

# Supporting Information

## Biocatalytic Construction of Chiral Pyrrolidines and Indolines *via* Intramolecular C(sp<sup>3</sup>)-H Amination

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## I. General Procedures

### **(A) General**

Unless otherwise noted, all chemicals and reagents were obtained from commercial suppliers (Millipore Sigma, VWR, Alfa Aesar, Ambeed, Combi-Blocks, TCI America, and Fisher Scientific) and used without further purification. Silica-gel chromatography was carried out using AMD Silica Gel 60, 230–400 mesh.  $^1\text{H}$  and  $^{13}\text{C}$  NMR spectra were recorded on a Varian Inova 300 MHz or Bruker 400 MHz instrument in  $\text{CDCl}_3$ . Data for  $^1\text{H}$  NMR are reported as follows: chemical shift ( $\delta$  ppm), multiplicity (s = singlet, d = doublet, t = triplet, q = quartet, hept = heptet, m = multiplet), coupling constant (Hz), and integration. Chemical reactions were monitored using thin-layer chromatography (Merck 60 silica gel plates) and a UV lamp for visualization. Sonication was performed using a Qsonica Q500 sonicator. High-resolution mass spectra HRMS were acquired from the Caltech Mass Spectral Facility using Field Desorption (FD-MS) with a JEOL AccuTOF GC-Alpha (JMS-T2000GC) mass spectrometer (enabled by funds from DOW next generation instrumentation). High-performance liquid-chromatography mass spectroscopy (HPLC-MS) for analysis was carried out using Agilent 1200 series instruments, with C18 (Kromasil®,  $4.6 \times 50$  mm,  $5 \mu\text{m}$ ) columns. Water and acetonitrile containing 0.1% acetic acid were used as eluents. Normal-phase chiral HPLC was performed using Daicel Chiralpak IC column ( $4.6 \times 250$  mm,  $5 \mu\text{m}$ ) with hexane and isopropanol as the mobile phase. Distilled water was utilized for growth media while double-distilled water was employed for all buffer preparations.

The M9-N buffer described in this study was prepared as follows:

A 5X stock solution was prepared by dissolving  $\text{Na}_2\text{HPO}_4$  (34 g),  $\text{KH}_2\text{PO}_4$  (15 g) and  $\text{NaCl}$  (2.5 g) in 1 L of water followed by sterilization by autoclaving. A 1X stock was then prepared by diluting 200 mL of the 5X solution to 1 L, followed by addition of 1 mL  $\text{CaCl}_2$  (0.1 M), 2 mL  $\text{MgSO}_4$  (1.0 M), and adjusting the pH to 7.4 or 8.4 by the addition of 6.0 M aqueous  $\text{NaOH}$ .

In all cases, commercially available cyclic amines (Sigma, Enamine, Ambeed, Combi-Blocks) were utilized as amine standards without further purification. These were acetylated with benzoyl chloride to give the corresponding acetyl amides for use as amide standards for enantioselectivity.

### **(B) Cloning, mutagenesis, and expression of enzymes**

Expression vector pET22b(+) (Novagen) was used for cloning and expression of all variants described in this paper. Site-saturation mutagenesis was performed using a modified QuikChange™ mutagenesis protocol using the 22-codon trick.<sup>1</sup> The PCR products were purified with New England Biolabs gel purification kit, and the gaps were repaired using Gibson Mix™.<sup>2</sup> Without further purification, 1  $\mu\text{L}$  of the Gibson product was used to transform 50  $\mu\text{L}$  of electrocompetent *Escherichia coli* cells. Electrocompetent *E. coli* BL21 *E. cloni*® (Lucigen) cells were utilized for all experiments. Luria-Bertani (LB) media were used for growth.

*E. coli* transformed with pET22b(+) constructs encoding various P411 variants were grown overnight (14 h to 16 h) in 5-mL LB medium supplemented with ampicillin ( $\text{LB}_{\text{amp}}$ ). Subsequently, 1 mL of this preculture was used to inoculate 49 mL of Hyper-Broth™ (HB, AthenaES) medium

in a 150-mL Erlenmeyer flask, supplemented with ampicillin (HB<sub>amp</sub>) and Glucose Mix for expression. The expression culture was incubated at 37 °C and shaken at 220 rpm for 2 hours until the optical cell density at 600 nm (OD<sub>600</sub>) was ~0.9–1.1. Then, the expression culture was cooled in an ice bath for 45–60 minutes and was treated with 1 mM 5-aminolevulinic acid (ALA) and 0.5 mM isopropyl β-D-1-thiogalactopyranoside (IPTG) (final concentrations). Cells were grown at 22 °C and 140 rpm for 20–24 hours, and the shaking radius was 25 mm. Once expression was finished, the cultures were centrifuged (4,000g, 6 minutes, 4 °C) and the pellets were resuspended to an OD<sub>600</sub> of 30–40 (or other appropriate OD as necessary) in M9-N buffer with pH adjusted to 8.4. This cell suspension was utilized to setup whole-cell reactions. Aliquots of the cell suspension (3–4 mL) were used to determine protein concentration after lysis by sonication.

### **(C) Determination of hemoprotein concentration**

The concentration of P411 enzymes in whole-cell experiments was determined from ferrous carbon monoxide binding difference spectra using the previously reported extinction coefficient for serine-ligated enzymes ( $\epsilon = 103,000 \text{ M}^{-1}\cdot\text{cm}^{-1}$ ).<sup>3</sup> Lysate was obtained by sonication (2 minutes, 1 second on, 1 second off, 30% amplitude, on wet ice). The cell debris was removed by centrifugation (14,000 × g, 10 minutes, 4 °C), and 180 μL of the supernatant were then transferred to a well in a 96-well UV-vis flat bottom plate (measurements were performed in quadruplicate). To each well, 20 μL of freshly prepared 0.5 M sodium dithionite aqueous solution were added. Absorbance measurements were performed on a Tecan Spark instrument before and after CO binding. The following formula was used for estimating protein concentration.

$$[\text{Enzyme}] (\mu\text{M}) = 1.1 * \frac{\Delta 411_{\text{CO-red}} - \Delta 490_{\text{CO-red}}}{0.74 \text{ cm} * 0.103 \mu\text{M}^{-1}\text{cm}^{-1}}$$

### **(D) Analytic reaction setup and product quantification**

All biocatalytic reactions were set up in an anaerobic chamber (oxygen level: <40 ppm).

- For pyrrolidine construction, 300 μL of resuspended cells (diluted to OD<sub>600</sub> = 40 with M9-N minimal buffer, pH = 8.4) were added to 2-mL screw cap vials, followed by addition of D-glucose (90 μL, 500 mM in M9-N buffer), M9-N buffer, and the azide substrate (10 μL of 100 mM stock solution in EtOH). Final concentrations were 2.5 mM alkyl azide and 112.5 mM D-glucose; final reaction volume was 400 μL. The vials were capped and then shaken inside coy chamber (600 rpm) at room temperature for 12–20 hours (overnight). After the reaction was completed and the vials were removed from the shaker, 400 μL of 2.5 mM internal standard (ethyl benzoate) acetonitrile solution were added. The mixture was transferred to a 2.0-mL Eppendorf tube and then subjected to vortexing (20 s × 2) and centrifugation (14,000 × g, 5 min, 4 °C). A sample of the supernatant (0.2 mL) was transferred to a vial with an insert for LC-MS analysis. Products were identified and quantified based on the corresponding reference compounds (**Section V** and **VI**). To further determine the enantiomeric excess (*ee*), the remaining supernatants of three parallel analytical reactions were combined and transferred to a 2-dram vial and the solvent was removed by blowing air. To the remaining residues from air blowing were added benzoyl chloride (60 μL of 1 M stock solution in acetonitrile) and 60 μL saturated NaHCO<sub>3</sub> solution. After shaking the vials overnight, the benzoyl-protected pyrrolidines were extracted to a solution of hexane and EtOAc mixture (1:1) and subjected to normal-phase HPLC to determine the *ee*.

• For indoline construction, 360  $\mu\text{L}$  of resuspended cells (diluted to  $\text{OD}_{600} = 45$  with M9-N minimal buffer,  $\text{pH} = 8.4$ ) were added to 2-mL screw cap vials, followed by D-glucose (30  $\mu\text{L}$ , 500 mM in M9-N buffer), M9-N buffer the azide substrate (10  $\mu\text{L}$  of 200 mM stock solution in EtOH). Final concentrations were 5.0 mM alkyl azide and 37.5 mM D-glucose; final reaction volume was 400  $\mu\text{L}$ . The vials were capped and then shaken inside coy chamber (600 rpm) at room temperature for 12–20 hours (overnight). After the reaction was completed and the vials were removed from the shaker, 400  $\mu\text{L}$  of 5.0 mM internal standard (1,2,3-trimethoxylbenzene) acetonitrile solution were added. The mixture was transferred to a 2.0-mL Eppendorf tube and then subjected to vortexing (20 s  $\times$  2) and centrifugation (14,000  $\times$  g, 5 min, 4  $^{\circ}\text{C}$ ). A sample of the supernatant (0.2 mL) was transferred to a vial with an insert for LC-MS analysis. Products were identified and quantified based on the corresponding reference compounds (**Section V** and **VI**). To further determine the enantiomeric excess (*ee*), the remaining supernatants of three parallel analytical reactions were combined and transferred to a 2-dram vial and the solvent was removed by blowing air. After shaking the vials for 1 hour, the indolines were extracted to a solution of hexane and EtOAc mixture (1:1) and subjected to normal-phase HPLC to determine the *ee*.

#### **(E) Reaction screening in 96-well plate in whole-cell format**

After a single-site saturation mutagenesis (SSM) library was generated, 88 single colonies were randomly picked and cultured in 300  $\mu\text{L}$  of LB medium with 0.1 mg/mL ampicillin ( $\text{LB}_{\text{amp}}$ ) in a sterilized 96-well culture plate. The plate typically contained six wells inoculated with single colonies expressing the parent enzyme and two sterile wells. The cultures were grown at 37  $^{\circ}\text{C}$ , 250 rpm, and 80% relative humidity for 13–15 hours. A separate, sterilized 96-well culture plate was filled with 950  $\mu\text{L}$  of Hyperbroth medium containing 0.1 mg/mL ampicillin ( $\text{HB}_{\text{amp}}$ ) in each well. Likewise, a glycerol stock replica plate of the preculture (50  $\mu\text{L}$  of preculture added to 50  $\mu\text{L}$  of 50% glycerol per well) was also prepared and stored at -80  $^{\circ}\text{C}$  for future reference. The plate with  $\text{HB}_{\text{amp}}$  was inoculated with the LB preculture (50  $\mu\text{L}$ /well), and incubated at 37  $^{\circ}\text{C}$ , 250 rpm, and 80% relative humidity for 2.5 hours. The plate was cooled on ice for 1 hour, induced with 0.5 mM IPTG and 1 mM ALA (final concentrations), and then expressed at 22  $^{\circ}\text{C}$  and 220 rpm for 21–23 hours. The cells were pelleted (4,000g, 6 minutes), and after removal of the supernatant, 390  $\mu\text{L}$  of M9-N ( $\text{pH} 7.4$ , 20 mM D-glucose) were added to each well. After the cell pellets were fully resuspended by shaking at 500 rpm, the 96-well plate was transferred to an anaerobic chamber. Inside the anaerobic chamber, to each well were added 10  $\mu\text{L}$  of a reactant stock solution in ethanol (100 or 200 mM stock solution, 2.5 or 5.0 mM final concentration). The plate was sealed with aluminum foil tape and shaken at 600 rpm in the anaerobic chamber at room temperature overnight.

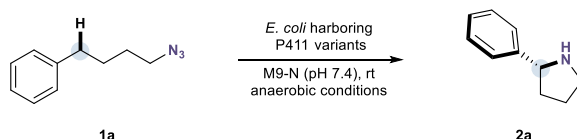
Once the plate was taken out of the anaerobic chamber and the seal was removed, ethanol (400  $\mu\text{L}$ /well) was added. The resulting suspension in the wells was mixed by vortexing and shaking. The plate was then centrifuged (5,000g, 5 minutes) to precipitate proteins and cell debris. The supernatant (200  $\mu\text{L}$ /well) was transferred to a shallow 96-well plate for reverse-phase HPLC-MS analysis. The MS product signals from each well were compared, and wells showing signals higher than the parent wells were identified. These ‘hits’ were recultured using the wells from the frozen replica glycerol stock plate and then sequenced. Among these, the activities of candidates showing mutations at the targeted site were revalidated in analytical scale reactions. In this way,

the best variant was selected as the final hit and was used as the parent for the next round of site-saturation mutagenesis.

## II. Directed Evolution of P411-PYS-5149 and P411-INS-5151 for Intramolecular C(sp<sup>3</sup>)-H Amination

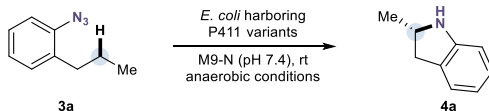
### Discovery of Initial Activity

The Arnold lab collection of heme enzymes (including P450s, P411s, protoglobins, and cytochromes *c*) was screened in 96-well-plate whole-cell reactions for product formation (see Section I.E). The collection consisted of nearly 400 distinct variants accumulated from prior directed evolution campaigns. For pyrrolidine synthesis, one variant from a previous carbene transferring lineage showed the highest product formation as assayed by LCMS. For indoline synthesis, the pyrrolidine synthase lineage showed the most promising results, and the 7<sup>th</sup> generation showed highest activity as assayed by LCMS. No product was detected in control reactions with free heme.



Pyrrolidine synthesis variants showing product formation:

Variant	Ion Count
P450-BM3 (WT)	0
P411-A330Y	2786747
<b>P411-M177L</b>	<b>4420892</b>



Indoline synthesis variants showing product formation:

Variant	Ion Count
P450-BM3 (WT)	0
P411-PYS-5146	2027686
<b>P411-PYS-5148</b>	<b>8380970</b>

**Table S1.** Detailed information of the evolutionary lineage for **PY**rrolidine Synthase (**PYS**).

P411-PYS variant	Yield (%)	<i>er</i>
<b>P411-M177L (P411-PYS-5141)</b>	4 ± 0.8	84:16
<b>P411-PYS-5141- L75E (P411-PYS-5142)</b>	13 ± 0.2	91:9
<b>P411-PYS-5141- L75E Q437L (P411-PYS-5143)</b>	13 ± 1.0	90:10
<b>P411-PYS-5141- L75E Q437L A330Q (P411-PYS-5144)</b>	20 ± 0.9	91:9
<b>P411-PYS-5141- L75E Q437L A330Q M118V(P411-PYS-5145)</b>	29 ± 1.6	93:7

<b>P411-PYS-5141-</b> L75E Q437L A330Q M118V F77C ( <b>P411-PYS-5146</b> )	31 ± 1.0	91:9
<b>P411-PYS-5141-</b> L75E Q437L A330Q M118V F77C S72W ( <b>P411-PYS-5147</b> )	53 ± 0.6	90:10
<b>P411-PYS-5141-</b> L75E Q437L A330Q M118V F77C S72W Q73A ( <b>P411-PYS-5148</b> )	54 ± 1.6	91:9
<b>P411-PYS-5141-</b> L75E Q437L A330Q M118V F77C S72W Q73A L436R ( <b>P411-PYS-5149</b> )	66 ± 3.5	91:9

**Table S2.** Detailed information of the evolutionary lineage for **IN**doline Synthase (**INS**).

<b>P411-INS</b> variant	<b>Yield (%)</b>	<b><i>er</i></b>
<b>P411-PYS-5148</b>	46 ± 3.2	51:49
<b>P411-PYS-5148-</b> L437P ( <b>P411-INS-5150</b> )	49 ± 1.7	88:12
<b>P411-PYS-5148-</b> L437P L181N ( <b>P411-INS-5151</b> )	52 ± 1.0	91:9

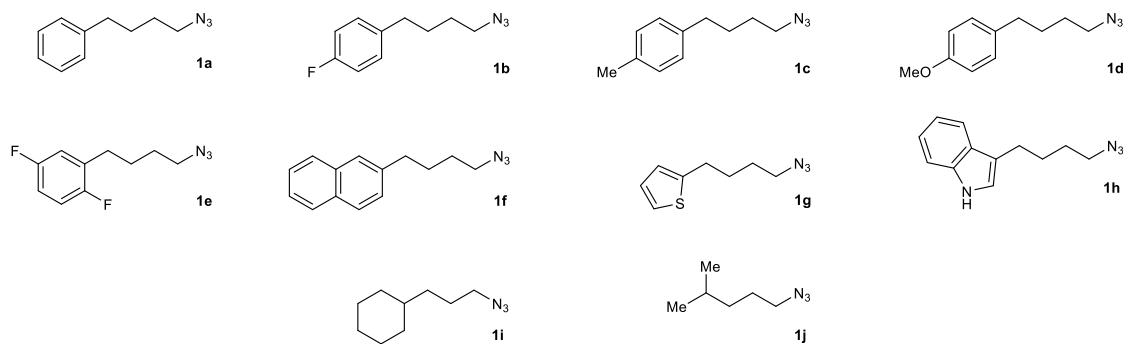
**Table S3.** Further information on directed evolution experiments.

<b>Round #</b>	<b>Parent</b>	<b>Sites targeted for SSM</b>	<b>Screen for activity or enantioselectivity</b>
1	<b>P411-PYS-5141</b>	75X	<b>activity</b>
2	<b>P411-PYS-5142</b>	78X, 87X, 263X, 268X, 327X, 328X, <b>437X</b>	<b>activity</b>
3	<b>P411-PYS-5143</b>	86X, 267X, <b>330X</b> , 400X	<b>activity</b>
4	<b>P411-PYS-5144</b>	82X, <b>118X</b> , 181X, 395X, 438X, 401X	<b>activity</b>
5	<b>P411-PYS-5145</b>	<b>77X</b> , 177X, 266X, 326X, 409X, 436X	<b>activity</b>
6	<b>P411-PYS-5146</b>	<b>72X</b> , 88X, 162X, 264X, 333X, 435X	<b>activity</b>
7	<b>P411-PYS-5147</b>	70X, 71X, <b>73X</b> , 74X, 76X, 178X, 269X, 331X, 332X	<b>activity</b>
8	<b>P411-PYS-5148</b>	87X, 267X, 268X, 327X, <b>436X</b> , 437X	<b>activity</b>
9	<b>P411-PYS-5148</b>	87X, 267X, 268X, 327X,	<b>both</b>

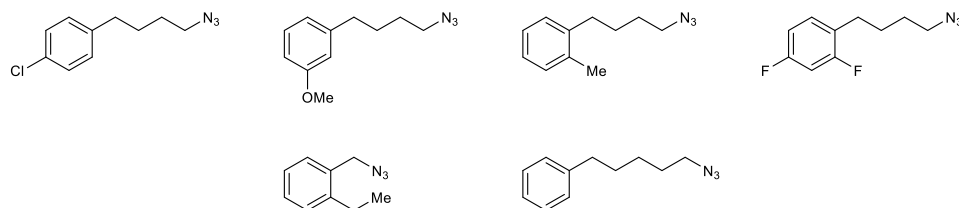
	<b>(for indoline synthesis)</b>	436X, <b>437X</b>	
10	<b>P411-INS-5149</b>	72X, 78X, 82X, <b>181X</b> , 188X, 438X	<b>both</b>



### III. Supporting Experimental Figures and Miscellaneous Experiments

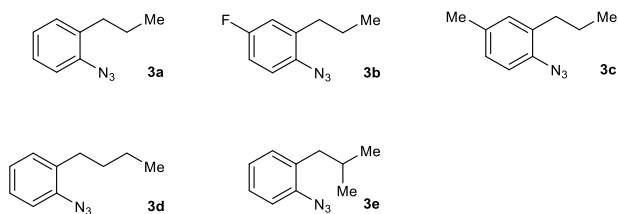


**Figure S1.** Summary of alkyl azide substrates (**1a–1j**).

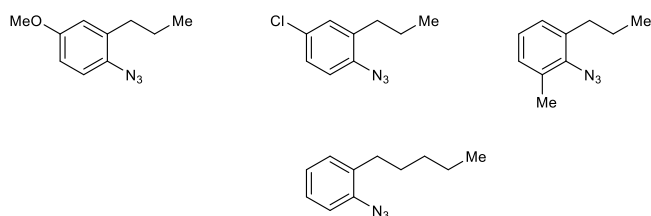


**Figure S2.** Other substrates tested for intramolecular alkyl nitrene  $\text{C}(\text{sp}^3)\text{--H}$  amination reaction.

*Notes:* The alkyl azide substrates listed here have been tested briefly for the intramolecular  $\text{C}(\text{sp}^3)\text{--H}$  amination chemistry catalyzed by **P411-PYS-5149**. However, these substrates only gave low activity, as preliminarily analyzed by LC-MS and chiral HPLC. These results are noteworthy, but they cannot be used for drawing final conclusions before further validation.

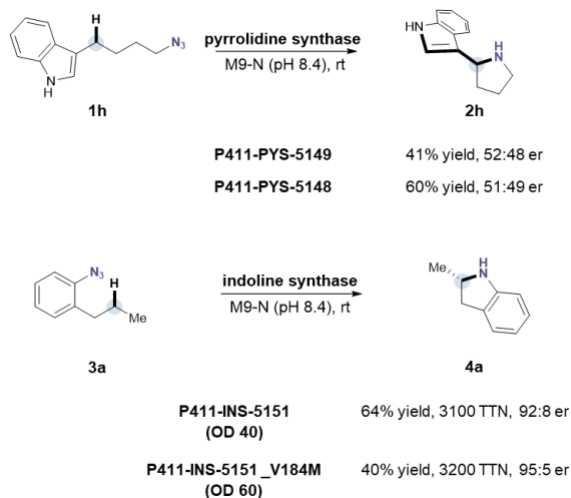


**Figure S3.** Summary of aryl azide substrates (**1a–1j**).



**Figure S4.** Other substrates tested for intramolecular aryl nitrene C(sp<sup>3</sup>)–H amination reaction.

*Notes:* The aryl azide substrates listed here have been tested briefly for the intramolecular C(sp<sup>3</sup>)–H amination chemistry catalyzed by **P411-INS-5151**. However, these substrates only gave low activity, as preliminarily analyzed by LC-MS and chiral HPLC. These results are noteworthy, but they cannot be used for drawing final conclusions before further validation.



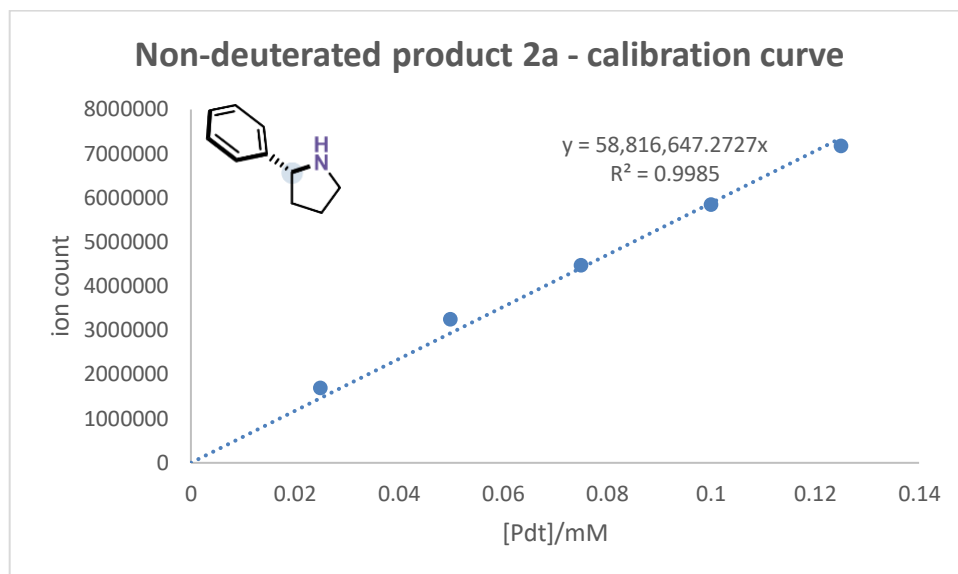
**Figure S5.** Variants that showed improved activity or selectivity for examples **1h** and **3a**.

*Notes:* Variant **P411-PYS-5148** (CA-G7) is the seventh generation of ‘pyrrolidine synthase’ lineage. Variant **P411-INS-5151\_V184M** has one mutation (V184M) relative to **P411-INS-5151** (AN-G2).

### Kinetic Isotope Effect (KIE) studies

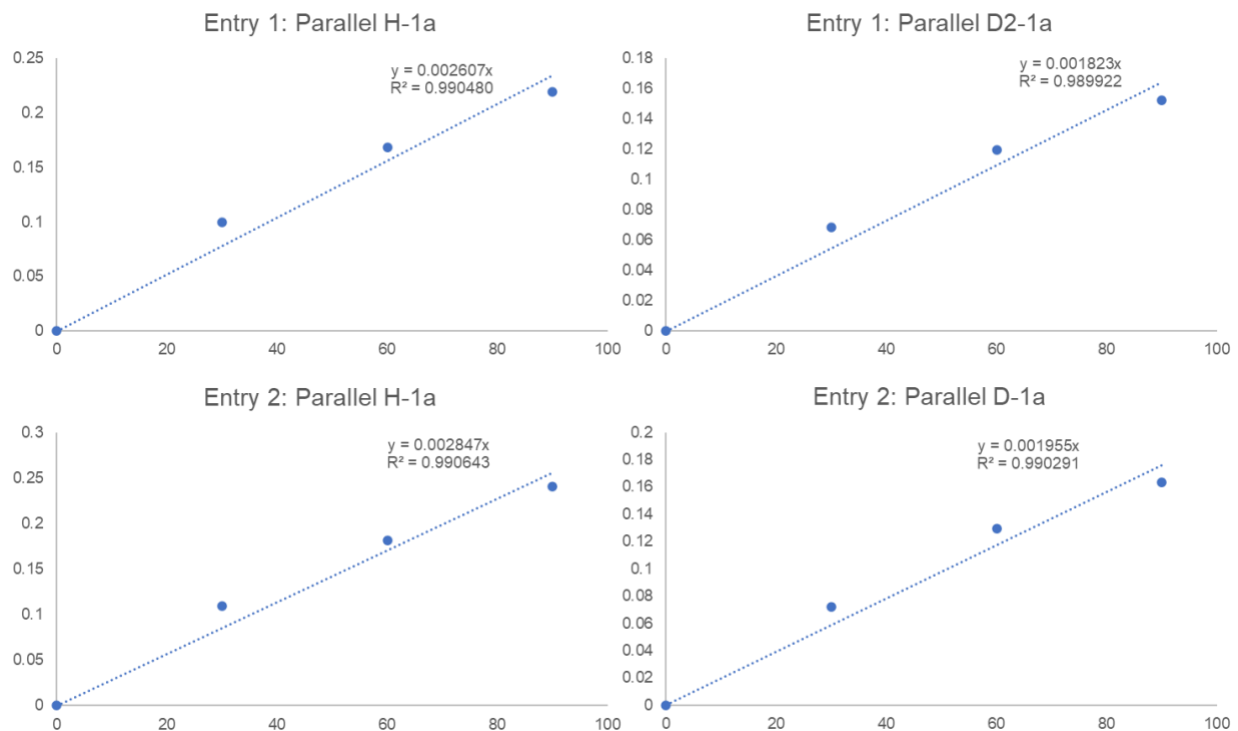
From a freshly streaked plate of *E. coli* cells with the **P411-PYS-5149** plasmid, two single colonies were inoculated into two separate, 4-mL LB media tubes for ~14 h at 37 °C. These were utilized for duplicate experiments. After growing the overnight culture for ~14 h, 1 mL of the starter culture was transferred to 49 mL HB media (supplemented with Ampicillin and Glucose Mix) in a 150-mL Erlenmeyer flask and grown with vigorous shaking at 37 °C (230 rpm) for 2 h, by which time the cell optical density (OD<sub>600</sub>) was 0.8 to 1.0. The flask was chilled on ice for 45 min. ALA (1 mM) and IPTG (0.5 mM) were supplemented, and the flask shaken at 22 °C (140 rpm) for 22 h. The culture was centrifuged (4,000g, 6 min), and the cell pellets were resuspended in 12 mL of M9-N buffer (pH 8.4) to give a suspension with OD<sub>600</sub>~40. All manipulations were done on ice. Reaction setup follows the standard procedure mentioned in **Section I (D)**.

- Calibration curve of non-deuterated product **2a** at low yields (using ion count in single-mass channel to quantify)



- Non-competitive KIE Experiments

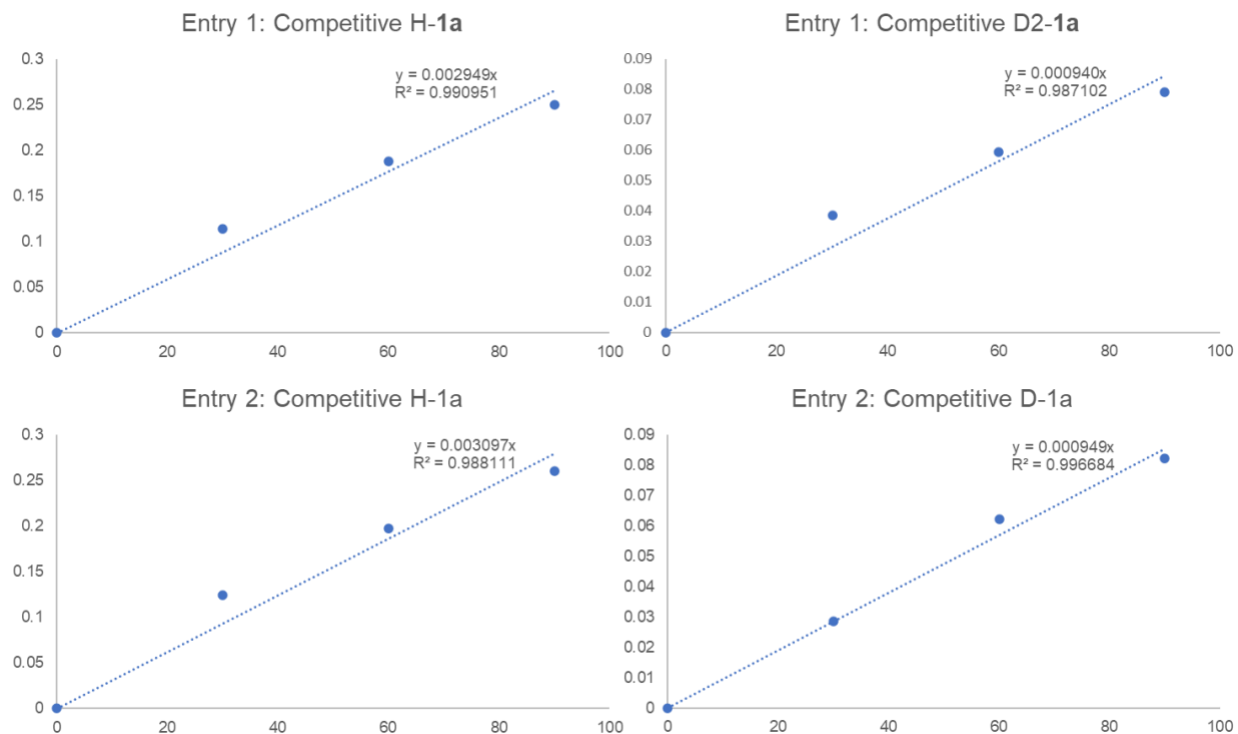
Entry	Subs	Ion Count			Yield (%)			$K_{H/D}$	KIE ( $K_H/K_D$ )
		30 s	60 s	90 s	30 s	60 s	90 s		
1	H-1a	146156	247766	176056	0.099	0.169	0.220	0.00261	1.43
	D-1a	100606	176056	224437	0.068	0.120	0.153	0.00182	
2	H-1a	161435	267685	353785	0.110	0.182	0.241	0.00285	1.45
	D-1a	105536	190294	240509	0.072	0.129	0.164	0.00196	



**Figure S6.** Duplicate of non-competitive kinetic isotope effect (KIE) experiments

• Competitive KIE Experiments

Entry	Subs	Ion Count			Yield (%)			$K_{H/D}$	KIE ( $K_H/K_D$ )
		30 s	60 s	90 s	30 s	60 s	90 s		
1	1:1	167110	276341	367201	0.114	0.188	0.250	0.00295	3.14
	H/D-1a	56674	87321	116399	0.039	0.059	0.079	0.00094	
2	1:1	182657	290499	382915	0.124	0.198	0.260	0.00310	3.26
	H/D-1a	42133	91205	120526	0.028	0.062	0.082	0.00095	



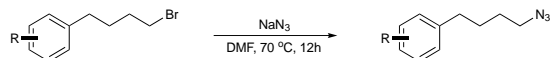
**Figure S7.** Duplicate of competitive kinetic isotope effect (KIE) experiments

• KIE Experiments Summary

Entry		KIE	Avg. KIE	SD KIE	KIE
Non-competitive KIE	1	1.43	1.44	0.01	$1.44 \pm 0.01$
	2	1.45			
Competitive KIE	1	3.14	3.20	0.08	$3.20 \pm 0.08$
	2	3.26			

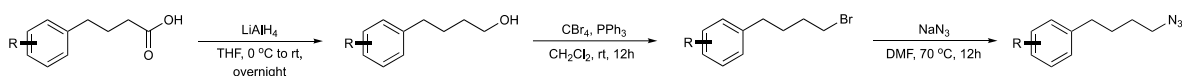
## IV. Preparation and Characterization of the Azide Substrates

### General procedure A:<sup>4</sup>



To a 100-mL flask were added alkyl bromide (5.0 mmol, 1.0 equiv.), sodium azide (487.6 mg, 7.5 mmol, 1.5 equiv.), and anhydrous DMF (50 mL). The mixture was stirred at 70 °C for 12 h, then cooled to room temperature, and diluted with diethyl ether/water (50 mL, 1:1). The product was extracted by diethyl ether (30 mL  $\times$  3), and the combined organic layer was washed with brine (50 mL). The organic phase was further dried over Na<sub>2</sub>SO<sub>4</sub> and concentrated to afford a yellow residue. Flash column chromatography was performed to afford pure product in 60% to 80% yield.

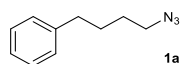
### General procedure B:



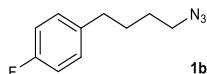
**LAH reduction:**<sup>5</sup> To a round-bottom flask containing carboxylic acids (1.0 equiv.) and anhydrous THF (0.1 M) at 0 °C was slowly added LiAlH<sub>4</sub> (5.0 equiv.). The mixture was gradually warmed to room temperature and stirred for 18 h. Fieser method was conducted to workup the LAH reduction. After filtration, the organic phase was dried over Na<sub>2</sub>SO<sub>4</sub>, and further concentrated to afford a yellow residue. Flash column chromatography was performed to afford pure product in quantitative yield.

**Bromination:**<sup>6</sup> To a round-bottom flask containing alcohols (1.0 equiv.) and anhydrous dichloromethane (DCM, 0.3 M) was added CBr<sub>4</sub> (1.2 equiv.) and PPh<sub>3</sub> (1.2 equiv.) sequentially. The mixture was stirred at room temperature for 4 h before quenching with saturated aqueous NaHCO<sub>3</sub> and extracted with DCM ( $\times$  3). The combined organic layer was washed with brine, further dried with Na<sub>2</sub>SO<sub>4</sub>, and concentrated to afford a colored residue. Flash column chromatography was performed to afford pure product in 70% to 80% yield.

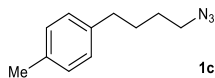
**Azidation:** To a round-bottom flask were added alkyl bromide (1.0 equiv.), sodium azide (1.5 equiv.), and anhydrous DMF (0.1 M). The mixture was stirred at 70 °C for 12 h, then cooled to room temperature, and diluted with diethyl ether/water (1:1). The product was extracted by diethyl ether ( $\times$  3), and the combined organic layer was washed with brine (50 mL). The organic phase was further dried over Na<sub>2</sub>SO<sub>4</sub> and concentrated to afford a yellow residue. Flash column chromatography was performed to afford pure product in 60% to 80% yield.



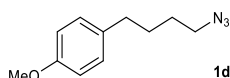
**1a (4-azidobutyl)benzene (1a):** The synthesis was conducted through general procedure A. <sup>1</sup>H NMR (400 MHz, CDCl<sub>3</sub>)  $\delta$  7.33 – 7.24 (m, 2H), 7.23 – 7.13 (m, 3H), 3.29 (t,  $J$  = 6.6 Hz, 2H), 2.65 (t,  $J$  = 7.4 Hz, 2H), 1.78 – 1.58 (m, 4H). <sup>13</sup>C NMR (101 MHz, CDCl<sub>3</sub>)  $\delta$  142.0, 128.5, 128.5, 126.0, 51.5, 35.5, 28.6.



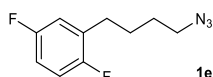
**1b 1-(4-azidobutyl)-4-fluorobenzene (1b):** The synthesis was conducted through general procedure B.  $^1\text{H}$  NMR (400 MHz,  $\text{CDCl}_3$ )  $\delta$  7.15 – 7.03 (m, 4H), 3.28 (t,  $J$  = 6.7 Hz, 2H), 2.61 (t,  $J$  = 7.3 Hz, 2H), 2.32 (s, 3H), 1.78 – 1.57 (m, 4H).  $^{13}\text{C}$  NMR (101 MHz,  $\text{CDCl}_3$ )  $\delta$  161.4 (d,  $J$  = 243.5 Hz), 137.5 (d,  $J$  = 3.2 Hz), 129.8 (d,  $J$  = 7.7 Hz), 115.3 (d,  $J$  = 21.2 Hz), 51.4, 34.7, 28.7, 28.5.  $^{19}\text{F}$  NMR (376 MHz,  $\text{CDCl}_3$ )  $\delta$  -117.6.



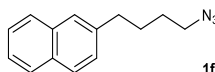
**1c 1-(4-azidobutyl)-4-methylbenzene (1c):** The synthesis was conducted through general procedure B.  $^1\text{H}$  NMR (400 MHz,  $\text{CDCl}_3$ )  $\delta$  7.14 – 7.02 (m, 4H), 3.28 (t,  $J$  = 6.5 Hz, 2H), 2.61 (t,  $J$  = 7.2 Hz, 2H), 2.32 (s, 3H), 1.76 – 1.57 (m, 4H).  $^{13}\text{C}$  NMR (101 MHz,  $\text{CDCl}_3$ )  $\delta$  138.9, 135.5, 129.2, 128.4, 51.5, 35.0, 28.7, 28.6, 21.1.



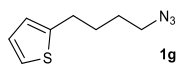
**1d 1-(4-azidobutyl)-4-methoxybenzene (1d):** The synthesis was conducted through general procedure A.  $^1\text{H}$  NMR (400 MHz,  $\text{CDCl}_3$ )  $\delta$  7.13 – 7.06 (m, 2H), 6.87 – 6.79 (m, 2H), 3.79 (s, 3H), 3.28 (t,  $J$  = 6.5 Hz, 2H), 2.59 (t,  $J$  = 7.2 Hz, 2H), 1.74 – 1.56 (m, 4H).  $^{13}\text{C}$  NMR (101 MHz,  $\text{CDCl}_3$ )  $\delta$  158.0, 134.0, 129.4, 113.9, 55.4, 51.5, 34.6, 28.8, 28.5.



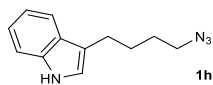
**1e 2-(4-azidobutyl)-1,4-difluorobenzene (1e):** The synthesis was conducted through general procedure B.  $^1\text{H}$  NMR (400 MHz,  $\text{CDCl}_3$ )  $\delta$  6.96 (td,  $J$  = 8.8, 4.4 Hz, 1H), 6.92 – 6.80 (m, 2H), 3.30 (t,  $J$  = 6.5 Hz, 2H), 2.65 (t,  $J$  = 6.7 Hz, 2H), 1.74 – 1.60 (m, 4H).  $^{13}\text{C}$  NMR (101 MHz,  $\text{CDCl}_3$ )  $\delta$  158.7 (d,  $J$  = 239.4 Hz), 157.2 (d,  $J$  = 240.6 Hz), 130.5 (dd,  $J$  = 18.7, 7.7 Hz), 116.9 (dd,  $J$  = 23.6, 5.3 Hz), 116.3 (dd,  $J$  = 25.4, 8.8 Hz), 114.0 (dd,  $J$  = 24.0, 8.6 Hz), 51.3, 28.6, 28.5, 27.1.  $^{19}\text{F}$  NMR (376 MHz,  $\text{CDCl}_3$ )  $\delta$  -119.6 (d,  $J$  = 18.0 Hz), -125.0 (d,  $J$  = 18.0 Hz).



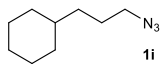
**1f 2-(4-azidobutyl)naphthalene (1f):** The synthesis was conducted through general procedure B.  $^1\text{H}$  NMR (400 MHz,  $\text{CDCl}_3$ )  $\delta$  7.79 (ddd,  $J$  = 10.9, 7.7, 1.1 Hz, 3H), 7.61 (dd,  $J$  = 1.8, 0.9 Hz, 1H), 7.55 – 7.38 (m, 2H), 7.33 (dd,  $J$  = 8.5, 1.7 Hz, 1H), 3.31 (t,  $J$  = 6.8 Hz, 2H), 2.82 (t,  $J$  = 7.7 Hz, 2H), 1.87 – 1.74 (m, 2H), 1.74 – 1.59 (m, 2H).  $^{13}\text{C}$  NMR (101 MHz,  $\text{CDCl}_3$ )  $\delta$  139.4, 133.7, 132.2, 128.1, 127.8, 127.6, 127.3, 126.6, 126.1, 125.3, 51.5, 35.6, 28.6, 28.4.



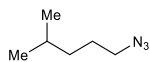
**1g 2-(4-azidobutyl)thiophene (1g):** The synthesis was conducted through general procedure B.  $^1\text{H}$  NMR (400 MHz,  $\text{CDCl}_3$ )  $\delta$  7.13 (dd,  $J$  = 5.1, 1.2 Hz, 1H), 6.92 (dd,  $J$  = 5.1, 3.4 Hz, 1H), 6.79 (dq,  $J$  = 3.2, 1.0 Hz, 1H), 3.30 (t,  $J$  = 6.7 Hz, 2H), 2.87 (td,  $J$  = 7.3, 1.0 Hz, 2H), 1.83 – 1.72 (m, 2H), 1.72 – 1.61 (m, 2H).  $^{13}\text{C}$  NMR (101 MHz,  $\text{CDCl}_3$ )  $\delta$  144.7, 126.9, 124.4, 123.3, 51.4, 29.5, 28.9, 28.4.



**1h 3-(4-azidobutyl)-1H-indole (1h):** The synthesis was conducted through general procedure B.  $^1\text{H}$  NMR (400 MHz,  $\text{CDCl}_3$ )  $\delta$  7.92 (s, 1H), 7.61 (dq,  $J$  = 7.8, 0.9 Hz, 1H), 7.37 (dt,  $J$  = 8.1, 0.9 Hz, 1H), 7.21 (ddd,  $J$  = 8.1, 7.0, 1.2 Hz, 1H), 7.13 (ddd,  $J$  = 8.0, 7.0, 1.1 Hz, 1H), 6.99 (dt,  $J$  = 2.0, 0.9 Hz, 1H), 3.31 (t,  $J$  = 6.8 Hz, 2H), 2.81 (td,  $J$  = 7.4, 0.9 Hz, 2H), 1.86 – 1.76 (m, 2H), 1.76 – 1.66 (m, 2H).  $^{13}\text{C}$  NMR (101 MHz,  $\text{CDCl}_3$ )  $\delta$  136.5, 127.6, 122.1, 121.3, 119.3, 119.0, 116.3, 111.2, 51.6, 28.8, 27.3, 24.8.

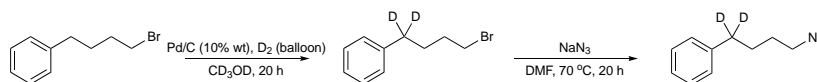


**1i (3-azidopropyl)cyclohexane (1i):** The synthesis was conducted through general procedure A.  $^1\text{H}$  NMR (400 MHz,  $\text{CDCl}_3$ )  $\delta$  3.24 (t,  $J$  = 7.0 Hz, 2H), 1.75 – 1.51 (m, 7H), 1.27 – 1.08 (m, 6H), 0.89 (tt,  $J$  = 11.6, 6.4 Hz, 2H).  $^{13}\text{C}$  NMR (101 MHz,  $\text{CDCl}_3$ )  $\delta$  52.0, 37.5, 34.6, 33.4, 26.7, 26.5, 26.4.



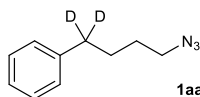
**1j 1-azido-4-methylpentane (1j):** The synthesis was conducted through general procedure A.  $^1\text{H}$  NMR (400 MHz,  $\text{CDCl}_3$ )  $\delta$  3.25 (t,  $J$  = 7.0 Hz, 2H), 1.68 – 1.51 (m, 3H), 1.30 – 1.20 (m, 2H), 0.90 (d,  $J$  = 6.6 Hz, 6H).  $^{13}\text{C}$  NMR (101 MHz,  $\text{CDCl}_3$ )  $\delta$  51.9, 36.0, 27.9, 26.9, 22.6.

### General procedure C:<sup>7</sup>



A mixture of (4-bromobutyl)benzene (0.53 g, 2.5 mmol, 1.0 equiv.) and Pd/C (10 wt%, 0.33 g, 60 mol%) in  $\text{CD}_3\text{OD}$  (5 mL) was placed under nitrogen and equipped with a deuterium balloon. After 20 h of reaction the mixture was filtered over celite, and the product diluted with diethyl ether (20 mL). The solution was washed with water (20 mL) and a saturated aqueous solution of sodium bicarbonate ( $\times$  2). The organic fraction was dried over  $\text{MgSO}_4$  filtered and solvent removed to yield 4-bromo-1,1-bisdeutero-1-phenylbutane as a colorless oil which was used in the next step without additional purification.

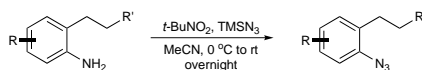
The obtained 4-bromo-1,1-bisdeutero-1-phenylbutane was dissolved in DMF (10 mL) and sodium azide was added to the stirred solution. After heating at 70 °C for 20 hours the mixture was cooled to room temperature and water (20 mL) was added. The product was extracted with diethyl ether (20 mL), and the organic fraction was washed with water ( $5 \times 30$  mL), dried over  $\text{MgSO}_4$ , filtered and concentrated to afford a yellow residue. Flash column chromatography was performed to afford pure product as a colorless oil (0.25 g, 1.4 mmol, 90% deuteration rate, 56% overall yield).



**1aa (4-azidobutyl-1,1-d<sub>2</sub>)benzene (1aa):** The synthesis was conducted through general procedure C (90% deuteration rate).  $^1\text{H}$  NMR (400 MHz,  $\text{CDCl}_3$ )  $\delta$  7.29 (tt,  $J$  = 6.9, 0.9 Hz, 2H), 7.23 – 7.16 (m, 3H), 3.29 (t,  $J$  = 6.6 Hz, 2H), 1.75 – 1.59 (m, 3H).  $^{13}\text{C}$  NMR (101 MHz,  $\text{CDCl}_3$ )  $\delta$  141.8, 128.4, 128.4, 125.9, 51.4, 35.2 – 34.4, 28.4, 28.3.

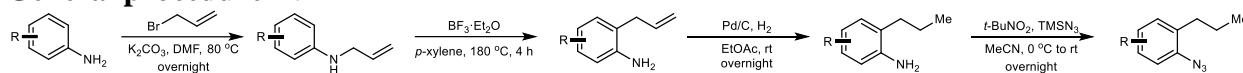


### General procedure D:<sup>8</sup>



To a 100-mL flask at 0 °C were added aniline (1.0 equiv.), MeCN (0.4 M), *t*-BuNO<sub>2</sub> (4.0 equiv.), and TMSN<sub>3</sub> (3.0 equiv.) dropwise, then the flask was warmed to room temperature and stirred overnight. De-ionized water was added after completion, the reaction mixture was extracted by diethyl ether (× 3), and the combined organic layer was washed with brine. The organic phase was further dried over Na<sub>2</sub>SO<sub>4</sub> and concentrated to afford a yellow residue. Flash column chromatography was performed to afford pure product in 50% to 70% yield.

### General procedure E:<sup>9</sup>

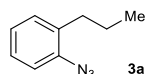


**Allylation:** To a 100-mL round-bottom flask were added aniline (1.0 equiv.), K<sub>2</sub>CO<sub>3</sub> (2.4 equiv.), DMF (0.4 M) and allyl bromide (1.0 equiv.) dropwise. The solution was sealed and heated to 80 °C overnight. The reaction mixture was filtered, washed with H<sub>2</sub>O, and extracted with ethyl acetate twice. The combined organic layer was washed with brine, then dried over Na<sub>2</sub>SO<sub>4</sub> and concentrated to afford a yellow residue. The crude product was purified by flash column chromatography (eluent: 10% Hex in EtOAc) to afford corresponding allyl aniline as a yellow oil with 40% to 50% yield.

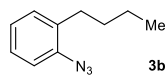
**Aza-Claisen rearrangement:** To a 50-mL Schlenk tube were added allyl aniline (1.0 equiv.), *p*-xylene (2.0 M) and then added BF<sub>3</sub>·Et<sub>2</sub>O (1.0 equiv.) dropwise. The Schlenk tube was sealed and heated to 180 °C for 4 h (sometimes longer based on how fast the rearrangement is).

**Hydrogenation:** To a 25-mL round-bottom flask were added corresponding aniline (1.0 equiv.) ethyl acetate (0.2 M) and Pd/C (100 mg/g of aniline) and then the mixture was degassed and recharged with a balloon of hydrogen. The reaction was vigorously stirred at room temperature overnight. After the reaction was completed, the mixture was filtered through a pad of celite before being concentrated to afford a yellow residue. The residue was directly used for the next step without any further purification.

**Azidation:** Same as General Procedure C described above.

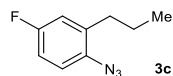


**1-azido-2-propylbenzene (3a):** The synthesis was conducted through general procedure C. <sup>1</sup>H NMR (400 MHz, CDCl<sub>3</sub>) δ 7.28 – 7.19 (m, 1H), 7.14 (ddd, *J* = 12.2, 7.7, 1.4 Hz, 2H), 7.06 (td, *J* = 7.4, 1.3 Hz, 1H), 2.58 – 2.50 (m, 2H), 1.66 – 1.52 (m, 2H), 0.94 (t, *J* = 7.3 Hz, 3H). <sup>13</sup>C NMR (101 MHz, CDCl<sub>3</sub>) δ 138.1, 134.3, 130.6, 127.3, 124.7, 118.2, 33.4, 23.6, 14.1.

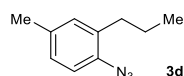


**1-azido-2-butylbenzene (3b):** The synthesis was conducted through general procedure C. <sup>1</sup>H NMR (400 MHz, CDCl<sub>3</sub>) δ 7.23 (td, *J* = 7.6, 1.7 Hz, 1H), 7.14 (ddd, *J* = 13.8, 7.7, 1.4 Hz, 2H), 7.06 (td, *J* = 7.4, 1.2 Hz, 1H), 2.56 (t, *J* = 7.6 Hz, 2H), 1.60 – 1.48 (m, 2H), 1.35

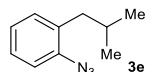
(dq,  $J = 14.6, 7.3$  Hz, 2H), 0.93 (t,  $J = 7.3$  Hz, 3H).  **$^{13}\text{C}$  NMR** (101 MHz,  $\text{CDCl}_3$ )  $\delta$  138.0, 134.5, 130.5, 127.2, 124.8, 118.2, 32.6, 31.1, 22.7, 14.1.



**3c 1-azido-4-fluoro-2-propylbenzene (3c):** The synthesis was conducted through general procedure D.  **$^1\text{H}$  NMR** (400 MHz,  $\text{CDCl}_3$ )  $\delta$  7.06 (dd,  $J = 8.7, 4.8$  Hz, 1H), 6.98 – 6.84 (m, 2H), 2.55 – 2.49 (m, 2H), 1.64 – 1.53 (m, 2H), 0.94 (t,  $J = 7.4$  Hz, 3H).  **$^{13}\text{C}$  NMR** (101 MHz,  $\text{CDCl}_3$ )  $\delta$  159.9 (d,  $J = 243.7$  Hz), 136.4 (d,  $J = 7.4$  Hz), 133.8 (d,  $J = 2.8$  Hz), 119.3 (d,  $J = 8.7$  Hz), 117.2 (d,  $J = 22.4$  Hz), 113.9 (d,  $J = 23.2$  Hz), 33.3 (d,  $J = 1.4$  Hz), 23.3, 14.0.  **$^{19}\text{F}$  NMR** (376 MHz,  $\text{CDCl}_3$ )  $\delta$  -118.5.



**3d 1-azido-4-methyl-2-propylbenzene (3d):** The synthesis was conducted through general procedure D.  **$^1\text{H}$  NMR** (400 MHz,  $\text{CDCl}_3$ )  $\delta$  7.05 – 6.99 (m, 2H), 6.96 (s, 1H), 2.54 – 2.43 (m, 2H), 2.30 (s, 3H), 1.64 – 1.51 (m, 2H), 0.94 (t,  $J = 7.4$  Hz, 3H).  **$^{13}\text{C}$  NMR** (101 MHz,  $\text{CDCl}_3$ )  $\delta$  135.2, 134.4, 134.0, 131.3, 127.8, 118.1, 33.4, 23.7, 21.0, 14.1.

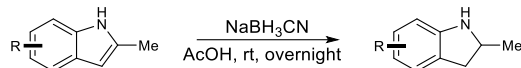


**3e 1-azido-2-isobutylbenzene (3e):** The synthesis was conducted through general procedure C.  **$^1\text{H}$  NMR** (400 MHz,  $\text{CDCl}_3$ )  $\delta$  7.26 – 7.20 (m, 1H), 7.12 (ddd,  $J = 7.6, 3.6, 1.5$  Hz, 2H), 7.05 (td,  $J = 7.4, 1.2$  Hz, 1H), 2.44 (d,  $J = 7.2$  Hz, 2H), 1.95 – 1.82 (m, 1H), 0.89 (d,  $J = 6.6$  Hz, 6H).  **$^{13}\text{C}$  NMR** (101 MHz,  $\text{CDCl}_3$ )  $\delta$  138.3, 133.4, 131.5, 127.3, 124.5, 118.2, 40.5, 29.3, 22.5.

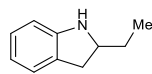
## V. Preparation and Characterization of the Racemic Standards of Products

**Notes:** All the pyrrolidine derivative standard products were commercially available and purchased from vendors mentioned in **Section I**. Unless otherwise noted, indoline derivative standard products were commercially available and purchased from vendors.

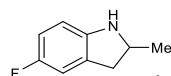
### General procedure F:<sup>10</sup>



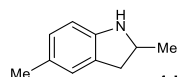
To a round-bottom flask at 0 °C were added indole (1.0 equiv.), AcOH (0.2 M), and NaBH<sub>3</sub>CN (6.0 equiv.). The mixture was gradually warmed to room temperature and stirred overnight. After completion detected by TLC analysis, water and additional NaOH pellets were added until pH >12 before extracting with diethyl ether (three times). After extraction, the organic phase was combined, further dried over Na<sub>2</sub>SO<sub>4</sub>, and concentrated to afford a yellow residue. Flash column chromatography was performed to afford pure product in 50% to 60% yield.



**4b 2-ethylindoline (4b):** <sup>1</sup>H NMR (400 MHz, CDCl<sub>3</sub>) δ 7.11 – 7.04 (m, 1H), 7.01 (dddd, *J* = 7.7, 6.8, 1.3, 0.7 Hz, 1H), 6.70 (td, *J* = 7.4, 1.0 Hz, 1H), 6.63 (d, *J* = 7.7 Hz, 1H), 3.79 (tt, *J* = 8.5, 6.6 Hz, 1H), 3.13 (dd, *J* = 15.5, 8.6 Hz, 1H), 2.69 (dd, *J* = 15.5, 8.4 Hz, 1H), 1.65 (dtd, *J* = 13.8, 7.3, 3.0 Hz, 2H), 0.98 (t, *J* = 7.4 Hz, 3H). <sup>13</sup>C NMR (101 MHz, CDCl<sub>3</sub>) δ 150.7, 129.2, 127.4, 124.8, 118.9, 109.5, 61.7, 35.9, 29.6, 10.9. **HRMS** (FD) Calcd for C<sub>10</sub>H<sub>13</sub>N [M] 147.1048, found 147.1038.



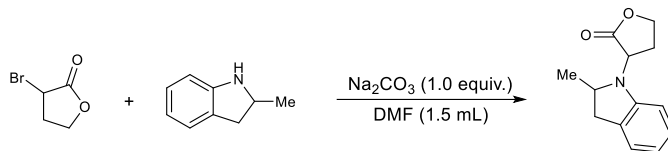
**4c 5-fluoro-2-methylindoline (4c):** <sup>1</sup>H NMR (400 MHz, CDCl<sub>3</sub>) δ 6.80 (ddt, *J* = 8.5, 2.5, 1.2 Hz, 1H), 6.70 (dddt, *J* = 9.3, 8.4, 2.7, 0.8 Hz, 1H), 6.53 (ddd, *J* = 8.4, 4.4, 1.1 Hz, 1H), 4.08 – 3.94 (m, 1H), 3.13 (dd, *J* = 16.3, 8.9 Hz, 1H), 2.63 (dd, *J* = 15.4, 7.6 Hz, 1H), 1.30 (d, *J* = 6.3 Hz, 3H). <sup>13</sup>C NMR (101 MHz, CDCl<sub>3</sub>) δ 157.3 (d, *J* = 235.2 Hz), 146.6 (d, *J* = 1.5 Hz), 131.0 (d, *J* = 8.2 Hz), 113.3 (d, *J* = 23.1 Hz), 112.3 (d, *J* = 23.7 Hz), 109.8 (d, *J* = 8.4 Hz), 56.1, 38.1 (d, *J* = 1.8 Hz), 22.2. <sup>19</sup>F NMR (376 MHz, CDCl<sub>3</sub>) δ -126.3. **HRMS** (FD) Calcd for C<sub>9</sub>H<sub>10</sub>NF [M] 151.0797, found 151.0798.



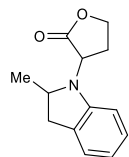
**4d 2,5-dimethylindoline (4d):** <sup>1</sup>H NMR (400 MHz, CDCl<sub>3</sub>) δ 6.92 (s, 1H), 6.83 (d, *J* = 7.8 Hz, 1H), 6.54 (d, *J* = 7.8 Hz, 1H), 3.98 (ddq, *J* = 8.4, 7.8, 6.2 Hz, 1H), 3.11 (dd, *J* = 15.4, 8.4 Hz, 1H), 2.61 (dd, *J* = 15.4, 7.8 Hz, 1H), 2.25 (s, 3H), 1.29 (d, *J* = 6.3 Hz, 3H). <sup>13</sup>C NMR (101

MHz, CDCl<sub>3</sub>)  $\delta$  148.0, 129.7, 128.6, 127.7, 125.7, 109.8, 55.6, 37.9, 22.2, 21.0. **HRMS** (FD) Calcd for C<sub>10</sub>H<sub>13</sub>N [M] 147.1048, found 147.1046.

### General procedure G:<sup>11</sup>



To a 40-mL dram vial were added a solution of alkylamine (2.2 mmol) in DMF (1.5 mL) and  $\alpha$ -bromo- $\gamma$ -butyrolactone (330 mg, 0.185 mL, 2 mmol). The resulting mixture was stirred at room temperature for 24 h. After reaction completion, the mixture was extracted with ethyl acetate (7 mL  $\times$  3), and the combined organic layer was washed with saturated NaHCO<sub>3</sub> solution (15 mL) and brine (15 mL). The organic phase was further dried over Na<sub>2</sub>SO<sub>4</sub> and concentrated to afford a brown residue. The final product was purified through silica gel column chromatography.



**5 3-(2-methylindolin-1-yl)dihydrofuran-2(3H)-one (5):** <sup>1</sup>H NMR (400 MHz, CDCl<sub>3</sub>)  $\delta$  7.09 – 6.98 (m, 2H), 6.70 (dtd,  $J$  = 12.4, 7.4, 0.9 Hz, 1H), 6.30 (dd,  $J$  = 11.4, 7.9 Hz, 1H), 4.55 (tdd,  $J$  = 9.2, 6.7, 1.7 Hz, 1H), 4.39 – 4.22 (m, 2H), 4.07 – 3.70 (m, 1H), 3.28 – 3.13 (m, 1H), 2.77 – 2.45 (m, 2H), 2.43 – 2.29 (m, 1H), 1.34 (dd,  $J$  = 41.8, 6.2 Hz, 3H). <sup>13</sup>C NMR (101 MHz, CDCl<sub>3</sub>)  $\delta$  175.2, 174.8, 148.7, 148.2, 129.7, 129.1, 127.4, 127.3, 125.0, 124.9, 119.1, 118.6, 108.8, 107.0, 65.7, 65.5, 60.0, 59.5, 55.0, 54.4, 37.3, 37.2, 24.7, 22.7, 20.3, 20.2. **HRMS** (FD) Calcd for C<sub>13</sub>H<sub>15</sub>NO<sub>2</sub> [M] 217.1103, found 217.1108.

## VI. Analytic Scale Enzymatic Reactions and Calibration Curves for Products

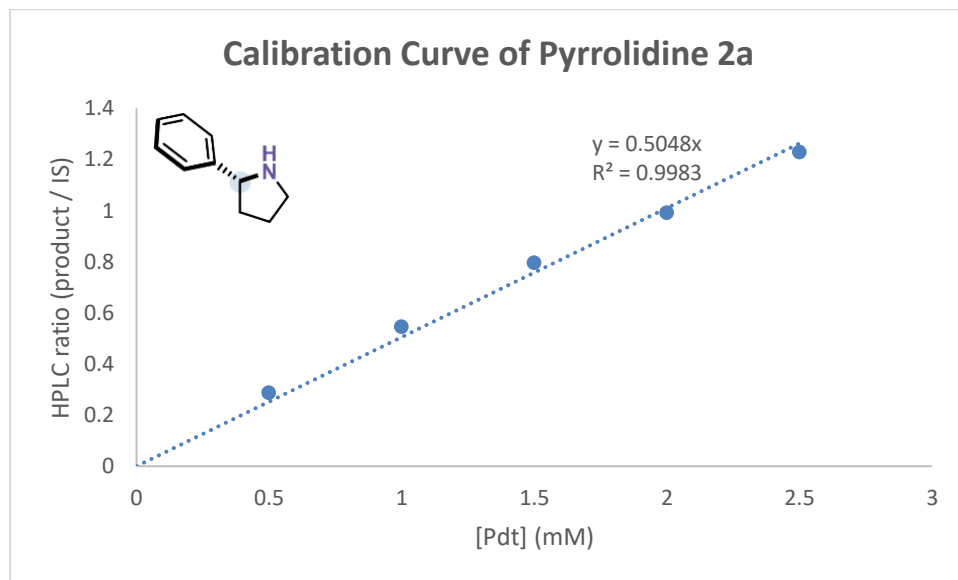
All enzymatic reactions for intramolecular alkyl/aryl nitrene C–H insertion on analytical scale were conducted following the general procedure described in **Section I (D)**. Reactions for every substrate were set up in triplicate. Product formation was quantified by LC-MS based on the calibration curve of the corresponding racemic standard compound (**Section IV**). All TTNs for different products were calculated as the concentration of products divided by the concentration of hemoproteins measured by the CO binding assay (**Section I (C)**).

### LC-MS calibration curve:

Calibration curves of synthesized reference compounds were created for the determination of yield and TTN. For each substrate, five different concentrations of product (1.00, 2.00, 3.00, 4.00, and 5.00 mM) in 400- $\mu$ L *E. coli* cell solutions were quenched, each with 400  $\mu$ L of 5.00 mM internal standard (ethyl benzoate or 1,2,3-trimethoxylbenzene) acetonitrile solution. The mixtures were vortexed and then analyzed by LC-MS based on UV absorbance at 254 or 210 nm. All data points represent the average of duplicate runs. The calibration curves depict the ratio of product area to internal standard area (y-axis) against product concentration in mM (x-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.

### 2-Phenylpyrrolidine (2a)



Data analysis for **P411-PYS-5141** catalyzed intramolecular C–H insertion with **1a** (2.5 mM, OD<sub>600</sub> = 30):

Entry	Pdt	IS	Pdt/IS	[Pdt]/mM	[PC]/ $\mu$ M	Avg. TTN	SD TTN	Avg. Yield [%]	SD Yield [%]
1	50.6	967.3	0.0523	0.10	1.95	54	10	4	0.8
2	40.9	945.9	0.0432	0.086	1.95				
3	60.3	952.1	0.0633	0.13	1.95				

Data analysis for **P411-PYS-5142** catalyzed intramolecular C–H insertion with **1a** (2.5 mM, OD<sub>600</sub> = 30):

Entry	Pdt	IS	Pdt/IS	[Pdt]/mM	[PC]/ $\mu$ M	Avg. TTN	SD TTN	Avg. Yield [%]	SD Yield [%]
1	159.7	964.7	0.166	0.33	1.58	210	3	13	0.2
2	161.9	952	0.170	0.34	1.58				
3	160.3	956.1	0.168	0.33	1.58				

Data analysis for **P411-PYS-5143** catalyzed intramolecular C–H insertion with **1a** (2.5 mM, OD<sub>600</sub> = 30):

Entry	Pdt	IS	Pdt/IS	[Pdt]/mM	[PC]/ $\mu$ M	Avg. TTN	SD TTN	Avg. Yield [%]	SD Yield [%]
1	159.6	972.7	0.164	0.32	2.38	142	10	14	1.0
2	155.2	956	0.162	0.32	2.38				
3	179.5	970.8	0.185	0.37	2.38				

Data analysis for **P411-PYS-5144** catalyzed intramolecular C–H insertion with **1a** (2.5 mM, OD<sub>600</sub> = 30):

Entry	Pdt	IS	Pdt/IS	[Pdt]/mM	[PC]/ $\mu$ M	Avg. TTN	SD TTN	Avg. Yield [%]	SD Yield [%]
1	241.6	932.6	0.259	0.51	2.21	224	10	20	0.9
2	240.9	951.2	0.253	0.50	2.21				
3	225.4	946.2	0.238	0.47	2.21				

Data analysis for **P411-PYS-5145** catalyzed intramolecular C–H insertion with **1a** (2.5 mM, OD<sub>600</sub> = 30):

Entry	Pdt	IS	Pdt/IS	[Pdt]/mM	[PC]/ $\mu$ M	Avg. TTN	SD TTN	Avg. Yield [%]	SD Yield [%]
1	344.2	907.4	0.379	0.75	1.73	420	24	29	1.6
2	361.8	957.5	0.378	0.75	1.73				
3	329.4	960.3	0.343	0.68	1.73				

Data analysis for **P411-PYS-5146** catalyzed intramolecular C–H insertion with **1a** (2.5 mM, OD<sub>600</sub> = 30):

Entry	Pdt	IS	Pdt/IS	[Pdt]/mM	[PC]/ $\mu$ M	Avg. TTN	SD TTN	Avg. Yield [%]	SD Yield [%]
1	369.4	916.5	0.403	0.80	1.68	463	15	31	1.0
2	368.8	931.8	0.396	0.78	1.68				
3	353	933.8	0.378	0.75	1.68				

Data analysis for **P411-PYS-5147** catalyzed intramolecular C–H insertion with **1a** (2.5 mM, OD<sub>600</sub> = 30):

Entry	Pdt	IS	Pdt/IS	[Pdt]/mM	[PC]/ $\mu$ M	Avg. TTN	SD TTN	Avg. Yield [%]	SD Yield [%]
1	608.4	927.9	0.656	1.30	3.76	350	4	53	0.6
2	637.8	952.7	0.669	1.33	3.76				
3	628.5	938.6	0.670	1.33	3.76				

Data analysis for **P411-PYS-5148** catalyzed intramolecular C–H insertion with **1a** (2.5 mM, OD<sub>600</sub> = 30):

Entry	Pdt	IS	Pdt/IS	[Pdt]/mM	[PC]/ $\mu$ M	Avg. TTN	SD TTN	Avg. Yield [%]	SD Yield [%]
1	635.7	958.9	0.663	1.31	3.76	361	11	54	1.6
2	645.5	938.4	0.688	1.36	3.76				
3	676.4	961.4	0.704	1.39	3.76				

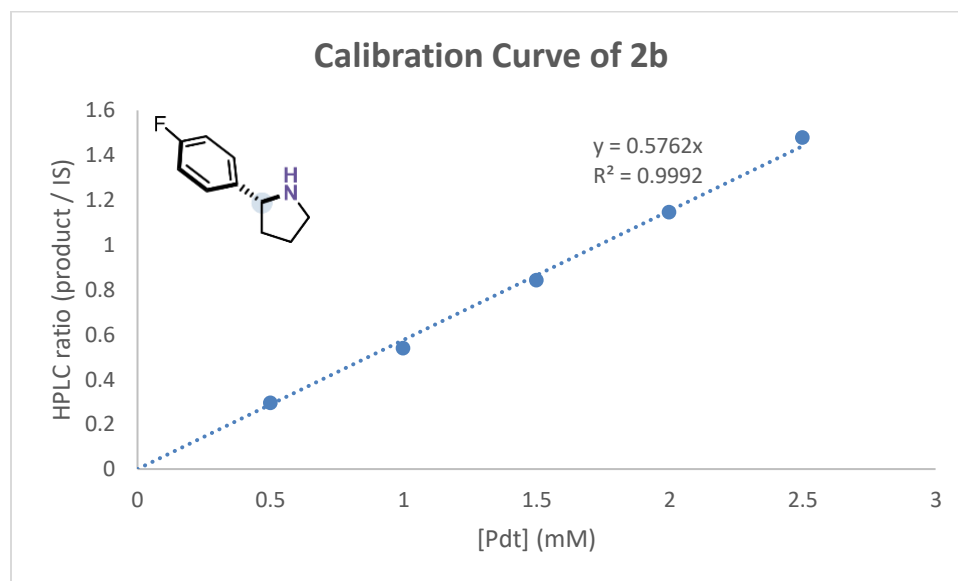
Data analysis for **P411-PYS-5149** catalyzed intramolecular C–H insertion with **1a** (2.5 mM, OD<sub>600</sub> = 30):

Entry	Pdt	IS	Pdt/IS	[Pdt]/mM	[PC]/ $\mu$ M	Avg. TTN	SD TTN	Avg. Yield [%]	SD Yield [%]
1	725.9	927.9	0.782	1.55	3.44	479	25	66	3.5
2	797.5	940.6	0.848	1.68	3.44				
3	812.8	938.3	0.866	1.72	3.44				

Data analysis for **P411-PYS-5149** (M9-N, pH = 8.4) catalyzed intramolecular C–H insertion with **1a** (2.5 mM, OD<sub>600</sub> = 30):

Entry	Pdt	IS	Pdt/IS	[Pdt]/mM	[PC]/ $\mu$ M	Avg. TTN	SD TTN	Avg. Yield [%]	SD Yield [%]
1	874.9	930.6	0.940	1.86	3.74	494	4	74	0.7
2	877.2	949.8	0.924	1.83	3.74				
3	877.7	940.7	0.933	1.85	3.74				

### 2-(4-Fluorophenyl)pyrrolidine (3b)



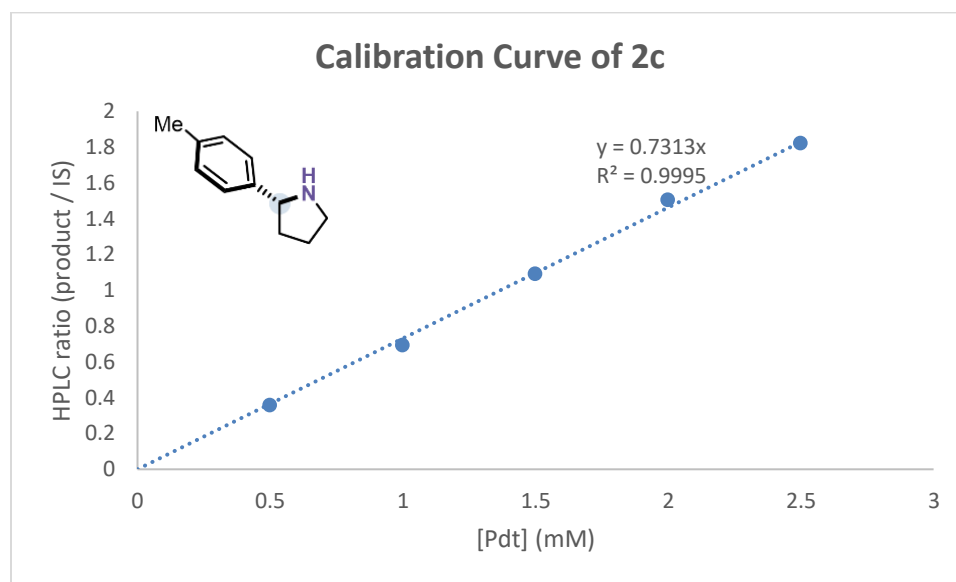
Data analysis for **P411-PYS-5149** (M9-N, pH = 8.4) catalyzed intramolecular C–H insertion with **1b** (2.5 mM, OD<sub>600</sub> = 30):

Entry	Pdt	IS	Pdt/IS	[Pdt]/mM	[PC]/ $\mu$ M	Avg. TTN	SD TTN	Avg. Yield [%]	SD Yield [%]
1	307	965.9	0.249	0.43	2.21	290	37	26	3.2



2	395.6	966.9	0.320	0.56	2.21				
3	371.1	974	0.301	0.52	2.21				

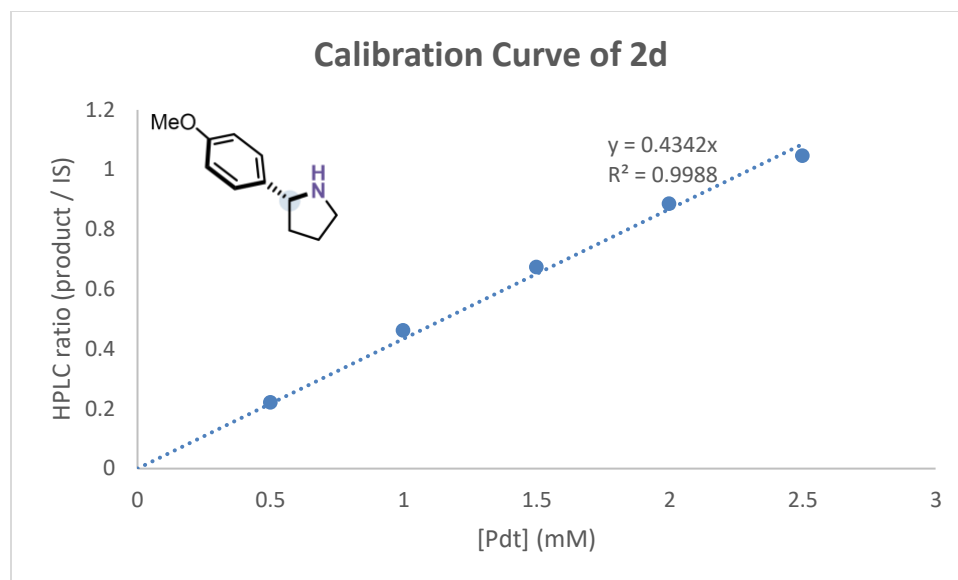
### 2-(*p*-Tolyl)pyrrolidine (2c)



Data analysis for **P411-PYS-5149** (M9-N, pH = **8.4**) catalyzed intramolecular C–H insertion with **1c** (2.5 mM, OD<sub>600</sub> = 30):

Entry	Pdt	IS	Pdt/IS	[Pdt]/mM	[PC]/μM	Avg. TTN	SD TTN	Avg. Yield [%]	SD Yield [%]
1	560.1	902.7	0.620	0.85	2.21	414	43	37	3.8
2	681.4	911	0.748	1.02	2.21				
3	576.7	902	0.639	0.87	2.21				

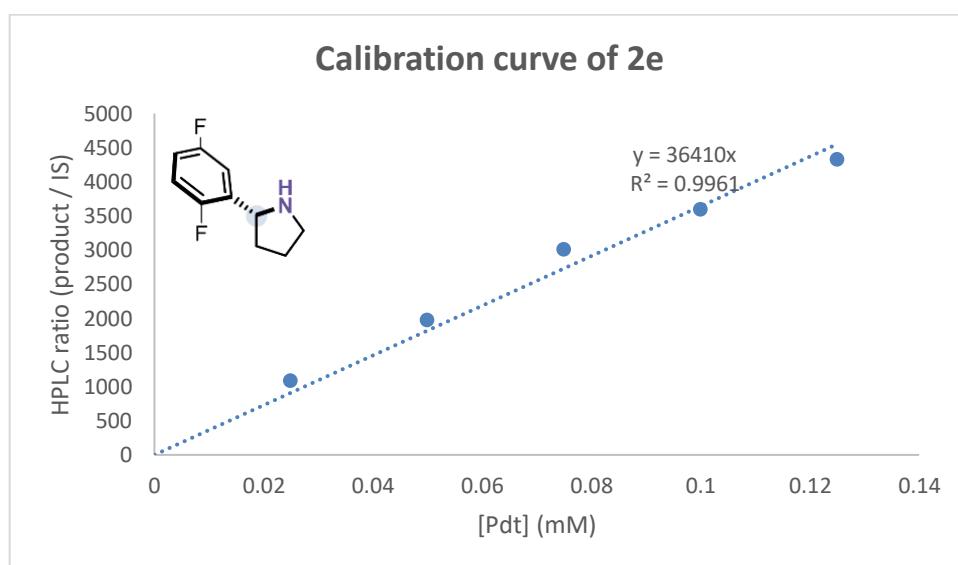
### 2-(4-Methoxyphenyl)pyrrolidine (2d)



Data analysis for **P411-PYS-5149** (M9-N, pH = 8.4) catalyzed intramolecular C–H insertion with **1d** (2.5 mM, OD<sub>600</sub> = 30):

Entry	Pdt	IS	Pdt/IS	[Pdt]/mM	[PC]/μM	Avg. TTN	SD TTN	Avg. Yield [%]	SD Yield [%]
1	659.8	928.2	0.711	1.64	2.21	761	30	67	2.7
2	697.7	913.9	0.763	1.76	2.21				
3	656.5	916.3	0.716	1.65	2.21				

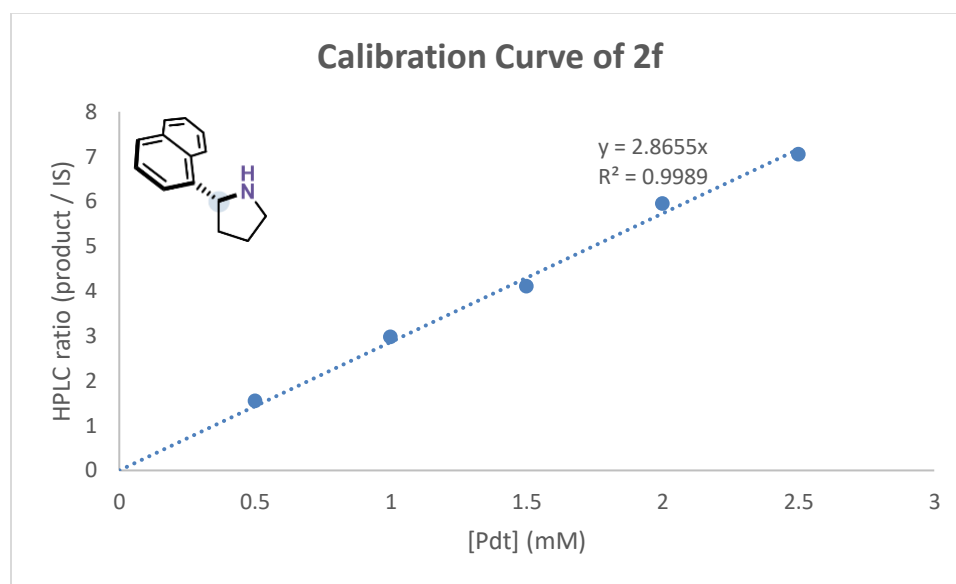
### 2-(2,5-Difluorophenyl)pyrrolidine (2e)



Data analysis for **P411-PYS-5149** (M9-N, pH = **8.4**) catalyzed intramolecular C–H insertion with **1e** (2.5 mM, OD<sub>600</sub> = 30):

Entry	Pdt (Ion Count)	IS	Pdt/IS	[Pdt]/mM	[PC]/μM	Avg. TTN	SD TTN	Avg. Yield [%]	SD Yield [%]
1	2730675.0	919.7	2969.1	0.082	1.44	58	1	3.3	0.06
2	2790964.8	915.6	3048.2	0.084	1.44				
3	2751191.0	895.4	3072.6	0.084	1.44				

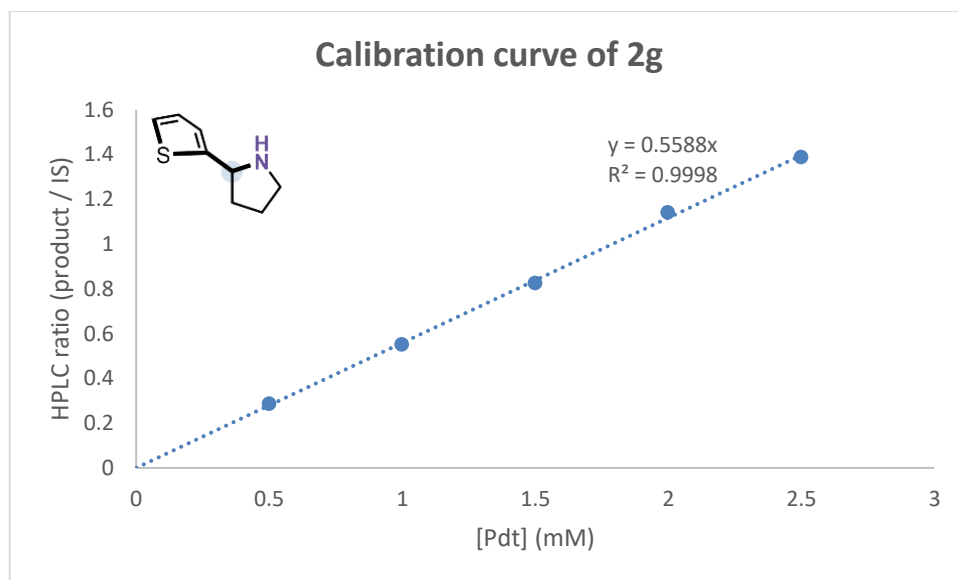
### 2-(Naphthalen-2-yl)pyrrolidine (2f)



Data analysis for **P411-PYS-5149** (M9-N, pH = **8.4**) catalyzed intramolecular C–H insertion with **1f** (2.5 mM, OD<sub>600</sub> = 30):

Entry	Pdt	IS	Pdt/IS	[Pdt]/mM	[PC]/μM	Avg. TTN	SD TTN	Avg. Yield [%]	SD Yield [%]
1	166.8	212.1	0.786	0.27	1.44	211	19	12	1.1
2	162.5	183.0	0.888	0.31	1.44				
3	155.6	165.8	0.938	0.33	1.44				

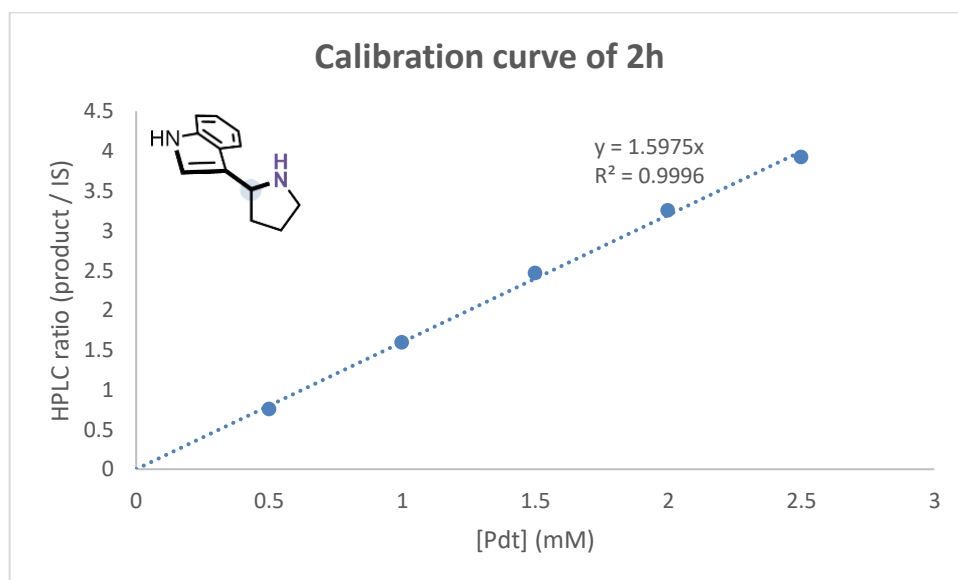
### 2-(Thiophen-2-yl)pyrrolidine (2g)



Data analysis for **P411-PYS-5149** (M9-N, pH = **8.4**) catalyzed intramolecular C–H insertion with **1g** (2.5 mM, OD<sub>600</sub> = 30):

Entry	Pdt	IS	Pdt/IS	[Pdt]/mM	[PC]/μM	Avg. TTN	SD TTN	Avg. Yield [%]	SD Yield [%]
1	76.5	184.5	0.415	0.74	2.21	360	23	32	2.0
2	84.3	178.9	0.471	0.84	2.21				
3	80.4	179.9	0.447	0.80	2.21				

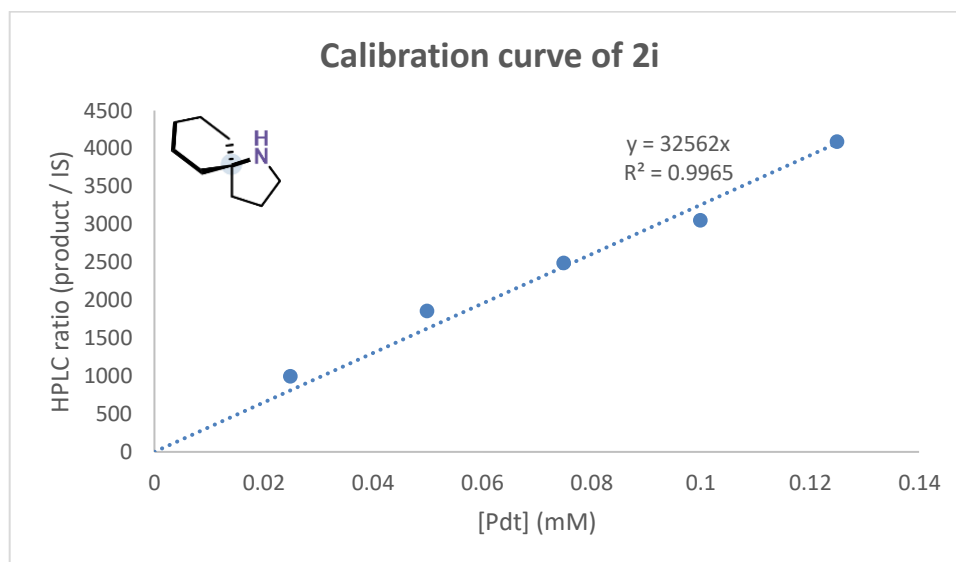
### 3-(Pyrrolidin-2-yl)-1H-indole (2h)



Data analysis for **P411-PYS-5149** (M9-N, pH = 8.4) catalyzed intramolecular C–H insertion with **1h** (2.5 mM, OD<sub>600</sub> = 30):

Entry	Pdt	IS	Pdt/IS	[Pdt]/mM	[PC]/μM	Avg. TTN	SD TTN	Avg. Yield [%]	SD Yield [%]
1	254.4	177.8	1.43	0.90	2.21	461	49	41	4.3
2	306.1	175.4	1.75	1.09	2.21				
3	290.4	170.1	1.71	1.07	2.21				

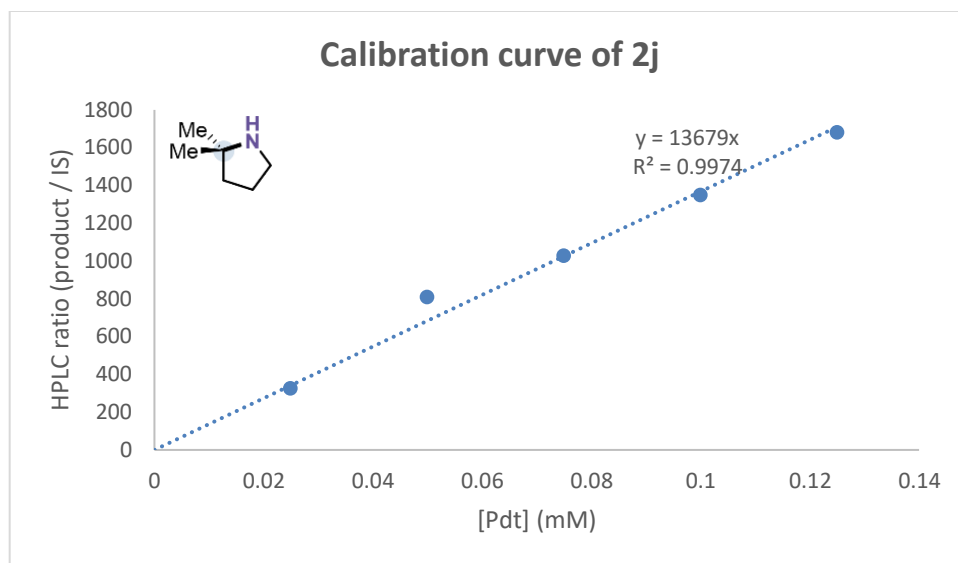
### 1-Azaspiro[4.5]decane (2i)



Data analysis for **P411-PYS-5149** (M9-N, pH = 8.4) catalyzed intramolecular C–H insertion with **1i** (2.5 mM, OD<sub>600</sub> = 30):

Entry	Pdt (Ion Count)	IS	Pdt/IS	[Pdt]/mM	[PC]/μM	Avg. TTN	SD TTN	Avg. Yield [%]	SD Yield [%]
1	2544228.3	931.9	2730.1516	0.084	1.44	57	2	3.3	0.1
2	2383615.3	931.8	2558.0761	0.079	1.44				
3	2489055.3	931.6	2671.8069	0.082	1.44				

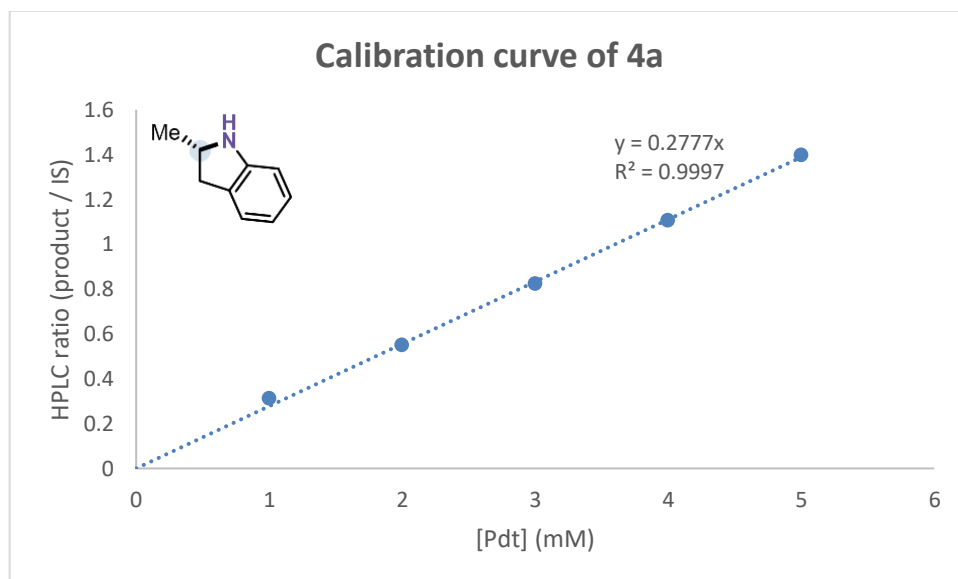
### 2,2-Dimethylpyrrolidine (2j)



Data analysis for **P411-PYS-5149** (M9-N, pH = 8.4) catalyzed intramolecular C–H insertion with **1j** (2.5 mM, OD<sub>600</sub> = 30):

Entry	Pdt (Ion Count)	IS	Pdt/IS	[Pdt]/mM	[PC]/μM	Avg. TTN	SD TTN	Avg. Yield [%]	SD Yield [%]
1	657275.0	896.6	733.1	0.054	1.44	36	1	2.0	0.08
2	631301.0	915.8	689.3	0.050	1.44				
3	622256.9	916	679.3	0.050	1.44				

## 2-Methylindoline (4a)



Data analysis for **P411-PYS-5148** (M9-N, pH = **7.4**) catalyzed intramolecular C–H insertion with **3a** (5.0 mM, OD<sub>600</sub> = 40):

Entry	Pdt	IS	Pdt/IS	[Pdt]/mM	[PC]/μM	Avg. TTN	SD TTN	Avg. Yield [%]	SD Yield [%]
1	59.3	97.6	0.61	2.18	4.71	488	34	46	3.2
2	68.8	99.7	0.69	2.48	4.71				
3	58.2	94.2	0.62	2.22	4.71				

Data analysis for **P411-INS-5150** (M9-N, pH = **7.4**) catalyzed intramolecular C–H insertion with **3a** (5.0 mM, OD<sub>600</sub> = 40):

Entry	Pdt	IS	Pdt/IS	[Pdt]/mM	[PC]/μM	Avg. TTN	SD TTN	Avg. Yield [%]	SD Yield [%]
1	66.3	95.2	0.70	2.51	3.29	742	25	49	1.7
2	63.7	97.7	0.65	2.35	3.29				
3	63.8	93.2	0.68	2.47	3.29				

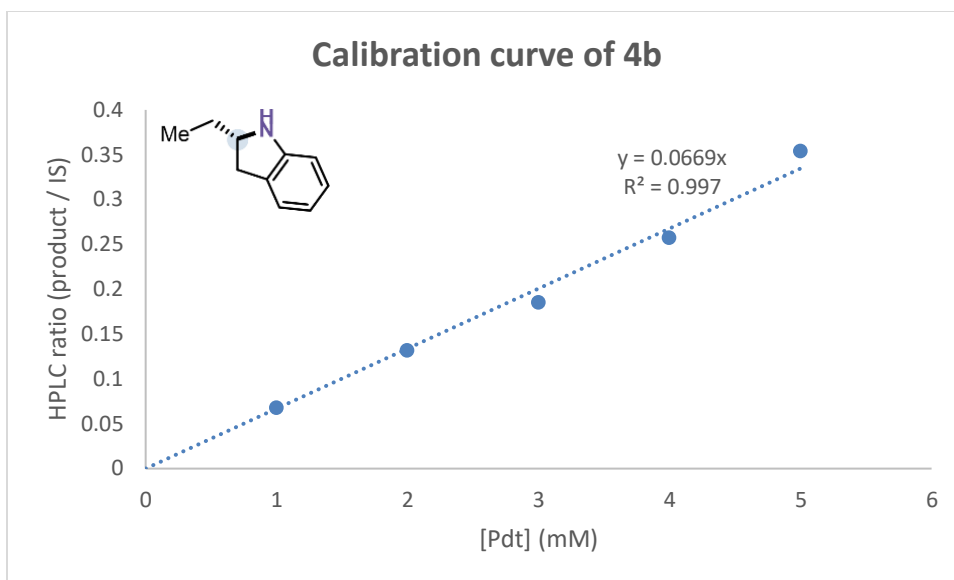
Data analysis for **P411-INS-5151** (M9-N, pH = **7.4**) catalyzed intramolecular C–H insertion with **3a** (5.0 mM, OD<sub>600</sub> = 40):

Entry	Pdt	IS	Pdt/IS	[Pdt]/mM	[PC]/μM	Avg. TTN	SD TTN	Avg. Yield [%]	SD Yield [%]
1	72.8	100.1	0.73	2.62	0.97	2690	49	52	1.0
2	67.8	92.3	0.73	2.65	0.97				
3	67.7	95.5	0.71	2.55	0.97				

Data analysis for **P411-INS-5151** (M9-N, pH = **8.4**) catalyzed intramolecular C–H insertion with **3a** (5.0 mM, OD<sub>600</sub> = 40):

Entry	Pdt	IS	Pdt/IS	[Pdt]/mM	[PC]/μM	Avg. TTN	SD TTN	Avg. Yield [%]	SD Yield [%]
1	82.4	91.8	0.90	3.23	1.04	3100	48	64	1.0
2	88.5	97.5	0.91	3.27	1.04				
3	83.7	95.1	0.88	3.17	1.04				

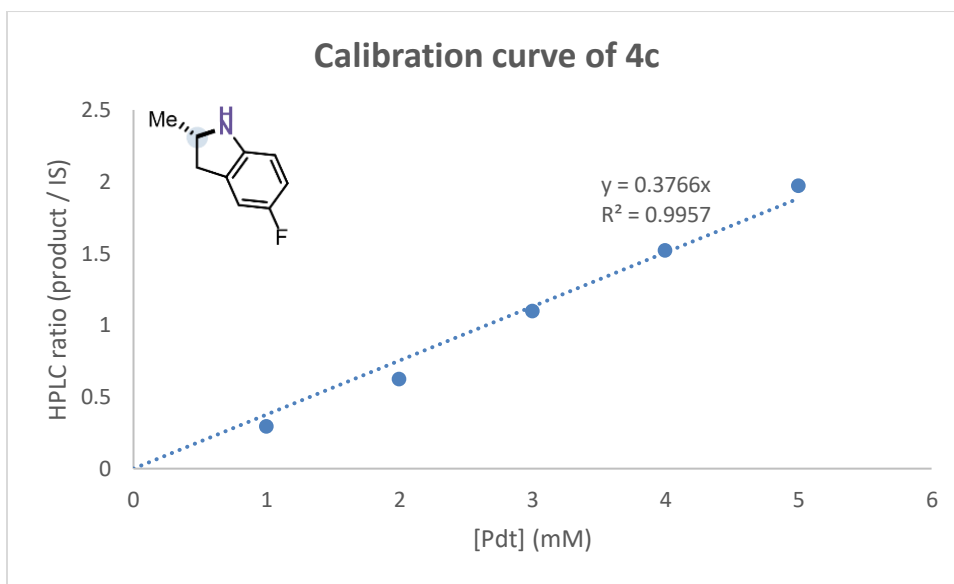
### Ethylindoline (4b)



Data analysis for **P411-INS-5151** (M9-N, pH = **8.4**) catalyzed intramolecular C–H insertion with **3c** (5.0 mM, OD<sub>600</sub> = 40):

Entry	Pdt	IS	Pdt/IS	[Pdt]/mM	[PC]/μM	Avg. TTN	SD TTN	Avg. Yield [%]	SD Yield [%]
1	258.0	5814.1	0.044	0.66	0.49	1310	57	13	0.6
2	261.0	5945.0	0.044	0.66	0.49				
3	232.6	5684.5	0.041	0.61	0.49				

### 5-Fluoro2-methylindoline (4c)

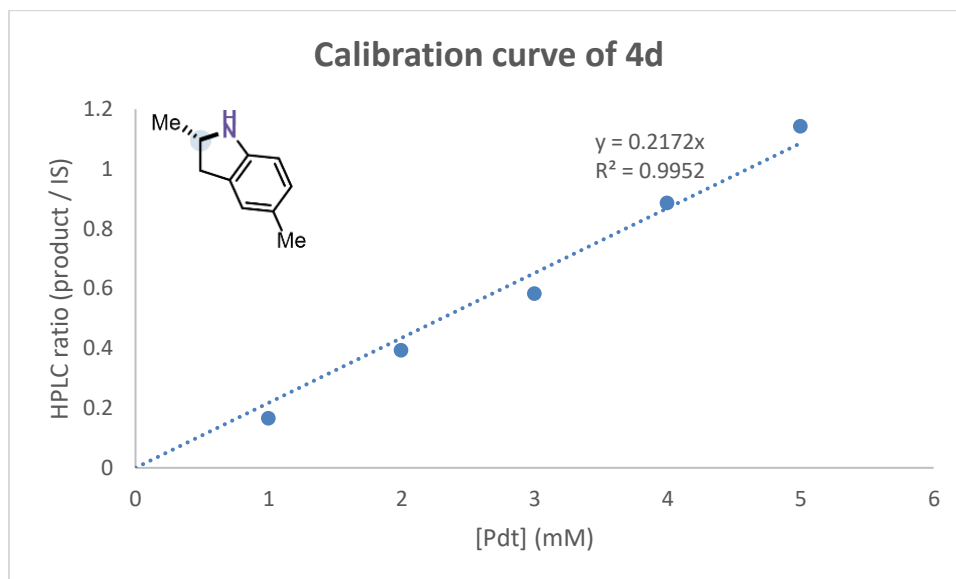




Data analysis for **P411-INS-5151** (M9-N, pH = **8.4**) catalyzed intramolecular C–H insertion with **3b** (5.0 mM, OD<sub>600</sub> = 40):

Entry	Pdt	IS	Pdt/IS	[Pdt]/mM	[PC]/μM	Avg. TTN	SD TTN	Avg. Yield [%]	SD Yield [%]
1	17.9	95.3	0.19	0.51	0.49	1050	43	10	0.4
2	17.4	93.9	0.19	0.50	0.49				
3	19.1	95.5	0.20	0.54	0.49				

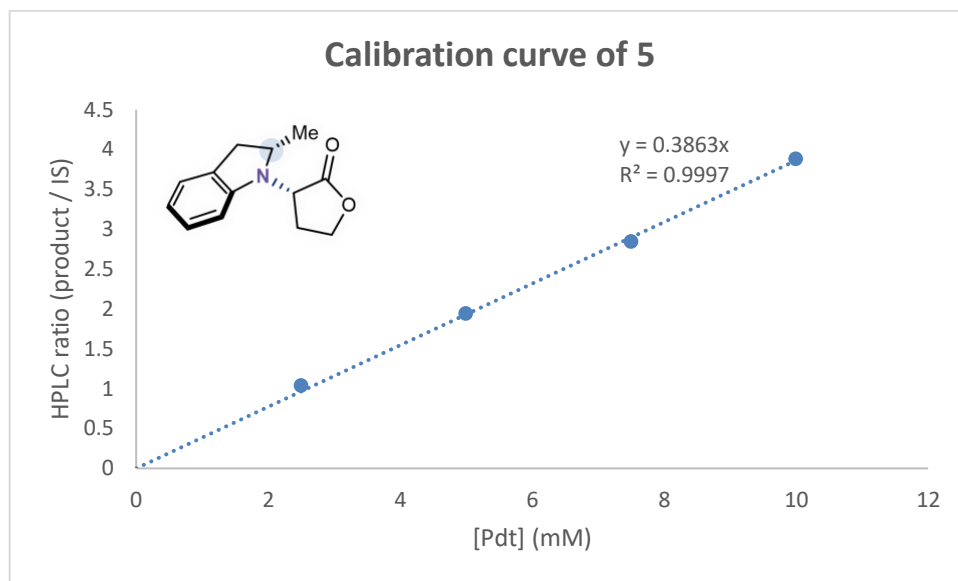
### 2,5-Dimethylindoline (4d)



Data analysis for **P411-INS-5151** (M9-N, pH = **8.4**) catalyzed intramolecular C–H insertion with **3c** (5.0 mM, OD<sub>600</sub> = 40):

Entry	Pdt	IS	Pdt/IS	[Pdt]/mM	[PC]/μM	Avg. TTN	SD TTN	Avg. Yield [%]	SD Yield [%]
1	48.2	6019.7	0.0080	0.11	0.49	211	18	2	0.2
2	40.1	5831.5	0.0069	0.10	0.49				
3	41.4	5869.6	0.0071	0.10	0.49				

### 3-(2-Methylindolin-1-yl)dihydrofuran-2(3H)-one (5)



Data analysis for **L7\_FL** (M9-N, pH = **7.4**) catalyzed intermolecular N–H insertion with **4a** (10.0 mM, OD<sub>600</sub> = 30):

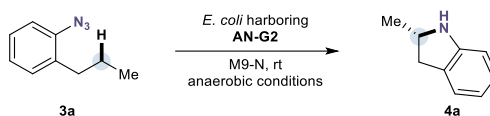
Entry	Pdt	IS	Pdt/IS	[Pdt]/mM	[PC]/μM	Avg. TTN	SD TTN	Avg. Yield [%]	SD Yield [%]
1	697.6	359.4	1.94	0.90	2.38	1985	115	47	2.7
2	621.8	357.6	1.74	1.09	2.38				
3	640.6	358.8	1.79	1.07	2.38				

## VII. Preparative-Scale Enzymatic Synthesis

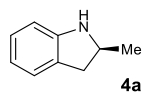
### General procedure for 1-mmol scale enzymatic intramolecular C–H aminations with **3a**:

In a 500-mL flask, a suspension of 150 mL *E. coli* expressing variant **P411-INS-5151** ( $OD_{600} = 40$ ) in M9-N (pH = 8.4), 45 mL D-glucose (500 mM in M9-N, pH = 8.4), and 5 mL 1-azido-2-propylbenzene **3a** (161.2 mg, 200 mM in EtOH) were added sequentially under anaerobic conditions. The flask was capped and sealed with parafilm inside the anaerobic chamber. The mixture was shaken at 250 rpm in a shaker outside of an anaerobic chamber overnight.

After the reaction was completed, the reaction mixture was transferred to two 500-mL centrifuge bottles. The aqueous phase was extracted with organic solvent (hexane/EtOAc = 1:2, 120 mL  $\times$  4). The organic layers were combined in an Erlenmeyer flask, dried over  $Na_2SO_4$ , and concentrated under reduced pressure. Purification by preparative TLC with dichloromethane (with 0.5%  $NEt_3$ ) as eluents afforded the cyclized product as a dark oil. TTNs were calculated based on measured protein concentration using CO binding and isolated product yield.



### (S)-2-Methylindoline

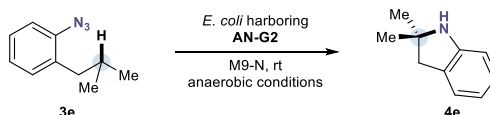


largescale (S)-**4a**: 79.8 mg, 60% yield, 2900 TTN, 92:8 *er*  $^1H$  NMR (400 MHz,  $CDCl_3$ )  $\delta$  7.08 (d,  $J = 7.3$  Hz, 1H), 7.02 (dddd,  $J = 9.1, 7.6, 1.4, 0.8$  Hz, 1H), 6.71 (td,  $J = 7.4, 1.0$  Hz, 1H), 6.64 (d,  $J = 7.8$  Hz, 1H), 4.01 (ddq,  $J = 8.5, 7.7, 6.2$  Hz, 1H), 3.15 (dd,  $J = 15.3, 8.4$  Hz, 1H), 2.65 (dd,  $J = 15.4, 7.7$  Hz, 1H), 1.31 (d,  $J = 6.2$  Hz, 3H).  $^{13}C$  NMR (101 MHz,  $CDCl_3$ )  $\delta$  150.6, 129.2, 127.4, 124.9, 119.0, 109.7, 55.4, 37.9, 22.3.

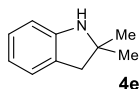
### General procedure for 1-mmol scale enzymatic intramolecular C–H aminations with **3e**:

In a 500-mL flask, a suspension of 150 mL *E. coli* expressing variant **P411-INS-5151** ( $OD_{600} = 40$ ) in M9-N (pH = 8.4), 45 mL D-glucose (500 mM in M9-N, pH = 8.4), and 5 mL 1-azido-2-propylbenzene **3a** (175.2 mg, 200 mM in EtOH) were added sequentially under anaerobic conditions. The flask was capped and sealed with parafilm inside the anaerobic chamber. The mixture was shaken at 250 rpm in a shaker outside of an anaerobic chamber overnight.

After the reaction was completed, the reaction mixture was transferred to two 500-mL centrifuge bottles. The aqueous phase was extracted with organic solvent (hexane/EtOAc = 1:2, 120 mL  $\times$  4). The organic layers were combined in an Erlenmeyer flask, dried over  $Na_2SO_4$ , and concentrated under reduced pressure. Purification by preparative TLC with EtOAc/hexanes (10% hexanes in EtOAc) as eluents afforded the cyclized product as a dark oil. TTNs were calculated based on measured protein concentration using CO binding and isolated product yield.



## 2,2-Dimethylindoline

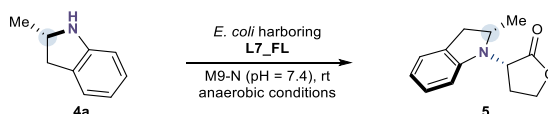


largescale **4e**: 58.6 mg, 40% yield, 1470 TTN **<sup>1</sup>H NMR** (400 MHz, CDCl<sub>3</sub>) δ 7.06 (d, *J* = 7.3 Hz, 1H), 7.01 (t, *J* = 7.6 Hz, 1H), 6.69 (t, *J* = 7.4 Hz, 1H), 6.58 (d, *J* = 7.7 Hz, 1H), 2.85 (s, 2H), 1.33 (s, 6H). **<sup>13</sup>C NMR** (101 MHz, CDCl<sub>3</sub>) δ 129.7, 127.6, 125.3, 120.2, 117.5, 111.2, 62.3, 44.1, 28.9. **HRMS** (FD) Calcd for C<sub>10</sub>H<sub>13</sub>N [M] 147.1048, found 147.1046.

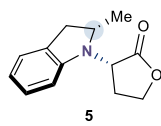
### General procedure for 0.5-mmol scale enzymatic N–H insertion reactions:

In a 250-mL flask, a suspension of 45 mL *E. coli* expressing variant **L7\_FL** (OD<sub>600</sub> = 40) in M9-N (pH = 7.4), 2.5 mL D-glucose (500 mM in M9-N, pH = 7.4), 1.25 mL (*S*)-2-methylindoline **4a** (66.6 mg, 1.0 equiv. 400 mM in EtOH), and 1.25 mL lactone diazo (LAD, 67.2 mg, 1.2 equiv. 480 mM in EtOH) were added sequentially under anaerobic conditions. The flask was capped and sealed with parafilm inside the anaerobic chamber. The mixture was shaken at 250 rpm in a shaker outside of an anaerobic chamber overnight.

After the reaction was completed, the reaction mixture was transferred to four 50-mL Eppendorf tubes. The aqueous phase was extracted with organic solvent (hexane/EtOAc = 1:2, 120 mL × 4). The organic layers were combined in an Erlenmeyer flask, dried over Na<sub>2</sub>SO<sub>4</sub>, and concentrated under reduced pressure. Purification by silica column chromatography with EtOAc/hexanes as eluents afforded the desired product. TTNs were calculated based on measured protein concentration using CO binding and isolated product yield.



### (S)-3-((S)-2-Methylindolin-1-yl)dihydrofuran-2(3H)-one

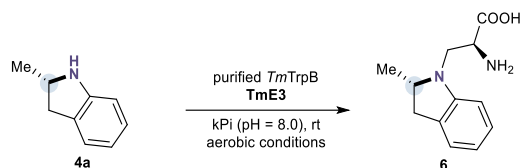


**5**: 46.6 mg, 43% yield, 2770 TTN, 98:2 *er*, >96:4 *dr* **<sup>1</sup>H NMR** (400 MHz, CDCl<sub>3</sub>) δ 7.11 – 6.97 (m, 2H), 6.72 (t, *J* = 7.4 Hz, 1H), 6.30 (d, *J* = 7.9 Hz, 1H), 4.54 (td, *J* = 9.2, 1.6 Hz, 1H), 4.36 – 4.20 (m, 2H), 3.76 (ddq, *J* = 9.5, 8.7, 6.1 Hz, 1H), 3.18 (dd, *J* = 15.5, 8.6 Hz, 1H), 2.71 (dd, *J* = 15.4, 9.4 Hz, 1H), 2.60 – 2.43 (m, 1H), 2.42 – 2.29 (m, 1H), 1.40 (d, *J* = 6.1 Hz, 3H). **<sup>13</sup>C NMR** (101 MHz, CDCl<sub>3</sub>) δ 174.8, 148.1, 129.8, 127.4, 124.9, 119.2, 108.8, 65.7, 60.0, 55.1, 37.3, 22.7, 20.2. **HRMS** (FD) Calcd for C<sub>13</sub>H<sub>15</sub>NO<sub>2</sub> [M] 217.1103, found 217.1104.

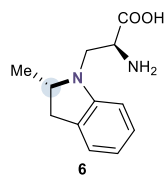
### General procedure for 0.5-mmol scale enzymatic non-canonical amino acid synthesis:

In a 100-mL flask, a suspension of 25 mL kPi (pH = 8.0), L-serine (52.5 mg as a solid), (*S*)-2-methylindoline **4a** (66.6 mg, 1.0 equiv. 400 mM in EtOH), and 300 μL purified *Tm*TrpB synthase **TmE3** (238 μM in KPi buffer, 2.856 μM final concentration) were added sequentially under aerobic conditions. The flask was capped and sealed with parafilm. The mixture was shaken at 250 rpm in a shaker overnight.

After the reaction was completed, the reaction mixture was transferred to a 100-mL round-bottom flask. The aqueous phase was concentrated under reduced pressure. Purification by reverse column chromatography with EtOAc/hexanes as eluents afforded the desired product. TTNs were calculated based on measured protein concentration using CO binding and isolated product yield.



**(2S)-2-Amino-3-(2-methylindolin-1-yl)propanoic acid**



**6:** 32.5 mg, 30% yield, 2100 TTN, >94:6 *dr* **<sup>1</sup>H NMR** (400 MHz, D<sub>2</sub>O) δ 7.14 (tdd, *J* = 7.7, 4.2, 1.3 Hz, 2H), 6.73 (t, *J* = 7.4 Hz, 1H), 6.62 (d, *J* = 7.8 Hz, 1H), 3.82 – 3.72 (m, 1H), 3.69 (dd, *J* = 7.4, 5.5 Hz, 1H), 3.43 (qd, *J* = 14.8, 6.4 Hz, 2H), 3.15 (dd, *J* = 15.7, 8.4 Hz, 1H), 2.61 (dd, *J* = 15.7, 7.5 Hz, 1H), 1.23 (d, *J* = 6.2 Hz, 3H). **<sup>13</sup>C NMR** (101 MHz, D<sub>2</sub>O) δ 178.3, 151.8, 129.6, 127.5, 124.7, 118.0, 106.8, 61.3, 55.3, 50.0, 36.4, 17.8. **HRMS** (FD) Calcd for C<sub>12</sub>H<sub>16</sub>N<sub>2</sub>O<sub>2</sub> [M] 220.1211, found 220.1214.

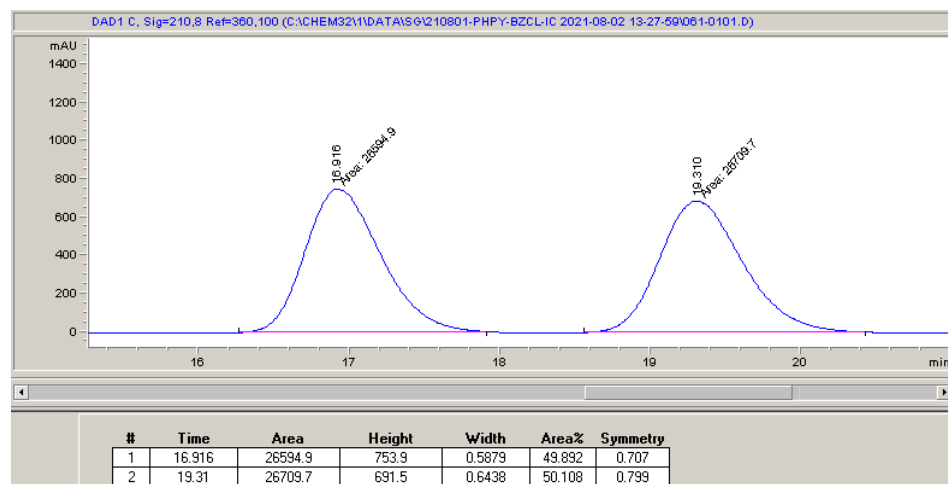
## VIII. Chiral-Phase HPLC Traces

The absolute stereochemistry for enzymatic products **2a** and **4a** were assigned to be *R* and *S*, respectively, by comparing with their optical pure standard product. All other products **2b–2g**, **2j**, **4b–4d** were assigned by analogy. Before analysis of *ee*, all pyrrolidine products were protected by the benzoyl group, while indoline products were not.

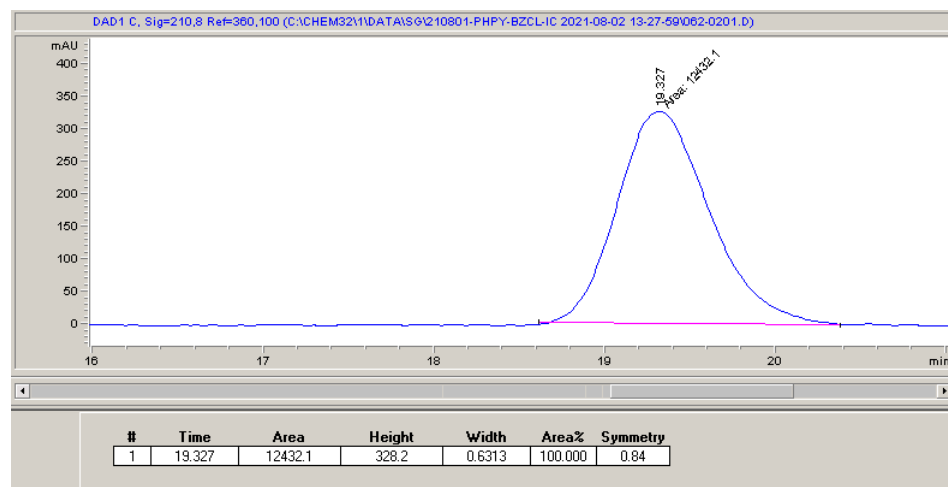
Determination of absolute stereochemistry for **2a**:

Chiral-phase HPLC conditions: Chiralpak IC, 25% *i*-PrOH in hexane, 1.5 mL/min, 25 °C, 210 nm

### Racemic 2-Phenylpyrrolidine:



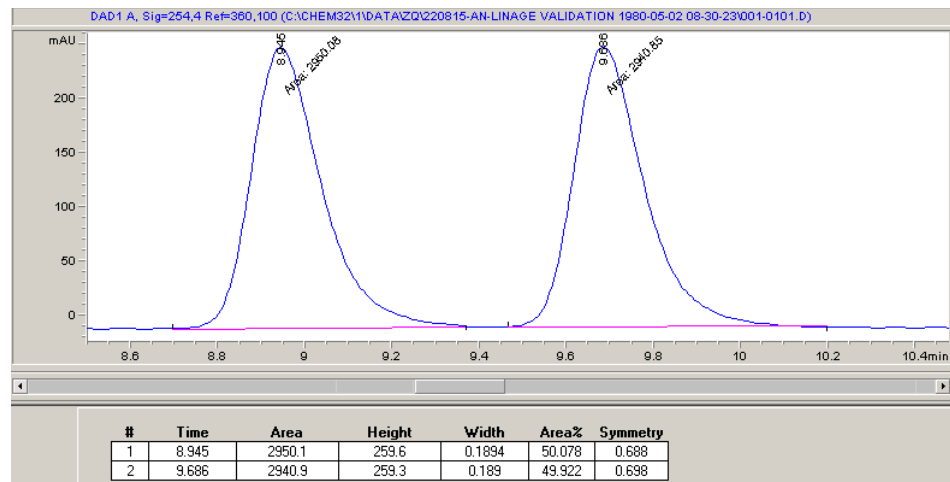
### (*S*)-Phenylpyrrolidine: commercially available enantiopure compound



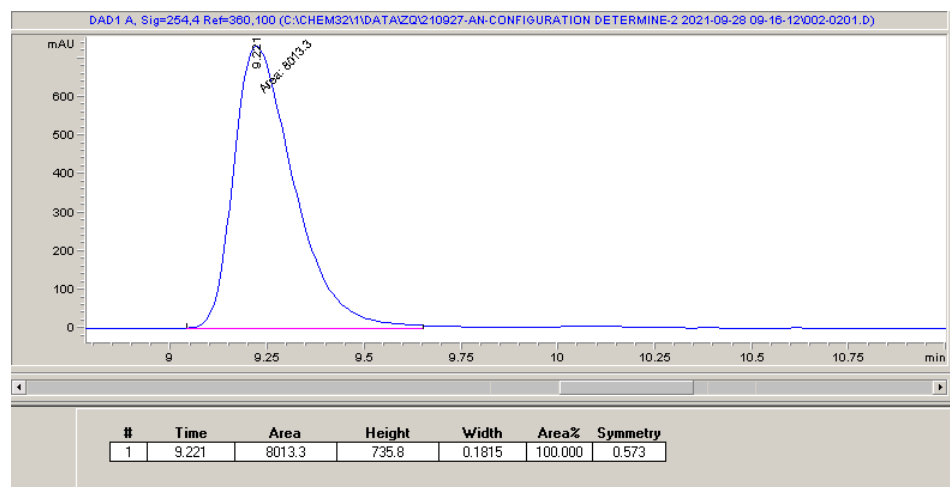
Determination of absolute stereochemistry for **4a**:

Chiral-phase HPLC conditions: Chiralpak IB, 2% *i*-PrOH in hexane, 1.0 mL/min, 25 °C, 254 nm

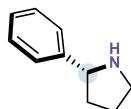
**Racemic 2-Methylindoline:**



**(R)- 2-Methylindoline:** commercially available enantiopure compound



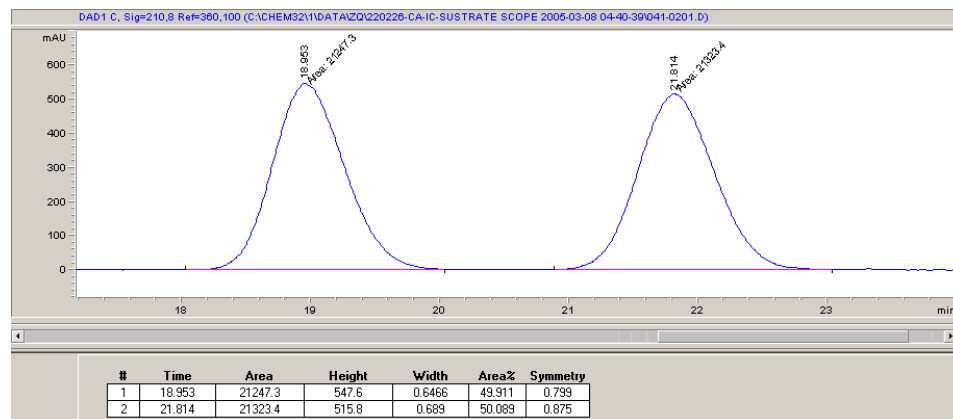
Determination of stereochemistry for all products:



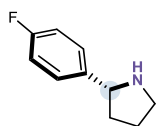
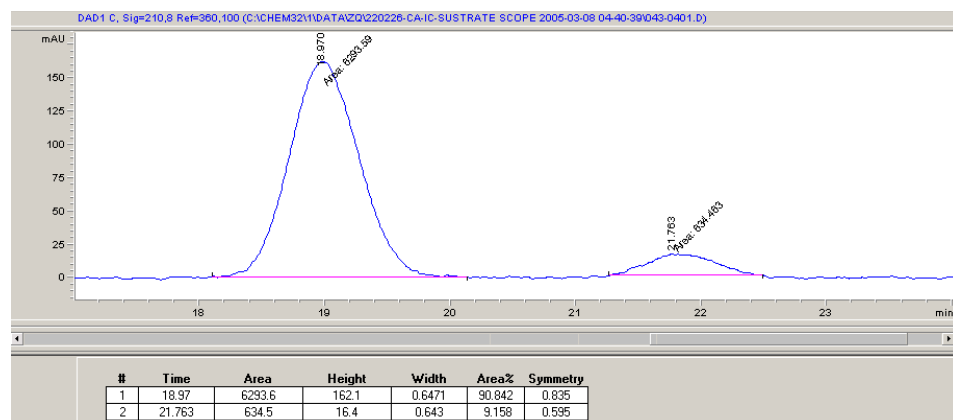
**(R)-2-Phenylpyrrolidine (2a)**

Chiral-phase HPLC conditions: Chiralpak IC, 25% *i*-PrOH in hexane, 1.5 mL/min, 25 °C, 210 nm

### Racemic 2a:



### Enzymatic preparation of 2a with P411-PYS-5149: 91:9 *er*

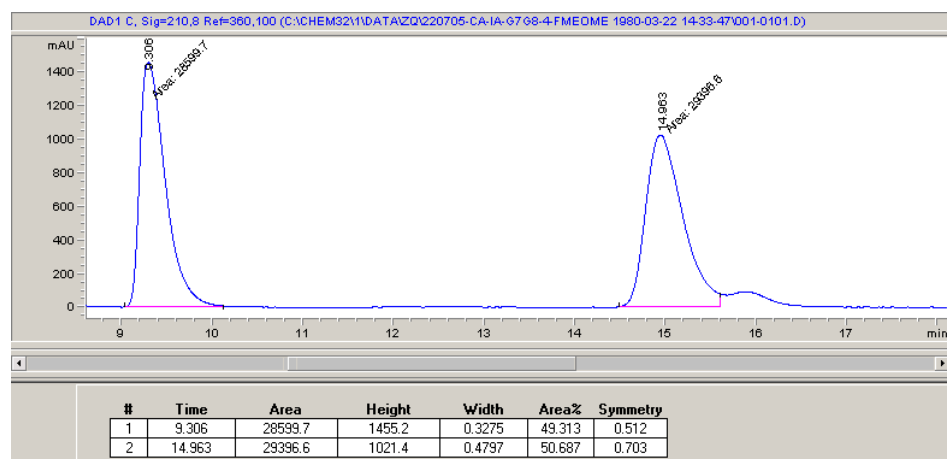


### 2-(4-Fluorophenyl)pyrrolidine (2b)

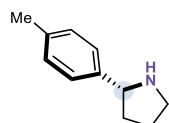
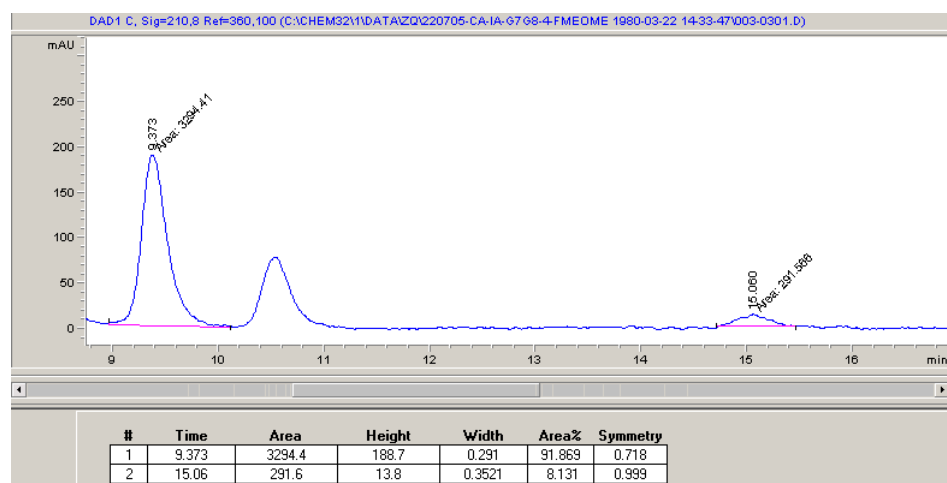
Chiral-phase HPLC conditions: Chiralpak IA, 10% *i*-PrOH in hexane, 1.5 mL/min, 25 °C, 210 nm

### Racemic 2b:





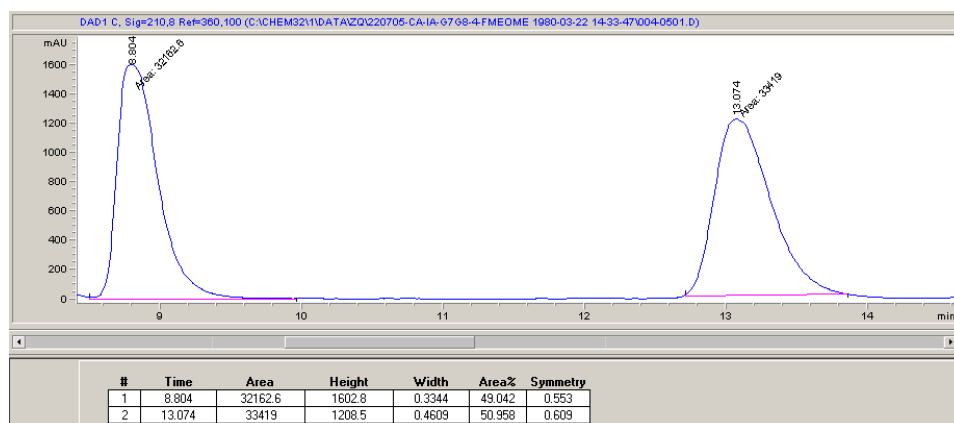
### Enzymatic preparation of 2b with P411-PYS-5149: 92:8 *er*



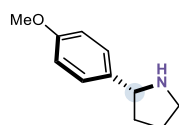
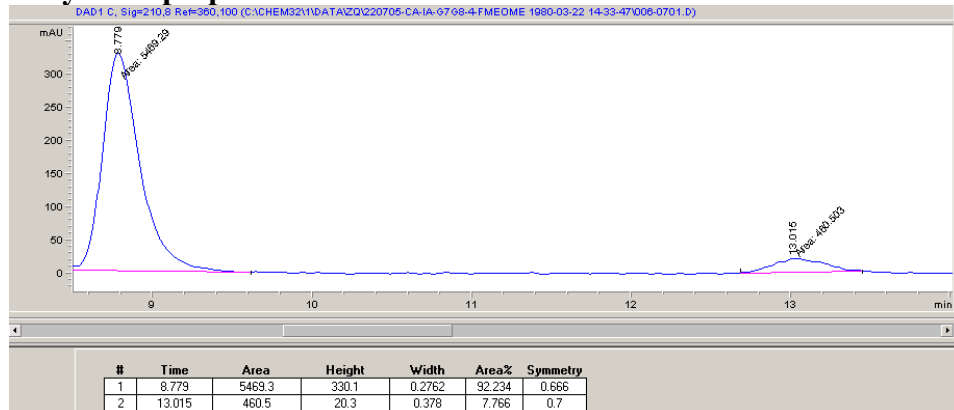
### 2-(*p*-Tolyl)pyrrolidine (2c)

Chiral-phase HPLC conditions: Chiralpak IA, 10% *i*-PrOH in hexane, 1.5 mL/min, 25 °C, 210 nm

### Racemic 2c:



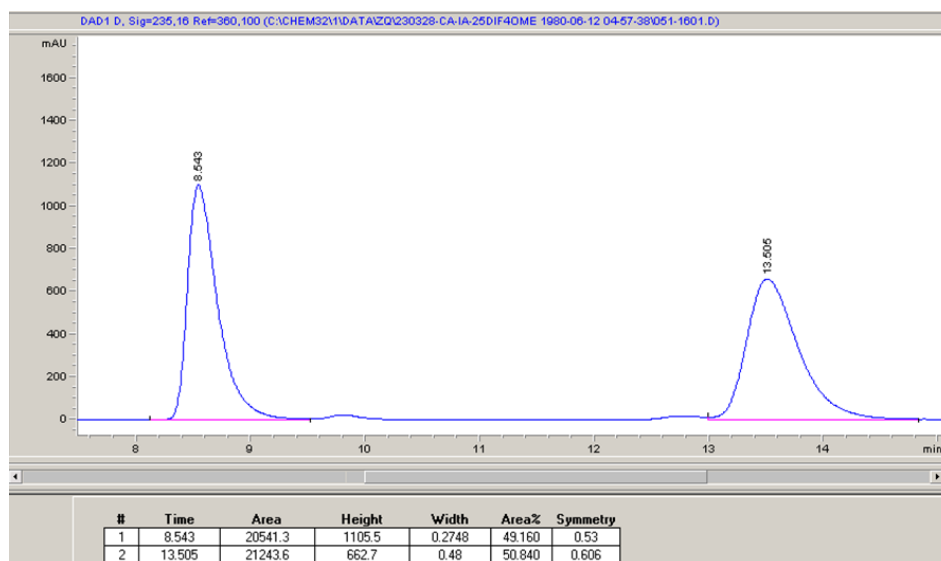
### Enzymatic preparation of 2c with P411-PYS-5149: 92:8 *er*



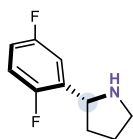
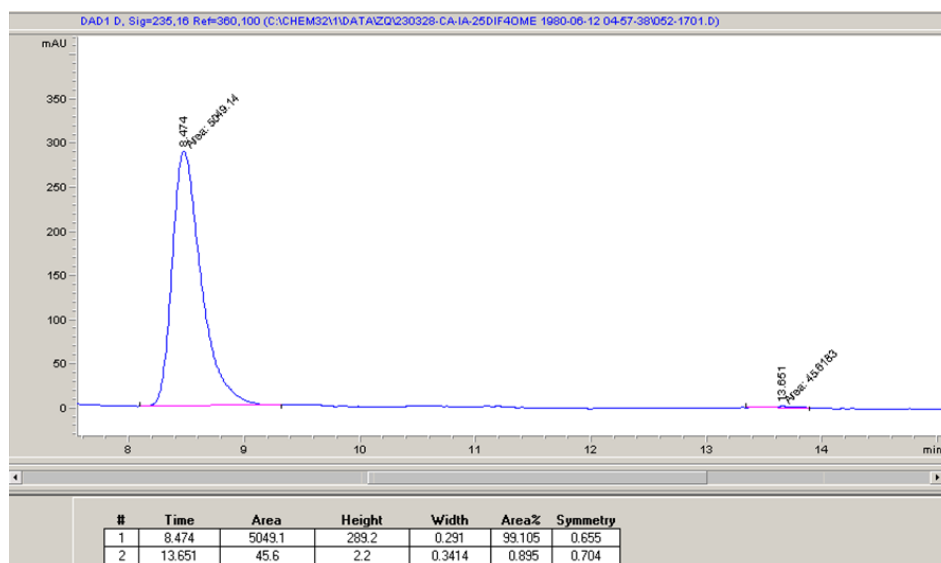
### (*R*)-2-(4-Methoxyphenyl)pyrrolidine (2d)

Chiral-phase HPLC conditions: Chiralpak IA, 15% *i*-PrOH in hexane, 1.5 mL/min, 25 °C, 210 nm

**Racemic 2d:**



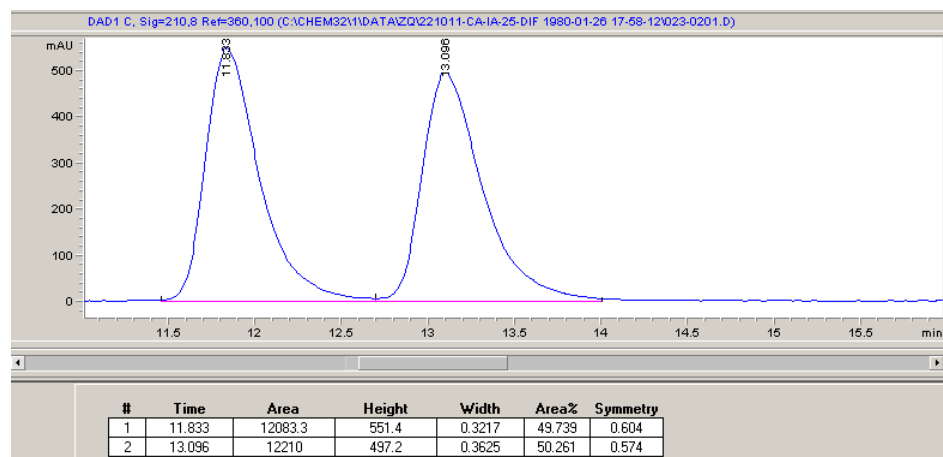
**Enzymatic preparation of 2d with P411-PYS-5149: 99:1 *er***



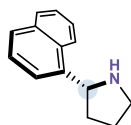
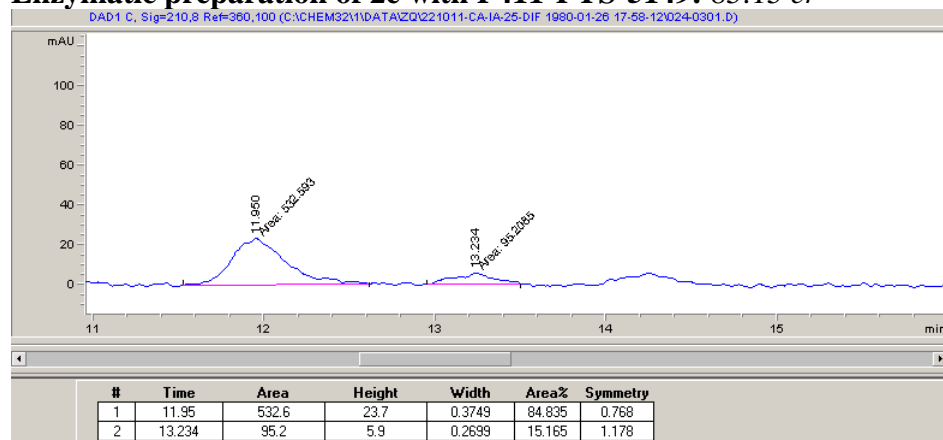
**(*R*)-2-(2,5-Difluorophenyl)pyrrolidine (2e)**

Chiral-phase HPLC conditions: Chiralpak IA, 7% *i*-PrOH in hexane, 1.5 mL/min, 25 °C, 210 nm

**Racemic 2e:**



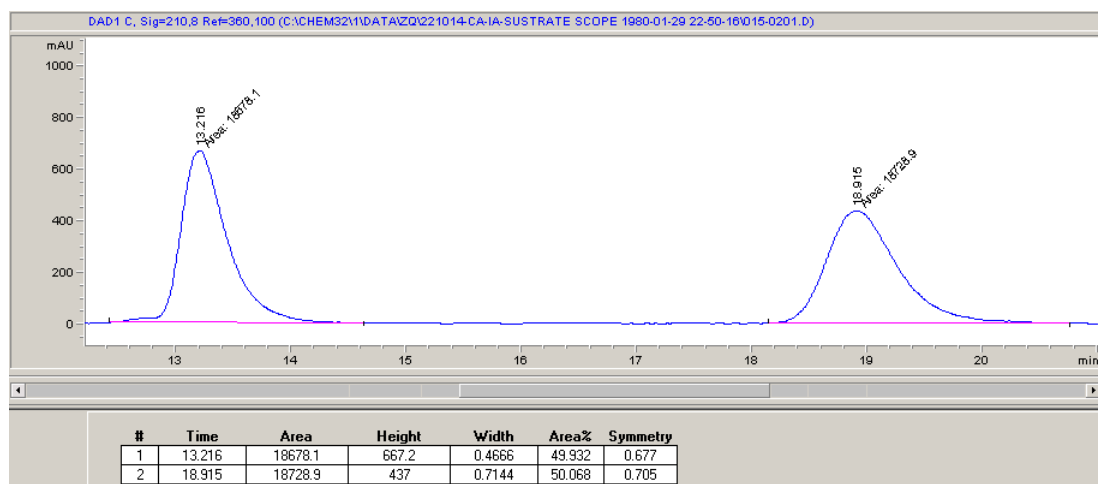
### Enzymatic preparation of 2e with P411-PYS-5149: 85:15 *er*



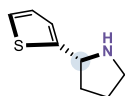
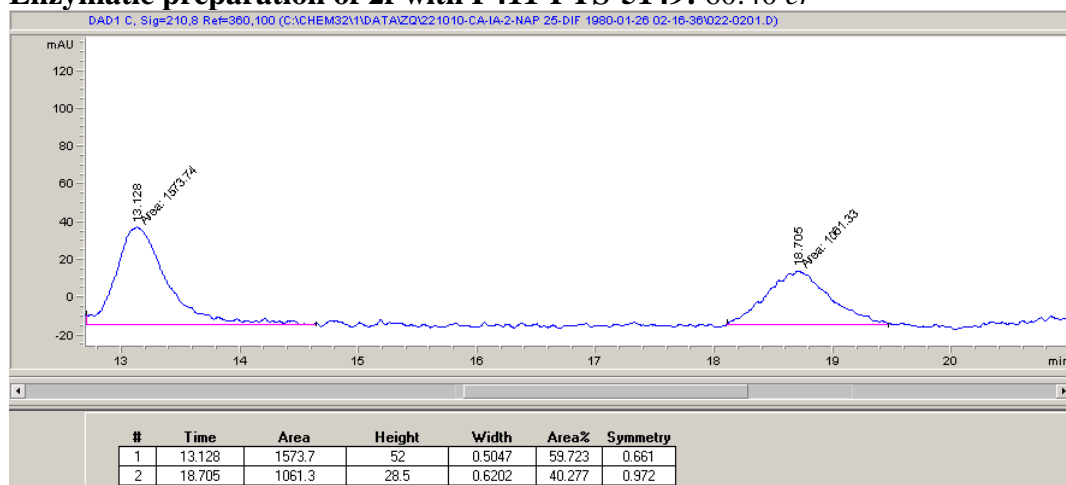
### (*R*)-2-(Naphthalen-2-yl)pyrrolidine (2f)

Chiral-phase HPLC conditions: Chiralpak IA, 10% *i*-PrOH in hexane, 1.5 mL/min, 25 °C, 210 nm

### Racemic 2f:



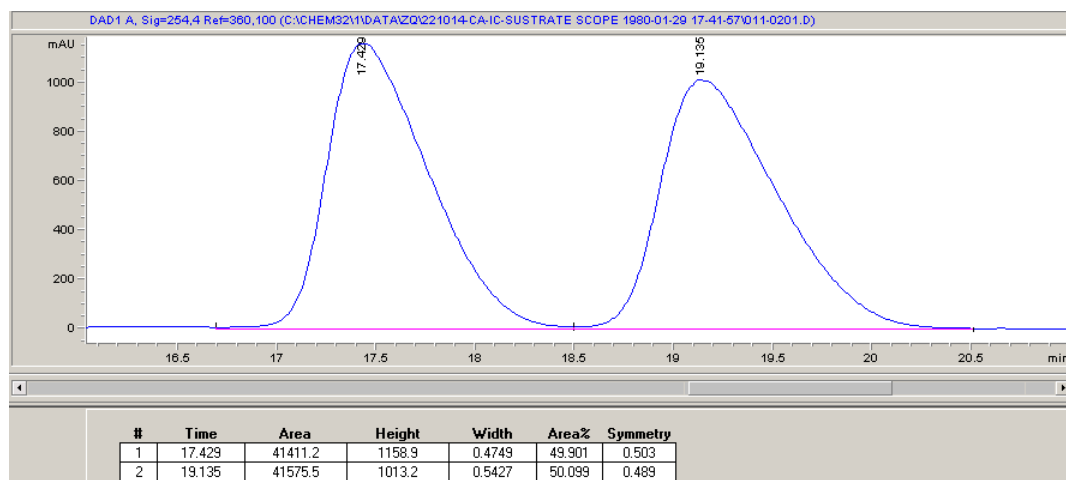
### Enzymatic preparation of 2f with P411-PYS-5149: 60:40 *er*



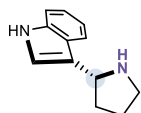
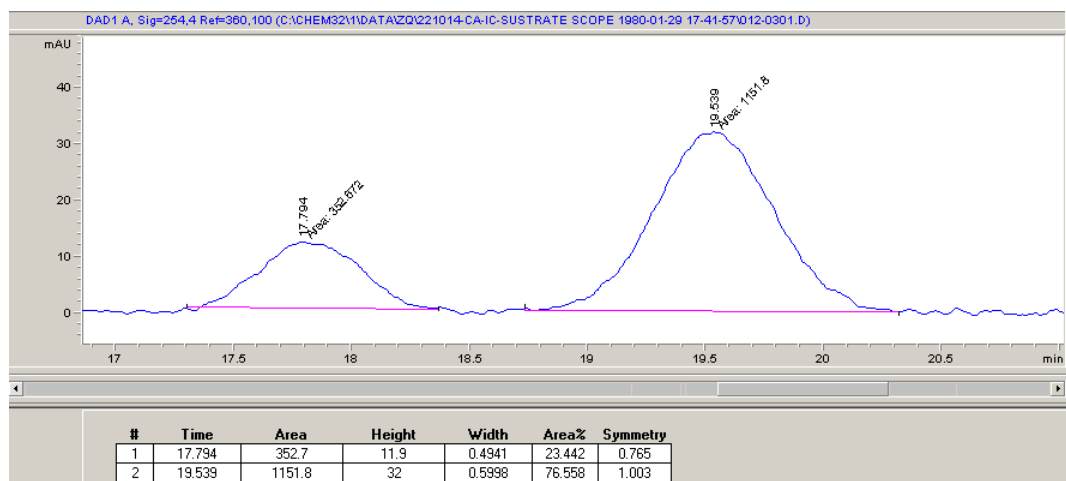
### 2-(Thiophen-2-yl)pyrrolidine (2g)

Chiral-phase HPLC conditions: Chiralpak IC, 25% *i*-PrOH in hexane, 1.5 mL/min, 25 °C, 254 nm

**Racemic 2g:**



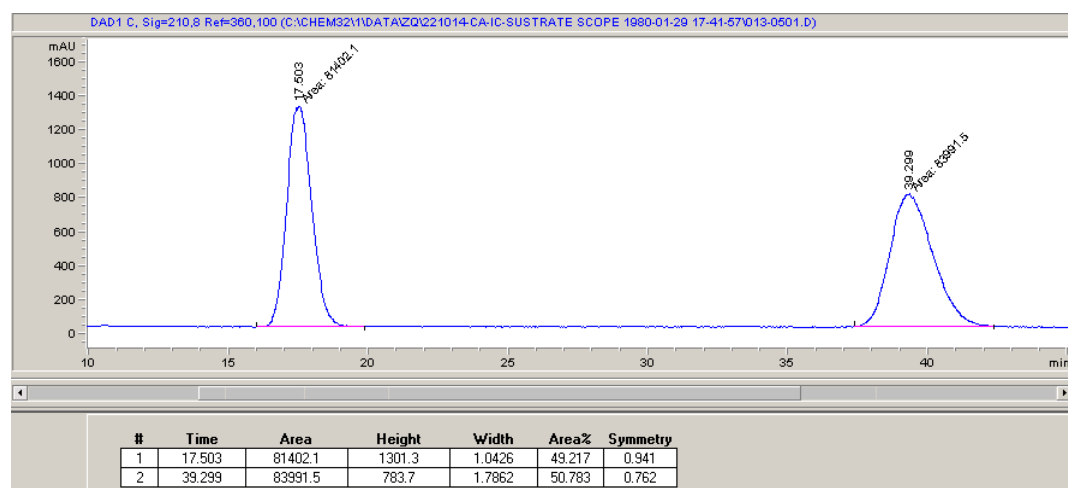
**Enzymatic preparation of 2g with P411-PYS-5149: 23:77 *er***



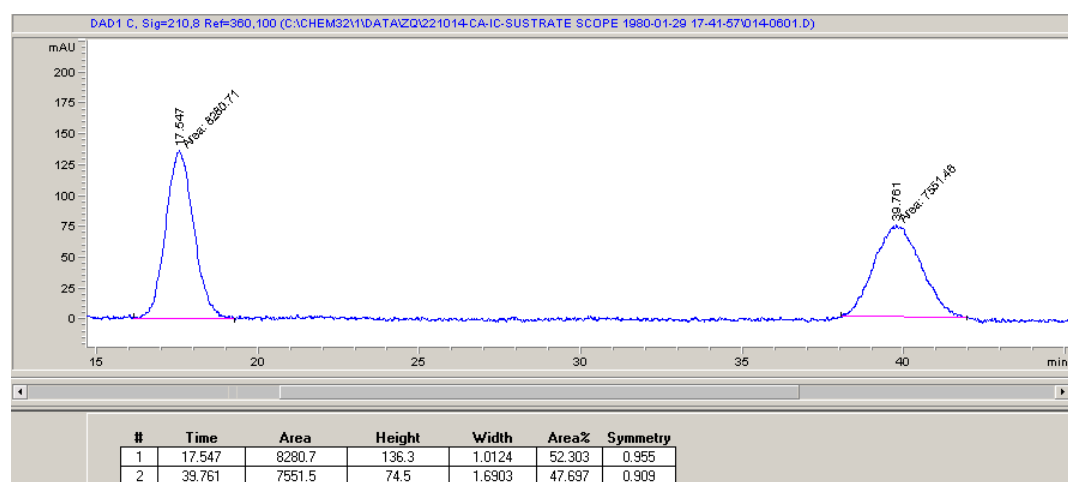
### 3-(Pyrrolidin-2-yl)-1H-indole (2h)

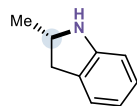
Chiral-phase HPLC conditions: Chiralpak IC, 20% *i*-PrOH in hexane, 1.5 mL/min, 25 °C, 210 nm

**Racemic 2h:**



Enzymatic preparation of 2h with P411-PYS-5149: 52:48 *er*

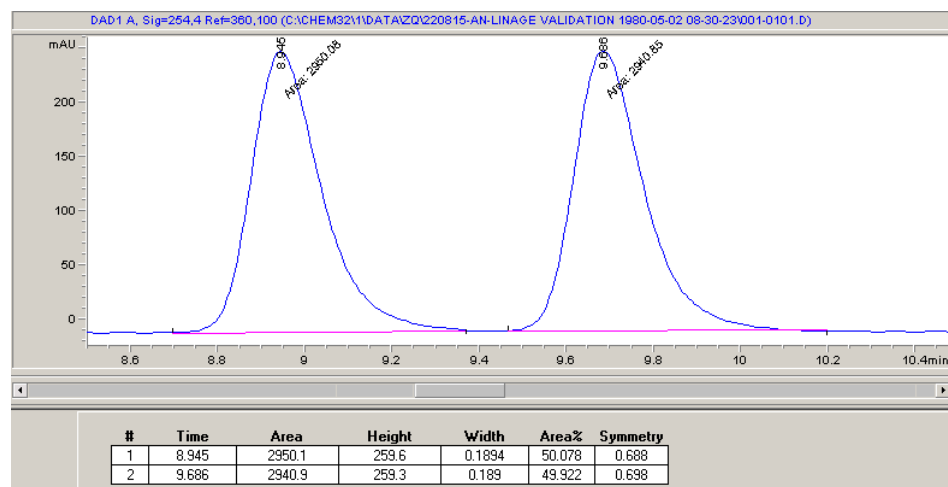




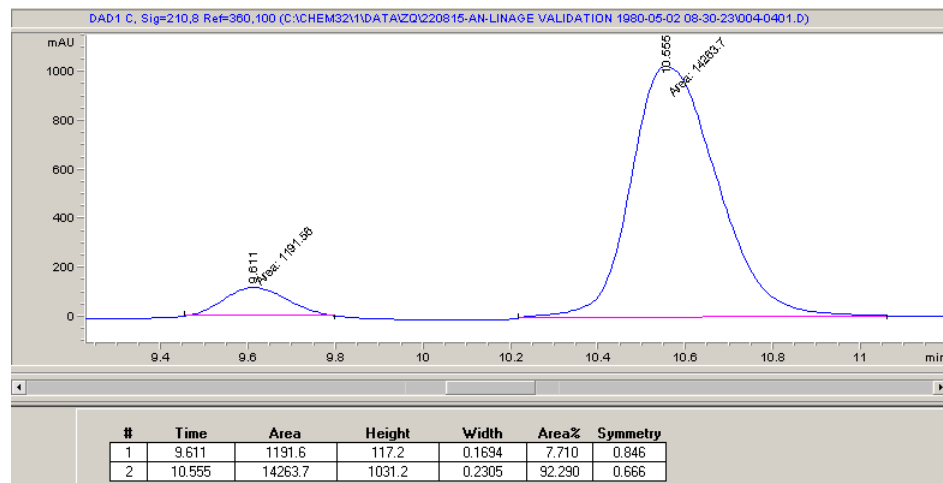
### (S)-2-Methylindoline (4a)

Chiral-phase HPLC conditions: Chiralpak IB, 2% *i*-PrOH in hexane, 1.0 mL/min, 25 °C, 254 nm

#### Racemic 4a:

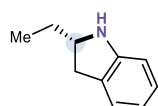
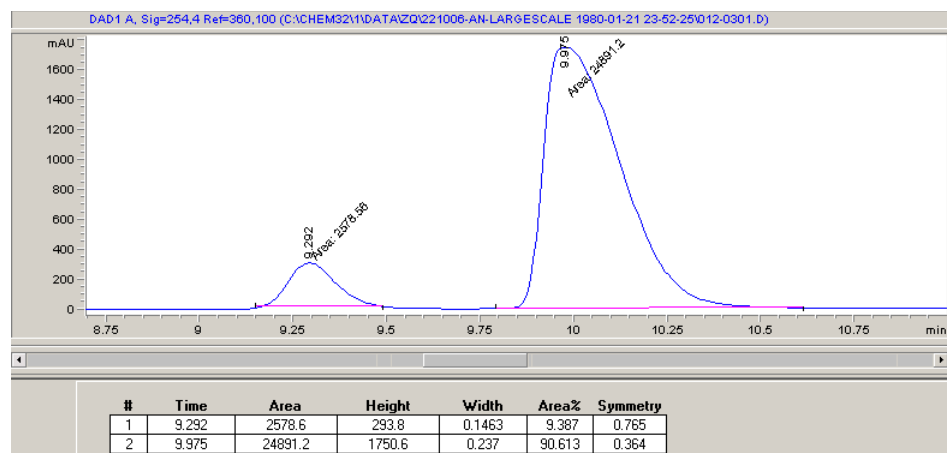


#### Enzymatic preparation of 4a with P411-INS-5151: 8:92 *er*



#### Preparative scale enzymatic preparation of 4a with P411-INS-5151: 9:91 *er*

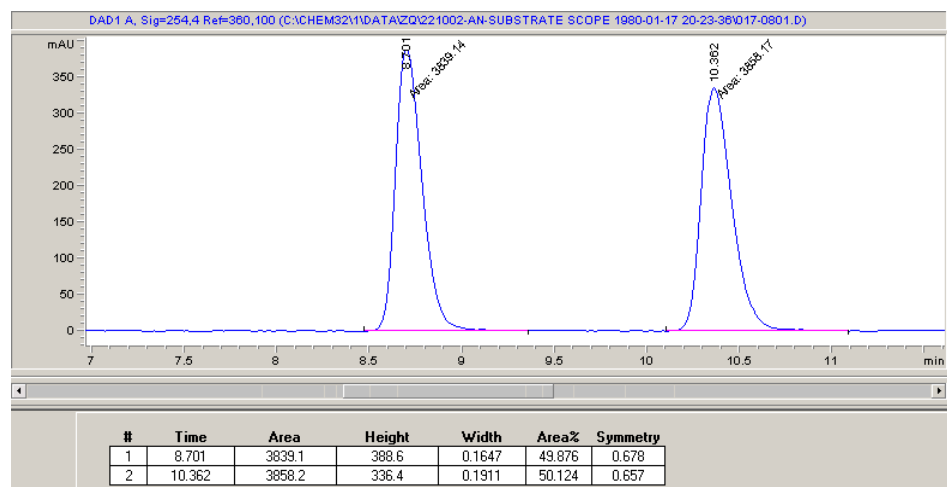




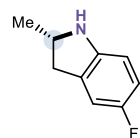
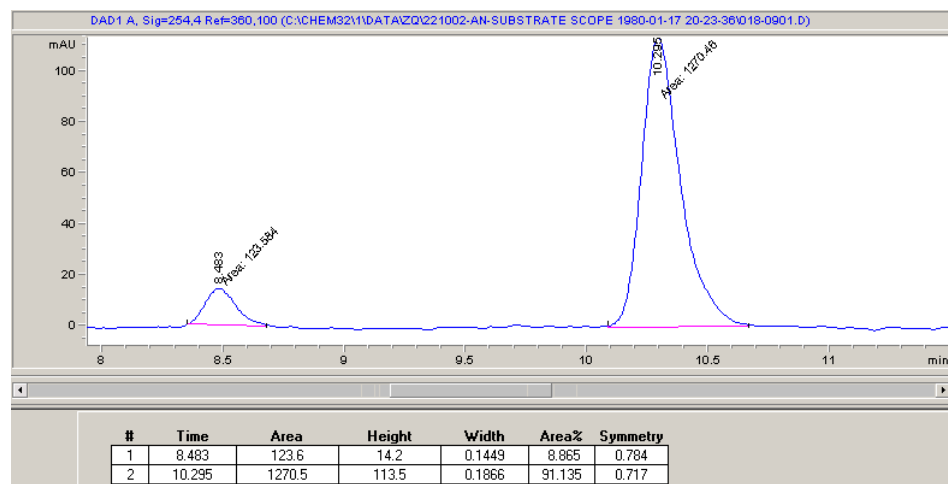
### (S)-2-Ethylindoline (4b)

Chiral-phase HPLC conditions: Chiralpak IB, 2% *i*-PrOH in hexane, 1.0 mL/min, 25 °C, 254 nm

### Racemic 4b:



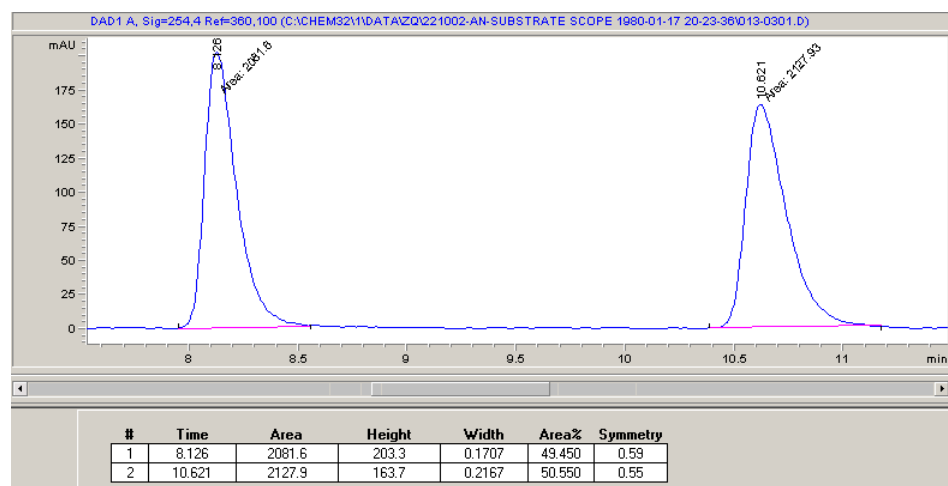
Enzymatic preparation of 4b with P411-INS-5151: 9:91 *er*



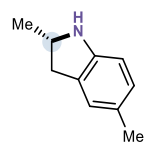
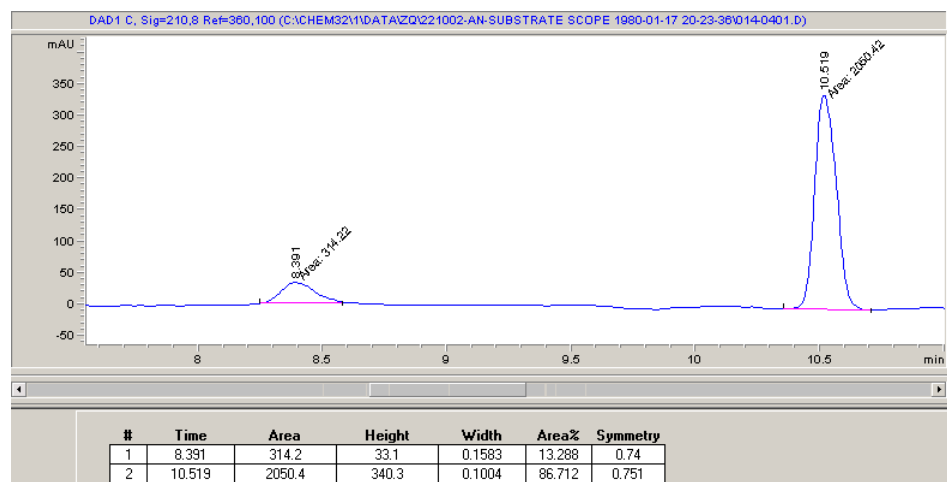
### (S)-5-Fluoro-2-methylindoline (4c)

Chiral-phase HPLC conditions: Chiralpak IB, 2% *i*-PrOH in hexane, 1.0 mL/min, 25 °C, 254 nm

### Racemic 4c:



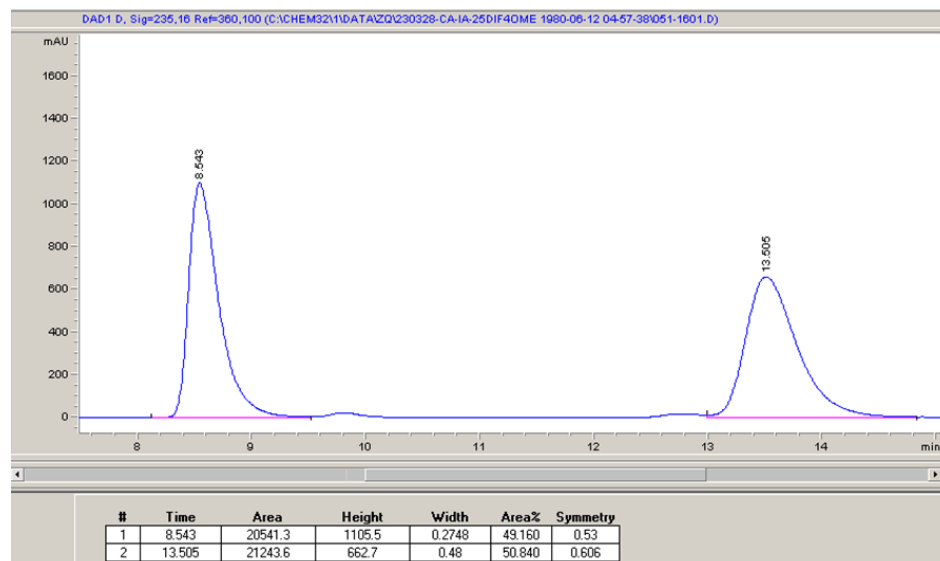
Enzymatic preparation of 4c with P411-INS-5151: 13:87 *er*



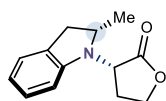
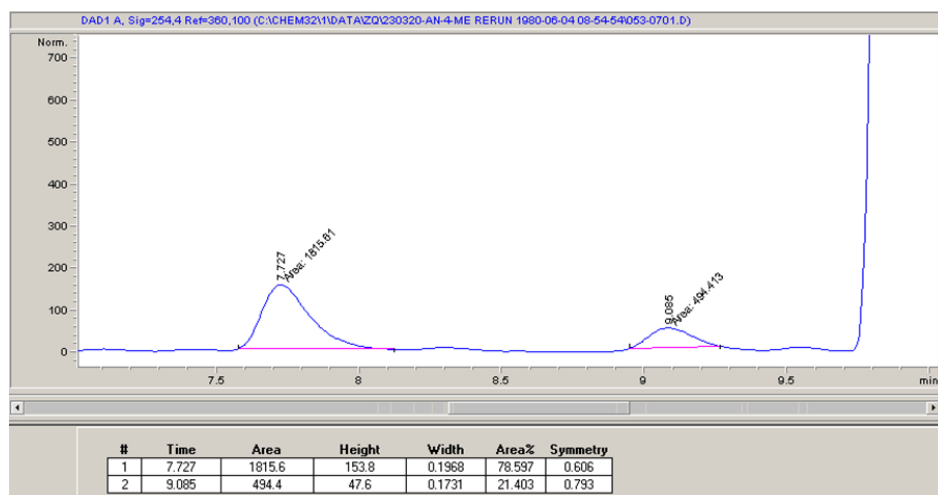
#### (S)-2,5-Dimethylindoline (4d)

Chiral-phase HPLC conditions: Chiralpak IB, 2% *i*-PrOH in hexane, 1.0 mL/min, 25 °C, 254 nm

#### Racemic 4d:



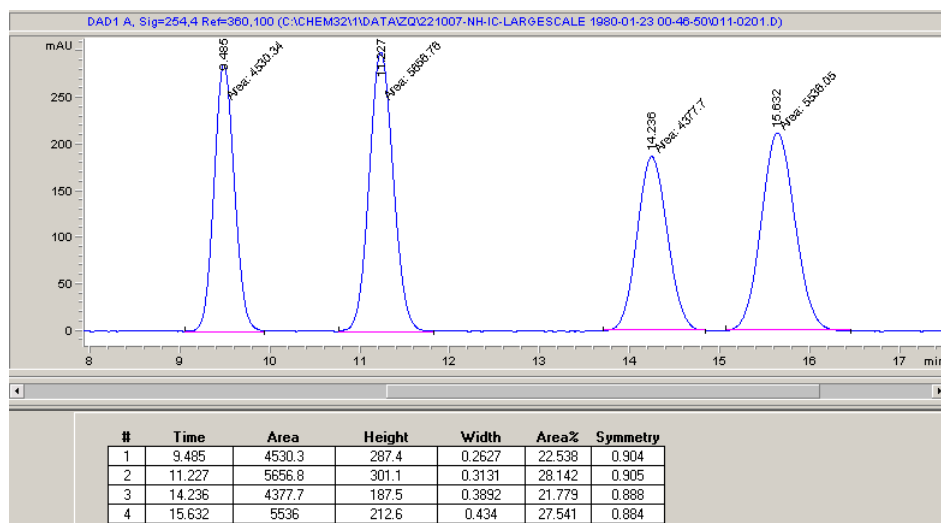
Enzymatic preparation of 4d with P411-INS-5151: 79:21 *er*



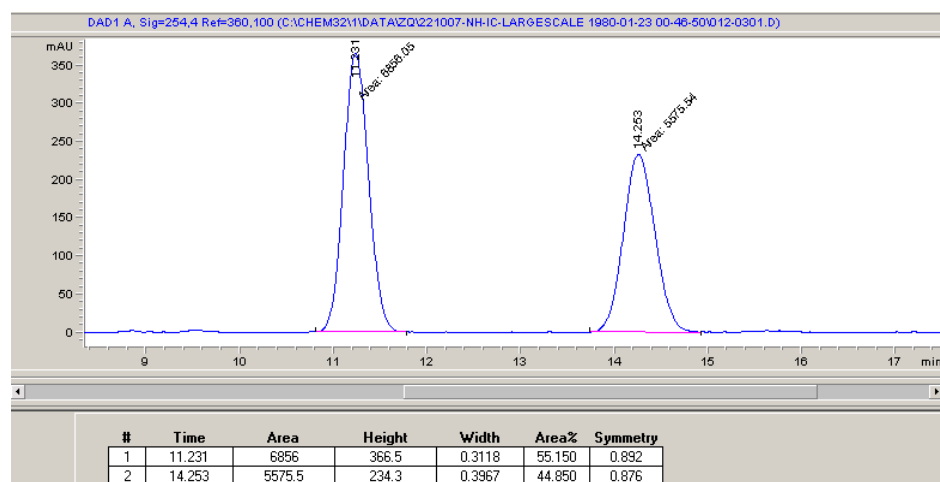
**(S)-3-((S)-2-Methylindolin-1-yl)dihydrofuran-2(3H)-one (5):**

Chiral-phase HPLC conditions: Chiralpak IC, 25% *i*-PrOH in hexane, 1.5 mL/min, 25 °C, 254 nm

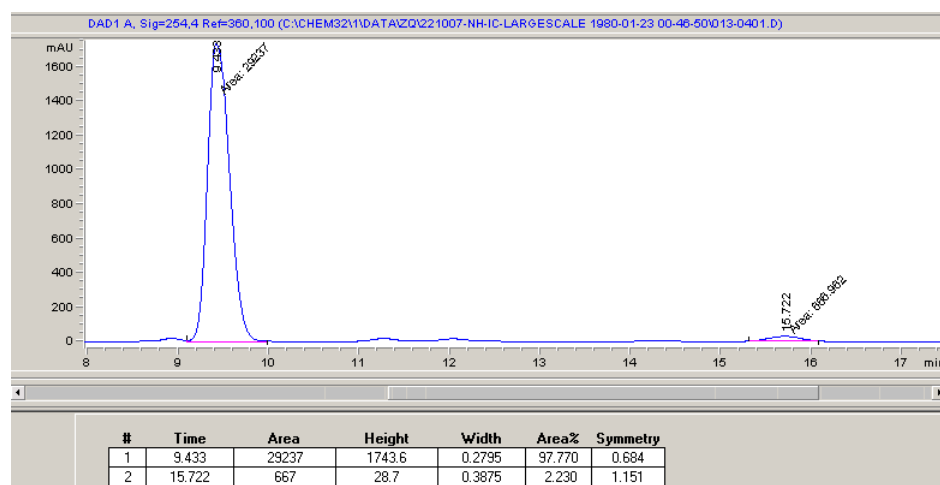
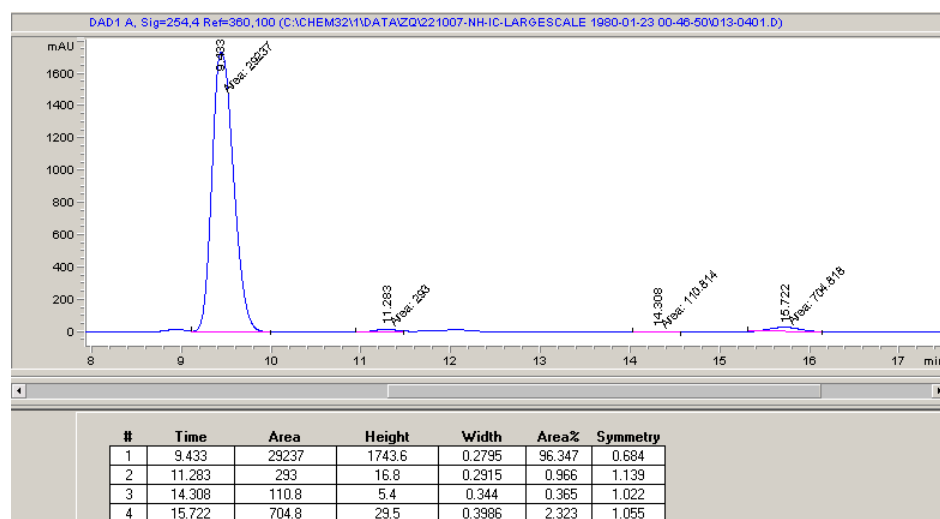
**Racemic 5:**



**Racemic 3-((S)-2-methylindolin-1-yl)dihydrofuran-2(3H)-one:**



**Preparative scale enzymatic preparation of 5 with L7\_FL: 98:2 *er* and >24:1 *dr***



## IX. Sequence Information

### Mutations present in P411 variants described in this study:

P411 variant	Mutations relative to wild-type P450 <sub>BM3</sub>
P411-M177L (P411-PYS-5141)	A74G V78L A82L F87A P142S T175I M177L A184V S226R H236Q E252G I263Y H266V T268G A290V T327I A328V L353V I366V C400S T436L L437Q E442K
P411-PYS-5142	A74G <b>L75E</b> V78L A82L F87A P142S T175I M177L A184V S226R H236Q E252G I263Y H266V T268G A290V T327I A328V L353V I366V C400S T436L L437Q E442K
P411-PYS-5143	A74G <b>L75E</b> V78L A82L F87A P142S T175I M177L A184V S226R H236Q E252G I263Y H266V T268G A290V T327I A328V L353V I366V C400S T436L E442K
P411-PYS-5144	A74G <b>L75E</b> V78L A82L F87A P142S T175I M177L A184V S226R H236Q E252G I263Y H266V T268G A290V T327I A328V <b>A330Q</b> L353V I366V C400S T436L E442K
P411-PYS-5145	A74G <b>L75E</b> V78L A82L F87A <b>M118V</b> P142S T175I M177L A184V S226R H236Q E252G I263Y H266V T268G A290V T327I A328V <b>A330Q</b> L353V I366V C400S T436L E442K
P411-PYS-5146	A74G <b>L75E F77C</b> V78L A82L F87A <b>M118V</b> P142S T175I M177L A184V S226R H236Q E252G I263Y H266V T268G A290V T327I A328V <b>A330Q</b> L353V I366V C400S T436L E442K
P411-PYS-5147	<b>S72W</b> A74G <b>L75E F77C</b> V78L A82L F87A <b>M118V</b> P142S T175I M177L A184V S226R H236Q E252G I263Y H266V T268G A290V T327I A328V <b>A330Q</b> L353V I366V C400S T436L E442K
P411-PYS-5148	<b>S72W Q73A</b> A74G <b>L75E F77C</b> V78L A82L F87A <b>M118V</b> P142S T175I M177L A184V S226R H236Q E252G I263Y H266V T268G A290V T327I A328V <b>A330Q</b> L353V I366V C400S T436L E442K
P411-PYS-5149	<b>S72W Q73A</b> A74G <b>L75E F77C</b> V78L A82L F87A <b>M118V</b> P142S T175I M177L A184V S226R H236Q E252G I263Y H266V T268G A290V T327I A328V <b>A330Q</b> L353V I366V C400S <b>T436R</b> E442K
P411-INS-5150	<b>S72W Q73A</b> A74G <b>L75E F77C</b> V78L A82L F87A <b>M118V</b> P142S T175I M177L A184V S226R H236Q E252G I263Y H266V T268G A290V T327I A328V <b>A330Q</b> L353V I366V C400S T436L <b>L437P</b> E442K
P411-INS-5151	<b>S72W Q73A</b> A74G <b>L75E F77C</b> V78L A82L F87A <b>M118V</b> P142S T175I M177L <b>L181N</b> A184V S226R H236Q E252G I263Y H266V T268G A290V T327I A328V <b>A330Q</b> L353V I366V C400S T436L <b>L437P</b> E442K

**Nucleotide and amino acid sequences of P411-M177L (P411-PYS-5141):**

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### Nucleotide and amino acid sequences of P411-PYS-5142:

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### **Nucleotide and amino acid sequences of P411-PYS-5143:**

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TTGCGTCGAAGTATCTTGCCGAGCTGCAAGAAGGAGATACGATTACGTGCTTTATTTCCACACCGCAGTC  
AGAATTTACGCTGCCAAAAGACCCTGAAACGCCGCTTATCATGGTCGGACCGGGAACAGGCGTCGCGCCG  
TTTAGAGGCTTTGTGACGGCGCGCAAACAGCTAAAAGAACAAGGACAGTCACTTGGAAGACACATTTAT  
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CATCATTACGCTTCATACCGCTTTTTTCTCGCATGCCAAATCAGCCGAAAACATACGTTTCAGCACGTAATG  
GAACAAGACGGCAAGAAATTGATTGAACTTCTTGATCAAGGAGCGCACTTCTATATTTGCGGAGACGGAA  
GCCAAATGGCACCTGCCGTTGAAGCAACGCTTATGAAAAGCTATGCTGACGTTACCAAGTGAGTGAAGC  
AGACGCTCGCTTATGGCTGCAGCAGCTAGAAGAAAAAGGCCGATACGCAAAGACGTGTGGGCTGGGCTC  
GAGCACCACCACCACCACCACTGA

MTIKEMPQPKTFGELKNLPLLNTDKPVQALMKIADDELGEIFKFEAPGRVTRYLSSQRLIKEACDESRFDK  
NLSQGEKFLRDFLDGLATSWTHEKNWKKAHNILLPSFSQAMKGYHAMMVDAVQLVQKWERLNADDEHI  
EVSEDMTRLTLDTIGLCGFNYRFNSFYRDQPHFPIISLVRALDEV MNKLQRANPDDPAYDENKRQFQEDI  
KVMNDLVDKIIADRKARGEQSDDLTLQMLNGKDPETGEPLDDGNIRYQIIITFLYAGVEGTSGLLSFALYF  
LVKNPHVLQKVAEEAARVLVDPVPSYKQVKQLKYVGMVLNEALRLWPVPAFSLYAKEDTVLGGEYPLEK  
GDEVMLIPQLHRDKTVWGDDVEEFRPERFENPSAIPQHAFKPFNGQORASIGQQFALHEATLVLGMMMLK  
HFDFEDHTNYELDIKELLTLKPKGFVVKAKSKKIPLGGIPSPSTEQS AKKVRKKAENAHNTPLLVLVYGSN  
MGTAEGTARDLADIAMSKGFAPQVATLDSHAGNLPREGAVLIVTASYNHPPDNAKQFVDWLDQASADEV  
KGVRYSVFGCGDKNWATTYQKVPAFIDETLAAGAENIADRGEADASDDFEGTYEEWREHMWSDVAA YFN  
LDIENSEDNKSTLSLQFVDSAADMPLAKMHGAFSTNVVASKELQQPGSARSTRHLEIELPKEASYQEGDH  
LGVIPRNYEGIVNRVTARFGLDASQQIRLEAEEEEKLAHLPLAKTVSVEELLQYVELQDPVTRTQLRAMAA  
KTVCPPHKVELEALLEKQAYKEQVLAKRLTMLELLEKYPACEMKFSEFIALLPISIRPRYYSISSSPRVDE  
KQASITVSVVSGEAWSGYGEYKGIASNYLAELQEGDTITCFISTPQSEFTLPKDPETPLIMVGP GTGVAP  
FRGFVQARKQLKEQGQSLGEAHL YFGCRSPHEDYLYQEEL ENAQSEGIITLHTAFSRMPNQPKTYVQHVM  
EQDGKKLIELLDQGAHFYICGDGSQMAPAVEATLMKSYADVHVQSEADARLWLQQLEEKGRYAKDVWAGL  
EHHHHHH

#### **Nucleotide and amino acid sequences of P411-PYS-5144:**

ATGACAATTAAAGAAATGCCTCAGCCAAAACGTTTGGAGAGCTTAAAAATTTACCGTTATTAAACACAG  
ATAAACCGGTTCAAGCTTTGATGAAAATTGCGGATGAATTAGGAGAAATCTTTAAATTCGAGGCGCCTGG  
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AACTTAAGTCAAGGTGAGAAATTTCTGCGTGATTTTCTTGGAGACGGGTTAGCCACAAGCTGGACGCATG  
AAAAAAATTGGGAAAAAAGCGCATAATATCTTACTTCCAAGCTTTAGTCAGCAGGCAATGAAAGGCTATC  
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TGAAGTATCGGAAGACATGACACGTTTAAACGCTTGATACAATTGGTCTTTGCGGCTTTAACTATCGCTTT

AACAGCTTTTACCGAGATCAGCCTCATCCATTTATTATAAGTCTGGTCCGTGCACTGGATGAAGTAATGA  
ACAAGCTGCAGCGAGCAAATCCAGACGACCCAGCTTATGATGAAAAACAAGCGCCAGTTTCAAGAAGATAT  
CAAGGTGATGAACGACCTAGTAGATAAAATTATTGCAGATCGCAAAGCAAGGGGTGAACAAAGCGATGAT  
TTATTAACGCAGATGCTAAACGGAAAAGATCCAGAAACGGGTGAGCCGCTTGATGACGGGAACATTCGCT  
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CTTAGTGAAAAATCCACATGTATTACAAAAAGTAGCAGAAGAAGCAGCAGAGTTCTAGTAGATCCTGTT  
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CAATTGTTCCCTCAGTTTTTCCCTATATGCAAAAGAAGATACGGTGCTTGGAGGAGAATATCCTTTAGAAAA  
AGGCGACGAAGTAATGGTTCTGATTCTCAGCTTCACCGTGATAAAACAGTTTGGGGAGACGATGTGGAG  
GAGTTCCGTCCAGAGCGTTTTTGAAAATCCAAGTGCATTCCGCAGCATGCGTTTAAACCGTTTGGAACG  
GTCAGCGTGCGTCTATCGGTGAGCAGTTTCGCTCTTCATGAAGCAACGCTGGTACTTGGTATGATGCTAAA  
ACACTTTGACTTTGAAGATCATACAAACCTACGAGCTCGATATTAAAGAACTGCTGACGTTAAACCTAAA  
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GCTTTTATCGATGAAACGCTTGCCGCTAAAGGGGCAGAAAACATCGCTGACCGCGGTGAAGCAGATGCAA  
GCGACGACTTTGAAGGCACATATGAAGAATGGCGTGAACATATGTGGAGTGACGTAGCAGCCTACTTTAA  
CCTCGACATTGAAAACAGTGAAGATAATAAATCTACTCTTTCACCTCAATTTGTGACAGCGCCGCGGAT  
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ATTGCGTCGAACTATCTTGCCGAGCTGCAAGAAGGAGATACGATTACGTGCTTTATTTCCACACCGCAGT  
CAGAATTTACGCTGCCAAAAGACCCTGAAACGCCGCTTATCATGGTTCGACCGGGAACAGGCGTCGCGCC  
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TACTTCGGCTGCCGTTACCTCATGAAGACTATCTGTATCAAGAAGAGCTTGAAAACGCCCAAAGCGAAG  
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GGAACAAGACGGCAAGAAATTGATTGAACTTCTTGATCAAGGAGCGCACTTCTATATTTGCGGAGACGGA  
AGCCAAATGGCACCTGCCGTTGAAGCAACGCTTATGAAAAGCTATGCTGACGTTACCAAGTGAGTGAAG  
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MTIKEMPQPKTFGELKNLPLLNTDKPVQALMKIADELGEIFKFEAPGRVTRYLSSQRLIKEACDESFRDK  
NLSQGEKFLRDFLDGLATSWTHEKNWKAHNILLPSFSQQAMKGYHAMMVDAIVQLVQKWERLNADEHI  
EVSEDMTRLTLDTIGLCGFNYRFNSFYRDQPHPFIISLVRALDEV MNKLQRANPDDPAYDENKRQFQEDI  
KVMNDLVDKIIADRKARGEQSDDLTLQMLNGKDPETGEPLDDGNIRYQIITFLYAGVEGTSGLLSFALYF  
LVKNPHVLQKVAEEAARVLVDPVPSYKQVKQLKYVGMVLNEALRLWPIVPQFSLYAKEDTVLGGEYPLEK  
GDEVMLIPQLHRDKTVWGDDVEEFRPERFENPSAIPQHAFKPFNGQRASIGQQFALHEATLVLGMLLK  
HFD FEDHTNYELDIKELLTLKPKGFVVKAKSKKIPLGGIPSPSTEQSAKKVRKKAENAHNTPLLVLVYGSN  
MGTAEGTARDLADIAMSKGFAPQVATLDSHAGNLPREGAVLIVTASYNHPPDNAKQFVDWLDAQASADEV  
KGVRYSVFGCDKNWATTYQKVPFIDETLAAKGAENIADRGEADASDDFEGTYEEWREHMWSDVAAAYFN  
LDIENSEDNKSTLSLQFVDSADMP LAKMHGAFSTNVVASKELQQPGSARSTRHLEIELPKEASYQEGDH  
LGVIPRNYEGIVNRVTARFLDASQQIRLEAEEEKLAHLPLAKTVSVEELLQYVELQDPVTRTQLRAMAA  
KTVCPPHKVELEALLEKQAYKEQVLAKRLTMLELLEKYPACEMKFSEFIALLP S I R P R Y Y S I S S S P R V D E

KQASITVSVVSGEAWSGYGEYKGIASNYLAELQEGDTITCFISTPQSEFTLPKDPETPLIMVGP GTGVAP  
FRGFVQARKQLKEQGQSLGEAHL YFGCRSPHEDYLYQEEL ENAQSEGIITLHTAFSRMPNQPKTYVQHVM  
EQDGKKLIELLDQGAHFYICGDGSQMAPAVEATLMKSYADVHQVSEADARLWLQQLEEKGRYAKDVWAGL  
EHHHHHH

**Nucleotide and amino acid sequences of P411-PYS-5145:**

ATGACAATTAAAGAAATGCCTCAGCCAAAAACGTTTGGAGAGCTTAAAAATTTACCGTTATTAAACACAG  
ATAAACCGGTTCAAGCTTTGATGAAAATTGCGGATGAATTAGGAGAAATCTTTAAATTCGAGGCGCCTGG  
TCGTGTAACGCGCTACTTATCAAGTCAGCGTCTAATTAAAGAAGCATGCGATGAATCACGCTTTGATAAA  
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AAAAAAATTGGGAAAAAAGCGCATAATATCTTACTTCCAAGCTTTAGTCAGCAGGCAATGAAAGGCTATC  
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AACAGCTTTTACCGAGATCAGCCTCATCCATTTATTATAAGTCTGGTCCGTGCACTGGATGAAGTAATGA  
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CAAGGTGATGAACGACCTAGTAGATAAAATTATTGCAGATCGCAAAGCAAGGGGTGAACAAAGCGATGAT  
TTATTAACGCAGATGCTAAACGGAAAAAGATCCAGAAACGGGTGAGCCGCTTGATGACGGGAACATTCGCT  
ATCAAAATTATTACATTCTTATATGCGGGAGTTGAAGGTACAAGTGGTCTTTTATCATTTGCGCTGTATTT  
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AGGCGACGAAGTAATGGTTCTGATTCCTCAGCTTCACCGTGATAAAACAGTTTGGGGAGACGATGTGGAG  
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GCGACGACTTTGAAGGCACATATGAAGAATGGCGTGAACATATGTGGAGTGACGTAGCAGCCTACTTTAA  
CCTCGACATTGAAAACAGTGAAGATAATAAATCTACTCTTTCACCTCAATTTGTGCGACAGCGCCGCGGAT  
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ATTGCGTCGAACTATCTTGCCGAGCTGCAAGAAGGAGATACGATTACGTGCTTTATTTCCACACCGCAGT  
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CGAGCACCACCACCACCACCTGA

MTIKEMPQPKTFGELKNLPLLNTDKPVQALMKIADDELGEIFKFEAPGRVTRYLSSQRLIKEACDESFRDK  
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EVSEDMTRLTLDTIGLCGFNYRFNSFYRDQPHFPIISLVRALDEV MNKLQRANPDDPAYDENKRQFQEDI  
KVMNDLVDKIIADRKARGEQSDDLTLQMLNGKDPETGEPLDDGNIRYQIITFLYAGVEGTSGLLSFALYF  
LVKNPHVLQKVAEEAARVLVDPVPSYKQVKQLKYVGMVLNEALRLWP IVPQFSLYAKEDTVLGGEYPLEK  
GDEVMLIPLQLHRDKTVWGDDVEEFRPERFENPSAIPQHAFKPFNGQRASIGQQFALHEATLVLGMMMLK  
HFD FEDHTNYELDIKELLTLKPKGFVVKAKSKKIPLGGIPSPSTEQSAKKVRKKAENAHNTPLLVLVLYGSN  
MGTAEGTARDLADIAMSKGFAPQVATLDSHAGNLPREGAVLIVTASYNHPPDNAKQFVDWLDQASADEV  
KGVRYSVFGCGDKNWATTYQKVPAFIDETLAAKGAENIADRGEADASDDFEGTYEEWREHMWSDVAAYFN  
LDIENSEDNKSTLSLQFVDSAADMPLAKMHGAFSTNVVASKELQQPGSARSTRHLEIELPKEASYQEGDH  
LGVIPRNYEGIVNRVTARFGLDASQQIRLEAEEEKLAHLPLAKTVSVEELLQYVELQDPVTRTQLRAMAA  
KTVCPPHKVELEALLEKQAYKEQVLAKRLTMLELLEKYPACEMKFSEFIALLP SIRPRYYSISSSPRVDE  
KQASITVSVVSGEAWSGYGEYKGIASNYLAELQEGDTITCFISTPQSEFTLPKDPETPLIMVGPGTGVAP  
FRGFVQARKQLKEQGQSLGEAHL YFGCRSPHEDYLYQEELENAQSEGIITLHTAFSRMPNQPKTYVQHVM  
EQDGKKLIELLDQGAHFYICGDSQMAPAVEATLMKSYADVHVQVSEADARLWLQQL EEKGRYAKDVWAGL  
EHHHHHH

**Nucleotide and amino acid sequences of P411-PYS-5146:**

ATGACAATTAAAGAAATGCCTCAGCCAAAAACGTTTGGAGAGCTTAAAAATTTACCGTTATTAAACACAG  
ATAAACCGGTTCAAGCTTTGATGAAAATTGCGGATGAATTAGGAGAAATCTTTAAATTCGAGGCGCCTGG  
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AACAGCTTTTTACCGAGATCAGCCTCATCCATTTATTATAAGTCTGGTCCGTGCACTGGATGAAGTAATGA  
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ATCAAAATTATTACATTCTTATATGCGGGAGTTGAAGGTACAAGTGGTCTTTTATCATTTGCGCTGTATTT  
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GCGACGACTTTGAAGGCACATATGAAGAATGGCGTGAACATATGTGGAGTGACGTAGCAGCCTACTTTAA  
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TTTAGGTGTTATTCCTCGCAACTATGAAGGAATAGTAAACCGTGTAACAGCAAGGTTCCGCCTAGATGCA

TCACAGCAAATCCGTCTGGAAGCAGAAGAAGAAAAATTAGCTCATTGCCACTCGCTAAAACAGTATCCG  
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GCATCATTACGCTTCATACCGCTTTTCTCGCATGCCAAATCAGCCGAAAACATACGTTTACGACGTAAT  
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MTIKEMPQPKTFGELKNLPLLNTDKPVQALMKIADELGEIFKFEAPGRVTRYLSSQRLIKEACDESFRDK  
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GDEVMLIPQLHRDKTVWGDDVEEFRPERFENPSAIPQHAFKPFNGQRASIGQQFALHEATLVLGMLLK  
HFD FEDHTNYELDIKELLTLKPKGFVVKAKSKKIPGGIPSPSTEQSAKKVRKKAENAHNTPLLVLVYGSN  
MGTAEGTARDLADIAMSKGFAPQVATLDSHAGNLPREGAVLIVTASYNHPPDNAKQFVDWLDQASADEV  
KGVRYSVFGCGDKNWATTYQKVPAFIDETLAAKGAENIADRGEADASDDFEGTYEEWREHMWSDVAAYFN  
LDIENSEDNKSTLSLQFVDSAADMPLAKMHGAFSTNVVASKELQQPGSARSTRHLEIELPKEASYQEGDH  
LGVIPRNYEGIVNRVTARFLDASQQIRLEAEEEEKLAHLPLAKTVSVEELLQYVELQDPVTRTQLRAMAA  
KTVCPPHKVELEALLEKQAYKEQVLAKRLTMLELLEKYPACEMKFSEFIALLPISIRPRYSSISSSPRVDE  
KQASITVSVVSGEAWSGYGEYKGIASNYLAELQEGDTITCFISTPQSEFTLPKDPETPLIMVGPGTGVP  
FRGFVQARKQLKEQGQSLGEAHLVFGCRSPHEDYLYQEELNAQSEGIITLHTAFSRMPNQPKTYVQHVM  
EQDGKKLIELLDQGAHFYICGDSQMAPAVEATLMKSYADVHQVSEADARLWLQQLLEEKGRYAKDVWAGL  
EHHHHHH

#### **Nucleotide and amino acid sequences of P411-PYS-5147:**

ATGACAATTAAAGAAATGCCTCAGCCAAAACGTTTGAGAGAGCTTAAAAATTTACCGTTATTAAACACAG  
ATAAACCGGTTCAAGCTTTGATGAAAATTGCGGATGAATTAGGAGAAATCTTTAAATTCGAGGCGCCTGG  
TCGTGTAACGCGCTACTTATCAAGTCAGCGTCTAATTAAAGAAGCATGCGATGAATCACGCTTTGATAAA  
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AAAAAAATTGGGAAAAAAGCGCATAATATCTTACTTCCAAGCTTTAGTCAGCAGGCAATGAAAGGCTATC  
ATGCGGTGATGGTCGATATCGCCGTGCAGCTTGTTCAAAAGTGGGAGCGTCTAAATGCAGATGAGCATAT  
TGAAGTATCGGAAGACATGACACGTTTAAACGCTTGATACAATTGGTCTTTGCGGCTTTAACTATCGCTTT  
AACAGCTTTTACCAGATCAGCCTCATCCATTTATTATAAGTCTGGTCCGTGCACTGGATGAAGTAATGA  
ACAAGCTGCAGCGAGCAAATCCAGACGACCCAGCTTATGATGAAAACAAGCGCCAGTTTCAAGAAGATAT  
CAAGGTGATGAACGACCTAGTAGATAAAATTATTGCAGATCGCAAAGCAAGGGGTGAACAAAGCGATGAT  
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AGGCGACGAAGTAATGGTTCTGATTCCTCAGCTTCACCGTGATAAAACAGTTTGGGGAGACGATGTGGAG  
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 KVMNDLVDKIIADRKARGEQSDDLTLQMLNGKDPETGEPLDDGNIRYQIITFLYAGVEGTSGLLSFALYF  
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 GDEVMLIPLHRDKTVWGDDVEEFRPERFENPSAIPQHAFKPFNGQQRASIGQQFALHEATLVLGMLLK  
 HFDFFEDHTNYELDIKELLTLKPKGFVVKAKSKKIPLGGIPSPSTEQSAKKVRKKAENAHNTPLLVLYGSN  
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 LDIENSEDNKSTLSLQFVDSAADMPLAKMHGAFSTNVVASKELQQPGSARSTRHLEIELPKEASYQEGDH  
 LGVIPRNYEGIVNRVTARFGLDASQQIRLEAEKEKLAHLPLAKTVSVEELLQYVELQDPVTRTQLRAMAA  
 KTVCPPHKVELEALLEKQAYKEQVLAKRLTMLELLEKYPACEMKFSEFIALLPISIRPRYSSISSSPRVDE  
 KQASITVSVVSGEAWSGYGEYKGIASNYLAELQEGDTITCFISTPQSEFTLPKDPETPLIMVGPPTGVAP  
 FRGFVQARKQLKEQGQSLGEAHLFYGCRSPHEDYLYQEELNAQSEGIITLHTAFSRMPNQPKTYVQHVM  
 EQDGKKLIELLDQGAHFYICGDGSQMAPAVEATLMKSYADVHQVSEADARLWLQQLLEEKGRYAKDVWAGL  
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# **Nucleotide and amino acid sequences of P411-PYS-5148:**

ATGACAATTAAAGAAATGCCTCAGCCAAAAACGTTTGGAGAGCTTAAAAATTTACCGTTATTAAACACAG  
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CAAGCTACAAACAAGTCAAACAGCTTAAATATGTGCGCATGGTCTTAAACGAAGCGCTGCGCTTATGGCC  
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GCCAAATGGCACCTGCCGTTGAAGCAACGCTTATGAAAAGCTATGCTGACGTTACCAAGTGAGTGAAGC  
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KVMNDLVDKIIADRKARGEQSDDLTLQMLNGKDPETGEPLDDGNIRYQIITFLYAGVEGTSGLLSFALYF  
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GDEVMLIPLQHRDKTVWGDDVEEFRPERFENPSAIPQHAFKPFNGQQRASIGQQFALHEATLVLGMLLK  
HFDFFEDHTNYELDIKELLTLKPKGFVVKAKSKKIPLGGIPSPSTEQSAKKVRKKAENAHNTPLLVLVYGSN  
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KGVRYSVFGCGDKNWATTYQKVPAFIDETLAAKGAENIADRGEADASDDFEGTYEEWREHMWSDVAAYFN  
LDIENSEDNKSTLSLQFVDSAADMPLAKMHGAFSTNVVASKELQQPGSARSTRHLEIELPKEASYQEGDH  
LGVI PRNYEGIVNRVTARFGLDASQQIRLEAEEEEKLAHLPLAKTVSVEELLQYVELQDPVTRTQLRAMAA  
KTVCPPHKVELEALLEKQAYKEQVLAKRLTMLELLEKYPACEMKFSEFIALLPsirpryysissSPRVDE  
KQASITVSVVSGEAWSGYGEYKGIASNYLAELQEGDTITCFISTPQSEFTLPKDPETPLIMVGP GTGVAP  
FRGFVQARKQLKEQGQSLGEAHL YFGCRSPHEDYLYQEELENAQSEGIITLHTAFSRMPNQPKTYVQHVM  
EQDGKKLIELLDQGAHFYICGDGSQMAPAVEATLMKSYADVHQVSEADARLWLQQL EEKGRYAKDVWAGL  
EHHHHHH

### **Nucleotide and amino acid sequences of P411-PYS-5149:**

ATGACAATTAAAGAAATGCCTCAGCCAAAAACGTTTGGAGAGCTTAAAAATTTACCGTTATTAAACACAG  
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KVMNDLVDKIIADRKARGEQSDDLTLTQMLNGKDPETGEPLDDGNIRYQIITFLYAGVEGTSGLLSFALYF  
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GDEV MVLI PQLHRDKTVWGDDVEEFRPERFENPSAIPQHAFKPFNGNGQRASIGQQFALHEATLVLGMMMLK  
HFD FEDHTNYELDIKERLTLKPKGFVVKAKSKKIPLGGIPSPSTEQSAKKVRKKAENAHNTPLLVL YGSN  
MGTAEGTARDLADIAMSKGFAPQVATLDSHAGNLPREGAVLIVTASYNHPPDNAKQFVDWLDQASADEV  
KGVRYSVFGCGDKNWATTYQKVPAFIDETLAAKGAENIADRGEADASDDFEGTYEEWREHMWSDVAAYFN  
LDIENSEDNKSTLSLQFVDSAADMPLAKMHGAFSTNVVASKELQQPGSARSTRHLEIELPKEASYQEGDH  
LGVIPRNYEGIVNRVTARFGLDASQQIRLEAEEEEKLAHLPLAKTVSVEELLQYVELQDPVTRTQLRAMAA  
KTVCPPHKVELEALLEKQAYKEQVLAKRLTMLELLEKY PACEMKFSEFIALLP SIRPRYSSISSSPRVDE  
KQASITVSVVSGEAWSGYGEYKGIASNYLAELQEGDITTCFISTPQSEFTLPKDPETPLIMVGPGTGVP  
FRGFVQARKQLKEQGQSLGEAHL YFGCRSPHEDYLYQEELENAQSEGIITLHTAFSRMPNQPKTYVQHVM  
EQDGK KLI ELLDQGAHFYICGDGSQMAPAVEATLMKSYADVHQVSEADARLWLQQLEEKGRYAKDVWAGL  
EHHHHHH

#### **Nucleotide and amino acid sequences of P411-INS-5150:**

ATGACAATTAAAGAAATGCCTCAGCCAAAAACGTTTGGAGAGCTTAAAAATTTACCGTTATTAAACACAG  
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AACTTATGGGCGGGTGAGAAATGTCTGCGTGATTTTCTTGGAGACGGGTTAGCCACAAGCTGGACGCATG  
AAAAAAATTGGAAGAAAAGCGCATAATATCTTACTTCCAAGCTTTAGTCAGCAGGCAATGAAAGGCTATCA  
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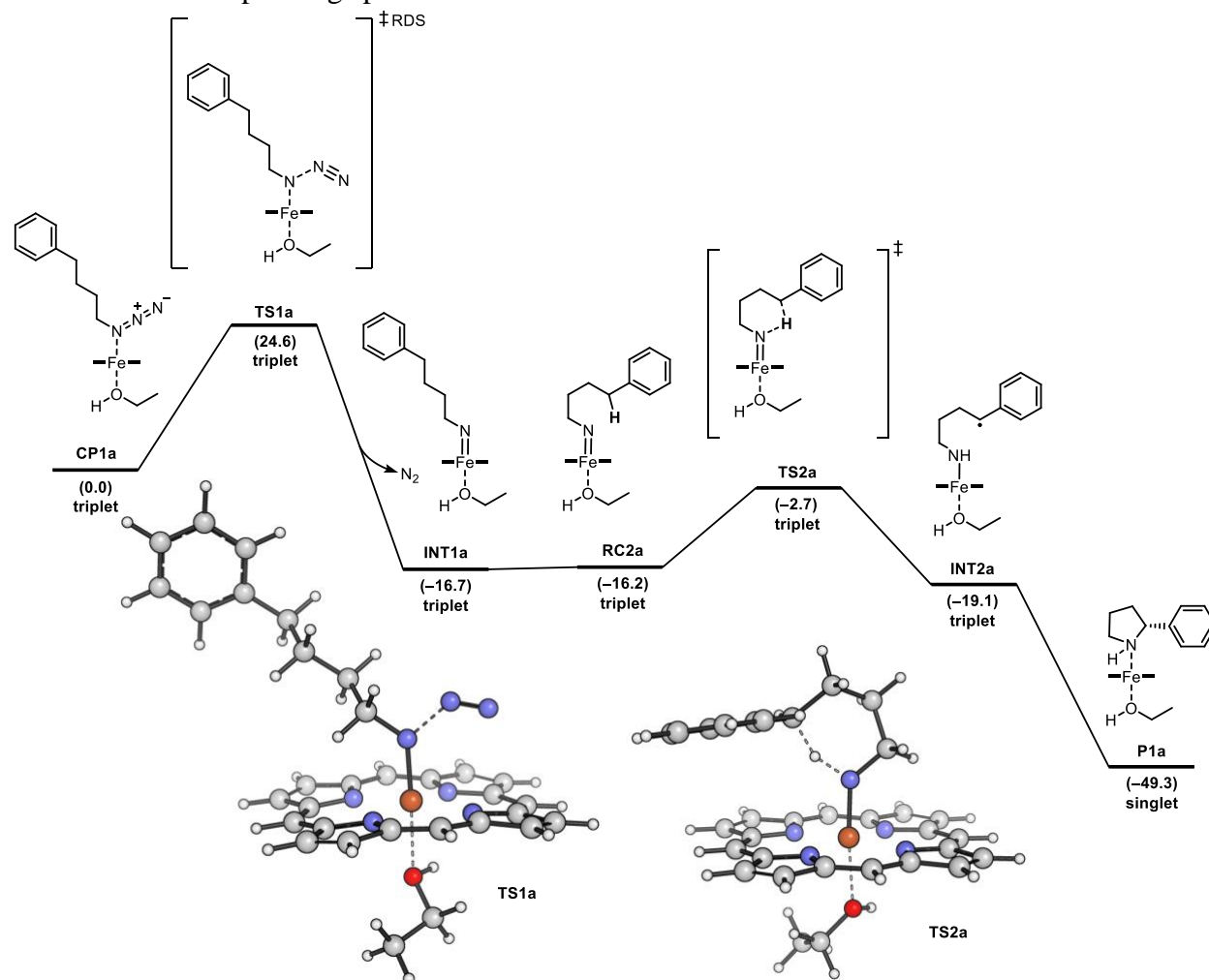
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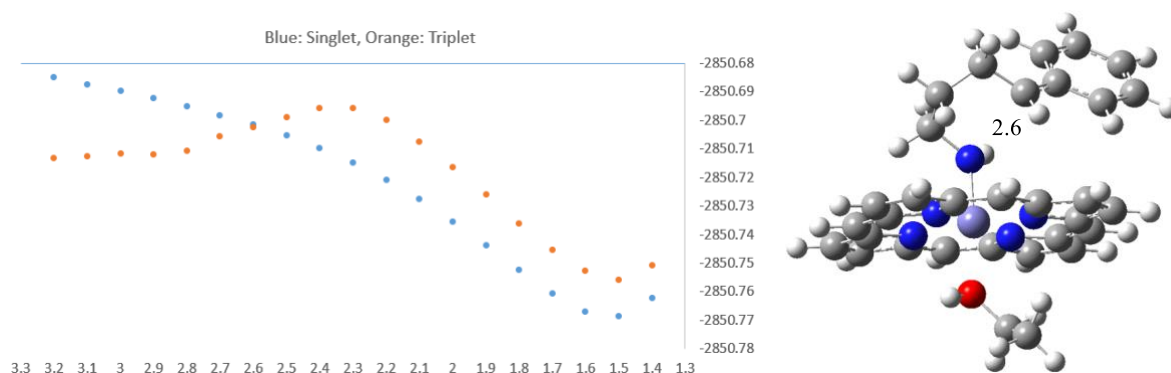
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## X. Computational Methods

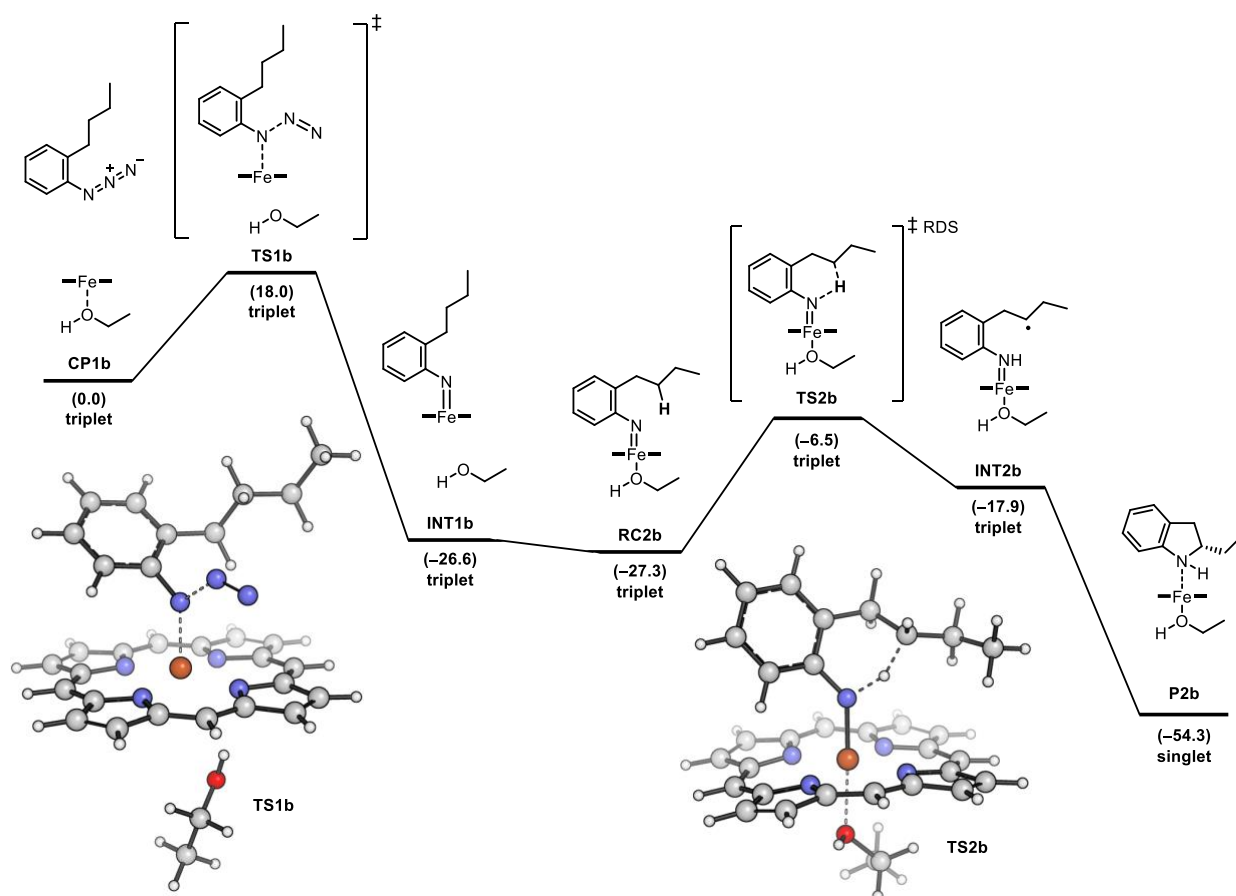
### DFT Calculations

A conformational search was conducted using CREST of the XTB program (with the searching parameters -rthr 0.5 -metac -T 8).<sup>12</sup> DFT calculation of each low-energy conformer was performed using Gaussian 09 program package.<sup>13</sup> The structure of each species was submitted for geometry optimization at the level of B3LYP/(SDD for Fe and 6-31G(d) for other atoms) for singlet state and uB3LYP/(SDD for Fe and 6-31G(d) for other atoms) for triplet state, with CPCM solvation model for diethyl ether with the integration grid set to ultrafine level, followed by frequency calculation at the same theoretical level. All reported Gibbs free energies are for 298K and are after quasi-harmonic correction using the GoodVibes program.<sup>14</sup> Single point energy calculations of the optimized geometries were performed at uB3LYP-D3/DEF2TZVP level with CPCM solvation model for diethyl ether and with the integration grid set to ultrafine level. We have calculated energies for singlet, triplet, and quintet. All reported energies are in the lowest energy states of the corresponding species.





**Figure S8.** Calculated reaction pathway for the alkyl azide substrate **1a**. The MECP for triplet **INT2a** to singlet **P1a** occurs when the bond forming distance is 2.6 Angstrom.



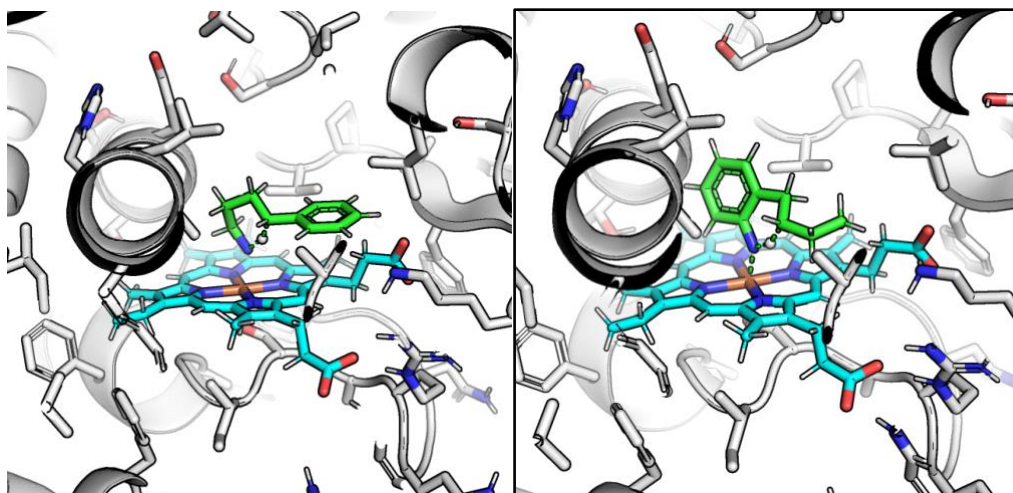
**Figure S9.** Calculated reaction pathway for the aryl azide substrate **3b**.

### Molecular Dynamics Simulations

Molecular dynamics (MD) simulations were performed using the Amber 16 program and AmberTools 16 packages.<sup>15</sup> For the MD simulations of proteins with substrates, the structures resulting from the docking calculations were used for the simulations (where the intrinsically preferred antipode led to docked poses, whereas the opposite antipode does not provide any reasonable docking pose). The protonation state of each protein was first determined from the

PDB2PQR Server using PROPKA<sup>16</sup> to assign protonation states at pH 7.3. MD simulations in explicit water were performed using the GPU-accelerated code (*pmemd*). For the protein scaffold, an evolved version of the Stony Brook modification of the Amber 99 force field (*ff14SB*)<sup>17</sup> parameters were applied. TIP3P<sup>18</sup> parameters were assigned to water molecules. MCPB.py<sup>19</sup> was applied to prepare for the force field of the ligand and Fe atom. The partial charges of the ligand were set to fit the electrostatic potential generated at the HF/6-31 G(d) level by the RESP (restrained electrostatic potential) model.<sup>20</sup> The charges were calculated according to the Merz-Singh-Kollman scheme using the Gaussian 09 program package. For the simulations involving a transition state bound, the two bond-forming distances of the ligand were restrained to the distances according to the QM optimized transition state structure, respectively, applying a harmonic constraint with a force constant with the number corresponding to the imaginary frequency obtained from DFT calculations. For the simulations not involving a transition state bound, no constraint was applied. Each protein complex was placed in a pre-equilibrated cubic box with a 12-Å buffer of TIP3P water molecules using the *leap* module. The systems were neutralized by the addition of explicit counter ions (Na<sup>+</sup>). Long-range electrostatic effects were modeled using the particle mesh Ewald method with periodic boundary conditions.<sup>21</sup> An 8-Å cutoff was applied to Lennard-Jones and electrostatic interactions. Molecular dynamics simulations were performed according to the following steps:

- (1) Each system was minimized with a maximum cycle of 50000 and with the steepest descent algorithm for the first 25000 cycles, with a periodic boundary for constant volume (NVT) and without the SHAKE algorithm activated. Positional restraint of 2 kcal mol<sup>-1</sup> Å<sup>-2</sup> was applied on the protein backbone atoms (C and N) and heavy atoms of the ligand.
- (2) A 1 ns heating process was performed with a periodic boundary for constant volume (NVT) with the SHAKE algorithm turned on such that the angle between the hydrogen atoms was kept fixed. The temperature increased from 0 K to 300 K in a time period of 1 ns with Langevin dynamics with the collision frequency of 5 ps<sup>-1</sup>. Positional restraint of 2 kcal mol<sup>-1</sup> Å<sup>-2</sup> was applied on the protein backbone atoms (C and N) and heavy atoms of the ligand.
- (3) a 2 ns equilibrium process was performed with a periodic boundary for constant pressure (NPT) and with a constant temperature of 300 K. Positional restraint of 2 kcal mol<sup>-1</sup> Å<sup>-2</sup> was applied on the protein backbone atoms (C and N) and heavy atoms of the ligand.
- (4) a 2 ns equilibrium process was performed for constant pressure (NPT) and with a constant temperature of 300 K. Positional restraint of 0.5 kcal mol<sup>-1</sup> Å<sup>-2</sup> was applied on the protein backbone atoms (C and N), and heavy atoms of the ligand.
- (5) A 1000 ns production was performed by applying the standard simulation condition for constant pressure (NPT) and with a constant temperature of 300K.



**Figure S10.** Reaction model of the hydrogen abstraction step derived from MD simulations.

### **XYZ coordinates and energies for the DFT calculations**

#### **CP1a**

E[M06-2X/6-31G(d,p)/CPCM(ether)]= -  
1820.51428283

Zero-point correction= 0.575950

Thermal correction to Energy= 0.614033

Thermal correction to Enthalpy= 0.614978

Thermal correction to Gibbs Free Energy=  
0.495862

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N	-0.410546	1.502004	1.966395
N	-0.913242	-1.031899	0.779858
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**CP1b**

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Thermal correction to Energy= 0.613114

Thermal correction to Enthalpy= 0.614058

Thermal correction to Gibbs Free Energy=  
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<b>INT1a</b>			
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Thermal correction to Energy = 0.601098			
Thermal correction to Enthalpy = 0.602043			
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C	1.295182	4.000415	-1.262034
C	2.375679	-2.834131	-1.909762
C	1.959103	3.205494	-2.147717
C	2.743023	-1.726873	-2.610991
C	-1.382560	3.173635	2.898959
C	-0.316957	-3.653241	2.242660
C	-1.753440	2.069145	3.604652
C	-0.982298	-2.864726	3.131932
H	1.187888	5.077835	-1.271787
H	2.613142	-3.871260	-2.110749
H	2.508379	3.496869	-3.034229
H	3.345179	-1.664650	-3.508796
H	-1.604104	4.213002	3.106449
H	-0.202683	-4.729925	2.248956
H	-2.342630	2.013909	4.511446
H	-1.527732	-3.159558	4.019612
C	-0.037693	3.546733	0.818335
C	1.009865	-3.202215	0.164226
C	-1.358814	-0.391283	3.324420
C	2.324645	0.730391	-2.335119
H	-0.215533	4.612858	0.921663
H	1.177961	-4.270360	0.065357

H	-1.939082	-0.567852	4.224979
H	2.900633	0.904830	-3.239003
C	-5.781002	-0.616728	-2.241241
H	-5.640410	0.232635	-2.922563
H	-5.451819	-1.512998	-2.783214
C	-4.877441	-0.420641	-1.006412
H	-5.204980	0.475511	-0.461023
C	-2.498950	-0.097446	-0.128886
H	-2.827438	0.802234	0.420784
H	-5.018597	-1.267985	-0.320929
H	-2.640295	-0.948146	0.559939
C	-3.393122	-0.291384	-1.369494
H	-3.061361	-1.188279	-1.909430
H	-3.247211	0.558640	-2.049379
N	-1.122212	0.025542	-0.490115
O	2.368370	0.432244	1.585157
C	2.572706	0.573569	3.007924
H	1.665313	0.981738	3.467539
H	3.393025	1.281849	3.176407
H	2.474364	1.301998	1.162034
C	2.917261	-0.783595	3.596274
H	3.070464	-0.691820	4.677562
H	3.835926	-1.178136	3.148835
H	2.109174	-1.500051	3.421831
C	-7.246990	-0.746704	-1.884222
C	-8.068543	0.386478	-1.791037
C	-7.810910	-1.999770	-1.602079
C	-9.411712	0.273644	-1.425063
H	-7.651051	1.366676	-2.012248
C	-9.153399	-2.118834	-1.235623
H	-7.191402	-2.891334	-1.675039
C	-9.959348	-0.981017	-1.145277
H	-10.031219	1.164772	-1.363062
H	-9.570745	-3.100340	-1.025333
H	-11.005092	-1.071644	-0.863794

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### INT1b

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E[M06-2X/6-31G(d,p)/CPCM(ether)]= -  
1711.01292976

Zero-point correction= 0.565376

Thermal correction to Energy= 0.600836

Thermal correction to Enthalpy= 0.601781

Thermal correction to Gibbs Free Energy=  
0.492742

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Fe	0.798039	1.359037	-0.028810
N	2.496994	2.360066	-0.355661
N	1.382009	-0.048803	-1.329699
N	0.504028	2.487562	1.639396
N	-0.616973	0.051963	0.665665
C	2.889336	3.547120	0.229815
C	0.690507	-1.187699	-1.691335
C	3.465602	2.075432	-1.295513
C	2.498039	-0.023941	-2.138993
C	1.148354	3.658120	1.963876
C	-1.076195	-1.076681	0.018404
C	-0.513013	2.360218	2.559142
C	-1.505038	0.269931	1.699663
C	4.112297	4.021948	-0.367996
C	1.379149	-1.877621	-2.754252
C	4.475564	3.103944	-1.305494
C	2.505542	-1.162663	-3.023716
C	0.536099	4.273119	3.117169
C	-2.253743	-1.589382	0.670970
C	-0.492696	3.463803	3.490405
C	-2.516290	-0.757144	1.718785
H	4.625085	4.929987	-0.077463
H	1.040253	-2.800749	-3.206895
H	5.345888	3.103410	-1.949284
H	3.282562	-1.372718	-3.747600
H	0.869473	5.196924	3.572675
H	-2.792571	-2.476253	0.362646
H	-1.183160	3.584985	4.315474
H	-3.316351	-0.819712	2.445455
C	2.250100	4.170286	1.291784
C	-0.470996	-1.652345	-1.090732
C	-1.448632	1.333909	2.590901
C	3.477818	0.959213	-2.120802
H	2.669702	5.104838	1.650746
H	-0.917677	-2.554943	-1.495819
H	-2.204806	1.372666	3.369023
H	4.308341	0.854145	-2.811675
N	-0.249871	2.266870	-1.072772
O	1.882506	-1.145173	2.165330
C	1.819875	-1.061666	3.590640
H	1.031634	-1.724592	3.979936
H	1.576756	-0.036562	3.907584
C	3.170227	-1.475175	4.153271
H	3.158227	-1.433643	5.248038

H	3.959502	-0.807823	3.789669
H	3.417307	-2.498090	3.848292
C	-0.384827	2.906300	-2.243737
C	-0.785738	4.274266	-4.687009
C	-1.581187	3.690405	-2.450799
C	0.578809	2.842603	-3.296183
C	0.375864	3.516278	-4.491169
C	-1.742620	4.349077	-3.666574
H	1.474383	2.256072	-3.140814
H	1.125073	3.453257	-5.276190
H	-2.640779	4.943774	-3.819920
H	-0.944746	4.804806	-5.621432
C	-2.644719	3.768867	-1.381135
H	-3.240010	4.678027	-1.536375
H	-2.171060	3.857173	-0.395952
C	-3.591375	2.549580	-1.366632
H	-2.996690	1.636713	-1.233189
H	-4.083215	2.464369	-2.346129
C	-4.653996	2.633405	-0.263603
H	-5.241134	3.553997	-0.392745
H	-4.153121	2.722247	0.710947
H	1.031186	-0.844820	1.801674
C	-5.594148	1.423180	-0.244488
H	-6.345932	1.513455	0.548447
H	-6.126219	1.319399	-1.198427
H	-5.035309	0.495123	-0.071864

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### INT2a

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E[M06-2X/6-31G(d,p)/CPCM(ether)]= -  
1710.99829055

Zero-point correction= 0.565464

Thermal correction to Energy= 0.600051

Thermal correction to Enthalpy= 0.600995

Thermal correction to Gibbs Free Energy=  
0.495476

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N	-2.112991	23.301363	-28.790109
C	-3.118253	22.256637	-28.815395
C	-2.815304	21.136593	-29.830413
C	-1.609679	20.237523	-29.478909
C	-0.272067	20.892529	-29.644284
O	-2.576940	27.017087	-27.334655
H	-3.426271	27.342246	-27.677051
N	-0.766257	24.743747	-26.871507
N	-3.628050	24.458580	-26.729969

N	-0.995661	25.745808	-29.513620
C	1.107589	25.466882	-28.283790
C	-2.031759	23.872309	-24.953880
C	-5.741345	24.811318	-27.929977
C	-2.587873	26.248990	-31.318790
C	0.570603	24.960712	-27.103701
C	-3.315943	23.989170	-25.478387
C	-5.205337	25.286709	-29.123500
C	-1.305164	26.164579	-30.783893
C	1.347724	24.578724	-25.945861
C	-4.522643	23.648974	-24.757423
C	-5.979053	25.661862	-30.284535
C	-0.099690	26.527750	-31.497221
C	0.465135	24.123990	-25.014023
C	-5.566564	23.920959	-25.588441
C	-5.089054	26.056995	-31.237675
C	0.940072	26.318821	-30.642579
C	-0.852504	24.229292	-25.600901
C	-4.998358	24.424213	-26.818786
C	-3.770774	25.927544	-30.658856
C	0.370158	25.824626	-29.408881
N	-3.863430	25.459538	-29.369722
Fe	-2.306646	24.997162	-28.157029
H	-4.078790	22.709910	-29.079867
H	-3.256651	21.792374	-27.820370
H	-2.667007	21.580369	-30.824421
H	-3.706133	20.497377	-29.898055
H	-1.654371	19.351703	-30.137326
H	-1.738738	19.851971	-28.459466
H	-1.185919	22.921305	-28.599654
H	-0.155065	21.528910	-30.520788
H	2.186269	25.581018	-28.334001
H	-1.943899	23.482511	-23.943953
H	-6.821997	24.727292	-27.864036
H	-2.674057	26.605940	-32.341033
H	-6.626691	23.801519	-25.402589
H	-7.059570	25.622985	-30.345183
H	-5.289473	26.408962	-32.242052
H	-0.072598	26.894107	-32.515985
H	1.997520	26.477032	-30.814352
H	2.425458	24.655025	-25.874287
H	0.668257	23.750831	-24.017959
H	-4.547756	23.259927	-23.747119
C	-1.718201	29.095769	-28.360859



H	-0.998097	29.907301	-28.204648
H	-1.486977	28.601333	-29.308465
H	-2.715207	29.548617	-28.435413
C	-1.649528	28.114829	-27.200082
H	-1.856812	28.623755	-26.250052
H	-0.665653	27.648213	-27.130891
C	0.876137	20.710588	-28.832623
C	2.085342	21.399868	-29.157417
C	0.907640	19.860170	-27.686239
C	3.232888	21.250626	-28.393482
H	2.092394	22.055150	-30.025373
C	2.063455	19.717861	-26.929555
H	0.016669	19.309233	-27.402105
C	3.235448	20.407747	-27.271197
H	4.136020	21.789577	-28.668748
H	2.056870	19.060847	-26.063328
H	4.135385	20.290221	-26.674397

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### INT2b

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E[M06-2X/6-31G(d,p)/CPCM(ether)]= -  
1710.99422569

Zero-point correction= 0.564434

Thermal correction to Energy= 0.599336

Thermal correction to Enthalpy= 0.600280

Thermal correction to Gibbs Free Energy=  
0.496860

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Fe	0.608653	0.502097	0.267943
N	2.257584	1.597183	-0.061896
N	1.223090	-0.805456	-1.141506
N	0.111133	1.672213	1.841079
N	-0.929898	-0.739622	0.757636
C	2.577565	2.782706	0.552635
C	0.535593	-1.912804	-1.578099
C	3.272018	1.345508	-0.954372
C	2.372263	-0.750304	-1.896323
C	0.720923	2.852463	2.187808
C	-1.336204	-1.843643	0.041748
C	-0.941094	1.516323	2.708769
C	-1.860494	-0.571075	1.757910
C	3.820872	3.298638	0.025146
C	1.265743	-2.565735	-2.640876
C	4.256166	2.401987	-0.902998
C	2.409546	-1.850862	-2.830949
C	0.035400	3.457394	3.308440

C	-2.544144	-2.389543	0.613897
C	-0.991613	2.625214	3.635946
C	-2.864934	-1.605691	1.682361
H	4.290525	4.220320	0.345095
H	0.936496	-3.460100	-3.154886
H	5.154889	2.436917	-1.505904
H	3.210670	-2.034323	-3.535921
H	0.321885	4.391738	3.774686
H	-3.063117	-3.263233	0.239981
H	-1.724591	2.735478	4.425291
H	-3.701101	-1.704174	2.363220
C	1.854862	3.381780	1.580254
C	-0.663624	-2.383467	-1.050030
C	-1.856752	0.467735	2.683942
C	3.342991	0.241674	-1.799026
H	2.231739	4.323698	1.967427
H	-1.092965	-3.269189	-1.508609
H	-2.648901	0.478535	3.426342
H	4.204680	0.166999	-2.455350
N	-0.520196	1.512391	-0.796246
O	1.671873	-0.716801	1.762683
C	2.968801	-1.358871	1.669530
H	3.209655	-1.522254	0.615066
H	2.903130	-2.333432	2.165423
C	4.011472	-0.486239	2.345925
H	4.996032	-0.961870	2.270289
H	3.774109	-0.348150	3.406165
H	4.066282	0.496599	1.869141
C	-0.405678	2.388908	-1.858259
C	-0.231358	4.133931	-4.088125
C	-1.268199	3.526315	-1.958246
C	0.531916	2.171895	-2.893799
C	0.618195	3.029528	-3.986241
C	-1.162376	4.363429	-3.070892
H	1.176146	1.305436	-2.834414
H	1.348076	2.826793	-4.766635
H	-1.822374	5.226605	-3.134688
H	-0.171320	4.806176	-4.939495
C	-2.273064	3.846140	-0.866971
H	-2.675171	4.858228	-1.058215
H	-1.762476	3.927564	0.107089
C	-3.411073	2.871726	-0.743629
H	-1.372325	1.688273	-0.268680
H	-3.738514	2.357709	-1.647180

C	-4.345296	2.919772	0.424413
H	-4.958046	3.841039	0.373607
H	-3.766602	3.016912	1.355979
H	0.976945	-1.395138	1.816792
C	-5.282318	1.707922	0.517566
H	-4.712512	0.780221	0.643355
H	-5.968204	1.803063	1.366964
H	-5.887287	1.609099	-0.391886

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<b>P1a</b>			
E[M06-2X/6-31G(d,p)/CPCM(ether)] = -			
1711.05336838			
Zero-point correction = 0.572279			
Thermal correction to Energy = 0.605238			
Thermal correction to Enthalpy = 0.606182			
Thermal correction to Gibbs Free Energy =			
0.508138			

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N	-0.479298	23.466083	-29.370636
C	-1.116416	22.801133	-30.558550
C	-0.314385	21.501090	-30.826803
C	0.888969	21.590578	-29.867910
C	0.328480	22.408297	-28.674216
O	-2.143906	27.012356	-27.650766
N	0.547127	25.871634	-28.235337
N	-1.375273	24.562051	-26.562160
N	-1.385131	26.001687	-30.347243
C	0.913329	26.866100	-30.452579
C	0.919408	25.157747	-25.913756
C	-3.684805	23.735646	-26.445459
C	-3.682469	25.415950	-30.988395
C	1.326672	26.517147	-29.167184
C	-0.341319	24.621870	-25.656606
C	-4.075280	24.028774	-27.750961
C	-2.434853	25.986637	-31.233610
C	2.635816	26.797377	-28.617842
C	-0.755029	24.065345	-24.386510
C	-5.401468	23.788089	-28.283533
C	-2.055442	26.634038	-32.471404
C	2.636342	26.318170	-27.342050
C	-2.052038	23.674681	-24.533185
C	-5.399582	24.256374	-29.561983
C	-0.761274	27.034493	-32.324353
C	1.328562	25.742303	-27.111954
C	-2.430557	23.986677	-25.894138

C	-4.073341	24.786153	-29.808035
C	-0.351252	26.635633	-30.994511
N	-3.279018	24.617052	-28.701298
Fe	-1.360438	25.208944	-28.482379
H	-1.083259	23.498891	-31.396253
H	-2.166907	22.604484	-30.342600
H	-0.003982	21.415465	-31.872378
H	-0.922636	20.621414	-30.592278
H	1.637017	27.373990	-31.084249
H	1.642800	25.132162	-25.103298
H	-4.426077	23.274758	-25.798396
H	-4.420537	25.479826	-31.783398
H	-2.704202	23.216578	-23.799631
H	-6.215326	23.330834	-27.734013
H	-6.211649	24.264026	-30.278864
H	-2.705038	26.756980	-33.329493
H	-0.131754	27.554645	-33.036093
H	3.435201	27.299987	-29.148677
H	3.436542	26.347017	-26.612443
H	-0.125850	23.995786	-23.507493
C	-2.365015	29.395628	-27.143967
H	-1.922756	30.380440	-27.334356
H	-3.399508	29.405179	-27.503281
H	-2.377052	29.237922	-26.058521
C	-1.555902	28.316577	-27.848290
H	-0.515756	28.305885	-27.504859
H	-1.554953	28.462312	-28.929650
C	-0.395883	21.497929	-27.694938
C	0.383756	20.871014	-26.707970
C	-1.751191	21.154390	-27.778880
C	-0.165035	19.926096	-25.841364
H	1.438009	21.126249	-26.621910
C	-2.304923	20.206561	-26.912716
H	-2.393357	21.641097	-28.502870
C	-1.516368	19.584455	-25.944552
H	0.461523	19.458890	-25.085933
H	-3.360452	19.960631	-26.996338
H	-1.949211	18.847375	-25.273476
H	1.125776	22.923362	-28.132316
H	0.243010	24.065565	-29.768392
H	1.276320	20.612646	-29.568926
H	1.710903	22.150538	-30.332190
H	-2.071988	26.771726	-26.709862

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**P2b**

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E[M06-2X/6-31G(d,p)/CPCM(ether)]= -  
1711.05390925

Zero-point correction= 0.570621

Thermal correction to Energy= 0.603943

Thermal correction to Enthalpy= 0.604888

Thermal correction to Gibbs Free Energy=  
0.507355

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Fe	0.379977	0.444249	0.402194
N	1.685154	1.914431	-0.025457
N	1.099485	-0.650282	-1.141213
N	-0.214956	1.445068	2.046765
N	-0.873815	-1.079988	0.871035
C	1.801414	3.124436	0.612285
C	0.633240	-1.863154	-1.590122
C	2.645943	1.909863	-1.006721
C	2.169662	-0.334479	-1.943904
C	0.183156	2.697390	2.439268
C	-1.111389	-2.220612	0.135913
C	-1.039612	0.979692	3.040233
C	-1.664408	-1.179947	1.993428
C	2.843341	3.919913	-0.004191
C	1.426780	-2.321498	-2.710453
C	3.375601	3.160752	-1.001456
C	2.390227	-1.379647	-2.919040
C	-0.425873	3.045088	3.707148
C	-2.102334	-3.041696	0.795003
C	-1.173402	1.971938	4.087483
C	-2.434776	-2.402850	1.952906
H	3.128957	4.916147	0.310790
H	1.264747	-3.249568	-3.245013
H	4.184460	3.407556	-1.678247
H	3.174263	-1.373095	-3.666404
H	-0.274915	3.981447	4.230382
H	-2.467259	-3.990600	0.421336
H	-1.770101	1.849619	4.983200
H	-3.133150	-2.718971	2.718194
C	1.086460	3.502859	1.747584
C	-0.426643	-2.574332	-1.026276
C	-1.715271	-0.238920	3.020200
C	2.895122	0.853529	-1.879859
H	1.298967	4.483517	2.164374
H	-0.700588	-3.514151	-1.497441
H	-2.360939	-0.462218	3.865098

H	3.704301	0.979724	-2.593799
N	-1.264076	1.238403	-1.064572
O	1.730624	-0.588704	1.704762
C	3.169617	-0.700975	1.564856
H	3.435370	-0.604635	0.508491
H	3.465906	-1.698002	1.910202
C	3.840335	0.372358	2.403282
H	4.928622	0.297804	2.295751
H	3.588446	0.252840	3.462609
H	3.528666	1.369349	2.079463
C	-0.755986	1.842696	-2.275908
C	0.041532	3.413035	-4.428171
C	-1.000460	3.224113	-2.267161
C	-0.176663	1.224030	-3.378855
C	0.225904	2.028503	-4.453617
C	-0.589082	4.017551	-3.331618
H	-0.045569	0.149007	-3.419234
H	0.681463	1.560351	-5.322362
H	-0.782547	5.087592	-3.328729
H	0.358672	4.018777	-5.272701
C	-1.817444	3.553054	-1.040833
H	-2.585015	4.311436	-1.220939
H	-1.189646	3.892433	-0.204871
C	-2.419853	2.167787	-0.728826
H	-1.617911	0.298662	-1.239449
H	-3.186343	1.974712	-1.497682
C	-3.078395	1.991996	0.632252
H	-2.422932	2.374016	1.415685
H	-3.219926	0.923474	0.830093
H	1.329514	-1.463531	1.570928
C	-4.437092	2.704100	0.700596
H	-4.337308	3.785344	0.548573
H	-5.129651	2.323175	-0.060464
H	-4.901792	2.551017	1.680837

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### RC2a

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E[M06-2X/6-31G(d,p)/CPCM(ether)]= -  
1710.99898058

Zero-point correction= 0.566426

Thermal correction to Energy= 0.600994

Thermal correction to Enthalpy= 0.601938

Thermal correction to Gibbs Free Energy=  
0.495824

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N	-2.221773	23.404981	-29.402152
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C	-3.230321	22.393327	-29.399256
C	-2.730665	21.074100	-30.027097
C	-1.543698	20.417509	-29.305986
C	-1.856530	19.937657	-27.872357
O	-2.239508	27.177436	-28.059422
H	-1.982523	27.716344	-28.826163
N	-0.316512	24.849912	-27.949450
N	-2.987802	24.515711	-27.038393
N	-1.305792	25.854403	-30.454189
C	1.061211	25.601839	-29.840793
C	-0.962634	23.964355	-25.756853
C	-5.355326	24.801674	-27.633114
C	-3.325701	26.296703	-31.773075
C	0.890175	25.085541	-28.559653
C	-2.341875	24.056365	-25.914041
C	-5.182735	25.270554	-28.930919
C	-1.946122	26.259807	-31.600891
C	1.976905	24.723750	-27.676075
C	-3.304896	23.697971	-24.898759
C	-6.264187	25.625672	-29.821763
C	-0.981111	26.642592	-32.605580
C	1.410770	24.259723	-26.527559
C	-4.538307	23.945105	-25.421242
C	-5.693787	26.033753	-30.988797
C	0.251218	26.453062	-32.056887
C	-0.021410	24.340666	-26.710159
C	-4.331852	24.448861	-26.759300
C	-4.262762	25.934680	-30.810929
C	0.039718	25.951370	-30.717963
N	-3.973369	25.465911	-29.552023
Fe	-2.160528	25.037488	-28.791710
H	-4.111684	22.741943	-29.965126
H	-3.585363	22.211336	-28.371185
H	-2.447852	21.273288	-31.068835
H	-3.578487	20.374787	-30.058088
H	-0.703287	21.122442	-29.274040
H	-1.204901	19.555888	-29.896567
H	-2.722340	19.262499	-27.903104
H	-2.146428	20.796006	-27.253998
H	2.081025	25.732906	-30.190325
H	-0.592697	23.580696	-24.810812
H	-6.374388	24.697192	-27.273051
H	-3.702097	26.646282	-32.729704
H	-5.507423	23.805506	-24.958834

H	-7.315247	25.567081	-29.568076
H	-6.178718	26.382092	-31.892080
H	-1.231145	27.006109	-33.594451
H	1.222319	26.627065	-32.503344
H	3.027632	24.819906	-27.919680
H	1.899605	23.898088	-25.631589
H	-3.051226	23.315549	-23.918024
C	-0.349435	28.357728	-26.985710
H	-0.035619	28.809210	-26.037405
H	0.367634	27.577039	-27.254690
H	-0.316279	29.142591	-27.752239
C	-1.753842	27.788498	-26.847249
H	-2.460389	28.573734	-26.547979
H	-1.788024	26.996327	-26.096823
C	-0.683342	19.229763	-27.226953
C	-0.555641	17.834717	-27.294857
C	0.323930	19.957161	-26.574609
C	0.543780	17.183455	-26.730236
H	-1.328991	17.252813	-27.792216
C	1.425520	19.311306	-26.009312
H	0.240742	21.040118	-26.507142
C	1.539773	17.920488	-26.084983
H	0.619814	16.100685	-26.791105
H	2.192983	19.894039	-25.505898
H	2.394672	17.416114	-25.642374

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### RC2b

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E[M06-2X/6-31G(d,p)/CPCM(ether)]= -  
1711.01513944

Zero-point correction= 0.565739

Thermal correction to Energy= 0.600543

Thermal correction to Enthalpy= 0.601487

Thermal correction to Gibbs Free Energy=  
0.497100

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Fe	0.786754	0.745042	0.382055
N	2.569022	1.604411	0.052759
N	1.143164	-0.588652	-1.087902
N	0.547975	1.898892	2.038420
N	-0.871468	-0.335526	0.911561
C	3.100057	2.685519	0.716185
C	0.310767	-1.596472	-1.517316
C	3.483276	1.264646	-0.915639
C	2.244476	-0.629712	-1.910564
C	1.340297	2.945272	2.431154



C	-1.449281	-1.362807	0.202774
C	-0.500079	1.861438	2.921852
C	-1.734295	-0.052511	1.944449
C	4.378771	3.040376	0.144290
C	0.898773	-2.280463	-2.646359
C	4.619776	2.155037	-0.862336
C	2.100504	-1.686435	-2.885391
C	0.781001	3.588000	3.600984
C	-2.696402	-1.753259	0.817155
C	-0.359965	2.912473	3.907989
C	-2.870809	-0.943583	1.900501
H	5.002437	3.855196	0.489997
H	0.442557	-3.113394	-3.166502
H	5.480233	2.094950	-1.516895
H	2.833812	-1.928103	-3.644552
H	1.221402	4.436710	4.109140
H	-3.339713	-2.547041	0.458586
H	-1.053534	3.092365	4.719910
H	-3.687897	-0.936326	2.610989
C	2.526058	3.324605	1.810272
C	-0.902189	-1.949780	-0.934159
C	-1.558244	0.957193	2.886294
C	3.342481	0.221238	-1.826105
H	3.061705	4.171203	2.229158
H	-1.455668	-2.764122	-1.391972
H	-2.320292	1.056154	3.653729
H	4.147750	0.069121	-2.538432
N	-0.109743	1.857245	-0.634967
O	1.744478	-0.715759	1.811570
C	2.947997	-1.499794	1.630327
H	3.136556	-1.626403	0.559346
H	2.784979	-2.489585	2.071808
C	4.109598	-0.799195	2.313161
H	5.027689	-1.380959	2.171944
H	3.924900	-0.699136	3.388113
H	4.265055	0.198066	1.891559
C	-0.226131	2.590591	-1.745789
C	-0.537901	4.173015	-4.073794
C	-1.342985	3.502296	-1.865073
C	0.706080	2.514361	-2.829557
C	0.545851	3.291069	-3.966457
C	-1.461204	4.264426	-3.023964
H	1.542991	1.834382	-2.740325
H	1.268553	3.214628	-4.774989

H	-2.298188	4.954676	-3.108981
H	-0.662209	4.785756	-4.962143
C	-2.377167	3.603039	-0.768993
H	-2.843968	4.596034	-0.809383
H	-1.890385	3.512927	0.209024
C	-3.482974	2.530889	-0.873512
H	-3.021370	1.535675	-0.834683
H	-3.971425	2.613018	-1.855047
C	-4.536418	2.651302	0.234916
H	-4.984603	3.654838	0.202443
H	-4.040250	2.567009	1.212019
H	0.971389	-1.305676	1.794715
C	-5.640102	1.593025	0.130415
H	-5.221766	0.581804	0.205000
H	-6.381577	1.708266	0.929875
H	-6.169160	1.665415	-0.828154

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**TS1a**


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E[M06-2X/6-31G(d,p)/CPCM(ether)]= -  
1820.47131100

Zero-point correction= 0.574028

Thermal correction to Energy= 0.610724

Thermal correction to Enthalpy= 0.611668

Thermal correction to Gibbs Free Energy=  
0.501557

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Fe	0.602248	0.899615	0.650682
N	2.276997	1.800920	1.362247
N	1.728081	-0.185175	-0.617423
N	-0.447485	1.786858	2.129557
N	-0.992118	-0.225822	0.181386
C	2.386741	2.658158	2.436419
C	1.320562	-1.229928	-1.410765
C	3.525227	1.761106	0.780542
C	3.052495	0.026592	-0.915654
C	0.017207	2.628486	3.113360
C	-1.047399	-1.266122	-0.715987
C	-1.808284	1.709647	2.309499
C	-2.279096	-0.033964	0.623988
C	3.734866	3.160196	2.536037
C	2.416366	-1.689272	-2.232448
C	4.436263	2.617432	1.500623
C	3.487796	-0.903297	-1.933072
C	-1.077989	3.091722	3.932598
C	-2.402431	-1.752161	-0.830586

C	-2.212500	2.535799	3.423647
C	-3.168012	-0.980480	-0.008884
H	4.081812	3.845945	3.298680
H	2.355432	-2.506727	-2.939824
H	5.478772	2.760261	1.245345
H	4.489979	-0.944670	-2.340799
H	-0.974904	3.762114	4.776543
H	-2.710754	-2.573064	-1.465696
H	-3.232541	2.647702	3.769146
H	-4.233533	-1.041245	0.173626
C	1.342588	3.013555	3.282465
C	0.031917	-1.752649	-1.446861
C	-2.669588	0.888725	1.588918
C	3.882824	0.954242	-0.294392
H	1.568094	3.689579	4.101408
H	-0.154459	-2.580357	-2.124250
H	-3.724436	0.927422	1.843302
H	4.910159	1.013017	-0.640818
N	0.190468	3.756522	-0.407423
N	0.478678	4.343733	0.535013
C	1.498448	2.457953	-5.534200
H	1.737188	3.522856	-5.413750
H	2.422761	1.902636	-5.327408
C	0.436336	2.064048	-4.486771
H	-0.491268	2.616735	-4.692374
C	-0.179681	1.946013	-2.012533
H	-1.102207	2.510166	-2.215657
H	0.193885	0.998691	-4.606898
H	-0.428176	0.887621	-2.119701
C	0.892060	2.330376	-3.046543
H	1.809053	1.766818	-2.834527
H	1.136939	3.394502	-2.927044
N	0.218222	2.143913	-0.624297
O	1.253086	-0.723308	2.193337
C	0.503872	-1.192974	3.338102
H	-0.199637	-0.414579	3.653618
H	1.205050	-1.378766	4.160301
H	1.975664	-0.152108	2.505798
C	-0.226669	-2.471401	2.966904
H	-0.795100	-2.836492	3.829868
H	0.482389	-3.249791	2.665079
H	-0.924532	-2.296992	2.142958
C	1.052792	2.193314	-6.957049
C	0.350468	3.165882	-7.684217

C	1.299200	0.956188	-7.570749
C	-0.094822	2.911446	-8.983312
H	0.154994	4.134128	-7.227844
C	0.856365	0.695899	-8.869594
H	1.848159	0.191156	-7.025366
C	0.156466	1.673743	-9.581126
H	-0.633687	3.681260	-9.529908
H	1.062036	-0.268499	-9.327241
H	-0.185911	1.474789	-10.593170

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**TS1b**


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E[M06-2X/6-31G(d,p)/CPCM(ether)] = -  
1820.47606862

Zero-point correction = 0.571115

Thermal correction to Energy = 0.609387

Thermal correction to Enthalpy = 0.610331

Thermal correction to Gibbs Free Energy =  
0.494222

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Fe	0.472053	0.724918	-0.091014
N	2.047016	1.906103	-0.507624
N	1.303865	-0.725289	-1.247118
N	0.018152	1.942403	1.465165
N	-0.731546	-0.681746	0.714060
C	2.304207	3.160232	0.007663
C	0.819123	-1.997389	-1.461629
C	3.013133	1.698020	-1.470461
C	2.356816	-0.578734	-2.123974
C	0.536509	3.193861	1.714129
C	-0.944124	-1.970505	0.250048
C	-1.004295	1.777649	2.374018
C	-1.659781	-0.501951	1.727312
C	3.441113	3.749091	-0.649606
C	1.578359	-2.657956	-2.492547
C	3.881319	2.841792	-1.565754
C	2.532723	-1.777228	-2.903873
C	-0.169741	3.823754	2.800300
C	-1.997835	-2.602815	0.993540
C	-1.126671	2.944789	3.209622
C	-2.442475	-1.692938	1.906413
H	3.844442	4.726800	-0.419214
H	1.396270	-3.667494	-2.838104
H	4.720969	2.919854	-2.244421
H	3.297577	-1.912795	-3.657764
H	0.054919	4.808208	3.190245

H	-2.342502	-3.615431	0.827889
H	-1.851217	3.056674	4.005963
H	-3.225389	-1.806371	2.645185
C	1.596927	3.772204	1.031733
C	-0.231574	-2.582856	-0.769798
C	-1.798141	0.645757	2.493295
C	3.155077	0.550260	-2.236572
H	1.909245	4.766287	1.334517
H	-0.506025	-3.598692	-1.034723
H	-2.568253	0.648985	3.257752
H	3.959851	0.527954	-2.964169
N	-2.278724	0.897173	-1.675805
N	-2.822355	-0.006486	-1.227480
N	-0.822599	1.474569	-1.412616
O	1.823966	-1.118795	2.600593
C	2.548151	-2.321369	2.330500
H	2.815206	-2.379990	1.264955
H	1.931786	-3.202439	2.567204
C	3.805768	-2.322555	3.184482
H	4.385053	-3.236344	3.011965
H	3.548987	-2.271212	4.248345
H	4.437013	-1.460687	2.941135
C	-0.652425	2.644011	-2.199688
C	-0.166653	4.914201	-3.789704
C	-1.299780	3.868025	-1.891420
C	0.209287	2.582836	-3.311452
C	0.464393	3.705357	-4.095334
C	-1.039076	4.981667	-2.703040
H	0.680594	1.632411	-3.541347
H	1.140917	3.635883	-4.943169
H	-1.527495	5.925396	-2.467811
H	0.017985	5.798748	-4.393778
C	-2.271654	4.000829	-0.739465
H	-2.079395	4.947704	-0.216181
H	-2.096675	3.195635	-0.020230
C	-3.750673	3.979749	-1.179891
H	-3.952586	3.049608	-1.727131
H	-3.928904	4.800045	-1.889895
C	-4.725196	4.102309	-0.001612
H	-4.513697	5.030344	0.548942
H	-4.541614	3.279704	0.704234
H	1.042405	-1.094578	2.022342
C	-6.195530	4.087338	-0.433589
H	-6.866968	4.175047	0.428600

H	-6.416441	4.918770	-1.114598
H	-6.444096	3.155801	-0.957084

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**TS2a**


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E[M06-2X/6-31G(d,p)/CPCM(ether)] = -  
1710.96742569

Zero-point correction = 0.561017

Thermal correction to Energy = 0.594784

Thermal correction to Enthalpy = 0.595729

Thermal correction to Gibbs Free Energy =  
0.493900

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N	-2.320466	23.136089	-28.743342
C	-3.365418	22.149725	-28.883638
C	-3.021034	21.117013	-29.976439
C	-1.661420	20.460265	-29.697354
C	-0.555557	21.508286	-29.634766
O	-2.555857	26.902471	-27.328292
H	-3.293448	27.276051	-27.839131
N	-0.839605	24.529244	-26.786562
N	-3.704328	24.352614	-26.697945
N	-0.977378	25.488019	-29.459843
C	1.084471	25.174758	-28.167384
C	-2.169842	23.718449	-24.886828
C	-5.775072	24.815059	-27.933249
C	-2.509436	26.067648	-31.292306
C	0.506954	24.704612	-26.992267
C	-3.437853	23.880593	-25.436974
C	-5.199092	25.264578	-29.118788
C	-1.241212	25.918766	-30.736444
C	1.248643	24.316015	-25.813081
C	-4.672750	23.605868	-24.735055
C	-5.938262	25.669288	-30.292229
C	-0.007529	26.237200	-31.421724
C	0.334249	23.895308	-24.896282
C	-5.686783	23.924847	-25.585850
C	-5.018688	26.012157	-31.237764
C	1.003086	25.999759	-30.539377
C	-0.967029	24.032066	-25.513121
C	-5.072124	24.390629	-26.809493
C	-3.715533	25.821462	-30.643354
C	0.386847	25.530322	-29.318251
N	-3.847204	25.373867	-29.348747
Fe	-2.340639	24.808187	-28.118376
H	-4.309436	22.650361	-29.136735

H	-3.534645	21.618042	-27.929141
H	-2.997963	21.619909	-30.952803
H	-3.812239	20.358524	-30.019258
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H	-1.722706	19.906650	-28.752134
H	-1.227271	22.501890	-29.053891
H	-0.368896	21.960770	-30.614550
H	2.166749	25.257507	-28.193243
H	-2.115447	23.335270	-23.871993
H	-6.859582	24.785933	-27.884964
H	-2.562509	26.422028	-32.317705
H	-6.754696	23.862750	-25.417057
H	-7.018603	25.683105	-30.366201
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H	0.057067	26.600919	-32.439775
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H	2.326452	24.361804	-25.719852
H	0.505229	23.527780	-23.892081
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H	-0.665863	27.387273	-26.797379
C	0.699617	21.234566	-28.903881
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C	0.735130	20.505810	-27.696040
C	3.124234	21.508159	-28.730239
H	1.921179	22.304373	-30.325503
C	1.936629	20.280555	-27.025557
H	-0.186169	20.114789	-27.273989
C	3.139278	20.776638	-27.538595
H	4.051685	21.898240	-29.142022
H	1.934392	19.713951	-26.097796
H	4.074836	20.595824	-27.016387

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### TS2b

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Zero-point correction= 0.560320

Thermal correction to Energy= 0.594318

Thermal correction to Enthalpy= 0.595262

Thermal correction to Gibbs Free Energy=  
0.494675

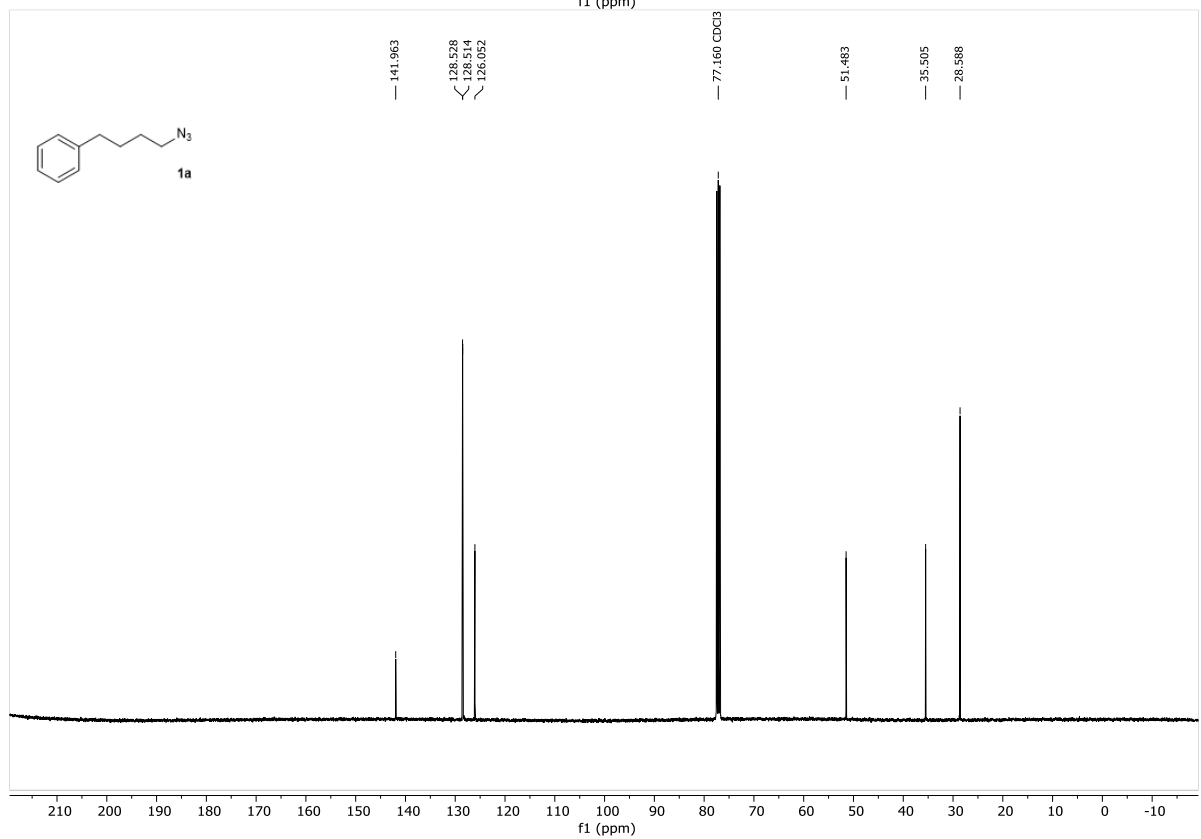
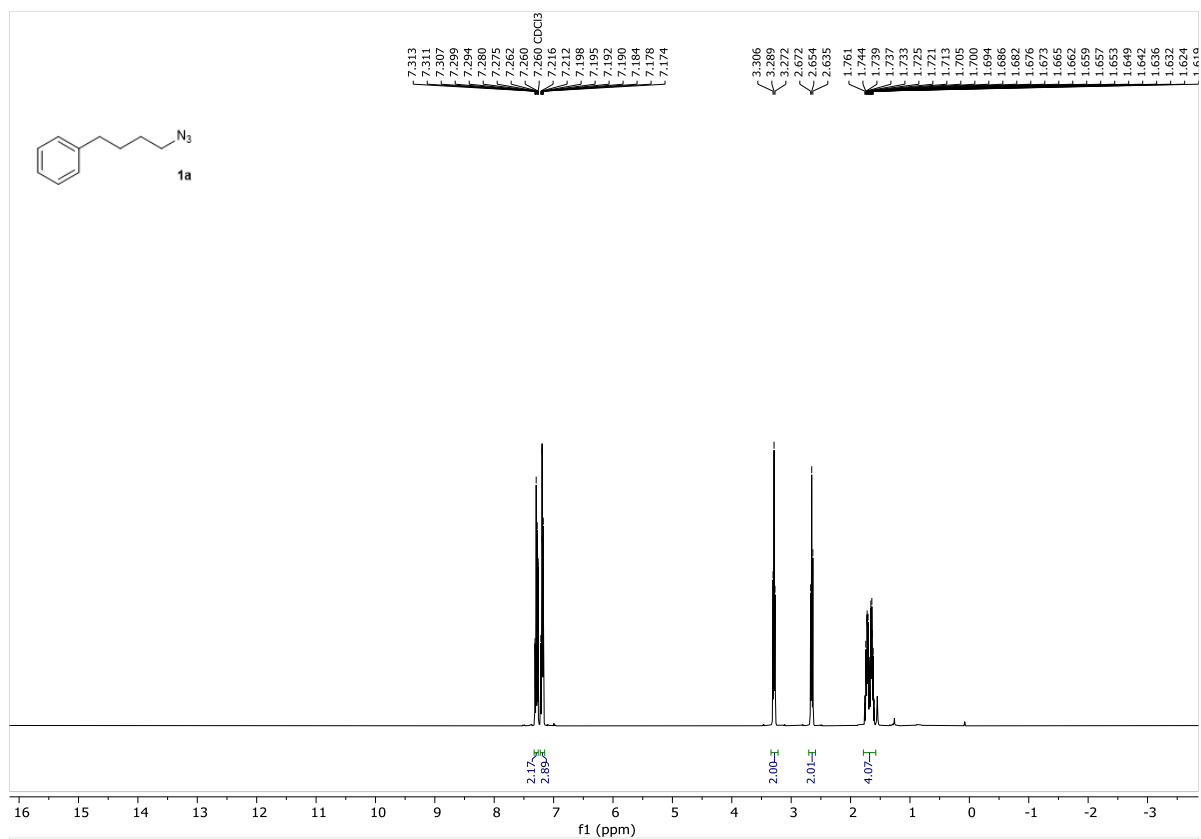
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N	0.175881	2.107824	1.723854
N	-0.712041	-0.421593	0.782901
C	2.369420	3.429112	0.181384
C	0.674952	-1.546665	-1.618089
C	3.146972	1.960414	-1.252372
C	2.417501	-0.266216	-2.035293
C	0.660170	3.369598	1.966944
C	-1.063456	-1.584118	0.140003
C	-0.727350	1.844866	2.723511
C	-1.500971	-0.354688	1.905665
C	3.530955	4.027339	-0.439390
C	1.412148	-2.176535	-2.687533
C	4.022205	3.109736	-1.317068
C	2.500203	-1.392509	-2.934033
C	0.042134	3.920127	3.152695
C	-2.110811	-2.261972	0.870553
C	-0.806946	2.967794	3.631212
C	-2.369971	-1.508190	1.975411
H	3.918612	5.010439	-0.203353
H	1.132535	-3.108041	-3.163562
H	4.892457	3.186325	-1.956824
H	3.289155	-1.545342	-3.659790
H	0.255370	4.900021	3.561240
H	-2.562001	-3.200523	0.573727
H	-1.439570	3.007883	4.509190
H	-3.082797	-1.696782	2.768435
C	1.654810	4.004426	1.227955
C	-0.447987	-2.090911	-1.001941
C	-1.494583	0.688054	2.827639
C	3.299164	0.810385	-2.022434
H	1.946569	5.002690	1.540319
H	-0.831065	-3.025224	-1.401238
H	-2.172224	0.612164	3.672637
H	4.144418	0.772653	-2.702947
N	-0.588502	1.824327	-0.936974
O	2.207934	-0.141701	1.377177
C	2.126444	-0.587631	2.750802
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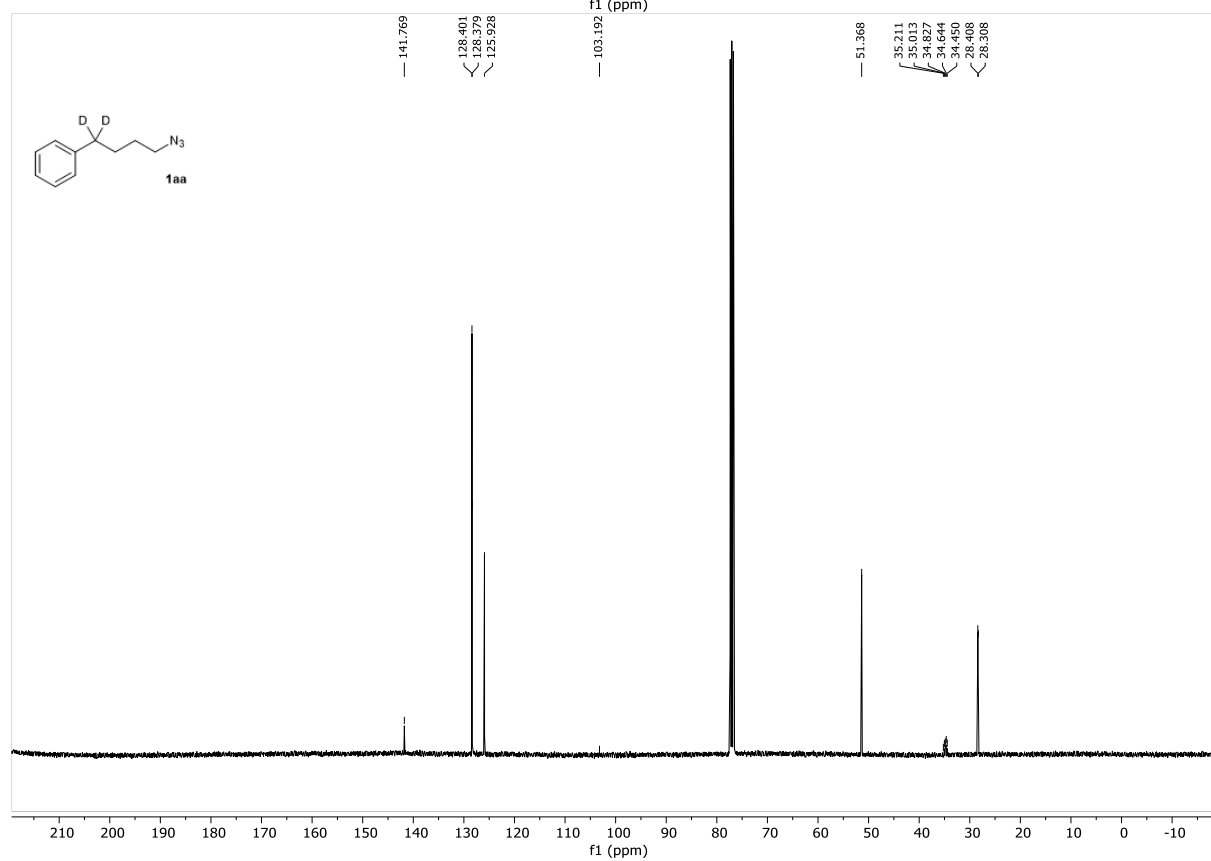
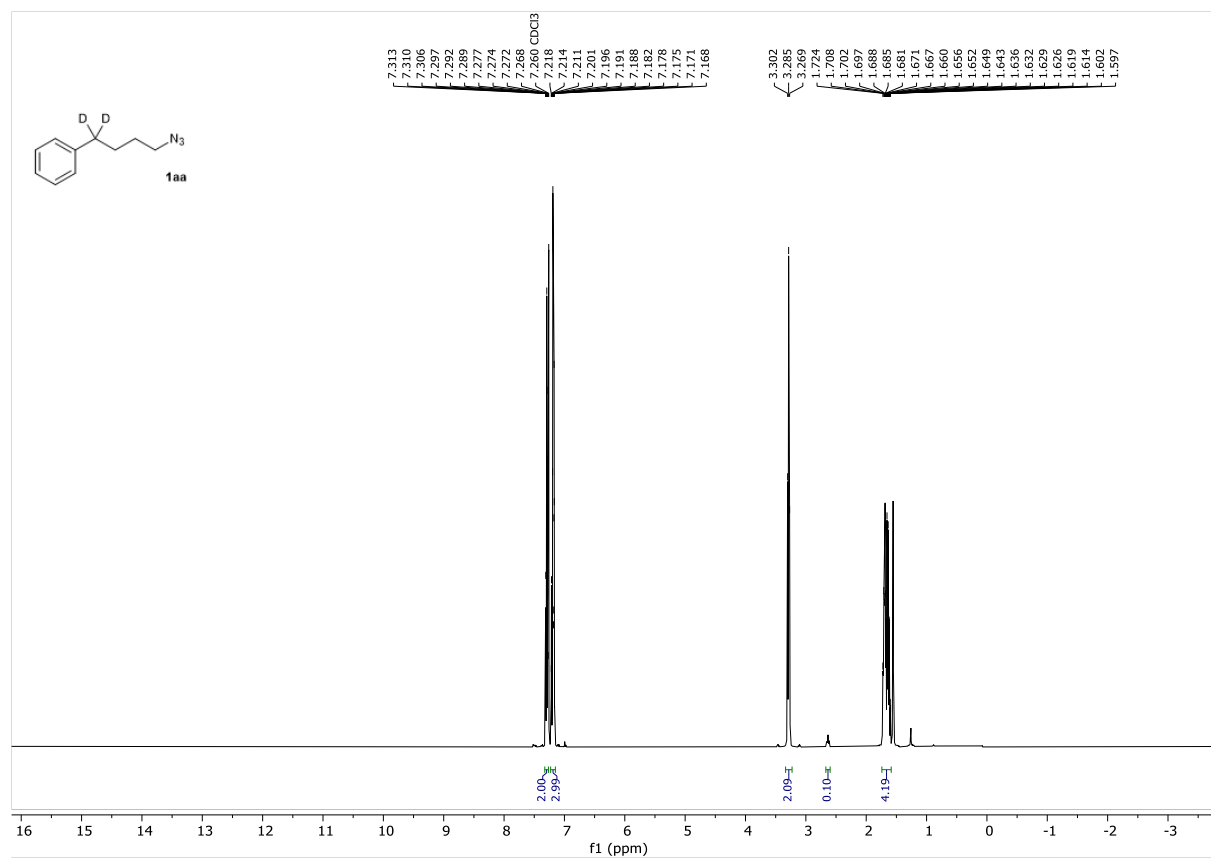


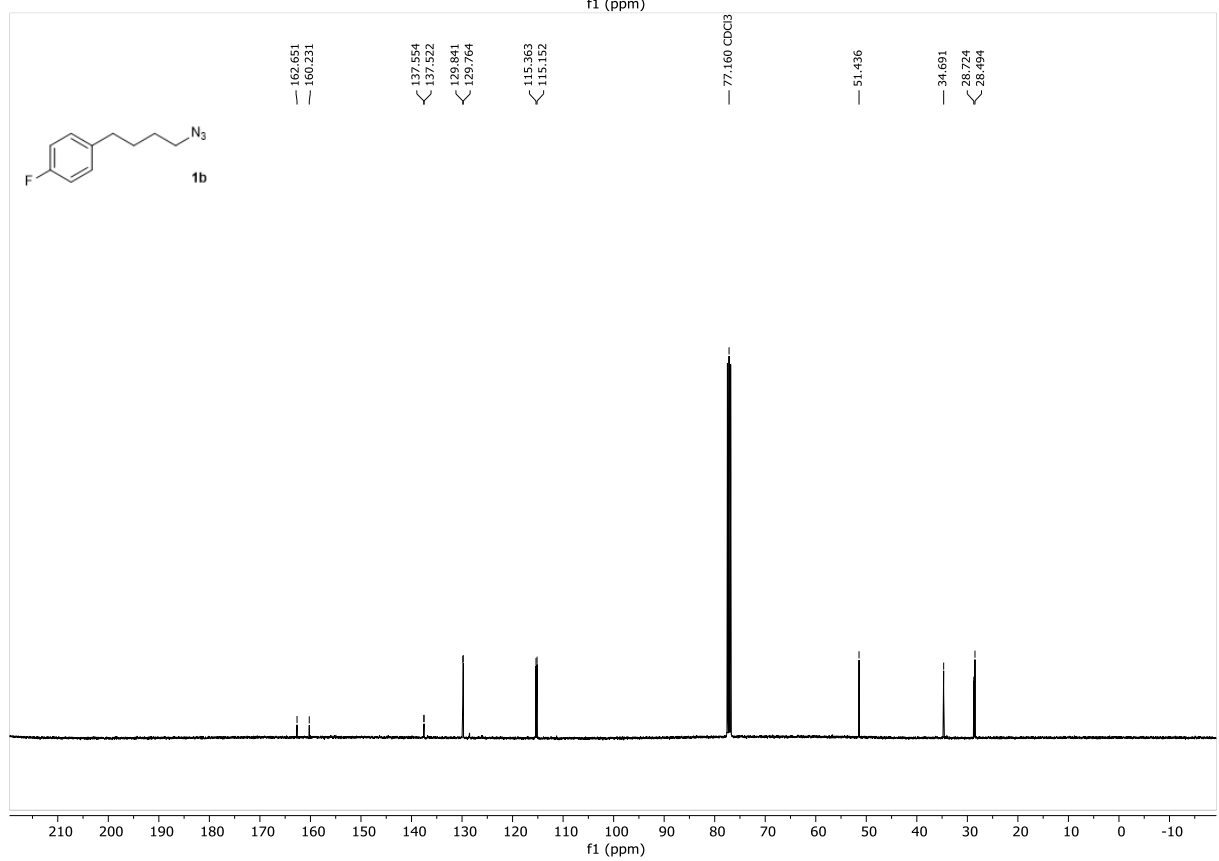
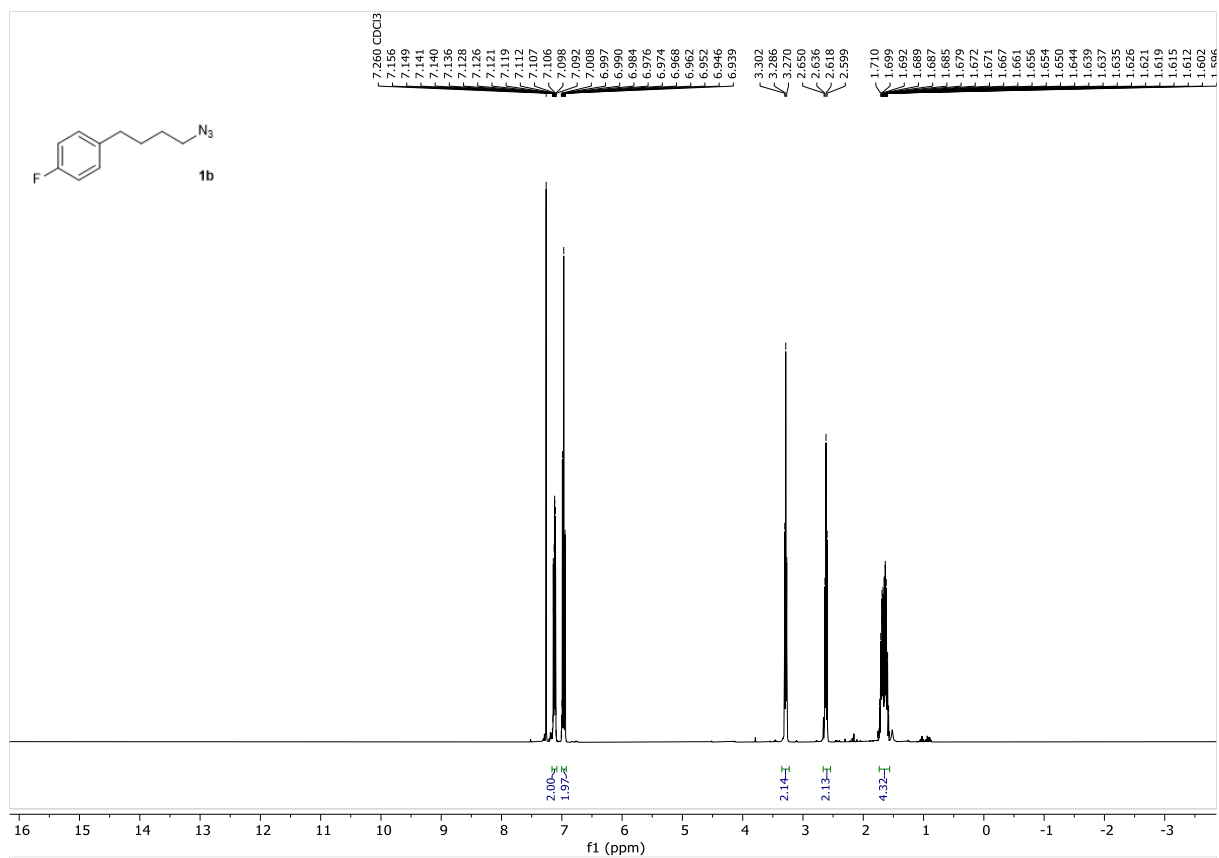
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H	2.708069	0.129446	4.696124
H	2.276354	1.417055	3.551457
H	3.834321	0.575460	3.395057
C	-0.522769	2.615806	-2.068954
C	-0.461940	4.249249	-4.386854
C	-1.401009	3.737536	-2.197422
C	0.356456	2.337631	-3.142485
C	0.390355	3.147962	-4.274072
C	-1.356458	4.523059	-3.347377
H	1.001081	1.473209	-3.078007
H	1.080242	2.906539	-5.079237
H	-2.035347	5.369651	-3.428681
H	-0.441779	4.877686	-5.272818
C	-2.366260	4.020865	-1.071386
H	-3.166554	4.690185	-1.421113
H	-1.854527	4.549405	-0.251352
C	-2.943866	2.725620	-0.529105
H	-1.743611	2.055944	-0.456154
H	-3.449055	2.141245	-1.308045
C	-3.726935	2.806956	0.765003
H	-4.359292	3.711028	0.724027
H	-3.045098	2.967155	1.610360
H	2.189378	-0.915003	0.788635
C	-4.622510	1.591715	1.028285
H	-4.037322	0.667894	1.076263
H	-5.162695	1.697303	1.976356
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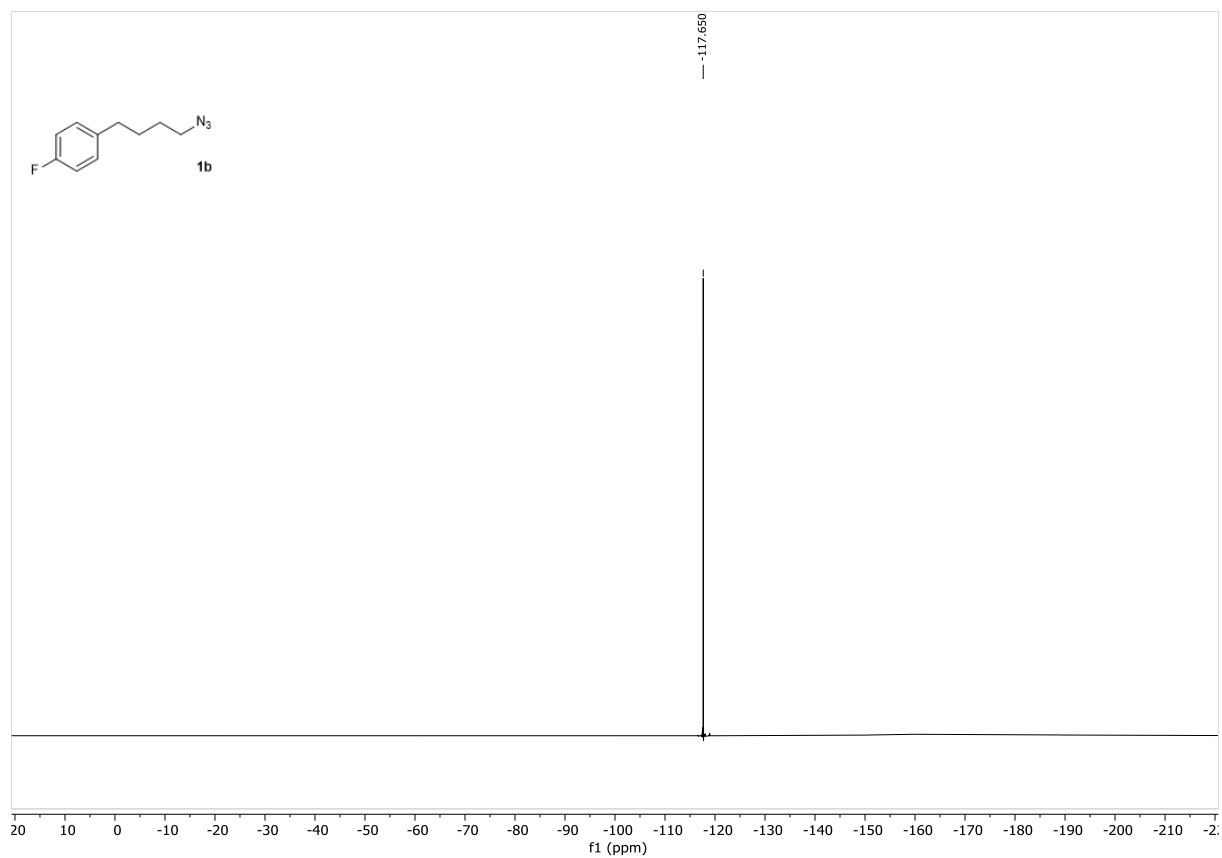
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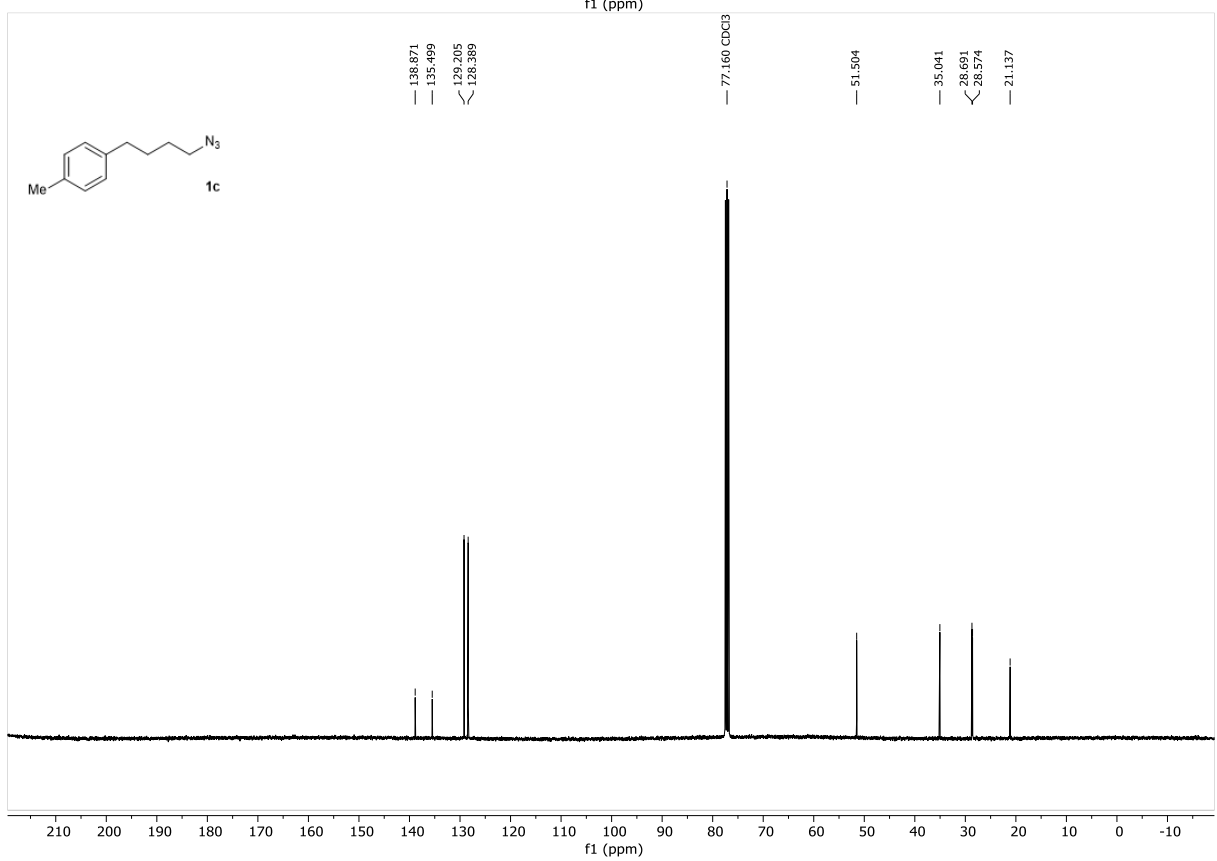
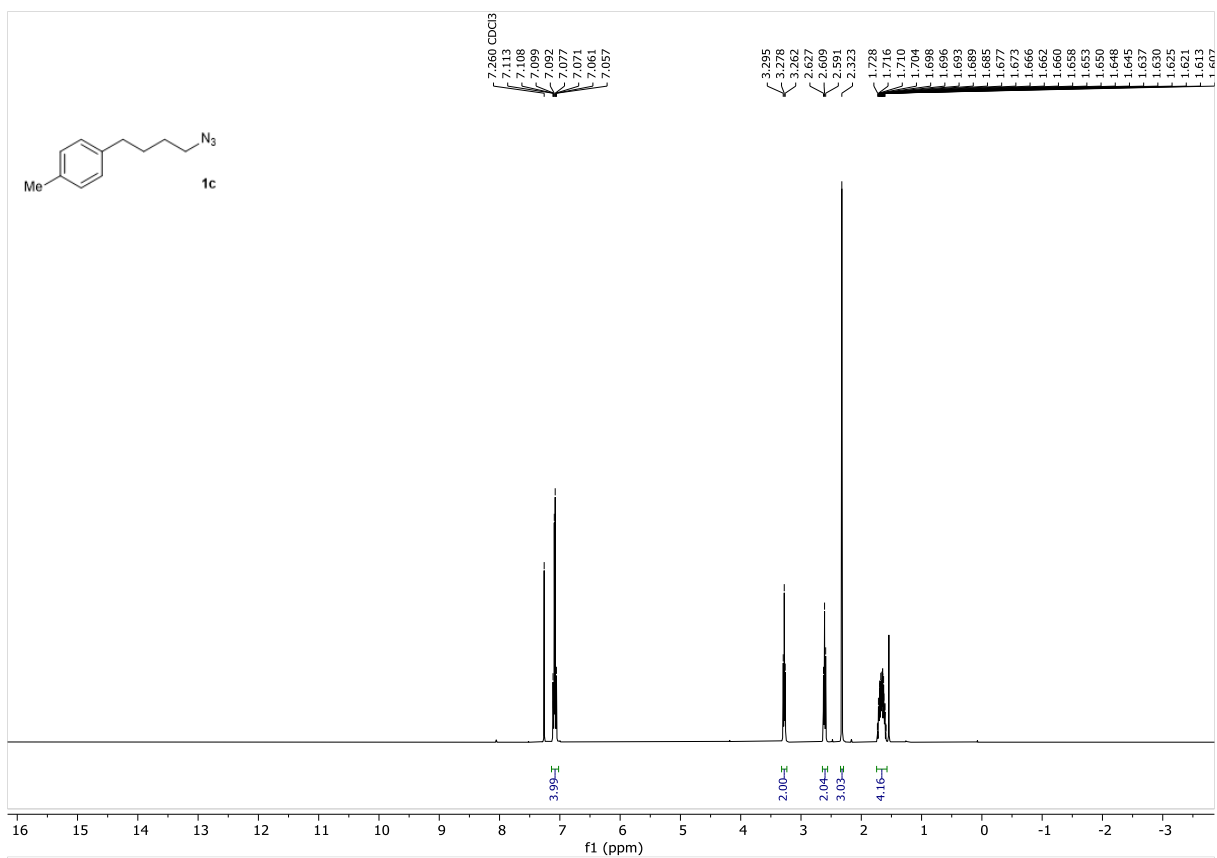
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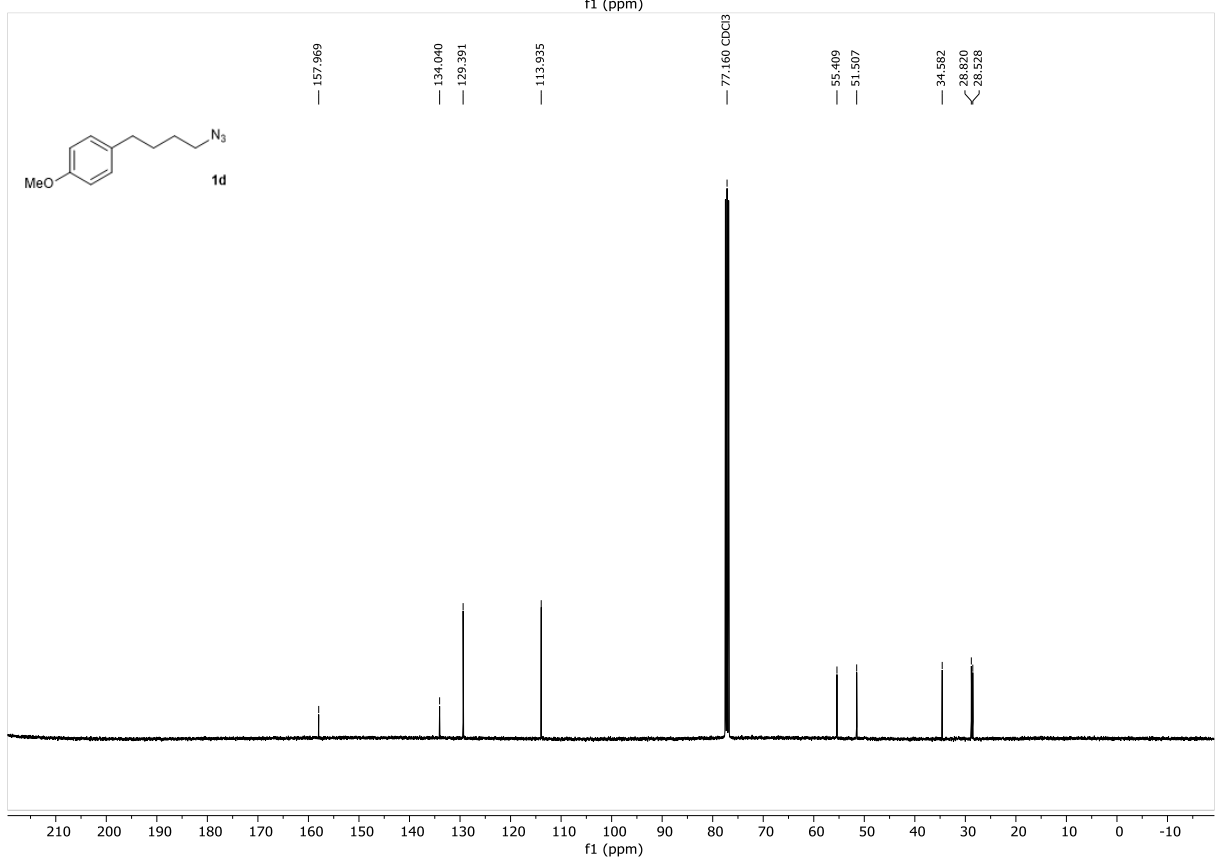
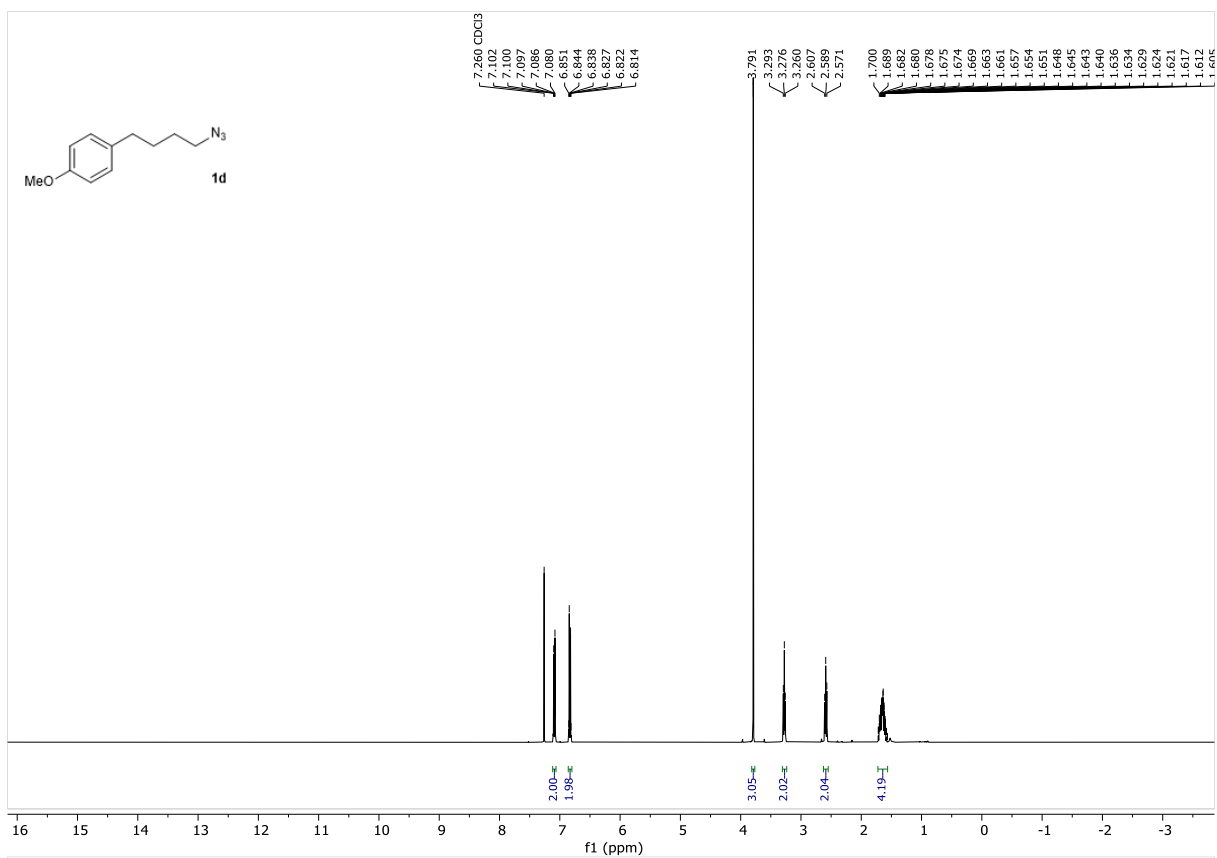


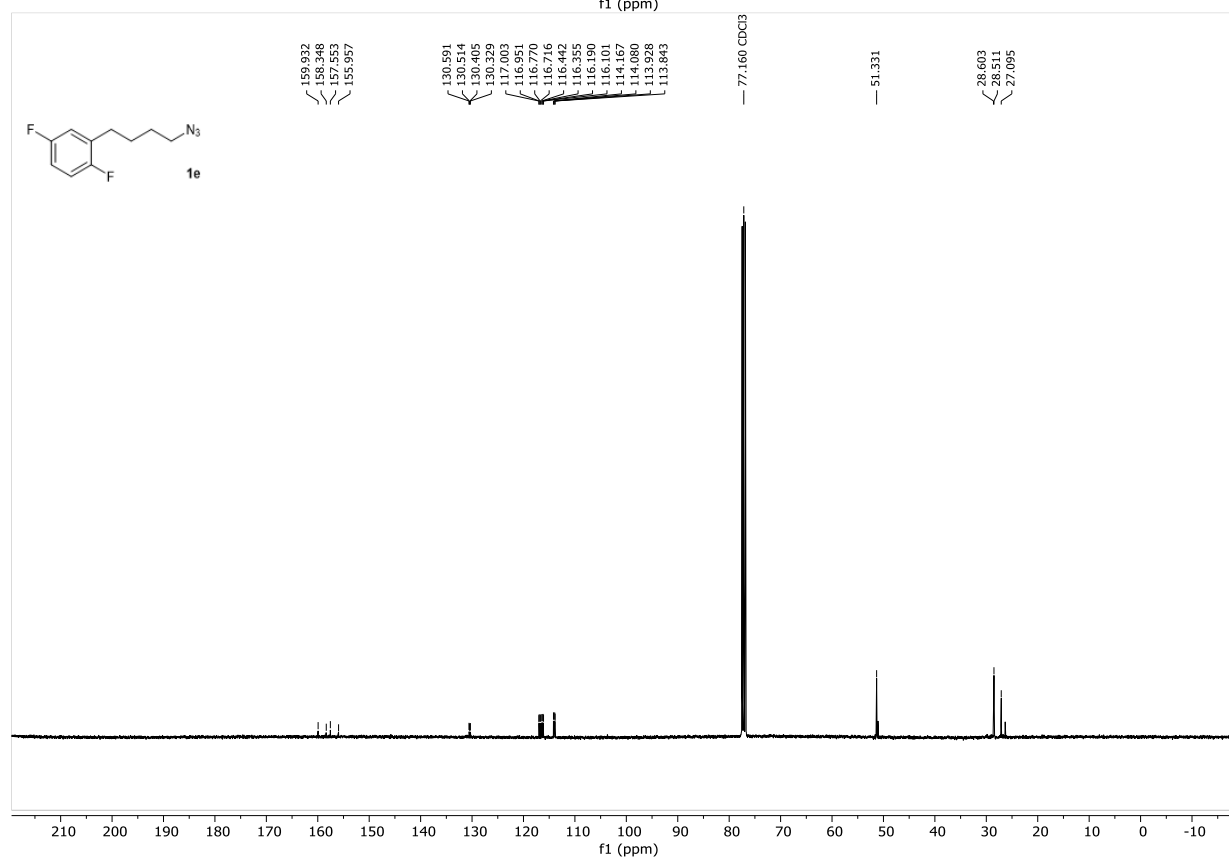
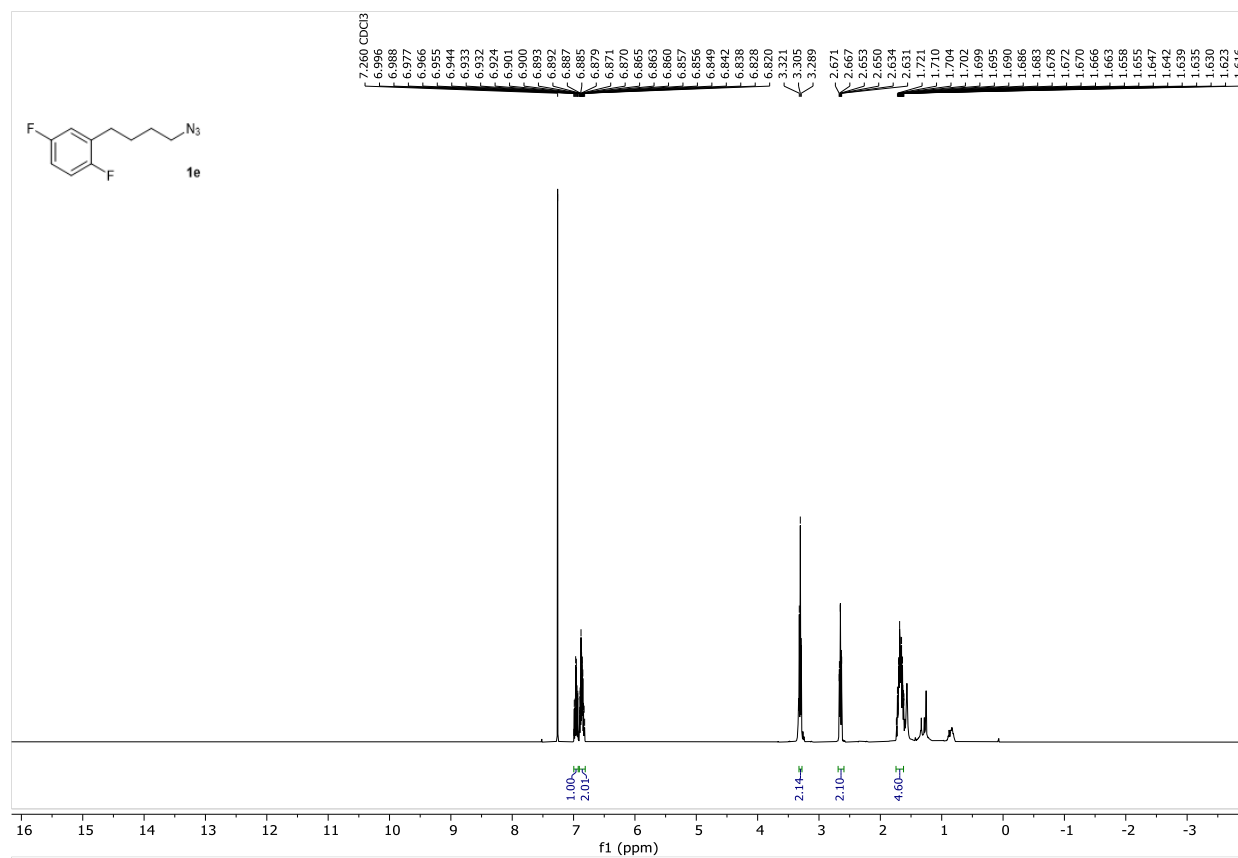




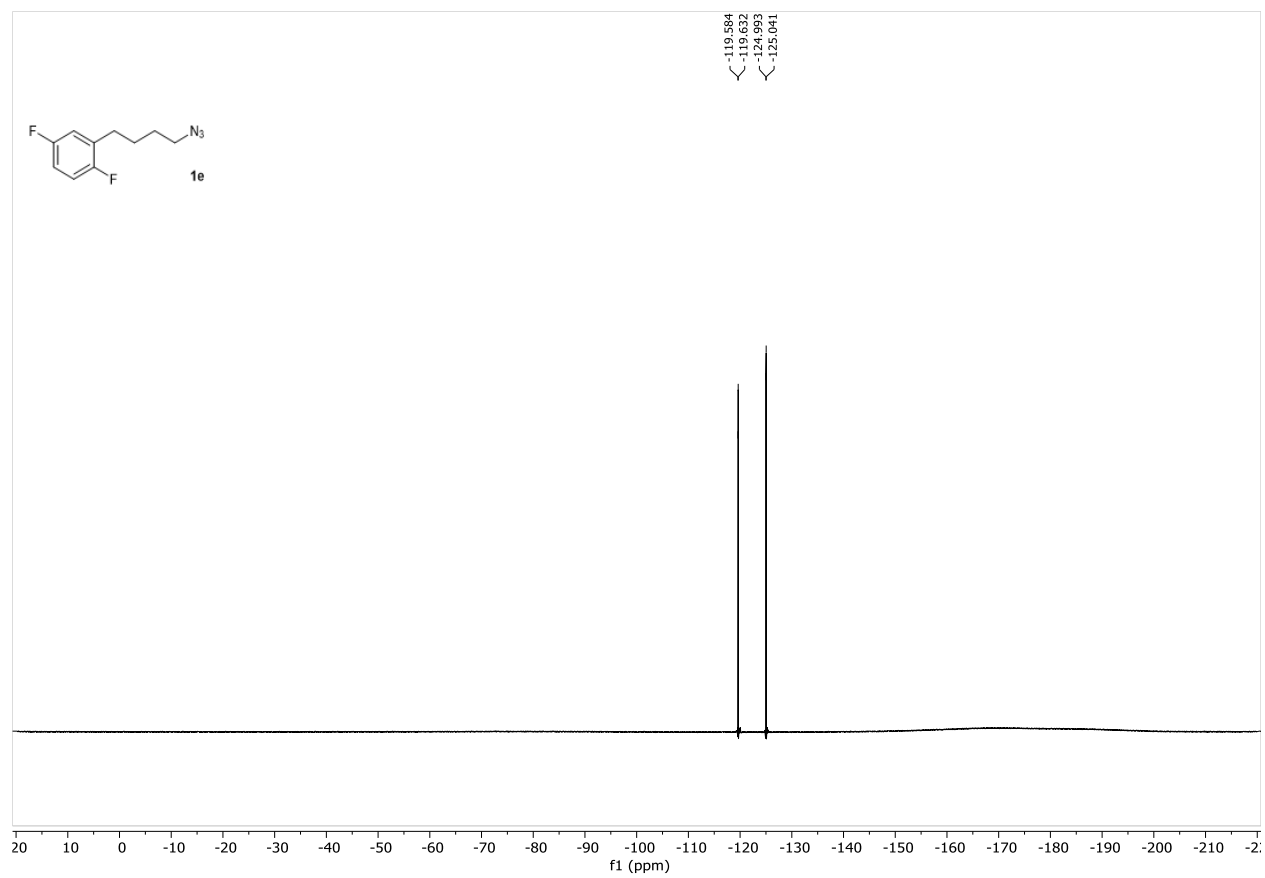


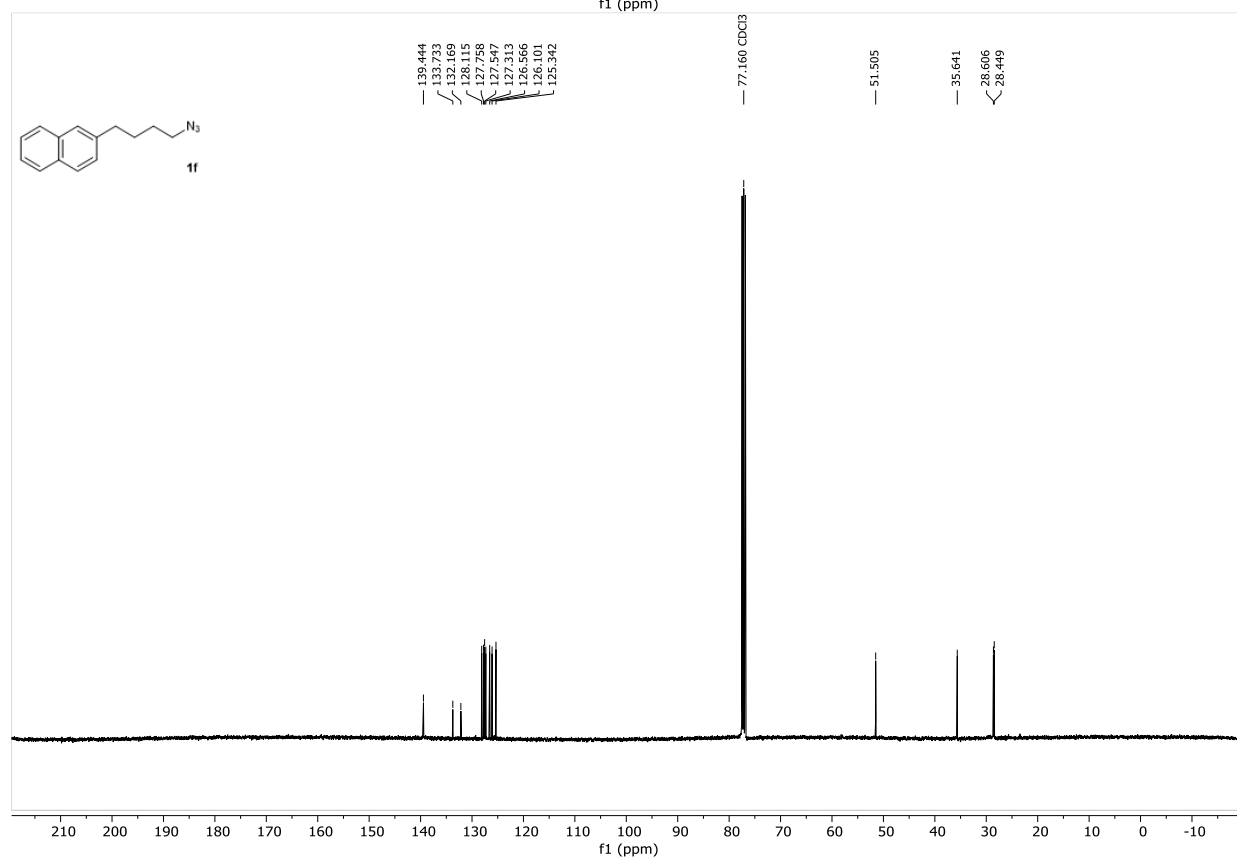
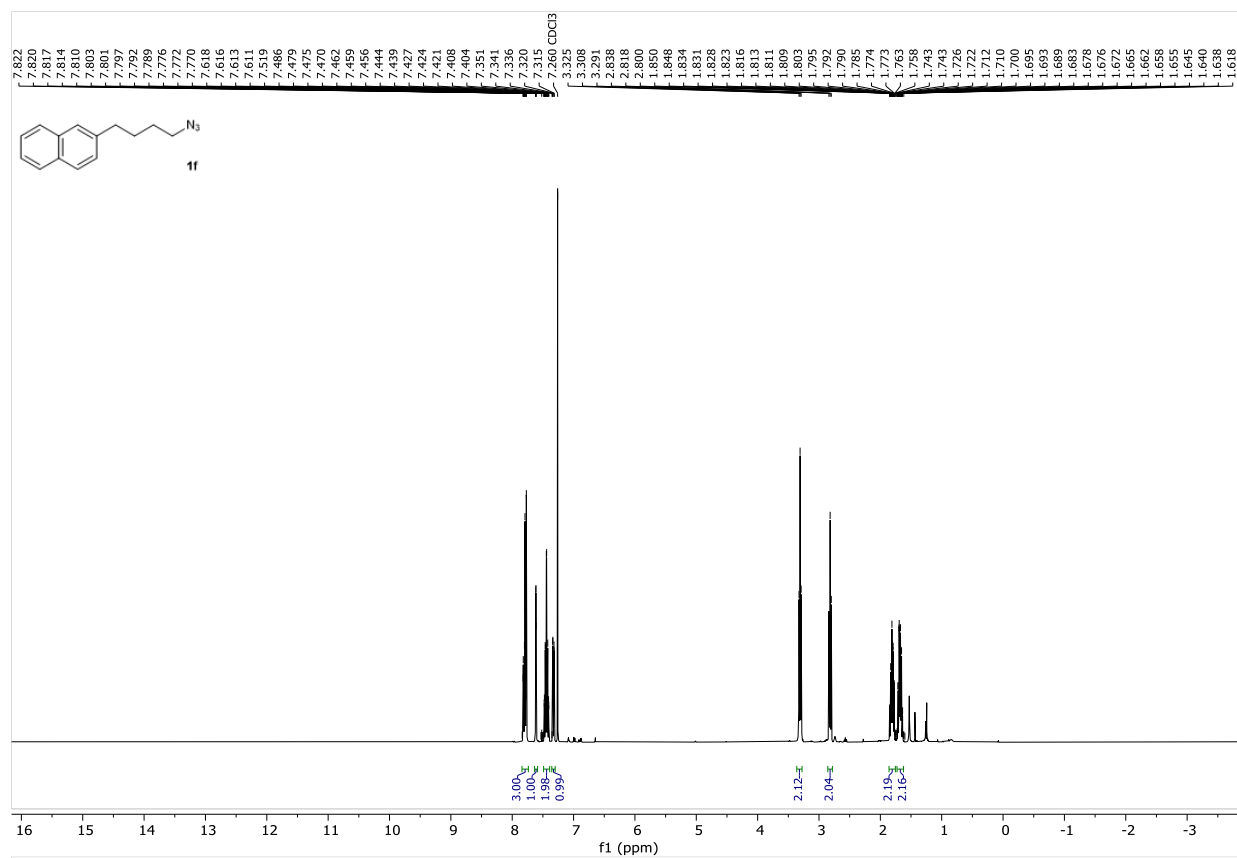


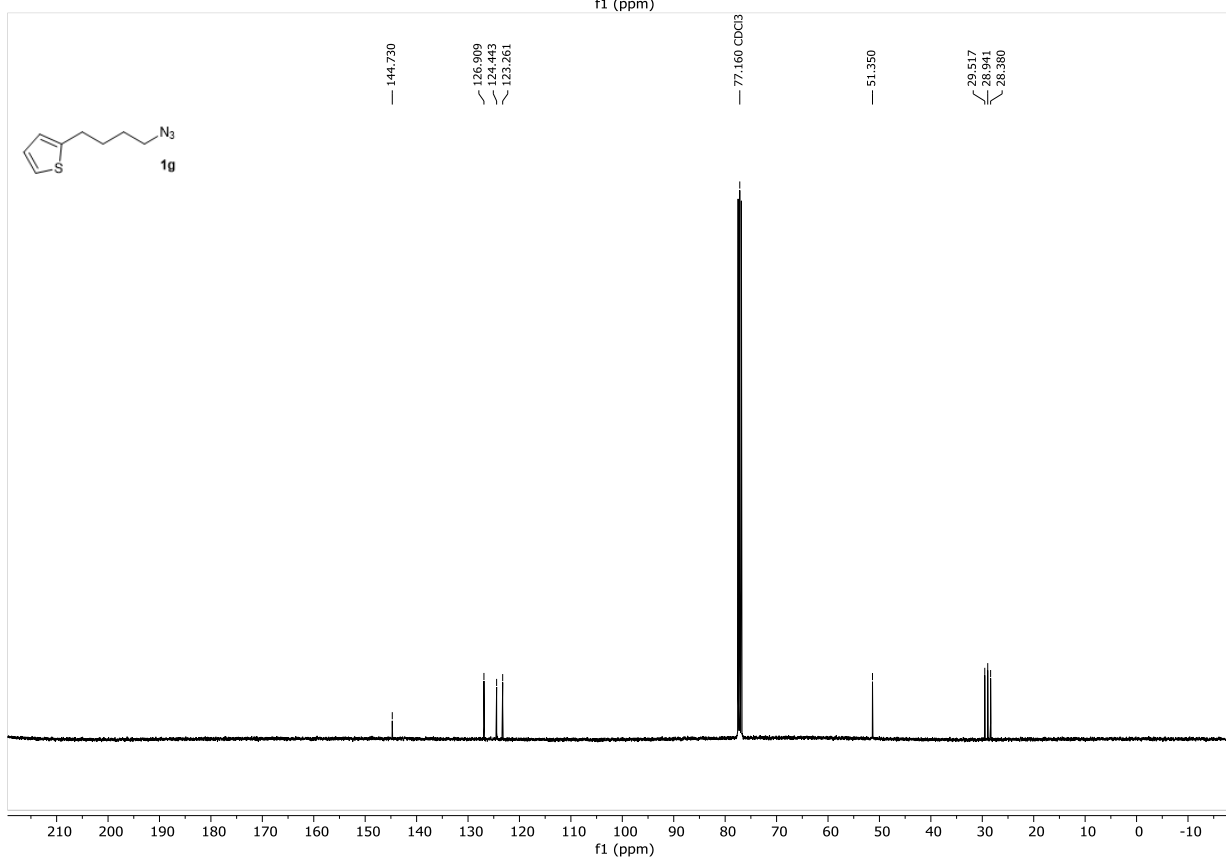
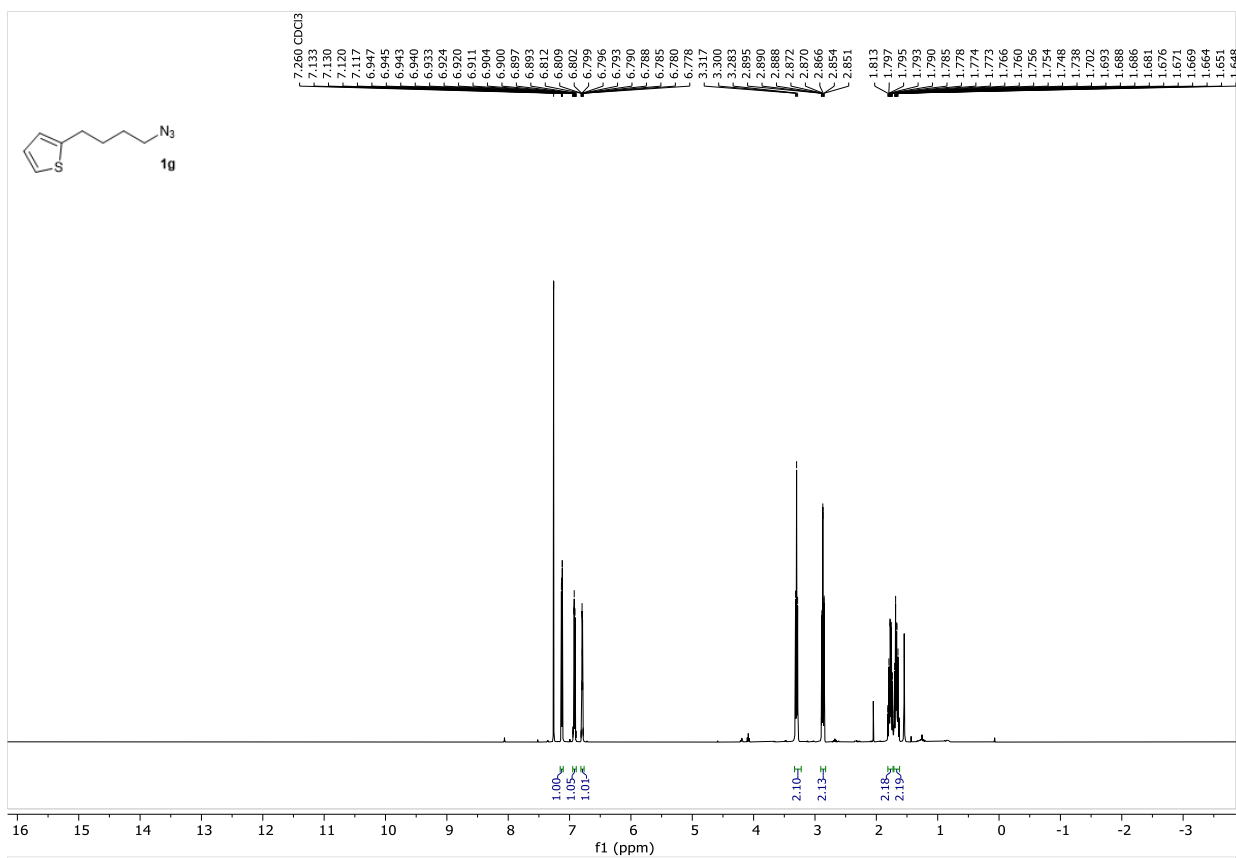


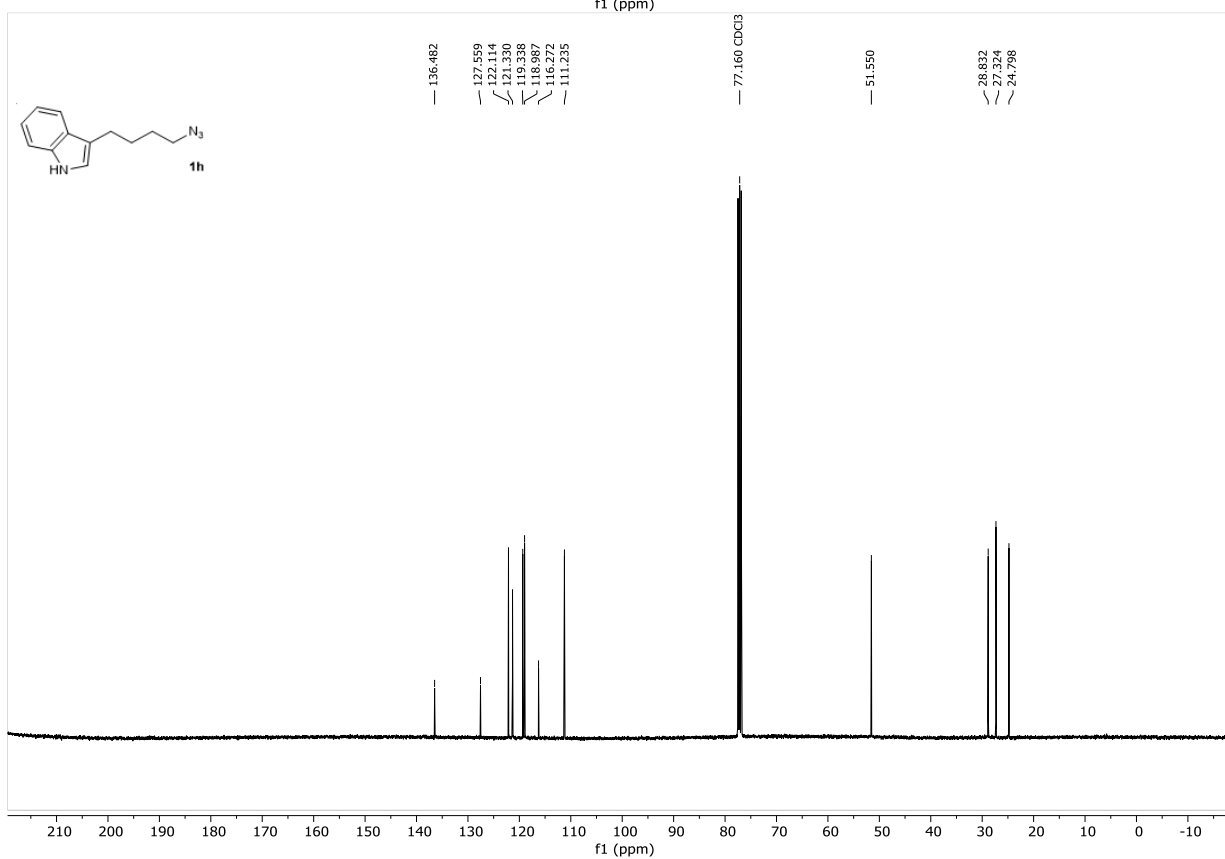
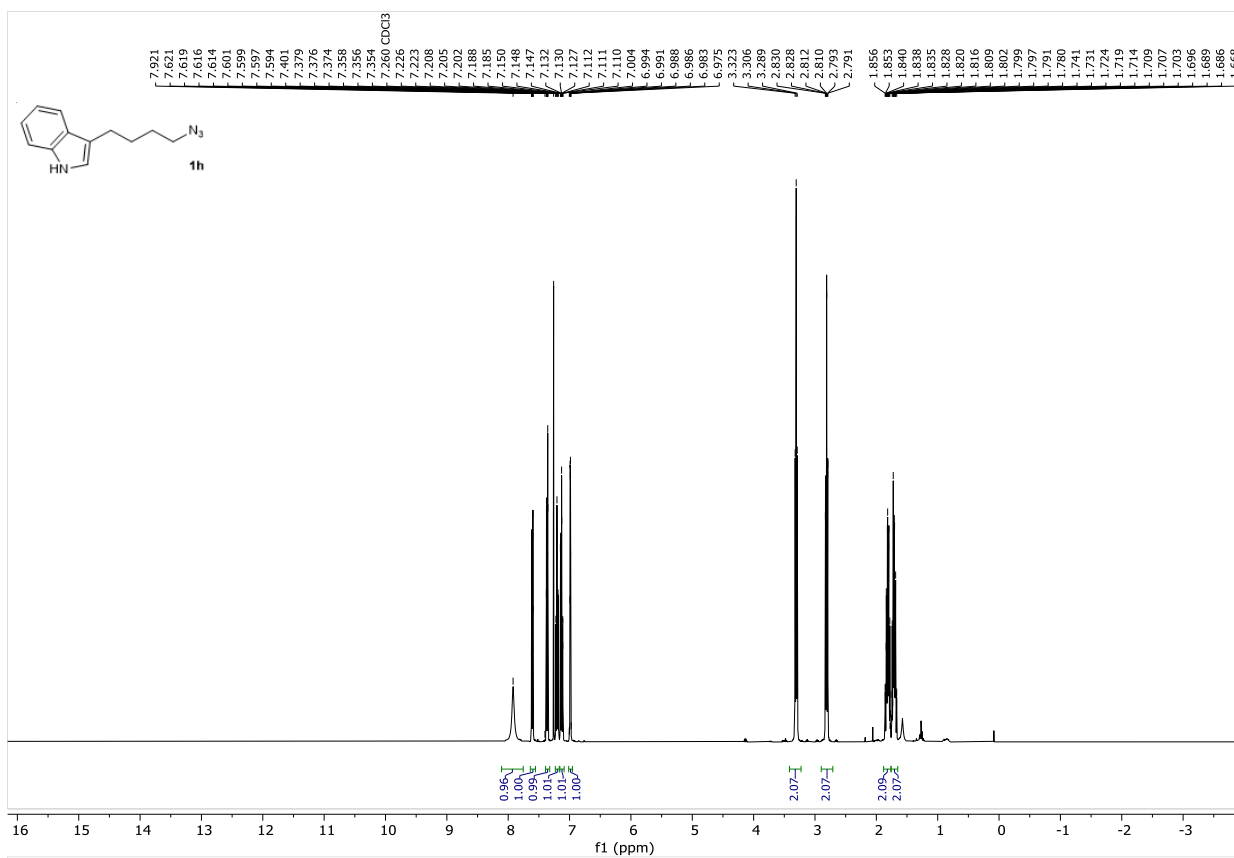


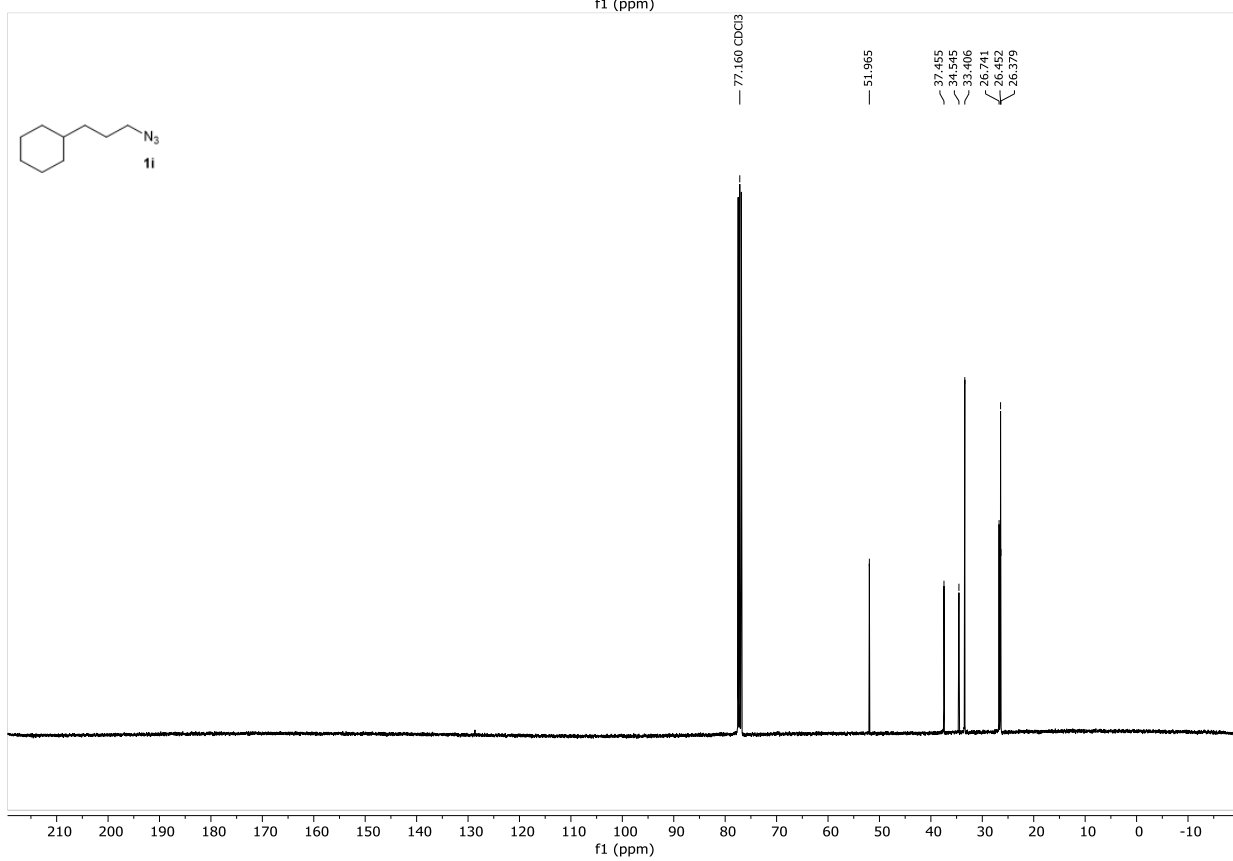
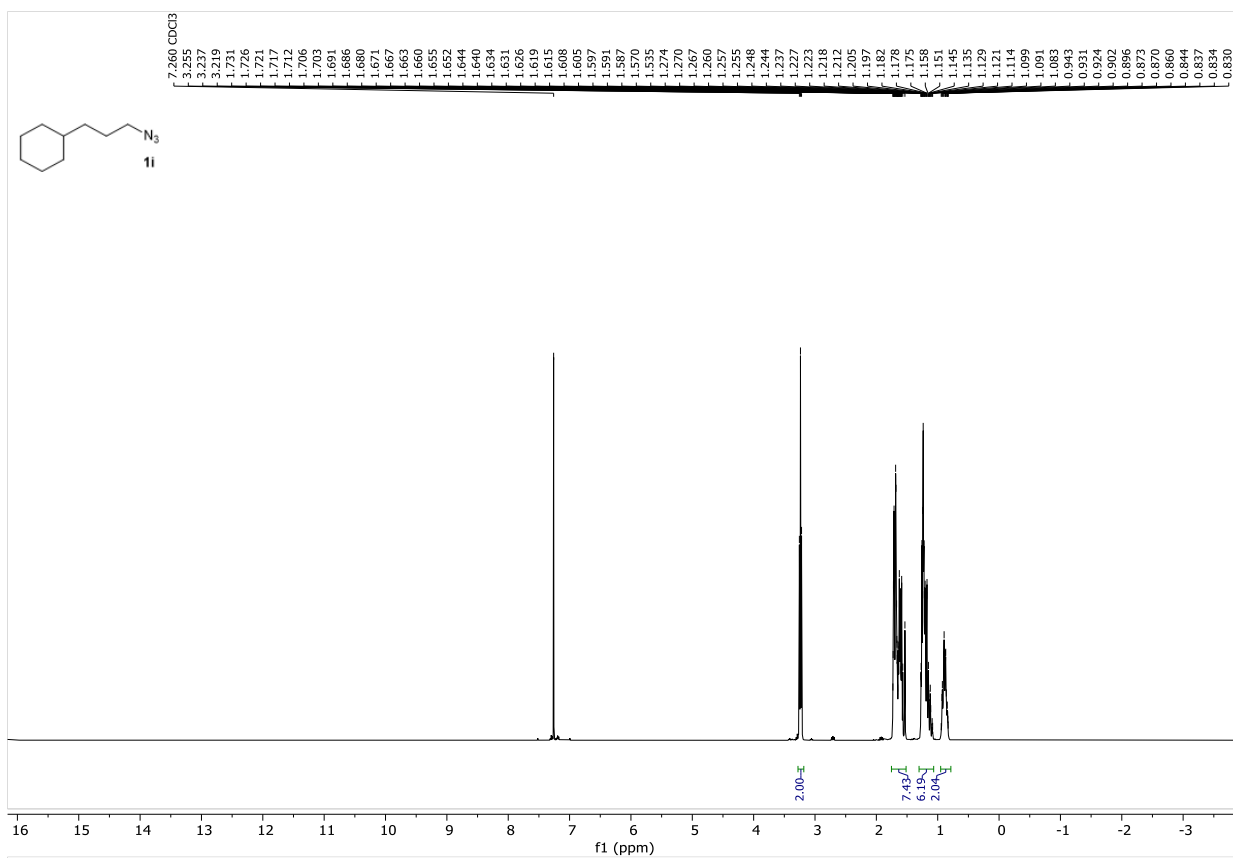


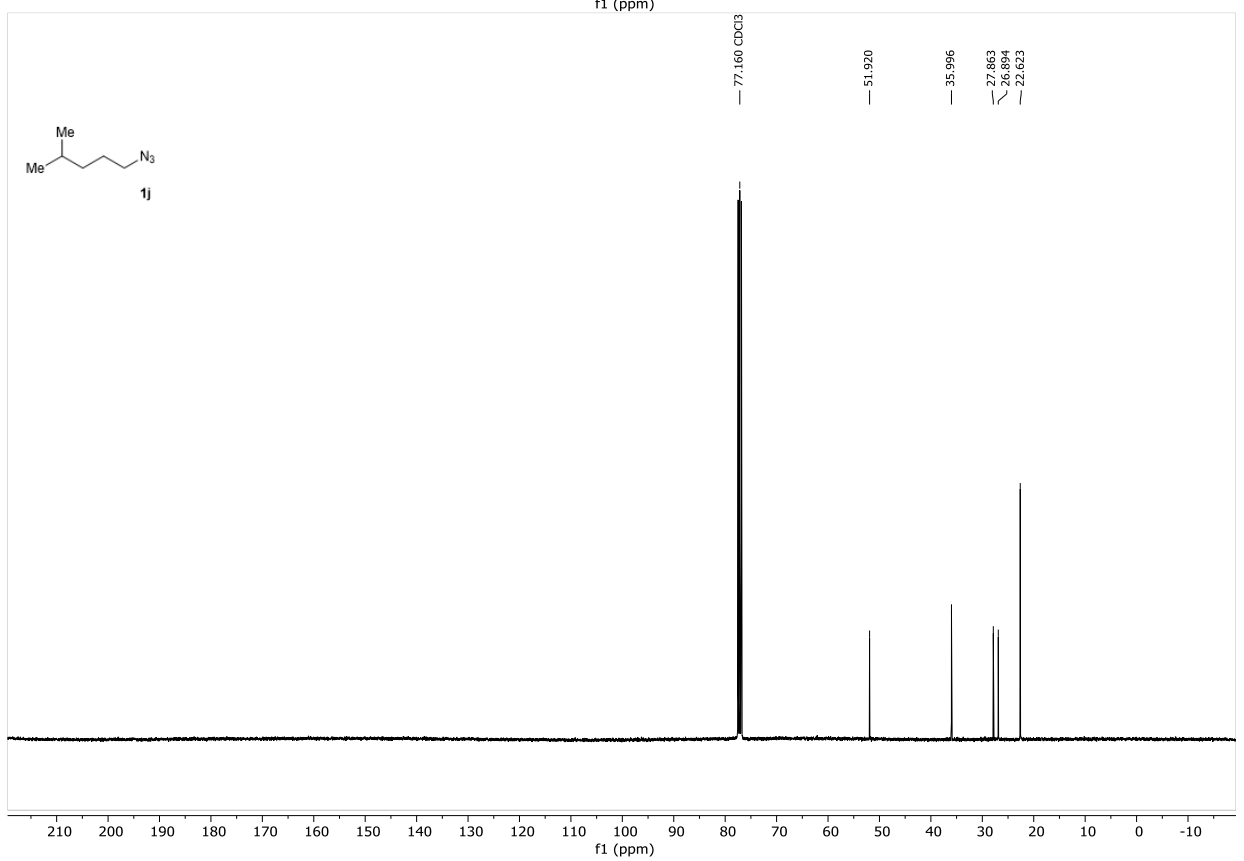
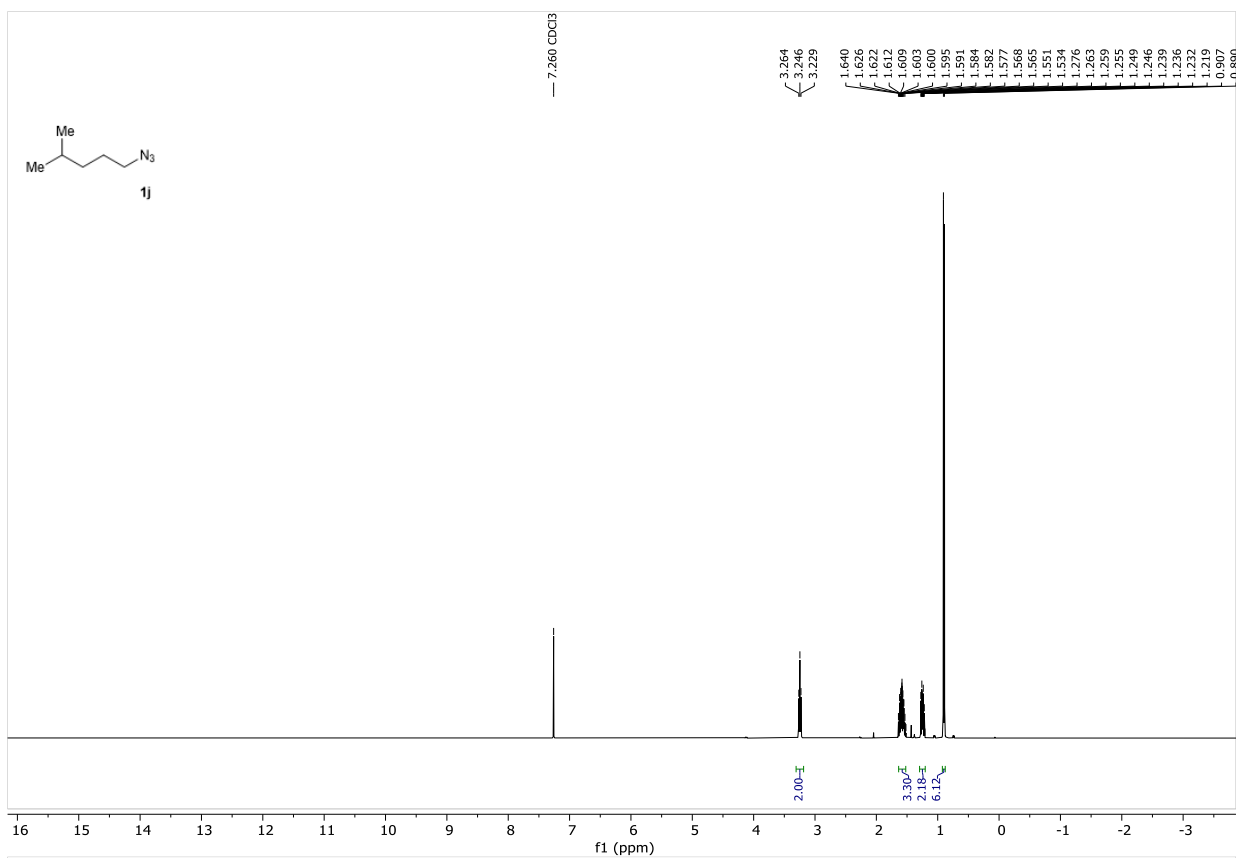


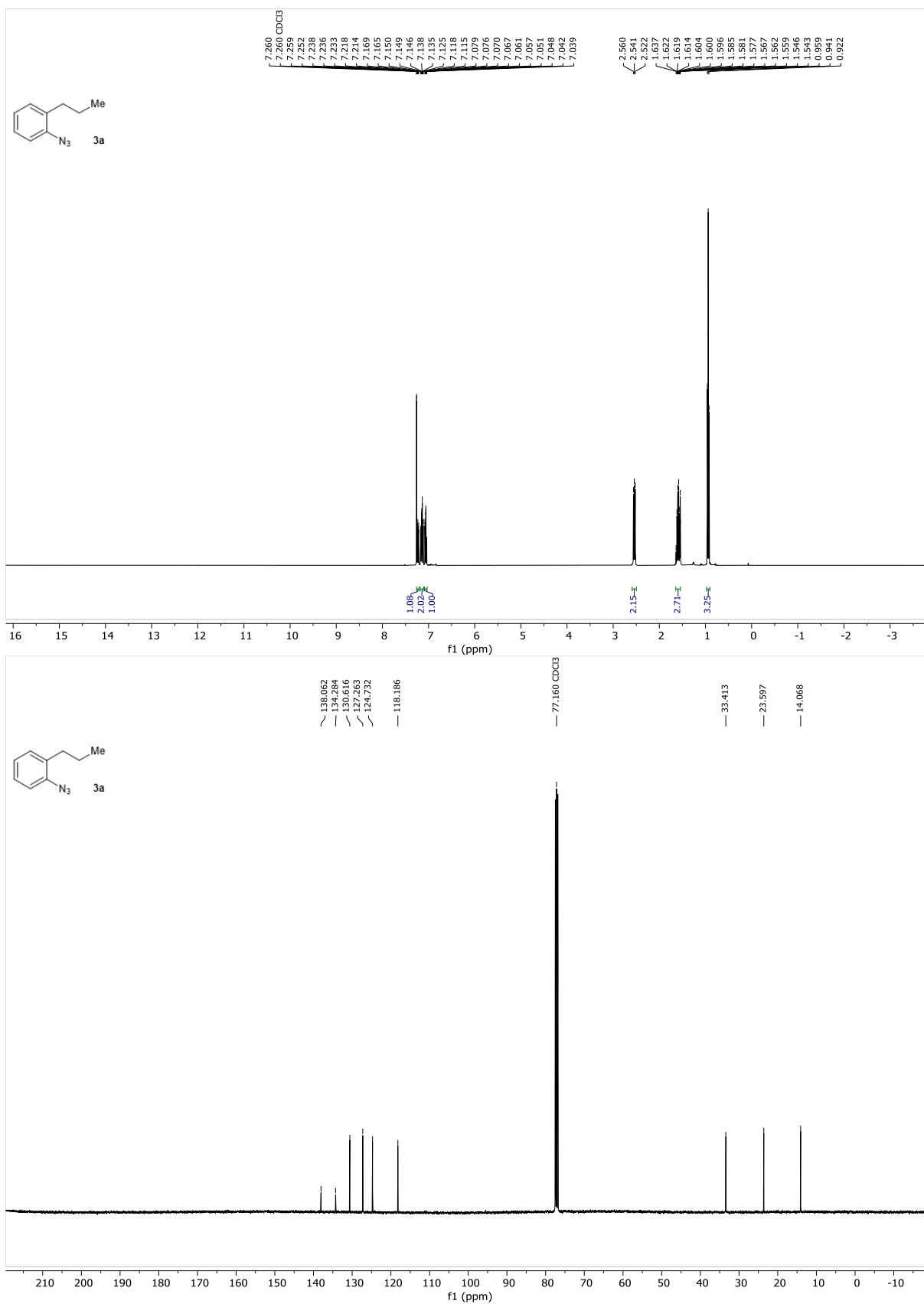


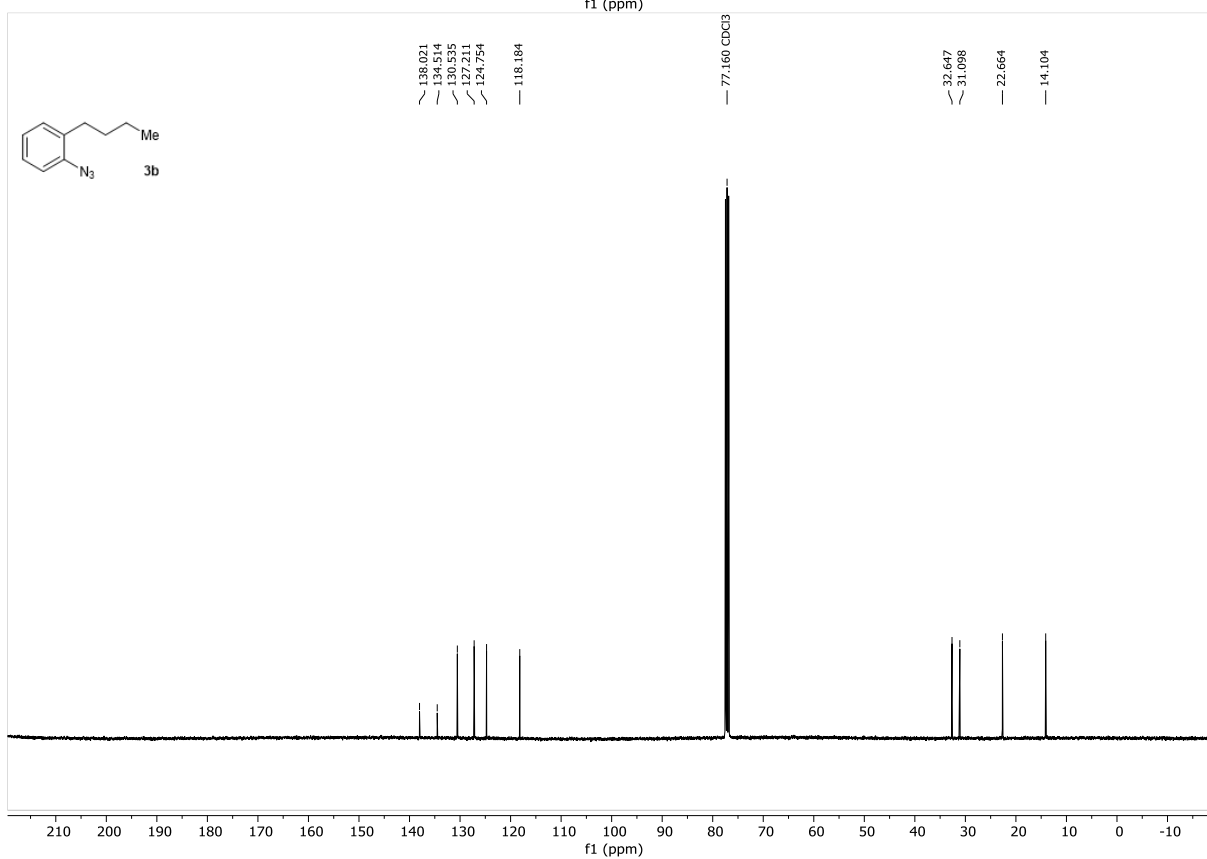
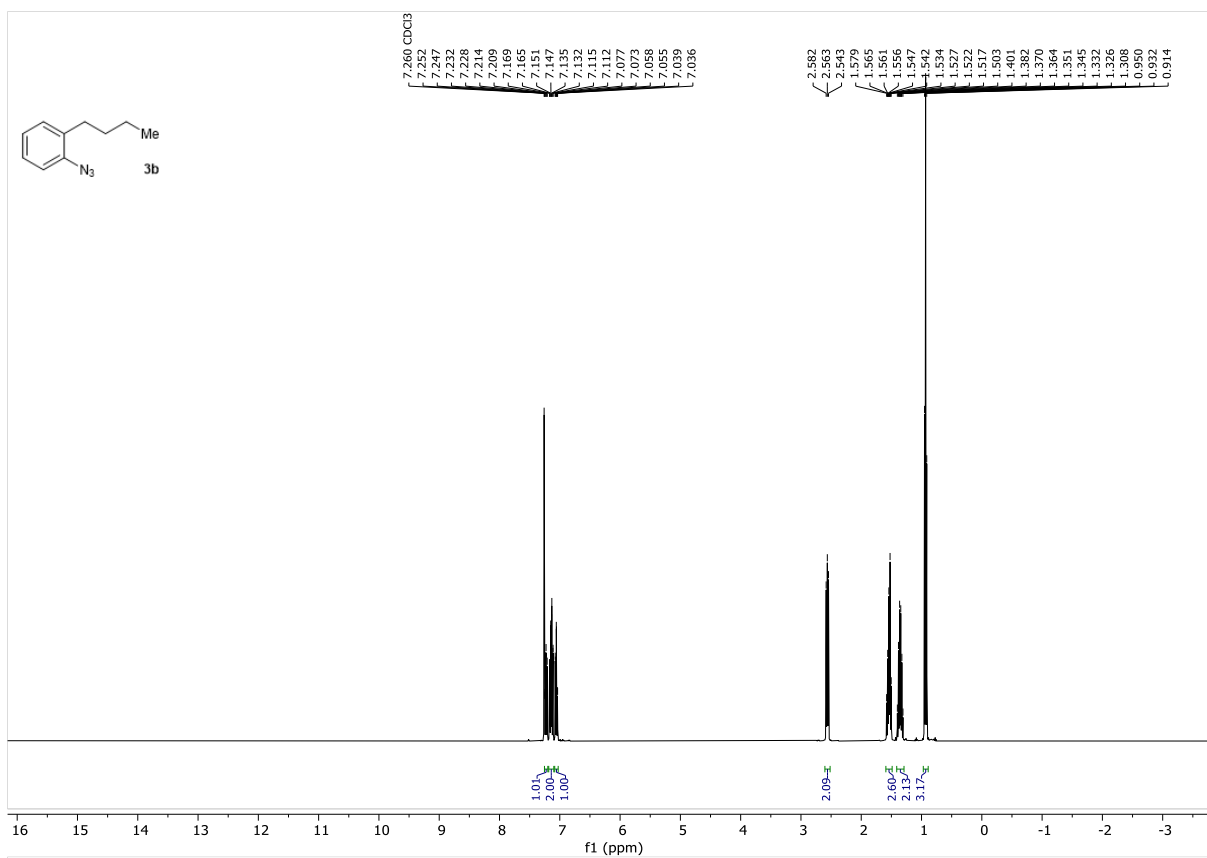




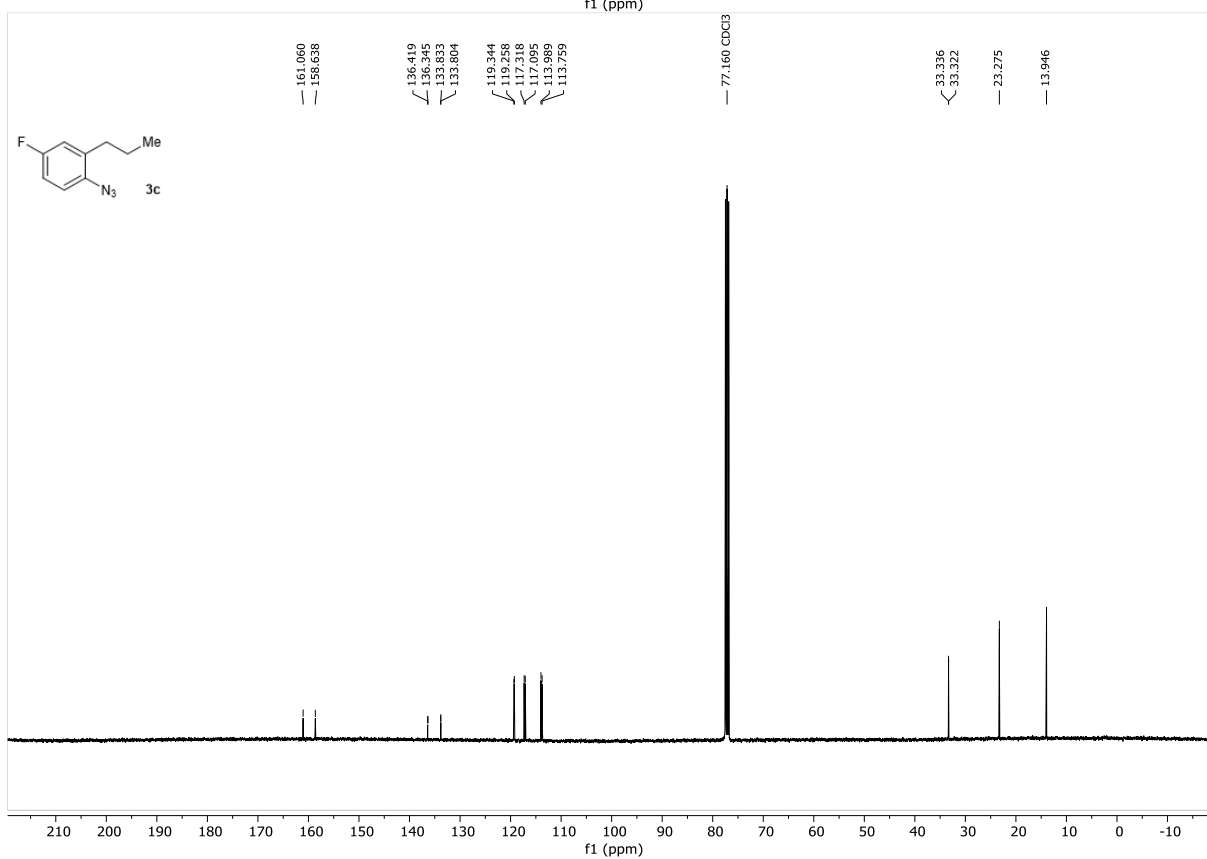
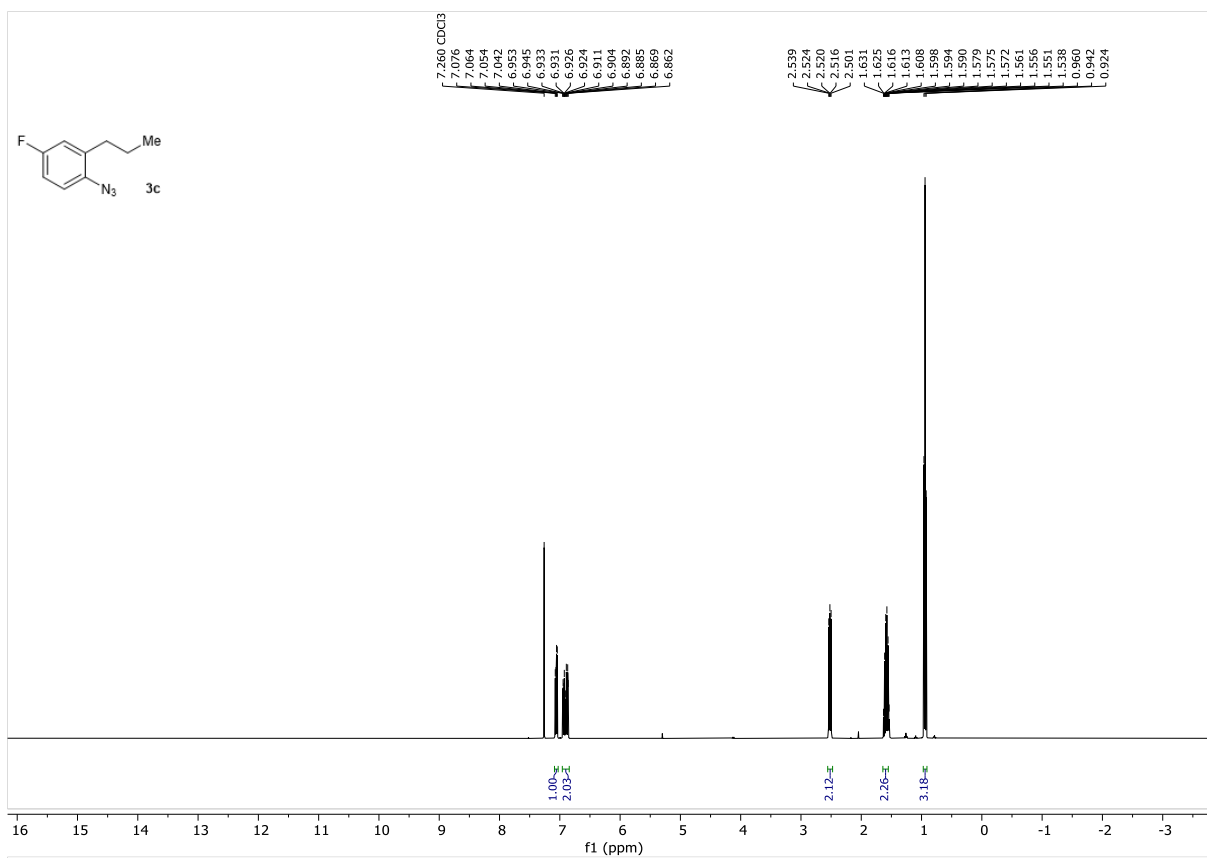


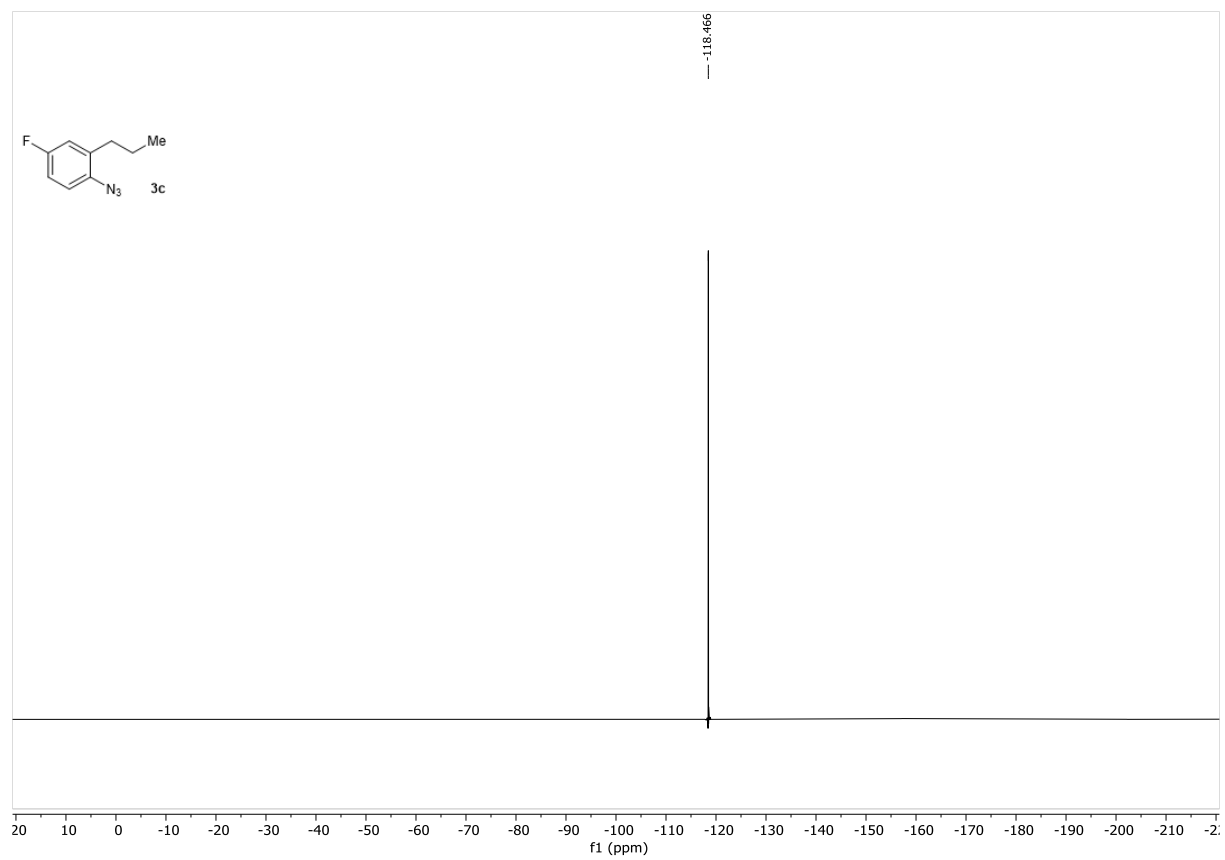


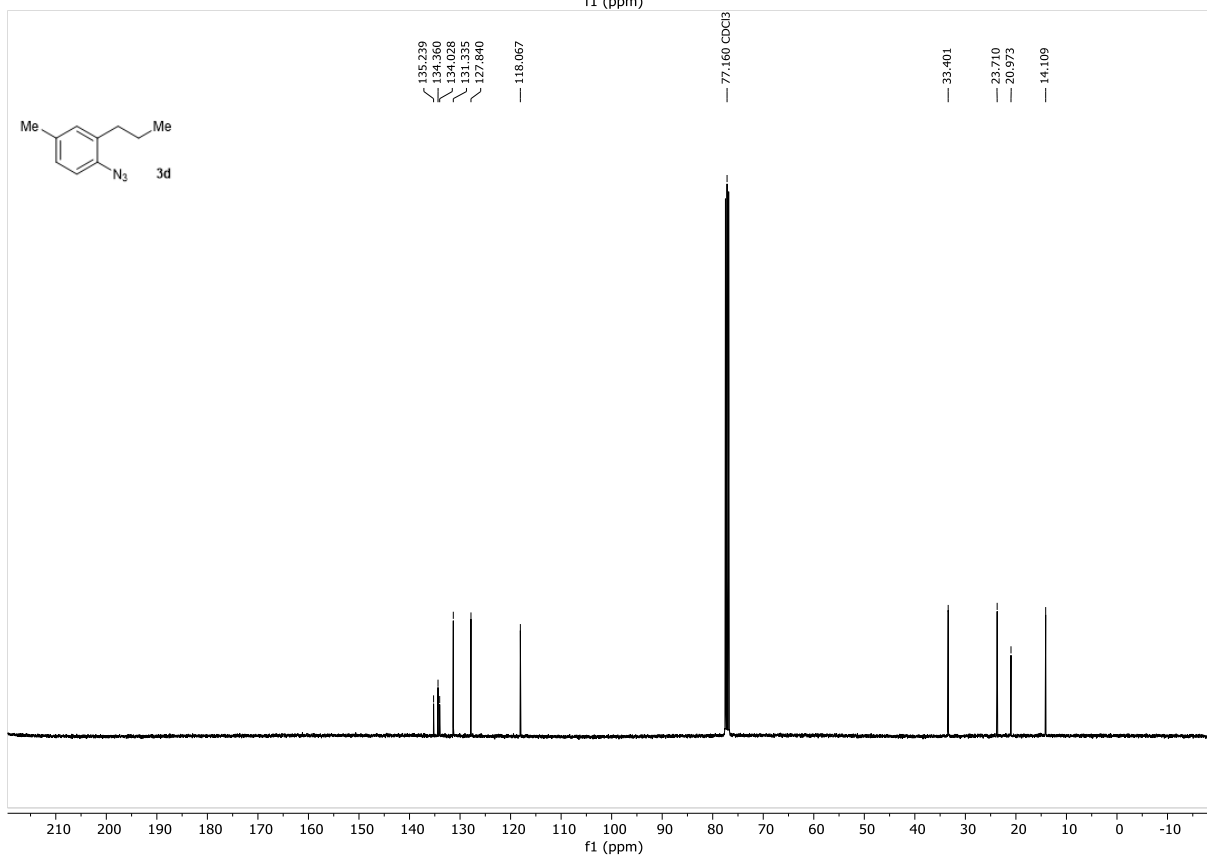
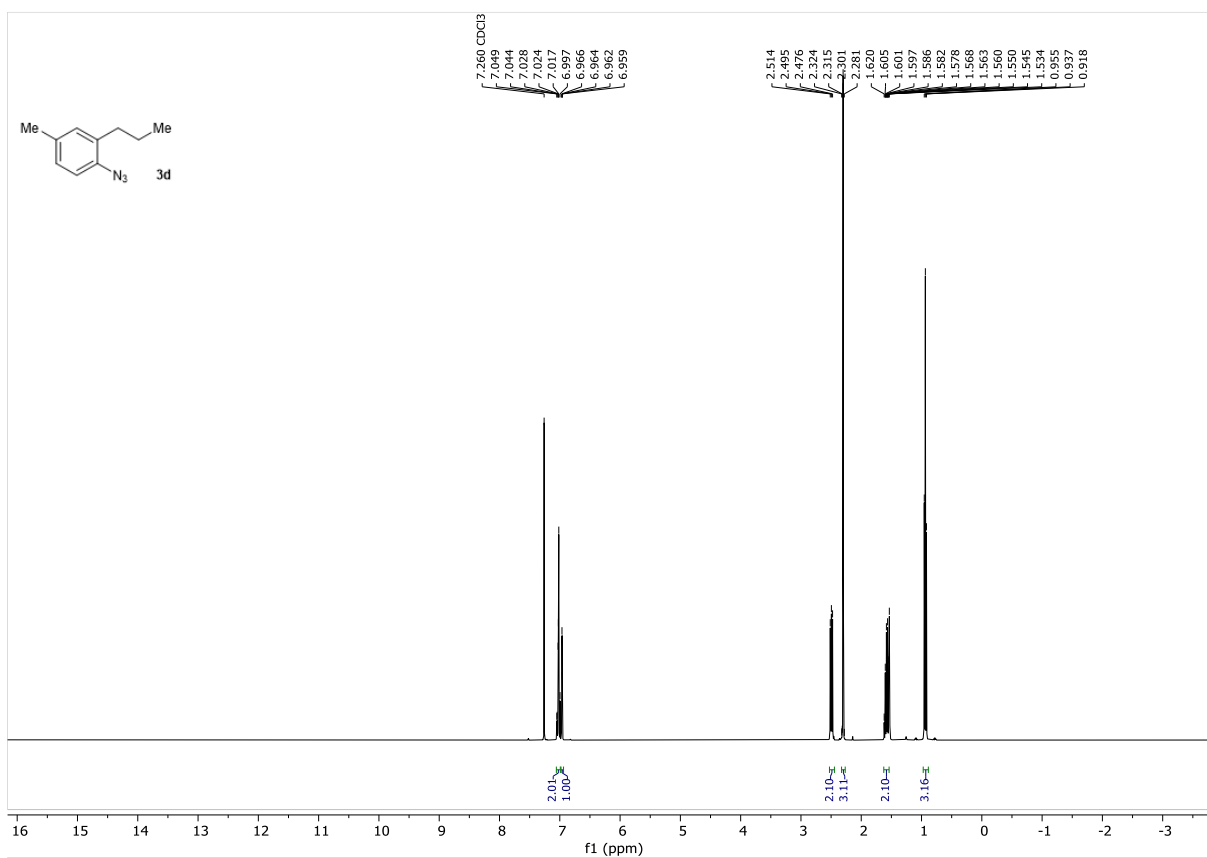


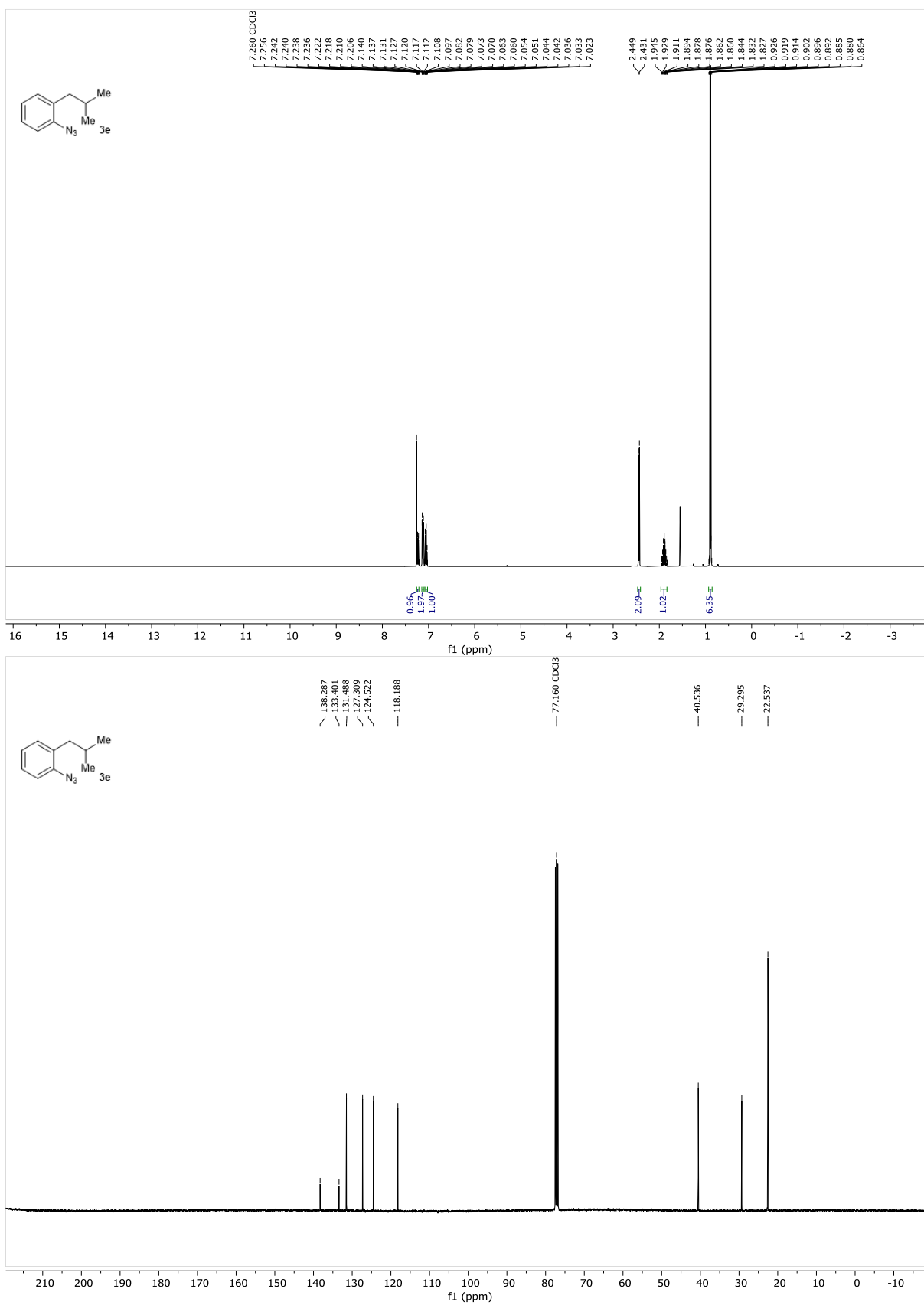




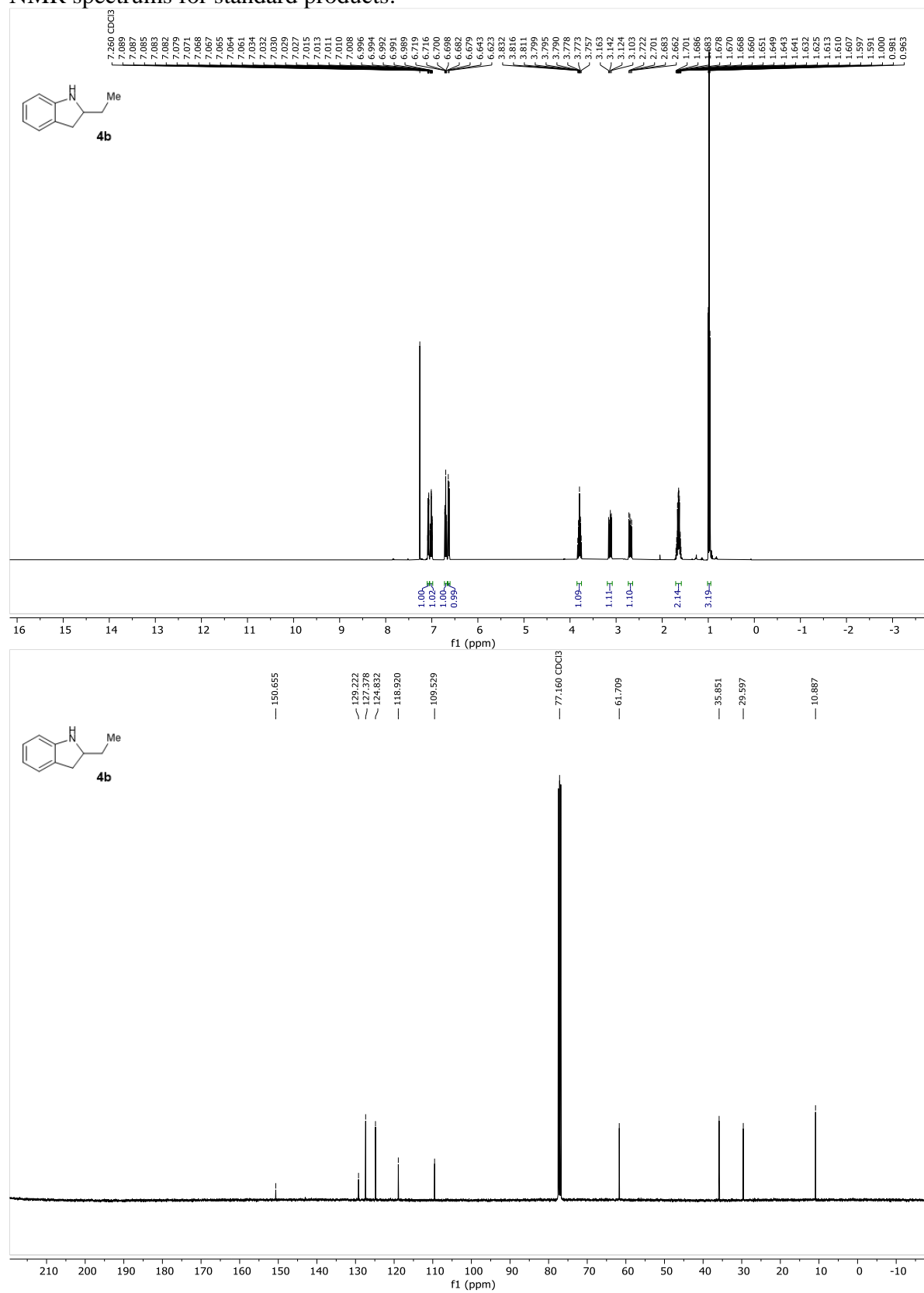


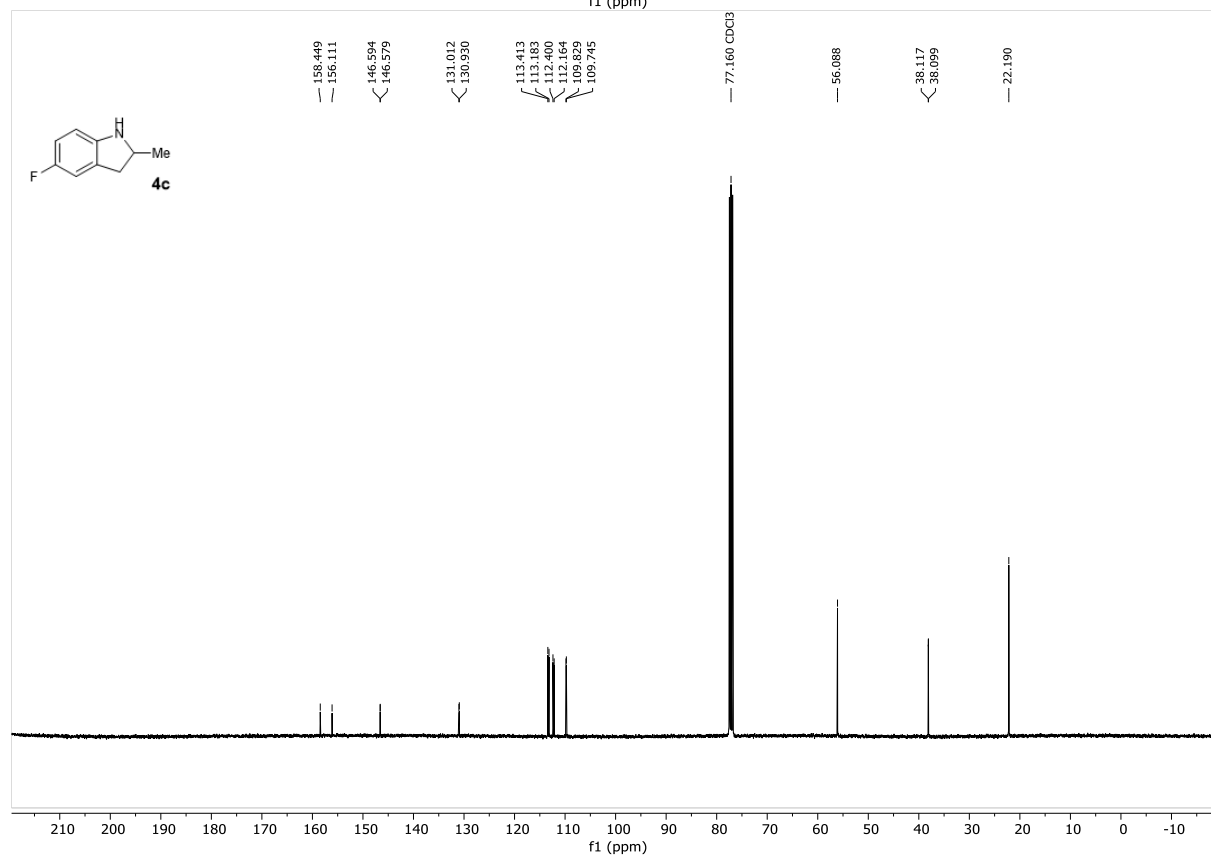
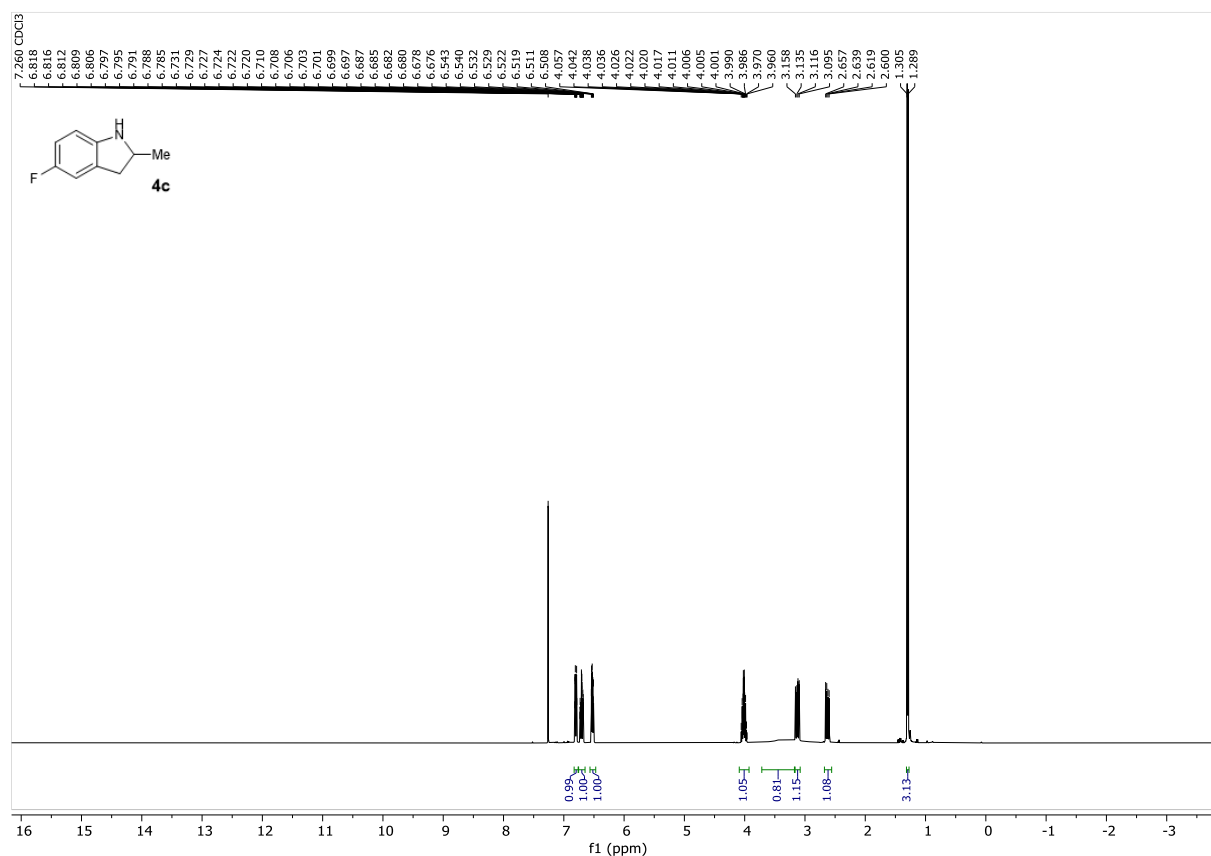


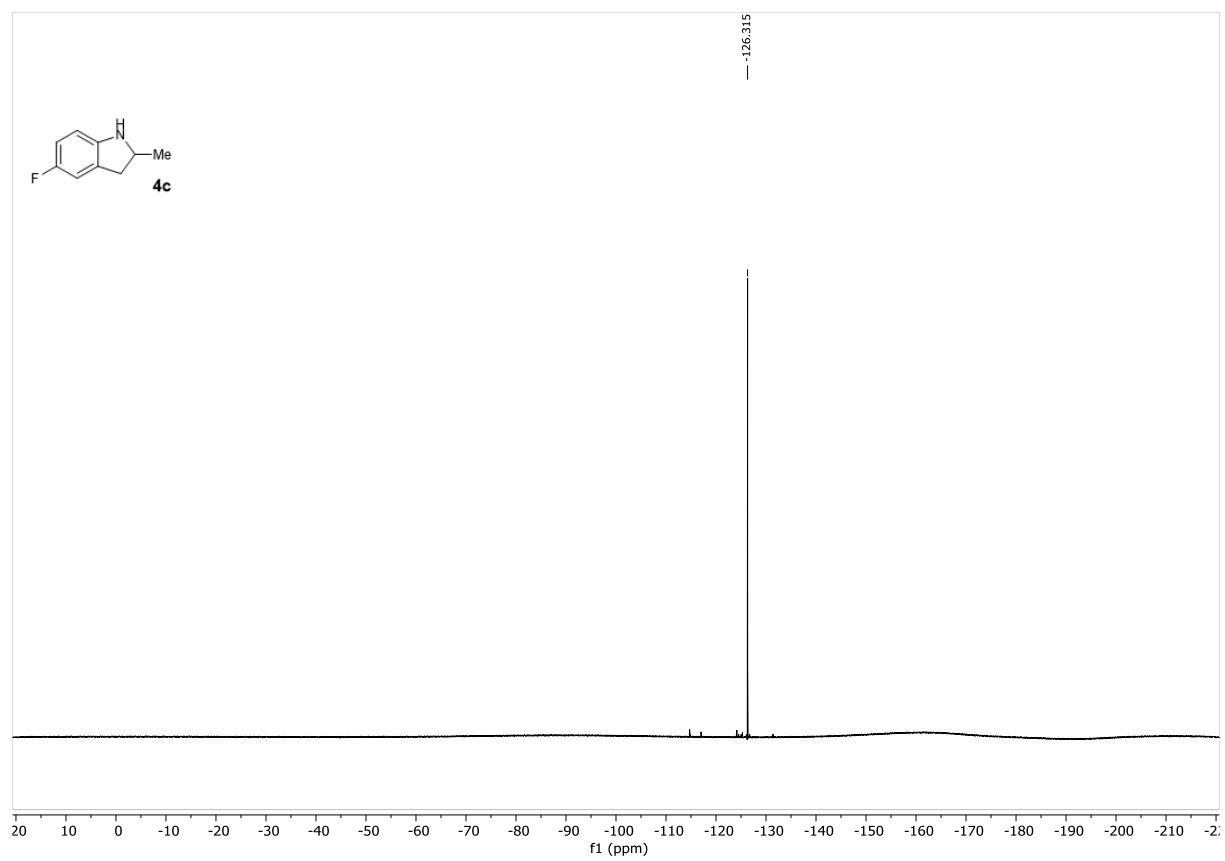


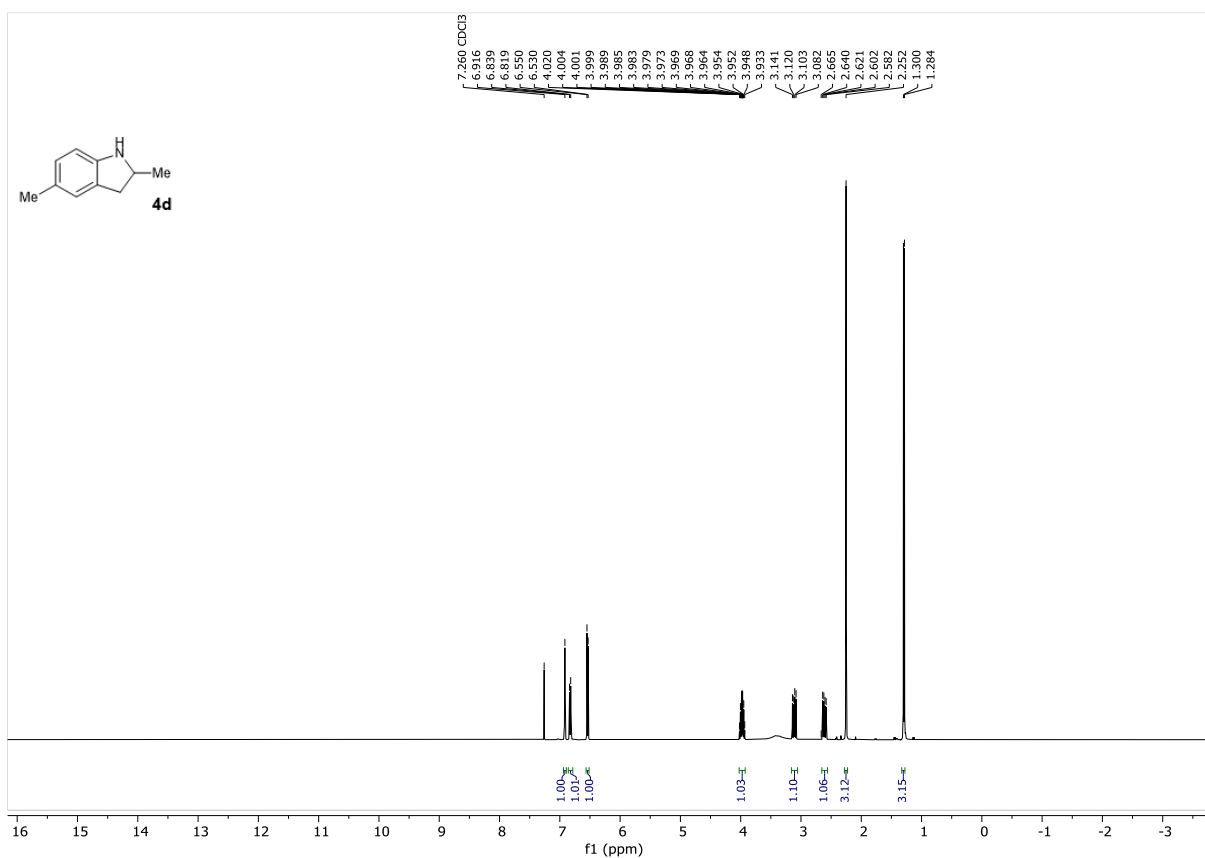


NMR spectra for standard products:

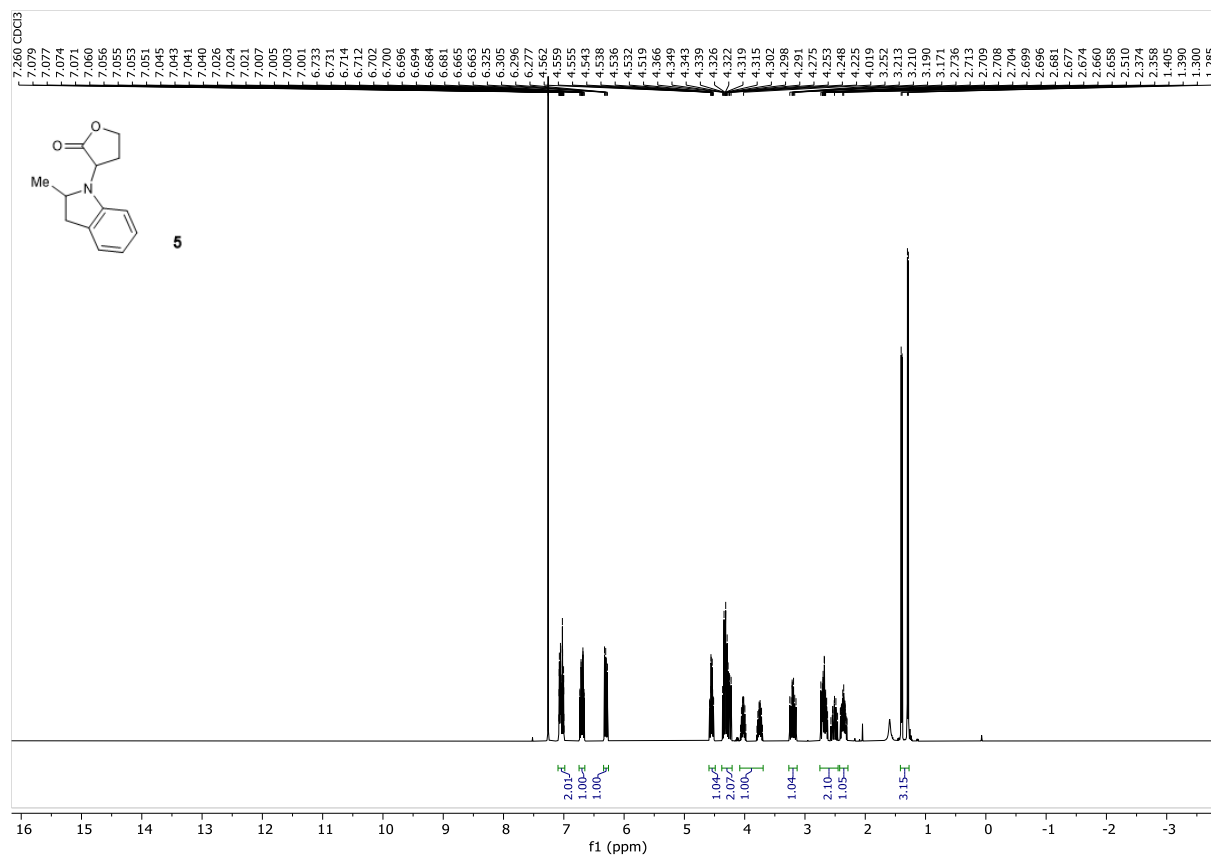
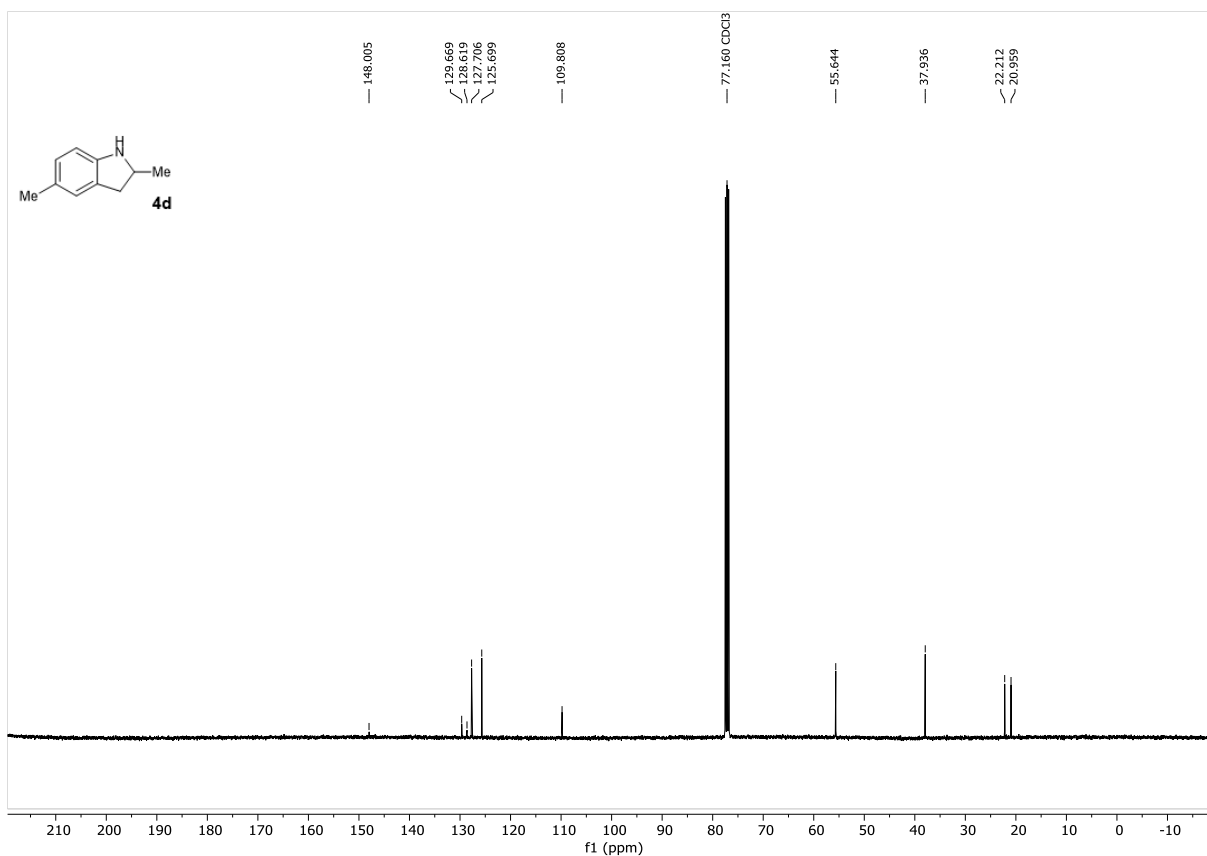


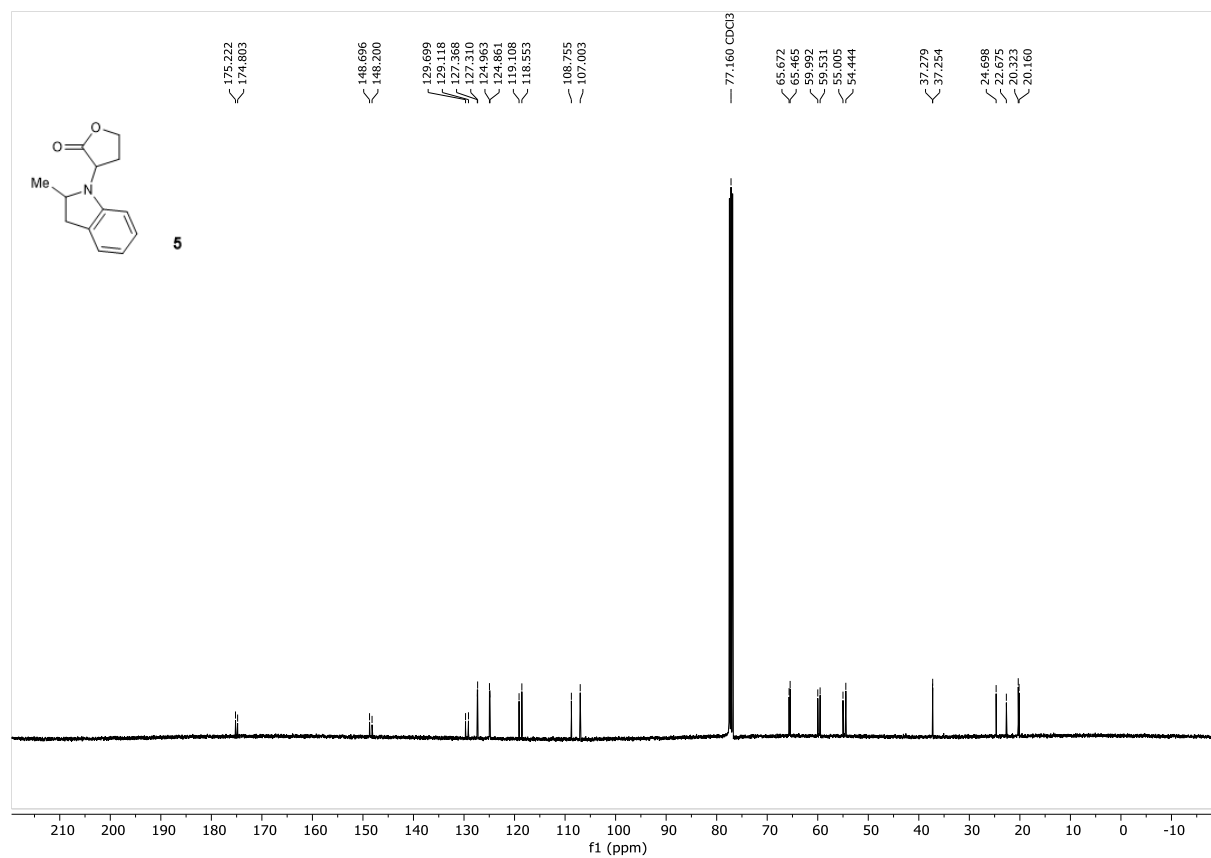






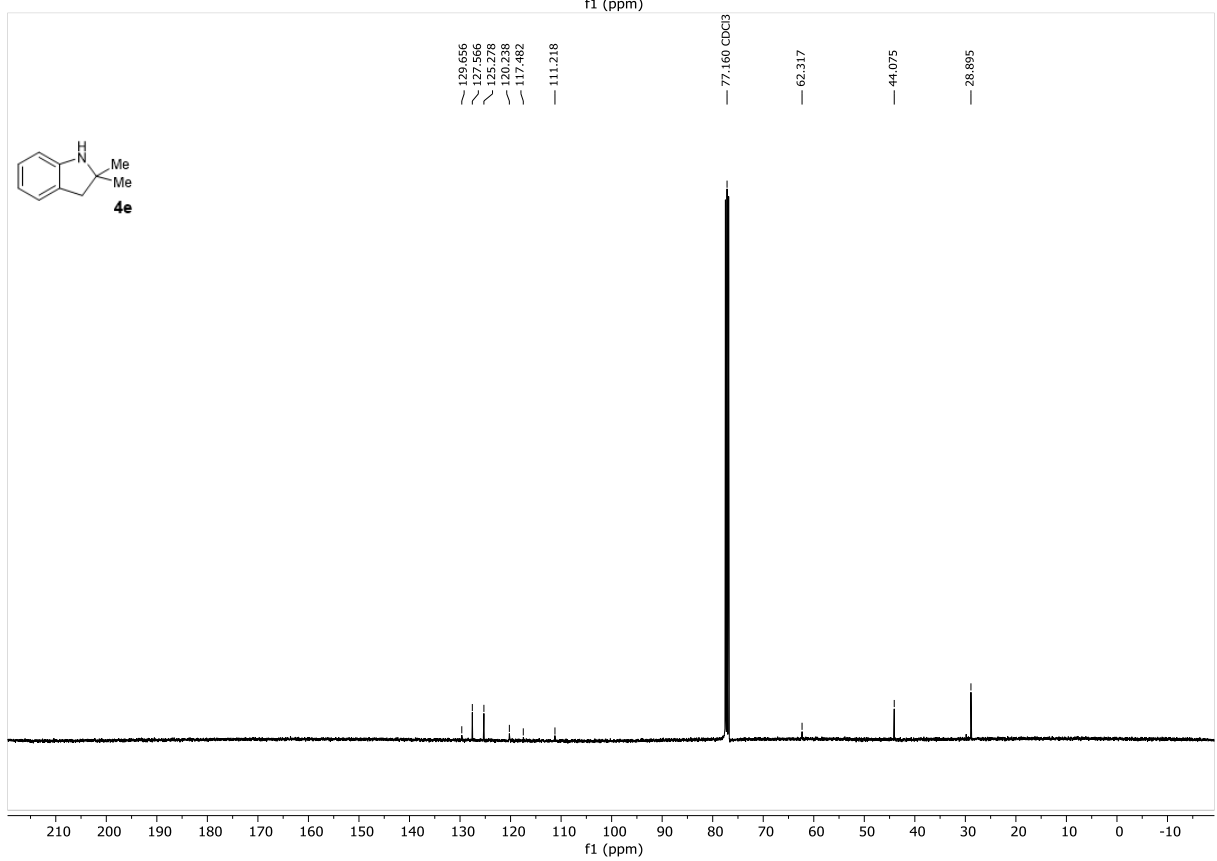
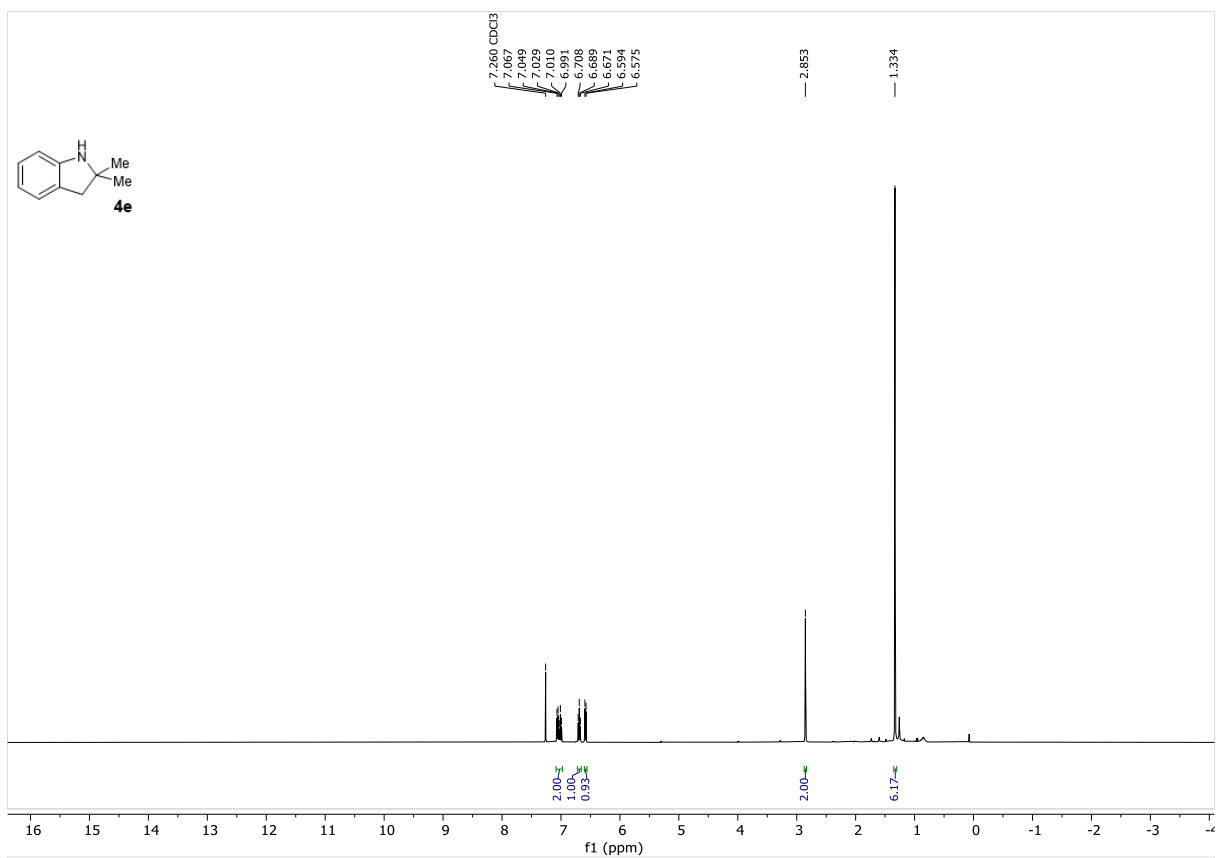


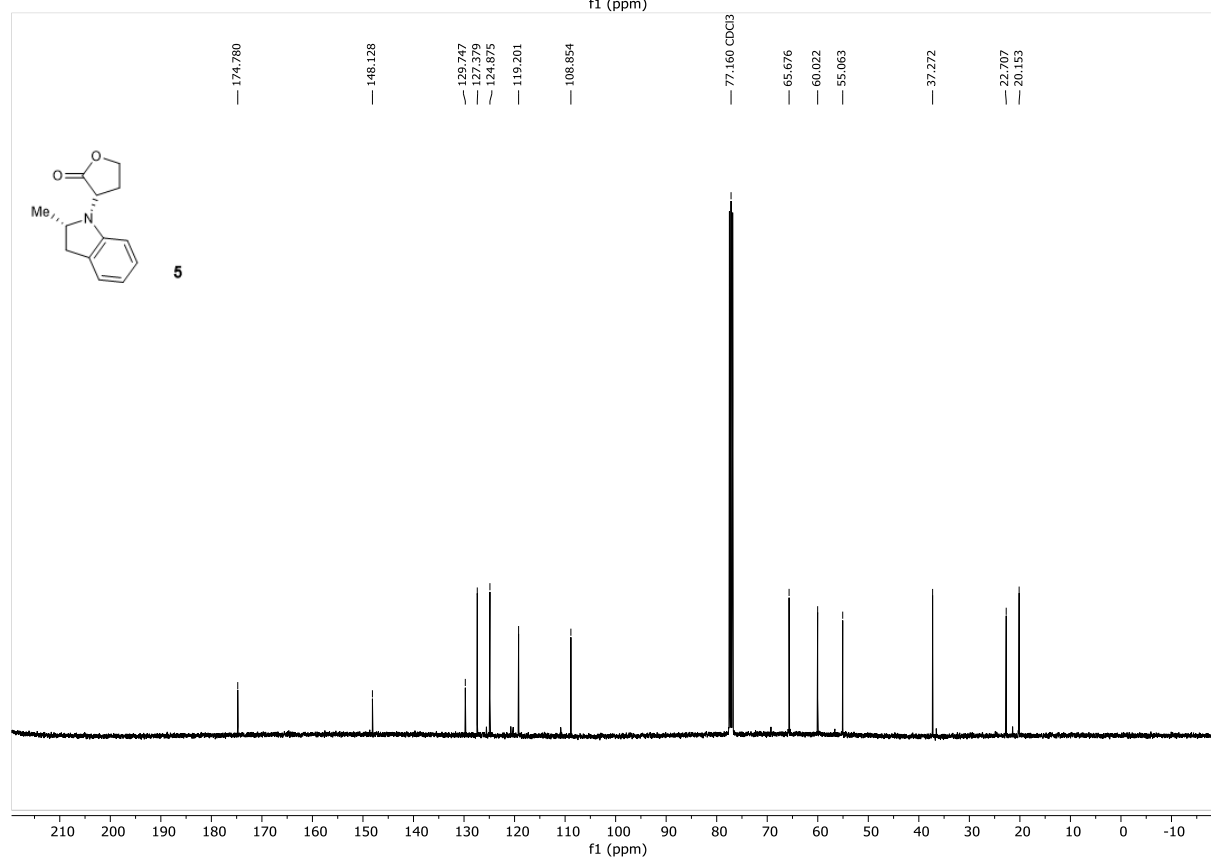
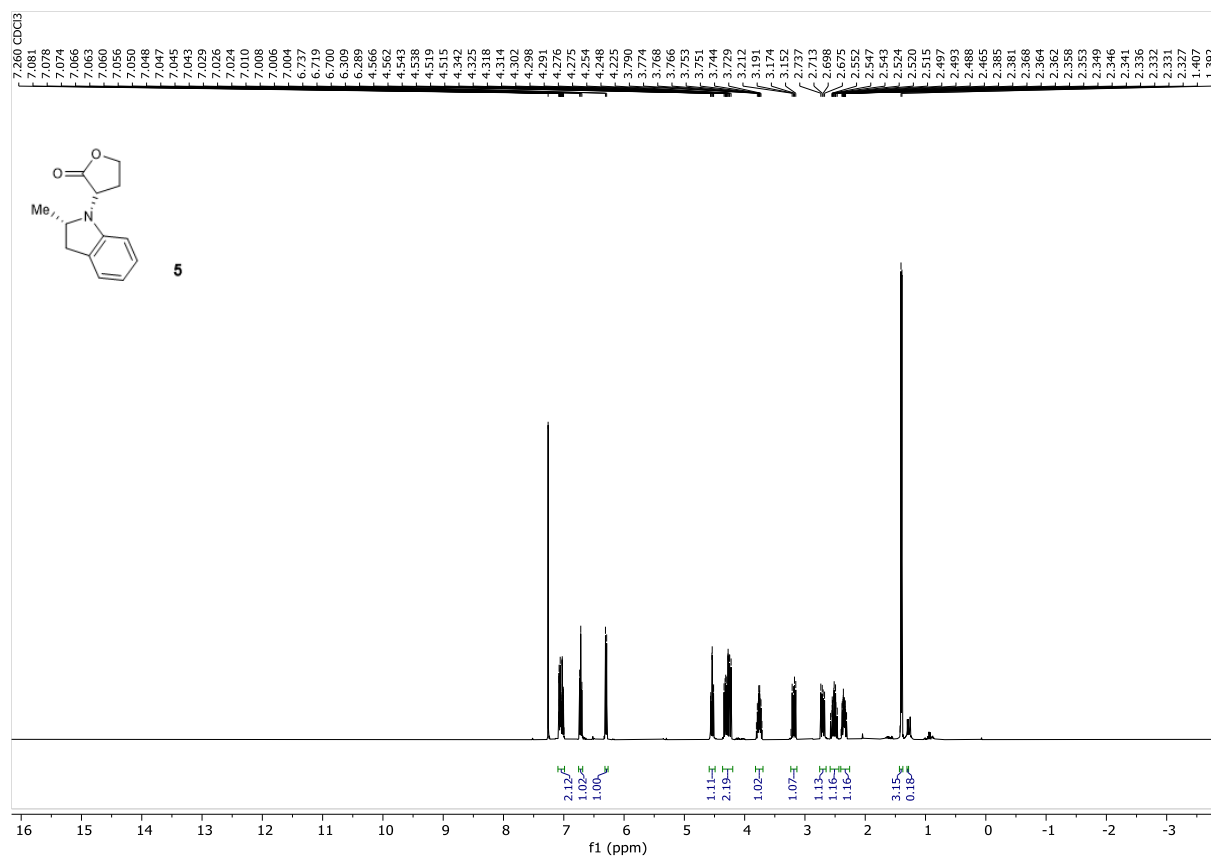


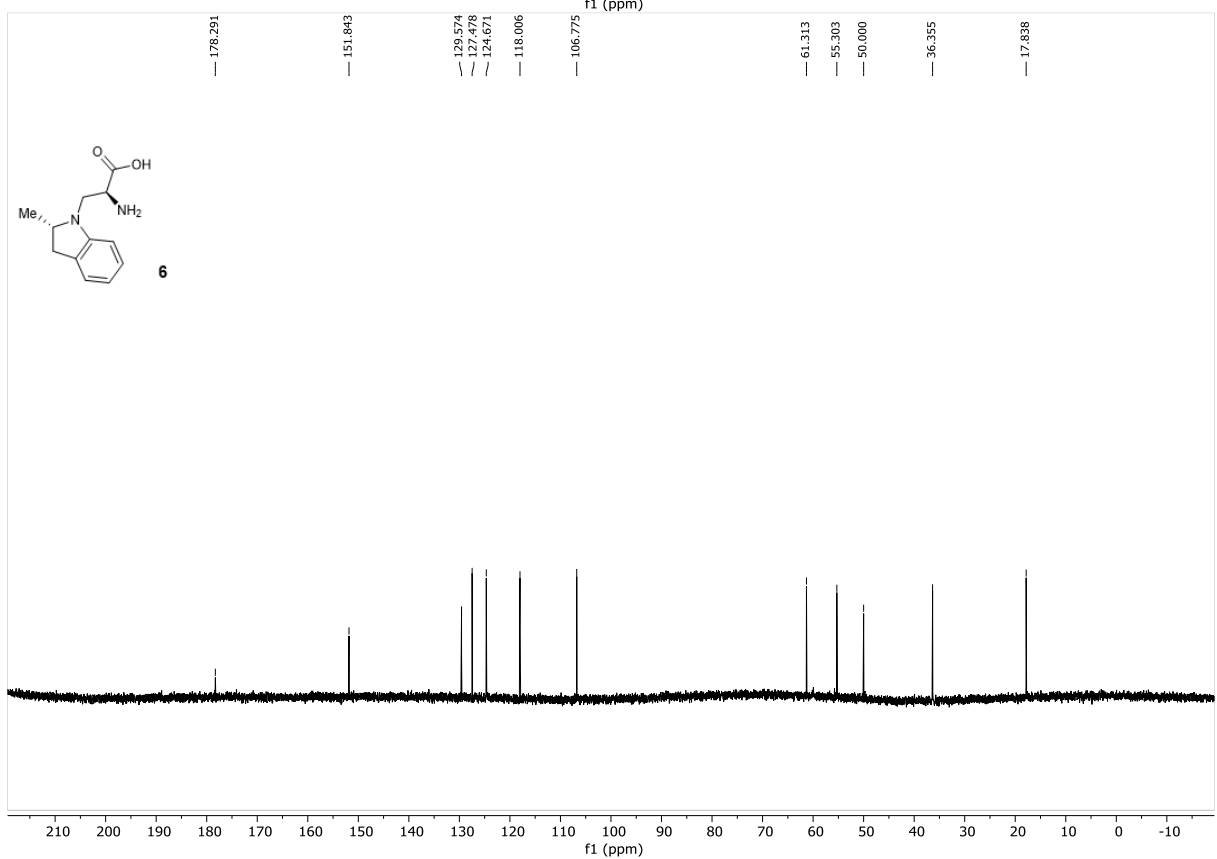
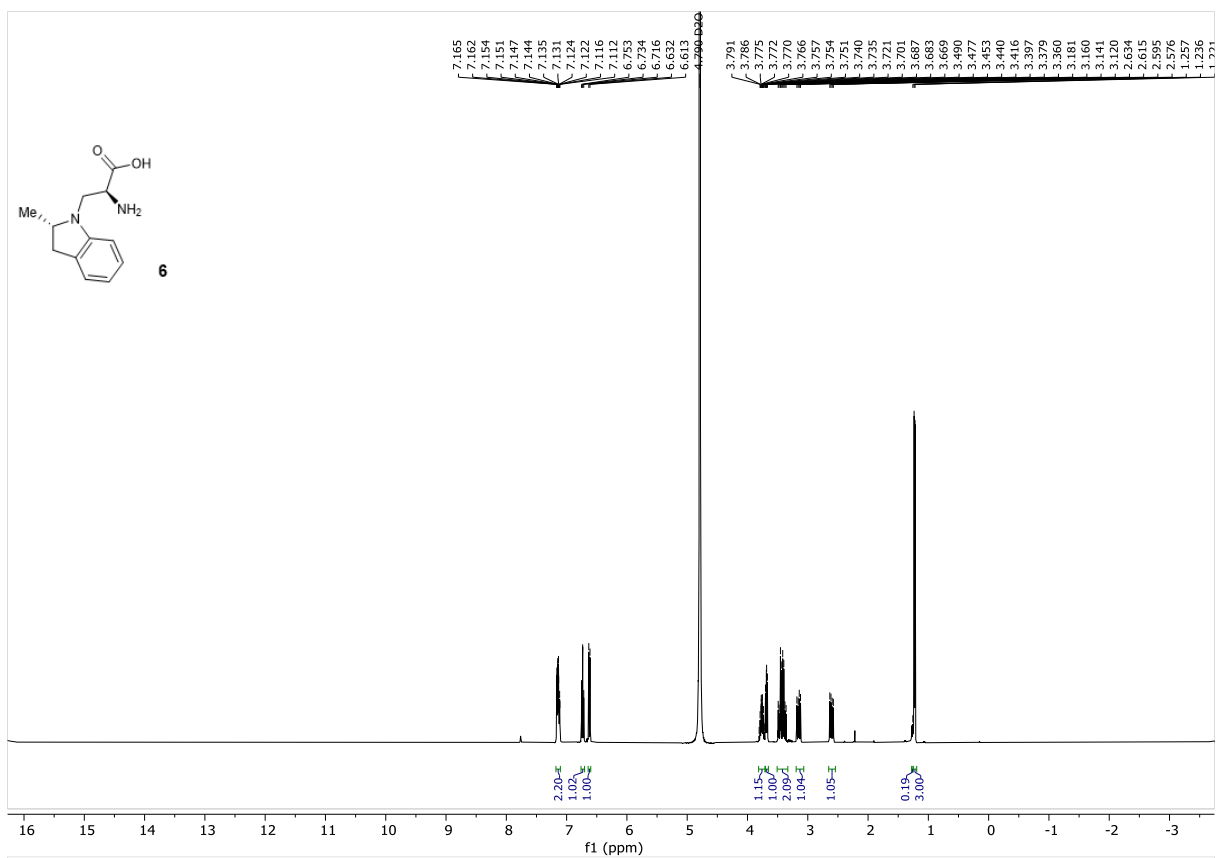


NMR for the preparative-scale enzymatic reaction:









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