resuspended in M9-N buffer (360 μL, pH 7.4) by gentle vortexing. The 96-well plates were then transferred to an anaerobic chamber. To deep-well plates of cell suspensions was added the substrate (20 μL/well, 200 mM in acetonitrile). The plates were sealed with aluminum sealing foil immediately after the addition and shaken in the anaerobic chamber at room temperature and 600 rpm. After 24 hours, the seals were removed and acetonitrile (600 μL/well) was added. The

plates were tightly sealed with silicone mats, vigorously vortexed, and centrifuged (4,500 g, 5 min) to precipitate proteins and cell debris. The supernatant (200 μ L/well) was filtered through an AcroPrep 96-well filter plate (0.2 μ m) into a 96-well assay plate for reverse-phase HPLC analysis to determine the yield.

1.5 Flask Expression of P411 Variants

E. coli (*E. coli* BL21(DE3)) cells carrying plasmid encoding the appropriate P411 variant were grown overnight in 5 mL Luria-Bertani medium supplemented with 0.1 mg/mL ampicillin (LB_{amp}). The preculture (1 mL) was used to inoculate 50 mL of Hyperbroth medium supplemented with 0.1 mg/mL ampicillin (HB_{amp}) in a 125-mL Erlenmeyer flask. This culture was incubated at 37 $^{\circ}$ C and 230 rpm for 2.5 hours. The culture was then cooled on ice for 45 min and induced with 0.5 mM IPTG and 1.0 mM ALA (final concentrations). Expression was conducted at 24 $^{\circ}$ C, 140 rpm for 16–18 hours. Subsequently, the *E. coli* cells were pelleted by centrifugation (5,000 g, 5 min, and 4 $^{\circ}$ C). Media were removed, and the pellets were resuspended to an optical density at 600 nm (OD_{600}) of 30 in M9-N minimal medium. Aliquots of the cell suspension (3–4 mL) were used to determine protein concentration after lysis by sonication.

1.6 Hemochrome Assay for the Determination of Hemoprotein Concentration

Protein concentration in the cell was determined using the hemochrome assay on cell lysate.³ Lysate was obtained by sonication using a Qsonica Q500 sonicator (6 minutes, 1 second on, 2 seconds off, 35% amplitude, on wet ice). The cell debris was removed by centrifugation (14,000 g, 10 minutes, 4 $^{\circ}$ C). To a cuvette, 500 μ L of the lysate and 500 μ L of solution I [0.2 M NaOH, 40% (v/v) pyridine, 0.5 mM $K_3Fe(CN)_6$] were added. The UV-Vis spectrum (380–620 nm) of the oxidized state Fe(III) was recorded immediately. Sodium dithionite (10 μ L of 0.5 M solution in water) was added, and the UV-Vis spectrum of the reduced state Fe(II) was recorded immediately. The protein concentration was calculated using the extinction coefficient and dilution factor ($2\times$ dilution in volume): $\epsilon_{[557_{reduced} - 540_{oxidized}]} = 23.98 \text{ mM}^{-1}\text{cm}^{-1}$. The hemochrome assay detects total heme level, which is a good approximation of over-expressed heme enzyme.

1.7 Biotransformation Using Whole *E. coli* Cells

Suspension of *E. coli* (*E. coli* BL21(DE3)) cells expressing the appropriate hemoprotein variant in M9-N buffer (typically $OD_{600} = 2.5$) were transferred to a reaction vial. Enzymatic

reactions were then set up in an anaerobic chamber. To an Agilent's 2-mL screw top vial were added degassed suspension of *E. coli* expressing P411 variant (typically OD₆₀₀ = 2.5, 395 μ L) and substrate (typically 5 μ L of 200 mM stock solution in acetonitrile). The final volume of the biotransformation was set to be 400 μ L, with 1.25% (v/v) acetonitrile. The reaction vials were then capped and shaken in the anaerobic chamber at room temperature and 600 rpm for 24–48 hours. After the completion of the reaction, 600 μ L acetonitrile containing 0.67 mM 1,3,5-trimethoxybenzene internal standard were added to the vial. The resulting mixture was transferred to a 1.7-mL microcentrifuge tube, vigorously vortexed, and centrifuged (14,000 g, 5 min, 4 °C). A sample of the supernatant (0.6 mL) was transferred to a vial for HPLC analysis.

To determine the enantiomeric excess (e.e.), three parallel analytical reactions were conducted. Each reaction mixture was extracted with an equal volume of a hexane/ethyl acetate (3:1) solution. The organic extracts were combined and transferred to a 2-dram vial, and the solvent was removed by blowing air. Residue was resuspended in 100 μ L isopropanol and subjected to normal-phase HPLC to determine the e.e.

1.8 Enzymatic Preparative Synthesis

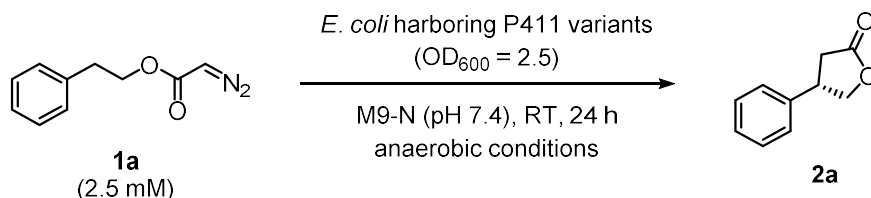
The *E. coli* cell suspension harboring a P411 variant was prepared as described in **Sections 1.5 and 1.6**. The cell suspension (*E. coli* whole cells harboring P411 variants, OD₆₀₀ = 2.5, suspended in M9-N aqueous buffer) was placed in a flask covered loosely with aluminum foil and then bubbled with argon for at least 15 minutes. The reaction flask was then transferred to an anaerobic chamber. To the reaction flask with cell suspension (OD₆₀₀ = 2.5), substrate (200 mM acetonitrile stock solution, final concentration = 2.5 mM, 1.0 equiv.) was added to make 1.25% v/v acetonitrile (co-solvent). The reaction vial was immediately capped and sealed with parafilm and stirred in the anaerobic chamber at room temperature for 48 hours. The reaction solution was filtered through celite then extracted with an equal volume of ethyl acetate (\times 3 times). The combined organic layer was then washed with brine and dried over anhydrous MgSO₄. The solvent was removed *in vacuo*, and the product was purified by flash chromatography.

Note: Many of the lactone standard products involved in this study are challenging to prepare using existing chemical methods, particularly those with 6-membered and 7-membered rings, and complex structures. Therefore, those challenging products were synthesized using enzymatic

catalysis developed in this work. However, for most of these preparative-scale biosyntheses, we did not use the final enzyme variants, but rather used variants earlier in the evolution trajectory. This is because: 1. We need to obtain standard products early on to draw HPLC standard curves and determine the activity of enzyme variants during directed evolution. 2. The final enzymes usually afford nearly enantiopure products, so we would have been unable to obtain two enantiomers and separate them using chiral HPLC. In order to obtain imperfect e.e. values, we used earlier enzyme variants to biosynthesize lactone standards in preparative scales. Therefore, most of the NMR spectra were obtained from products catalyzed by non-final (less active) enzyme variants.

2. Discovery of Initial Activity and Directed Evolution

Table S1. Initial activity screening with engineered P411s for γ -lactone synthesis.^a



A panel of cytochrome P450 and P411 (P450 with an axial serine ligand) variants previously engineered for carbene nitrene transformations were screened in whole *E. coli* cells against **1a** under anaerobic conditions.⁴⁻⁶ Among these, P411-LAS-5239 (**C10**), known for its promiscuous activities in different carbene-transfer reactions such as internal alkyne cyclopropanation⁵ and lactone-carbene C–H insertion,⁴ was effective in producing the γ -lactone product **2a** (8% yield).

Entry	Variant / Catalyst	Yield of 3a ^a	Standard deviation of yield	TTN	Standard deviation of TTN
1	P411-LAS-5239	7.5%	0.5%	530	35
2	^b hemin (20 μ M)	N.D.	-	N.D.	-
3	^c hemin (20 μ M) + Na ₂ S ₂ O ₄	N.D.	-	N.D.	-
4	^c hemin (20 μ M) + BSA (20 μ M)	N.D.	-	N.D.	-
5	^c hemin (20 μ M) + Na ₂ S ₂ O ₄ + BSA (20 μ M)	N.D.	-	N.D.	-
6	^d cellular background	N.D.	-	N.D.	-

^a Experiments were performed using whole *E. coli* cells according to the protocol described in **Sections 1.3** and **1.4**. The yields of **2a** were calculated based on comparing the signal integration ratio of the products and an added internal standard compound (see **section 6** for more details). All reactions were performed in triplicate, with the reported yields representing the average of three

experiments. The signal calibration curves correlating the products and the internal standard compound can be found in **Section 6**. To enhance systematic management of different enzyme variants within the Arnold lab, we recently implemented a new nomenclature system. Variants are named as follows: family name-chemistry abbreviation-entry code. All enzyme variants in this study follow this nomenclature.

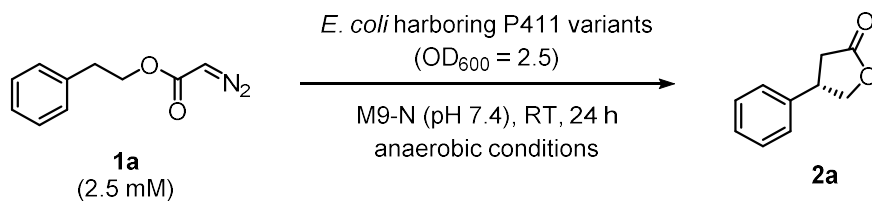
^b Negative control experiments (with free hemin) were performed without the addition of Na₂S₂O₄. Under this condition, the resting oxidation state of hemin in aqueous buffer should be Fe(III).

^c Negative control experiments using free hemin under reduced conditions (Fe(II)) were performed using an excess amount of Na₂S₂O₄ (20 mM).

^d Cellular background control experiments were performed in whole-cell format, using *E. coli* (*E. coli* BL21(DE3)) cells harboring an engineered tryptophan synthase β -subunit (Tm9D8*). The gene of this enzyme was also cloned into the pET22b(+) vector (Novagen) between restriction sites *Nde*I and *Xho*I. The protein expression protocol for this experiment followed the standard P411 expression conditions as described in **Sections 1.5, 1.6, and 1.7**.

N.D. – no product was detected.

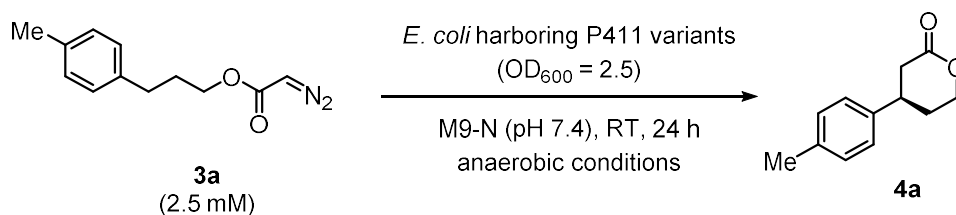
Table S2. Directed evolution of P411-LAS-5247 for γ -lactone synthesis.^a



Entry	Round #	Variant	Yield of 2a ^a	Standard deviation of yield	TTN	Standard deviation of TTN
1	0	P411-LAS-5239	7.5%	0.5%	530	35
2	1	P411-LAS-5240	14%	1.7%	2200	260
3	2	P411-LAS-5241	20%	0.1%	1100	8
4	3	P411-LAS-5242	35%	0.4%	2700	28
5	4	P411-LAS-5243	41%	1.5%	2900	200
6	5	P411-LAS-5244	52%	1.5%	3900	120
7	6	P411-LAS-5245	64%	2.9%	4100	190
8	7	P411-LAS-5246	65%	2.0%	4900	150
9	8	P411-LAS-5247	66%	0.8%	3800	49

^aExperiments were performed using a suspension of *E. coli* cells harboring enzyme variants prepared according to the protocol described in **Sections 1.5, 1.6, and 1.7**. Yields were calculated from HPLC calibration curves and the average of triplicate experiments (n = 3).

Table S3. Directed evolution of P411-LAS-5246 for δ -lactone **4a** synthesis.^a



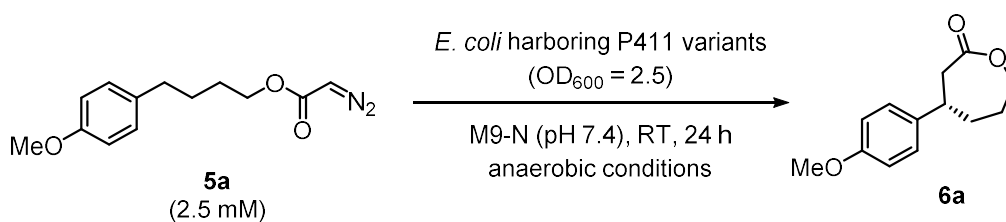
Entry	Round #	Variant	Yield of 4a ^a	Standard deviation of yield	TTN	Standard deviation of TTN
1	0	P411-LAS-5244 ^b	52%	12.4%	3900	930
2	1	P411-LAS-5248	50%	6.2%	2900	360
3	2	P411-LAS-5249 ^c	50%	1.1%	2800	60

^aExperiments were performed using a suspension of *E. coli* cells harboring enzyme variants prepared according to the protocol described in **Sections 1.5, 1.6, and 1.7**. Yields were calculated from HPLC calibration curves and the average of triplicate experiments (n = 3).

^b 46% e.e. for product **4a**.

^c 83% e.e. for product **4a**.

Table S4. Directed evolution of P411-LAS-5265 for ϵ -lactone **6a** synthesis.^a



Entry	Round #	Variant	Yield of 6a ^a	Standard deviation of yield	TTN	Standard deviation of TTN
1	0	P411-LAS-5250	16%	1.9%	940	110
2	1	P411-LAS-5251	26%	1.2%	1100	52
3	2	P411-LAS-5252	21%	0.5%	1100	28
4	3	P411-LAS-5253	31%	1.9%	1500	94
5	4	P411-LAS-5254	31%	4.0%	1300	170
6	5	P411-LAS-5255	36%	3.8%	1500	160
7	6	P411-LAS-5256	44%	2.3%	1700	90
8	7	P411-LAS-5257	52%	2.7%	2200	110
9	8	P411-LAS-5258	45%	2.2%	2300	120
10	9	P411-LAS-5259 ^b	58%	0.3%	2400	14
11	10	P411-LAS-5260 ^c	12%	0.3%	700	19

12	11	P411-LAS-5261	18%	0.8%	1200	51
13	12	P411-LAS-5262	33%	1.1%	2700	93
14	13	P411-LAS-5263	39%	2.2%	2900	160
15	14	P411-LAS-5264 ^d	54%	0.5%	3100	27

^aExperiments were performed using a suspension of *E. coli* cells harboring enzyme variants prepared according to the protocol described in **Sections 1.5, 1.6, and 1.7**. Yields were calculated from HPLC calibration curves and the average of triplicate experiments (n = 3).

^b 51% e.e. for product **6a**.

^c 96% e.e. for product **6a**.

^d 95% e.e. for product **6a**.

3. Nucleotide and Amino Acid Sequences

The genes encoding the heme proteins shown below were cloned using Gibson assembly¹ into vector pET-22b(+) (Novagen) between restriction sites *NdeI* and *XhoI* in frame with a C-terminal 6×His-tag.

Table S5. Mutations of the P411 variants in this study.

Name	Mutations relative to the wild-type P450 _{BM3}	Mutations relative to P411-C10
P411-LAS-5239	N70E, A74G, V78L, A82L, F87A, M118S, P142S, F162L, T175I, M177L, A184V, S226R, H236Q, E252G, I263Y, H266V, T268G, A290V, A328V, A330Y, L353V, I366V, C400S, I401L, T436L, L437Q, E442K, ΔFAD	-
P411-LAS-5240	N70E, A74G, V78L, A82L, F87A, M118S, P142S, F162L, T175I, M177L, A184V, S226R, H236Q, E252G, I263Y, H266V, T268G, A290V, A328V, A330Y, L353V, I366V, C400S, I401L, T436L, L437I , E442K, ΔFAD	Q437I
P411-LAS-5241	N70E, A74G, V78L, A82L, F87A, M118S, P142S, F162L, T175I, M177L, A184V, S226R, H236Q, E252G, I263Y, H266V, T268G, A290V, A328I , A330Y, L353V, I366V, C400S, I401L, T436L, L437I , E442K, ΔFAD	V328I, Q437I
P411-LAS-5242	N70E, A74G, V78M , A82L, F87A, M118S, P142S, F162L, T175I, M177L, A184V, S226R, H236Q, E252G,	L78M, V328I, Q437I

	I263Y, H266V, T268G, A290V, A328I , A330Y, L353V, I366V, C400S, I401L, T436L, L437I , E442K, ΔFAD	
P411-LAS-5243	N70E, A74G, V78M , A82L, F87A, M118S, P142S, F162L, T175I, M177L, A184V, S226R, H236Q, E252G, I263Y, H266V, T268G, A290V, A328I , A330Y, L353V, I366V, C400S, I401L, T436R , L437I , E442K, ΔFAD	L78M , V328I , L436R , Q437I
P411-LAS-5244	N70E, A74G, V78M , A82L, F87A, M118S, P142S, F162L, T175I, M177L, A184V, S226R, H236Q, E252G, I263Y, H266V, T268G, A290V, A328I , A330Y, L353V, I366V, C400S, I401V , T436R , L437I , E442K, ΔFAD	L78M , V328I , L401V , L436R , Q437I
P411-LAS-5245	N70E, A74G, V78M , A82L, F87A, M118S, P142S, F162I , T175I, M177L, A184V, S226R, H236Q, E252G, I263Y, H266V, T268G, A290V, A328I , A330Y, L353V, I366V, C400S, I401V , T436R , L437I , E442K, ΔFAD	L78M , L162I , V328I , L401V , L436R , Q437I
P411-LAS-5246	N70E, A74G, V78M , A82L, F87A, M118S, P142S, F162I , T175I, M177L, A184V, R190L , S226R, H236Q, E252G, I263Y, H266V, T268G, A290V, A328I , A330Y, L353V, I366V, C400S, I401V , T436R , L437I , E442K, ΔFAD	L78M , L162I , R190L , V328I , L401V , L436R , Q437I
P411-LAS-5247	N70S , A74G, V78M , A82L, F87A, M118S, P142S, F162I , T175I, M177L, A184V, R190L , S226R, H236Q, E252G, I263Y, H266V, T268G, A290V, A328I , A330Y, L353V, I366V, C400S, I401V , T436R , L437I , E442K, ΔFAD	E70S , L78M , L162I , R190L , V328I , L401V , L436R , Q437I
P411-LAS-5248	N70E, A74G, V78M , A82L, F87A, M118S, P142S, F162L, T175I, M177L, A184V, S226R, H236Q, E252G,	L78M , L401V , L436R , Q437I

	I263Y, H266V, T268G, A290V, A328V , A330Y, L353V, I366V, C400S, I401V , T436R , L437I , E442K, ΔFAD	
P411-LAS-5249	N70E, A74G, V78M , A82L, F87A, T88S , M118S, P142S, F162L, T175I, M177L, A184V, S226R, H236Q, E252G, I263Y, H266V, T268G, A290V, A328V , A330Y, L353V, I366V, C400S, I401V , T436R , L437I , E442K, ΔFAD	L78M , T88S , L401V , L436R , Q437I
P411-LAS-5250	N70E, S72F, V78L, A82L, F87A, M118S, P142S, F162L, T175I, M177L, A184V, S226R, H236Q, E252G, I263W, H266V, T268G, A290V, A328V, A330Y, S332G, L353V, I366V, C400S, I401L, T436R, L437I, E442K, ΔFAD	S72F , Y263W , S332G , L436R , Q437I
P411-LAS-5251	N70E, S72F, V78L, A82L, F87A, M118S, P142S, F162L, T175I, M177L, A184V, S226R, H236Q, E252G, I263W, H266V, T268G, A290V, T327P , A328V, A330Y, S332G, L353V, I366V, C400S, I401L, T436R, L437I, E442K, ΔFAD	S72F , Y263W , T327P , S332G , L436R , Q437I
P411-LAS-5252	N70E, S72V , V78L, A82L, F87A, M118S, P142S, F162L, T175I, M177L, A184V, S226R, H236Q, E252G, I263W, H266V, T268G, A290V, T327P , A328V, A330Y, S332G, L353V, I366V, C400S, I401L, T436R, L437I, E442K, ΔFAD	S72V , Y263W , T327P , S332G , L436R , Q437I
P411-LAS-5253	N70E, S72V , V78L, A82L, F87A, M118S, P142S, F162L, T175I, M177L, A184V, S226R, H236Q, E252G, I263W, H266V, T268G, A290V, T327P , A328V, P329P	S72V , Y263W , T327P , S332G , L436R , Q437I

	(silent mutation), A330Y, S332G, L353V, I366V, C400S, I401L, T436R, L437I, E442K, ΔFAD	
P411-LAS-5254	N70E, S72V , V78L, A82L, F87A, M118S, P142S, F162L, T175I, M177L, A184V, H236Q, E252G, I263W, H266V, T268G, A290V, T327P , A328V, A330Y, S332G, L353V, I366V, C400S, I401L, T436R, L437I, E442K, ΔFAD	S72V, R226S, Y263W, T327P, S332G, L436R, Q437I
P411-LAS-5255	N70E, S72V , V78L, A82L, F87A, H92F , M118S, P142S, F162L, T175I, M177L, A184V, H236Q, E252G, I263W, H266V, T268G, A290V, T327P , A328V, A330Y, S332G, L353V, I366V, C400S, I401L, T436R, L437I, E442K, ΔFAD	S72V, H92F, R226S, Y263W, T327P, S332G, L436R, Q437I
P411-LAS-5256	N70E, S72V , V78L, A82L, F87A, H92F , M118S, P142S, T175I, M177L, A184V, H236Q, E252G, I263W, H266V, T268G, A290V, T327P , A328V, A330Y, S332G, L353V, I366V, C400S, I401L, T436R, L437I, E442K, ΔFAD	S72V, H92F, L162F, R226S, Y263W, T327P, S332G, L436R, Q437I
P411-LAS-5257	N70E, S72V , V78L, A82L, F87A, H92F , M118S, P142S, T175I, M177L, A184V, H236Q, E252R , I263W, H266V, T268G, A290V, T327P , A328V, A330Y, S332G, L353V, I366V, C400S, I401L, T436R, L437I, E442K, ΔFAD	S72V, H92F, L162F, R226S, G252R, Y263W, T327P, S332G, L436R, Q437I
P411-LAS-5258	N70E, S72V , V78L, A82L, F87A, H92F , M118S, P142S, T175I, M177L, A184V, H236Q, E252R , I263W, H266V, T268G, A290V, T327P , A328V, A330Y, S332G, L353V, C400S, I401L, T436R, L437I, E442K, ΔFAD	S72V, H92F, L162F, R226S, G252R, Y263W, T327P, S332G,

		V366I, L436R, Q437I
P411-LAS-5259	N70E, S72V , V78L, A82L, F87A, H92F , M118S, P142G , T175I, M177L, A184V, H236Q, E252R , I263W, H266V, T268G, A290V, T327P , A328V, A330Y, S332G, L353V, C400S, I401L, T436R, L437I, E442K, ΔFAD	S72V, H92F, S142G, L162F, R226S, G252R, Y263W, T327P, S332G, V366I, L436R, Q437I
P411-LAS-5260	N70E, S72V , V78L, A82L, F87V , H92F , M118S, P142G , T175I, M177L, A184V, H236Q, E252R , I263W, H266V, T268G, A290V, T327P , A328V, A330Y, S332G, L353V, C400S, I401L, T436R, L437I, E442K, ΔFAD	S72V, A87V, H92F, S142G, L162F, R226S, G252R, Y263W, T327P, S332G, V366I, L436R, Q437I
P411-LAS-5261	N70E, S72V , V78L, A82L, F87V , H92F , M118S, P142G , T175I, M177L, A184V, H236Q, E252R , I263W, H266V, T268G, A290V, T327P , A328I , A330Y, S332G, L353V, C400S, I401L, T436R, L437I, E442K, ΔFAD	S72V, A87V, H92F, S142G, L162F, R226S, G252R, Y263W, T327P, V328I, S332G, V366I, L436R, Q437I
P411-LAS-5262	N70E, S72V , V78L, D80E , A82L, F87V , H92F , M118S, P142G , T175I, M177L, A184V, I219I (silent mutation) , H236Q, G240R , E252R , I263W, H266V, T268G, A290V, T327P , A328I , A330Y, S332G, L353V, C400S, I401L, T436R, L437I, E442K, ΔFAD	S72V, D80E, A87V, H92F, S142G, L162F, R226S, G240R, G252R, Y263W, T327P, V328I,

		S332G, V366I, L436R, Q437I
P411-LAS-5263	I2T, N70E, S72V, V78L, D80E, A82L, F87V, H92F, M118S, P142G, T175I, M177L, A184V, H236Q, G240R, E252R, I263W, H266V, T268G, F279L, A290V, T327P, A328I, A330Y, S332G, L353V, C400S, I401L, T436R, L437I, E442K, ΔFAD	I2T, S72V, D80E, A87V, H92F, S142G, L162F, R226S, G240R, G252R, Y263W, F279L, T327P, V328I, S332G, V366I, L436R, Q437I
P411-LAS-5264	I2T, N70E, S72V, V78L, D80E, A82L, F87V, H92F, M118S, P142G, T175I, M177L, A184V, A191A (silent mutation), H236Q, G240R, E252R, I263W, H266V, T268G, F279L, A290V, T327P, A328I, A330Y, S332G, L353V, C400S, I401L, T436R, L437I, E442K, ΔFAD	I2T, S72V, D80E, A87V, H92F, S142G, L162F, R226S, G240R, G252R, Y263W, F279L, T327P, V328I, S332G, V366I, L436R, Q437I
P411-LAS-5265	N70E, A74G, V78L, A82L, F87A, M118S, P142S, F162L, T175I, M177L, A184V, S226R, H236Q, E252G, I263W, H266V, T268G, A290V, A328V, A330Y, L353V, I366V, C400S, I401L, T436L, L437I, E442K, ΔFAD	Y263W, Q437I

P411-LAS-5266	N70E, A74G, V78L, A82L, F87P , M118S, P142S, F162L, T175I, M177L, A184V, S226R, H236Q, E252G, I263Y, A264S , H266V, E267D , T268G, A290V, T327P , A328V, A330Y, S332A , L353V, I366V, C400S, I401L, T436L, E442K ΔFAD	A87P , A264S , E267D , T327P , S332A , Q437L
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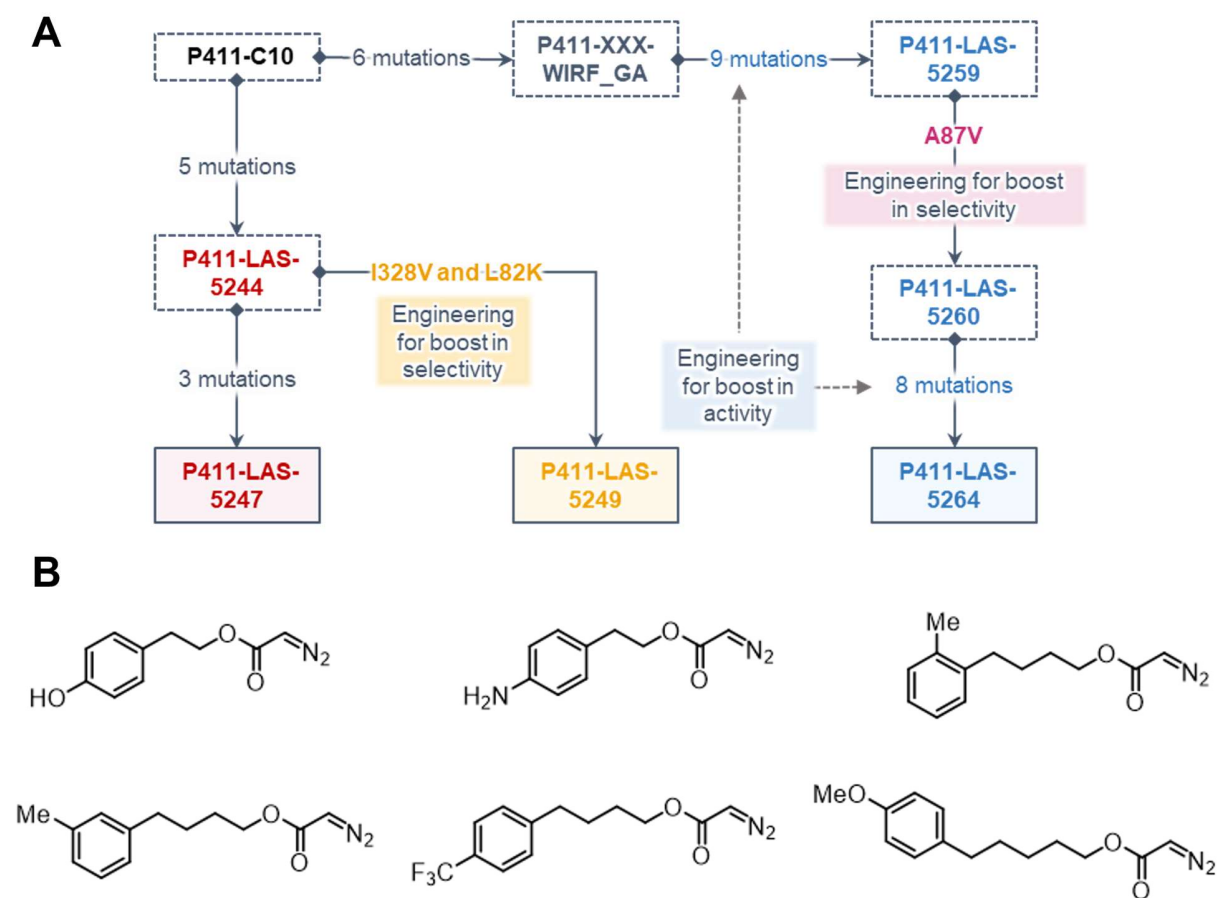


Figure S1. (A) Evolutionary trajectories of lactone synthases P411-LAS-5247, P411-LAS-5249, and P411-LAS-5264 from P411-C10. (B) Less reactive and unreactive substrates.

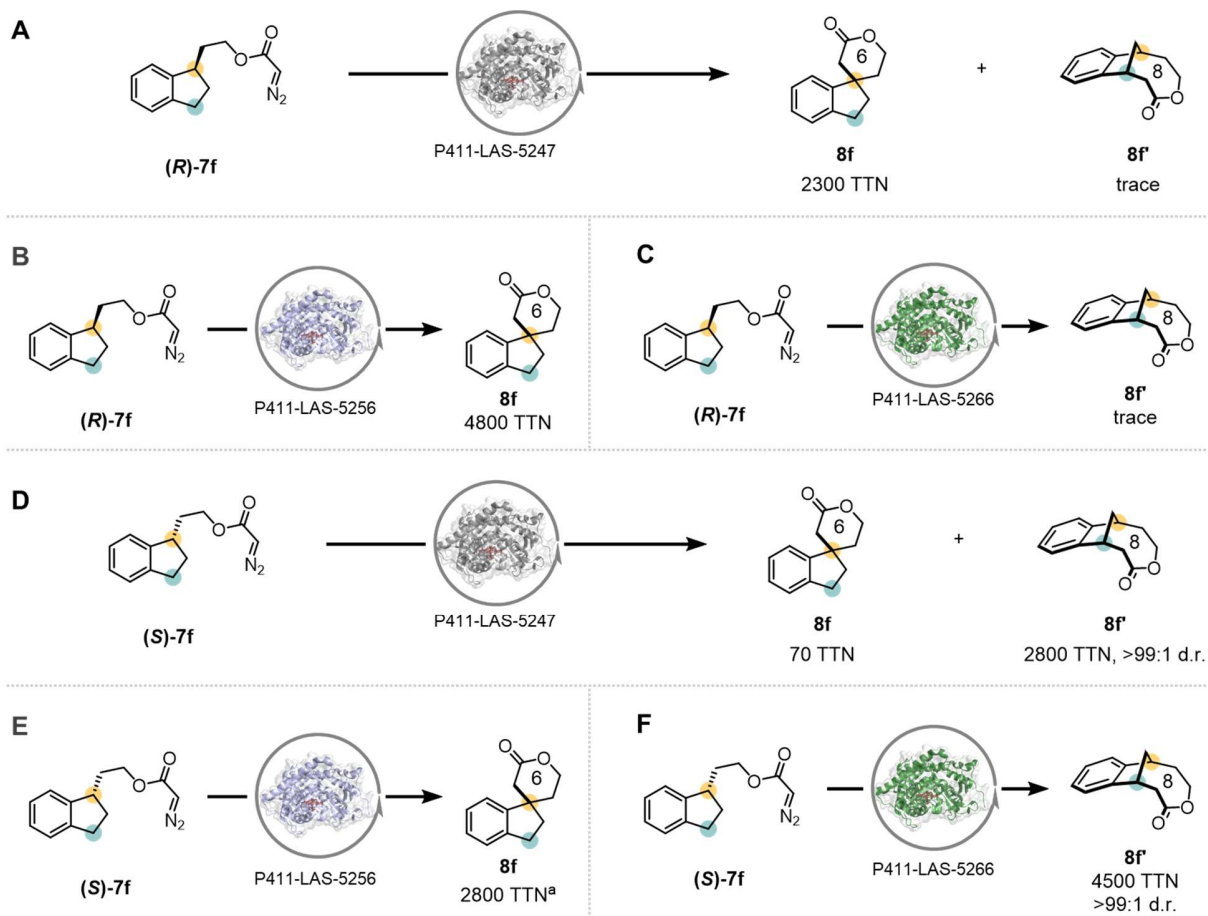


Figure S2. Reaction of stereopure 7f with P411-LAS-5247, P411-LAS-5256, and P411-LAS-5266.

^a550 TTN for product **8f'**

DNA and amino acid sequences of P411-LAS-5239 (P411-C10)⁵:

ATGACAATTAAAGAAATGCCTCAGCCAAAAACGTTTGGAGAGCTTAAAAATTTACCG
TTATTAAACACAGATAAACCGGTTCAAGCTTTGATGAAAATTGCGGATGAATTAGGA
GAAATCTTTAAATTCGAGGCGCCTGGTCGTGTAACGCGCTACTTATCAAGTCAGCGTC
TAATTAAAGAAGCATGCGATGAATCACGCTTTGATAAAGAGTTAAGTCAAGGTCTGA
AATTTCTGCGTGATTTTCTTGGAGACGGGTTAGCCACAAGCTGGACGCATGAAAAAA
ATTGGAAAAAGCGCATAATATCTTACTTCCAAGCTTTAGTCAGCAGGCAATGAAAG
GCTATCATGCGAGTATGGTCGATATCGCCGTGCAGCTTGTTCAAAGTGGGAGCGTCT
AAATGCAGATGAGCATATTGAAGTATCGGAAGACATGACACGTTTAACGCTTGATAC
AATTGGTCTTTGCGGCTTTAACTATCGCCTTAACAGCTTTTACCGAGATCAGCCTCAT
CCATTTATTATAAGTCTGGTCCGTGCACTGGATGAAGTAATGAACAAGCTGCAGCGA
GCAAATCCAGACGACCCAGCTTATGATGAAAACAAGCGCCAGTTTCAAGAAGATATC
AAGGTGATGAACGACCTAGTAGATAAAATTATTGCAGATCGCAAAGCAAGGGGTGA
ACAAAGCGATGATTTATTAACGCAGATGCTAAACGGAAAAGATCCAGAAACGGGTG
AGCCGCTTGATGACGGGAACATTCGCTATCAAATTATTACATTCTTATATGCGGGAGT
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GTATTACAAAAAGTAGCAGAAGAAGCAGCACGAGTTCTAGTAGATCCTGTTCCAAGC
TACAAACAAGTCAAACAGCTTAAATATGTCGGCATGGTCTTAAACGAAGCGCTGCGC
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GTGATAAAACAGTTTGGGGAGACGATGTGGAGGAGTTCCGTCCAGAGCGTTTTGAAA
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GTAAAACCTAAAGGCTTTGTGGTAAAAGCAAAATCGAAAAAAATTCCGCTTGCGCG
TATTCCTTCACCTAGCACTGAACAGTCTGCTAAAAAAGTACGCAAAAAGGCAGAAAA
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LVDPVPSYKQVKQLKYVGMVLNEALRLWPTVPYFSLYAKEDTVLGGEYPLEKGDEVMV
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SYNGHPPDNAKQFVDWLDQASADEVKGVRYSVFGCGDKNWATTYQKVPAFIDETLAA
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ADMPLAKMHGAFSTLEHHHHHHH*

DNA and amino acid sequences of P411-LAS-5244:

ATGACAATTAAAGAAATGCCTCAGCCAAAAACGTTTGGAGAGCTTAAAAATTTACCG
TTATTAAACACAGATAAACCGGTTCAAGCTTTGATGAAAATTGCGGATGAATTAGGA
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DNA and amino acid sequences of P411-LAS-5247:

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DNA and amino acid sequences of P411-LAS-5249:

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NAHNTPLLVLVYGSNMGTAEGTARDLADIAMSKGFAPQVATLDSHAGNLPREGAVLIVTA
SYNGHPPDNAKQFVDWLDQASADEVKGVRYSVFGCGDKNWATTYQKVPAFIDETLAA
KGAENIADRGEADASDDFEGTYEEWREHMWSDVAA YFNLDIENSEDNKSTLSLQFVDSA
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DNA and amino acid sequences of P411-LAS-5250 (P411-C10-WIRF_GA)⁵:

ATGACAATTAAAGAAATGCCTCAGCCAAAAACGTTTGGAGAGCTTAAAAATTTACCG
TTATTAAACACAGATAAACCGGTTCAAGCTTTGATGAAAATTGCGGATGAATTAGGA
GAAATCTTTAAATTCGAGGCGCCTGGTCGTGTAACGCGCTACTTATCAAGTCAGCGTC
TAATTAAAGAAGCATGCGATGAATCACGCTTTGATAAAGAGTTATTTCAAGCGCTGA
AATTTCTGCGTGATTTTCTTGGAGACGGGTTAGCCACAAGCTGGACGCATGAAAAAA
ATTGGAAAAAGCGCATAATATCTTACTTCCAAGCTTTAGTCAGCAGGCAATGAAAG
GCTATCATGCGAGTATGGTCGATATCGCCGTGCAGCTTGTTCAAAAGTGGGAGCGTCT
AAATGCAGATGAGCATATTGAAGTATCGGAAGACATGACACGTTTAACGCTTGATAC
AATTGGTCTTTGCGGCTTTAACTATCGCCTTAACAGCTTTTACCGAGATCAGCCTCAT
CCATTTATTATAAGTCTGGTCCGTGCACTGGATGAAGTAATGAACAAGCTGCAGCGA
GCAAATCCAGACGACCCAGCTTATGATGAAAACAAGCGCCAGTTTCAAGAAGATATC
AAGGTGATGAACGACCTAGTAGATAAAATTATTGCAGATCGCAAAGCAAGGGGTGA
ACAAAGCGATGATTTATTAACGCAGATGCTAAACGGAAAAAGATCCAGAAACGGGTG
AGCCGCTTGATGACGGGAACATTCGCTATCAAATTATTACATTCTTATGGGCGGGAGT
TGAAGGTACAAGTGGTCTTTTATCATTGCGCTGTATTTCTTAGTGAAAAATCCACAT
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TTATGGCCAACGGTTCCTTATTTTGGTCTATATGCAAAGAAGATACGGTGCTTGAG
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GTGATAAACAGTTTGGGGAGACGATGTGGAGGAGTTCCGTCCAGAGCGTTTTTGAAA
ATCCAAGTGCGATTCCGCAGCATGCGTTTAAACCGTTTGGAAACGGTCAGCGTGCGT
CTCTGGGTCAGCAGTTCGCTCTTCATGAAGCAACGCTGGTACTTGGTATGATGCTAAA
ACACTTTGACTTTGAAGATCATACAACTACGAGCTCGATATTAAAGAACGTATTAC
GTAAAACCTAAAGGCTTTGTGGTAAAAGCAAAATCGAAAAAAATTCCGCTTGCGCG
TATTCCTTCACCTAGCACTGAACAGTCTGCTAAAAAAGTACGCAAAAAGGCAGAAAA
CGCTCATAATACGCCGCTGCTTGTGCTATACGGTTCAAATATGGGTACCGCTGAAGGA
ACGGCGCGTGATTTAGCAGATATTGCAATGAGCAAAGGATTTGCACCGCAGGTGCGA
ACGCTTGATTCACACGCCGGAATCTTCCGCGCGAAGGAGCTGTATTAATTGTAACG
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AAGCGTCTGCTGATGAAGTAAAAGGCGTTCGCTACTCCGTATTTGGATGCGGCGATA
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TAAAGGGGCAGAAAACATCGCTGACCGCGGTGAAGCAGATGCAAGCGACGACTTTG
AAGGCACATATGAAGAATGGCGTGAACATATGTGGAGTGACGTAGCAGCCTACTTTA
ACCTCGACATTGAAAACAGTGAAGATAATAAATCTACTCTTTCACTTCAATTTGTCGA
CAGCGCCGCGGATATGCCGCTTGCGAAAATGCACGGTGCGTTTTCAACGCTCGAGCA
CCACCACCACCACCACTGA

MTIKEMPQPKTFGELKNLPLLNTDKPVQALMKIADELGEIFKFEAPGRVTRYLSSQRLIKE
ACDESRFDKELFQALKFLRDFLDGLATSWTHEKNWKKAHNILLPSFSQQAMKGYHAS
MVDIAVQLVQKWERLNADEHIEVSEDMTRLTLDITGLCGFNYRLNSFYRDQPHPFISLVR
ALDEVMNKLQRANPDDPAYDENKRQFQEDIKVMNDLVDKIIADRKARGEQSDDLTTQM
LNGKDPETGEPLDDGNIRYQIITFLWAGVEGTSGLLSFALYFLVKNPHVLQKVAEEAARV
LVDPVPSYKQVKQLKYVGMVLNEALRLWPTVPYFGLYAKEDTVLGGEYPLEKGDEVM
VLIPQLHRDKTVWGDDVEEFRPERFENPSAIPQHAFKPFNGNGQRASLGQQFALHEATLVL
GMMLKHFDHFEDHTNYELDIKERITLKPFGFVVKAKSKKIPLGGIPSPSTEQSAKKVRKKA
ENAHNTPLLVLVYGSNMGTAEGTARDLADIAMSKGFAPQVATLDSHAGNLPREGAVLIVT
ASYNGHPPDNAKQFVDWLDQASADEVKGVRYSVFGCGDKNWATTYQKVPAFIDETLA
AKGAENIADRGEADASDDFEGTYEEWREHMWSDVAAYFNLDIENSEDNKSTLSLQFVDS
AADMPLAKMHGAFSTLEHHHHHH*

DNA and amino acid sequences of P411-LAS-5256:

ATGACAATTAAAGAAATGCCTCAGCCAAAAACGTTTGGAGAGCTTAAAAATTTACCG
TTATTAAACACAGATAAACCGGTTCAAGCTTTGATGAAAATTGCGGATGAATTAGGA
GAAATCTTTAAATTCGAGGCGCCTGGTCGTGTAACGCGCTACTTATCAAGTCAGCGTC
TAATTAAAGAAGCATGCGATGAATCACGCTTTGATAAAGAGTTAGTGCAAGCGCTGA
AATTTCTGCGTGATTTTCTTGGAGACGGGTTAGCCACAAGCTGGACGTTTGAAAAAA
ATTGGAAAAAGCGCATAATATCTTACTTCCAAGCTTTAGTCAGCAGGCAATGAAAG
GCTATCATGCGAGTATGGTCGATATCGCCGTGCAGCTTGTTCAAAGTGGGAGCGTCT
AAATGCAGATGAGCATATTGAAGTATCGGAAGACATGACACGTTTAACGCTTGATAC
AATTGGTCTTTGCGGCTTTAACTATCGCTTTAACAGCTTTTACCGAGATCAGCCTCATC
CATTTATTATAAGTCTGGTCCGTGCACTGGATGAAGTAATGAACAAGCTGCAGCGAG
CAAATCCAGACGACCCAGCTTATGATGAAAACAAGCGCCAGTTTCAAGAAGATATCA
AGGTGATGAACGACCTAGTAGATAAAATTATTGCAGATCGCAAAGCAAGTGGTGAAC
AAAGCGATGATTTATTAACGCAGATGCTAAACGGAAAAGATCCAGAAACGGGTGAG
CCGCTTGATGACGGGAACATTCGCTATCAAATTATTACATTCTTATGGGCGGGAGTTG
AAGGTACAAGTGGTCTTTTATCATTTGCGCTGTATTTCTTAGTGAAAAATCCACATGT
ATTACAAAAAGTAGCAGAAGAAGCAGCACGAGTTCTAGTAGATCCTGTTCCAAGCTA
CAAACAAGTCAAACAGCTTAAATATGTCGGCATGGTCTTAAACGAAGCGCTGCGCTT
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AGAATATCCTTTAGAAAAAGGCGACGAAGTAATGGTTCTGATTCCTCAGCTTCACCGT
GATAAAACAGTTTGGGGAGACGATGTGGAGGAGTTCCGTCCAGAGCGTTTTGAAAAT
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TGGGTCAGCAGTTCGCTCTTCATGAAGCAACGCTGGTACTTGGTATGATGCTAAAACA
CTTTGACTTTGAAGATCATACAACTACGAGCTCGATATTAAAGAACGTATTACGTTA
AAACCTAAAGGCTTTGTGGTAAAAGCAAAATCGAAAAAAATTCCGCTTGGCGGTATT
CCTTCACCTAGCACTGAACAGTCTGCTAAAAAAGTACGCAAAAAGGCAGAAAACGCT
CATAATACGCCGCTGCTTGTGCTATACGGTTCAAATATGGGTACCGCTGAAGGAACG
GCGCGTGATTTAGCAGATATTGCAATGAGCAAAGGATTTGCACCGCAGGTGCAACG
CTTGATTCACACGCCGGAATCTTCCGCGCGAAGGAGCTGTATTAATTGTAACGGCGT
CTTATAACGGTCATCCGCCTGATAACGCAAAGCAATTTGTCGACTGGTTAGACCAAG

CGTCTGCTGATGAAGTAAAAGGCGTTCGCTACTCCGTATTTGGATGCGGGCGATAAAA
ACTGGGCTACTACGTATCAAAAAGTGCCTGCTTTTATCGATGAAACGCTTGCCGCTAA
AGGGGCAGAAAACATCGCTGACCGCGGTGAAGCAGATGCAAGCGACGACTTTGAAG
GCACATATGAAGAATGGCGTGAACATATGTGGAGTGACGTAGCAGCCTACTTTAACC
TCGACATTGAAAACAGTGAAGATAATAAATCTACTCTTTCACCTCAATTTGTCGACAG
CGCCGCGGATATGCCGCTTGCGAAAATGCACGGTGCGTTTTCAACGCTCGAGCACCA
CCACCACCACCACTGA

MTIKEMPQPKTFGELKNLPLLNTDKPVQALMKIADELGEIFKFEAPGRVTRYLSSQRLIKE
ACDESRFDKELVQALKFLRDFLGDLATSWTFEKNWKKAHNILLPSFSQQAMKGYHAS
MVDIAVQLVQKWERLNADEHIEVSEDMTRLTLDITGLCGFNRYRFSFYRDQPHPFISLVR
ALDEVMNKLQRANPDDPAYDENKRQFQEDIKVMNDLVDKIIADRKASGEQSDDLTLTQM
LNGKDPETGEPLDDGNIRYQIITFLWAGVEGTSGLLSFALYFLVKNPHVLQKVAEEAARV
LVDPVPSYKQVKQLKYVGMVLNEALRLWPPVPYFGLYAKEDTVLGGEYPLEKGDEV
VLIPQLHRDKTVWGDDVEEFRPERFENPSAIPQHAFKPFNGQQRASLGQQFALHEATLVL
GMMLKHFDHFDHTNYELDIKERITLKPFGFVVKAKSKKIPLGGIPSPSTEQSAKKVRKKA
ENAHNTPLLVLVYGSNMGTAEGTARDLADIAMSKGFAPQVATLDSHAGNLPREGAVLIVT
ASYNGHPPDNAKQFVDWLDQASADEVKGVRYSVFGCGDKNWATTYQKVPAFIDETLA
AKGAENIADRGEADASDDFEGTYEEWREHMWSDVAAYFNLDIENSEDNKSTLSLQFVDS
AADMPLAKMHGAFSTLEHHHHHH*

DNA and amino acid sequences of P411-LAS-5266:

ATGACAATTAAAGAAATGCCTCAGCCAAAAACGTTTGGAGAGCTTAAAAATTTACCG
TTATTAAACACAGATAAACCGGTTCAAGCTTTGATGAAAATTGCGGATGAATTAGGA
GAAATCTTTAAATTCGAGGCGCCTGGTCGTGTAACGCGCTACTTATCAAGTCAGCGTC
TAATTAAAGAAGCATGCGATGAATCACGCTTTGATAAAGAGTTAGTGCAAGCGCTGA
AATTTCTGCGTGATTTTCTTGGAGACGGGTTAGCCACAAGCTGGACGTTTGAAAAAA
ATTGGAAAAAGCGCATAATATCTTACTTCCAAGCTTTAGTCAGCAGGCAATGAAAG
GCTATCATGCGAGTATGGTCGATATCGCCGTGCAGCTTGTTCAAAGTGGGAGCGTCT
AAATGCAGATGAGCATATTGAAGTATCGGAAGACATGACACGTTTAACGCTTGATAC
AATTGGTCTTTGCGGCTTTAACTATCGCTTTAACAGCTTTTACCGAGATCAGCCTCATC
CATTTATTATAAGTCTGGTCCGTGCACTGGATGAAGTAATGAACAAGCTGCAGCGAG
CAAATCCAGACGACCCAGCTTATGATGAAAACAAGCGCCAGTTTCAAGAAGATATCA
AGGTGATGAACGACCTAGTAGATAAAATTATTGCAGATCGCAAAGCAAGTGGTGAAC
AAAGCGATGATTTATTAACGCAGATGCTAAACGGAAAAGATCCAGAAACGGGTGAG
CCGCTTGATGACCGTAACATTCGCTATCAAATTATTACATTCTTATGGGCGGGAGTTG
AAGGTACAAGTGGTCTTTTATCATTTGCGCTGTATTTCTTAGTGAAAAATCCACATGT
ATTACAAAAAGTAGCAGAAGAAGCAGCACGAGTTCTAGTAGATCCTGTTCCAAGCTA
CAAACAAGTCAAACAGCTTAAATATGTCGGCATGGTCTTAAACGAAGCGCTGCGCTT
ATGGCCACCGGTTCCGTATTTTGGTCTATATGCAAAAGAAGATACGGTGCTTGGAGG
AGAATATCCTTTAGAAAAAGGCGACGAAGTAATGGTTCTGATTCTCAGCTTCACCGT
GATAAAACAGTTTGGGGAGACGATGTGGAGGAGTTCCGTCCAGAGCGTTTTGAAAAT
CCAAGTGCGATTCCGCAGCATGCGTTTAAACCGTTTGGAAACGGTCAGCGTGCGTCTC
TGGGTCAGCAGTTTCGCTCTTCATGAAGCAACGCTGGTACTTGGTATGATGCTAAAACA
CTTTGACTTTGAAGATCATACAAACTACGAGCTCGATATTAAAGAACGTATTACGTTA
AAACCTAAAGGCTTTGTGGTAAAAGCAAAATCGAAAAAAATTCCGCTTGGCGGTATT
CCTTCACCTAGCACTGAACAGTCTGCTAAAAAAGTACGCAAAAAGGCAGAAAACGCT
CATAATACGCCGCTGCTTGTGCTATACGGTTCAAATATGGGTACCGCTGAAGGAACG
GCGCGTGATTTAGCAGATATTGCAATGAGCAAAGGATTTGCACCGCAGGTGCAACG
CTTGATTACACGCCGGAATCTTCCGCGCGAAGGAGCTGTATTAATTGTAACGGCGT
CTTATAACGGTCATCCGCCTGATAACGCAAAGCAATTTGTCGACTGGTTAGACCAAG

CGTCTGCTGATGAAGTAAAAGGCGTTCGCTACTCCGTATTTGGATGCGGGCGATAAAA
ACTGGGCTACTACGTATCAAAAAGTGCCTGCTTTTATCGATGAAACGCTTGCCGCTAA
AGGGGCAGAAAACATCGCTGACCGCGGTGAAGCAGATGCAAGCGACGACTTTGAAG
GCACATATGAAGAATGGCGTGAACATATGTGGAGTGACGTAGCAGCCTACTTTAACC
TCGACATTGAAAACAGTGAAGATAATAAATCTACTCTTTCACCTCAATTTGTCGACAG
CGCCGCGGATATGCCGCTTGCGAAAATGCACGGTGCGTTTTCAACGCTCGAGCACCA
CCACCACCACCACTGA

MTIKEMPQPKTFGELKNLPLLNTDKPVQALMKIADELGEIFKFEAPGRVTRYLSSQRLIKE
ACDESRFDKELVQALKFLRDFLGDLATSWTFEKNWKKAHNILLPSFSQQAMKGYHAS
MVDIAVQLVQKWERLNADEHIEVSEDMTRLTLDITGLCGFNRYRFSFYRDQPHPFISLVR
ALDEVMNKLQRANPDDPAYDENKRQFQEDIKVMNDLVDKIIADRKASGEQSDDLTLTQM
LNGKDPETGEPLDDRNIRYQIITFLWAGVEGTSGLLSFALYFLVKNPHVLQKVAEEAARV
LVDPVPSYKQVKQLKYVGMVLNEALRLWPPVPYFGLYAKEDTVLGGEYPLEKGDEV
VLIPQLHRDKTVWGDDVEEFRPERFENPSAIPQHAFKPFNGNGQRASLGQQFALHEATLVL
GMMLKHFDHFEDHTNYELDIKERITLKPFGFVVKAKSKKIPLGGIPSPSTEQSAKKVRKKA
ENAHNTPLLVLVYGSNMGTAEGTARDLADIAMSKGFAPQVATLDSHAGNLPREGAVLIVT
ASYNGHPPDNAKQFVDWLDQASADEVKGVRYSVFGCGDKNWATTYQKVPAFIDETLA
AKGAENIADRGEADASDDFEGTYEEWREHMWSDVAAYFNLDIENSEDNKSTLSLQFVDS
AADMPLAKMHGAFSTLEHHHHHHH*

DNA and amino acid sequences of P411-LAS-5259:

ATGACAATTAAAGAAATGCCTCAGCCAAAAACGTTTGGAGAGCTTAAAAATTTACCG
TTATTAAACACAGATAAACCGGTTCAAGCTTTGATGAAAATTGCGGATGAATTAGGA
GAAATCTTTAAATTCGAGGCGCCTGGTCGTGTAACGCGCTACTTATCAAGTCAGCGTC
TAATTAAAGAAGCATGCGATGAATCACGCTTTGATAAAGAGTTAGTGCAAGCGCTGA
AATTTCTGCGTGATTTTCTTGGAGACGGGTTAGCCACAAGCTGGACGTTTGAAAAAA
ATTGGAAAAAGCGCATAATATCTTACTTCCAAGCTTTAGTCAGCAGGCAATGAAAG
GCTATCATGCGAGTATGGTCGATATCGCCGTGCAGCTTGTTCAAAAGTGGGAGCGTCT
AAATGCAGATGAGCATATTGAAGTAGGTGAAGACATGACACGTTTAACGCTTGATAC
AATTGGTCTTTGCGGCTTTAACTATCGCTTTAACAGCTTTTACCGAGATCAGCCTCATC
CATTTATTATAAGTCTGGTCCGTGCACTGGATGAAGTAATGAACAAGCTGCAGCGAG
CAAATCCAGACGACCCAGCTTATGATGAAAACAAGCGCCAGTTTCAAGAAGATATCA
AGGTGATGAACGACCTAGTAGATAAAATTATTGCAGATCGCAAAGCAAGTGGTGAAC
AAAGCGATGATTTATTAACGCAGATGCTAAACGGAAAAGATCCAGAAACGGGTGAG
CCGCTTGATGACCGTAACATTCGCTATCAAATTATTACATTCTTATGGGCGGGAGTTG
AAGGTACAAGTGGTCTTTTATCATTTGCGCTGTATTTCTTAGTGAAAAATCCACATGT
ATTACAAAAAGTAGCAGAAGAAGCAGCACGAGTTCTAGTAGATCCTGTTCCAAGCTA
CAAACAAGTCAAACAGCTTAAATATGTCTGGCATGGTCTTAAACGAAGCGCTGCGCTT
ATGGCCACCGGTTCCGTATTTTGGTCTATATGCAAAAGAAGATACGGTGCTTGGAGG
AGAATATCCTTTAGAAAAAGGCGACGAAGTAATGGTTCTGATTCCTCAGCTTCACCGT
GATAAAACAATTTGGGGAGACGATGTGGAGGAGTTCCGTCCAGAGCGTTTTGAAAAT
CCAAGTGCGATTCCGCAGCATGCGTTTAAACCGTTTGGAACGGTCAGCGTGCGTCTC
TGGGTCAGCAGTTTCGCTCTTCATGAAGCAACGCTGGTACTTGGTATGATGCTAAAACA
CTTTGACTTTGAAGATCATACAACTACGAGCTCGATATTAAAGAACGTATTACGTTA
AAACCTAAAGGCTTTGTGGTAAAAGCAAAATCGAAAAAAATTCCGCTTGGCGGTATT
CCTTCACCTAGCACTGAACAGTCTGCTAAAAAAGTACGCAAAAAGGCAGAAAACGCT
CATAATACGCCGCTGCTTGTGCTATACGGTTCAAATATGGGTACCGCTGAAGGAACG
GCGCGTGATTTAGCAGATATTGCAATGAGCAAAGGATTTGCACCGCAGGTGCAACG
CTTGATTCACACGCCGGAATCTTCCGCGCGAAGGAGCTGTATTAATTGTAACGGCGT
CTTATAACGGTCATCCGCCTGATAACGCAAAGCAATTTGTCGACTGGTTAGACCAAG

CGTCTGCTGATGAAGTAAAAGGCGTTCGCTACTCCGTATTTGGATGCGGGCGATAAAA
ACTGGGCTACTACGTATCAAAAAGTGCCTGCTTTTATCGATGAAACGCTTGCCGCTAA
AGGGGCAGAAAACATCGCTGACCGCGGTGAAGCAGATGCAAGCGACGACTTTGAAG
GCACATATGAAGAATGGCGTGAACATATGTGGAGTGACGTAGCAGCCTACTTTAACC
TCGACATTGAAAACAGTGAAGATAATAAATCTACTCTTTCACCTCAATTTGTCGACAG
CGCCGCGGATATGCCGCTTGCGAAAATGCACGGTGCGTTTTCAACGCTCGAGCACCA
CCACCACCACCACTGA

MTIKEMPQPKTFGELKNLPLLNTDKPVQALMKIADELGEIFKFEAPGRVTRYLSSQRLIKE
ACDESRFDKELVQALKFLRDFLGDLATSWTFEKNWKKAHNILLPSFSQQAMKGYHAS
MVDIAVQLVQKWERLNADEHIEVGEDMTRLTLDTIGLCGFNYRFNSFYRDQPHPFIISLV
RALDEV MNKLQRANPDDPAYDENKRQFQEDIKVMNDLVDKIIADRKASGEQSDDLTTQ
MLNGKDPETGEPLDDRNIRYQIITFLWAGVEGTSGLLSFALYFLVKNPHVLQKVAEEAAR
VLVDPVPSYKQVKQLKYVGMVLNEALRLWPPVPYFGLYAKEDTVLGGEYPLEKGDEV
MVLIPQLHRDKTIWGDDVEEFRPERFENPSAIPQHAFKPFNGNGQRASLGQQFALHEATLV
LGMMLKHFDHFEDHTNYELDIKERITLKPFGFVVKAKSKKIPLGGIPSPSTEQSAKKVRKK
AENAHNTPLLVLVYGSNMGTAEGTARDLADIAMSKGFAPQVATLDSHAGNLPREGAVLIV
TASYNGHPPDNAKQFVDWLDQASADEVKGVRYSVFGCGDKNWATTYQKVPAFIDETLA
AKGAENIADRGEADASDDFEGTYEEWREHMWSDVAAYFNLDIENSEDNKSTLSLQFVDS
AADMPLAKMHGAFSTLEHHHHHH*

DNA and amino acid sequences of P411-LAS-5264:

ATGACAACCTAAAGAAATGCCTCAGCCAAAAACGTTTGGAGAGCTTAAAAATTTACCG
TTATTAAACACAGATAAACCGGTTCAAGCTTTGATGAAAATTGCGGATGAATTAGGA
GAAATCTTTAAATTCGAGGCGCCTGGTCGTGTAACGCGCTACTTATCAAGTCAGCGTC
TAATTAAAGAAGCATGCGATGAATCACGCTTTGATAAAGAGTTAGTGCAAGCGCTGA
AATTTCTGCGTGAATTTCTTGGAGACGGGTTAGTGACAAGCTGGACGTTTGAAAAAA
ATTGGAAAAAGCGCATAATATCTTACTTCCAAGCTTTAGTCAGCAGGCAATGAAAG
GCTATCATGCGAGTATGGTCGATATCGCCGTGCAGCTTGTTCAAAAGTGGGAGCGTCT
AAATGCAGATGAGCATATTGAAGTAGGTGAAGACATGACACGTTTAACGCTTGATAC
AATTGGTCTTTGCGGCTTTAACTATCGCTTTAACAGCTTTTACCGAGATCAGCCTCATC
CATTTATTATAAGTCTGGTCCGTGCACTGGATGAAGTAATGAACAAGCTGCAGCGAG
CGAATCCAGACGACCCAGCTTATGATGAAAACAAGCGCCAGTTTCAAGAAGATATCA
AGGTGATGAACGACCTAGTAGATAAAATCATTGCAGATCGCAAAGCAAGTGGTGAAC
AAAGCGATGATTTATTAACGCAGATGCTAAACAGAAAAGATCCAGAAACGGGTGAG
CCGCTTGATGACCGTAACATTCGCTATCAAATTATTACATTCTTATGGGCGGGAGTTG
AAGGTACAAGTGGTCTTTTATCATTTGCGCTGTATCTCTTAGTGAAAAATCCACATGT
ATTACAAAAAGTAGCAGAAGAAGCAGCACGAGTTCTAGTAGATCCTGTTCCAAGCTA
CAAACAAGTCAAACAGCTTAAATATGTCTGGCATGGTCTTAAACGAAGCGCTGCGCTT
ATGGCCACCGATTCCGTATTTTGGTCTATATGCAAAAGAAGATACGGTGCTTGGAGG
AGAATATCCTTTAGAAAAAGGCGACGAAGTAATGGTTCTGATTCCTCAGCTTCACCGT
GATAAAACAATTTGGGGAGACGATGTGGAGGAGTTCCGTCCAGAGCGTTTTGAAAAT
CCAAGTGCGATTCCGCAGCATGCGTTTAAACCGTTTGGAACGGTCAGCGTGCGTCTC
TGGGTCAGCAGTTTCGCTCTTCATGAAGCAACGCTGGTACTTGGTATGATGCTAAAACA
CTTTGACTTTGAAGATCATACAACTACGAGCTCGATATTAAAGAACGTATTACGTTA
AAACCTAAAGGCTTTGTGGTAAAAGCAAAATCGAAAAAAATTCCGCTTGGCGGTATT
CCTTCACCTAGCACTGAACAGTCTGCTAAAAAAGTACGCAAAAAGGCAGAAAACGCT
CATAATACGCCGCTGCTTGTGCTATACGGTTCAAATATGGGTACCGCTGAAGGAACG
GCGCGTGATTTAGCAGATATTGCAATGAGCAAAGGATTTGCACCGCAGGTGCAACG
CTTGATTCACACGCCGGAATCTTCCGCGCGAAGGAGCTGTATTAATTGTAACGGCGT
CTTATAACGGTCATCCGCCTGATAACGCAAAGCAATTTGTCGACTGGTTAGACCAAG

CGTCTGCTGATGAAGTAAAAGGCGTTCGCTACTCCGTATTTGGATGCGGGCGATAAAA
ACTGGGCTACTACGTATCAAAAAGTGCCTGCTTTTATCGATGAAACGCTTGCCGCTAA
AGGGGCAGAAAACATCGCTGACCGCGGTGAAGCAGATGCAAGCGACGACTTTGAAG
GCACATATGAAGAATGGCGTGAACATATGTGGAGTGACGTAGCAGCCTACTTTAACC
TCGACATTGAAAACAGTGAAGATAATAAATCTACTCTTTCACTTCAATTTGTCGACAG
CGCCGCGGATATGCCGCTTGCGAAAATGCACGGTGCGTTTTCAACGCTCGAGCACCA
CCACCACCACCACTGA

MTTKEMPQPKTFGELKNLPLLNTDKPVQALMKIADELGEIFKFEAPGRVTRYLSSQRLIKE
ACDESRFDKELVQALKFLREFLDGLVTSWTFEKNWKKAHNILLPSFSQQAMKGYHAS
MVDIAVQLVQKWERLNADEHIEVGEDMTRLTLDTIGLCGFNYRFNSFYRDQPHPFIISLV
RALDEV MNKLQRANPDDPAYDENKRQFQEDIKVMNDLVDKIIADRKASGEQSDDLTTQ
MLNRKDPETGEPLDDRNIRYQIITFLWAGVEGTSGLLSFALYLLVKNPHVLQKVAEEAAR
VLVDPVPSYKQVKQLKYVGMVLNEALRLWPPIPYFGLYAKEDTVLGGEYPLEKGDEVM
VLIPQLHRDKTIWGDDVEEFRPERFENPSAIPQHAFKPFNGQRASLGQQFALHEATLVLG
MMLKHFD FEDHTNYELDIKERITLKP KGFVVKAKSKKIPLGGIPSPSTEQSAKKVRKKAE
NAHNTPLLVLVYGSNMGTAEGTARDLADIAMSKGFAPQVATLDSHAGNLPREGAVLIVTA
SYNGHPPDNAKQFVDWLDQASADEVKGVRYSVFGCGDKNWATTYQKVPAFIDETLAA
KGAENIADRGEADASDDFEGTYEEWREHMWSDVAA YFNLDIENSEDNKSTLSLQFVDSA
ADMPLAKMHGAFSTLEHHHHHHH*

DNA and amino acid sequences of P411-LAS-5265 (P411-C10-WI)⁵:

ATGACAATTAAAGAAATGCCTCAGCCAAAAACGTTTGGAGAGCTTAAAAATTTACCG
TTATTAAACACAGATAAACCGGTTCAAGCTTTGATGAAAATTGCGGATGAATTAGGA
GAAATCTTTAAATTCGAGGCGCCTGGTCGTGTAACGCGCTACTTATCAAGTCAGCGTC
TAATTAAAGAAGCATGCGATGAATCACGCTTTGATAAAGAGTTAAGTCAAGGTCTGA
AATTTCTGCGTGATTTTCTTGGAGACGGGTTAGCCACAAGCTGGACGCATGAAAAAA
ATTGGAAAAAGCGCATAATATCTTACTTCCAAGCTTTAGTCAGCAGGCAATGAAAG
GCTATCATGCGAGTATGGTCGATATCGCCGTGCAGCTTGTTCAAAAGTGGGAGCGTCT
AAATGCAGATGAGCATATTGAAGTATCGGAAGACATGACACGTTTAACGCTTGATAC
AATTGGTCTTTGCGGCTTTAACTATCGCCTTAACAGCTTTTACCGAGATCAGCCTCAT
CCATTTATTATAAGTCTGGTCCGTGCACTGGATGAAGTAATGAACAAGCTGCAGCGA
GCAAATCCAGACGACCCAGCTTATGATGAAAACAAGCGCCAGTTTCAAGAAGATATC
AAGGTGATGAACGACCTAGTAGATAAAATTATTGCAGATCGCAAAGCAAGGGGTGA
ACAAAGCGATGATTTATTAACGCAGATGCTAAACGGAAAAGATCCAGAAACGGGTG
AGCCGCTTGATGACGGGAACATTCGCTATCAAATTATTACATTCTTATGGGCGGGAGT
TGAAGGTACAAGTGGTCTTTTATCATTGCGCTGTATTTCTTAGTGAAAAATCCACAT
GTATTACAAAAAGTAGCAGAAGAAGCAGCACGAGTTCTAGTAGATCCTGTTCCAAGC
TACAAACAAGTCAAACAGCTTAAATATGTCGGCATGGTCTTAAACGAAGCGCTGCGC
TTATGGCCAACGGTTCCTTATTTTTCCCTATATGCAAAGAAGATACGGTGCTTGAG
GAGAATATCCTTTAGAAAAAGGCGACGAAGTAATGGTTCTGATTCCTCAGCTTCACC
GTGATAAAACAGTTTGGGGAGACGATGTGGAGGAGTTCCGTCCAGAGCGTTTTGAAA
ATCCAAGTGCGATTCCGCAGCATGCGTTTAAACCGTTTGGAAACGGTCAGCGTGCGT
CTCTGGGTCAGCAGTTCGCTCTTCATGAAGCAACGCTGGTACTTGGTATGATGCTAAA
ACACTTTGACTTTGAAGATCATACAACTACGAGCTCGATATTAAAGAACTGATTAC
GTAAAACCTAAAGGCTTTGTGGTAAAAGCAAAATCGAAAAAAATTCCGCTTGCGCG
TATTCCTTCACCTAGCACTGAACAGTCTGCTAAAAAAGTACGCAAAAAGGCAGAAAA
CGCTCATAATACGCCGCTGCTTGTGCTATACGGTTCAAATATGGGTACCGCTGAAGGA
ACGGCGCGTGATTTAGCAGATATTGCAATGAGCAAAGGATTTGCACCGCAGGTGCGA
ACGCTTGATTCACACGCCGGAATCTTCCGCGCGAAGGAGCTGTATTAATTGTAACG
GCGTCTTATAACGGTCATCCGCCTGATAACGCAAAGCAATTTGTCGACTGGTTAGACC

AAGCGTCTGCTGATGAAGTAAAAGGCGTTCGCTACTCCGTATTTGGATGCGGCGATA
AAAAGTGGGCTACTACGTATCAAAAAGTGCCTGCTTTTATCGATGAAACGCTTGCCGC
TAAAGGGGCAGAAAACATCGCTGACCGCGGTGAAGCAGATGCAAGCGACGACTTTG
AAGGCACATATGAAGAATGGCGTGAACATATGTGGAGTGACGTAGCAGCCTACTTTA
ACCTCGACATTGAAAACAGTGAAGATAATAAATCTACTCTTTCACTTCAATTTGTCGA
CAGCGCCGCGGATATGCCGCTTGCGAAAATGCACGGTGCGTTTTCAACGCTCGAGCA
CCACCACCACCACCACTGA

MTIKEMPQPKTFGELKNLPLLNTDKPVQALMKIADELGEIFKFEAPGRVTRYLSSQRLIKE
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DNA and amino acid sequences of P411-LAS-5266:

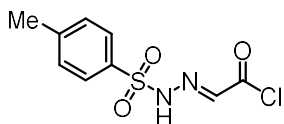
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4. Synthesis of Substrates

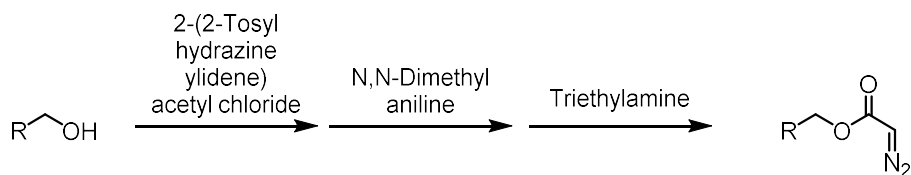
2-(2-Tosylhydrazineylidene)acetyl chloride



4-Methylbenzenesulfonohydrazide (55.9 g, 0.3 mol, 1.0 equiv.) was dissolved in aqueous hydrochloric acid (2 M, 180 mL) and warmed to 50 °C (solution 1). 2-Oxoacetic acid (44.4 g of 50% in water, 0.3 mol, 1.0 equiv.) was dissolved in water (300 mL) and heated to 50 °C (solution 2). Pre-warmed solution 1 was slowly transferred to solution 2. The reaction mixture was then stirred at 60 °C for 4 h until all the hydrozone product had crashed out. The mixture was cooled to 0 °C and kept for 2 h. The product 2-(2-tosylhydrazineylidene) acetic acid (~70 g, 97% yield) was collected by filtration, washed with hexane: ether (10:1, 20 mL \times 3) and dried under vacuum.

2-(2-Tosylhydrazineylidene)acetic acid (70 g, 0.29 mmol, 1.0 equiv.) was dissolved in dry dichloromethane (300 mL). Thionyl chloride (50 mL) and N,N-dimethyl formaldehyde (4 drops, cat.) were added to the solution. The reaction mixture was stirred at room temperature for 1 h and then heated to reflux (~ 50 °C) for 5 h until the starting material was completely dissolved and the reaction turned clear and light yellow. After the reaction was cooled to room temperature, organic solvent and the excess thionyl chloride were removed under reduced pressure. The resulting mixture was treated with ether (20 mL) and sonicated for 5 min. Hexane (150 mL) was then slowly added to the mixture to completely crash out the acyl chloride product. The mixture was cooled to 0 °C and kept for 2 h. The product 2-(2-tosylhydrazineylidene)acetyl chloride (~74 g, 98% yield, pale yellow) was collected by filtration, washed with hexane (20 mL \times 2) and dried under vacuum.

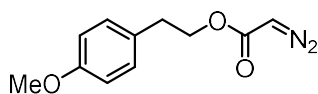
Diazo Synthesis



An alcohol substrate (1.0 equiv.) was dissolved in dry dichloromethane (conc. ~ 0.2–0.5 M) and kept at 0 °C. 2-(2-Tosylhydrazineylidene)acetyl chloride (1.05 equiv.) was then added to the solution. The mixture was stirred at 0 °C for 10 min before the addition of N,N-dimethyl aniline (1.3 equiv.). The resulting mixture was then stirred for another 10 min. Triethylamine (2.0 equiv.) was added to the reaction, which was then allowed to slowly warm up to room temperature over 20 min. The reaction was concentrated under reduced pressure and quenched by citric acid (saturated aqueous solution). The resulting mixture was transferred to a separatory funnel. Dichloromethane and water were used in minimum amount to wash the reaction container and transfer everything to the separatory funnel. Hexane/ethyl acetate (13:1) was used for extraction for three times. The combined organic layer was then washed with saturated citric acid solution and brine, dried over Na₂SO₄, filtered, and concentrated under reduced pressure. The resulting crude product was purified through a silica column using pentane/ether (1:0 to 10:1) as eluents. The yellow-colored fractions were concentrated to afford the diazo product as a yellow liquid (80–96% yield).

Compounds **1a**,⁷ **1b**,⁸ **1e**,⁹ **1f**,¹⁰ and **3b**¹¹ were known and spectral data were in accordance with literature values.

4-methoxyphenethyl 2-diazoacetate (1c)

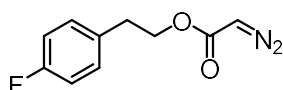


¹H NMR (400 MHz, Chloroform-*d*) δ 7.13 (d, J = 8.6 Hz, 2H), 6.85 (d, J = 8.6 Hz, 2H), 4.72 (s, 1H), 4.33 (t, J = 7.0 Hz, 2H), 3.79 (s, 3H), 2.89 (t, J = 7.0 Hz, 2H).

¹³C NMR (101 MHz, Chloroform-*d*) δ 158.46 , 130.02 , 129.78 , 114.06 , 65.67 , 55.40 , 46.33, 34.56 .

HRMS (FI): calcd for C₁₁H₁₂N₂O₃ [M]⁺ 220.08479; found 220.08468.

4-fluorophenethyl 2-diazoacetate (1d)

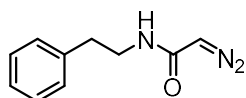


¹H NMR (400 MHz, Chloroform-*d*) δ 7.21 – 7.12 (m, 2H), 7.04 – 6.94 (m, 2H), 4.72 (s, 1H), 4.34 (t, J = 6.9 Hz, 2H), 2.92 (t, J = 6.9 Hz, 2H).

¹³C NMR (101 MHz, Chloroform-*d*) δ 161.86 (d, J = 244.6 Hz), 133.45 (d, J = 3.3 Hz), 130.47 (d, J = 8.0 Hz), 115.46 (d, J = 21.3 Hz), 65.30 , 46.35, 34.64 .

HRMS (FD): calcd for C₁₀H₉N₂O₂F [M]⁺ 208.06481; found 208.06525.

2-diazo-*N*-phenethylacetamide (1g)

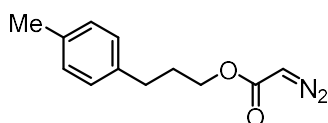


¹H NMR (400 MHz, Chloroform-*d*) δ 7.36 – 7.21 (m, 5H), 5.11 (s, 1H), 4.68 (s, 1H), 3.65 – 3.53 (m, 2H), 2.85 (t, J = 6.9 Hz, 2H).

¹³C NMR (101 MHz, Chloroform-*d*) δ 165.54 , 138.85 , 128.91 , 126.70 , 47.27 , 41.22 , 47.27, 36.15 .

HRMS (FI): calcd for C₇H₁₃N₂O₄ [M]⁺ 189.08753; found 189.09037.

3-(*p*-tolyl)propyl 2-diazoacetate (3a)

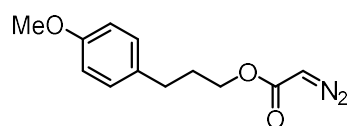


¹H NMR (400 MHz, Chloroform-*d*) δ 7.14 – 7.03 (m, 4H), 4.74 (s, 1H), 4.18 (t, *J* = 6.5 Hz, 2H), 2.65 (dd, *J* = 8.6, 6.7 Hz, 2H), 2.32 (s, 3H), 2.03 – 1.89 (m, 2H).

¹³C NMR (101 MHz, Chloroform-*d*) δ 138.13 , 135.62 , 129.26 , 128.40 , 64.35 , 46.30, 31.73 , 30.63 , 21.13 .

HRMS (FI): calcd for C₁₂H₁₄N₂O₂ [M]⁺• 218.10553; found 218.10529.

3-(4-methoxyphenyl)propyl 2-diazoacetate (3c)

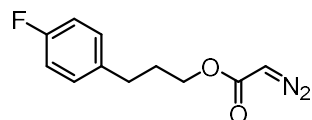


¹H NMR (400 MHz, Chloroform-*d*) δ 7.17 – 6.98 (m, 2H), 6.88 – 6.79 (m, 2H), 4.74 (s, 1H), 4.17 (t, *J* = 6.5 Hz, 2H), 3.79 (s, 3H), 2.63 (dd, *J* = 8.5, 6.8 Hz, 2H), 2.00 – 1.88 (m, 2H).

¹³C NMR (101 MHz, Chloroform-*d*) δ 158.05 , 133.27 , 129.43 , 114.00 , 64.32 , 55.41 , 46.31, 31.27 , 30.74 .

HRMS (FI): calcd for C₁₂H₁₄N₂O₃ [M]⁺• 234.10044; found 234.10034.

3-(4-fluorophenyl)propyl 2-diazoacetate (3d)

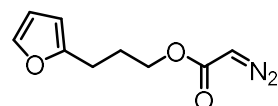


¹H NMR (400 MHz, Chloroform-*d*) δ 7.17 – 7.09 (m, 2H), 7.02 – 6.92 (m, 2H), 4.74 (s, 1H), 4.17 (t, *J* = 6.5 Hz, 2H), 2.66 (dd, *J* = 8.5, 6.8 Hz, 2H), 2.01 – 1.89 (m, 2H).

¹³C NMR (101 MHz, Chloroform-*d*) δ 161.49 (d, *J* = 243.6 Hz), 136.81 (d, *J* = 3.2 Hz), 129.85 (d, *J* = 7.8 Hz), 115.33 (d, *J* = 21.2 Hz), 64.13 , 46.31, 31.42 , 30.63 .

HRMS (FD): calcd for C₁₁H₁₁N₂O₂F [M]⁺• 222.08046; found 222.07990.

3-(furan-2-yl)propyl 2-diazoacetate (3e)



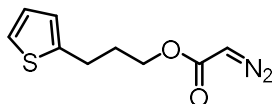
¹H NMR (400 MHz, Chloroform-*d*) δ 7.38 – 7.29 (m, 1H), 6.28 (dd, *J* = 3.2, 1.9 Hz, 1H), 6.01 (dt, *J* = 2.8, 0.9 Hz, 1H), 4.74 (s, 1H), 4.20 (t, *J* = 6.4 Hz, 2H), 2.76 – 2.69 (m, 2H), 2.00 (dq, *J* = 7.4, 6.4

Hz, 2H).

¹³C NMR (101 MHz, Chloroform-*d*) δ 154.89 , 141.21 , 110.29 , 105.40 , 64.15 , 46.31, 27.42 , 24.57 .

HRMS (ESI): calcd for C₉H₁₀N₂O₃Na [M+Na]⁺ 217.0613; found 217.0596.

3-(thiophen-2-yl)propyl 2-diazoacetate (3f)

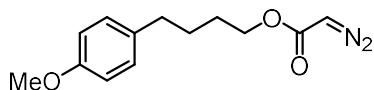


¹H NMR (400 MHz, Chloroform-*d*) δ 7.13 (dd, *J* = 5.1, 1.2 Hz, 1H), 6.92 (dd, *J* = 5.1, 3.4 Hz, 1H), 6.80 (dq, *J* = 3.3, 1.1 Hz, 1H), 4.75 (s, 1H), 4.22 (t, *J* = 6.4 Hz, 2H), 2.96 – 2.87 (m, 2H), 2.03 (dq, *J* = 7.5, 6.4 Hz, 2H).

¹³C NMR (101 MHz, Chloroform-*d*) δ 143.86 , 126.96 , 124.65 , 123.42 , 63.93 , 46.31, 30.85 , 26.34 .

HRMS (FI): calcd for C₉H₁₀N₂O₂S [M]⁺ 210.04630; found 210.04534.

4-(4-methoxyphenyl)butyl 2-diazoacetate (5a)

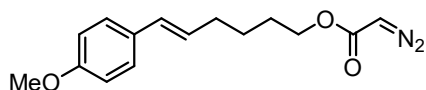


¹H NMR (400 MHz, Chloroform-*d*) δ 7.12 – 7.05 (m, 2H), 6.87 – 6.79 (m, 2H), 4.72 (s, 1H), 4.21 – 4.13 (m, 2H), 3.79 (s, 3H), 2.63 – 2.54 (m, 2H), 1.66 (d, *J* = 6.9 Hz, 4H).

¹³C NMR (101 MHz, Chloroform-*d*) δ 157.91 , 134.19 , 129.39 , 113.89 , 64.90 , 55.39 , 46.29, 34.62 , 28.45 , 27.95 .

HRMS (FI): calcd for C₁₃H₁₆N₂O₃ [M]⁺ 248.11609; found 248.11580.

(*E*)-6-(4-methoxyphenyl)hex-5-en-1-yl 2-diazoacetate (5b)

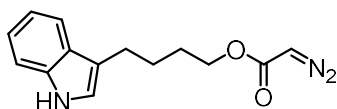


¹H NMR (400 MHz, Chloroform-*d*) δ 7.27 (d, *J* = 9.0 Hz, 2H), 6.84 (d, *J* = 8.7 Hz, 2H), 6.33 (d, *J* = 15.8 Hz, 1H), 6.11 – 5.96 (m, 1H), 4.73 (s, 1H), 4.18 (t, *J* = 6.6 Hz, 2H), 3.80 (s, 3H), 2.22 (q, *J* = 6.9 Hz, 2H), 1.70 (dt, *J* = 15.3, 6.8 Hz, 2H), 1.58 – 1.49 (m, 2H).

^{13}C NMR (101 MHz, Chloroform-*d*) δ 158.85 , 130.64 , 129.82 , 128.13 , 127.15 , 114.05 , 64.94 , 55.43 , 46.30, 32.64 , 28.45 , 25.83 .

HRMS (FI): calcd for $\text{C}_{15}\text{H}_{18}\text{N}_2\text{O}_3$ $[\text{M}]^{+}$ 274.13174; found 274.13224.

4-(1*H*-indol-3-yl)butyl 2-diazoacetate (5c)

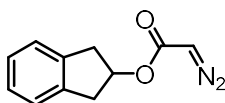


^1H NMR (400 MHz, Chloroform-*d*) δ 7.87 (s, 1H), 7.52 (dd, J = 8.0, 1.1 Hz, 1H), 7.28 (dd, J = 8.1, 0.9 Hz, 1H), 7.21 – 7.08 (m, 1H), 7.04 (ddd, J = 8.1, 7.0, 1.1 Hz, 1H), 6.93 – 6.87 (m, 1H), 4.64 (s, 1H), 4.13 (t, J = 6.2 Hz, 2H), 2.77 – 2.68 (m, 2H), 1.76 – 1.62 (m, 4H).

^{13}C NMR (101 MHz, Chloroform-*d*) δ 136.48 , 127.58 , 122.04 , 121.34 , 119.27 , 119.00 , 116.37 , 111.21 , 65.01 , 46.31, 28.75 , 26.45 , 24.84 .

HRMS (FI): calcd for $\text{C}_{14}\text{H}_{15}\text{N}_3\text{O}_2$ $[\text{M}]^{+}$ 257.11643; found 257.11652.

2,3-dihydro-1*H*-inden-2-yl 2-diazoacetate (7a)

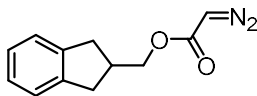


^1H NMR (400 MHz, Chloroform-*d*) δ 7.31 – 7.22 (m, 4H), 5.65 (dt, J = 6.5, 3.3 Hz, 1H), 4.75 (s, 1H), 3.36 (dd, J = 17.0, 6.5 Hz, 2H), 3.07 (dd, J = 17.0, 3.1 Hz, 2H).

^{13}C NMR (101 MHz, Chloroform-*d*) δ 140.31 , 126.80 , 124.65 , 75.91 , 46.51, 39.70 .

HRMS (FI): calcd for $\text{C}_{11}\text{H}_{10}\text{N}_2\text{O}_3$ $[\text{M}]^{+}$ 202.07423; found 202.07387.

(2,3-dihydro-1*H*-inden-2-yl)methyl 2-diazoacetate (7b)

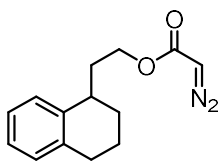


^1H NMR (400 MHz, Chloroform-*d*) δ 7.31 – 7.21 (m, 2H), 7.17 (dt, J = 5.2, 3.6 Hz, 2H), 4.78 (s, 1H), 4.23 (d, J = 6.8 Hz, 2H), 3.16 – 3.05 (m, 2H), 2.92 – 2.72 (m, 3H).

^{13}C NMR (101 MHz, Chloroform-*d*) δ 142.25 , 126.41 , 124.61 , 67.94 , 46.22, 38.40 , 35.89 .

HRMS (FI): calcd for $\text{C}_{12}\text{H}_{12}\text{N}_2\text{O}_2$ $[\text{M}]^{+}$ 216.08988; found 216.08981.

2-(1,2,3,4-tetrahydronaphthalen-1-yl)ethyl 2-diazoacetate (7c)

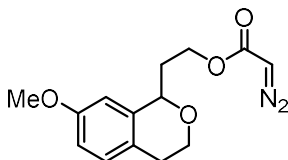


¹H NMR (δ 7.17 – 7.04 (m, 4H), 4.76 (s, 1H), 4.29 (ddd, J = 7.2, 6.3, 3.7 Hz, 2H), 2.92 (dd, J = 9.4, 4.9 Hz, 1H), 2.81 – 2.72 (m, 2H), 2.13 – 2.02 (m, 1H), 1.95 – 1.81 (m, 3H), 1.73 (dtd, J = 10.0, 5.9, 3.8 Hz, 2H).

¹³C NMR (101 MHz, Chloroform-*d*) δ 140.16 , 137.18 , 129.36 , 128.64 , 125.90 , 125.78 , 63.38 , 46.36, 35.78 , 34.50 , 29.63 , 27.68 , 19.72 .

HRMS (FI): calcd for C₁₄H₁₆N₂O₂ [M]⁺• 244.12118; found 244.12117.

2-(7-methoxyisochroman-1-yl)ethyl 2-diazoacetate (7d)

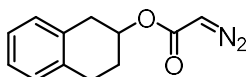


¹H NMR (400 MHz, Chloroform-*d*) δ 7.03 (d, J = 8.4 Hz, 1H), 6.74 (dd, J = 8.4, 2.6 Hz, 1H), 6.59 (d, J = 2.6 Hz, 1H), 4.81 (dd, J = 8.9, 2.9 Hz, 1H), 4.72 (s, 1H), 4.36 (ddd, J = 7.4, 5.9, 4.0 Hz, 2H), 3.82 – 3.67 (m, 4H), 2.96 – 2.83 (m, 1H), 2.63 (dt, J = 15.9, 3.8 Hz, 1H), 2.26 (ddd, J = 15.0, 7.3, 3.2 Hz, 1H), 2.13 (ddd, J = 9.0, 6.6, 5.3 Hz, 1H).

¹³C NMR (101 MHz, Chloroform-*d*) δ 158.07 , 138.55 , 130.02 , 126.08 , 112.59 , 109.91 , 72.84 , 63.51 , 61.87 , 55.46 , 46.32, 35.07 , 28.31 .

HRMS (FI): calcd for C₁₄H₁₆N₂O₄ [M]⁺• 276.1101; found 276.11068.

1,2,3,4-tetrahydronaphthalen-2-yl 2-diazoacetate (7e)

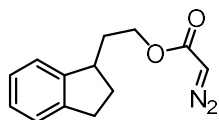


¹H NMR (400 MHz, Chloroform-*d*) δ 7.17 – 7.03 (m, 4H), 5.30 (dddd, J = 8.4, 7.0, 5.1, 3.2 Hz, 1H), 4.74 (s, 1H), 3.14 (dd, J = 16.7, 5.2 Hz, 1H), 2.99 – 2.80 (m, 3H), 2.12 – 1.92 (m, 2H).

¹³C NMR (101 MHz, Chloroform-*d*) δ 135.92 , 133.97 , 129.77 , 129.04 , 126.51 , 126.40 , 70.83 , 46.93, 35.15 , 28.44 , 26.81 .

HRMS (FI): calcd for C₁₂H₁₂N₂O₂ [M]⁺• 216.08988; found 216.08980.

2-(2,3-dihydro-1H-inden-1-yl)ethyl 2-diazoacetate (7f)



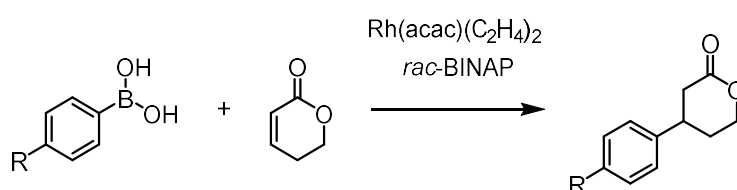
¹H NMR (400 MHz, Chloroform-*d*) δ 7.20 – 7.05 (m, 4H), 4.67 (s, 1H), 4.23 (t, *J* = 6.8 Hz, 2H), 3.17 – 3.08 (m, 1H), 2.91 – 2.71 (m, 2H), 2.31 – 2.07 (m, 2H), 1.75 – 1.53 (m, 2H).

¹³C NMR (101 MHz, Chloroform-*d*) δ 146.48 , 143.96 , 126.66 , 126.28 , 124.65 , 123.59 , 63.71 , 46.32, 41.73 , 33.98 , 32.27 , 31.51 .

HRMS (FI): calcd for C₁₃H₁₄N₂O₂ [M]⁺• 230.10553; found 230.10561.

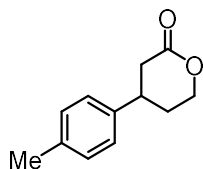
5. Synthesis of Reference Products

Compounds **2a–2g** and **4b** were purchased from commercial suppliers including Sigma-Aldrich, VWR, TCI America, Fischer Scientific, Alfa Aesar, Acros, and Combi Blocks and were used without additional purification. Other reference products were obtained using the method described below or through enzymatic preparative synthesis.



A typical procedure is given for the preparation of 6-membered lactones: 1,4-Dioxane (2.0 mL) was added to a flask charged with Rh(acac)(C₂H₄)₂ (12 μmol), *rac*-BINAP (14 μmol), and phenylboronic acid (2.00 mmol) and flushed with nitrogen, which was followed by addition of water (0.2 mL) and 5,6-dihydro-2H-pyran-2-one (0.40 mmol). The resulting mixture was then stirred at 100 °C for 3 h. After evaporation of the solvent, the residue was dissolved in ethyl acetate. The solution was washed with saturated aqueous sodium bicarbonate and dried over anhydrous Na₂SO₄. Chromatography on silica gel (hexane:EtOAc 2:1 to 1:1) gave products as a colorless oil.

4-(*p*-Tolyl)tetrahydro-2H-pyran-2-one (**4a**)

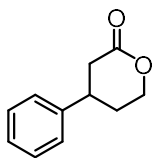


¹H NMR (400 MHz, Chloroform-*d*) δ 7.40 – 7.35 (m, 2H), 7.33 – 7.28 (m, 1H), 7.25 – 7.21 (m, 2H), 4.67 (dd, *J* = 9.1, 7.8 Hz, 1H), 4.28 (dd, *J* = 9.1, 7.9 Hz, 1H), 3.79 (p, *J* = 8.4 Hz, 1H), 2.93 (dd, *J* = 17.5, 8.7 Hz, 1H), 2.68 (dd, *J* = 17.5, 9.1 Hz, 1H).

¹³C NMR (101 MHz, Chloroform-*d*) δ 176.51 , 139.54 , 129.30 , 127.88 , 126.84 , 41.27 , 35.86 .

Spectral data were in accordance with literature values.¹²

4-Phenyltetrahydro-2H-pyran-2-one (4b)

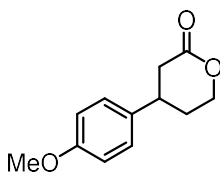


¹H NMR (400 MHz, Chloroform-*d*) δ 7.41 – 7.32 (m, 2H), 7.31 – 7.25 (m, 2H), 7.24 – 7.18 (m, 2H), 4.51 (ddd, J = 11.4, 4.9, 3.9 Hz, 1H), 4.40 (ddd, J = 11.4, 10.4, 3.8 Hz, 1H), 3.24 (tdd, J = 10.5, 5.9, 4.6 Hz, 1H), 2.93 (ddd, J = 17.7, 6.0, 1.7 Hz, 1H), 2.64 (dd, J = 17.6, 10.6 Hz, 1H), 2.19 (dq, J = 14.0, 3.9, 1.6 Hz, 1H), 2.11 – 1.99 (m, 1H).

¹³C NMR (101 MHz, Chloroform-*d*) δ 170.78 , 142.89 , 129.13 , 127.38 , 126.59 , 68.78 , 37.65 , 37.60 , 30.46 .

Spectral data were in accordance with literature values.¹³

4-(4-Methoxyphenyl)tetrahydro-2H-pyran-2-one (4c)

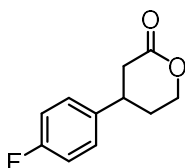


¹H NMR (400 MHz, Chloroform-*d*) δ 7.17 – 7.09 (m, 2H), 6.94 – 6.85 (m, 2H), 4.50 (ddd, J = 11.4, 4.9, 3.9 Hz, 1H), 4.38 (ddd, J = 11.4, 10.4, 3.8 Hz, 1H), 3.80 (s, 3H), 3.19 (tdd, J = 10.5, 5.9, 4.5 Hz, 1H), 2.90 (ddd, J = 17.6, 5.9, 1.7 Hz, 1H), 2.59 (dd, J = 17.7, 10.6 Hz, 1H), 2.15 (ddtd, J = 13.9, 4.5, 3.9, 1.7 Hz, 1H), 2.00 (dtd, J = 14.1, 10.5, 4.9 Hz, 1H).

¹³C NMR (101 MHz, Chloroform-*d*) δ 170.90 , 158.79 , 134.99 , 127.56 , 114.45 , 68.80 , 55.46 , 37.91 , 36.81 , 30.67 .

Spectral data were in accordance with literature values.¹⁴

4-(4-Fluorophenyl)tetrahydro-2H-pyran-2-one (4d)



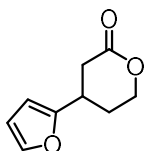
¹H NMR (400 MHz, Chloroform-*d*) δ 7.22 – 7.13 (m, 2H), 7.10 – 7.00 (m, 2H), 4.51 (ddd, J = 11.5, 4.9, 3.8 Hz, 1H), 4.39 (ddd, J = 11.5, 10.5, 3.7 Hz, 1H), 3.23 (tdd, J = 10.6, 5.9, 4.5 Hz, 1H), 2.91 (ddd, J = 17.6, 6.0, 1.7 Hz, 1H), 2.59 (dd, J = 17.6, 10.6 Hz, 1H), 2.21 – 2.13 (m, 1H), 2.01 (dtd, J = 14.1, 10.6, 4.9 Hz, 1H).

¹³C NMR (101 MHz, Chloroform-*d*) δ 170.51 , 163.21 , 160.76 , 138.60 , 128.13 , 128.05 , 116.09 , 115.88 , 68.68 , 37.82 , 36.98 , 30.56 .

¹⁹F NMR (376 MHz, Chloroform-*d*) δ -115.32 .

Spectral data were in accordance with literature values. ¹⁴

4-(Furan-2-yl)tetrahydro-2H-pyran-2-one (4e)

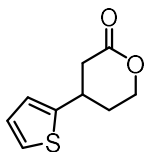


¹H NMR (400 MHz, Chloroform-*d*) δ 7.36 (dd, J = 2.0, 0.8 Hz, 1H), 6.32 (dd, J = 3.2, 1.8 Hz, 1H), 6.09 (dt, J = 3.2, 0.9 Hz, 1H), 4.47 – 4.33 (m, 2H), 3.37 (dddd, J = 11.6, 6.1, 3.6, 1.0 Hz, 1H), 2.93 (ddd, J = 17.5, 6.2, 1.2 Hz, 1H), 2.72 (dd, J = 17.5, 9.2 Hz, 1H), 2.28 – 2.20 (m, 1H), 2.04 (dtd, J = 13.8, 8.8, 4.7 Hz, 1H).

¹³C NMR (101 MHz, Chloroform-*d*) δ 170.13 , 155.53 , 142.13 , 110.38 , 105.20 , 68.08 , 34.60 , 31.14 , 27.99 .

Spectral data were in accordance with literature values. ¹⁵

4-(Thiophen-2-yl)tetrahydro-2H-pyran-2-one (4f)



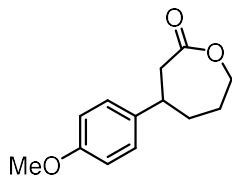
¹H NMR (400 MHz, Chloroform-*d*) δ 7.22 (dd, J = 5.2, 1.2 Hz, 1H), 6.98 (dd, J = 5.1, 3.5 Hz, 1H), 6.90 – 6.84 (m, 1H), 4.50 (dt, J = 11.6, 4.6 Hz, 1H), 4.39 (ddd, J = 11.7, 10.1, 3.8 Hz, 1H), 3.58 – 3.49 (m, 1H), 3.03 (ddd, J = 17.7, 5.9, 1.6 Hz, 1H), 2.70 (dd, J = 17.6, 10.3 Hz, 1H), 2.29 (ddq, J = 11.0, 4.2, 2.6, 2.1 Hz, 1H), 2.06 (dtd, J = 14.5, 10.1, 4.8 Hz, 1H).

¹³C NMR (101 MHz, Chloroform-*d*) δ 169.89 , 146.43 , 127.18 , 124.10 , 123.48 , 68.39 , 38.24 ,

33.19 , 31.46 .

Spectral data were in accordance with literature values.¹⁶

4-(4-Methoxyphenyl)oxepan-2-one (6a)

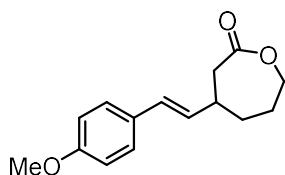


¹H NMR (400 MHz, Chloroform-*d*) δ 7.13 – 7.07 (m, 2H), 6.85 (d, J = 8.7 Hz, 2H), 4.42 – 4.20 (m, 2H), 3.79 (s, 3H), 3.05 – 2.71 (m, 3H), 2.21 – 2.01 (m, 2H), 1.99 – 1.70 (m, 2H).

¹³C NMR (101 MHz, Chloroform-*d*) δ 174.76 , 158.47 , 137.84 , 128.01 , 127.35 , 114.39 , 114.24 , 69.23 , 55.43 , 41.96 , 40.00 , 38.09 , 29.17 .

Spectral data were in accordance with literature values.¹⁷

(*E*)-4-(4-Methoxystyryl)oxepan-2-one (6b)

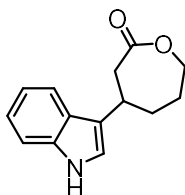


¹H NMR (400 MHz, Chloroform-*d*) δ 7.27 (d, J = 8.5 Hz, 3H), 6.88 – 6.82 (m, 2H), 6.40 (dd, J = 15.7, 1.1 Hz, 1H), 5.99 (dd, J = 15.9, 7.4 Hz, 1H), 4.38 – 4.27 (m, 1H), 4.23 (ddd, J = 12.7, 9.3, 1.1 Hz, 1H), 3.80 (s, 3H), 2.84 – 2.69 (m, 2H), 2.67 – 2.55 (m, 1H), 2.13 – 1.99 (m, 2H), 1.95 – 1.80 (m, 1H), 1.73 – 1.60 (m, 1H).

¹³C NMR (101 MHz, Chloroform-*d*) δ 174.69 , 159.29, 130.35 , 129.76 , 129.34 , 127.48 , 114.14 , 69.24 , 55.45 , 40.59 , 37.52 , 35.81 , 28.16 .

HRMS (FI): calcd for C₁₅H₁₈O₃ [M]⁺ 246.12559; found 246.12724.

4-(1*H*-Indol-3-yl)oxepan-2-one (6c)

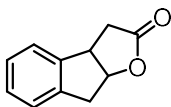


¹H NMR (400 MHz, Chloroform-*d*) δ 8.03 (s, 1H), 7.65 (dt, J = 7.8, 1.0 Hz, 1H), 7.38 (dt, J = 8.1, 0.9 Hz, 1H), 7.22 (ddd, J = 8.2, 7.1, 1.2 Hz, 1H), 7.14 (ddd, J = 8.0, 7.1, 1.1 Hz, 1H), 7.05 – 7.01 (m, 1H), 4.44 – 4.29 (m, 2H), 3.33 (ddd, J = 11.6, 7.8, 4.5 Hz, 1H), 3.09 – 2.99 (m, 2H), 2.40 – 2.27 (m, 1H), 2.19 – 2.06 (m, 1H), 2.05 – 1.95 (m, 2H).

¹³C NMR (101 MHz, Chloroform-*d*) δ 175.16 , 136.48 , 125.98 , 122.56 , 120.25 , 119.97 , 119.79 , 119.04 , 111.47 , 69.41 , 41.51 , 36.13 , 32.24 , 28.93 .

HRMS (FI): calcd for C₁₄H₁₅NO₂ [M]⁺ 229.11028; found 229.11145.

3,3a,8,8a-Tetrahydro-2*H*-indeno[2,1-*b*]furan-2-one (8a)

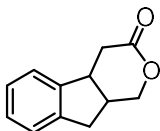


¹H NMR (400 MHz, Chloroform-*d*) δ 7.30 – 7.20 (m, 5H), 5.30 (ddd, J = 5.8, 3.8, 2.7 Hz, 1H), 4.02 (ddt, J = 9.3, 5.7, 1.3 Hz, 1H), 3.35 – 3.29 (m, 2H), 3.05 (dd, J = 17.8, 9.3 Hz, 1H), 2.75 (dd, J = 17.8, 1.5 Hz, 1H).

¹³C NMR (101 MHz, Chloroform-*d*) δ 142.15 , 128.46 , 127.85 , 125.43 , 124.79 , 84.43 , 45.58 , 39.07 , 35.48 .

HRMS (FI): calcd for C₁₁H₁₀O₂ [M]⁺ 174.06808; found 174.06856.

4,4a,9,9a-Tetrahydroindeno[2,1-*c*]pyran-3(1*H*)-one (8b)

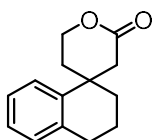


¹H NMR (400 MHz, Chloroform-*d*) δ 7.26 – 7.16 (m, 4H), 4.39 (dd, J = 11.4, 5.0 Hz, 1H), 4.09 (dd, J = 11.4, 8.8 Hz, 1H), 3.81 (dt, J = 9.8, 7.8 Hz, 1H), 3.30 (dd, J = 16.8, 9.7 Hz, 1H), 3.10 – 2.97 (m, 2H), 2.81 (dd, J = 16.8, 3.9 Hz, 1H), 2.58 (dd, J = 15.2, 7.8 Hz, 1H).

¹³C NMR (101 MHz, Chloroform-*d*) δ 172.79 , 143.96 , 141.31 , 127.91 , 127.56 , 125.06 , 124.27 , 70.26 , 41.04 , 35.81 , 34.93 , 34.90 .

HRMS (FI): calcd for C₁₂H₁₂O₂ [M]⁺⁺ 188.08373; found 188.08404.

3,4,5',6'-Tetrahydro-2*H*-spiro[naphthalene-1,4'-pyran]-2'(3'*H*)-one (8c)

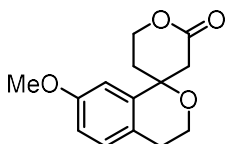


¹H NMR (400 MHz, Chloroform-*d*) δ 7.24 – 7.06 (m, 4H), 4.50 – 4.39 (m, 2H), 2.87 – 2.76 (m, 3H), 2.65 (dd, *J* = 16.7, 1.1 Hz, 1H), 2.26 (ddd, *J* = 14.2, 8.1, 5.8 Hz, 1H), 1.95 (dddd, *J* = 14.5, 5.3, 4.4, 1.1 Hz, 1H), 1.91 – 1.77 (m, 4H).

¹³C NMR (101 MHz, Chloroform-*d*) δ 172.01 , 142.44 , 136.63 , 126.81 , 126.68 , 77.48 , 66.40 , 37.20 , 36.23 , 18.98 .

HRMS (FI): calcd for C₁₂H₁₆O [M]⁺⁺ 176.12012; found 176.12080.

7-methoxy-5',6'-dihydrospiro[isochromane-1,4'-pyran]-2'(3'*H*)-one (8d)

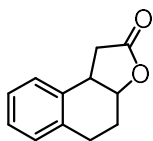


¹H NMR (400 MHz, Chloroform-*d*) δ 7.16 – 6.99 (m, 1H), 6.77 (ddd, *J* = 8.3, 2.7, 0.7 Hz, 1H), 6.58 (d, *J* = 2.7 Hz, 1H), 5.20 – 5.03 (m, 2H), 4.15 (dd, *J* = 11.2, 1.4 Hz, 1H), 3.92 – 3.85 (m, 2H), 3.82 (d, *J* = 1.5 Hz, 3H), 3.06 (d, *J* = 4.1 Hz, 1H), 2.68 (dd, *J* = 13.1, 5.3 Hz, 1H), 2.55 (ddd, *J* = 13.1, 2.6, 1.5 Hz, 1H), 2.51 – 2.41 (m, 1H), 2.41 – 2.27 (m, 1H).

¹³C NMR (101 MHz, Chloroform-*d*) δ 175.49 , 158.82 , 141.79 , 129.26 , 128.51 , 111.83 , 110.31 , 72.66 , 67.06 , 61.47 , 55.43 , 40.17 , 36.74 , 34.99 .

HRMS (FI): calcd for C₁₄H₁₆O₄ [M]⁺⁺ 248.10486; found 248.10591.

3a,4,5,9b-Tetrahydronaphtho[2,1-*b*]furan-2(1*H*)-one (8e)

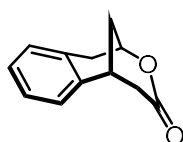


¹H NMR (400 MHz, Chloroform-*d*) δ 7.24 – 7.09 (m, 4H), 4.98 (td, J = 6.8, 3.4 Hz, 1H), 3.81 (dt, J = 9.6, 6.3 Hz, 1H), 3.09 (dd, J = 17.6, 9.5 Hz, 1H), 2.91 (ddd, J = 16.4, 9.5, 4.4 Hz, 1H), 2.75 – 2.65 (m, 1H), 2.58 (dd, J = 17.6, 5.6 Hz, 1H), 2.19 (dtd, J = 13.2, 6.4, 4.4 Hz, 1H), 1.99 (dddd, J = 14.0, 9.7, 4.6, 3.4 Hz, 1H).

¹³C NMR (101 MHz, Chloroform-*d*) δ 176.51 , 136.03 , 135.68 , 129.17 , 128.98 , 127.21 , 126.98 , 78.87, 37.86 , 37.74 , 26.54 , 24.67 .

HRMS (FI): calcd for C₁₂H₁₂O₂ [M]⁺⁺ 188.08373; found 188.08441.

1,2,5,6-tetrahydro-4*H*-2,6-methanobenzo[*d*]oxocin-4-one (8e')

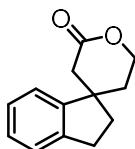


¹H NMR (400 MHz, Chloroform-*d*) δ 7.24 – 7.16 (m, 2H), 7.15 – 7.07 (m, 2H), 5.13 (dtd, J = 5.2, 3.6, 1.8 Hz, 1H), 3.35 – 3.21 (m, 2H), 3.10 (dd, J = 17.9, 3.8 Hz, 1H), 2.83 (dd, J = 17.9, 5.7 Hz, 1H), 2.65 (dt, J = 17.9, 2.2 Hz, 1H), 2.33 (ddt, J = 13.6, 4.7, 2.1 Hz, 1H), 2.23 – 2.10 (m, 1H).

¹³C NMR (101 MHz, Chloroform-*d*) δ 169.97 , 138.37 , 130.92 , 130.92 , 130.02 , 130.02 , 128.73 , 127.75 , 127.23 , 74.81 , 40.19 , 36.32 , 31.25 , 27.95 .

HRMS (FI): calcd for C₁₂H₁₂O₂ [M]⁺⁺ 188.08373; found 188.08414.

2,3,5',6'-Tetrahydrospiro[indene-1,4'-pyran]-2'(3'*H*)-one (8f)

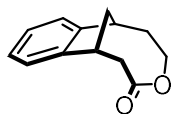


¹H NMR (400 MHz, Chloroform-*d*) δ 7.30 – 7.19 (m, 4H), 7.19 – 7.11 (m, 1H), 4.57 – 4.42 (m, 2H), 2.96 (tt, J = 6.8, 0.7 Hz, 2H), 2.73 – 2.59 (m, 2H), 2.26 – 2.13 (m, 1H), 2.08 (t, J = 7.1 Hz, 2H), 1.91 (dddd, J = 14.1, 5.8, 4.6, 1.1 Hz, 1H).

¹³C NMR (101 MHz, Chloroform-*d*) δ 170.86 , 147.65 , 142.73 , 127.63 , 127.04 , 125.03 , 122.29 , 77.23 , 67.00 , 45.58 , 41.67 , 38.82 , 33.76 , 29.62 .

HRMS (FI): calcd for C₁₃H₁₄O₂ [M]⁺⁺ 202.09938; found 202.09993.

(7)-1,5,6,7-Tetrahydro-1,7-methanobenzo[*e*]oxonin-3(2*H*)-one (8f')



¹H NMR (400 MHz, Chloroform-*d*) δ 7.30 – 7.13 (m, 5H), 4.14 – 3.97 (m, 2H), 3.68 (dt, J = 9.4, 4.9 Hz, 1H), 3.53 – 3.44 (m, 1H), 2.90 (dd, J = 12.5, 4.9 Hz, 1H), 2.66 – 2.55 (m, 2H), 2.39 (dddd, J = 14.8, 11.4, 5.0, 3.5 Hz, 1H), 2.22 (dt, J = 13.7, 1.0 Hz, 1H), 2.00 (ddt, J = 14.8, 4.5, 3.1 Hz, 1H).

¹³C NMR (101 MHz, Chloroform-*d*) δ 175.54 , 145.68 , 144.08 , 127.80 , 127.57 , 124.89 , 124.59 , 66.44 , 42.68 , 42.55 , 41.15 , 36.87 , 36.32 .

HRMS (FI): calcd for C₁₃H₁₄O₂ [M]⁺• 202.09938; found 202.10012.

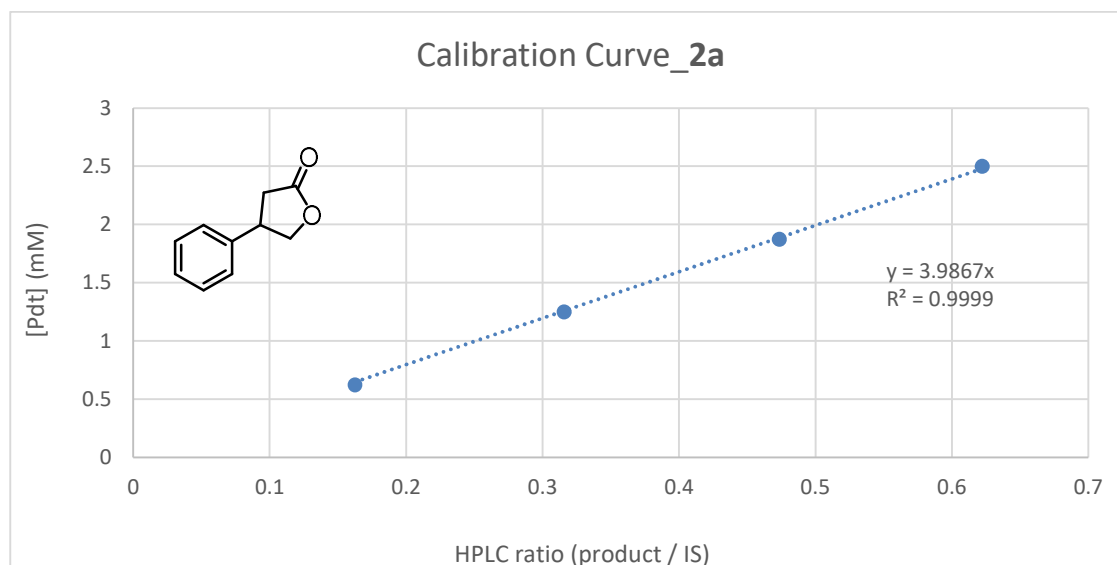
6. HPLC Calibration Curves

Calibration curves of synthesized reference compounds were created for the determination of yield and TTN.

For compounds **2a–6c**: For each substrate, four different concentrations of product (0.625, 1.25, 1.875, and 2.5 mM) with 0.67 mM internal standard in 600 μ L acetonitrile solutions were mixed each with 400 μ L water. The mixtures were vortexed and then analyzed by HPLC based on UV absorbance at 210 nm. All data points represent the average of duplicate runs. The calibration curves depict the ratio of product area to internal standard area (x-axis) against product concentration in mM (y-axis). Notes: Pdt = product area, IS = internal standard area, [Pdt] = product concentration in reaction, [PC] = protein concentration in reaction, Avg. TTN = average total turnover number, SD TTN = standard deviation of TTN, Avg. Yield = average yield, SD Yield = standard deviation of yield.

For compounds **8a–8f**: For each substrate, four different concentrations of product (0.625, 1.25, 1.875, and 2.5 mM) with 0.67 mM internal standard in 600 μ L hexane solutions were mixed each with 400 μ L water. The mixtures were vortexed and centrifuged. The supernatant was transferred to a new vial and analyzed by HPLC based on UV absorbance at 210 nm. All data points represent the average of duplicate runs. The calibration curves depict the ratio of product area to internal standard area (x-axis) against product concentration in mM (y-axis). Notes: Pdt = product area, IS = internal standard area, [Pdt] = product concentration in reaction, [PC] = protein concentration in reaction, Avg. TTN = average total turnover number, SD TTN = standard deviation of TTN, Avg. Yield = average yield, SD Yield = standard deviation of yield.

4-Phenyldihydrofuran-2(3H)-one (2a)



Data analysis for P411-LAS-5239-catalyzed lactonization of **1a**; Table S1, entry 1 and Table S2, entry 1:

Entry	Pdt	IS	Pdt/IS	[Pdt]/mM	[PC]/ μ M	Avg. Yield [%]	SD Yield [%]	Avg. TTN	SD TTN
1	264.9	6113.2	0.043	0.173	0.35	7.5%	0.5%	530	35
2	298.1	6053.8	0.049	0.196	0.35				
3	288.3	6053.9	0.048	0.190	0.35				

Data analysis for P411-LAS-5240-catalyzed lactonization of **1a**; Table S2, entry 2:

Entry	Pdt	IS	Pdt/IS	[Pdt]/mM	[PC]/ μ M	Avg. Yield [%]	SD Yield [%]	Avg. TTN	SD TTN
1	475.1	6152.5	0.077	0.308	0.16	14%	1.7%	2200	260
2	594.4	6115.2	0.097	0.388	0.16				
3	565.8	6111.0	0.093	0.369	0.16				

Data analysis for P411-LAS-5241-catalyzed lactonization of **1a**; Table S2, entry 3:

Entry	Pdt	IS	Pdt/IS	[Pdt]/mM	[PC]/ μ M	Avg. Yield [%]	SD Yield [%]	Avg. TTN	SD TTN
1	766.1	6119.3	0.125	0.499	0.45	20%	0.1%	1100	8
2	759.5	6120.2	0.124	0.495	0.45				

3	748.6	6070.1	0.123	0.492	0.45				
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Data analysis for P411-LAS-5242-catalyzed lactonization of **1a**; Table S2, entry 4:

Entry	Pdt	IS	Pdt/IS	[Pdt]/mM	[PC]/ μ M	Avg. Yield [%]	SD Yield [%]	Avg. TTN	SD TTN
1	1370.9	6197.7	0.221	0.882	0.33	35%	0.4%	2700	28
2	1346.0	6084.3	0.221	0.882	0.33				
3	1391.7	6177.4	0.225	0.898	0.33				

Data analysis for P411-LAS-5243-catalyzed lactonization of **1a**; Table S2, entry 5:

Entry	Pdt	IS	Pdt/IS	[Pdt]/mM	[PC]/ μ M	Avg. Yield [%]	SD Yield [%]	Avg. TTN	SD TTN
1	1578.8	6156.9	0.256	1.022	0.37	41%	1.5%	2900	200
2	1525.3	6143.5	0.248	0.990	0.37				
3	1610.5	6044.4	0.266	1.062	0.37				

Data analysis for P411-LAS-5244-catalyzed lactonization of **1a**; Table S2, entry 6:

Entry	Pdt	IS	Pdt/IS	[Pdt]/mM	[PC]/ μ M	Avg. Yield [%]	SD Yield [%]	Avg. TTN	SD TTN
1	1982.7	6142.6	0.323	1.287	0.33	52%	1.5%	3900	120
2	2099.3	6182.1	0.340	1.354	0.33				
3	1989.2	6160.0	0.323	1.287	0.33				

Data analysis for P411-LAS-5245-catalyzed lactonization of **1a**; Table S2, entry 7:

Entry	Pdt	IS	Pdt/IS	[Pdt]/mM	[PC]/ μ M	Avg. Yield [%]	SD Yield [%]	Avg. TTN	SD TTN
1	2383.0	6059.9	0.393	1.568	0.39	64%	2.9%	4100	190
2	2380.6	6097.7	0.390	1.556	0.39				
3	2610.4	6164.0	0.423	1.688	0.39				

Data analysis for P411-LAS-5246-catalyzed lactonization of **1a**; Table S2, entry 8:

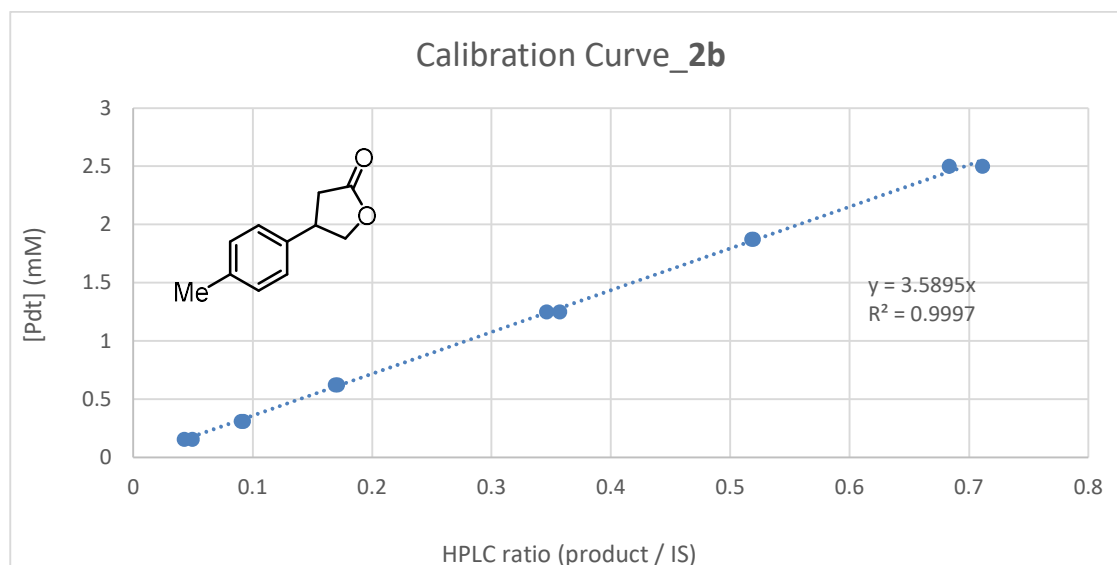
Entry	Pdt	IS	Pdt/IS	[Pdt]/mM	[PC]/ μ M	Avg. Yield [%]	SD Yield [%]	Avg. TTN	SD TTN
1	2412.5	6093.9	0.396	1.578	0.33	65%	2.0%	4900	150
2	2522.5	5995.2	0.421	1.677	0.33				

3	2523.0	6134.8	0.411	1.640	0.33				
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Data analysis for P411-LAS-5247-catalyzed lactonization of **1a**; Table S2, entry 9:

Entry	Pdt	IS	Pdt/IS	[Pdt]/mM	[PC]/ μ M	Avg. Yield [%]	SD Yield [%]	Avg. TTN	SD TTN
1	2548.7	6054.8	0.421	1.678	0.43	66%	0.8%	3800	49
2	2512.5	6114.5	0.411	1.638	0.43				
3	2513.1	6086.4	0.413	1.646	0.43				

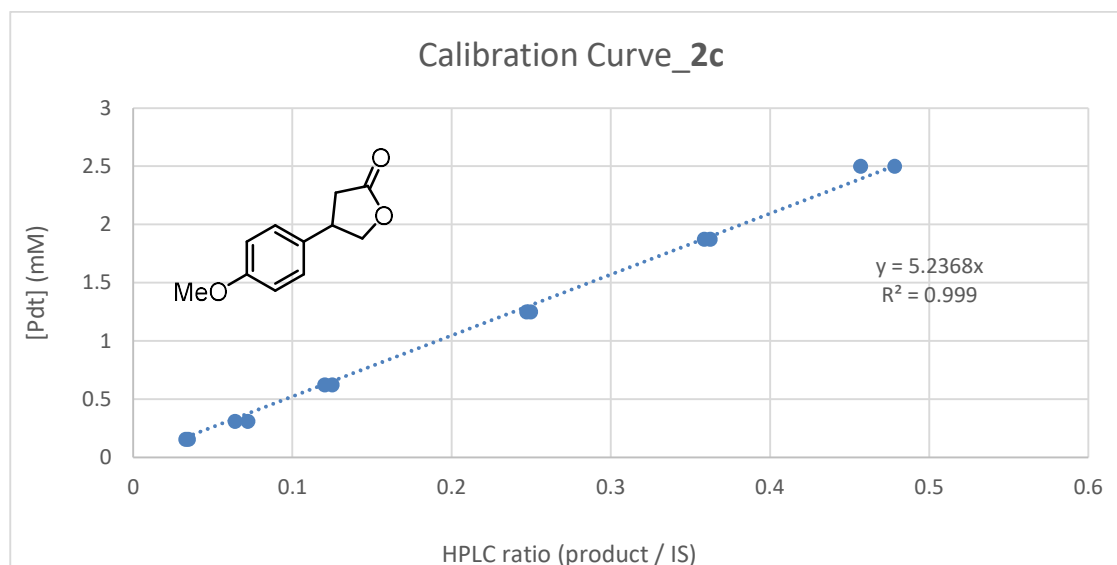
4-(*p*-Tolyl)dihydrofuran-2(3*H*)-one (2b)



Data analysis for P411-LAS-5247-catalyzed lactonization of **1b**:

Entry	Pdt	IS	Pdt/IS	[Pdt]/mM	[PC]/ μ M	Avg. Yield [%]	SD Yield [%]	Avg. TTN	SD TTN
1	1780.8	5986.7	0.297	1.068	0.36	41%	1.4%	2900	97
2	1780.8	6166.7	0.289	1.037	0.36				
3	1797.3	6465.0	0.278	0.998	0.36				

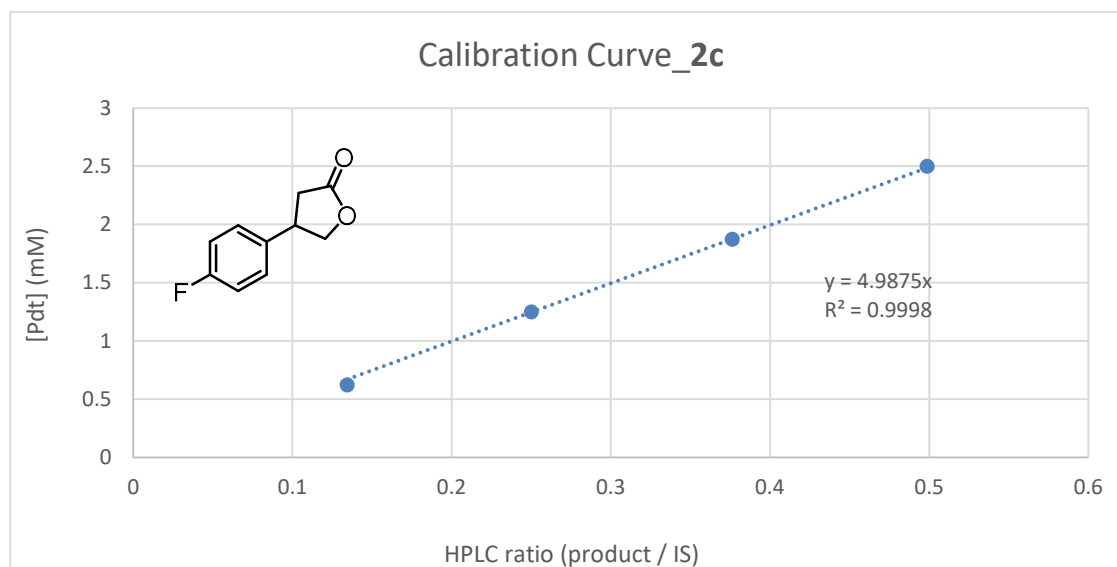
4-(4-Methoxyphenyl)dihydrofuran-2(3H)-one (2c)



Data analysis for P411-LAS-5247-catalyzed lactonization of **1c**:

Entry	Pdt	IS	Pdt/IS	[Pdt]/mM	[PC]/ μ M	Avg. Yield [%]	SD Yield [%]	Avg. TTN	SD TTN
1	1699.8	6305.0	0.270	1.412	0.36	57%	0.3%	3900	17
2	1771.9	6513.9	0.272	1.425	0.36				
3	1746.2	6448.6	0.271	1.418	0.36				

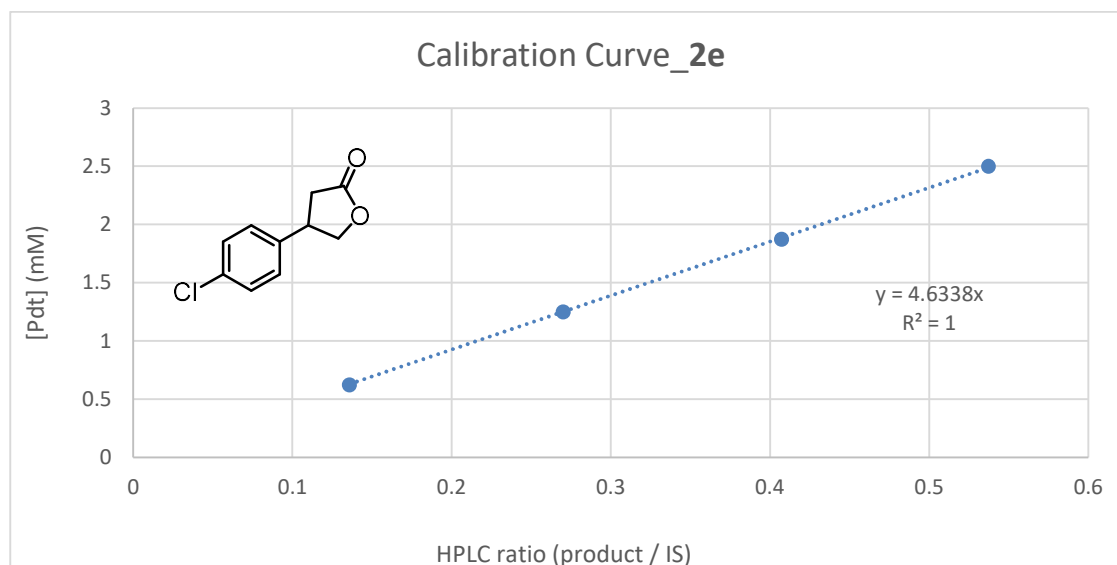
4-(4-Fluorophenyl)dihydrofuran-2(3H)-one (2d)



Data analysis for P411-LAS-5247-catalyzed lactonization of **1d**:

Entry	Pdt	IS	Pdt/IS	[Pdt]/mM	[PC]/ μ M	Avg. Yield [%]	SD Yield [%]	Avg. TTN	SD TTN
1	1853.3	6071.5	0.305	1.522	0.36	59%	2.6%	4100	180
2	1764.3	6291.9	0.280	1.399	0.36				
3	1863.3	6193.4	0.301	1.501	0.36				

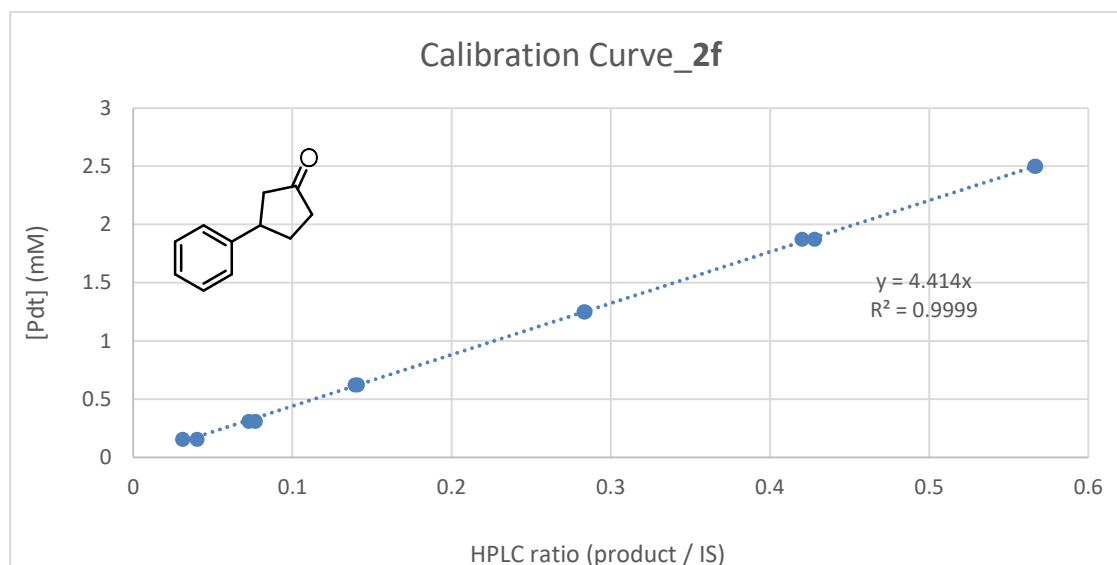
4-(4-Chlorophenyl)dihydrofuran-2(3H)-one (2e)



Data analysis for P411-LAS-5247-catalyzed lactonization of **1e**:

Entry	Pdt	IS	Pdt/IS	[Pdt]/mM	[PC]/ μ M	Avg. Yield [%]	SD Yield [%]	Avg. TTN	SD TTN
1	522.5	6060.0	0.086	0.400	0.36	16%	0.2%	1100	11
2	539.9	6222.4	0.087	0.402	0.36				
3	540.7	6154.0	0.088	0.407	0.36				

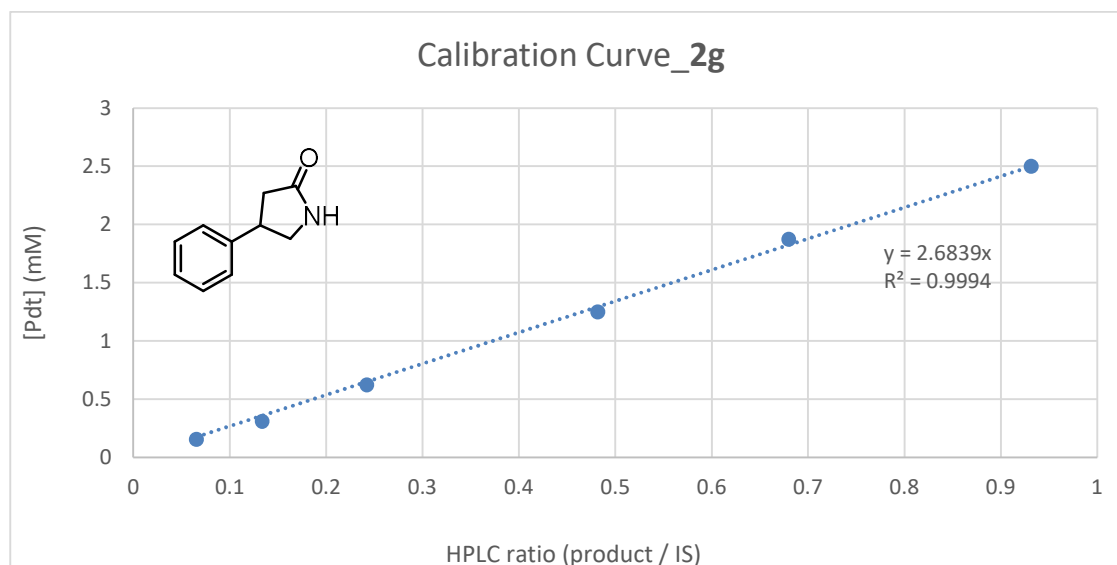
3-Phenylcyclopentan-1-one (2f)



Data analysis for P411-LAS-5247-catalyzed lactonization of **1f**:

Entry	Pdt	IS	Pdt/IS	[Pdt]/mM	[PC]/ μ M	Avg. Yield [%]	SD Yield [%]	Avg. TTN	SD TTN
1	3160.6	7132.0	0.443	1.956	0.36	80%	1.9%	5500	130
2	3265.6	7035.3	0.464	2.049	0.36				
3	3256.1	7160.5	0.455	2.007	0.36				

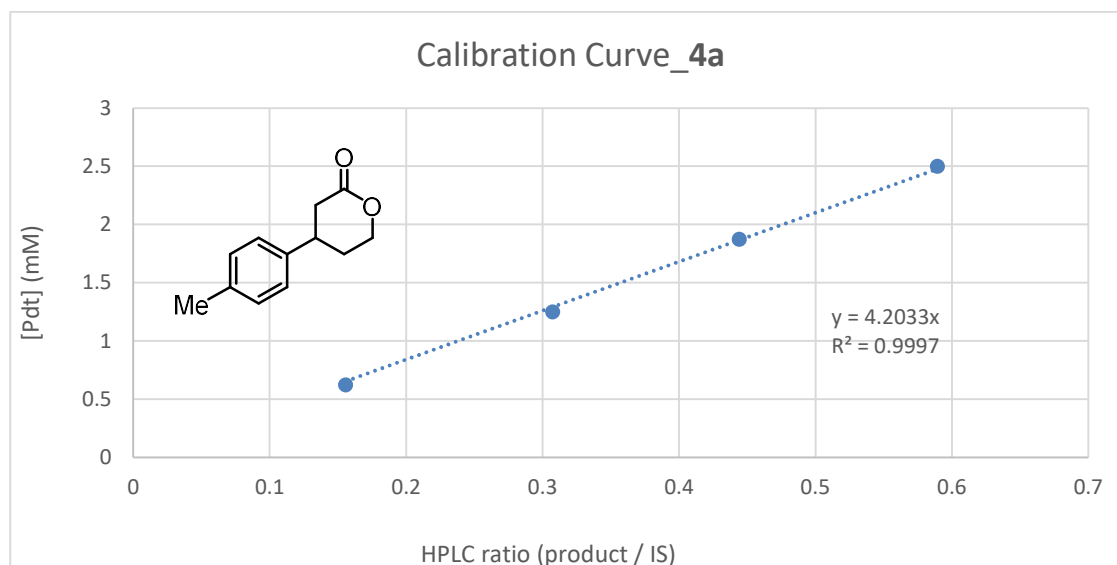
4-Phenylpyrrolidin-2-one (2g)



Data analysis for P411-LAS-5247-catalyzed lactonization of **1g**:

Entry	Pdt	IS	Pdt/IS	[Pdt]/mM	[PC]/ μ M	Avg. Yield [%]	SD Yield [%]	Avg. TTN	SD TTN
1	1094.2	4986.8	0.219	0.589	0.36	22%	1.7%	1500	120
2	1071.8	5423.0	0.198	0.530	0.36				
3	922.1	4884.8	0.189	0.507	0.36				

4-(*p*-Tolyl)tetrahydro-2*H*-pyran-2-one (4a)



Data analysis for P411-LAS-5244-catalyzed lactonization of **3a**:

Entry	Pdt	IS	Pdt/IS	[Pdt]/mM	[PC]/ μ M	Avg. Yield [%]	SD Yield [%]	Avg. TTN	SD TTN
1	1481.7	6087.0	0.243	1.023	0.33	52%	12%	3900	930
2	2345.7	6020.0	0.390	1.638	0.33				
3	1801.6	6036.7	0.298	1.254	0.33				

Data analysis for P411-LAS-5248-catalyzed lactonization of **3a**:

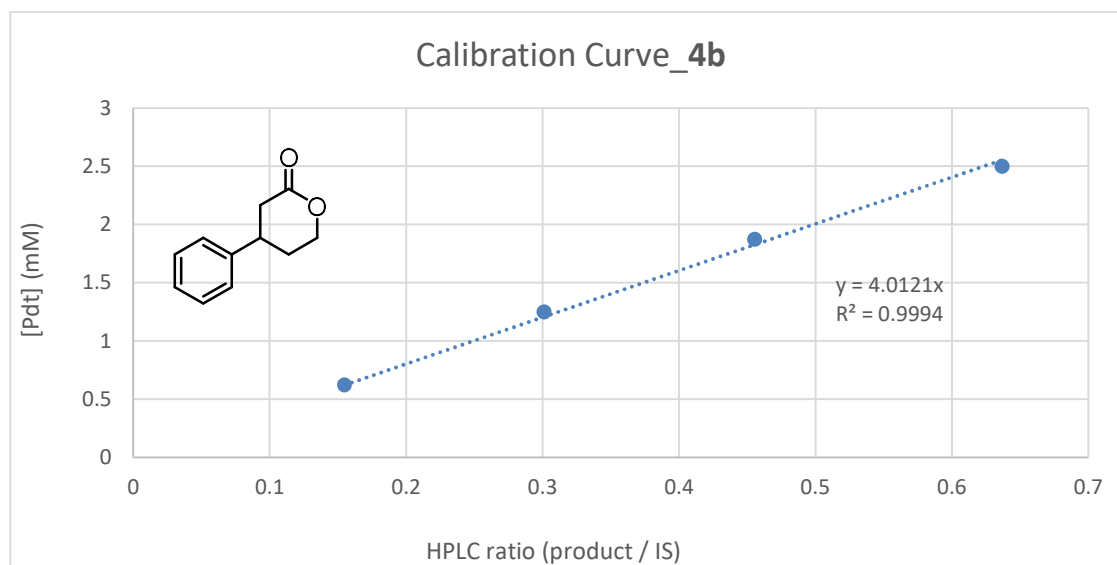
Entry	Pdt	IS	Pdt/IS	[Pdt]/mM	[PC]/ μ M	Avg. Yield [%]	SD Yield [%]	Avg. TTN	SD TTN
1	2084.1	6464.7	0.322	1.355	0.43	50%	6.2%	2900	360
2	1584.3	6192.3	0.256	1.075	0.43				
3	1950.1	6176.5	0.316	1.327	0.43				

Data analysis for P411-LAS-5249-catalyzed lactonization of **3a**:

Entry	Pdt	IS	Pdt/IS	[Pdt]/mM	[PC]/ μ M	Avg. Yield [%]	SD Yield [%]	Avg. TTN	SD TTN
1	1801.0	6187.4	0.291	1.223	0.44	50%	1.1%	2800	60
2	1862.7	6140.9	0.303	1.275	0.44				

3	1799.9	6114.0	0.294	1.237	0.44				
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4-Phenyltetrahydro-2H-pyran-2-one (4b)



Data analysis for P411-LAS-5244-catalyzed lactonization of **3b**:

Entry	Pdt	IS	Pdt/IS	[Pdt]/mM	[PC]/ μ M	Avg. Yield [%]	SD Yield [%]	Avg. TTN	SD TTN
1	1620.3	5949.3	0.272	1.093	0.33	48%	5.0%	3600	370
2	1978.5	5925.5	0.334	1.340	0.33				
3	1781.6	5974.4	0.298	1.196	0.33				

Data analysis for P411-LAS-5248-catalyzed lactonization of **3b**:

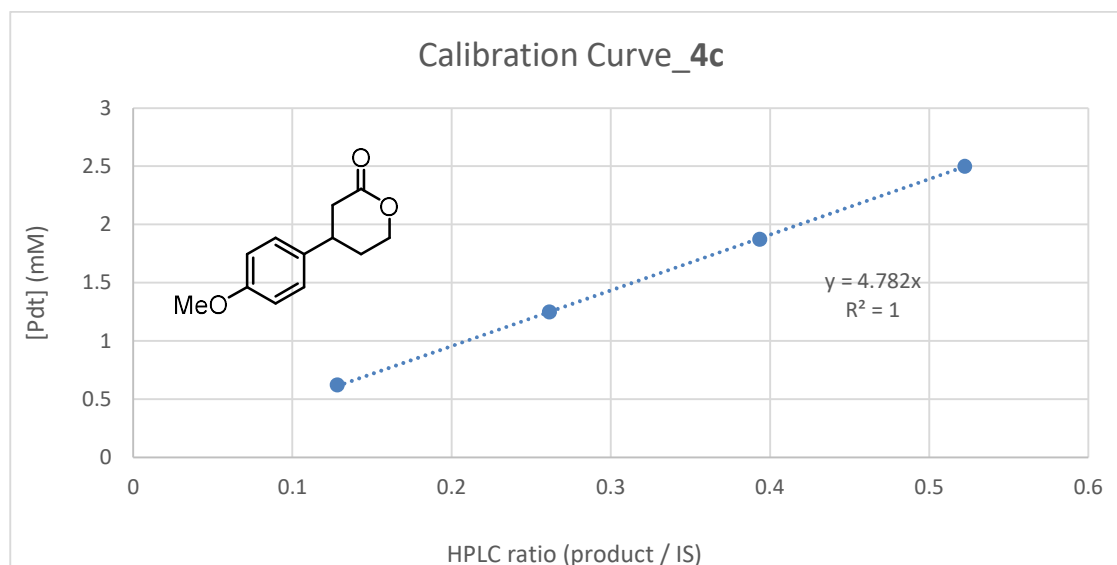
Entry	Pdt	IS	Pdt/IS	[Pdt]/mM	[PC]/ μ M	Avg. Yield [%]	SD Yield [%]	Avg. TTN	SD TTN
1	1677.7	6099.6	0.275	1.104	0.43	44%	0.7%	2600	39
2	1646.9	6092.6	0.270	1.085	0.43				
3	1691.7	6074.0	0.279	1.117	0.43				

Data analysis for P411-LAS-5249-catalyzed lactonization of **3b**:

Entry	Pdt	IS	Pdt/IS	[Pdt]/mM	[PC]/ μ M	Avg. Yield [%]	SD Yield [%]	Avg. TTN	SD TTN
1	997.9	6122.6	0.163	0.654	0.44	25%	1.2%	1400	69
2	937.9	6169.0	0.152	0.610	0.44				

3	908.2	6127.3	0.148	0.595	0.44				
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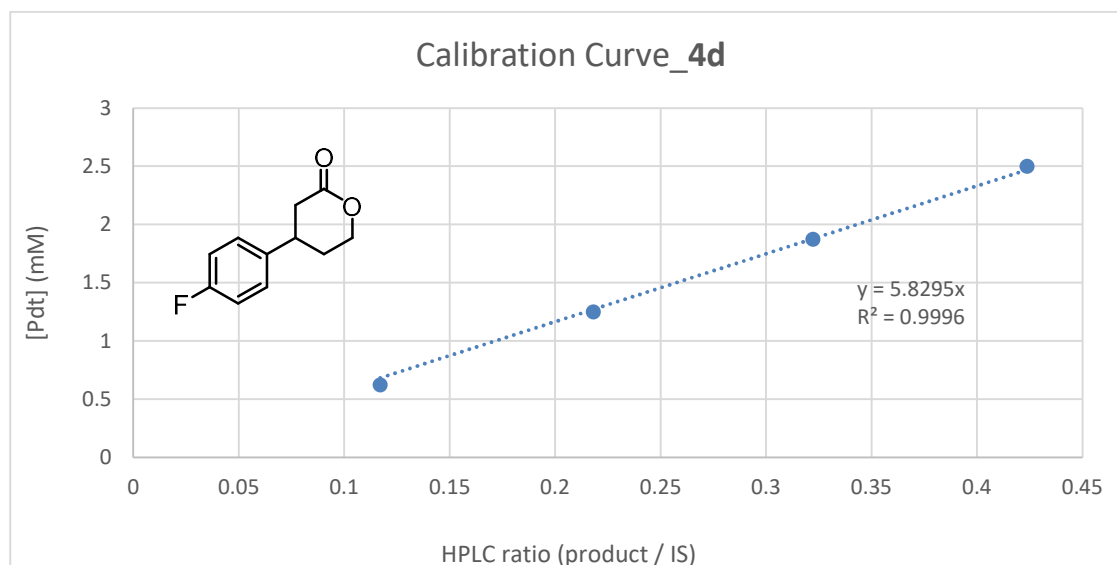
4-(4-Methoxyphenyl)tetrahydro-2H-pyran-2-one (4c)



Data analysis for P411-LAS-5249-catalyzed lactonization of **3c**:

Entry	Pdt	IS	Pdt/IS	[Pdt]/mM	[PC]/ μ M	Avg. Yield [%]	SD Yield [%]	Avg. TTN	SD TTN
1	1600.1	5835.8	0.274	1.311	0.44	53%	3.1%	3000	170
2	1744.1	5891.3	0.296	1.416	0.44				
3	1584.1	5987.1	0.265	1.265	0.44				

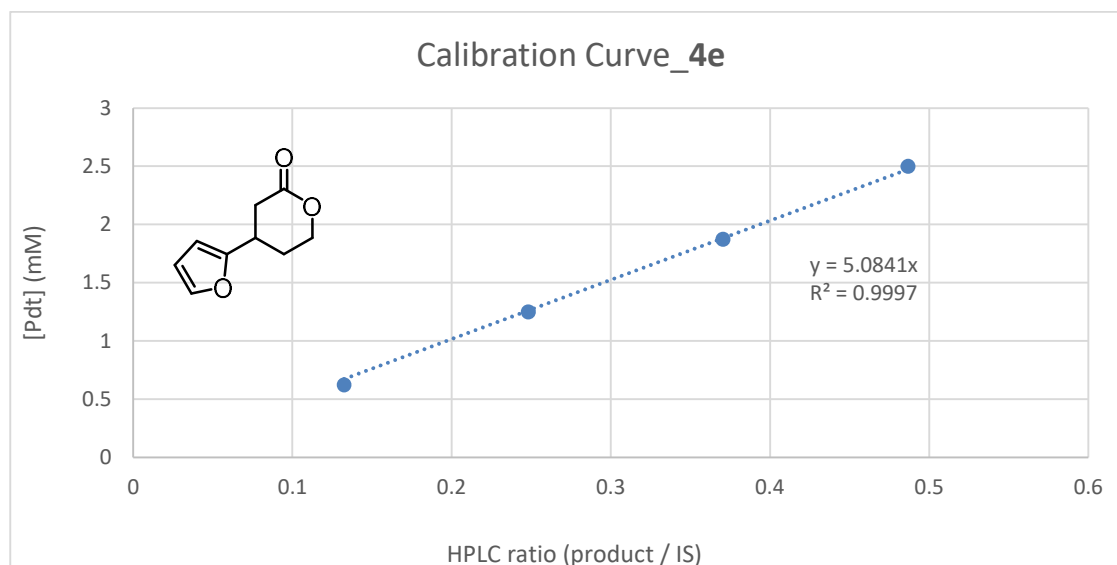
4-(4-Fluorophenyl)tetrahydro-2H-pyran-2-one (4d)



Data analysis for P411-LAS-5249-catalyzed lactonization of **3d**:

Entry	Pdt	IS	Pdt/IS	[Pdt]/mM	[PC]/ μ M	Avg. Yield [%]	SD Yield [%]	Avg. TTN	SD TTN
1	491.3	5720.4	0.086	0.501	0.44	21%	1.0%	1200	55
2	503.8	5389.0	0.093	0.545	0.44				
3	474.2	5481.1	0.087	0.504	0.44				

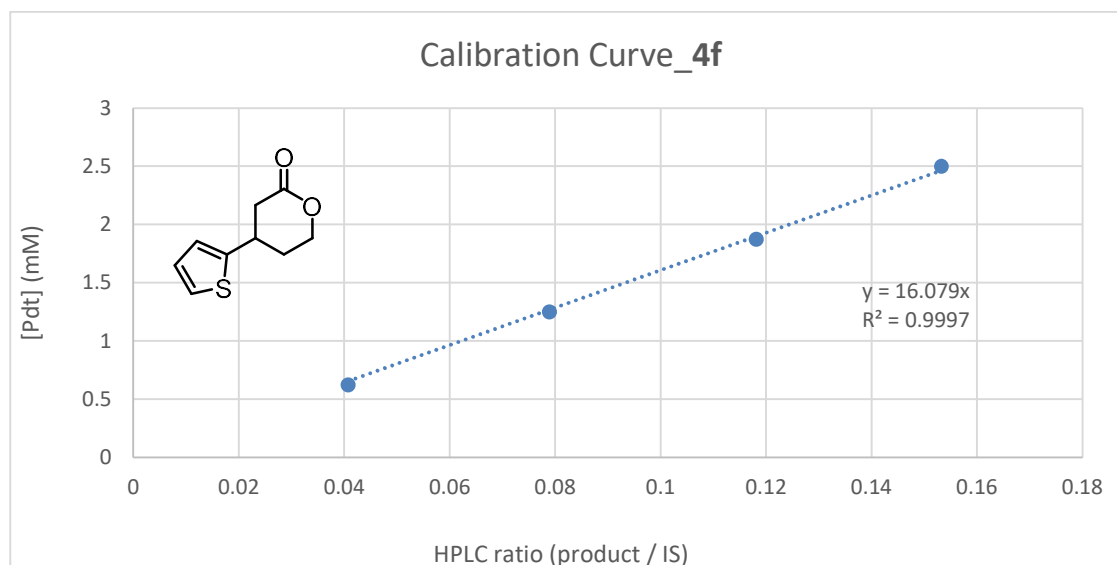
4-(Furan-2-yl)tetrahydro-2H-pyran-2-one (4e)



Data analysis for P411-LAS-5249-catalyzed lactonization of **3e**:

Entry	Pdt	IS	Pdt/IS	[Pdt]/mM	[PC]/ μ M	Avg. Yield [%]	SD Yield [%]	Avg. TTN	SD TTN
1	1286.9	7507.0	0.171	0.872	0.44	41%	5.1%	2300	290
2	1172.1	5582.4	0.210	1.067	0.44				
3	1187.0	5436.8	0.218	1.110	0.44				

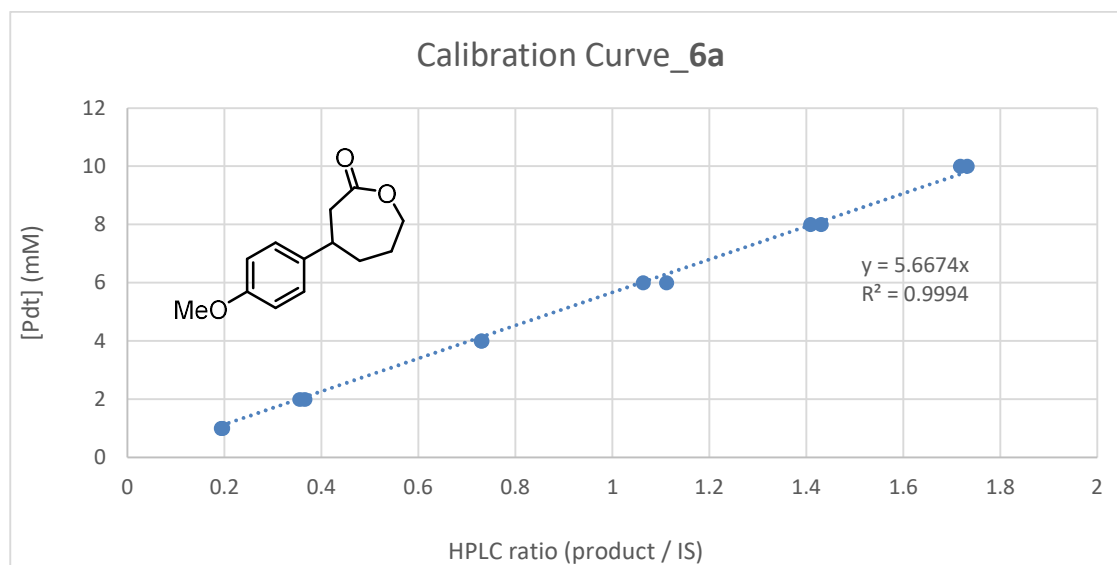
4-(Thiophen-2-yl)tetrahydro-2H-pyran-2-one (4f)



Data analysis for P411-LAS-5249-catalyzed lactonization of **3f**:

Entry	Pdt	IS	Pdt/IS	[Pdt]/mM	[PC]/ μ M	Avg. Yield [%]	SD Yield [%]	Avg. TTN	SD TTN
1	562.4	5383.0	0.104	1.680	0.44	71%	8.1%	4000	460
2	636.3	5093.9	0.125	2.009	0.44				
3	539.4	5284.6	0.102	1.641	0.44				

4-(4-Methoxyphenyl)oxepan-2-one (6a)



Data analysis for P411-LAS-5250-catalyzed lactonization of **5a**:

Entry	Pdt	IS	Pdt/IS	[Pdt]/mM	[PC]/ μ M	Avg. Yield [%]	SD Yield [%]	Avg. TTN	SD TTN
1	359.9	5927.4	0.061	0.344	0.42	16%	1.9%	940	111
2	452.7	6102.1	0.074	0.420	0.42				
3	484.2	6388.5	0.076	0.430	0.42				

Data analysis for P411-LAS-5251-catalyzed lactonization of **5a**:

Entry	Pdt	IS	Pdt/IS	[Pdt]/mM	[PC]/ μ M	Avg. Yield [%]	SD Yield [%]	Avg. TTN	SD TTN
1	732.6	6417.9	0.114	0.647	0.59	26%	1.2%	1100	52
2	718.9	6558.8	0.110	0.621	0.59				
3	788.2	6552.1	0.120	0.682	0.59				

Data analysis for P411-LAS-5252-catalyzed lactonization of **5a**:

Entry	Pdt	IS	Pdt/IS	[Pdt]/mM	[PC]/ μ M	Avg. Yield [%]	SD Yield [%]	Avg. TTN	SD TTN
1	603.8	6563.4	0.092	0.521	0.46	21%	0.5%	1100	28
2	600.4	6736.5	0.089	0.505	0.46				

3	625.1	6680.7	0.094	0.530	0.46				
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Data analysis for P411-LAS-5253-catalyzed lactonization of **5a**:

Entry	Pdt	IS	Pdt/IS	[Pdt]/mM	[PC]/ μ M	Avg. Yield [%]	SD Yield [%]	Avg. TTN	SD TTN
1	902.5	6670.6	0.135	0.767	0.51	31%	1.9%	1500	94
2	827.5	6557.1	0.126	0.715	0.51				
3	936.6	6551.0	0.143	0.810	0.51				

Data analysis for P411-LAS-5254-catalyzed lactonization of **5a**:

Entry	Pdt	IS	Pdt/IS	[Pdt]/mM	[PC]/ μ M	Avg. Yield [%]	SD Yield [%]	Avg. TTN	SD TTN
1	782.1	5819.3	0.134	0.762	0.59	31%	4.0%	1300	169
2	976.6	6180.9	0.158	0.895	0.59				
3	777.4	6307.1	0.123	0.699	0.59				

Data analysis for P411-LAS-5255-catalyzed lactonization of **5a**:

Entry	Pdt	IS	Pdt/IS	[Pdt]/mM	[PC]/ μ M	Avg. Yield [%]	SD Yield [%]	Avg. TTN	SD TTN
1	981.8	6519.0	0.151	0.854	0.59	36%	3.8%	1500	158
2	1161.9	6458.8	0.180	1.020	0.59				
3	1007.9	6633.7	0.152	0.861	0.59				

Data analysis for P411-LAS-5256-catalyzed lactonization of **5a**:

Entry	Pdt	IS	Pdt/IS	[Pdt]/mM	[PC]/ μ M	Avg. Yield [%]	SD Yield [%]	Avg. TTN	SD TTN
1	1234.1	6580.0	0.188	1.063	0.65	44%	2.3%	1700	90
2	1268.3	6630.9	0.191	1.084	0.65				
3	1341.1	6481.3	0.207	1.172	0.65				

Data analysis for P411-LAS-5257-catalyzed lactonization of **5a**:

Entry	Pdt	IS	Pdt/IS	[Pdt]/mM	[PC]/ μ M	Avg. Yield [%]	SD Yield [%]	Avg. TTN	SD TTN
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1	1536.3	6894.4	0.223	1.263	0.60	52%	2.7%	2200	110
2	1557.1	6936.0	0.225	1.272	0.60				
3	1585.7	6500.6	0.244	1.382	0.60				

Data analysis for P411-LAS-5258-catalyzed lactonization of **5a**:

Entry	Pdt	IS	Pdt/IS	[Pdt]/mM	[PC]/ μ M	Avg. Yield [%]	SD Yield [%]	Avg. TTN	SD TTN
1	1427.9	6825.7	0.209	1.186	0.48	45%	2.2%	2300	115
2	1299.7	6783.4	0.192	1.086	0.48				
3	1320.3	6846.9	0.193	1.093	0.48				

Data analysis for P411-LAS-5259-catalyzed lactonization of **5a**:

Entry	Pdt	IS	Pdt/IS	[Pdt]/mM	[PC]/ μ M	Avg. Yield [%]	SD Yield [%]	Avg. TTN	SD TTN
1	1701.9	6649.2	0.256	1.451	0.60	58%	0.3%	2400	14
2	1708.4	6745.3	0.253	1.435	0.60				
3	1686.3	6646.8	0.254	1.438	0.60				

Data analysis for P411-LAS-5260-catalyzed lactonization of **5a**:

Entry	Pdt	IS	Pdt/IS	[Pdt]/mM	[PC]/ μ M	Avg. Yield [%]	SD Yield [%]	Avg. TTN	SD TTN
1	459.3	8604.6	0.053	0.302	0.44	12%	0.3%	700	19
2	449.4	8536.2	0.053	0.298	0.44				
3	473.2	8540.4	0.055	0.314	0.44				

Data analysis for P411-LAS-5261-catalyzed lactonization of **5a**:

Entry	Pdt	IS	Pdt/IS	[Pdt]/mM	[PC]/ μ M	Avg. Yield [%]	SD Yield [%]	Avg. TTN	SD TTN
1	973.7	11628.9	0.084	0.475	0.38	18%	0.8%	1200	51
2	862.5	11202.6	0.077	0.436	0.38				
3	913.0	11158.4	0.082	0.464	0.38				

Data analysis for P411-LAS-5262-catalyzed lactonization of **5a**:

Entry	Pdt	IS	Pdt/IS	[Pdt]/mM	[PC]/ μ M	Avg. Yield [%]	SD Yield [%]	Avg. TTN	SD TTN
1	1004.5	6735.3	0.149	0.845	0.30	33%	1.1%	2700	93
2	957.7	6833.3	0.140	0.794	0.30				
3	1002.6	6763.7	0.148	0.840	0.30				

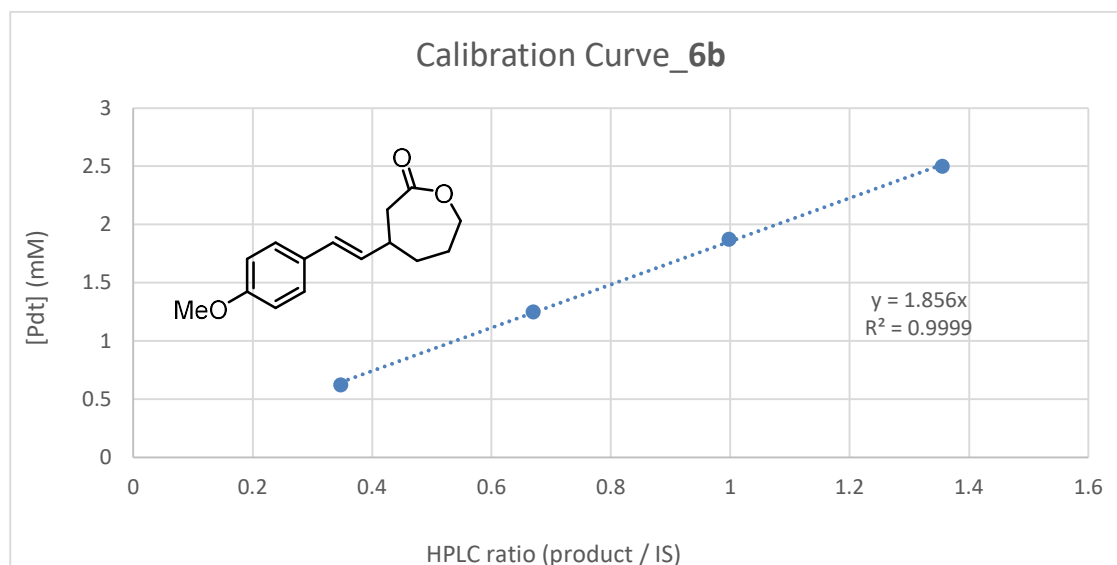
Data analysis for P411-LAS-5263-catalyzed lactonization of **5a**:

Entry	Pdt	IS	Pdt/IS	[Pdt]/mM	[PC]/ μ M	Avg. Yield [%]	SD Yield [%]	Avg. TTN	SD TTN
1	1237.1	6865.1	0.180	1.021	0.34	39%	2.2%	2900	160
2	1138.2	7037.4	0.162	0.917	0.34				
3	1242.0	7022.0	0.177	1.002	0.34				

Data analysis for P411-LAS-5264-catalyzed lactonization of **5a**:

Entry	Pdt	IS	Pdt/IS	[Pdt]/mM	[PC]/ μ M	Avg. Yield [%]	SD Yield [%]	Avg. TTN	SD TTN
1	1554.7	6540.6	0.238	1.347	0.43	54%	0.5%	3100	27
2	1589.5	6571.2	0.242	1.371	0.43				
3	1574.8	6557.0	0.240	1.361	0.43				

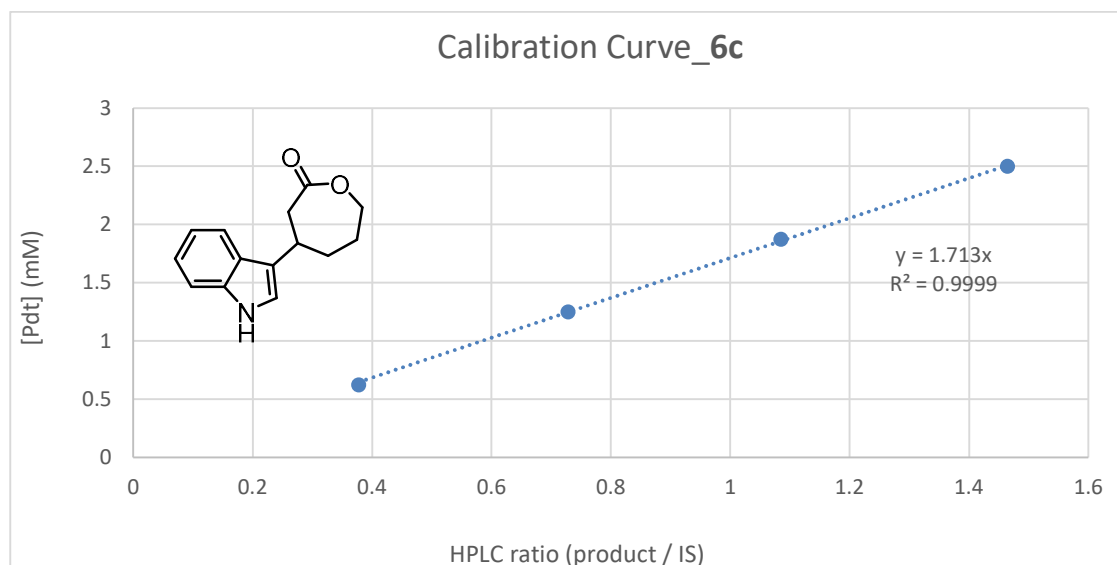
(E)-4-(4-Methoxystyryl)oxepan-2-one (6b)



Data analysis for P411-LAS-5264-catalyzed lactonization of **5b**:

Entry	Pdt	IS	Pdt/IS	[Pdt]/mM	[PC]/ μ M	Avg. Yield [%]	SD Yield [%]	Avg. TTN	SD TTN
1	4650.4	7286.5	0.638	1.185	0.38	51%	3.3%	3300	210
2	5572.1	7877.2	0.707	1.313	0.38				
3	5097.0	7072.8	0.721	1.338	0.38				

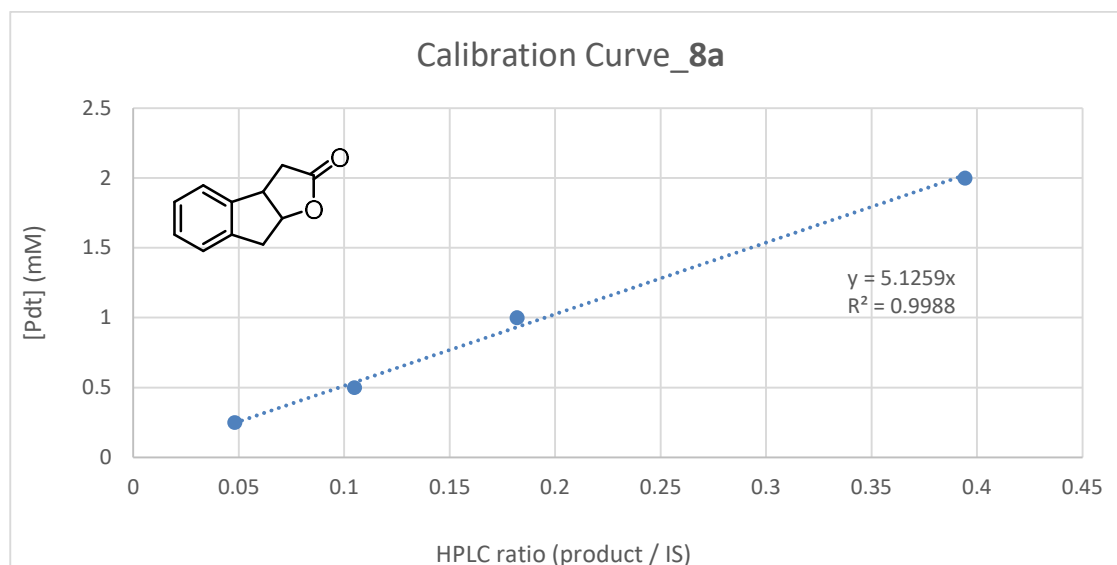
4-(1*H*-Indol-3-yl)oxepan-2-one (6c)



Data analysis for P411-LAS-5264-catalyzed lactonization of **5c**:

Entry	Pdt	IS	Pdt/IS	[Pdt]/mM	[PC]/ μ M	Avg. Yield [%]	SD Yield [%]	Avg. TTN	SD TTN
1	4710.8	7474.0	0.630	1.080	0.38	43%	3.3%	2800	220
2	5239.7	7653.6	0.685	1.173	0.38				
3	4474.1	7602.0	0.589	1.008	0.38				

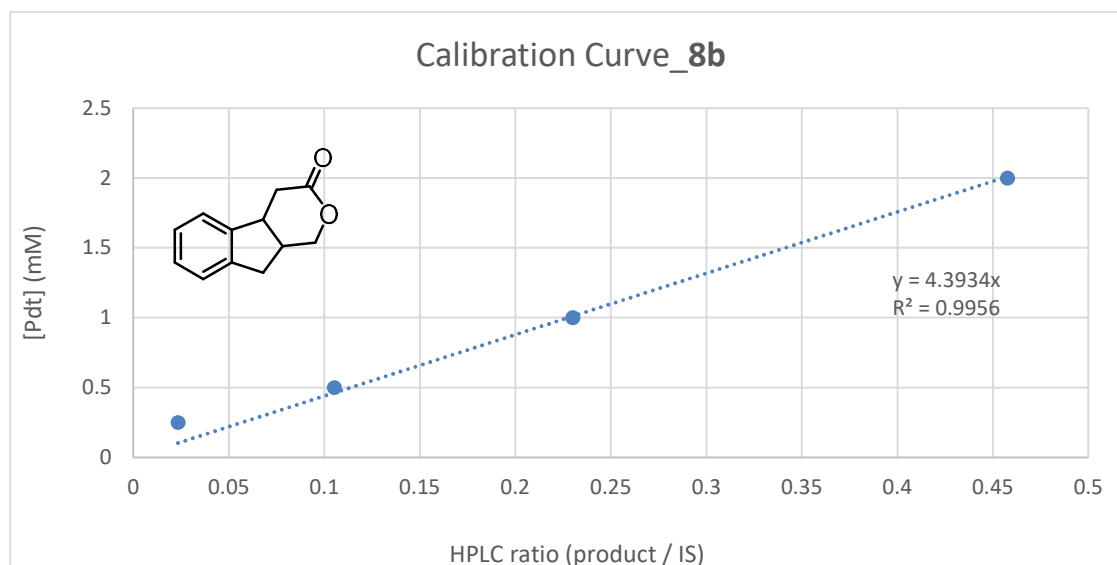
3,3a,8,8a-Tetrahydro-2*H*-indeno[2,1-*b*]furan-2-one (8a)



Data analysis for P411-LAS-5265-catalyzed lactonization of **7a**:

Entry	Pdt	IS	Pdt/IS	[Pdt]/mM	[PC]/ μ M	Avg. Yield [%]	SD Yield [%]	Avg. TTN	SD TTN
1	1751.0	3491.1	0.502	2.571	0.37	98%	4.2%	6500	280
2	1603.7	3452.6	0.464	2.381	0.37				
3	1624.4	3476.7	0.467	2.395	0.37				

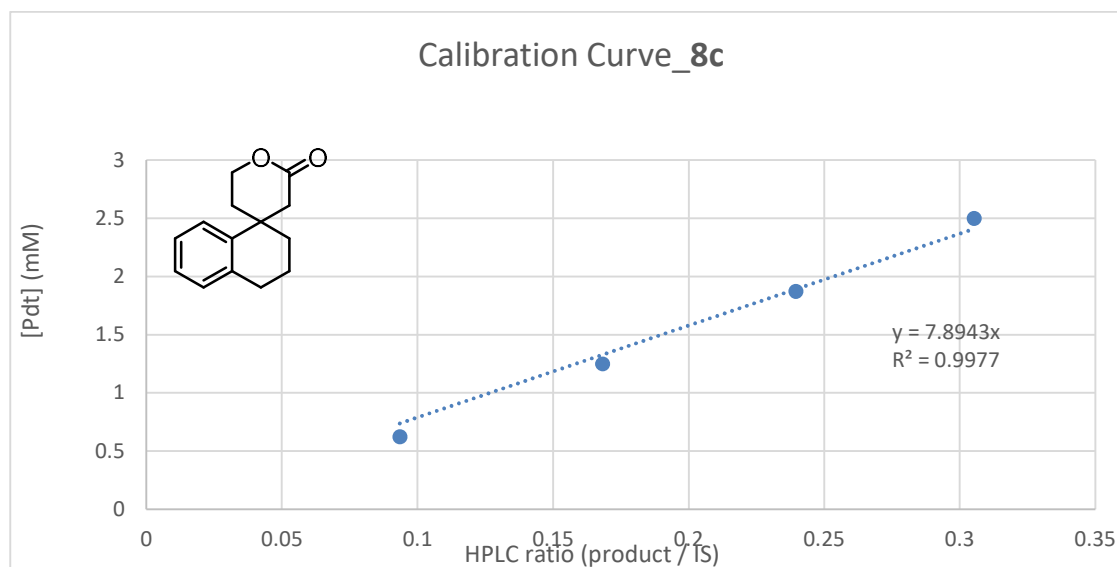
4,4a,9,9a-Tetrahydroindeno[2,1-c]pyran-3(1H)-one (8b)



Data analysis for P411-LAS-5265-catalyzed lactonization of **7b**:

Entry	Pdt	IS	Pdt/IS	[Pdt]/mM	[PC]/ μ M	Avg. Yield [%]	SD Yield [%]	Avg. TTN	SD TTN
1	1442.1	3458.6	0.417	1.832	0.37	73%	2.9%	4800	200
2	1360.2	3451.3	0.394	1.732	0.37				
3	1473.1	3452.3	0.427	1.875	0.37				

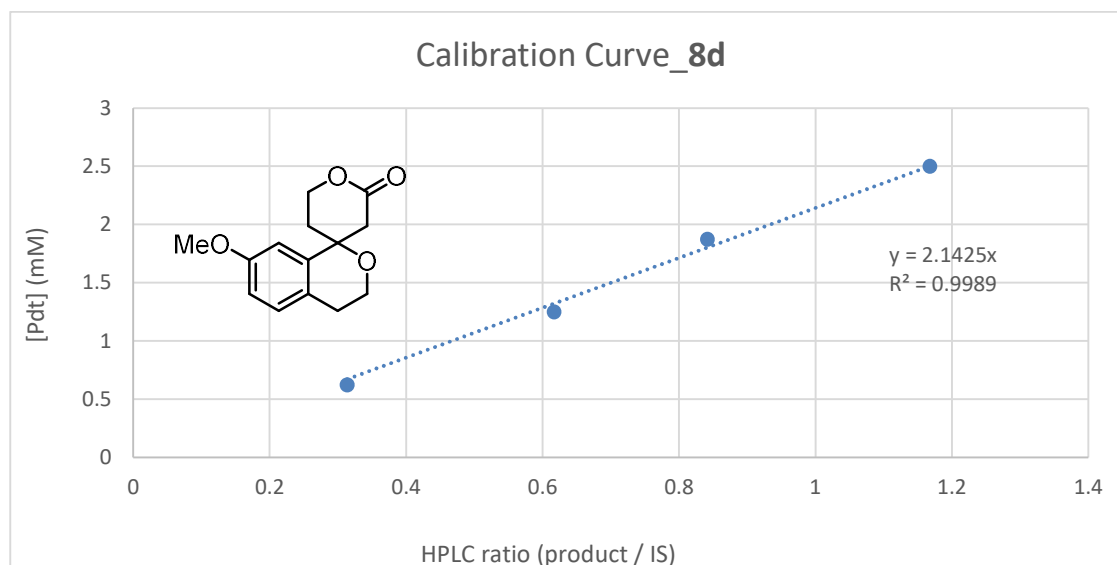
3,4,5',6'-Tetrahydro-2*H*-spiro[naphthalene-1,4'-pyran]-2'(3'*H*)-one (8c)



Data analysis for P411-LAS-5259-catalyzed lactonization of **7c**:

Entry	Pdt	IS	Pdt/IS	[Pdt]/mM	[PC]/ μ M	Avg. Yield [%]	SD Yield [%]	Avg. TTN	SD TTN
1	123.1	3824.5	0.032	0.254	0.46	11%	0.6%	591	31
2	134.5	3813.9	0.035	0.278	0.46				
3	136.4	3872.6	0.035	0.278	0.46				

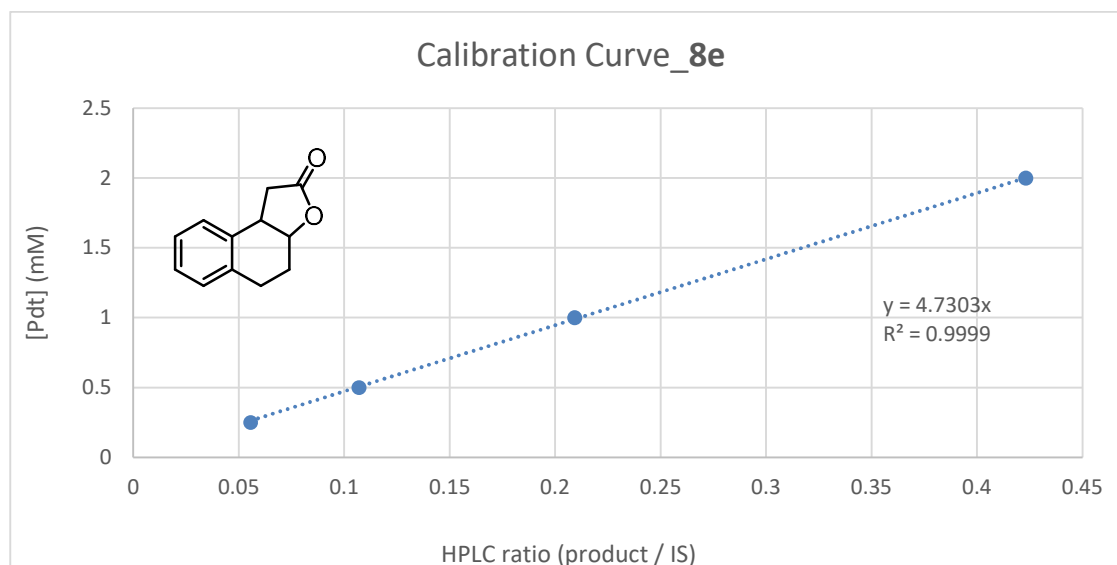
7-methoxy-5',6'-dihydrospiro[isochromane-1,4'-pyran]-2'(3'H)-one (8d)



Data analysis for P411-LAS-5257-catalyzed lactonization of **7d**:

Entry	Pdt	IS	Pdt/IS	[Pdt]/mM	[PC]/ μ M	Avg. Yield [%]	SD Yield [%]	Avg. TTN	SD TTN
1	1554.7	3507.3	0.443	0.950	0.40	39%	1.8%	2500	110
2	1589.3	3286.4	0.484	1.036	0.40				
3	1599.7	3530.1	0.453	0.971	0.40				

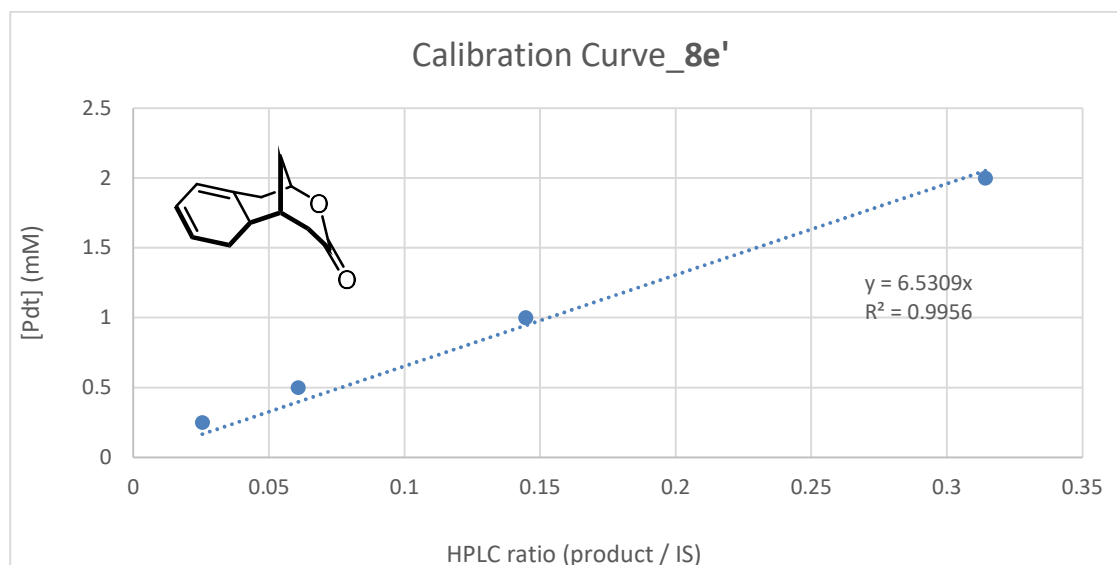
3a,4,5,9b-Tetrahydronaphtho[2,1-*b*]furan-2(1*H*)-one (8e)



Data analysis for P411-LAS-5259-catalyzed lactonization of **7e** toward the synthesis of **8e**:

Entry	Pdt	IS	Pdt/IS	[Pdt]/mM	[PC]/ μ M	Avg. Yield [%]	SD Yield [%]	Avg. TTN	SD TTN
1	717.4	3203.8	0.224	1.059	0.38	43%	1.1%	2900	76
2	740.4	3138.2	0.236	1.116	0.38				
3	720.8	3151.0	0.229	1.082	0.38				

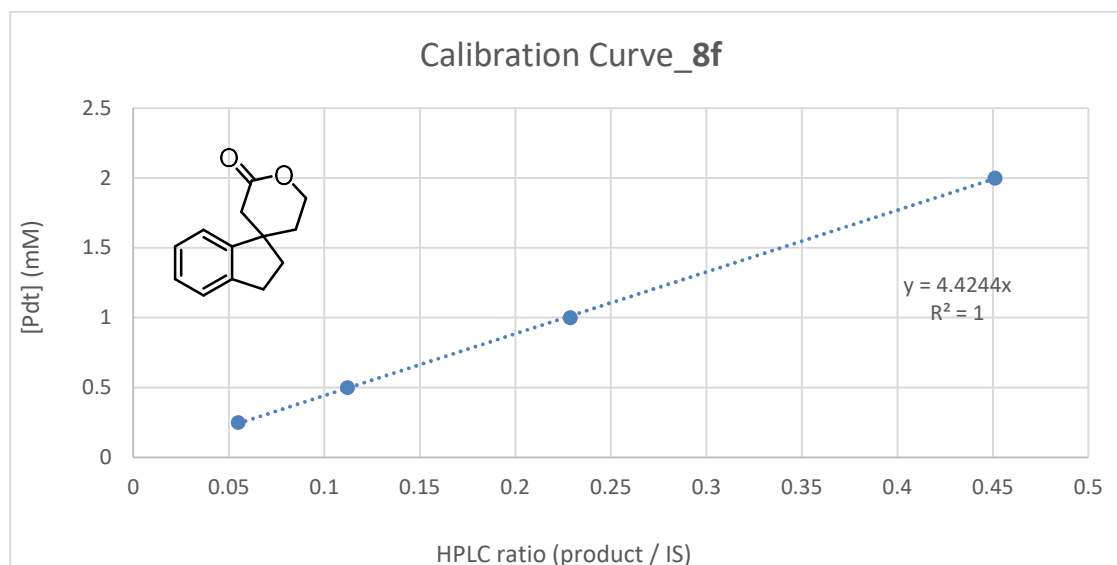
1,2,5,6-tetrahydro-4*H*-2,6-methanobenzo[*d*]oxocin-4-one (8e')



Data analysis for P411-LAS-5259-catalyzed lactonization of **7e** toward the synthesis of **8e'**:

Entry	Pdt	IS	Pdt/IS	[Pdt]/mM	[PC]/ μ M	Avg. Yield [%]	SD Yield [%]	Avg. TTN	SD TTN
1	619.5	3203.8	0.193	1.263	0.38	48%	2.3%	3200	150
2	571.5	3138.2	0.182	1.189	0.38				
3	554.6	3151.0	0.176	1.149	0.38				

2,3,5',6'-Tetrahydrospiro[indene-1,4'-pyran]-2'(3'H)-one (8f)



Data analysis for P411-LAS-5247-catalyzed lactonization of **7f** toward the synthesis of **8f**:

Entry	Pdt	IS	Pdt/IS	[Pdt]/mM	[PC]/ μ M	Avg. Yield [%]	SD Yield [%]	Avg. TTN	SD TTN
1	581.6	4155.9	0.140	0.619132	0.36	25%	2.3%	1700	160
2	532.8	4224.1	0.126	0.558086	0.36				
3	640.2	4219.2	0.152	0.671355	0.36				

Data analysis for P411-LAS-5256-catalyzed lactonization of **7f** toward the synthesis of **8f**:

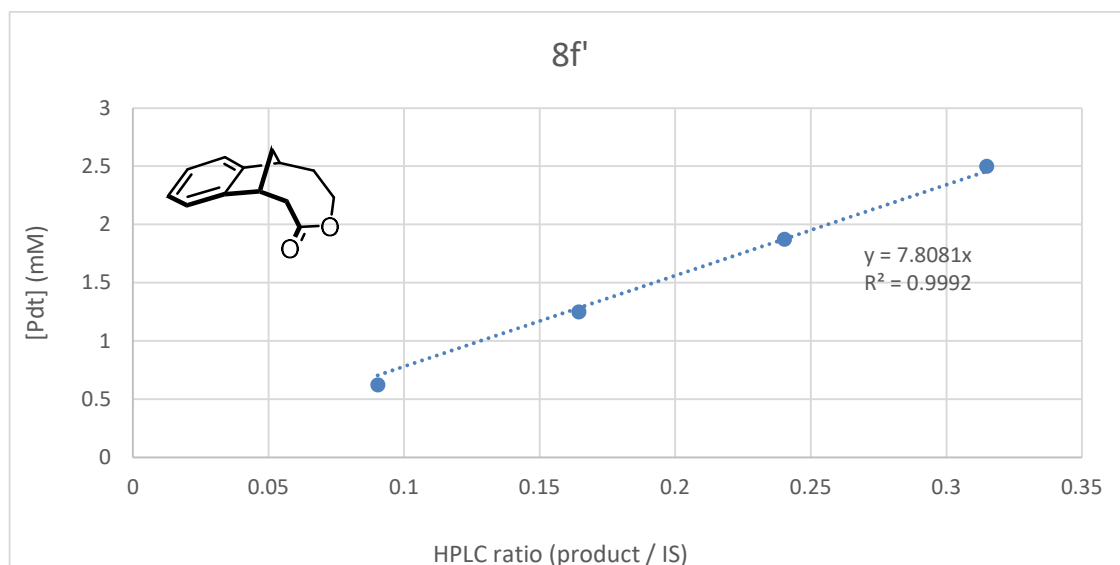
Entry	Pdt	IS	Pdt/IS	[Pdt]/mM	[PC]/ μ M	Avg. Yield [%]	SD Yield [%]	Avg. TTN	SD TTN
1	1280.4	4008.6	0.319	1.413	0.36	62%	4.9%	4300	340
2	1473.9	3961.7	0.372	1.646	0.36				
3	1448.6	4034.8	0.359	1.588	0.36				

Data analysis for P411-LAS-5266-catalyzed lactonization of **7f** toward the synthesis of **8f**:

Entry	Pdt	IS	Pdt/IS	[Pdt]/mM	[PC]/ μ M	Avg. Yield [%]	SD Yield [%]	Avg. TTN	SD TTN
1	0	3090.1	-	-	0.17	-	-	-	-
2	0	3288.8	-	-	0.17				

3	0	3269.2	-	-	0.17				
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(7)-1,5,6,7-Tetrahydro-1,7-methanobenzo[e]oxonin-3(2H)-one (8f')



Data analysis for P411-LAS-5247-catalyzed lactonization of **7f** toward the synthesis of **8f'**:

Entry	Pdt	IS	Pdt/IS	[Pdt]/mM	[PC]/ μ M	Avg. Yield [%]	SD Yield [%]	Avg. TTN	SD TTN
1	581.6	4155.9	0.121	0.945	0.36	34%	3.2%	2400	220
2	532.8	4224.1	0.109	0.848	0.36				
3	640.2	4219.2	0.101	0.787	0.36				

Data analysis for P411-LAS-5256-catalyzed lactonization of **7f** toward the synthesis of **8f'**:

Entry	Pdt	IS	Pdt/IS	[Pdt]/mM	[PC]/ μ M	Avg. Yield [%]	SD Yield [%]	Avg. TTN	SD TTN
1	0	4008.6	-	-	0.36	-	-	-	-
2	0	3961.7	-	-	0.36				
3	0	4034.8	-	-	0.36				

Data analysis for P411-LAS-5266-catalyzed lactonization of **7f** toward the synthesis of **8f'**:

Entry	Pdt	IS	Pdt/IS	[Pdt]/mM	[PC]/ μ M	Avg. Yield [%]	SD Yield [%]	Avg. TTN	SD TTN
1	205.0	3090.1	0.066	0.518	0.17	21%	0.3%	3100	39
2	221.8	3288.8	0.067	0.526	0.17				

3	222.3	3269.2	0.068	0.531	0.17				
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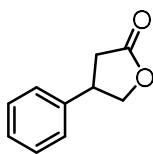
7. Enantioselectivity Determination

The absolute configuration of enzymatic product **2c** was assigned to be *S* by comparing the elution order of two enantiomers with a literature report under same elution conditions using the same column (Chiralpak IB).¹⁸ The other γ -lactone products **2a–2b**, **2d–2m** were assigned by analogy.

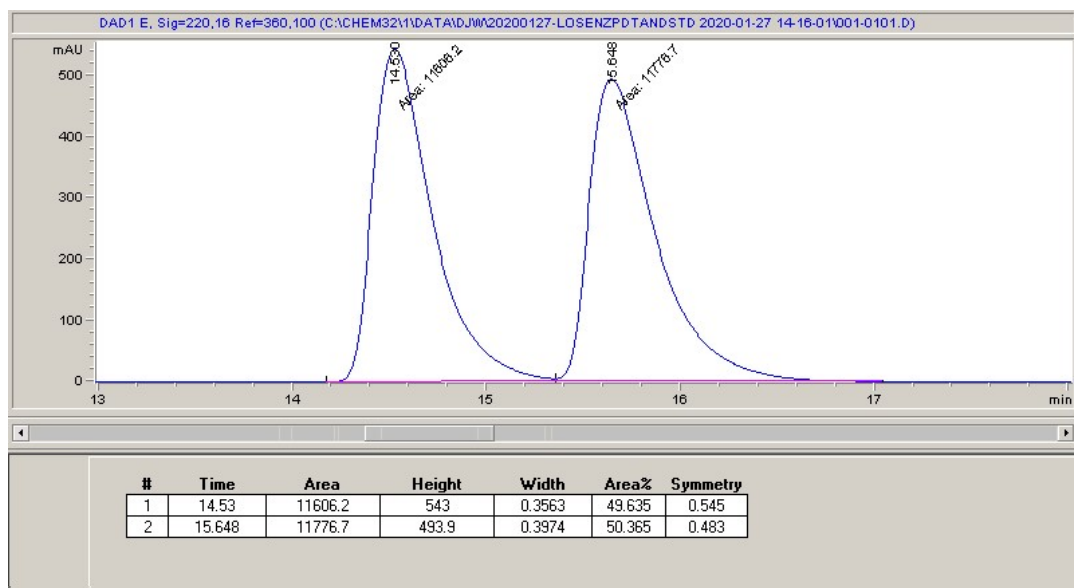
The absolute configuration of enzymatic product **4b** was assigned to be *R* by comparing the elution order of two enantiomers with a literature report under same elution conditions using the same column (Chiralpak AS-H).¹⁸ The other δ -lactone products **4a**, **4c–4f** were assigned by analogy.

The absolute stereochemistry for enzymatic product **6a** was assigned as *S* through X-ray crystallography (see section 8). The other ϵ -lactone products **6b** and **6c** were assigned by analogy.

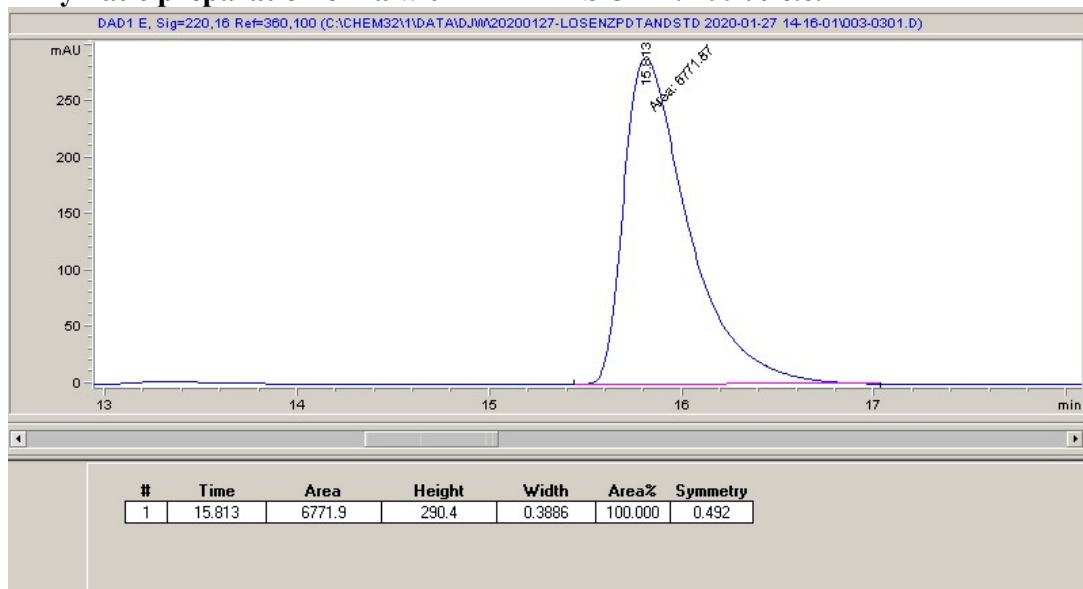
4-Phenyldihydrofuran-2(3H)-one (2a)



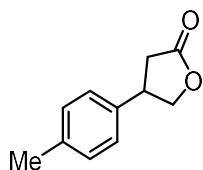
HPLC conditions: Chiralpak IA, 2.5% *i*-PrOH in hexane, 1.2 mL/min, 32 °C, 220 nm



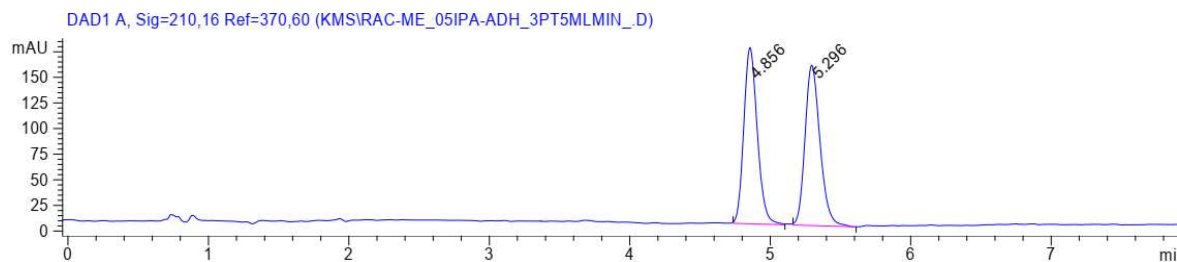
Enzymatic preparation of 2a with P411-LAS-5247: >99% e.e.



4-(*p*-Tolyl)dihydrofuran-2(3*H*)-one (2b)

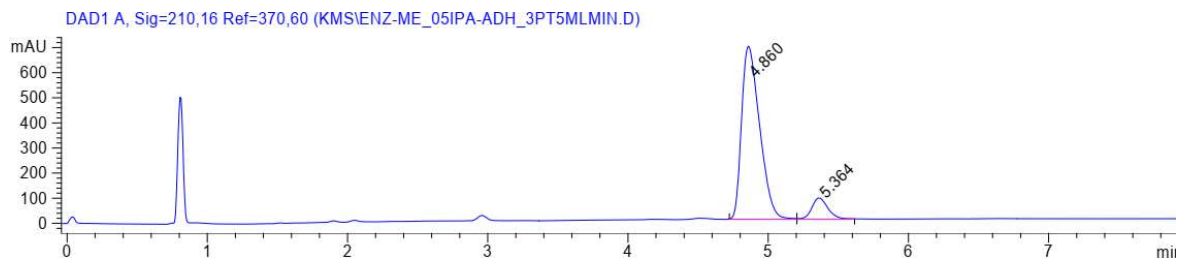


SFC conditions: Chiralpak AD-H, 5% *i*-PrOH in supercritical CO₂, 2.5 mL/min, 210 nm



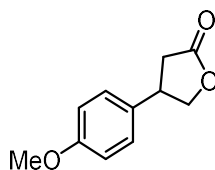
Peak #	RetTime [min]	Type	Width [min]	Area [mAU*s]	Height [mAU]	Area %
1	4.856	BB	0.1019	1146.25952	171.62752	49.6720
2	5.296	BB	0.1147	1161.39697	156.22182	50.3280

Enzymatic preparation of 2b with P411-LAS-5247: 80% e.e.

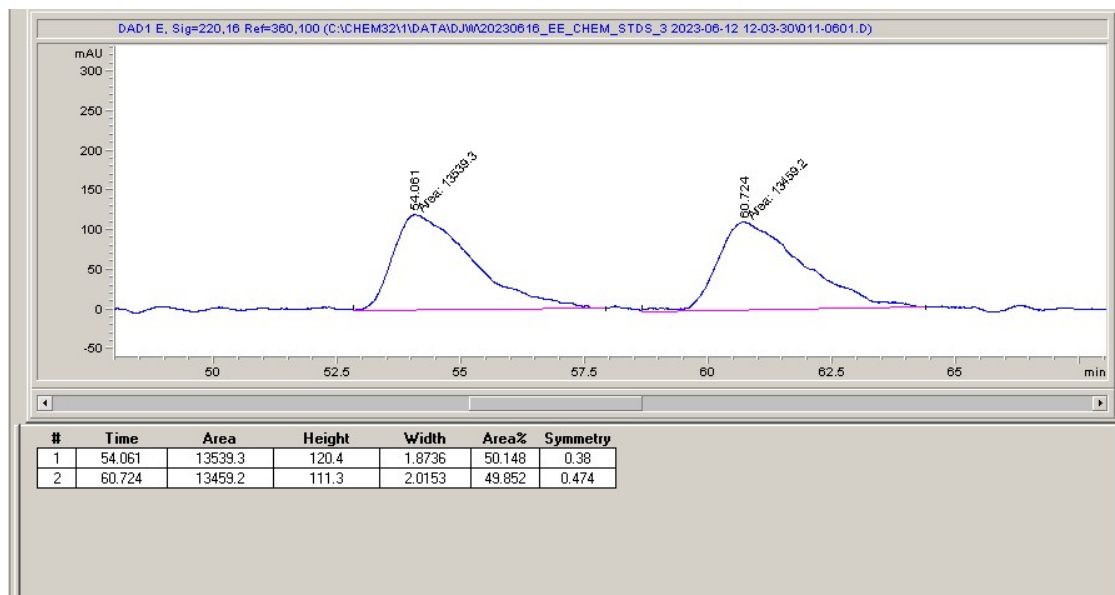


Peak #	RetTime [min]	Type	Width [min]	Area [mAU*s]	Height [mAU]	Area %
1	4.860	BV	0.1360	6139.50293	688.93280	90.1516
2	5.364	VB	0.1209	670.69690	84.23247	9.8484

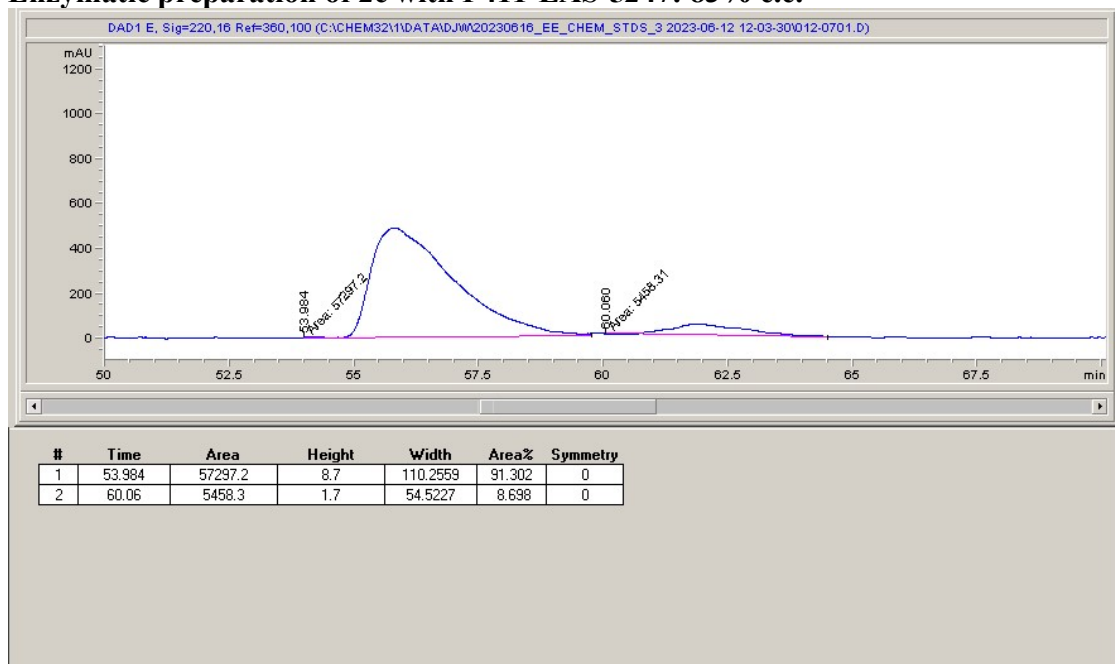
4-(4-Methoxyphenyl)dihydrofuran-2(3H)-one (2c)



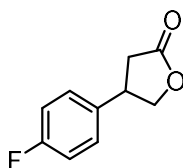
HPLC conditions: Chiralpak ODH, 2.5% *i*-PrOH in hexane, 1.2 mL/min, 32 °C, 220 nm



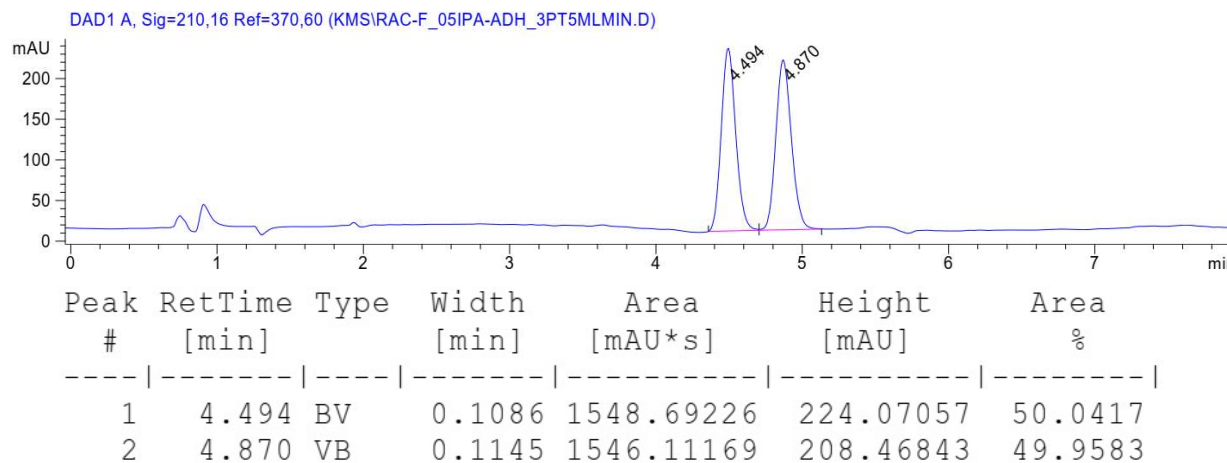
Enzymatic preparation of 2c with P411-LAS-5247: 83% e.e.



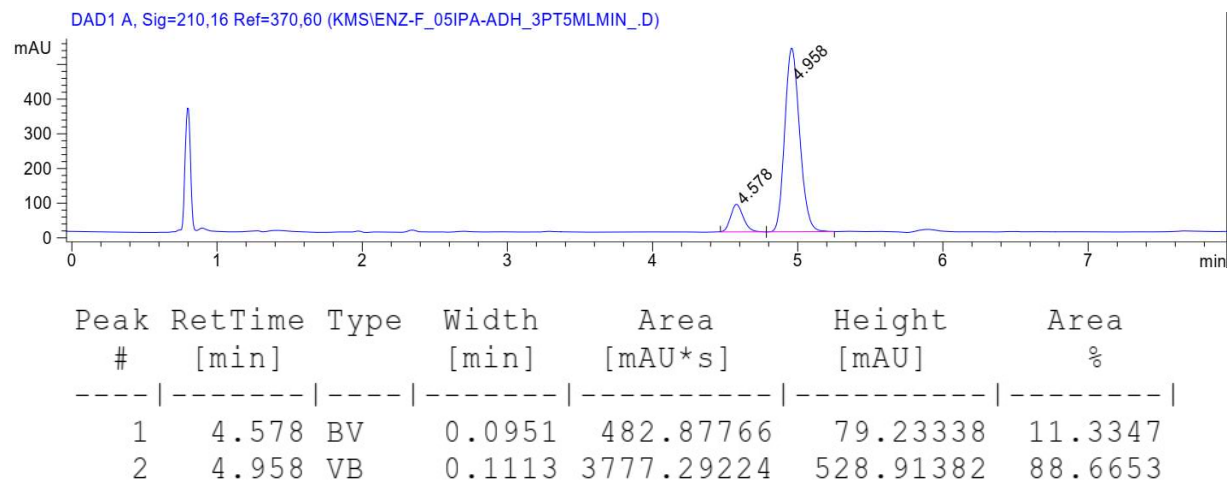
4-(4-Fluorophenyl)dihydrofuran-2(3H)-one (2d)



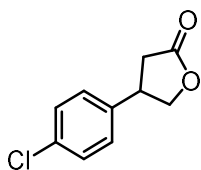
SFC conditions: Chiralpak AD-H, 5% *i*-PrOH in supercritical CO₂, 2.5 mL/min, 210 nm



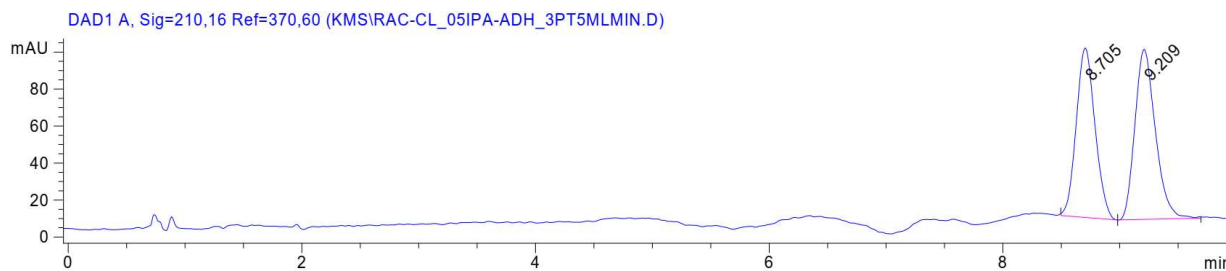
Enzymatic preparation of 2d with P411-LAS-5247: 77% e.e.



4-(4-Chlorophenyl)dihydrofuran-2(3H)-one (2e)

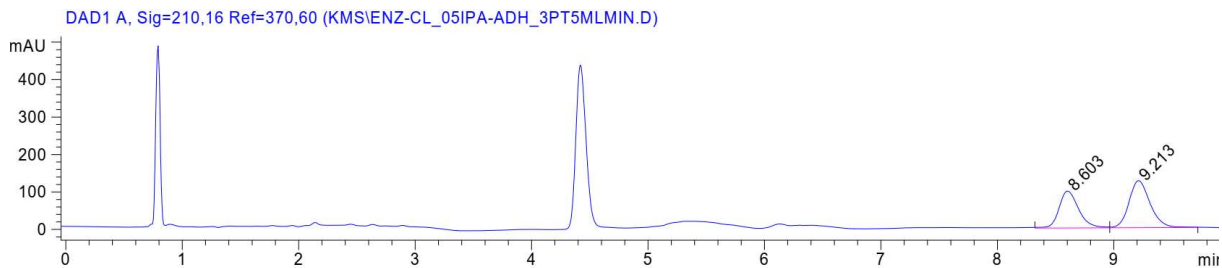


SFC conditions: Chiralpak AD-H, 5% *i*-PrOH in supercritical CO₂, 2.5 mL/min, 210 nm



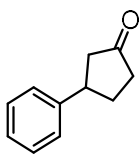
Peak #	RetTime [min]	Type	Width [min]	Area [mAU*s]	Height [mAU]	Area %
1	8.705	BV	0.1705	1023.10614	91.49740	47.7289
2	9.209	VB	0.1863	1120.47363	91.84954	52.2711

Enzymatic preparation of 2e with P411-LAS-5247: 16% e.e.

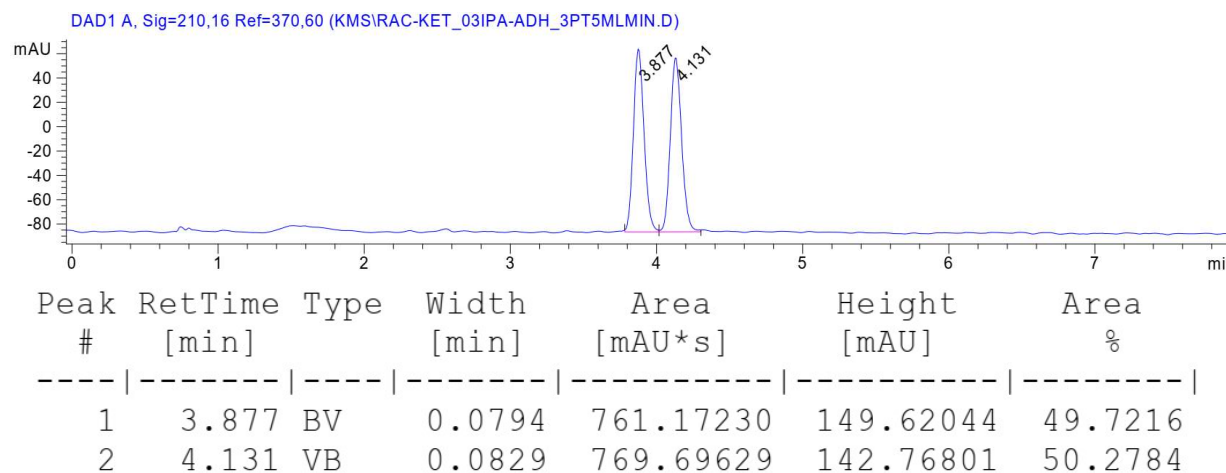


Peak #	RetTime [min]	Type	Width [min]	Area [mAU*s]	Height [mAU]	Area %
1	8.603	BV	0.1806	1152.80786	98.45173	42.0722
2	9.213	VB	0.1914	1587.26416	125.60918	57.9278

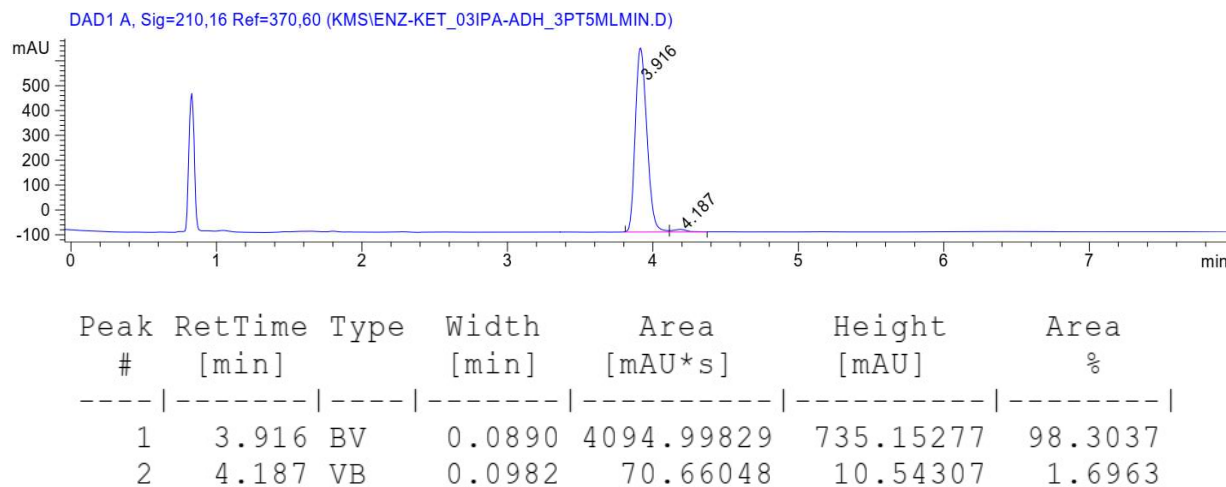
4-Phenyldihydrofuran-2(3H)-one (2f)



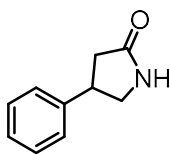
SFC conditions: Chiralpak AD-H, 5% *i*-PrOH in supercritical CO₂, 2.5 mL/min, 210 nm



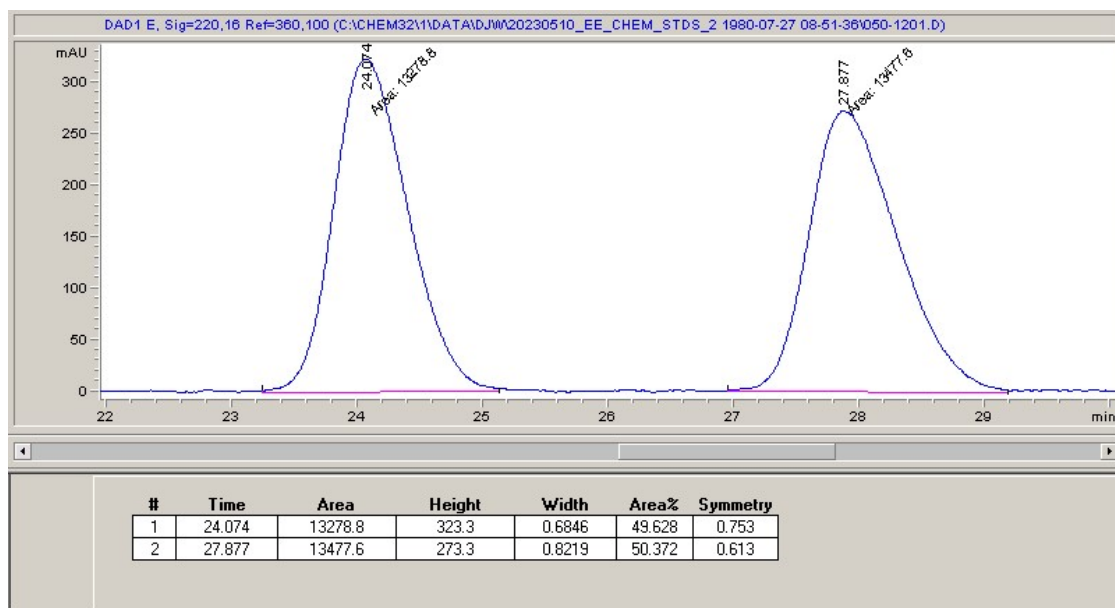
Enzymatic preparation of 2f with P411-LAS-5247: 97% e.e.



4-Phenylpyrrolidin-2-one (2g)

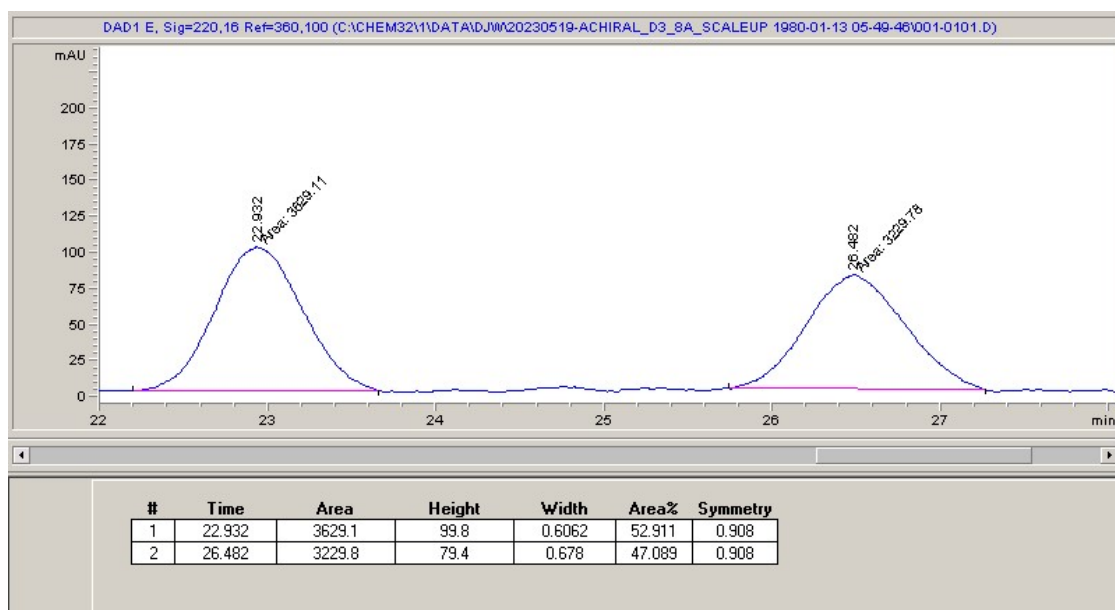


HPLC conditions: Chiralpak IC, 25% *i*-PrOH in hexane, 1.2 mL/min, 32 °C, 220 nm



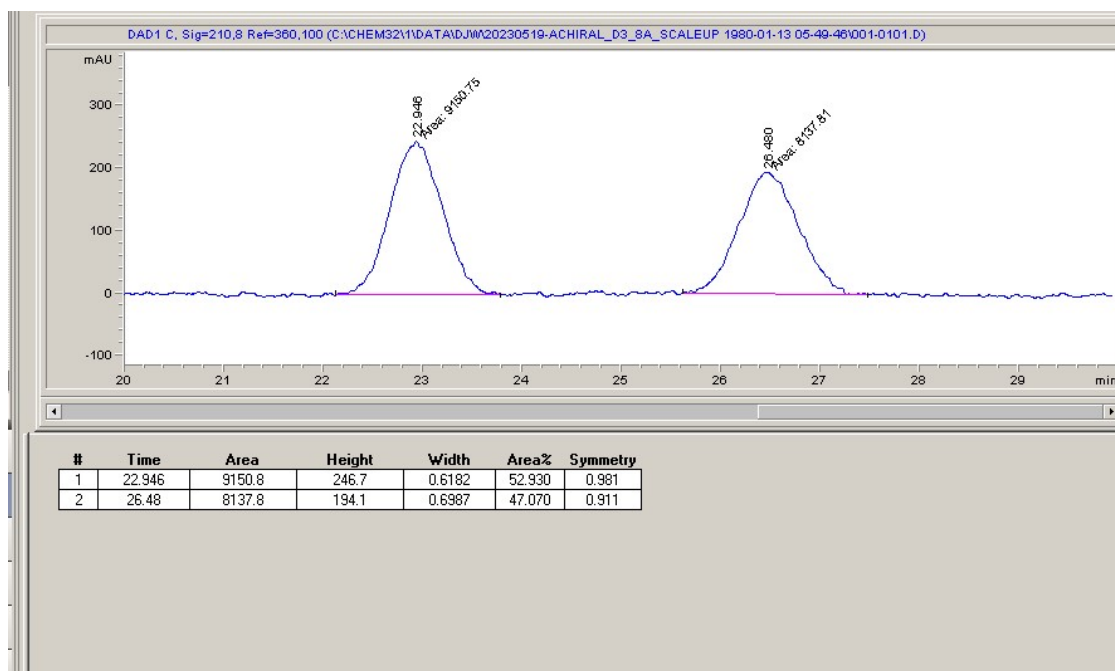
Enzymatic preparation of 2g with P411-LAS-5247, racemic

HPLC conditions: Chiralpak IC, 25% *i*-PrOH in hexane, 1.2 mL/min, 32 °C, 220 nm

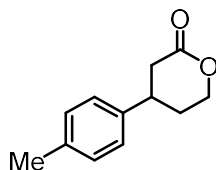


Enzymatic preparation of 2g with P411-LAS-5247, racemic

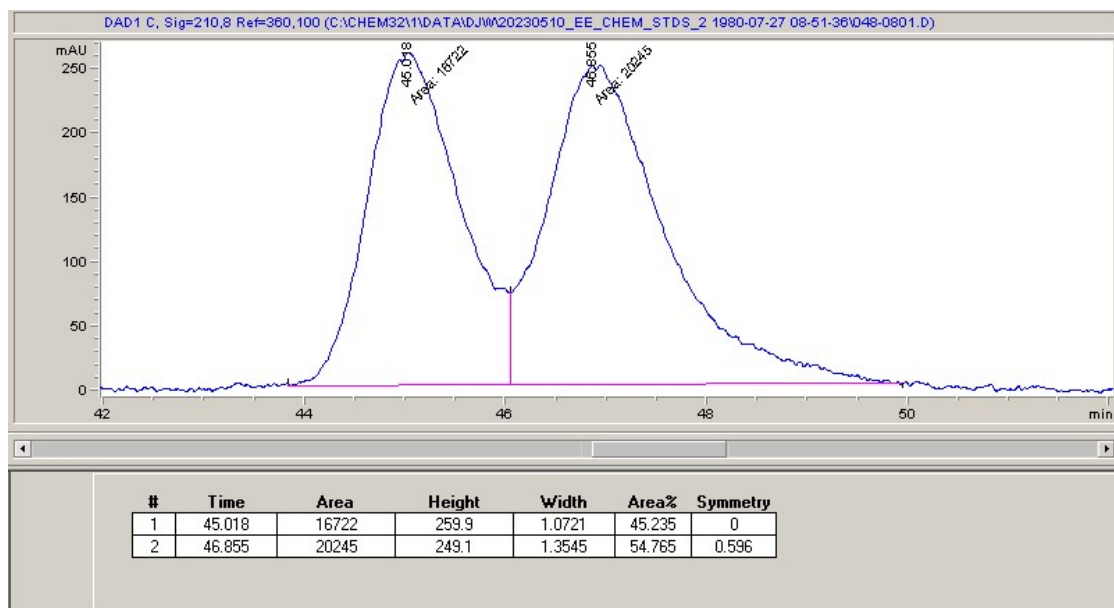
HPLC conditions: Chiralpak IC, 25% *i*-PrOH in hexane, 1.2 mL/min, 32 °C, 210 nm



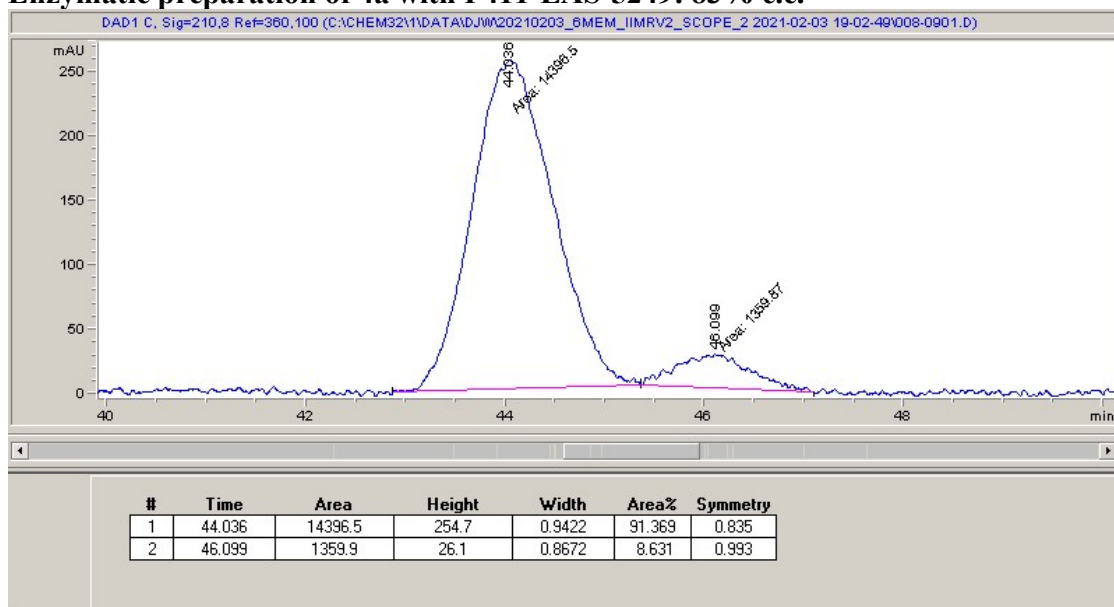
4-(*p*-Tolyl)tetrahydro-2*H*-pyran-2-one (4a)



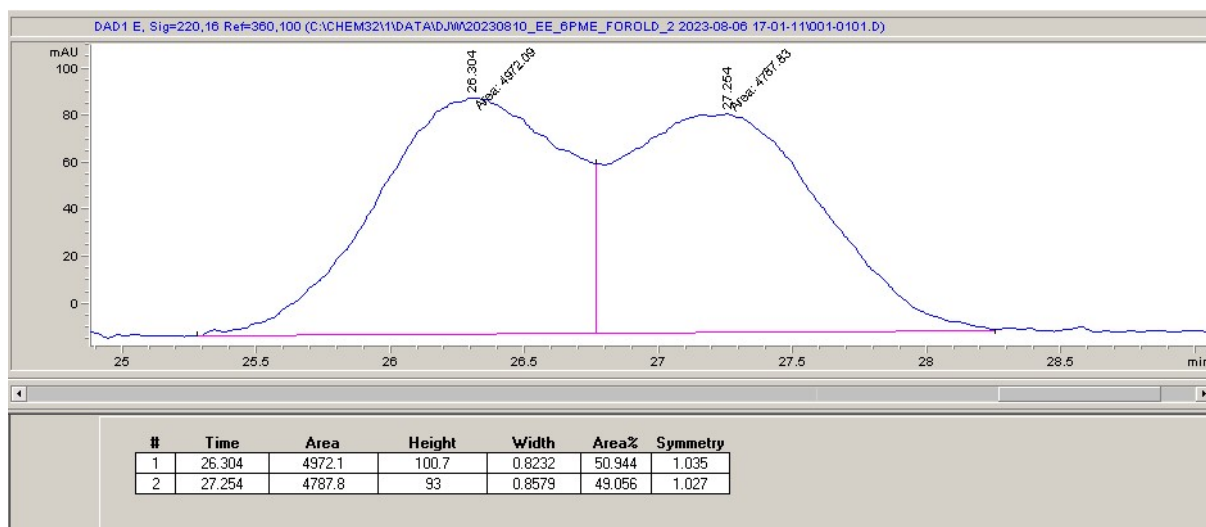
HPLC conditions: Chiralpak IC, 15% *i*-PrOH in hexane, 1.2 mL/min, 28 °C, 220 nm



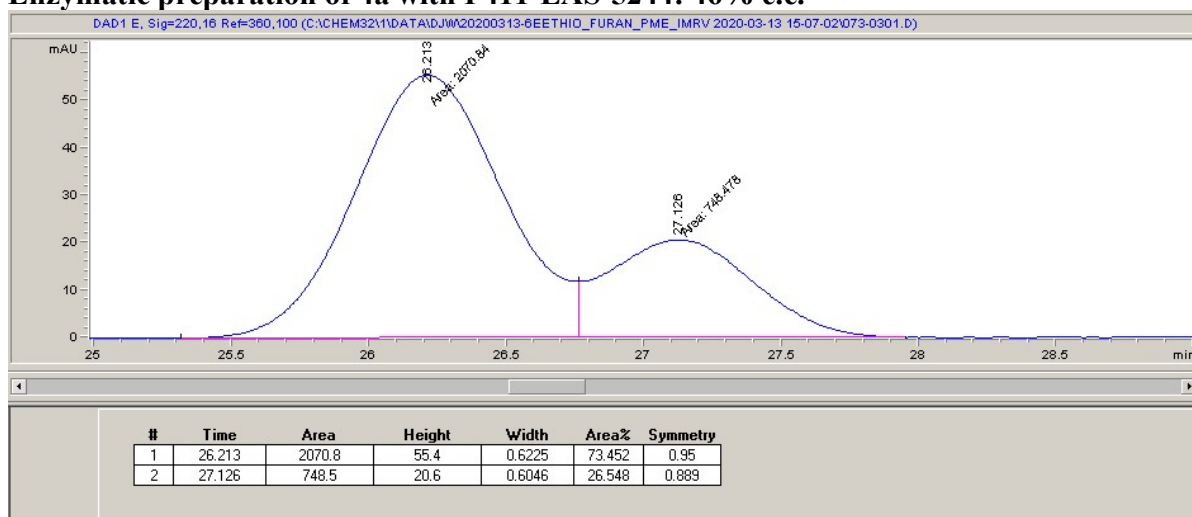
Enzymatic preparation of 4a with P411-LAS-5249: 83% e.e.



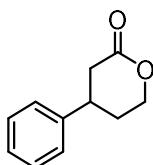
HPLC conditions: Chiralpak IC, 25% *i*-PrOH in hexane, 1.2 mL/min, 28 °C, 220 nm



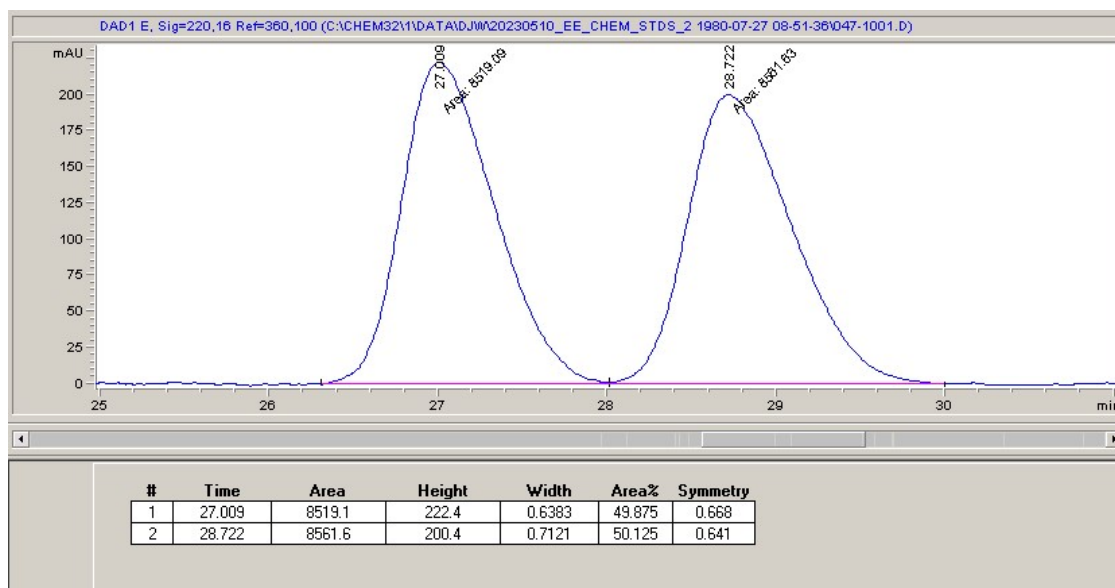
Enzymatic preparation of 4a with P411-LAS-5244: 46% e.e.



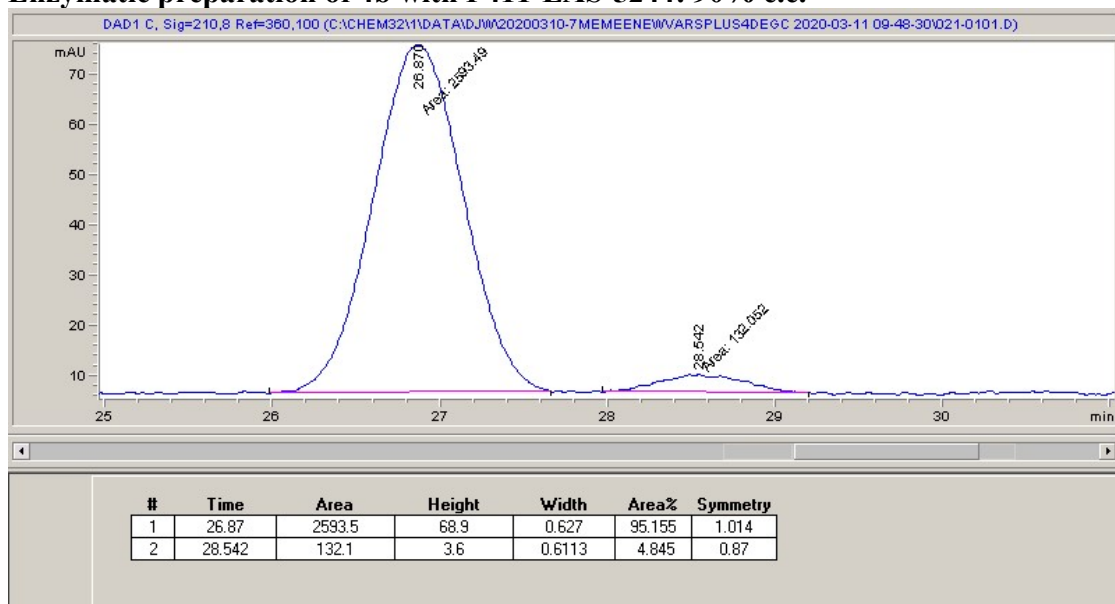
4-Phenyltetrahydro-2H-pyran-2-one (4b)



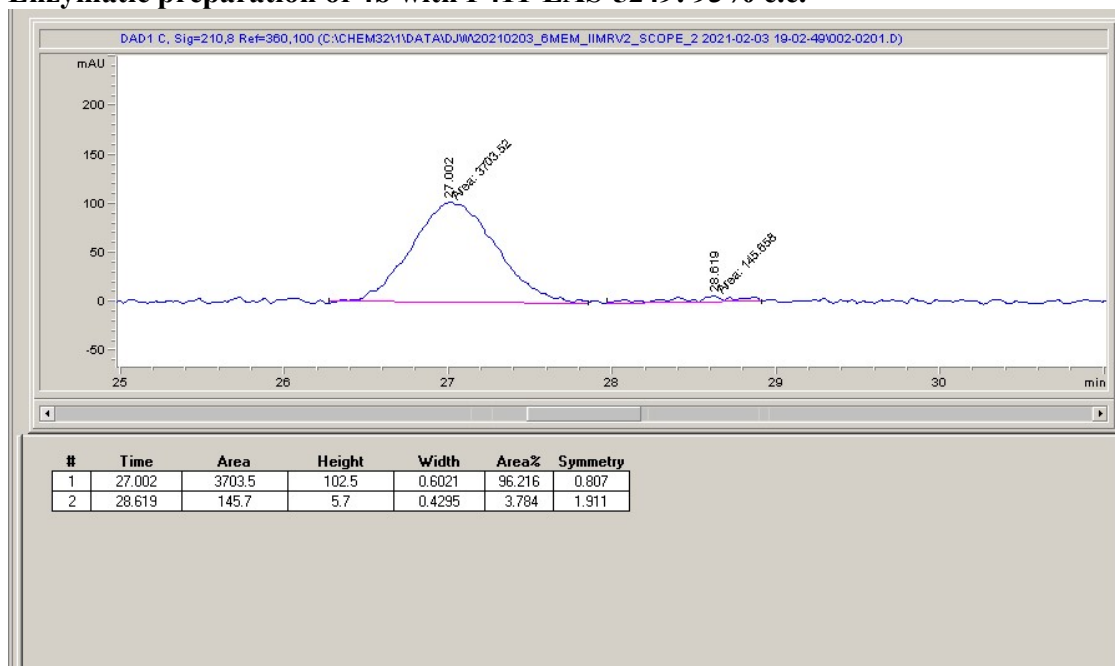
HPLC conditions: Chiralpak IC, 25% *i*-PrOH in hexane, 1.2 mL/min, 28 °C, 220 nm



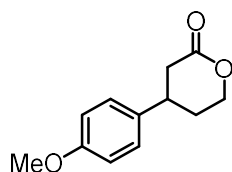
Enzymatic preparation of 4b with P411-LAS-5244: 90% e.e.



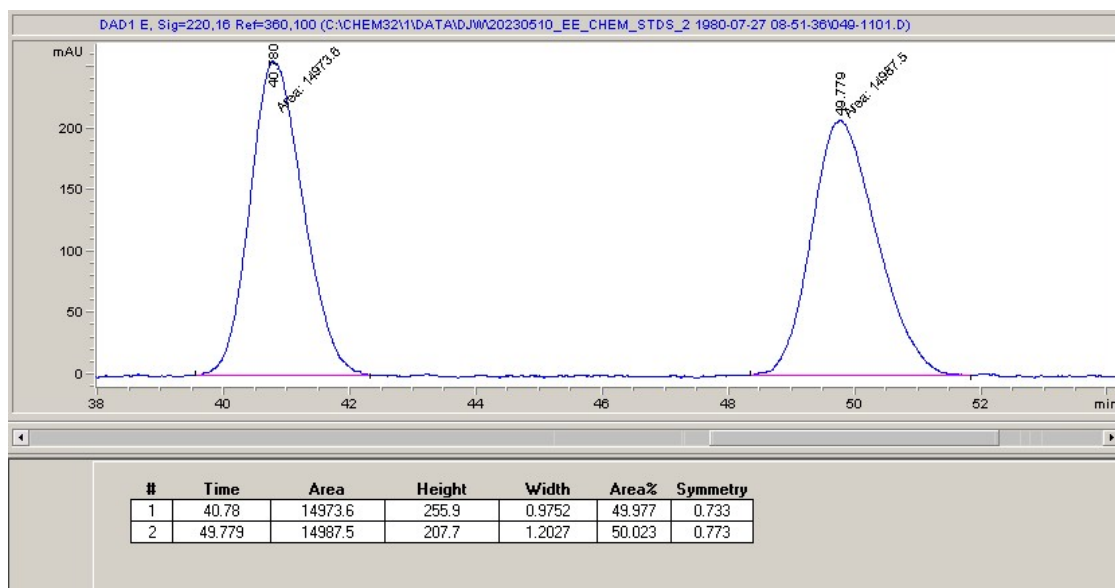
Enzymatic preparation of 4b with P411-LAS-5249: 93% e.e.



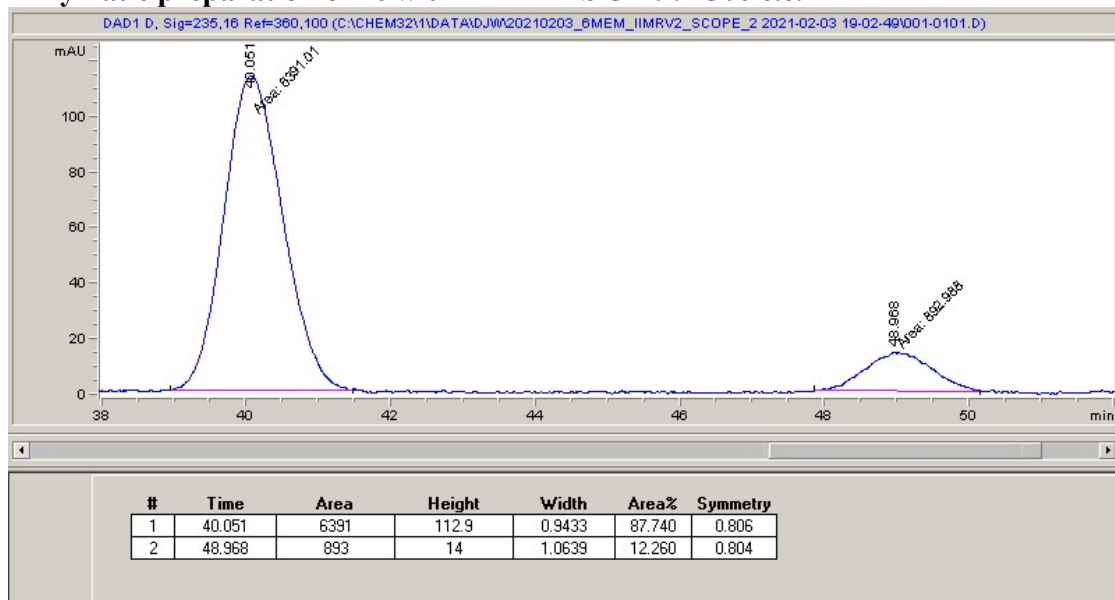
4-(4-Methoxyphenyl)tetrahydro-2H-pyran-2-one (4c)



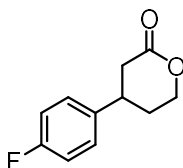
HPLC conditions: Chiralpak IC, 25% *i*-PrOH in hexane, 1.2 mL/min, 32 °C, 220 nm



Enzymatic preparation of 4c with P411-LAS-5249: 75% e.e.

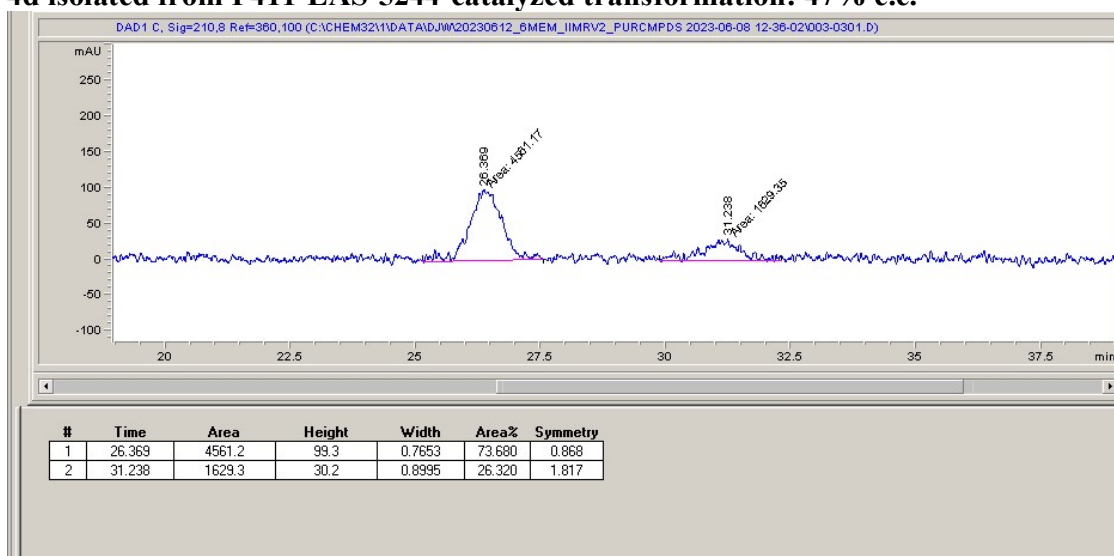


4-(4-Fluorophenyl)tetrahydro-2H-pyran-2-one (4d)

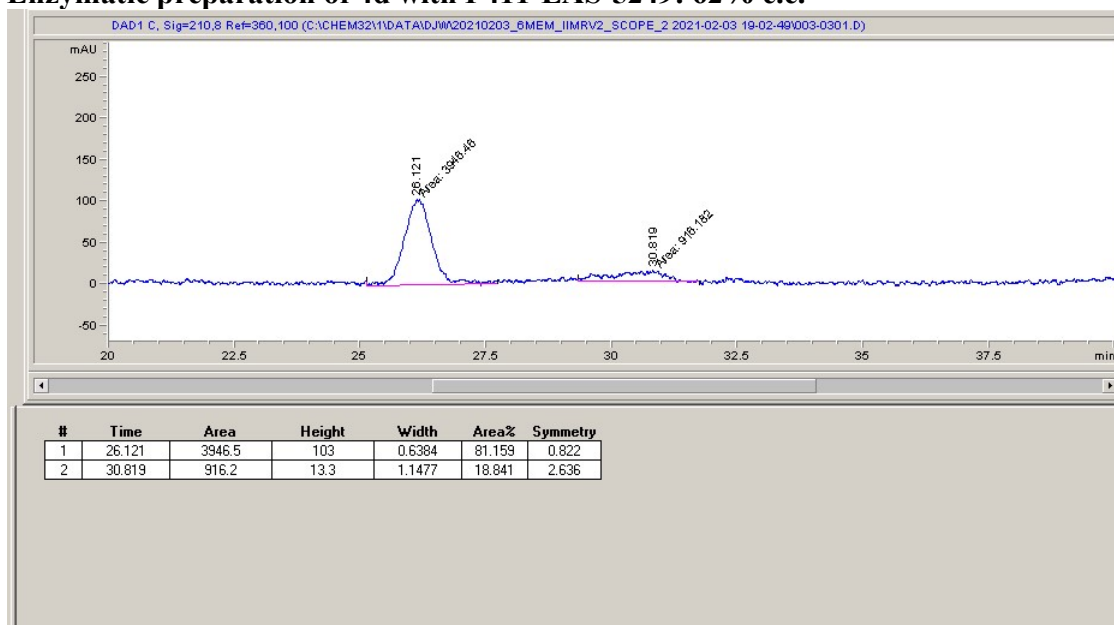


HPLC conditions: Chiralpak IC, 25% *i*-PrOH in hexane, 1.2 mL/min, 32 °C, 220 nm

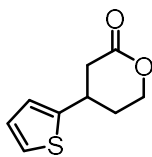
4d isolated from P411-LAS-5244-catalyzed transformation: 47% e.e.



Enzymatic preparation of 4d with P411-LAS-5249: 62% e.e.

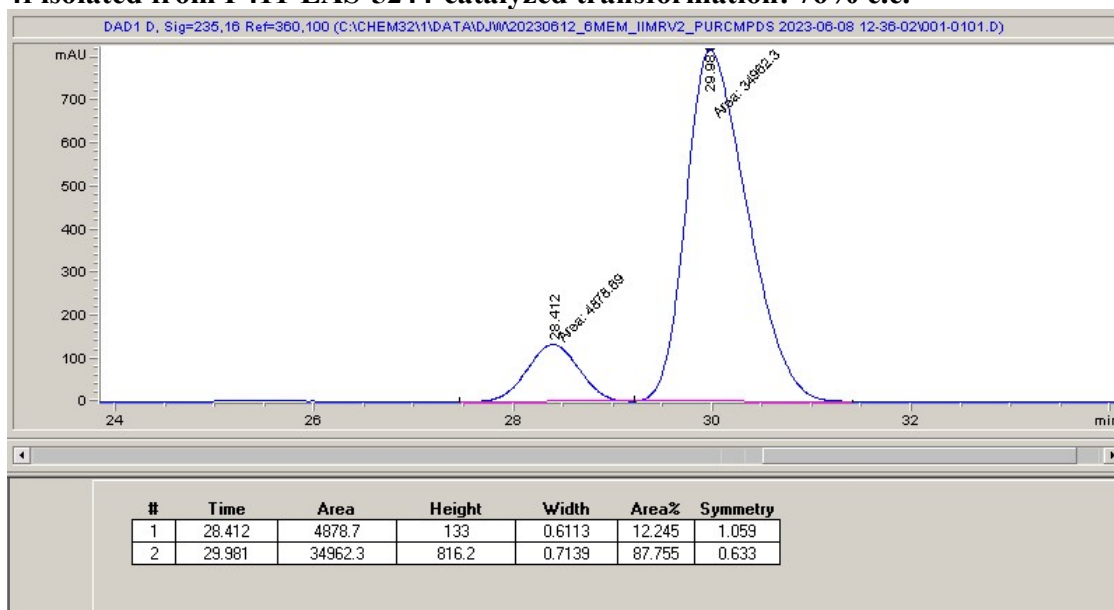


4-(Thiophen-2-yl)tetrahydro-2H-pyran-2-one (4f)

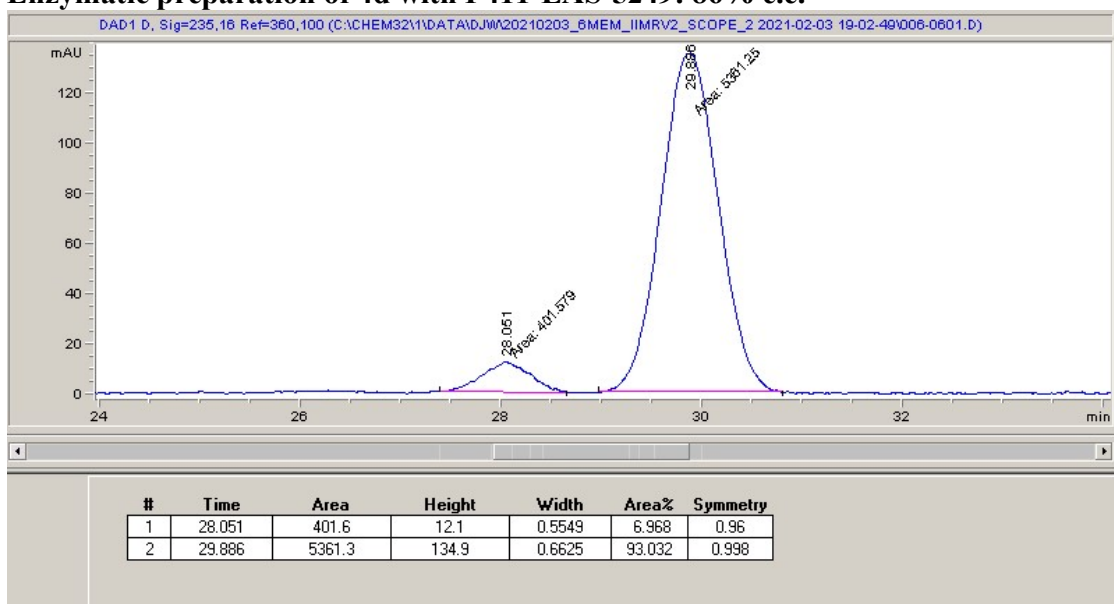


HPLC conditions: Chiralpak IC, 25% *i*-PrOH in hexane, 1.2 mL/min, 32 °C, 220 nm

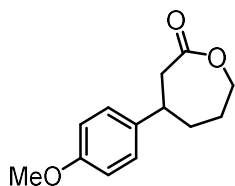
4f isolated from P411-LAS-5244-catalyzed transformation: 76% e.e.



Enzymatic preparation of 4d with P411-LAS-5249: 86% e.e.

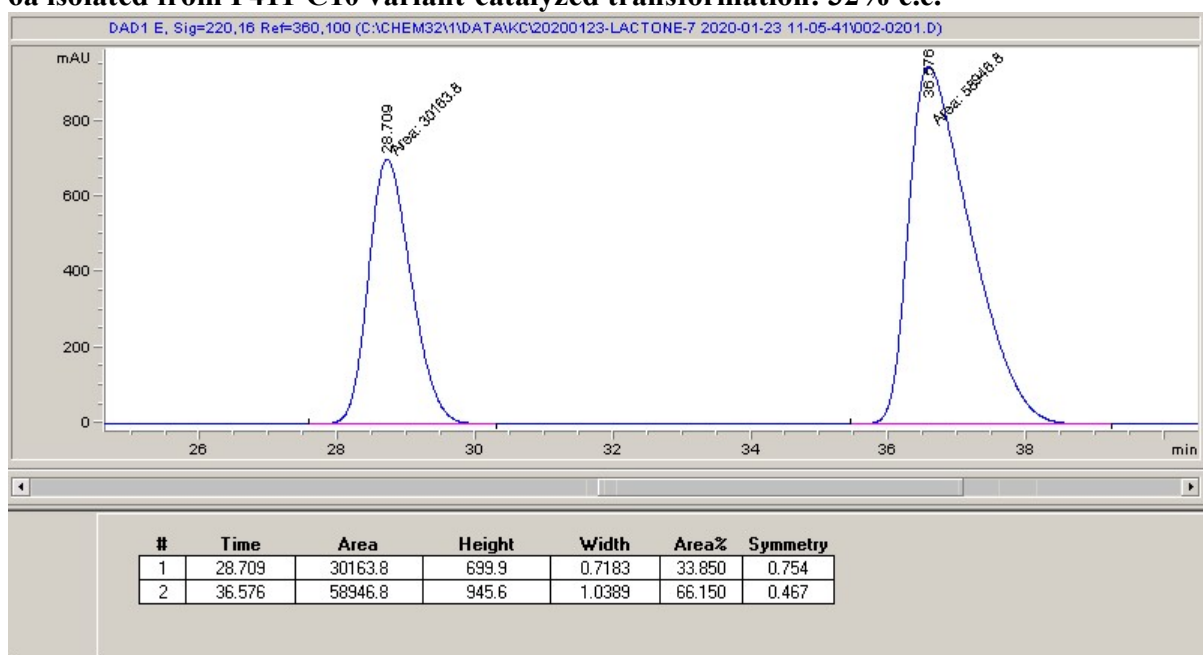


4-(4-Methoxyphenyl)oxepan-2-one (6a)

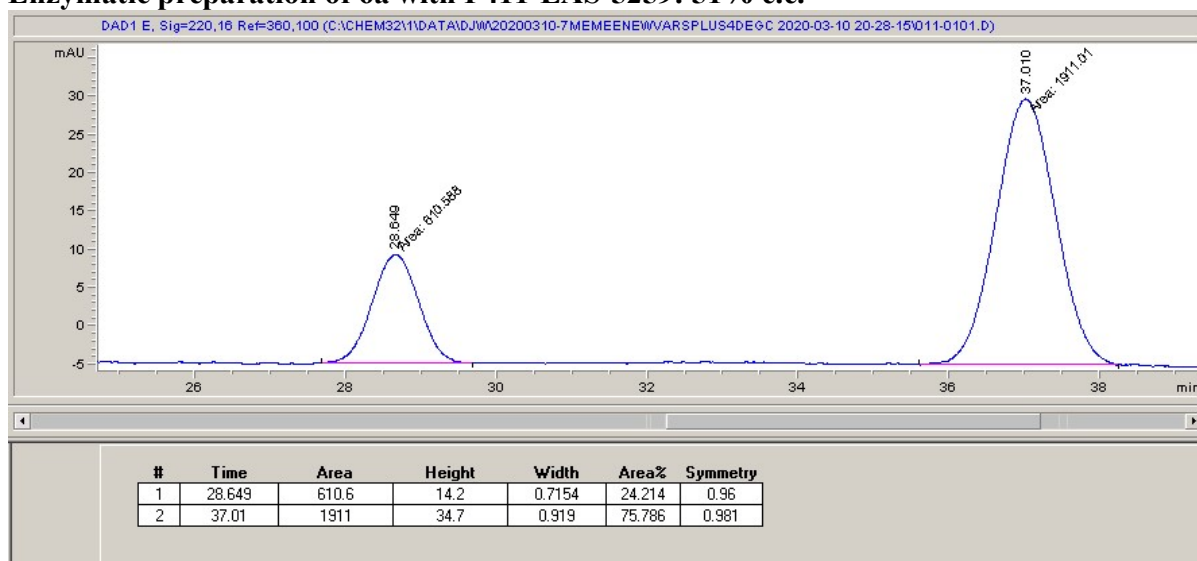


HPLC conditions: Chiralpak IC, 25% *i*-PrOH in hexane, 1.2 mL/min, 32 °C, 220 nm

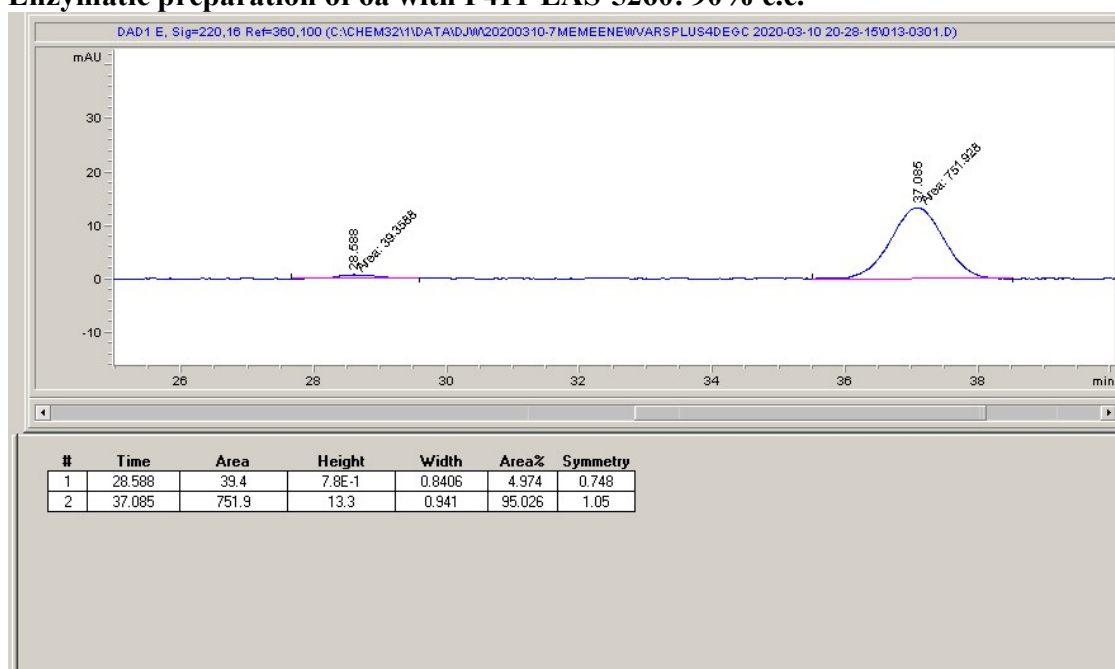
6a isolated from P411-C10 variant-catalyzed transformation: 32% e.e.



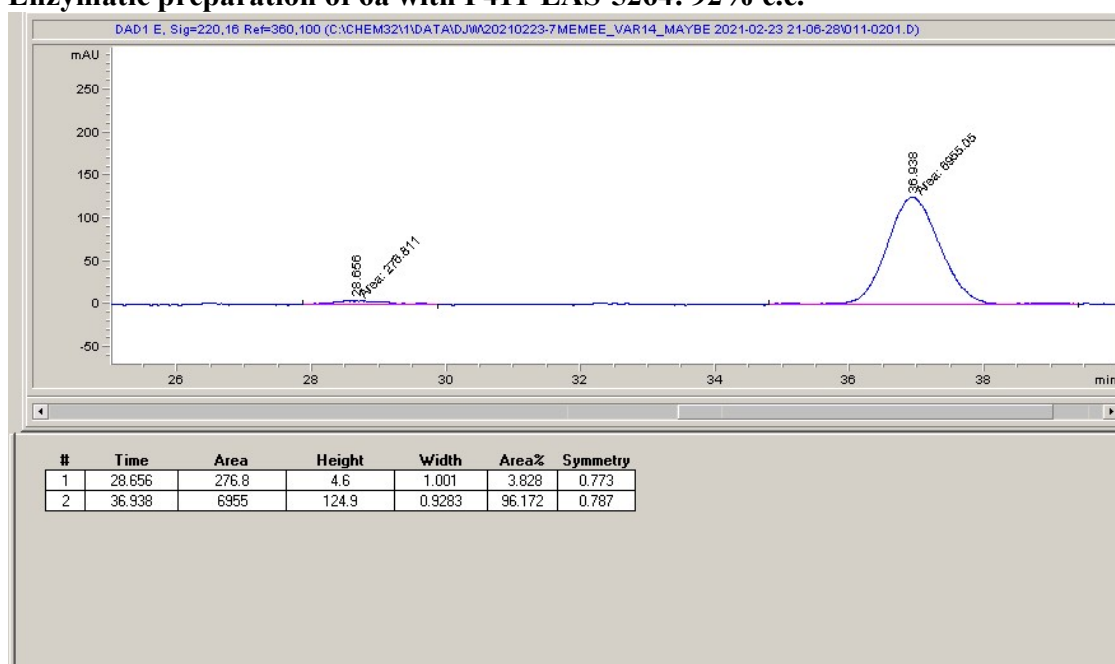
Enzymatic preparation of 6a with P411-LAS-5259: 51% e.e.



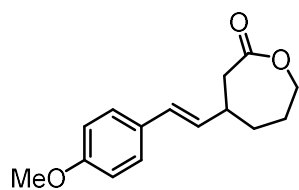
Enzymatic preparation of 6a with P411-LAS-5260: 90% e.e.



Enzymatic preparation of 6a with P411-LAS-5264: 92% e.e.

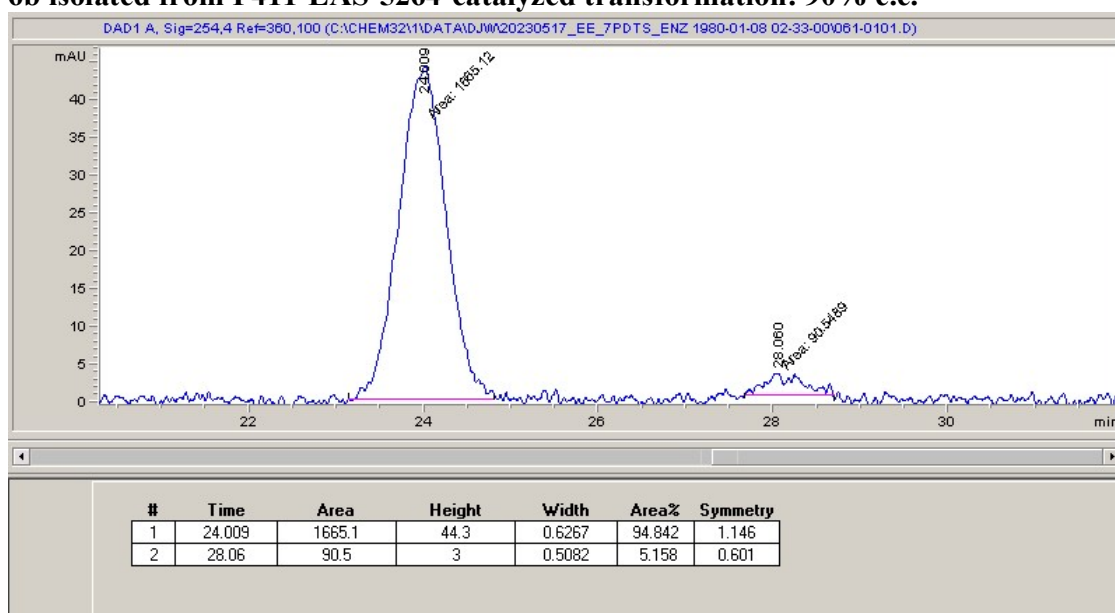


(E)-4-(4-Methoxystyryl)oxepan-2-one (6b)



HPLC conditions: Chiralpak IC, 35% *i*-PrOH in hexane, 1.2 mL/min, 32 °C, 220 nm

6b isolated from P411-LAS-5264-catalyzed transformation: 90% e.e.



8. X-ray Crystallography

Low-temperature diffraction data (ϕ - and ω -scans) were collected on a Bruker AXS D8 VENTURE KAPPA or Bruker APEX-II diffractometer coupled to a PHOTON II CPAD detector with Cu $K\alpha$ radiation ($\lambda = 1.54178 \text{ \AA}$) from an I μ S micro-source for the structure of compounds. The structure was solved by direct methods using SHELXS²⁰ and refined against F^2 on all data by full-matrix least squares with SHELXL-2019²¹ using established refinement techniques.²² All non-hydrogen atoms were refined anisotropically. Unless otherwise noted, all hydrogen atoms were included into the model at geometrically calculated positions and refined using a riding model. The isotropic displacement parameters of all hydrogen atoms were fixed to 1.2 times the U value of the atoms they are linked to (1.5 times for methyl groups).

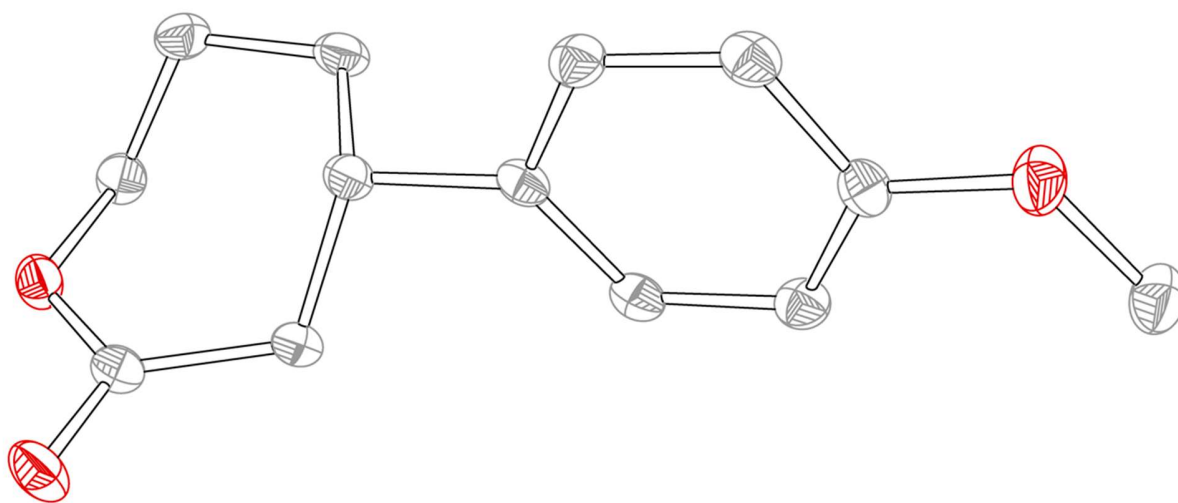


Figure S3. Displacement ellipsoid plot for **6a** plotted at 50% probability. Single crystals were obtained from slow evaporation of **6a** dissolved in CHCl_3 . Compound **6a** crystallizes in the orthorhombic space group $P2_12_12_1$ with one molecule in the asymmetric unit.

Table S6. X-ray experimental details of **6a** (CCDC 2288858).

Crystal data	
Chemical formula	C ₁₃ H ₁₆ O ₃
M_r	220.26
Crystal system, space group	Orthorhombic, $P2_12_12_1$
Temperature (K)	100
a, b, c (Å)	6.4683 (7), 9.5514 (11), 18.433 (2)
V (Å ³)	1138.8 (2)
Z	4
Radiation type	Cu $K\alpha$
μ (mm ⁻¹)	0.74
Crystal size (mm)	0.25 × 0.2 × 0.1
Data collection	
Diffractometer	Bruker <i>APEX</i> -II CCD
Absorption correction	
T_{\min}, T_{\max}	0.662, 0.754
No. of measured, independent and observed [$I > 2\sigma(I)$] reflections	14831, 2298, 2272
R_{int}	0.036
$(\sin \theta/\lambda)_{\max}$ (Å ⁻¹)	0.625
Refinement	
$R[F^2 > 2\sigma(F^2)], wR(F^2), S$	0.026, 0.066, 1.05
No. of reflections	2298
No. of parameters	146
H-atom treatment	H-atom parameters constrained
$\Gamma_{\max}, \Gamma_{\min}$ (e Å ⁻³)	0.14, -0.17
Absolute structure	Flack x determined using 932 quotients [(I+)-(I-)]/[(I+)+(I-)] (Parsons, Flack and Wagner, Acta Cryst. B69 (2013) 249-259).
Absolute structure parameter	-0.09 (6)

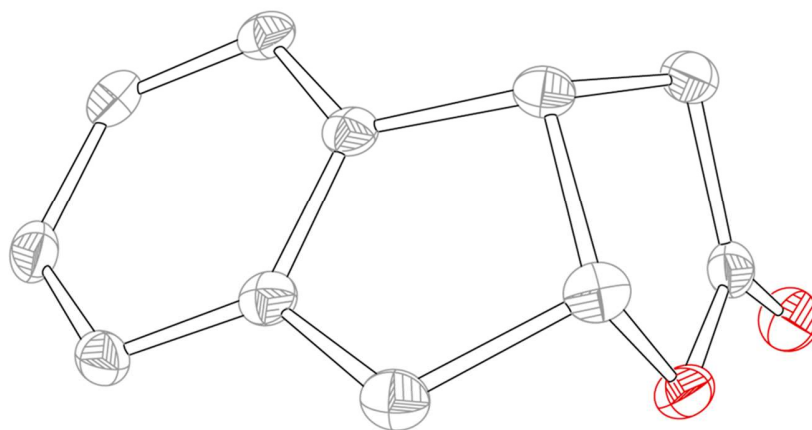


Figure S4. Displacement ellipsoid plot for **8a** plotted at 50% probability. Single crystals were obtained from evaporation of hexane into **8a** dissolved in ethyl acetate. Compound **8a** crystallizes in the orthorhombic space group $P2_12_12_1$ with one molecule in the asymmetric unit.

Table S7. X-ray experimental details of **8a** (CCDC 2287785).

Crystal data	
Chemical formula	C ₁₁ H ₁₀ O ₂
M_r	179.19
Crystal system, space group	Orthorhombic, $P2_12_12_1$
Temperature (K)	100
a, b, c (Å)	4.7240 (4), 12.2962 (14), 14.3829 (12)
V (Å ³)	835.46 (14)
Z	4
Radiation type	Cu $K\alpha$
μ (mm ⁻¹)	0.768
Crystal size (mm)	0.15 × 0.1 × 0.1
Data collection	
Diffractometer	Bruker D8 VENTURE Kappa Duo PHOTON II CPAD
Absorption correction	Multi-scan SADABS2016/2 (Sheldrick, 2014)
T_{\min}, T_{\max}	0.6762, 0.7538
No. of measured, independent and observed [$I > 2\sigma(I)$] reflections	15040, 1711, 1670
R_{int}	0.0367
$(\sin \theta/\lambda)_{\max}$ (Å ⁻¹)	0.625
Refinement	
$R[F^2 > 2\sigma(F^2)], wR(F^2), S$	0.0261, 0.0668, 1.079
No. of reflections	1711
No. of parameters	118
H-atom treatment	H-atom parameters constrained
$\Gamma_{\max}, \Gamma_{\min}$ (e Å ⁻³)	0.15, -0.15
Absolute structure	Flack x determined using 667 quotients [(I+)-(I-)]/[(I+)+(I-)] (Parsons, Flack and Wagner, Acta Cryst. B69 (2013) 249-259).
Absolute structure parameter	0.05 (7)

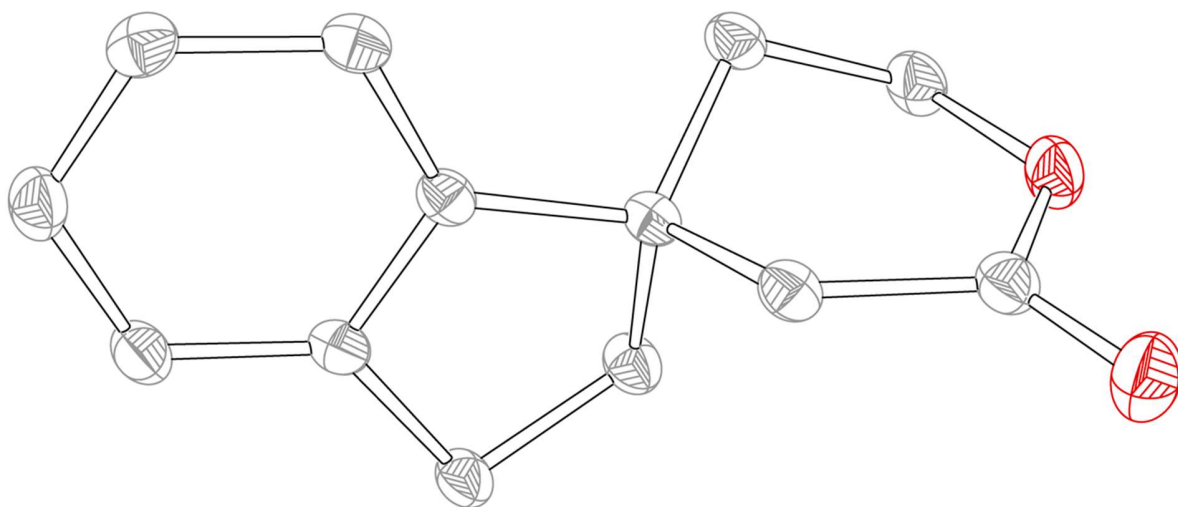


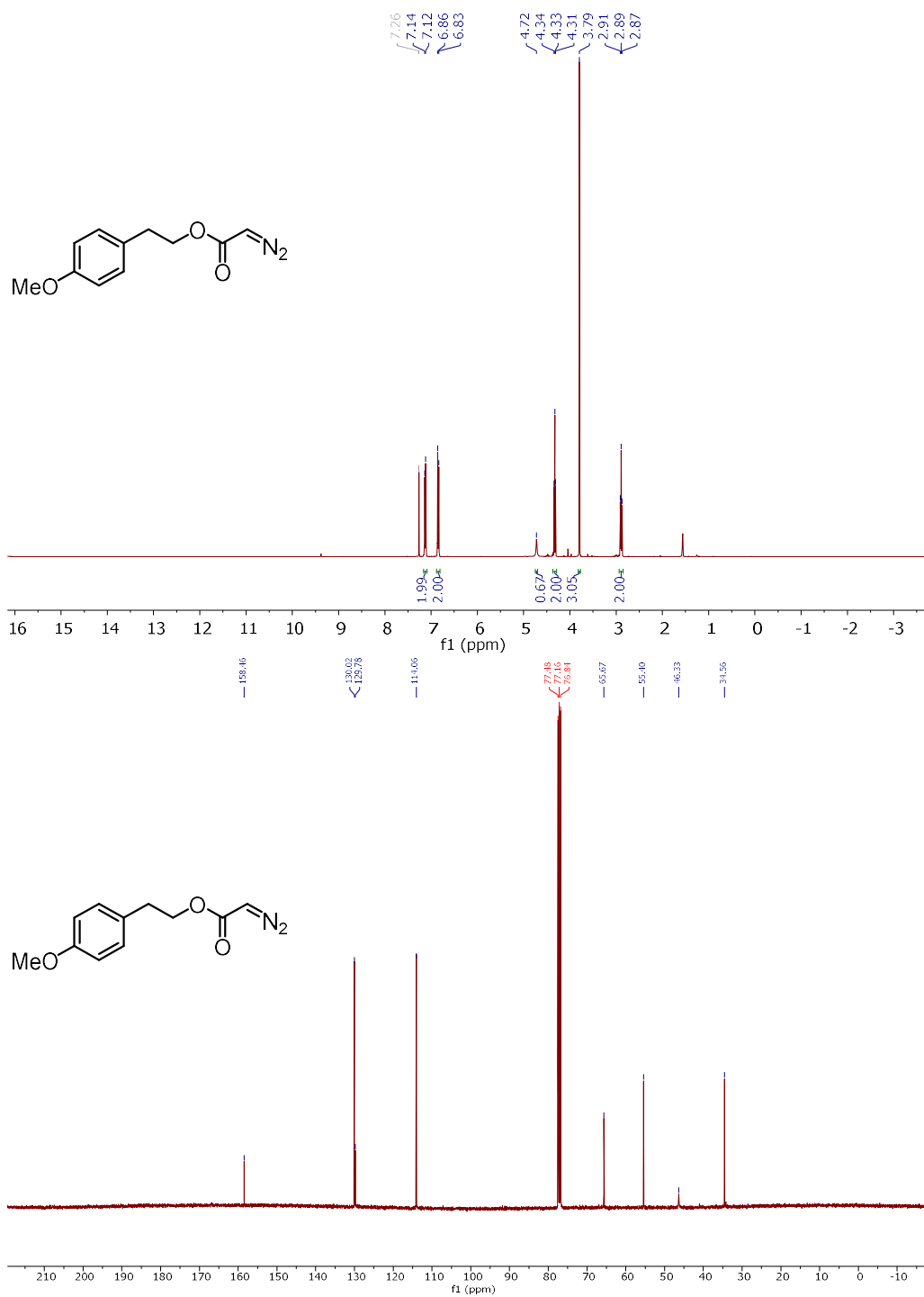
Figure S5. Displacement ellipsoid plot for **8f** plotted at 50% probability. Single crystals were obtained from evaporation of hexane into **8f** dissolved in ethyl acetate. Compound **8f** crystallizes in the monoclinic space group $P2_1/c$ with one molecule in the asymmetric unit.

Table S8. X-ray experimental details of **8f** (CCDC 2287784).

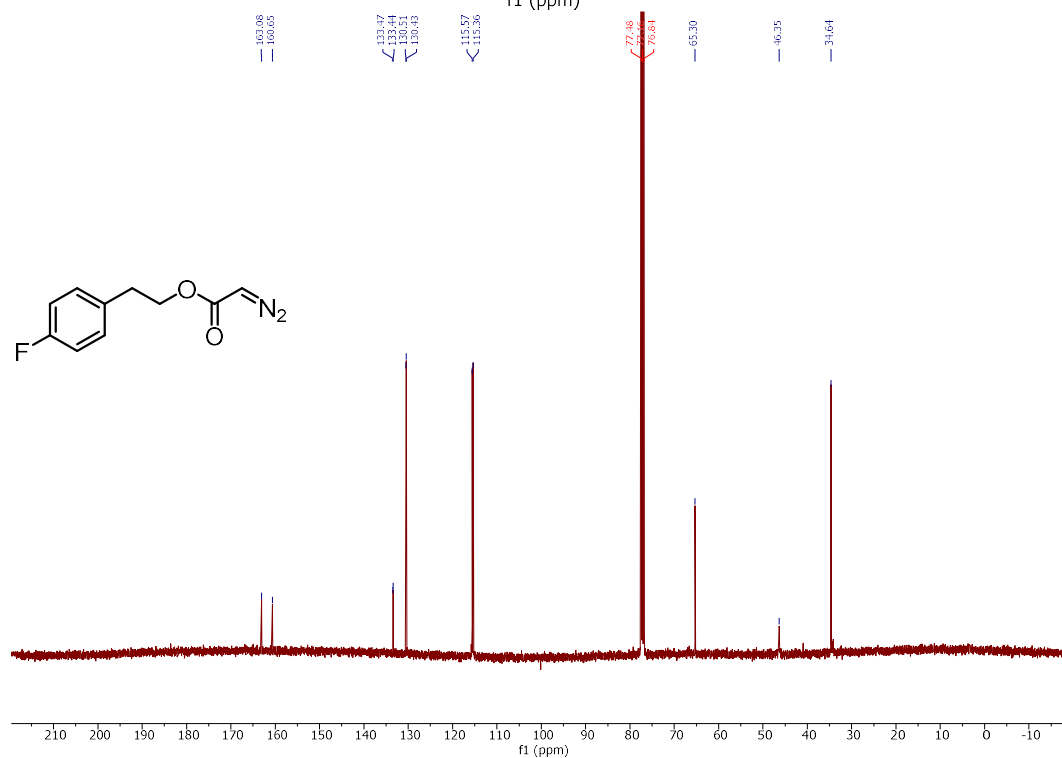
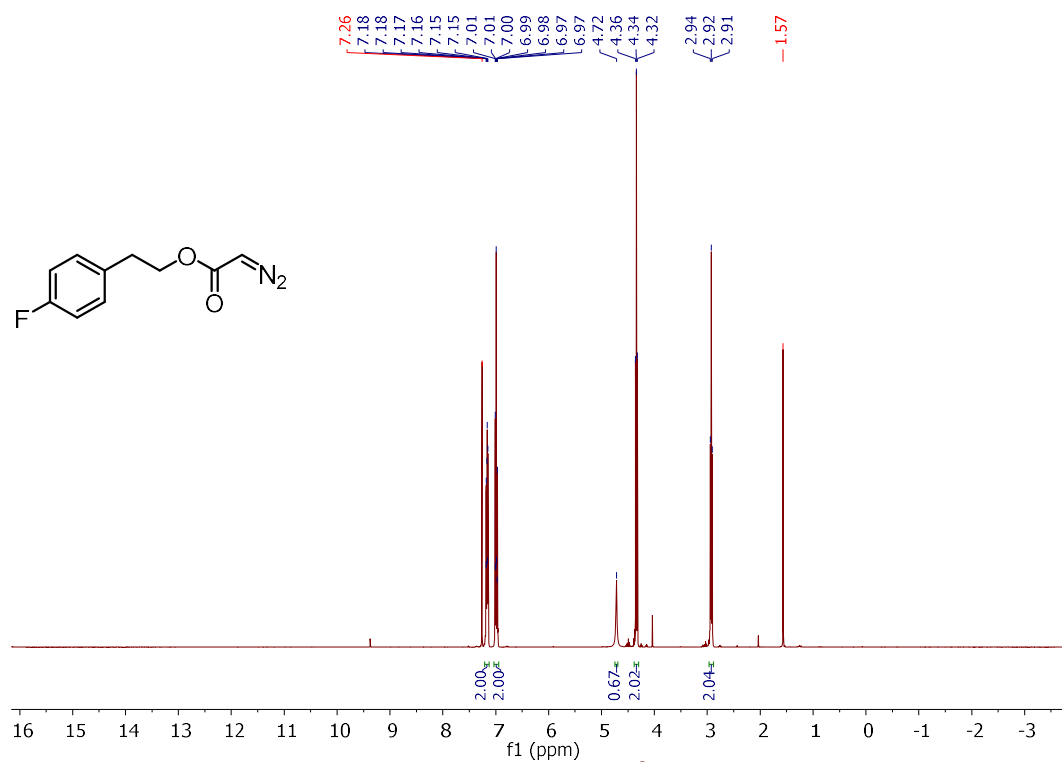
Crystal data	
Chemical formula	C ₁₃ H ₁₄ O ₂
M_r	202.24
Crystal system, space group	Monoclinic, $P2_1/c$
Temperature (K)	100
a, b, c (Å)	13.0013 (8), 6.6891 (6), 12.8888 (10)
α, β, γ (°)	90, 113.787 (3), 90
V (Å ³)	1025.68 (14)
Z	4
Radiation type	Cu $K\alpha$
μ (mm ⁻¹)	0.696
Crystal size (mm)	0.2 × 0.15 × 0.05
Data collection	
Diffractometer	Bruker D8 VENTURE Kappa Duo PHOTON II CPAD
Absorption correction	Multi-scan SADABS2016/2 (Sheldrick, 2014)
T_{\min}, T_{\max}	0.5155, 0.7538
No. of measured, independent and observed [$I > 2\sigma(I)$] reflections	13396, 2098, 1884
R_{int}	0.0632
$(\sin \theta/\lambda)_{\max}$ (Å ⁻¹)	0.625
Refinement	
$R[F^2 > 2\sigma(F^2)], wR(F^2), S$	0.0449, 0.1248, 1.07
No. of reflections	2098
No. of parameters	136
H-atom treatment	H-atom parameters constrained
$\Gamma_{\max}, \Gamma_{\min}$ (e Å ⁻³)	0.41, -0.23

9. NMR Spectra

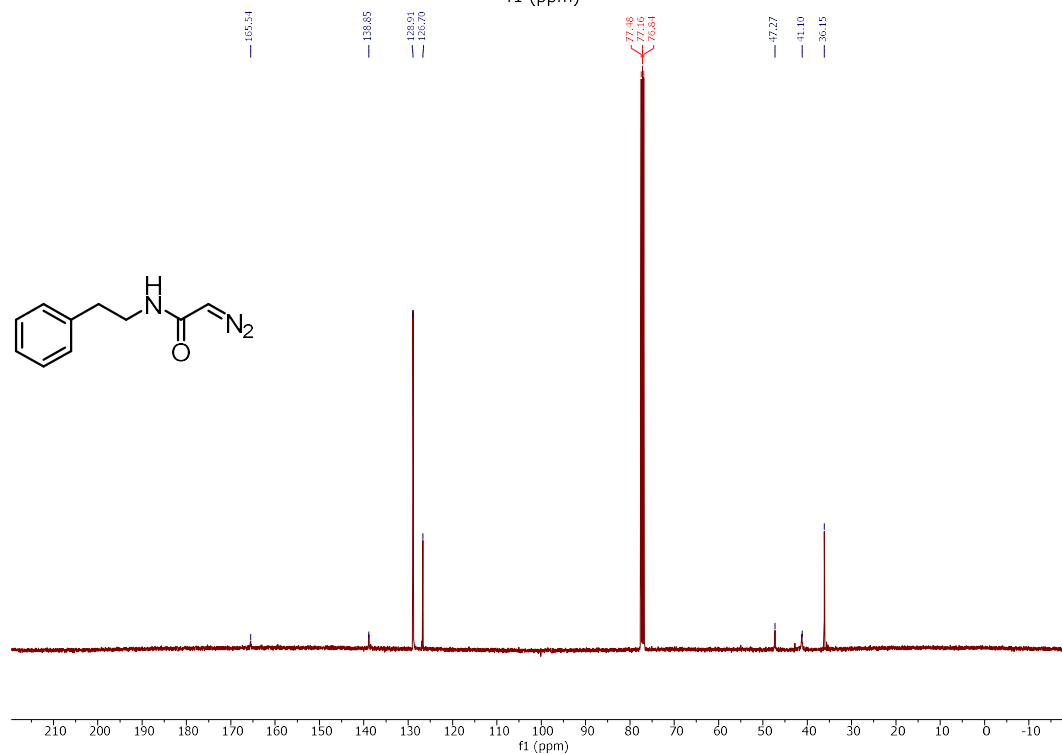
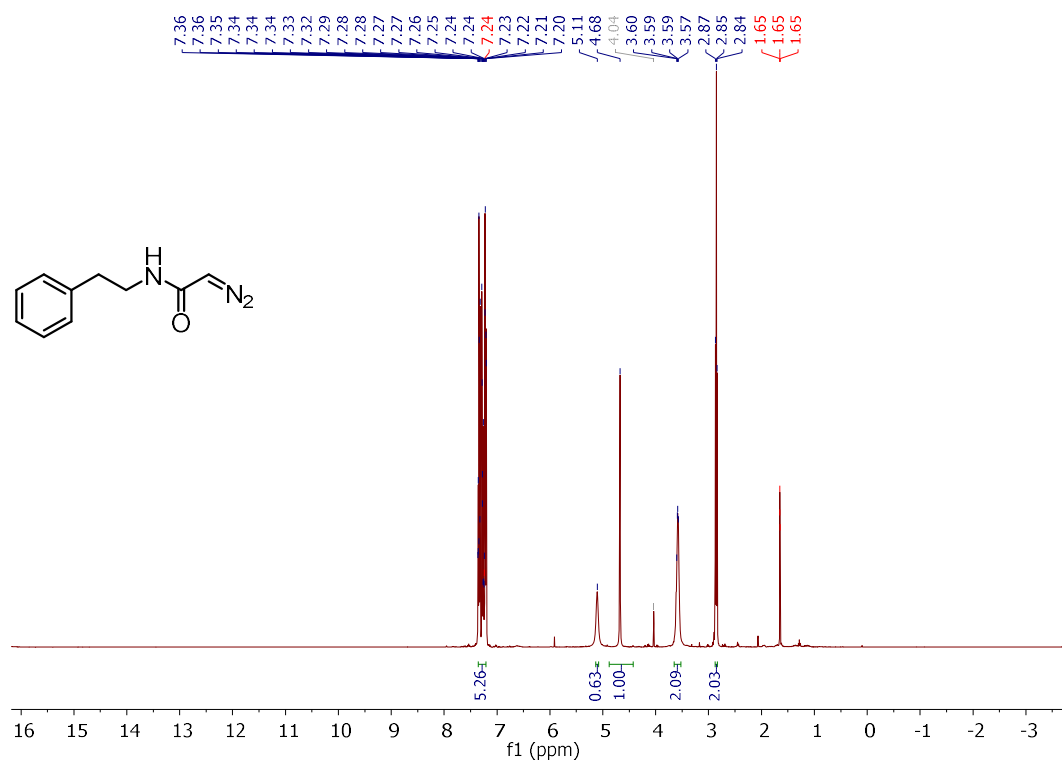
4-methoxyphenethyl 2-diazoacetate (1c)



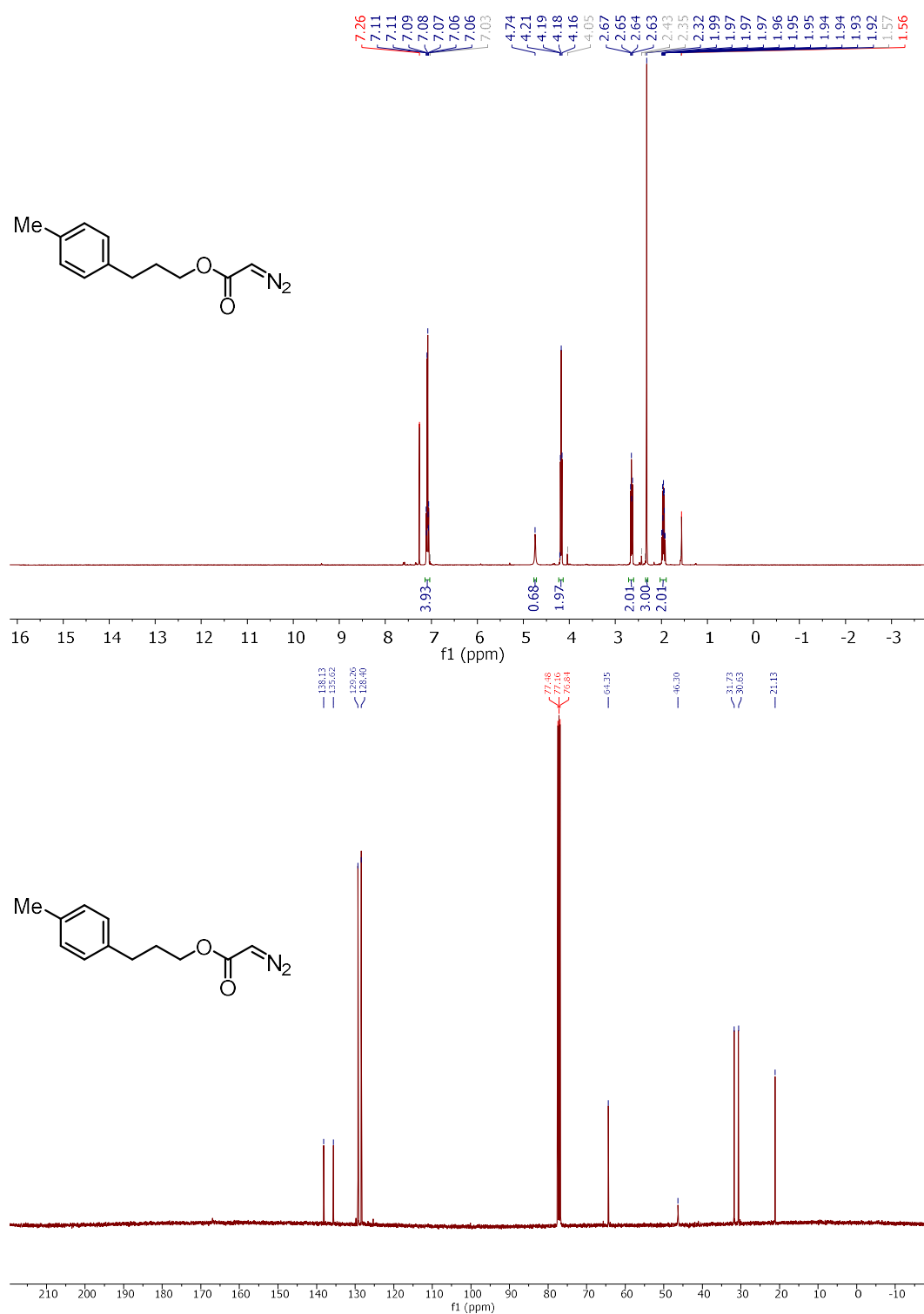
4-fluorophenethyl 2-diazoacetate (1d)



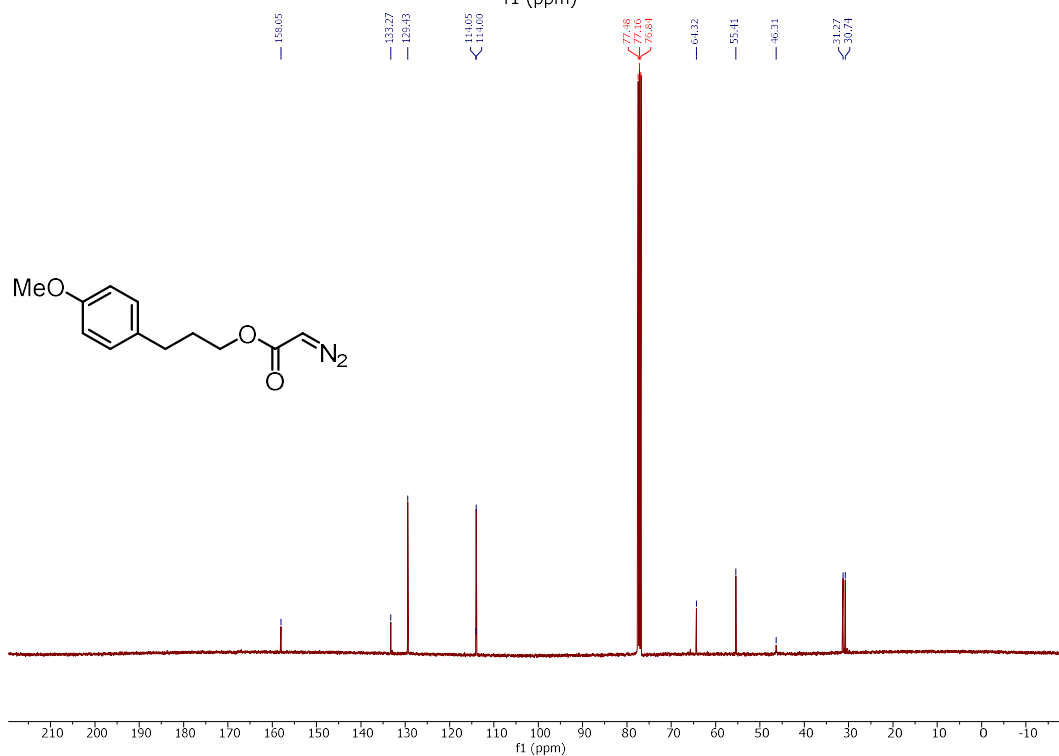
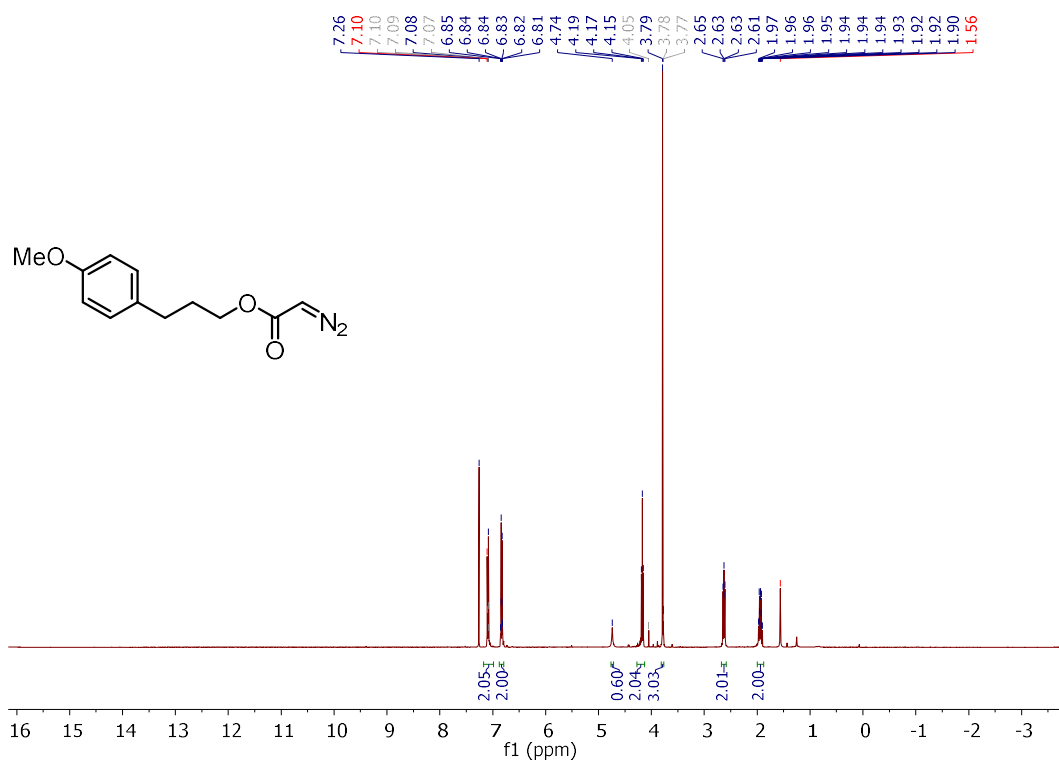
2-diazo-N-phenethylacetamide (1g)



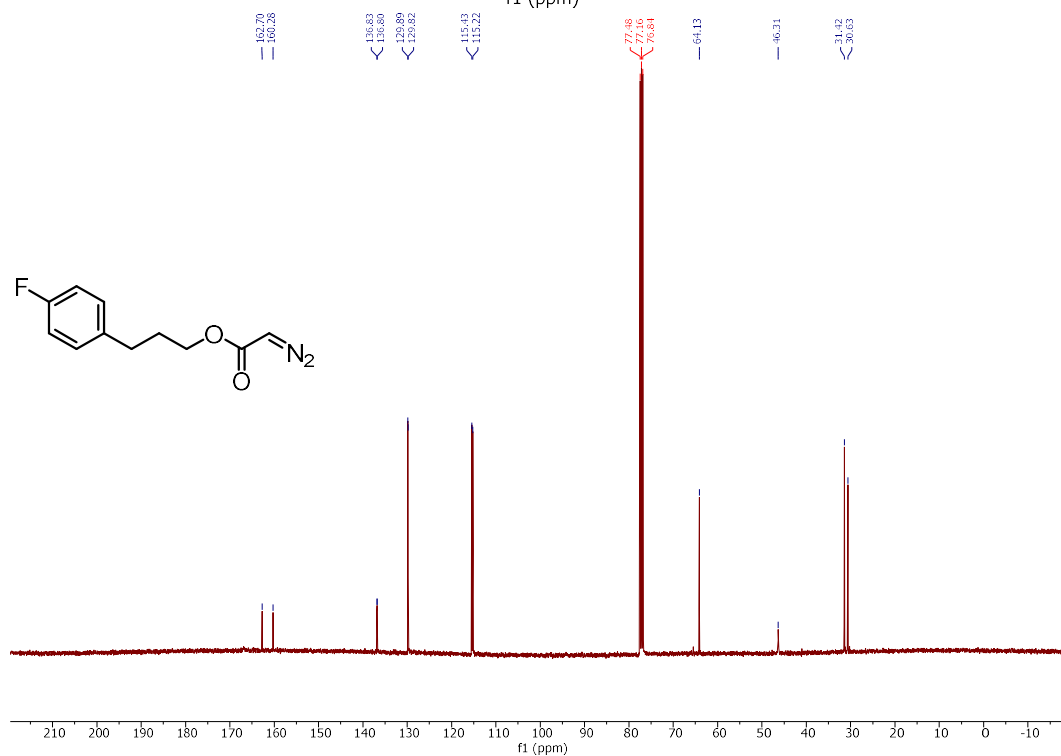
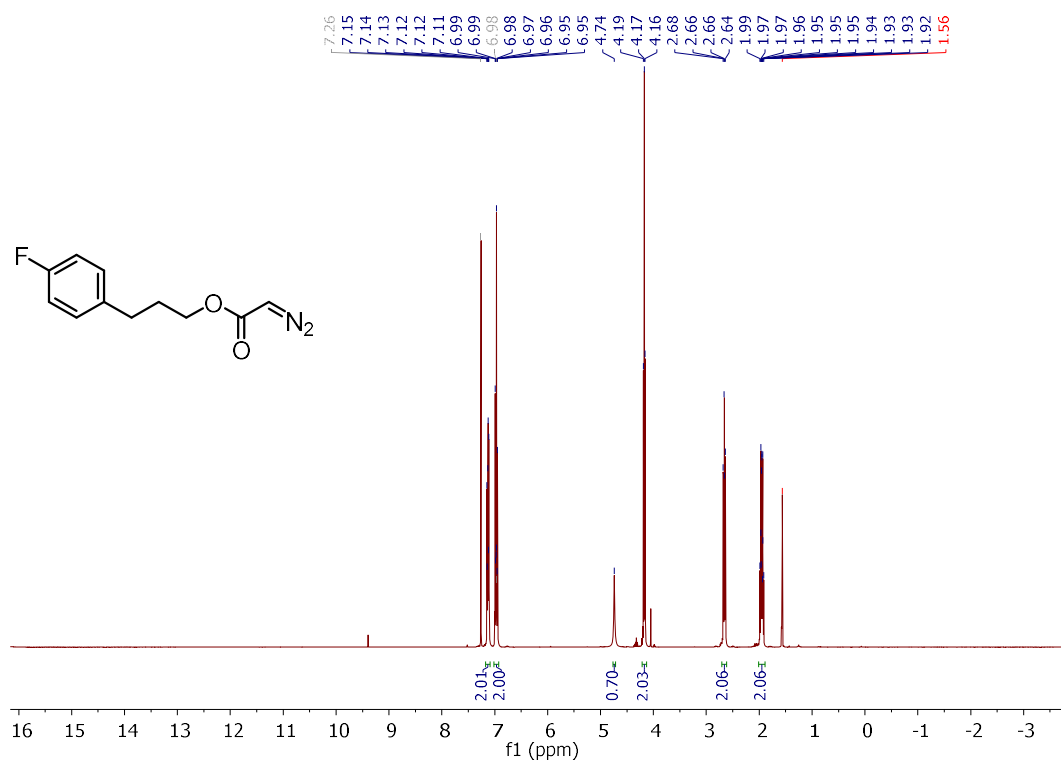
3-(*p*-tolyl)propyl 2-diazoacetate (3a)



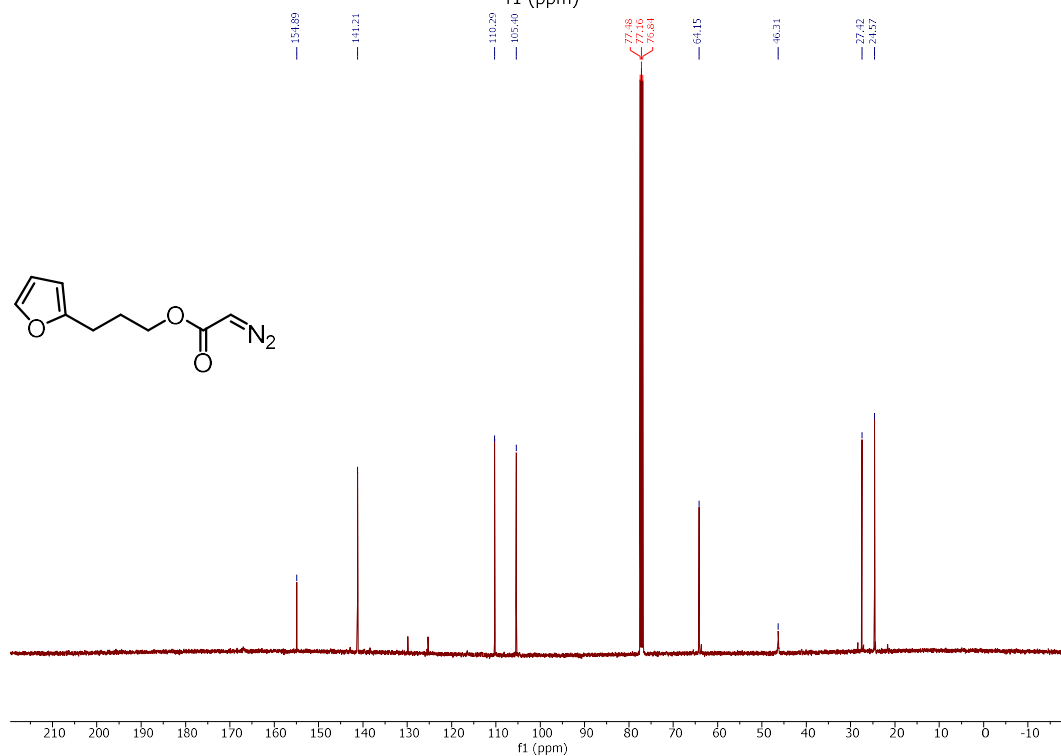
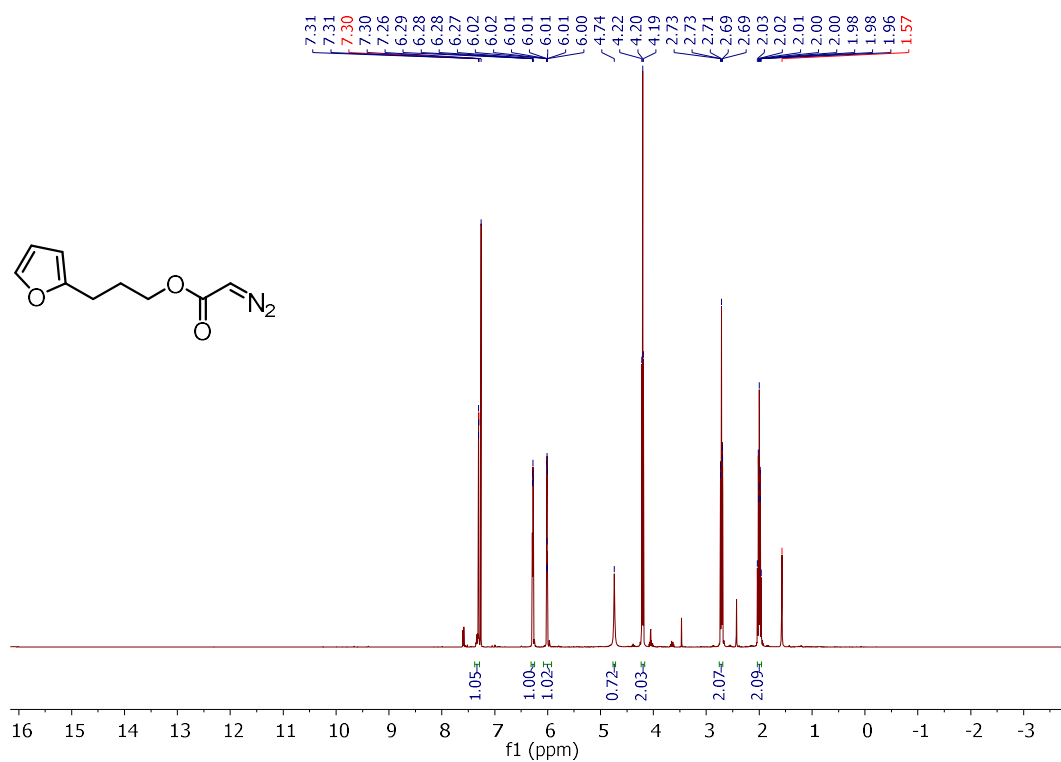
3-(4-methoxyphenyl)propyl 2-diazoacetate (3c)



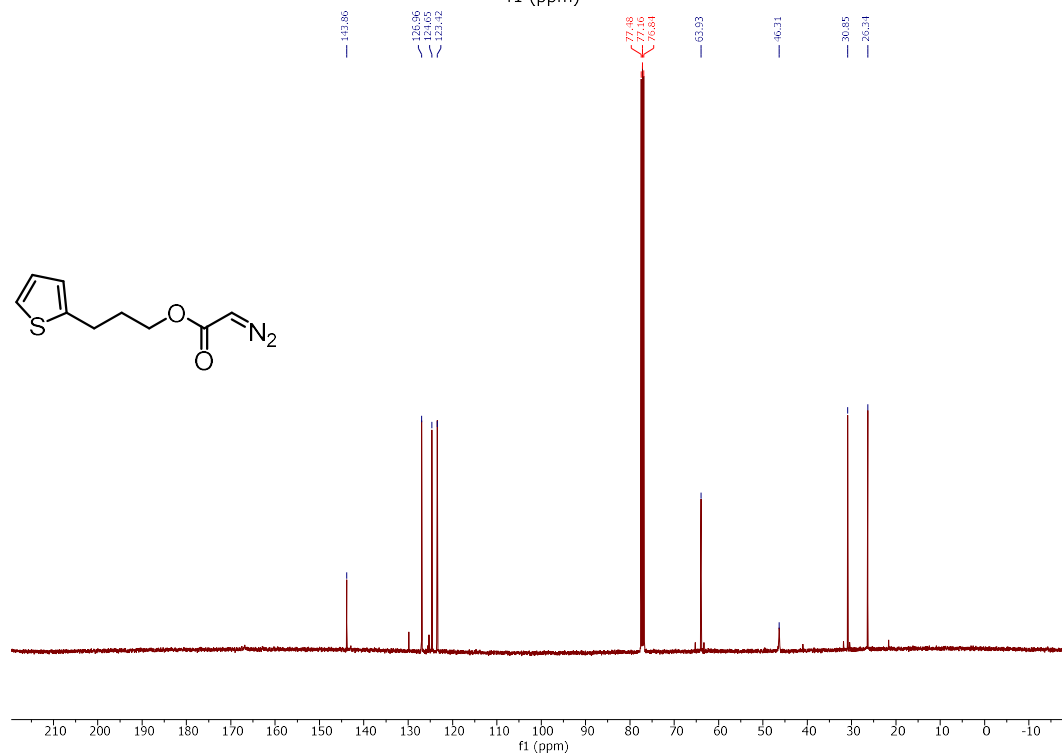
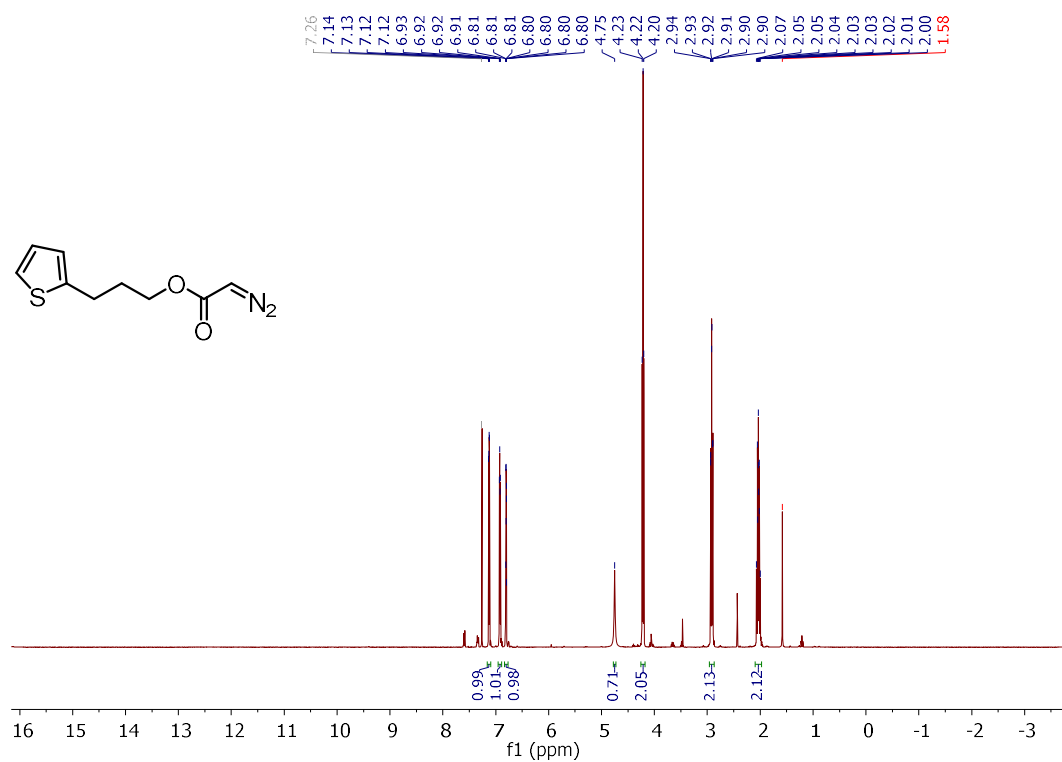
3-(4-fluorophenyl)propyl 2-diazoacetate (3d)



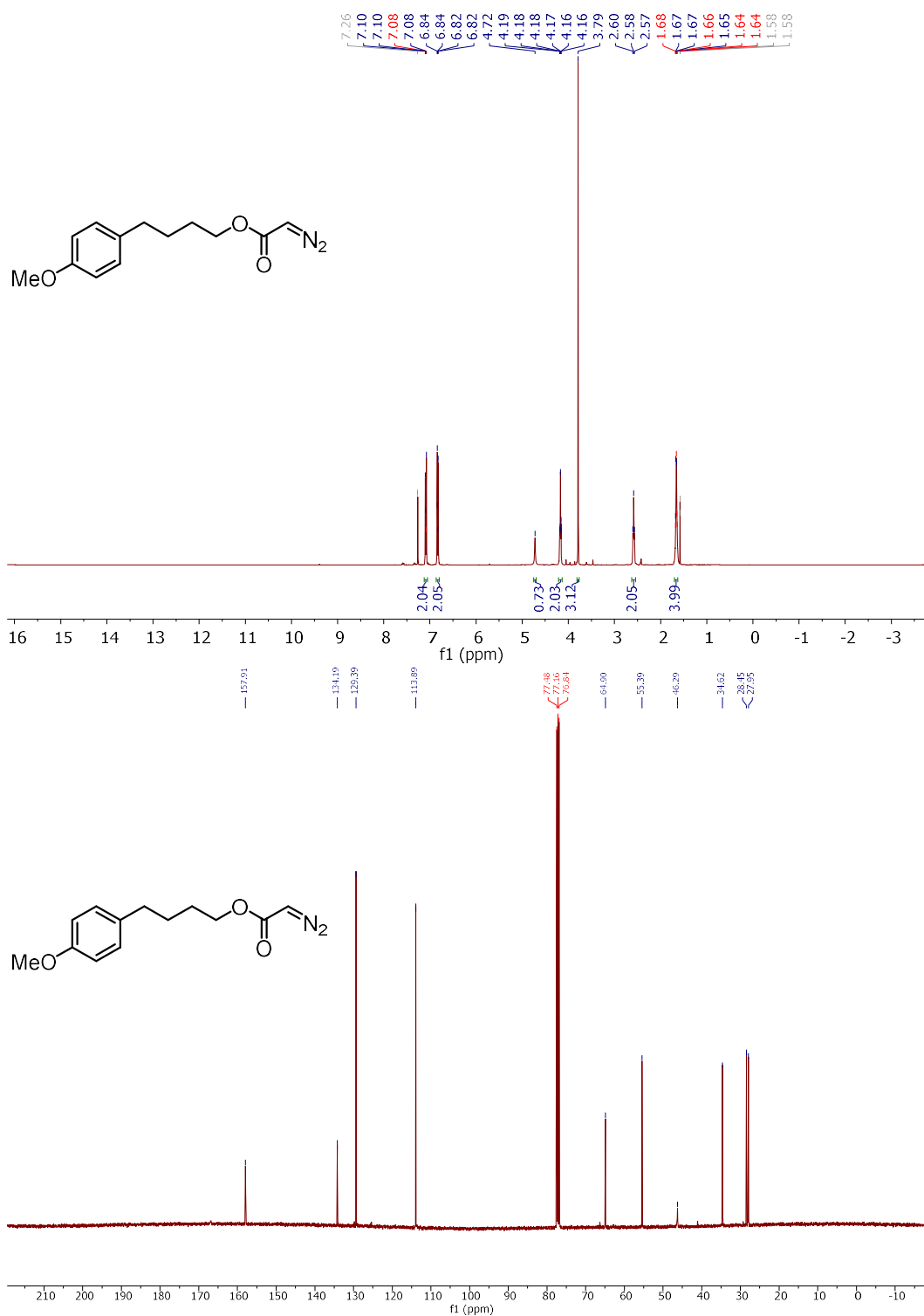
3-(furan-2-yl)propyl 2-diazoacetate (3e)



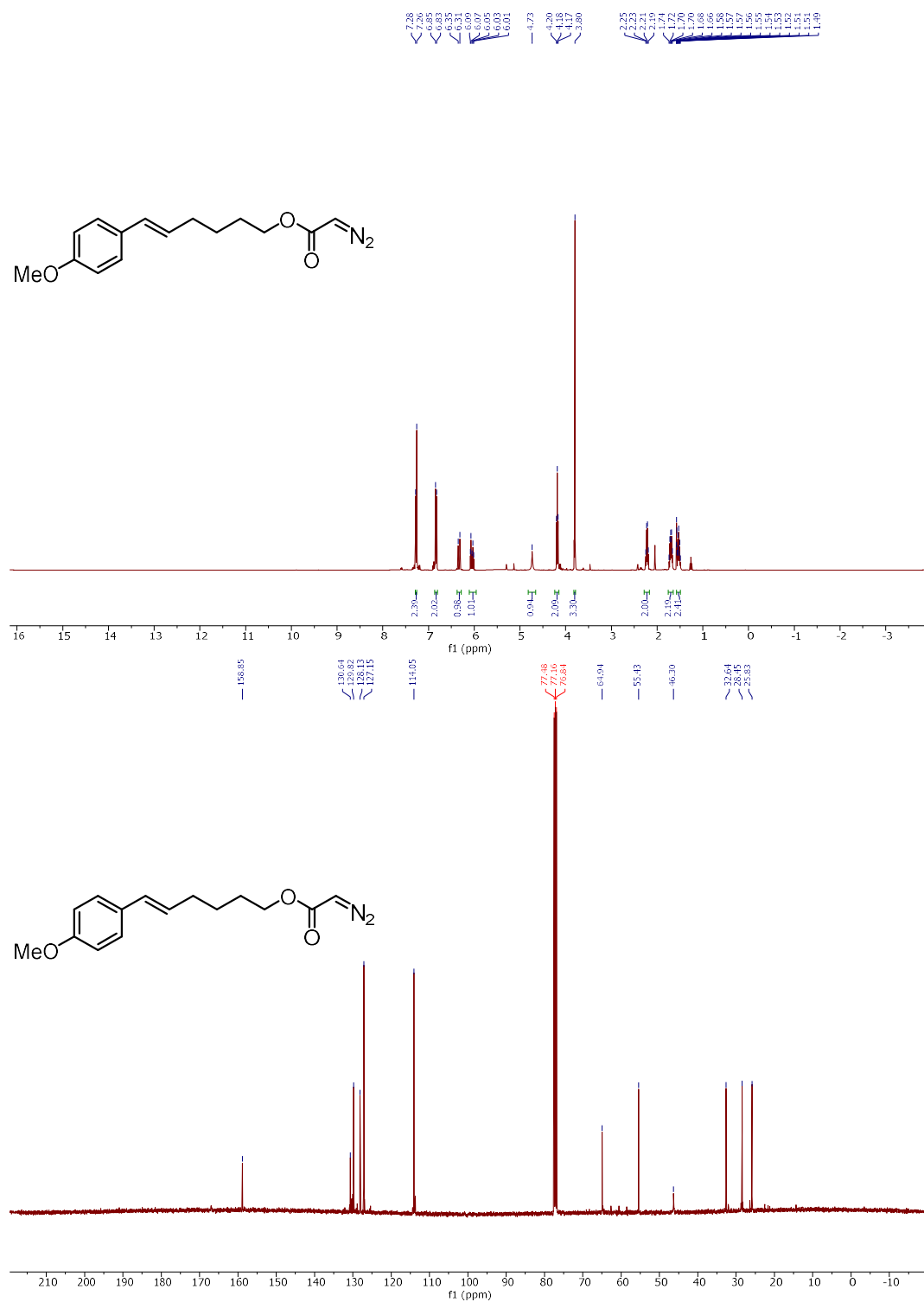
3-(thiophen-2-yl)propyl 2-diazoacetate (3f)



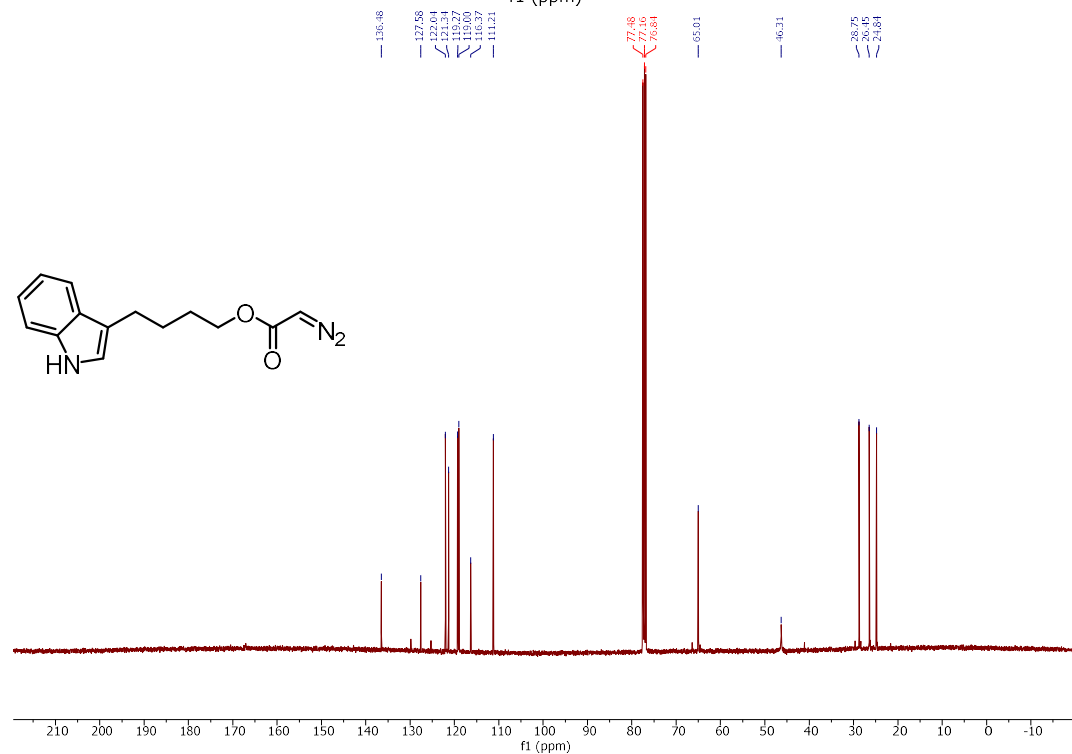
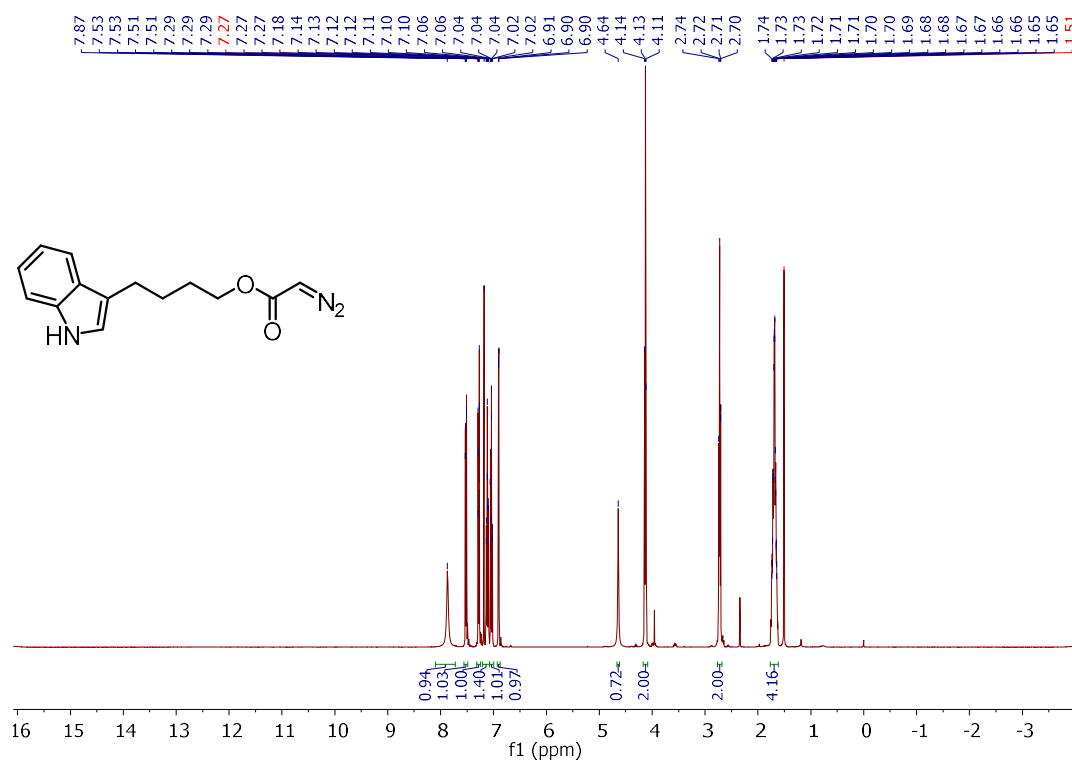
4-(4-methoxyphenyl)butyl 2-diazoacetate (5a)



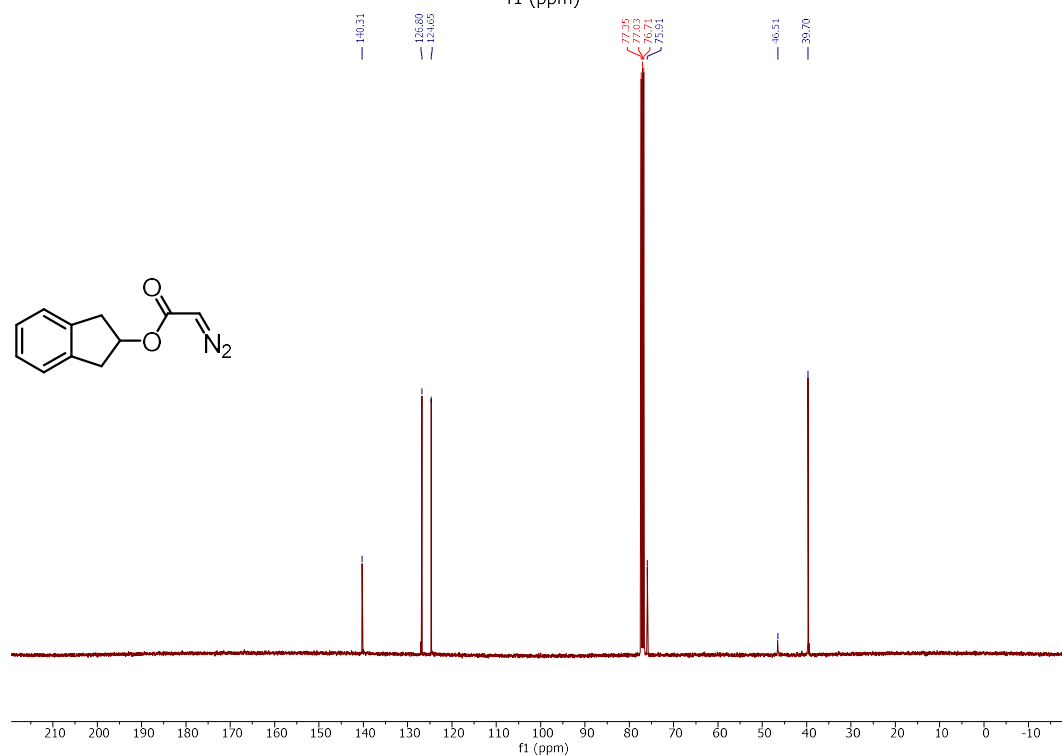
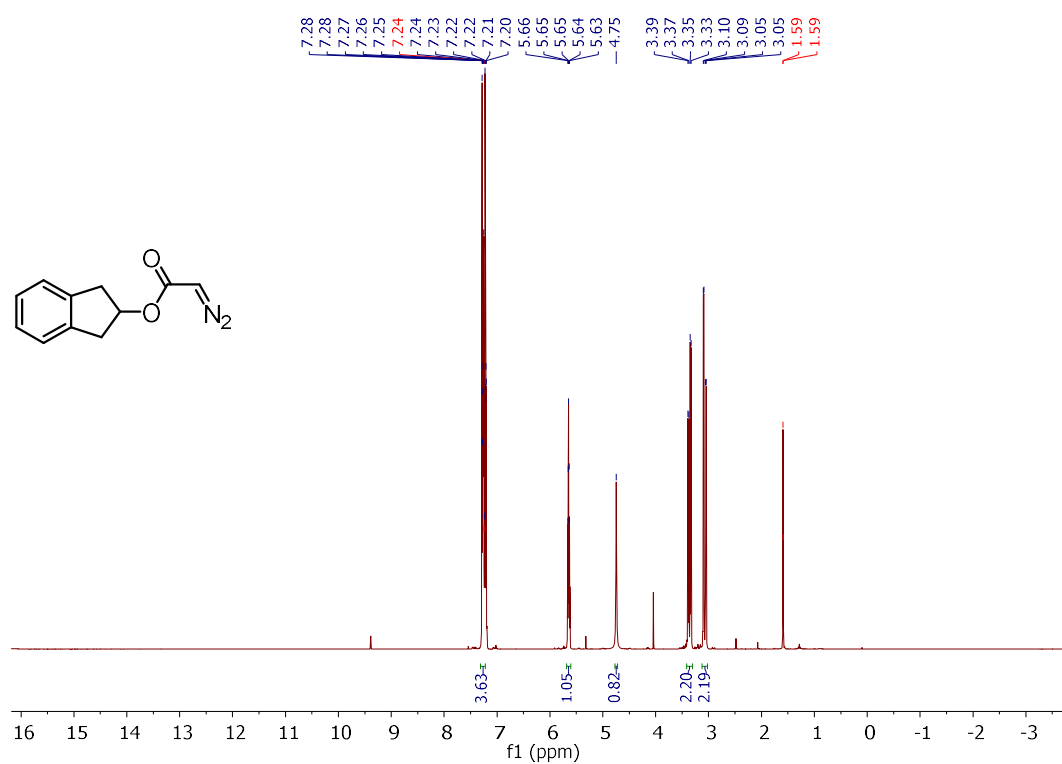
(*E*)-6-(4-methoxyphenyl)hex-5-en-1-yl 2-diazoacetate (5b)



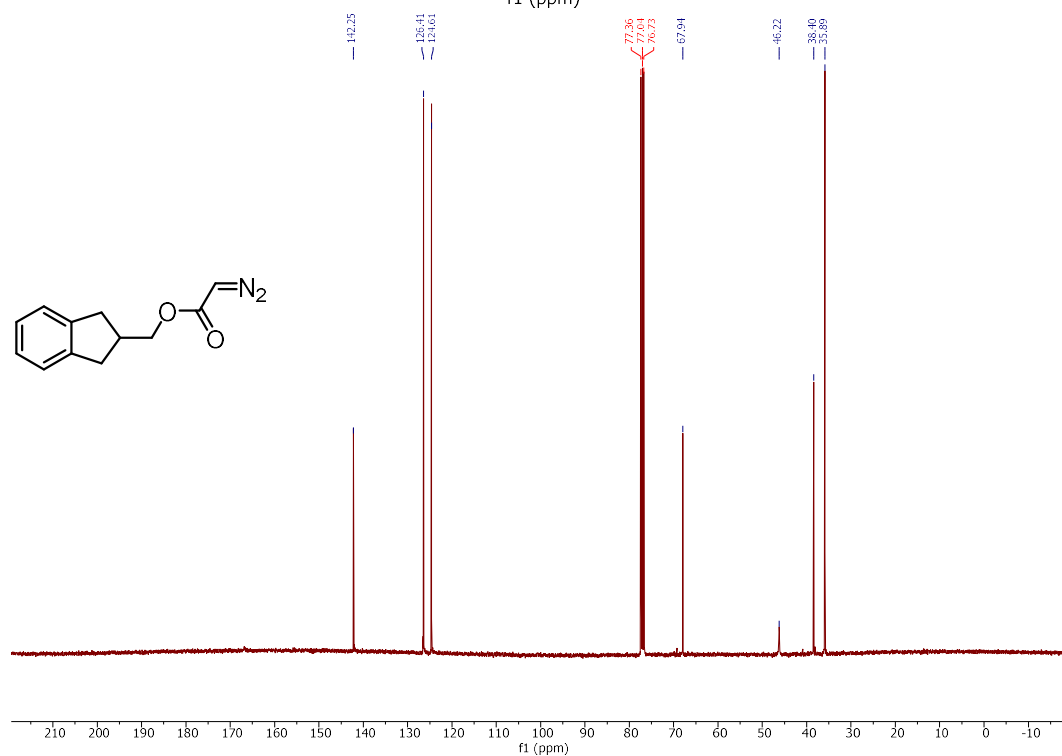
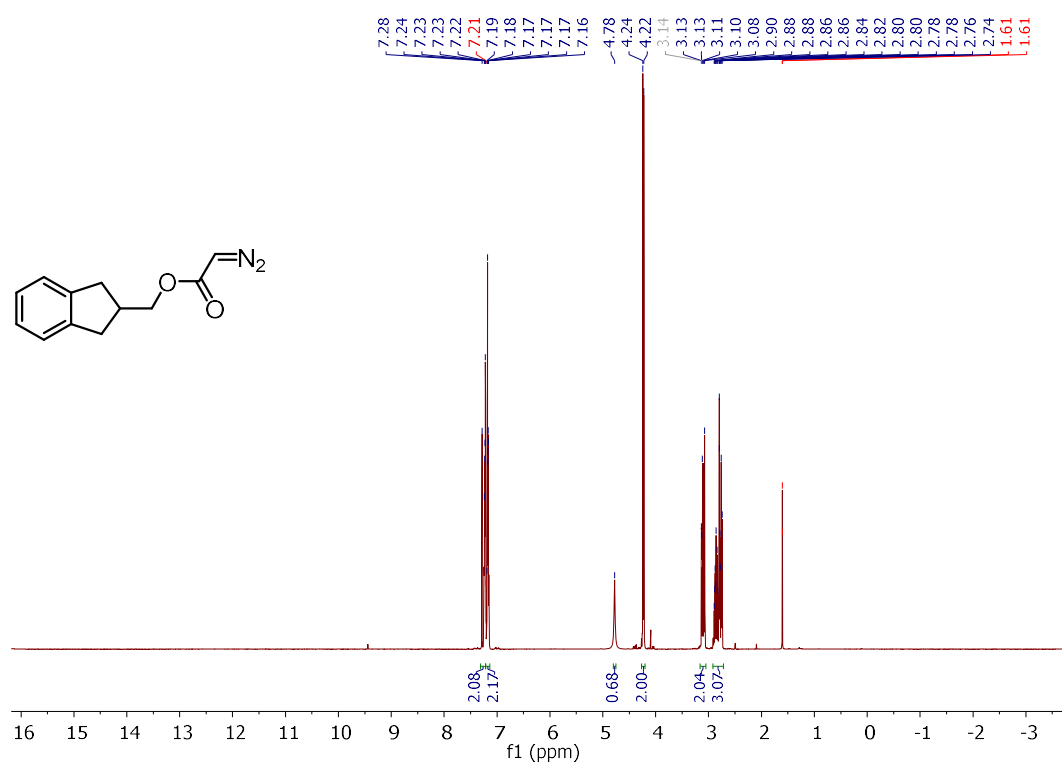
4-(1*H*-indol-3-yl)butyl 2-diazoacetate (5c)



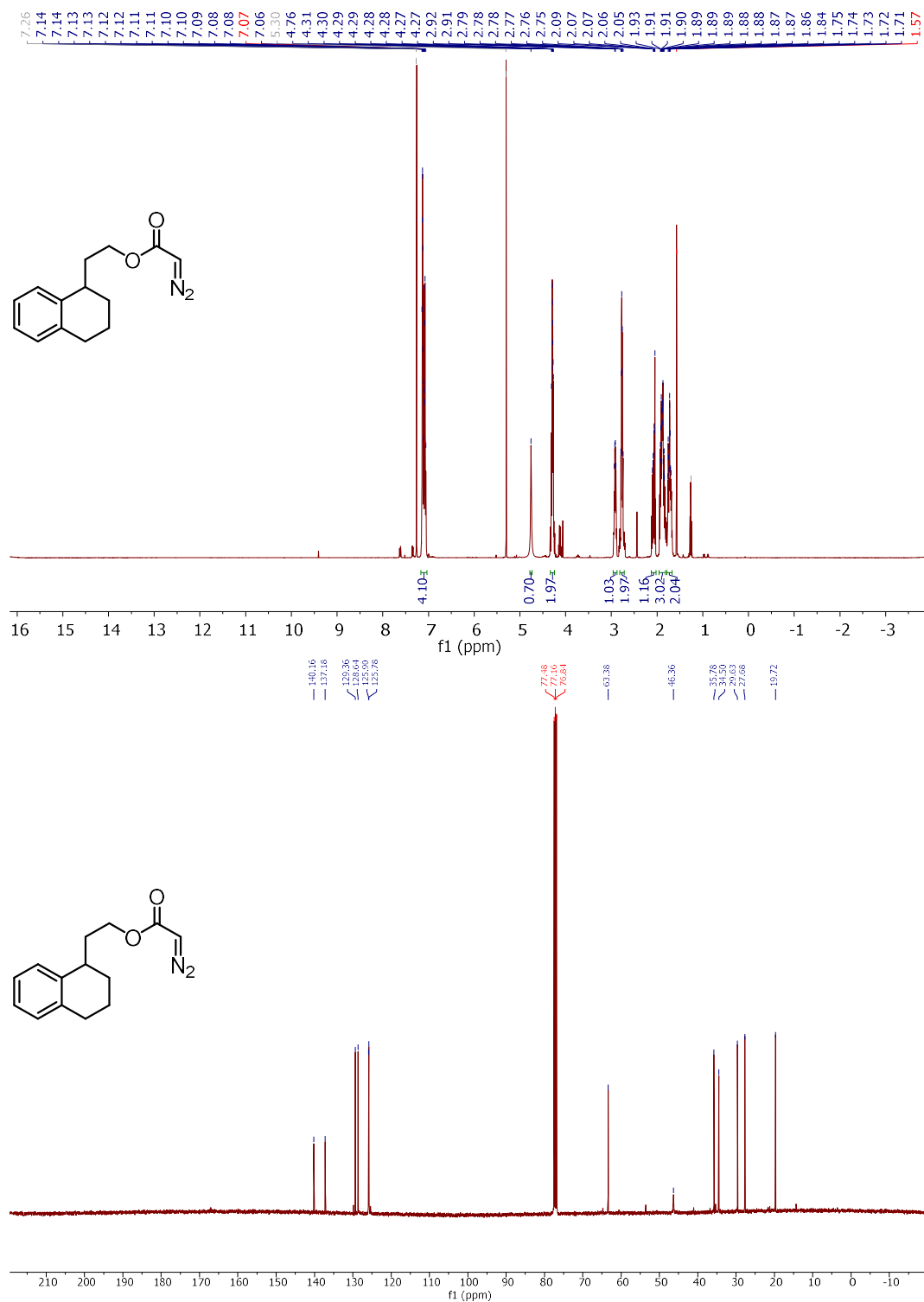
2,3-dihydro-1*H*-inden-2-yl 2-diazoacetate (7a)



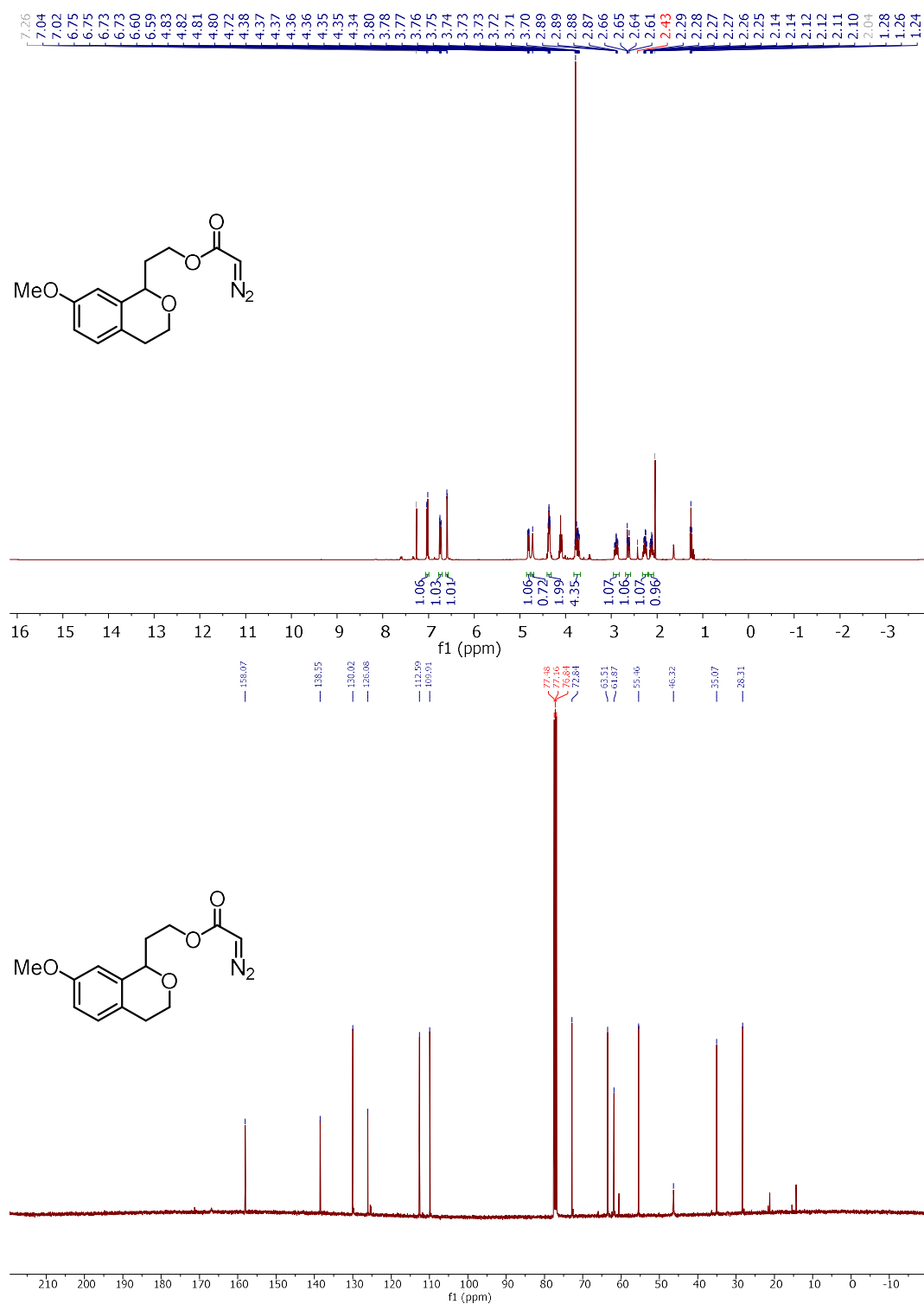
(2,3-dihydro-1*H*-inden-2-yl)methyl 2-diazoacetate (7b)



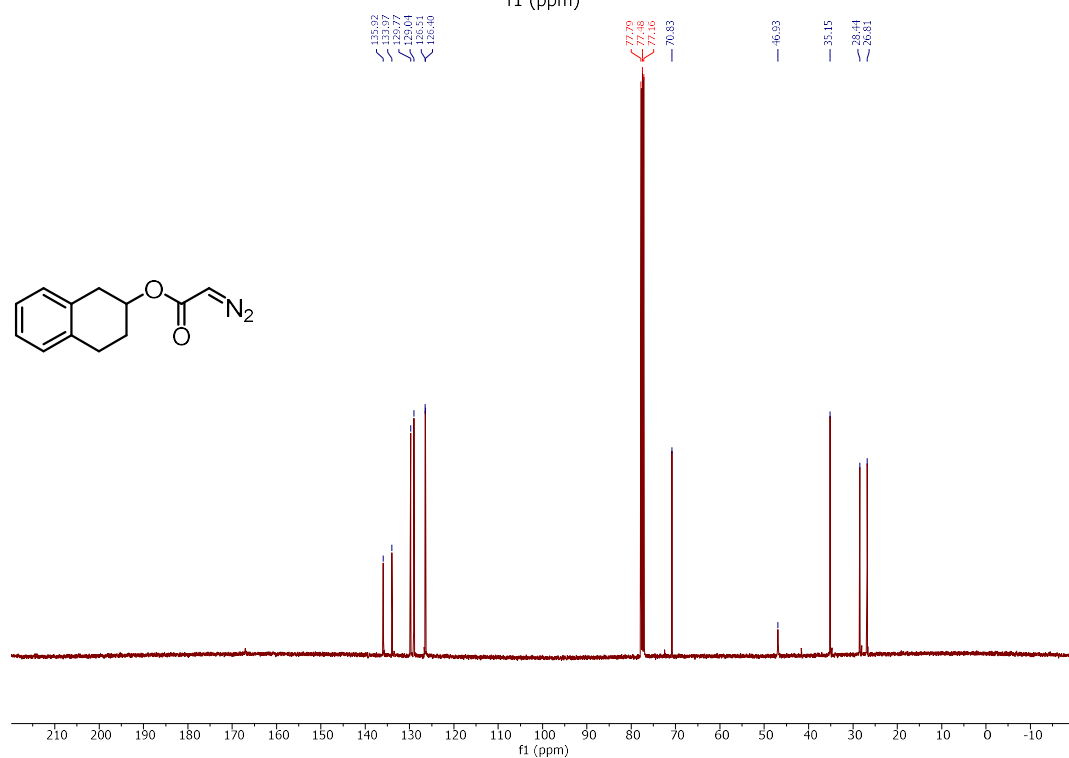
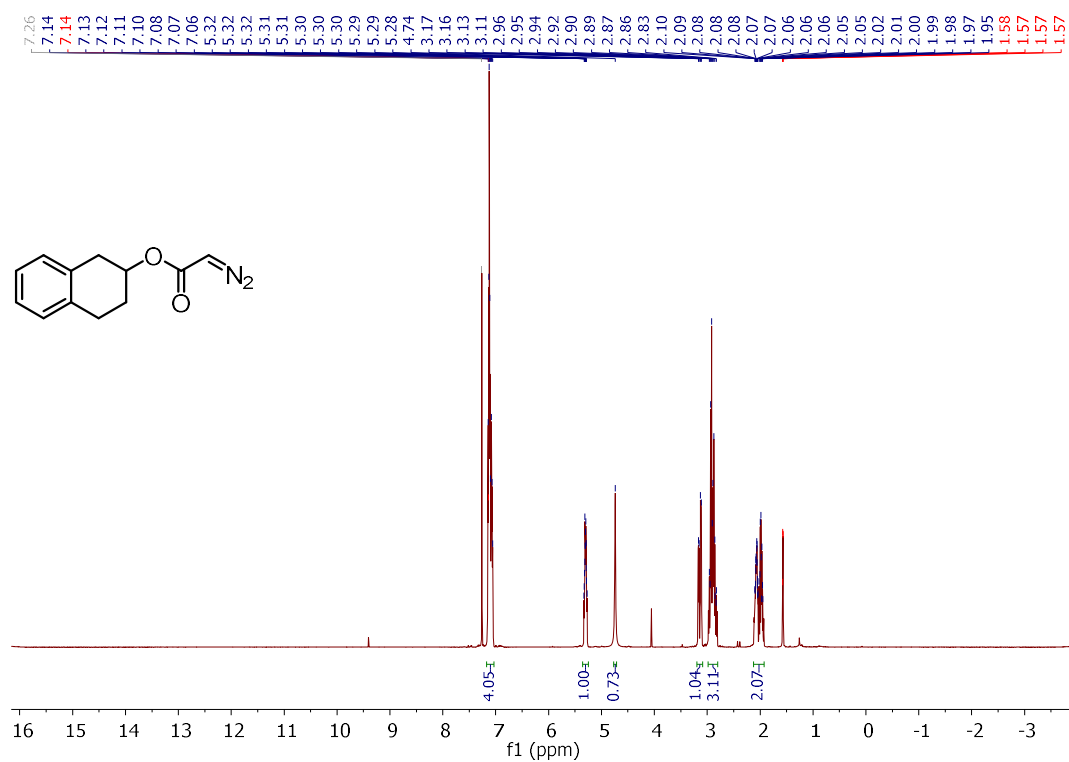
2-(1,2,3,4-tetrahydronaphthalen-1-yl)ethyl 2-diazoacetate (7c)



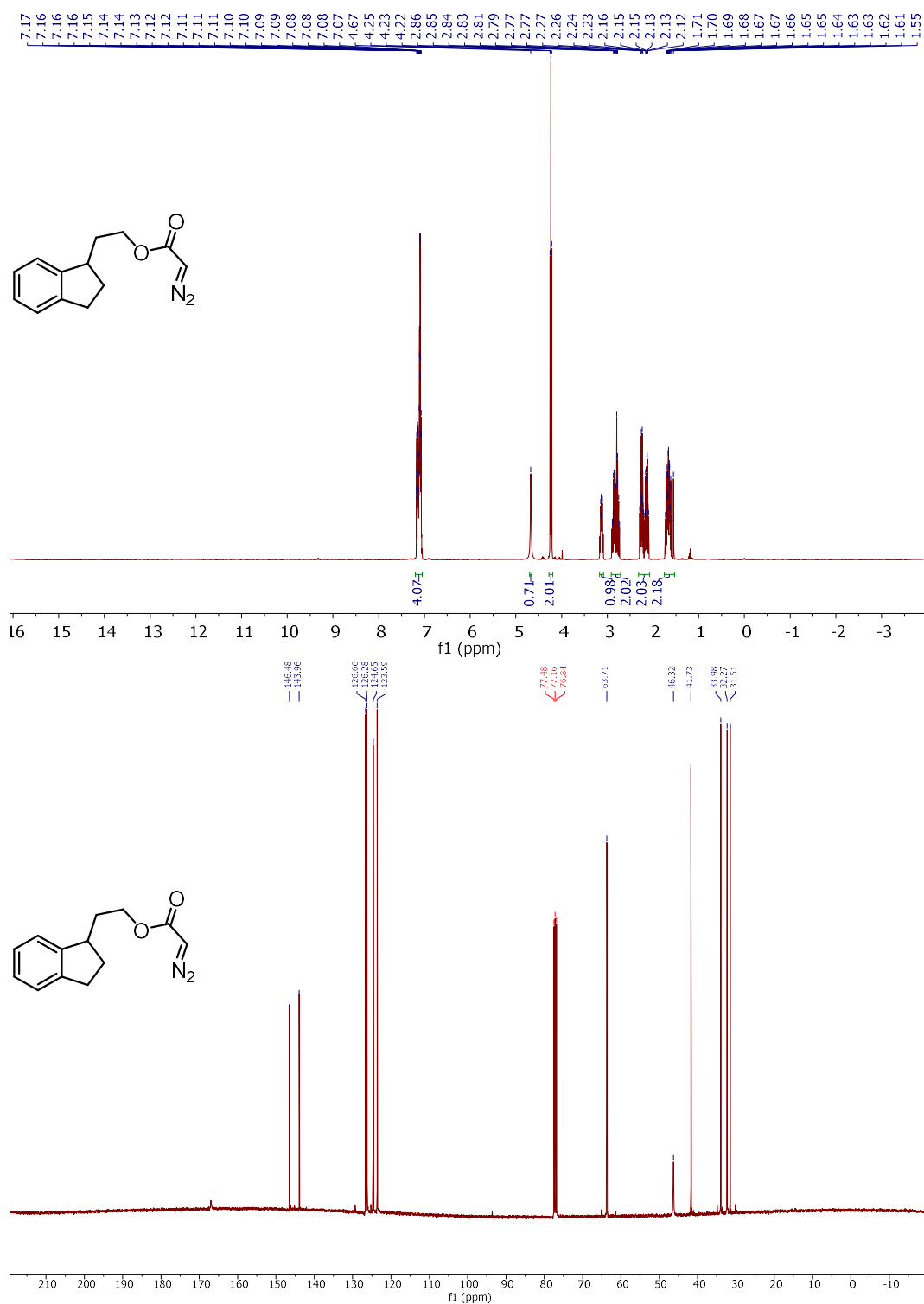
2-(7-methoxyisochroman-1-yl)ethyl 2-diazoacetate (7d)



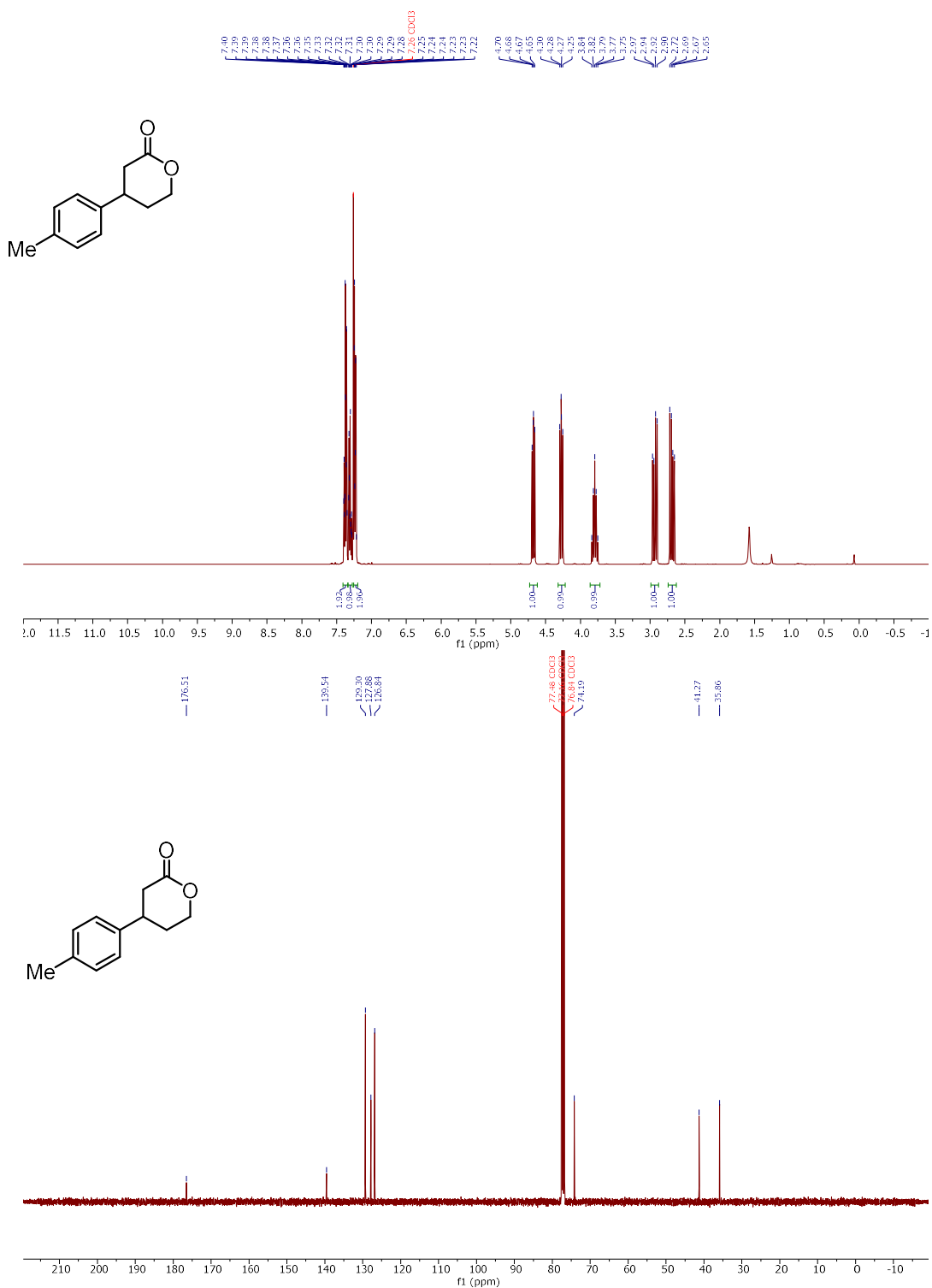
1,2,3,4-tetrahydronaphthalen-2-yl 2-diazoacetate (7e)



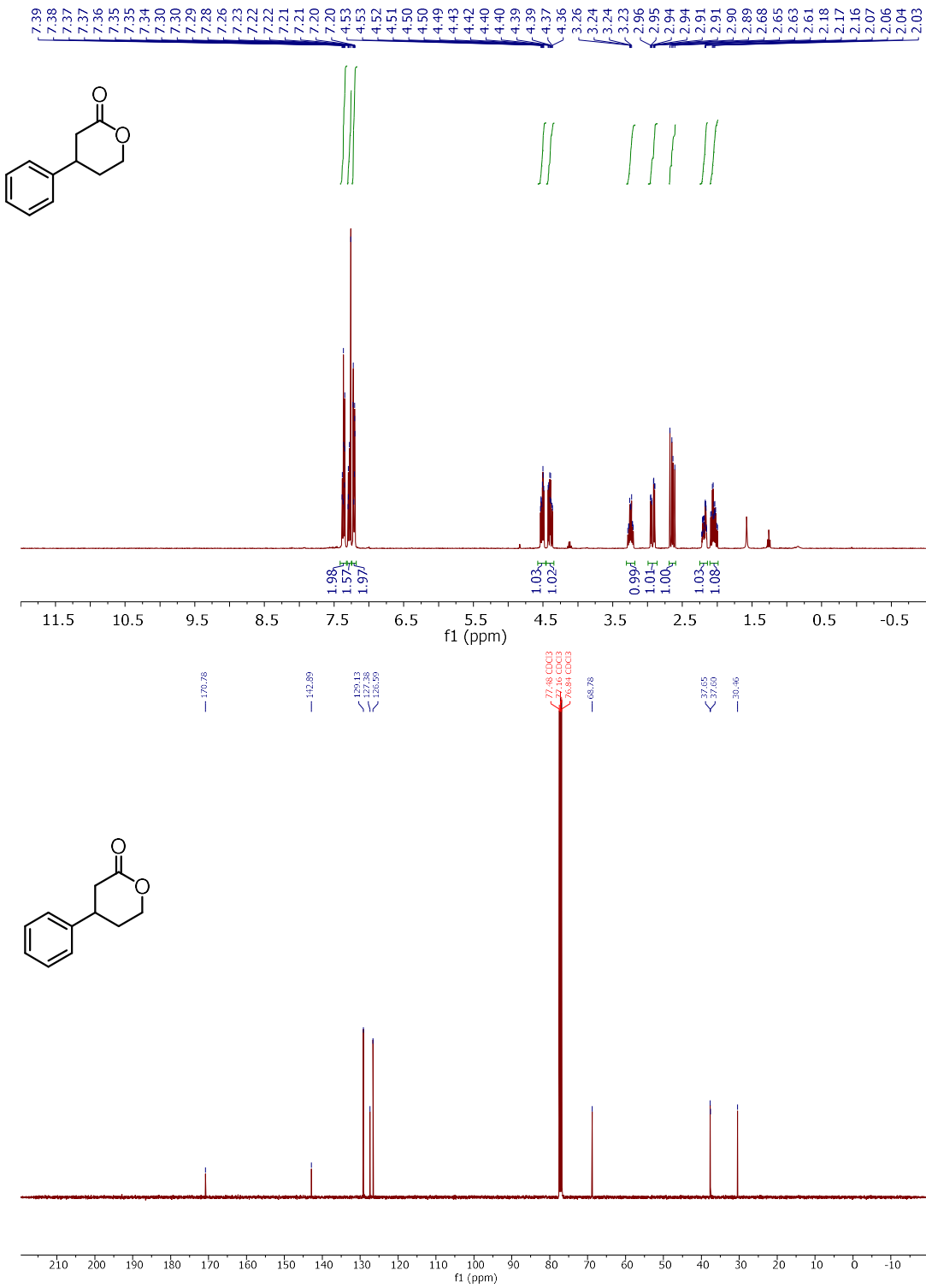
2-(2,3-dihydro-1H-inden-1-yl)ethyl 2-diazoacetate (7f)



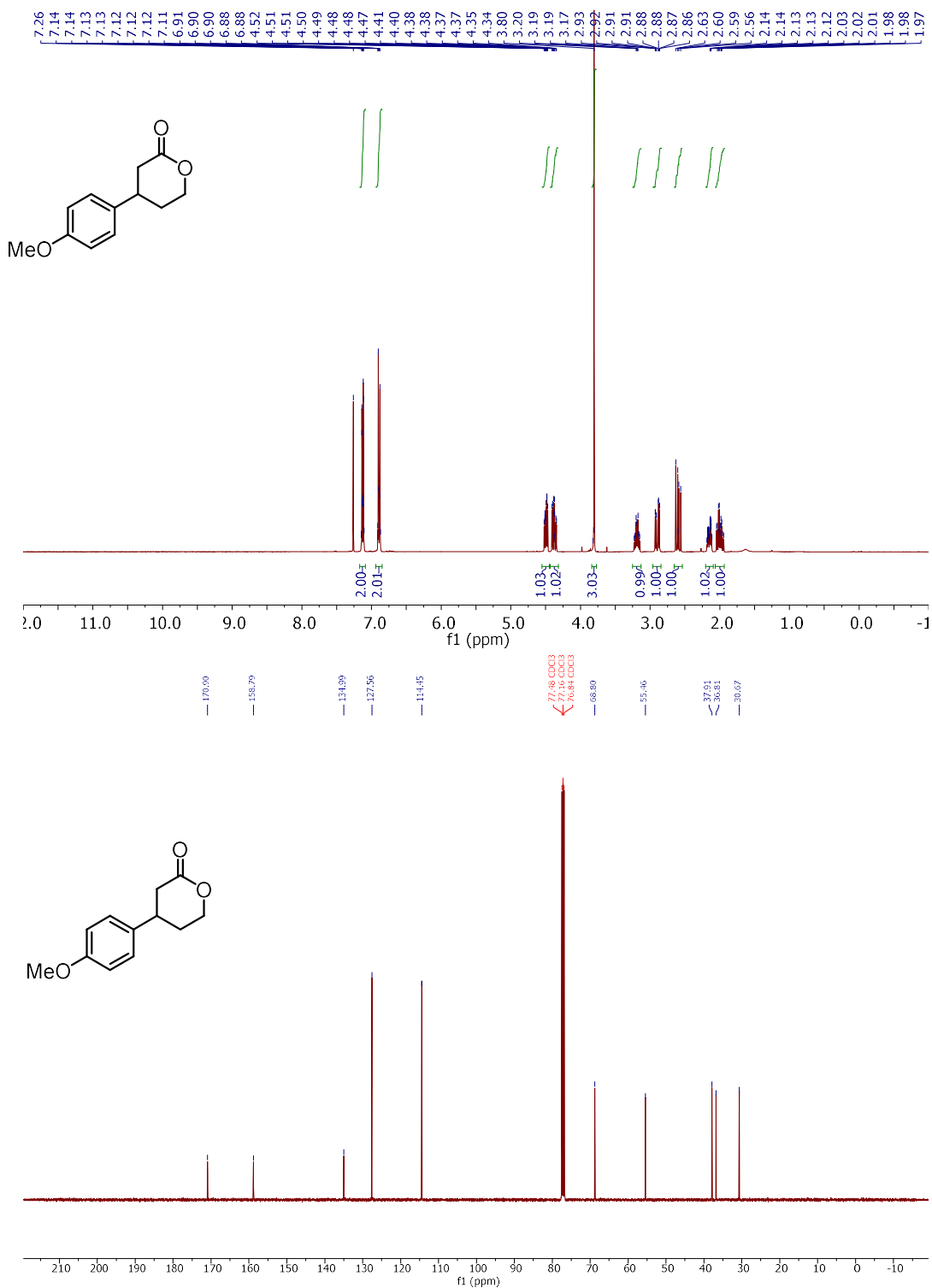
4-(*p*-tolyl)tetrahydro-2*H*-pyran-2-one (4a)



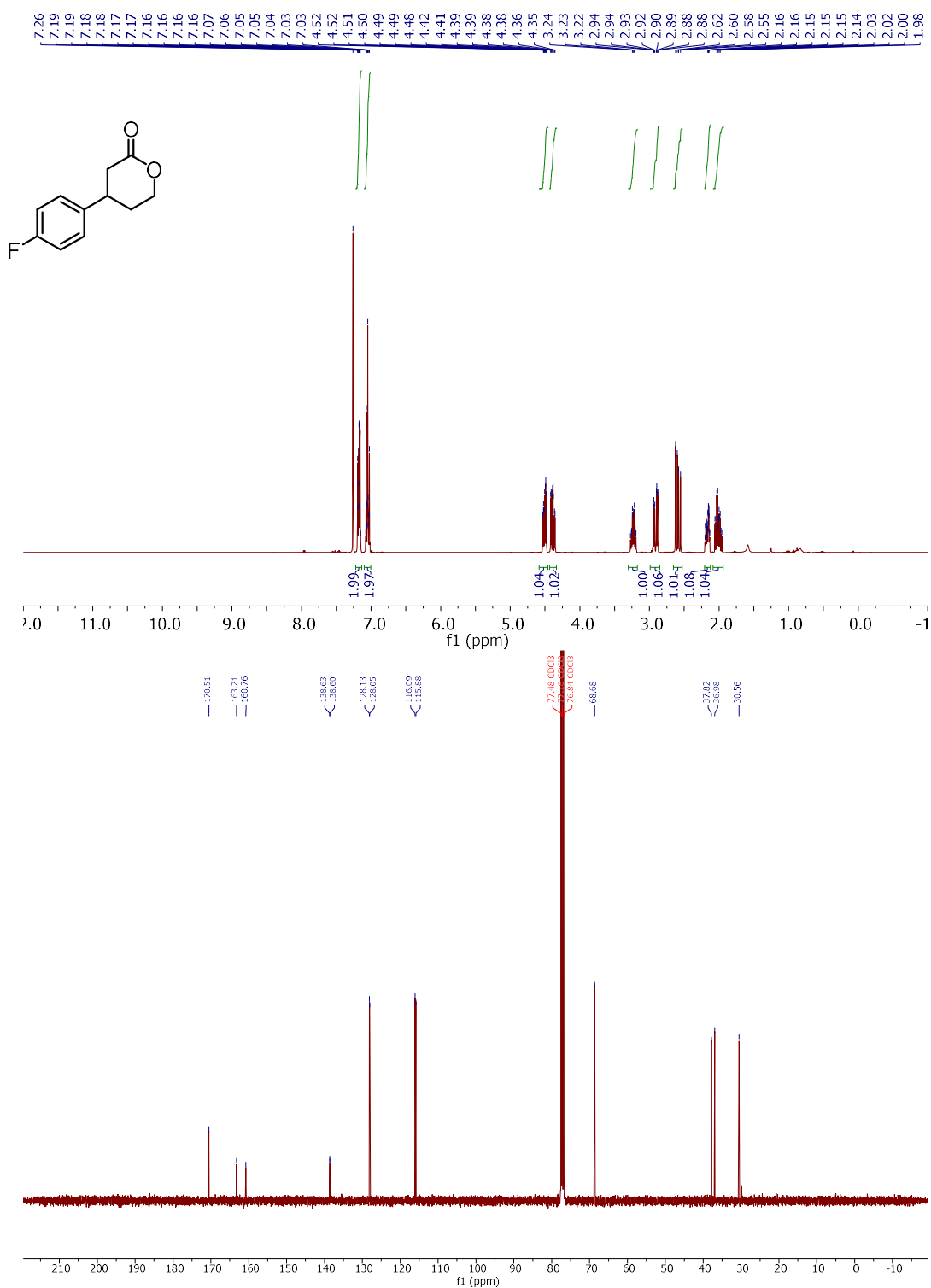
4-phenyltetrahydro-2H-pyran-2-one (4b)

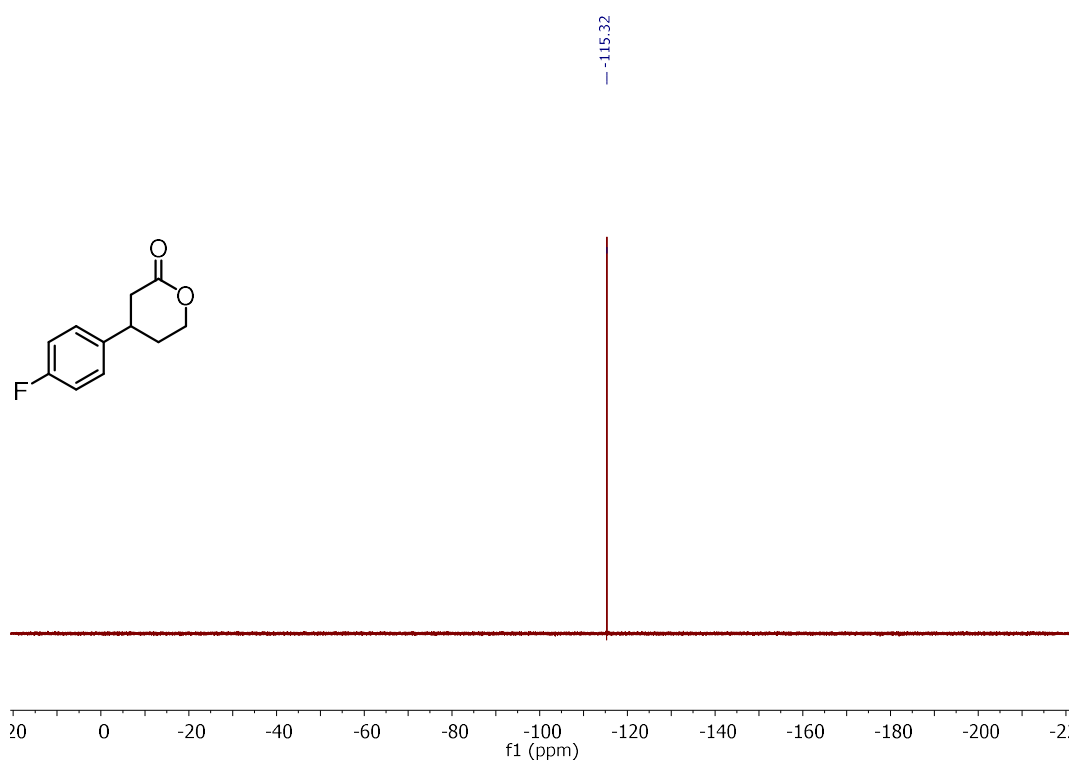


4-(4-methoxyphenyl)tetrahydro-2H-pyran-2-one (4c)

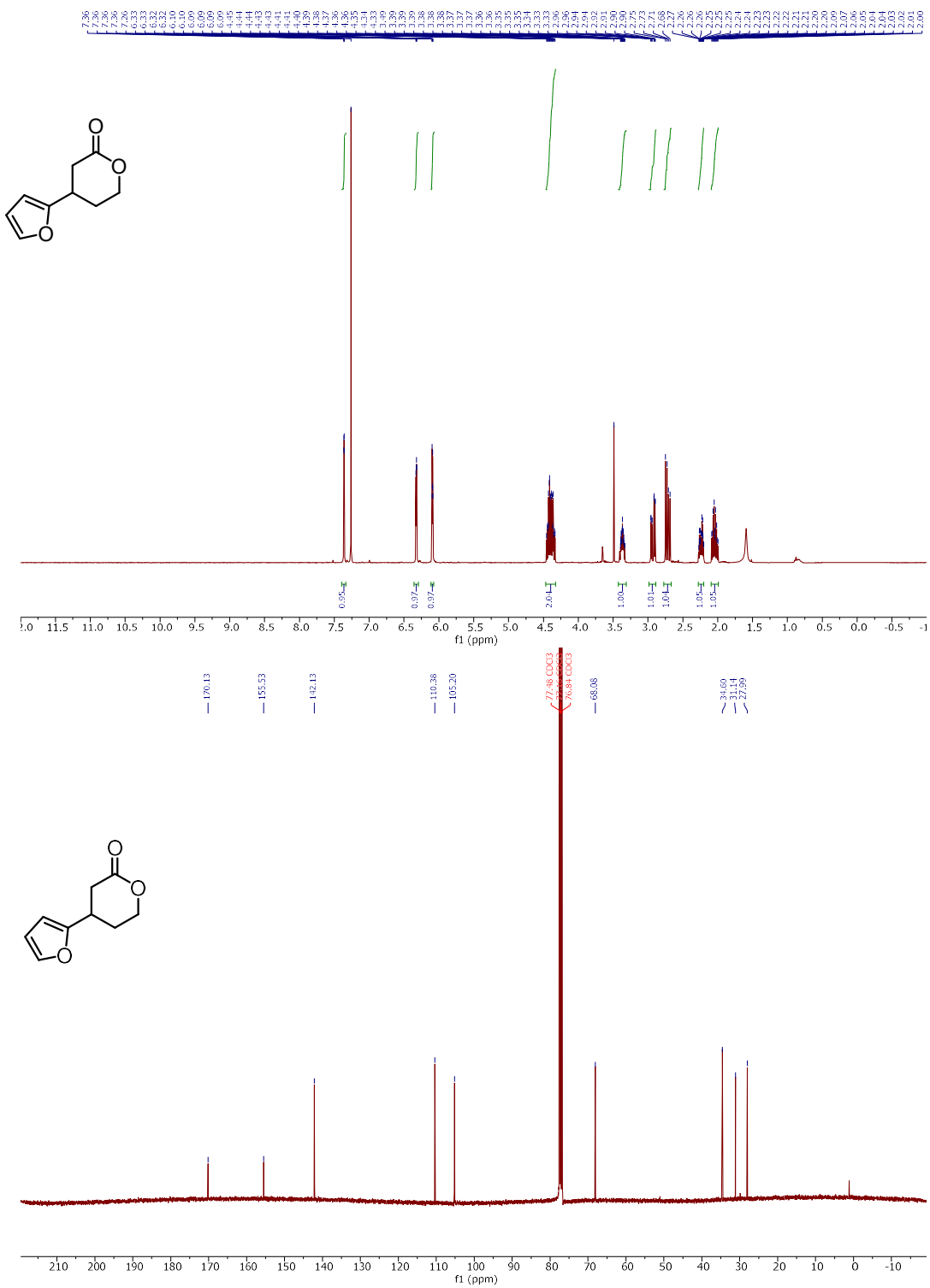


4-(4-fluorophenyl)tetrahydro-2H-pyran-2-one (4d)

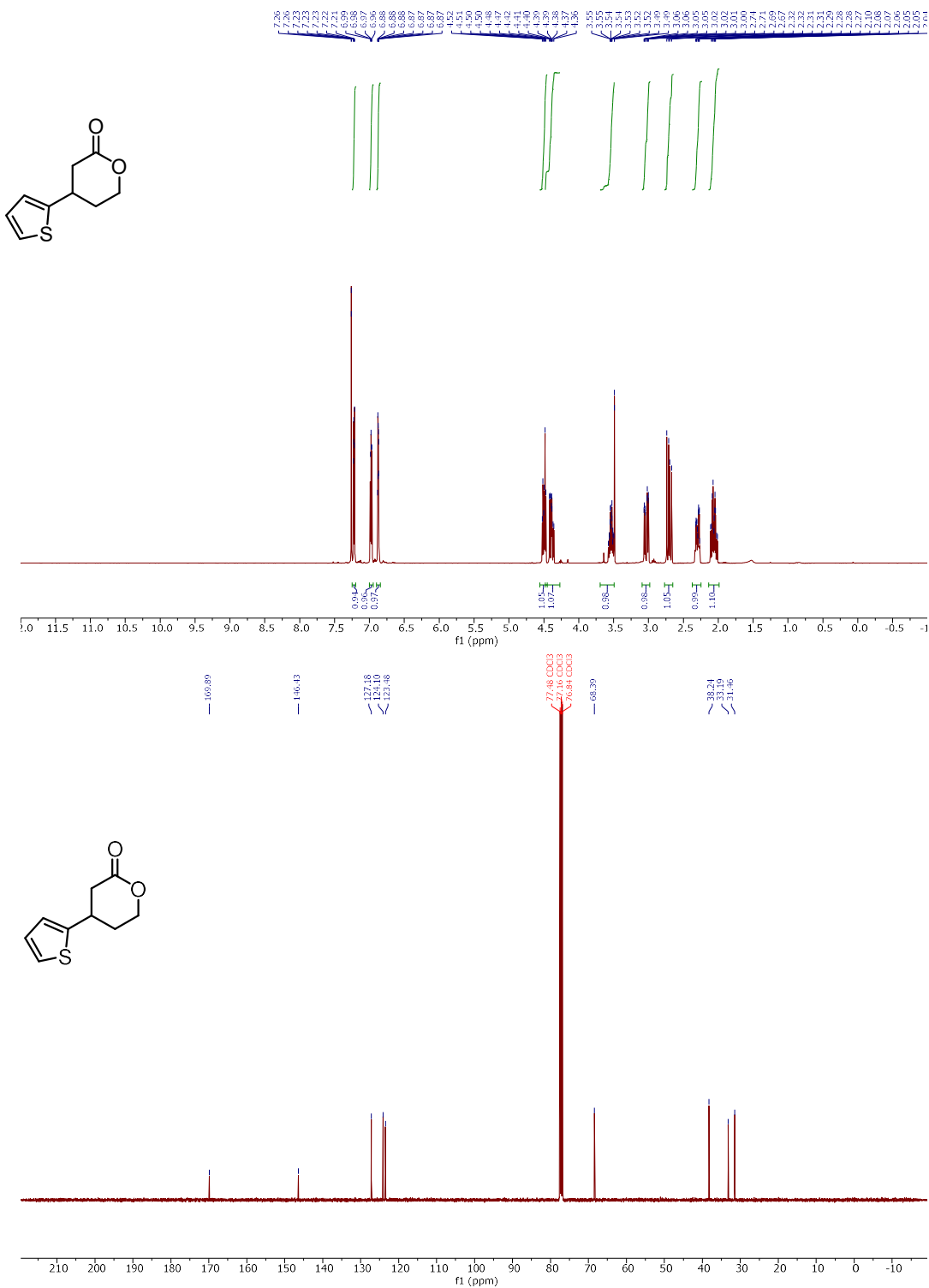




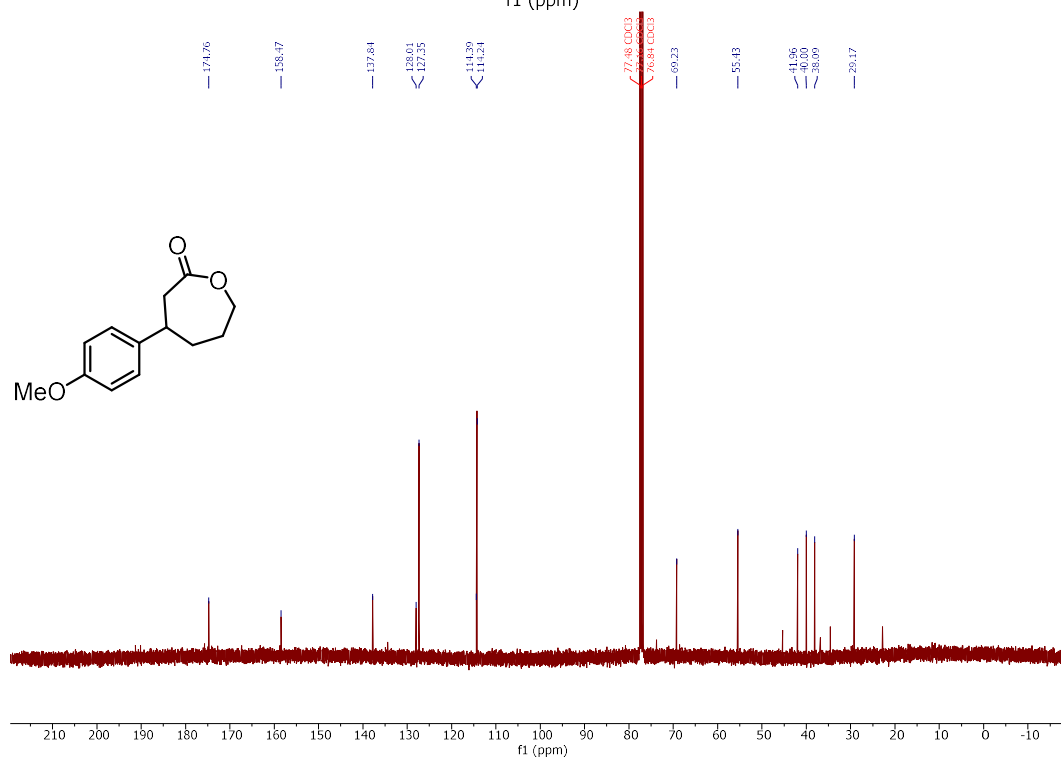
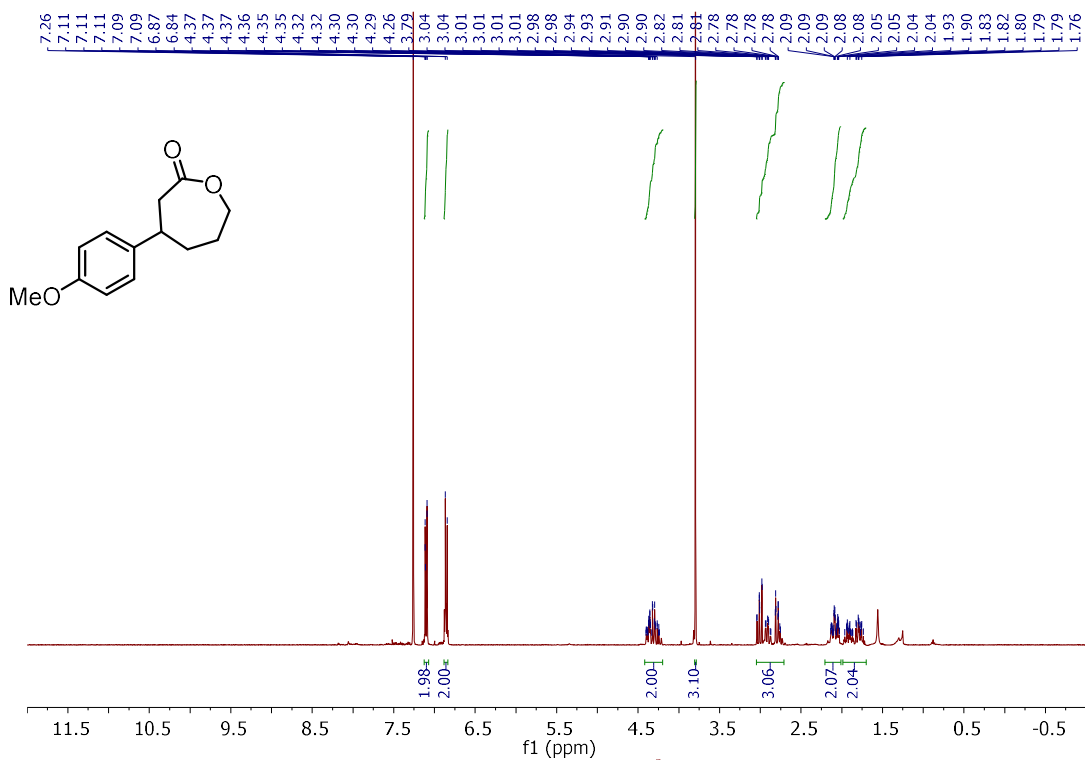
4-(furan-2-yl)tetrahydro-2*H*-pyran-2-one (4e)



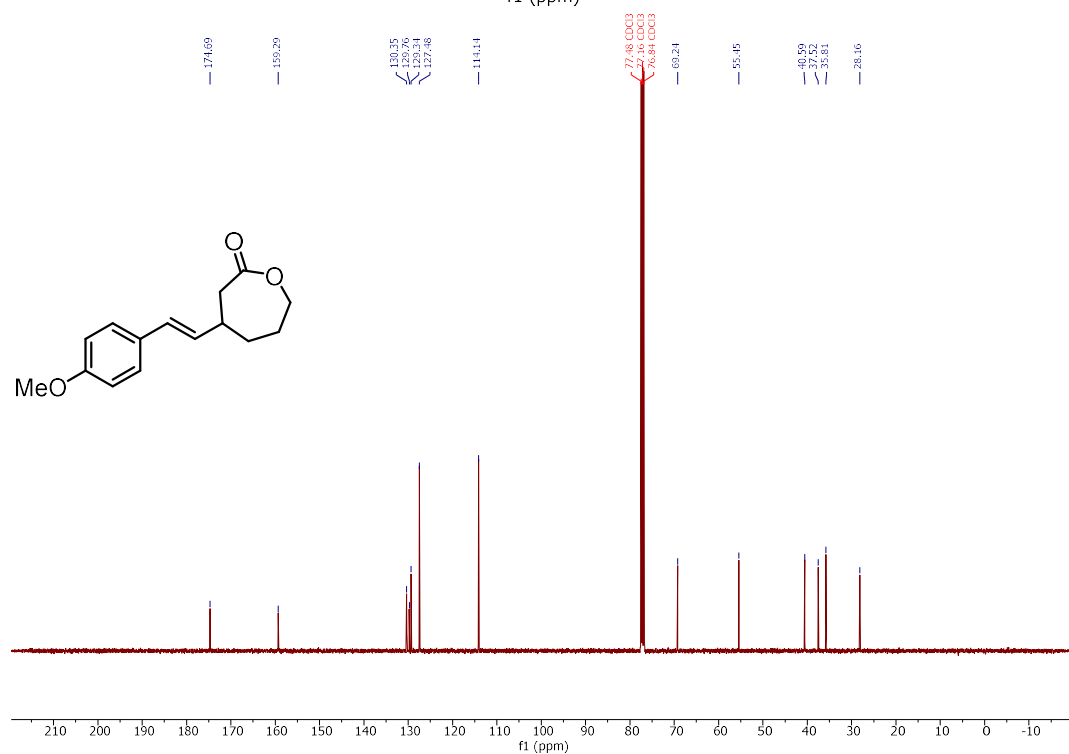
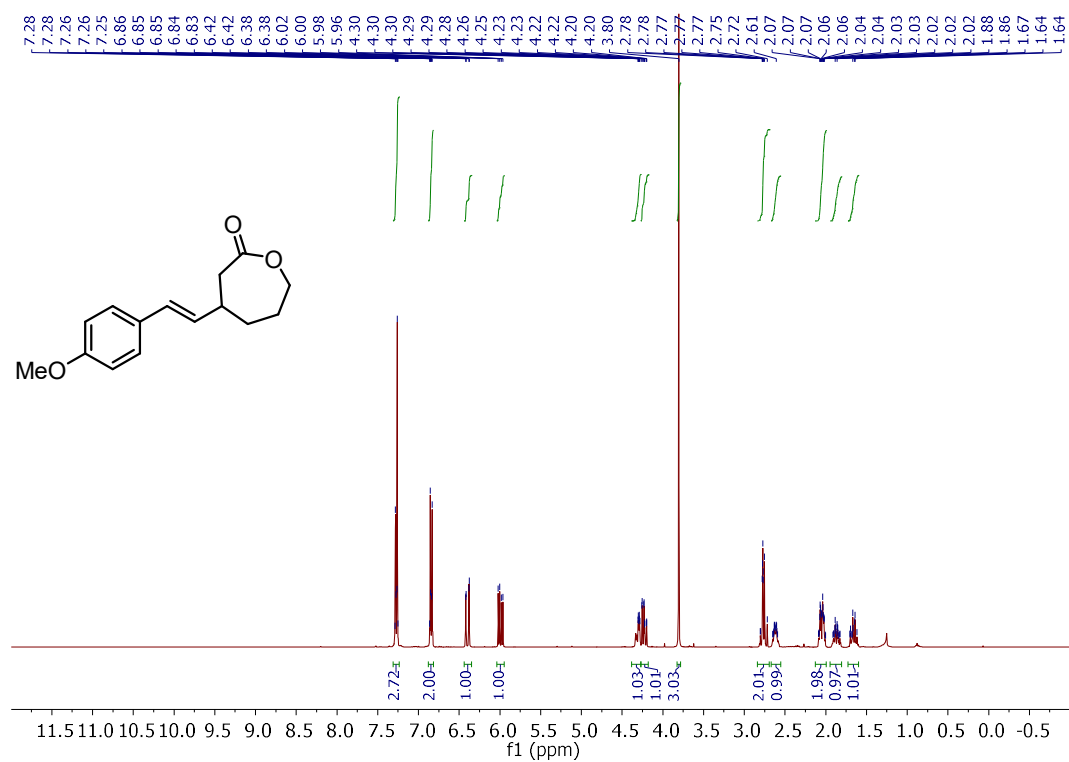
4-(thiophen-2-yl)tetrahydro-2*H*-pyran-2-one (4f)



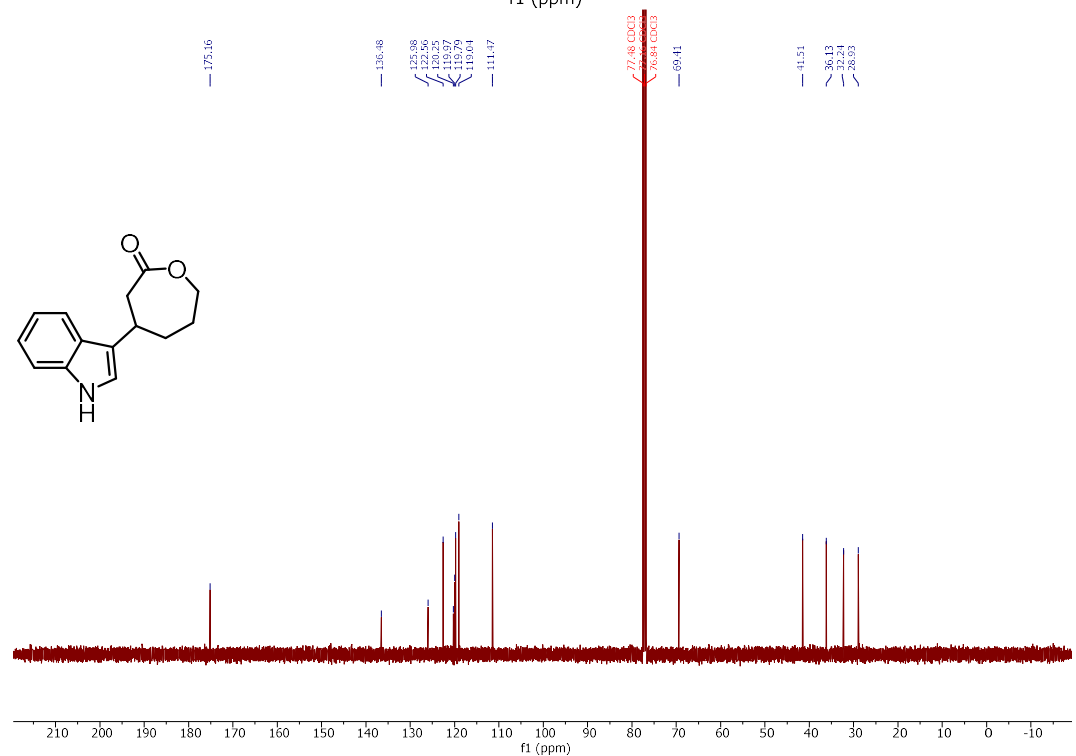
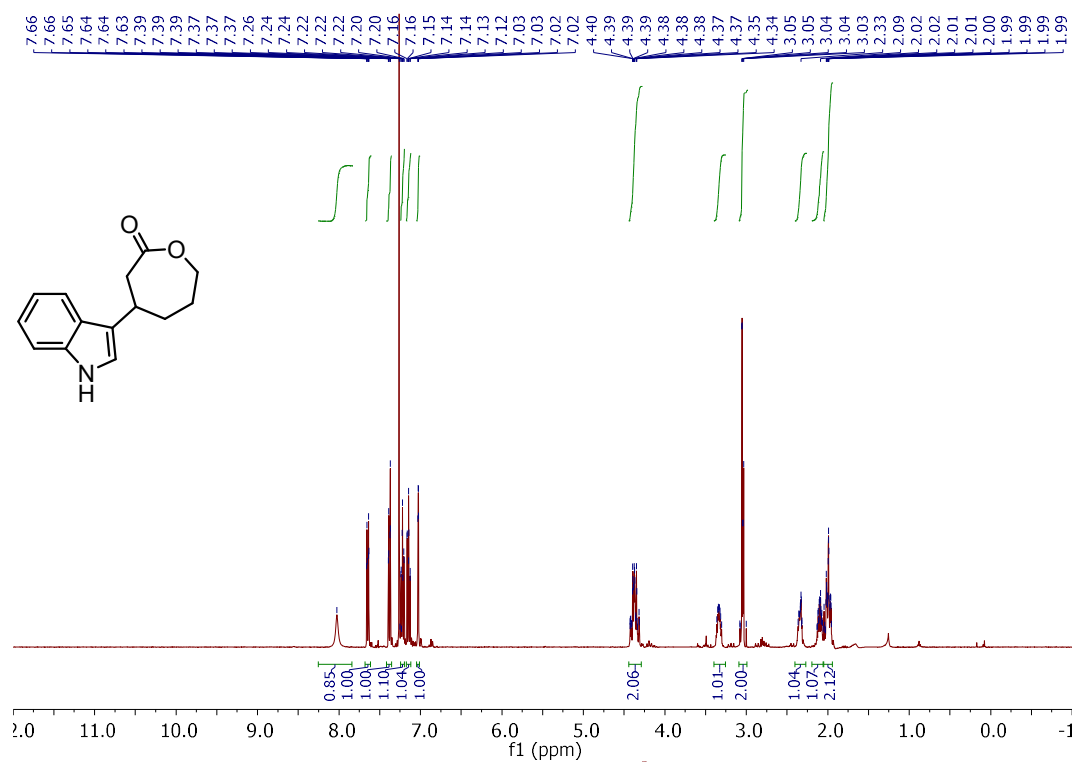
4-(4-methoxyphenyl)oxepan-2-one (6a)



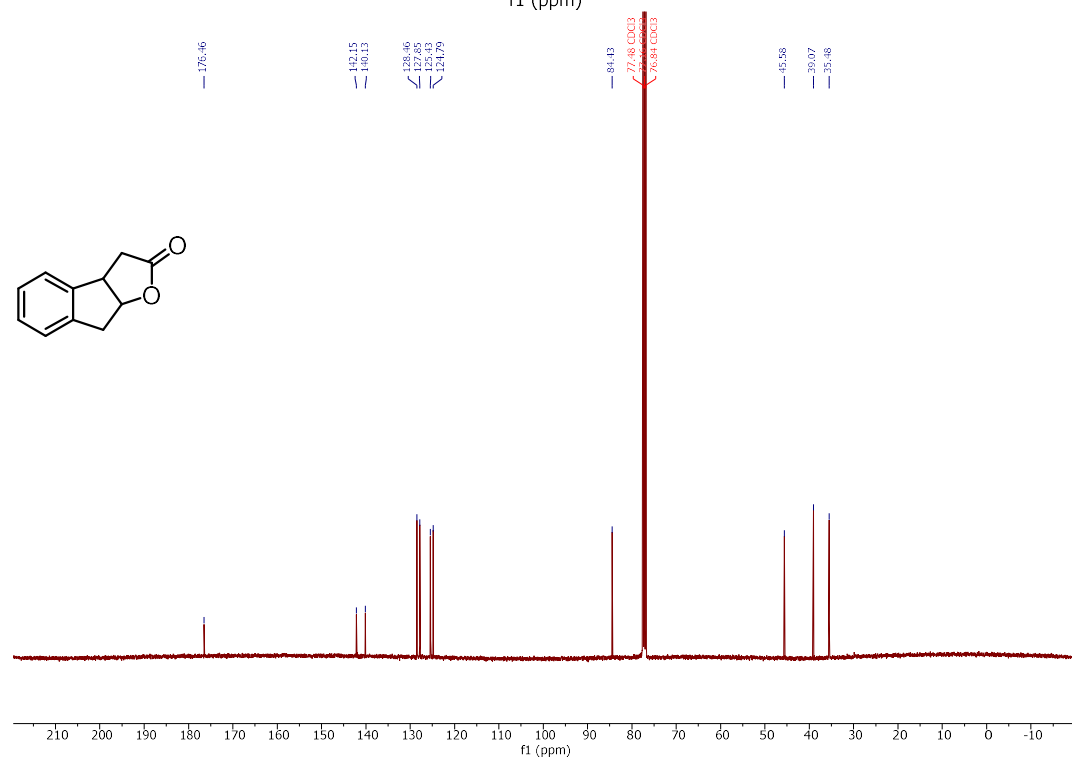
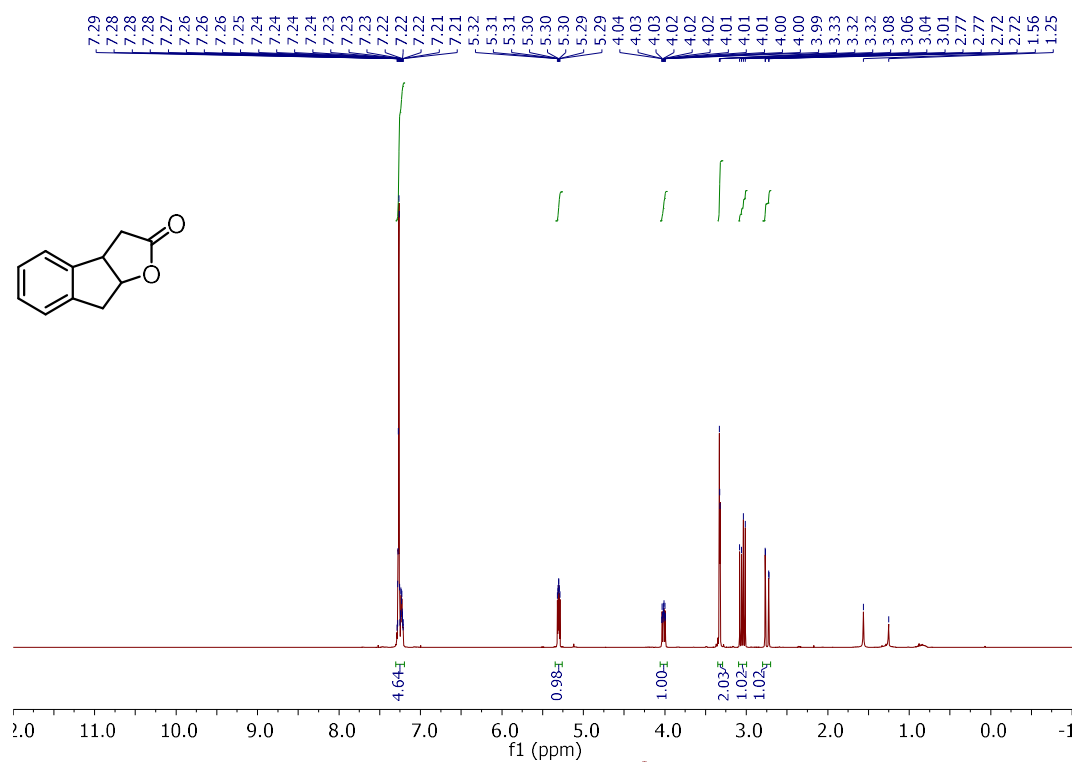
(E)-4-(4-methoxystyryl)oxepan-2-one (6b)



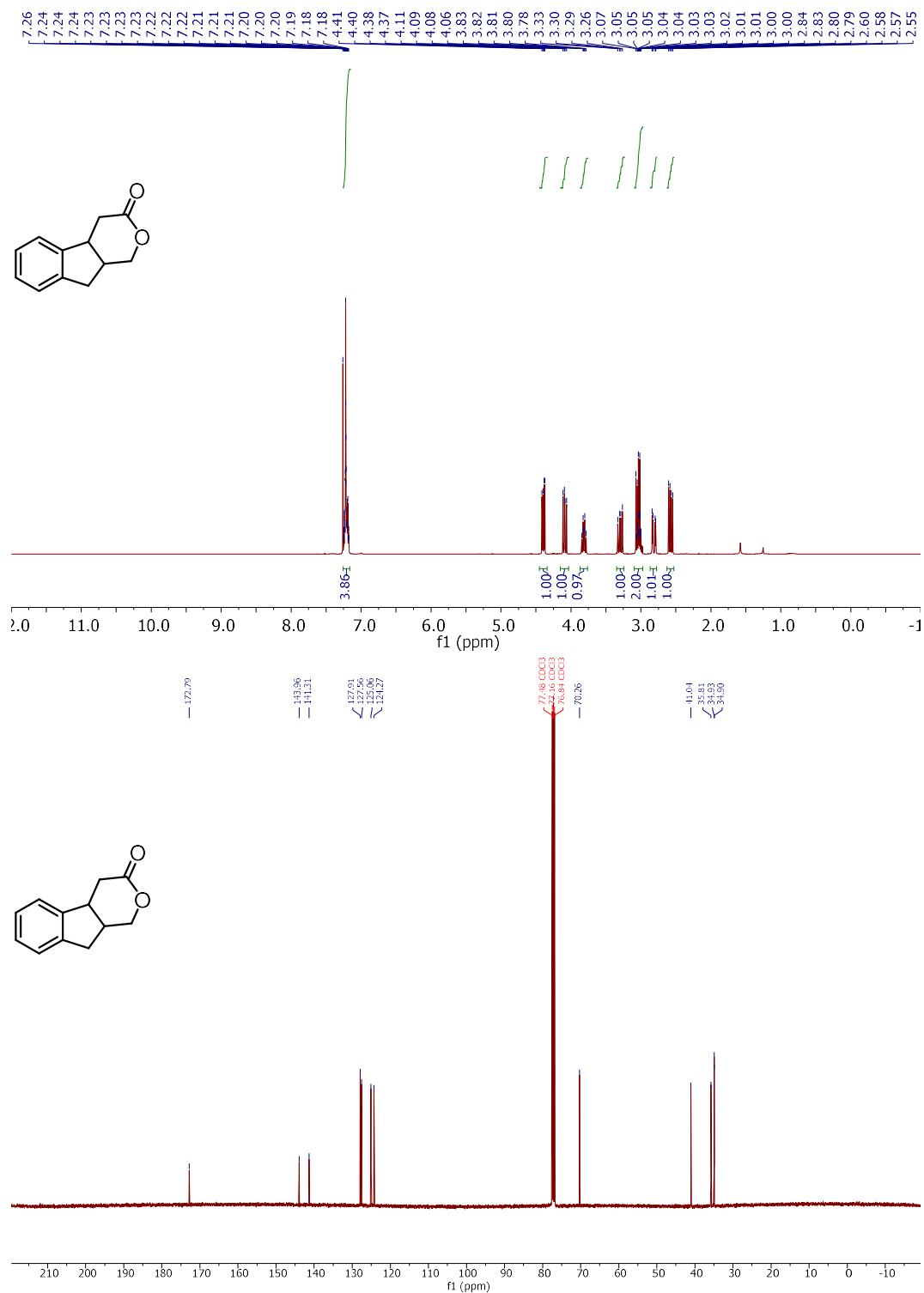
4-(1*H*-indol-3-yl)oxepan-2-one (6c)



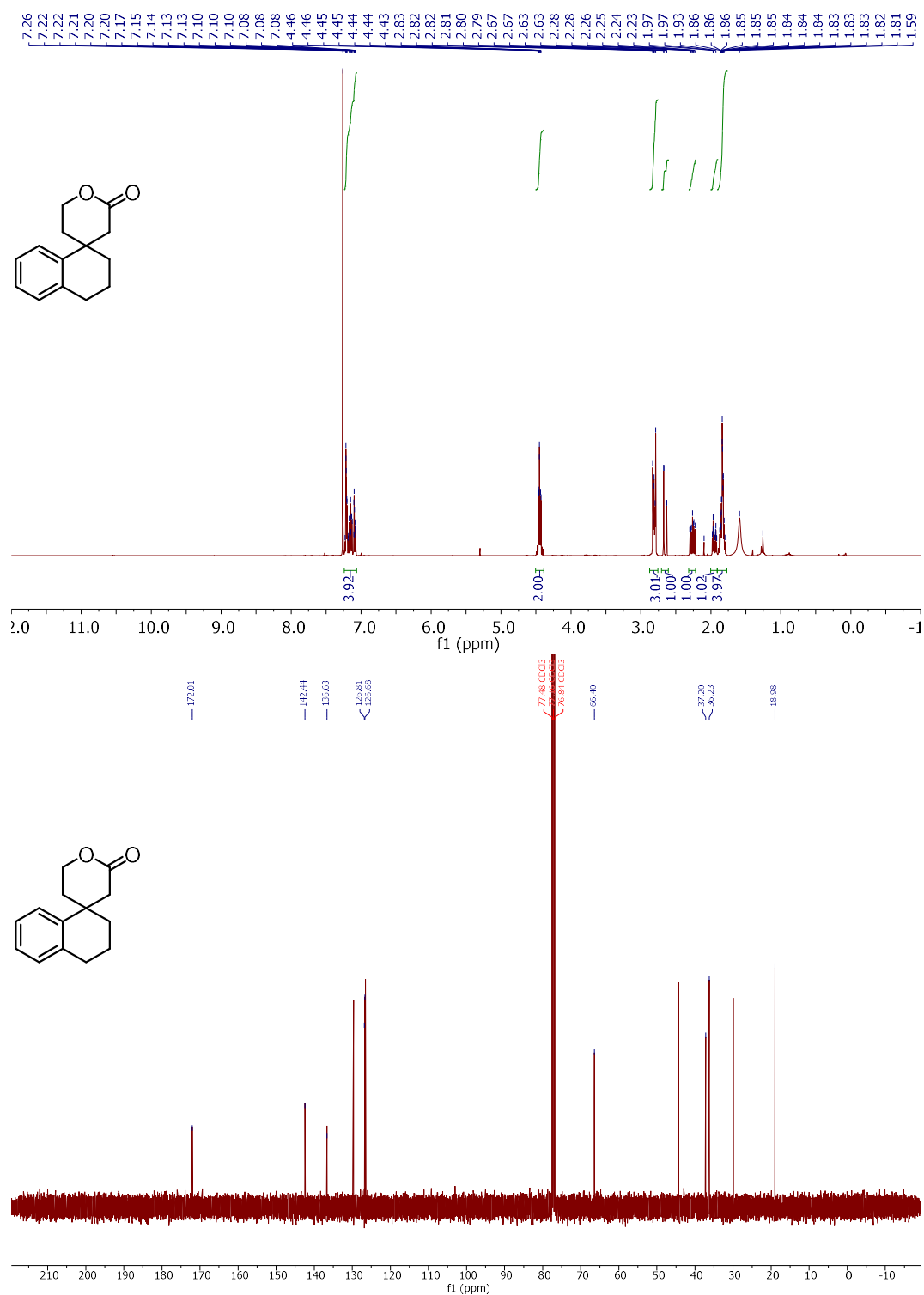
3,3a,8,8a-Tetrahydro-2*H*-indeno[2,1-*b*]furan-2-one (8a)



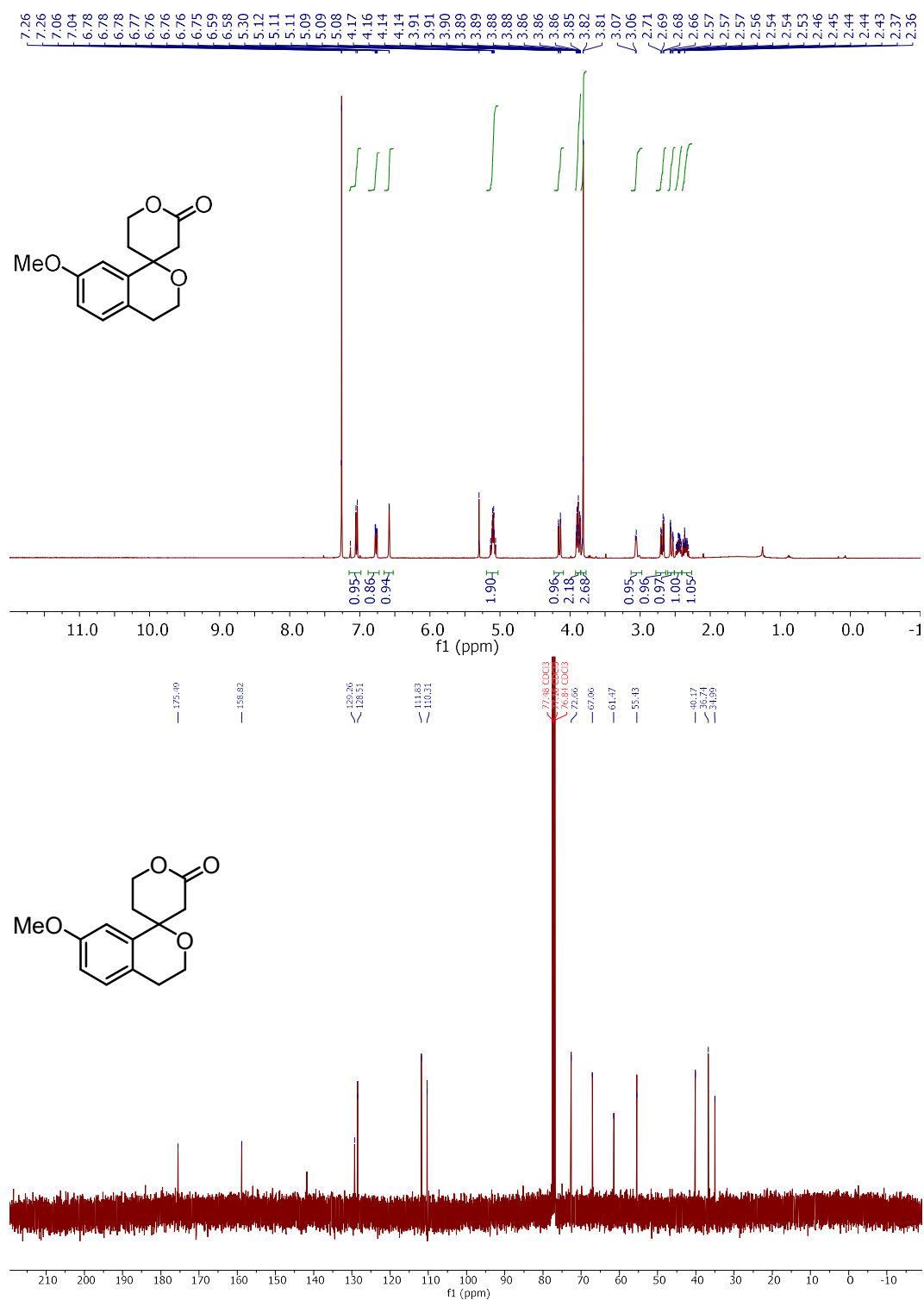
4,4a,9,9a-Tetrahydroindeno[2,1-c]pyran-3(1H)-one (8b)



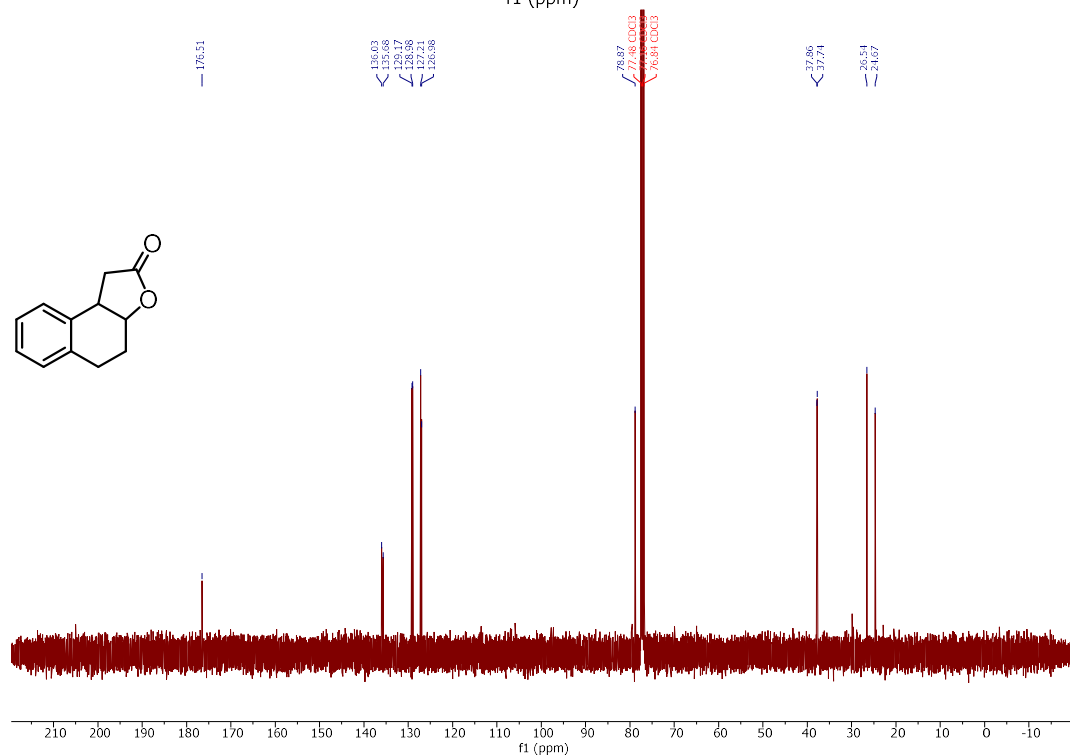
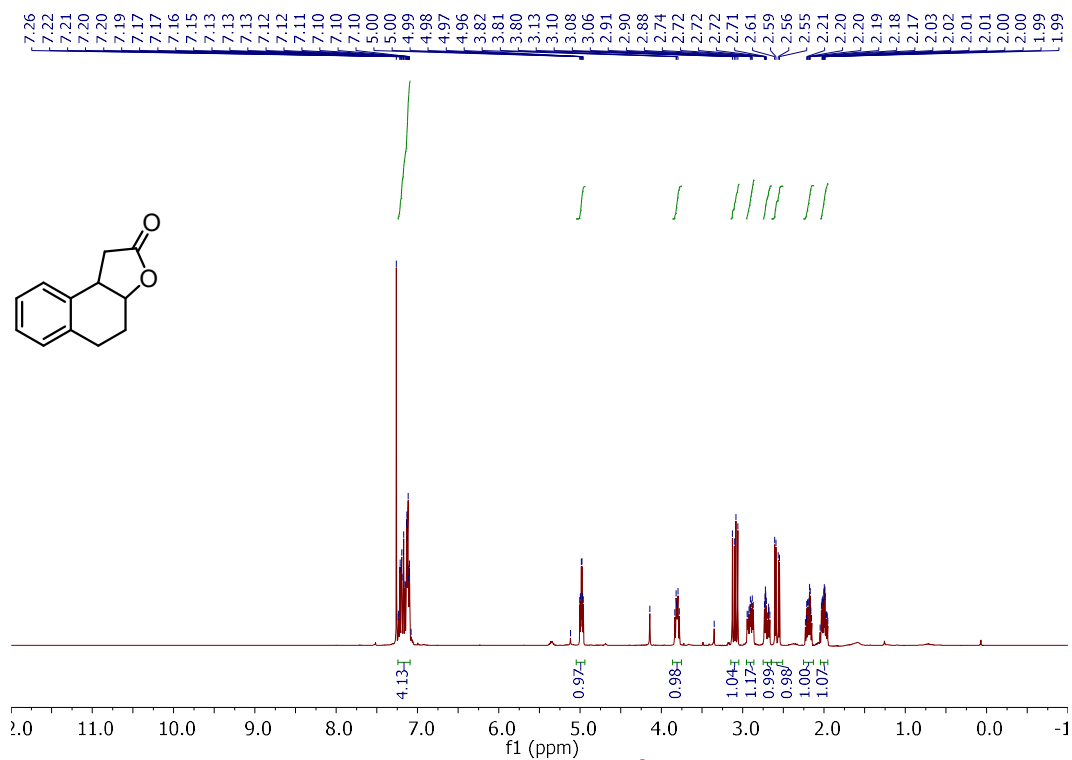
3,4,5',6'-tetrahydro-2H-spiro[naphthalene-1,4'-pyran]-2'(3'H)-one (8c)



7-methoxy-5',6'-dihydrospiro[isochromane-1,4'-pyran]-2'(3'H)-one (8d)

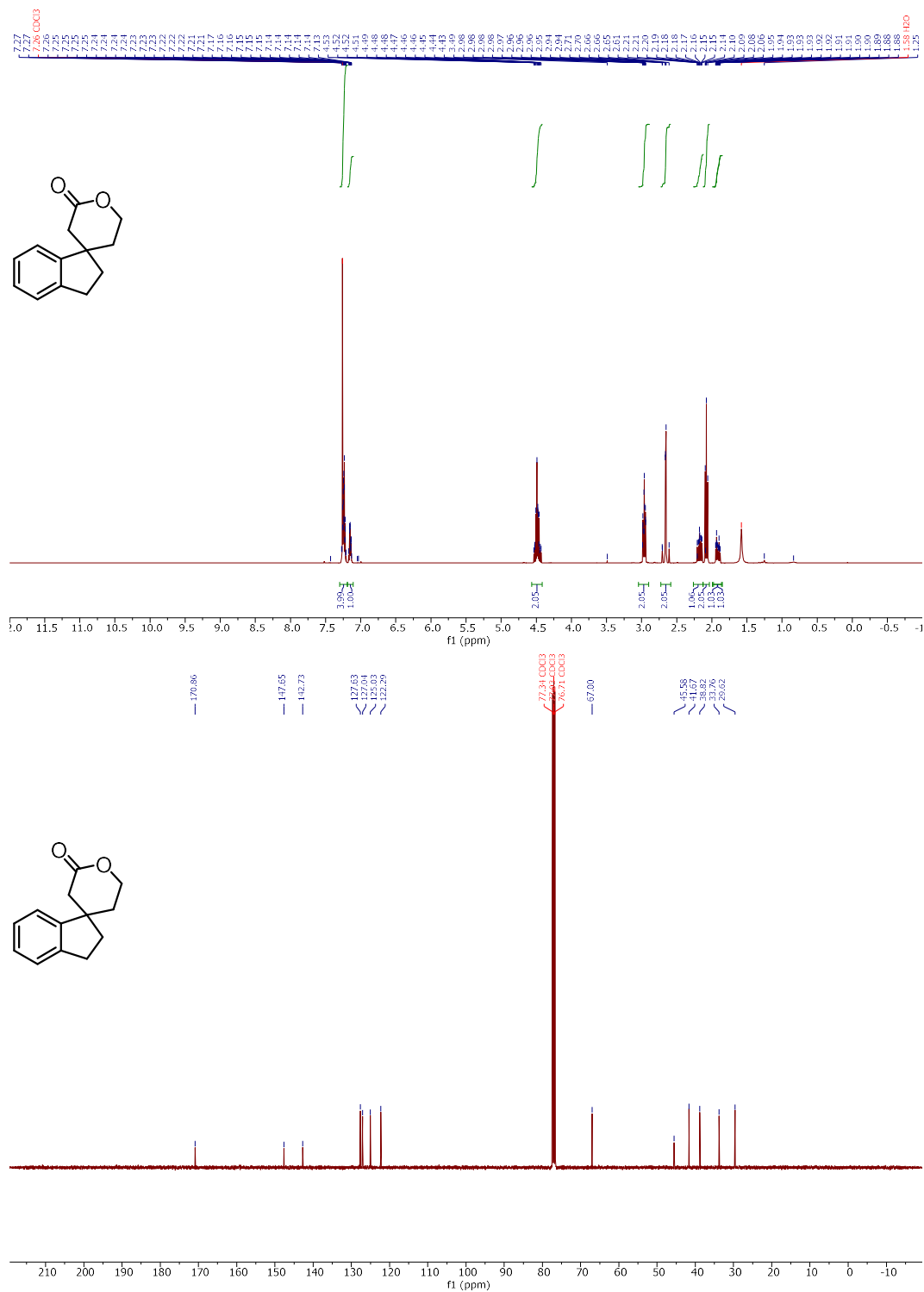


3a,4,5,9b-tetrahydronaphtho[2,1-*b*]furan-2(1*H*)-one (8e)

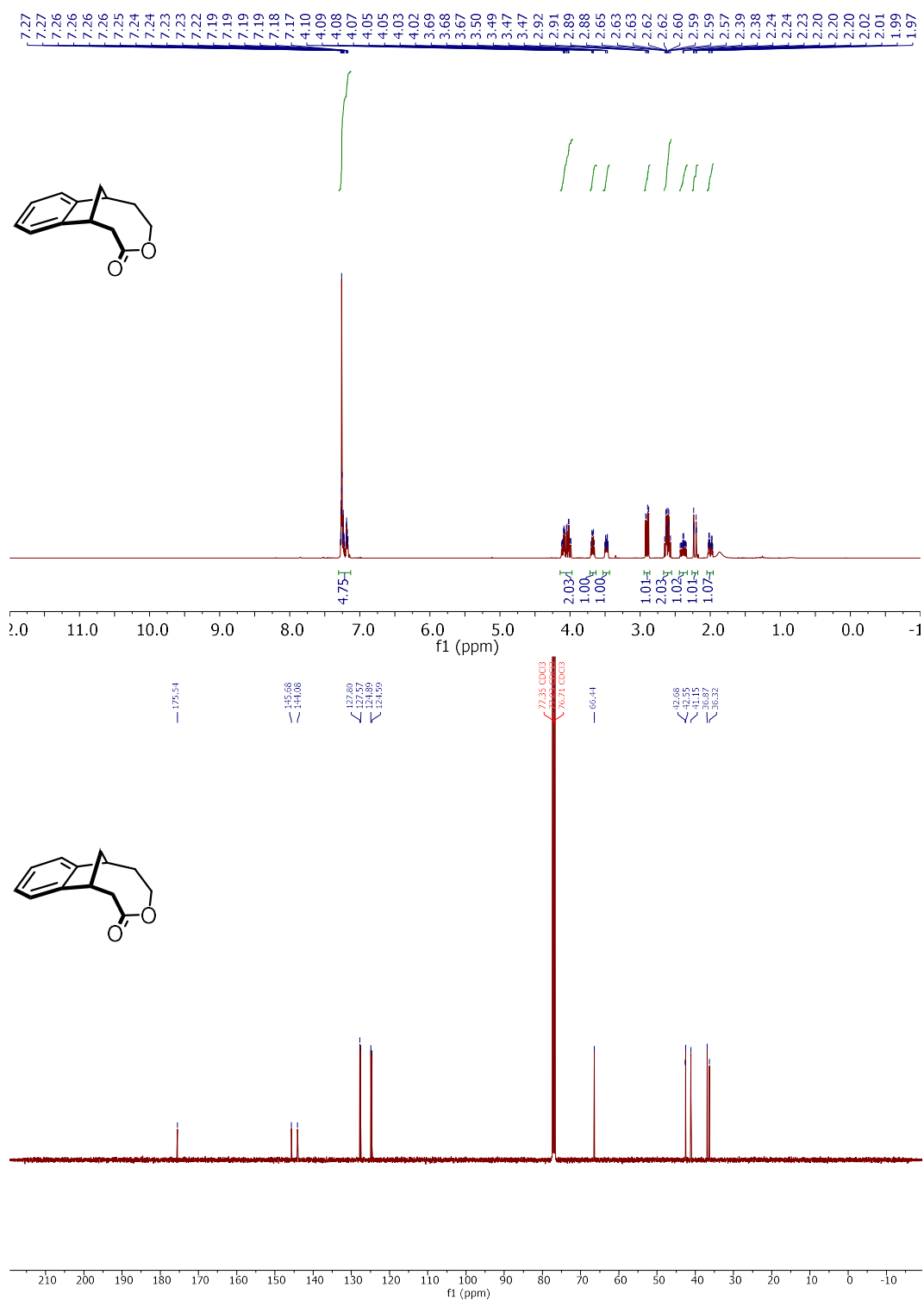


[illegible]

2,3,5',6'-tetrahydrospiro[indene-1,4'-pyran]-2'(3'*H*)-one (8f)



1,5,6,7-tetrahydro-1,7-methanobenzo[e]oxonin-3(2H)-one (8f')



10. References

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