

Supporting Information

Photochemical C–H Arylation of Heteroarenes for DNA-Encoded Library Synthesis

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1. General Considerations

1.1 General: All chemical transformations requiring inert atmospheric conditions were carried out using Schlenk line techniques with a 4- or 5-port dual-bank manifold. For blue light irradiation, two Kessil PR160-456 nm lamps (19 V DC 40 W Max) were placed 1.5 inches away from PCR tubes. NMR spectra (^1H , ^{13}C) were obtained at 298 °K using 400 or 500 MHz spectrometers. ^1H NMR spectra were referenced to residual CHCl_3 (δ 7.26 ppm) in CDCl_3 . ^{13}C NMR spectra were referenced to CDCl_3 (δ 77.3 ppm). Reactions were monitored by LC/MS, GC/MS, ^1H NMR, and/or TLC on silica gel plates (60 Å porosity, 250 μm thickness). TLC analysis was performed using hexanes/EtOAc as the eluent and visualized using ninhydrin, *p*-anisaldehyde stain, and/or UV light. Flash chromatography was accomplished using an automated system (CombiFlash®, UV detector, λ = 254 nm and 280 nm) with RediSep® R_f silica gel disposable flash columns (60 Å porosity, 40–60 μm) or RediSep R_f Gold® silica gel disposable flash columns (60 Å porosity, 20–40 μm). Accurate mass measurement analyses were conducted using electron ionization (EI) or electrospray ionization (ESI). The signals were mass measured against an internal lock mass reference of perfluorotributylamine (PFTBA) for EI-GCMS, and leucine enkephalin for ESI-LC/MS. IR spectra were recorded on an FT-IR using either neat oil or solid products. Solvents were purified with drying cartridges through a solvent delivery system. Melting points (°C) are uncorrected.

1.2 Chemicals: Deuterated NMR solvents were purchased and stored over 4Å molecular sieves. CH_2Cl_2 , DMF, EtOAc, hexanes, and DMSO were used as purchased. DIPEA, Et_3N , HATU (*N*-[(dimethylamino)-1*H*-1,2,3-triazolo-[4,5-*b*]pyridin-1-ylmethylene]-*N*-methylethanaminium hexafluorophosphate *N*-oxide), and (*E*)-3-(ethyldiazenyl)-*N,N*-dimethylpropan-1-amine were purchased from commercial suppliers and used without further purification. Synthesis of all new heteroarene derivatives and new on-DNA substrates is outlined here. Additional heteroarenes were purchased from commercial suppliers. The $\text{Ir}(\text{ppy})_3$ catalyst was purchased from commercial suppliers and used without further manipulation. All other reagents were purchased commercially and used as received. Photoredox-catalyzed reactions were performed using PCR 8-strip tubes (Ref. Fisher 781320) with PCR strips of 8 caps (Ref. Fisher 781340). DMSO was purchased and used as received. HyPure™ Molecular Biology Grade Water was purchased and used as received without further manipulation.

1.3 Analysis of “on-DNA” reactions: Analysis of on-DNA reactions was performed by LC/MS: After reaction completion, an aliquot of the reaction mixture was diluted with H_2O to approximately 0.05–0.13 mM. At this point, 3 μL aliquots of the LC/MS sample was injected onto a reverse-phase chromatography column (Clarity 2.6 μm Oligo-MS 100 Å 2.1x50 mm) and eluted (10-90% B over 4 min at 0.5 mL/min flow rate; Solvent A: 0.75% v/v HFIP / 0.038% TEA / 5 μM EDTA in H_2O ; Solvent B: 0.75% HFIP,

0.038% TEA, 5 μ M EDTA in 90/10 MeOH/deionized H₂O) with no UV monitoring. Effluent was analyzed on a Waters SQ Detector 2 ACQUITY UPLC System in Thermo Exactive Plus LC-esiMS with a Vanquish UHPLC. For the functionalized headpiece samples (the on-DNA aryl halides), % conversion was determined based on reported peak intensities following deconvolution (between 3,000-10,000 Da) of the DNA charge states using Intact MassTM by Protein Metrics Inc. (version 3.7-32x64). For the photoredox scope reactions, % conversion was determined using Intact MassTM by Protein Metrics Inc. (version 3.7-32x64). Data was scanned between 0.3-2.2 min and deconvoluted between 4,000-6,000 Da, with a mass tolerance window of 2.5-3 Da, with 5% of base peak threshold was set for reporting. For conversion calculations for each example, the peaks annotated with colored dots were used for the calculations. Na, K, NH₄, and HFIP adducts were included in the product percentage. Detailed parameters can be found later in the Supporting Information.

1.4 Materials for “on-DNA” synthesis: DNA headpiece HP-NH₂(5’-/5Phos/GAGTCA/iSp9/iUniAmM/iSp9/TGACTCCC-3’) was obtained from Biosearch Technologies, Novato, CA. The spacer-elongated AOP-Headpiece (Figure S1) was prepared via HATU coupling following the general procedure described later in this document with 5 equiv each of Fmoc-15-amino-4,7,10,13-tetraoxapentadecanoic acid (Fmoc-AOP), *i*-Pr₂NEt, and HATU. The lyophilized product of this reaction was then deprotected by exposure to a 10% piperidine in H₂O solution. After the reaction was deemed complete by LC/MS analysis, the reaction was precipitated following the EtOH protocol and is typically pure enough to be used without further purification.

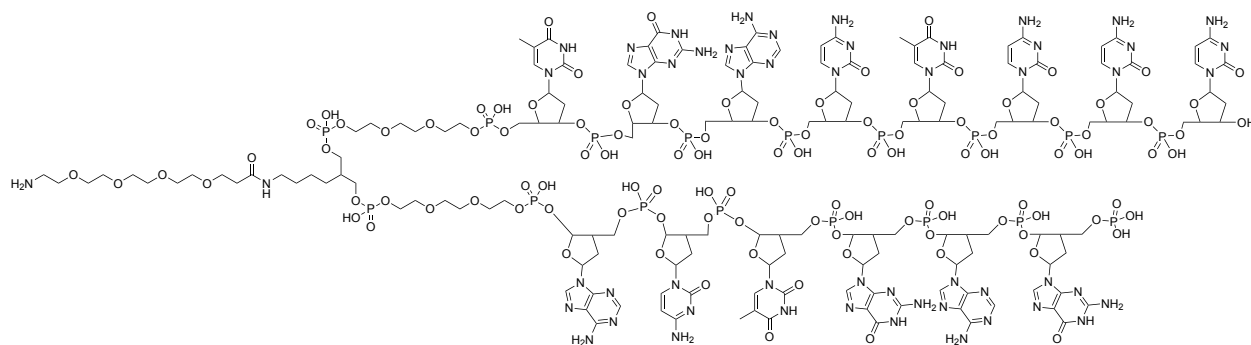
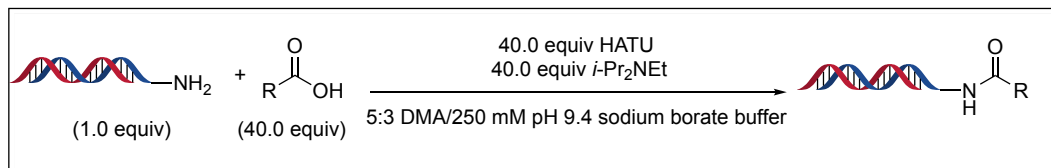


Figure S1. Sequence and structure of the AOP-headpiece (molecular weight = 5184.5220).

2. Preparation of on-DNA Substrates

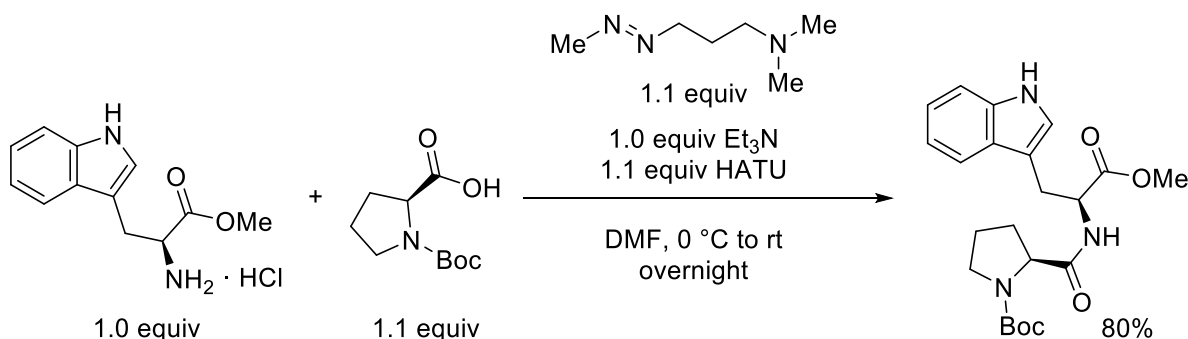


2.1 HATU premix protocol for acylation of DNA headpieces: The HATU (200 mM in DMA, 40.0 equiv), *i*-Pr₂NEt (200 mM in DMA, 40.0 equiv), and the corresponding carboxylic acid (200 mM in DMA, 40.0 equiv) solutions were individually cooled at 4 °C for 5 min. Once chilled, the acid, *i*-Pr₂NEt, and HATU solutions were added sequentially to a centrifuge tube, vortexed briefly, and allowed to react at 4 °C for 20 min. The oligomer solution (1 mM in 250 mM pH 9.4 sodium borate buffer) was then added, and the mixture was vortexed. The reaction was allowed to proceed at rt and monitored by LC/MS. Upon completion, the reaction was worked up following the EtOH precipitation protocol below.

2.2 EtOH precipitation protocol: The reaction mixture was transferred to a centrifuge tube where it filled at most 1/4 of the total volume. A volume of 5 M aq NaCl equal to 1/10 of the reaction volume was then added, followed by cold (–20 °C) EtOH equal to 2.5 reaction volumes. The resulting mixture was then left to stand in a –80 °C freezer for at least 1 h or overnight. The chilled mixture was then centrifuged for 30 min at 4 °C at 3,300 rpm. The supernatant was then decanted and allowed to dry under reduced pressure. The resulting pellet was re-dissolved in H₂O to give a theoretical concentration of 2 or 5 mM. Purity was assessed by LC/MS, and optical density was obtained via NanoDrop. For long term storage, solutions were frozen in liquid nitrogen and lyophilized to dryness to give a white solid. If purity was less than 90% by LC/MS, HPLC purification was performed: gradient of 95% A (50 mM TEAA, pH = 7.5)/5% B (1% H₂O in CH₃CN) to 60% A/40% B, through a Gemini C18 column (5 μm, 110 Å, 30x100 mm), with UV visualization at 260 nm.

3. Synthesis of Heteroarene Derivatives

Methyl (tert-Butoxycarbonyl)-L-prolinyl-L-tryptophan (2z)



Methyl (tert-Butoxycarbonyl)-L-prolinyl-L-tryptophan (2z). The compound was prepared according to a modified procedure from *Carpino et al.*¹ To a 100 mL flask equipped with a stir bar was added Boc-L-proline (651 mg, 3.0 mmol, 1.1 equiv), Et₃N (0.38 mL 2.75 mmol, 1.0 equiv), and L-tryptophan methyl ester hydrochloride (0.70 g, 2.75 mmol, 1.0 equiv). The reaction mixture was dissolved in DMF (20 mL) and stirred for 5 min. At this point, HATU (1.15 g, 3.0 mmol, 1.1 equiv) was added. Afterwards, the soln was cooled to 0 °C with an ice bath, and carbodiimide (0.39 g, 3.0 mmol, 1.1 equiv) was added portionwise. The soln was kept at 0 °C for 1 h and then stirred overnight. Upon completion, the reaction was diluted with EtOAc (25 mL) and transferred to a separatory funnel. After extraction with 1 M HCl (3 × 25 mL) and a 10% aq soln of NaHCO₃ (3 × 25 mL), the combined organic layers were washed with brine (25 mL) and then dried (Na₂SO₄). The solvent was removed under reduced pressure, and the crude product was purified using flash chromatography (gradient hexanes to 100% EtOAc) to give the title compound (910 mg, 2.19 mmol, 80%) as a colorless oil. ¹H NMR (400 MHz, CDCl₃), δ (ppm) = 8.74–8.66 (m, 1H), 7.51 (d, *J* = 8.1 Hz, 1H), 7.31 (d, *J* = 8.1 Hz, 1H), 7.15 (t, *J* = 7.5 Hz, 1H), 7.08 (t, *J* = 7.5 Hz, 1H), 7.01–6.97 (m, 1H), 6.52 (br s, 1H), 4.88 (br s, 1H), 4.28–4.11 (m, 1H), 3.66–3.63 (m, 3H), 3.47–3.08 (m, 3H), 1.99–1.91 (m, 3H), 1.84–1.59 (m, 1H), 1.38 (s, 9H). ¹³C NMR (101 MHz, CDCl₃), δ (ppm) = 171.7, 171.3, 154.6, 136.2, 127.6, 122.9, 122.1, 119.5, 118.3, 111.4, 109.7, 80.8, 60.5, 52.3, 30.7, 28.2 (3C), 27.8, 23.4, 21.3, 14.2. FT-IR (cm⁻¹, neat, ATR), $\tilde{\nu}$ = 3300, 2977, 1741, 1665, 1479, 1366, 1250, 850. HRMS (ESI) calc. for C₂₂H₃₀N₃O₅ [M+H]⁺: 416.2185, found: 416.2178.

4. Reaction Workflow

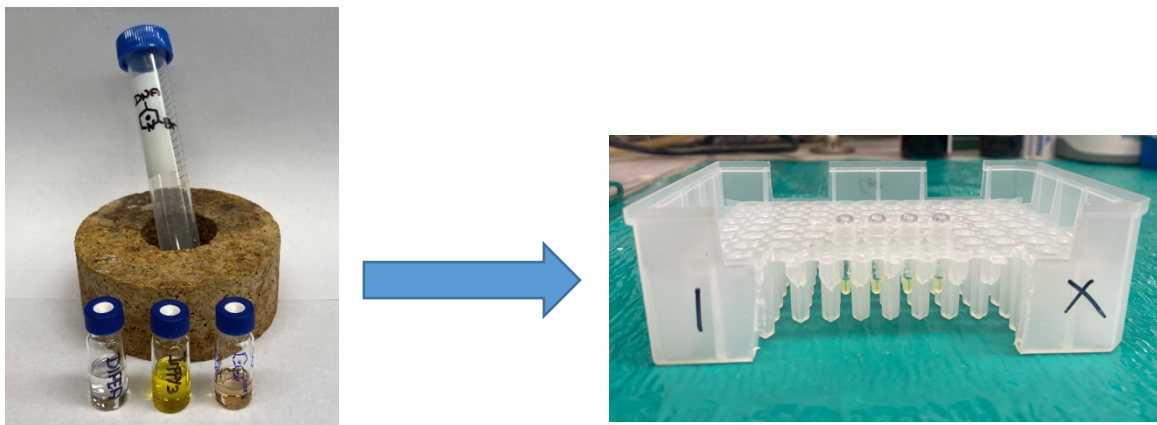


Figure S2. Photochemical reactions were conducted in PCR tubes under open-air conditions. Reagents were added as stock solutions.

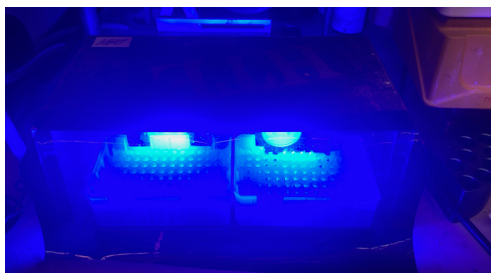


Figure S3. Reaction tubes were vortexed then positioned 1.5 inches away from two Kessil PR160 lamps ($\lambda = 456$ nm, 19 V DC 40 W Max) for the time designated for each experiment.

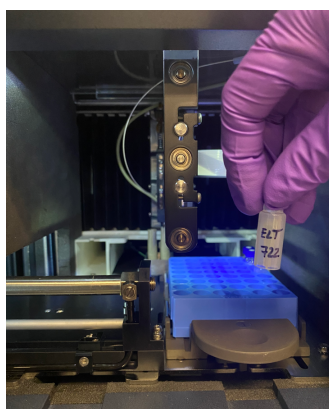
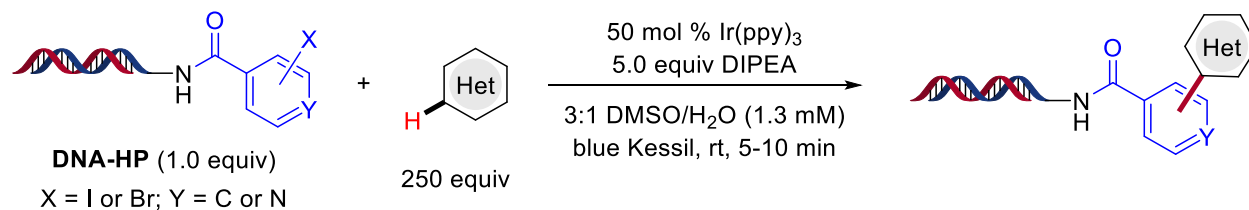


Figure S4. Upon completion, reactions were diluted with H₂O, filtered through MultiScreen[®] filter plates (Millipore) via centrifuge forces, and % conversion was determined using LC/MS analysis.

5. Procedures for Photoinduced Transformations

General Procedure I

Photoinduced on-DNA Minisci reaction via aryl radical formation



To a PCR Eppendorf tube was added DIPEA (2.5 μ L of a 50 nmol/ μ L soln in DMSO, 125 nmol, 5 equiv), *fac*-Ir(ppy)₃ (2.5 μ L of a 5 nmol/ μ L soln in DMSO, 12.5 nmol, 0.5 equiv), heteroarene (10 μ L of a 625 nmol/ μ L soln in DMSO, 6250 nmol, 250 equiv), and DNA-tethered aryl halide (5 μ L of a 5 nmol/ μ L soln in H₂O, 25 nmol, 1.0 equiv). The PCR tube was then capped, vortexed, and irradiated for 5-10 min with Kessil PR160 lamps at a distance of 1.5 inches. The reaction was then diluted with H₂O (150 μ L), filtered through MultiScreen[®] filter plates via centrifuge forces, and subsequently analyzed by LC/MS.

6. qPCR, PCR, and Sequencing

4-Cycle tag mimic sequence



4-Cycle tag synthesis (aryl iodide)

The top and bottom strands (purchased from IDT as lyophilized powders) of a control 4-cycle tag were annealed by combining 1.2 μmol of each strand (2 mM in H_2O), heating to 95 $^\circ\text{C}$ for 5 min, then cooling to rt. The annealed tag solution (1.2 equiv) was then added to the 4-chloro-3-iodobenzoic acid headpiece (500 μL , 2 mM in H_2O), followed by 400 μL of 10x T4 ligation buffer, 8 mL of H_2O , and 40 μL of T4 DNA ligase purchased from Syngene. The ligation solution was vortexed and allowed to sit at rt overnight. The ligation was precipitated for 30 min at -80 $^\circ\text{C}$ following addition of 0.8 mL of 5 M NaCl (aq) and 20 mL of cold EtOH. The precipitated soln was then centrifuged at 3,300 rpm at 4 $^\circ\text{C}$ for 30 min, and the solvent was decanted to afford the DNA pellet, which was dried on a lyophilizer for 30 min. The crude pellet was resuspended in 8 mL of H_2O and split into two 30,000 molecular weight cut-off spin filters. The spin filters were put on the centrifuge for 15 min (20 $^\circ\text{C}$, 3500 rpm), and the filtrate was collected. The original reaction flask was washed with 4 mL of H_2O and again split into the two-spin filter and put on the centrifuge for 15 min (20 $^\circ\text{C}$, 3500 rpm). The filtrate was then collected, and the wash process was repeated two more times. Once complete, the product was collected and lyophilized overnight. The resulting white pellet was dissolved in 500 μL of H_2O , and a QC was taken showing 36% starting material and 47% desired product (this was not seen on the μTOF QC that was taken before). The ligation was pushed with additional annealed control tag (300 nmol, 1 mM in H_2O) followed by 200 μL of 10x T4 ligation buffer, 4 mL of H_2O , and 20 μL of T4 DNA ligase purchased from Syngene. The reaction was again capped, vortexed, and left to react at rt overnight. The ligation was precipitated for 30 min at -80 $^\circ\text{C}$ following addition of 0.8 mL of 5 M NaCl (aq) and 20 mL of cold EtOH. The precipitated soln was then centrifuged at 3,300 rpm at 4 $^\circ\text{C}$ for 30 min, and the solvent was decanted to afford the DNA pellet, which was dried on a lyophilizer for 30 min. The crude pellet was resuspended in 8 mL of H_2O and spit into two 30,000 molecular weight cut-off spin filters. The spin filters were put on the centrifuge for 15 min (20 $^\circ\text{C}$, 3500 rpm), and the filtrate was collected. The original reaction flask was washed with 4 mL of H_2O and again split into the two-spin filter and put on the centrifuge for 15 min (20 $^\circ\text{C}$, 3500 rpm). The filtrate was then collected, and the wash process was repeated two more times. Once complete, the product was collected and lyophilized overnight. The

lyophilized product was analyzed by optical density using a composite extinction coefficient of 1023700 L/(mol-cm) to determine isolated yield (715 nmol, 71.5%). LCMS calcd: 34,521, found: 34,521

Closing primer ligation on reacted material

Top Strand: 5'-/5Phos/ACG ATG CCC GGT CTA CNN NNN NNN NNN NCT GAT GGC GCG AGG GAG GC-3'

Bottom Strand: 5'-GTA GAC CGG GCA TCG TAA-3'

To each of the six exemplar reaction samples (2 nmol aliquot, 0.04 mM in H₂O) was added the closing primer (5 nmol, 1 mM in H₂O), 10X ligation buffer (10 μ L), T4 DNA ligase (2 μ L, 10 mg/mL), and H₂O (33 μ L) for a final reaction volume of 100 μ L. Ligations were allowed to proceed overnight at rt. Samples were analyzed by gel electrophoresis, and all were determined to have gone to sufficient completion.

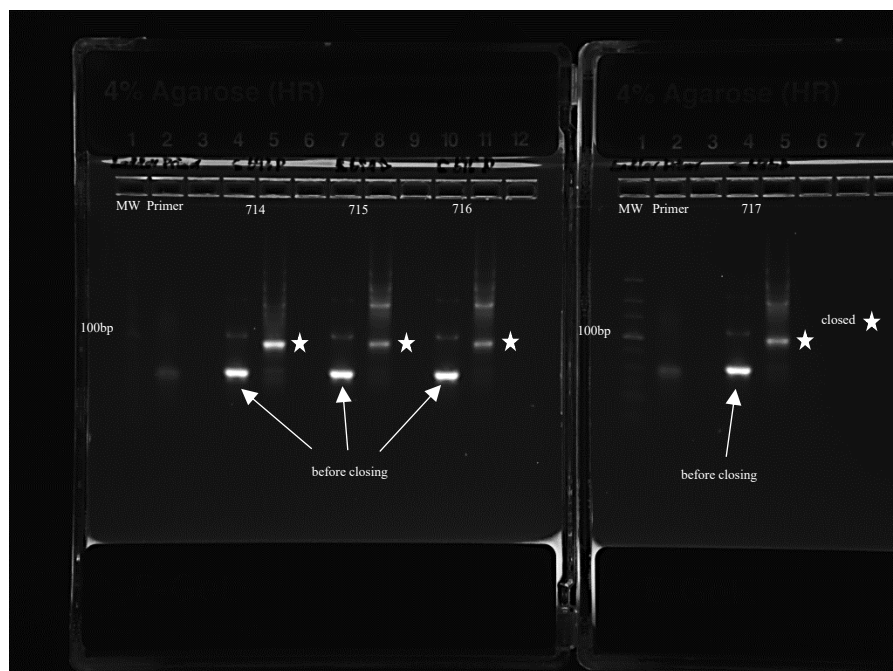


Figure S5. Gel electrophoresis of closing primer ligation on reacted material.

qPCR

qFor: 5'-GCT ACC TCT GAC TCC CAA ATC GAT GT -3'

qRev: 5'-ATA TTA GCC TCC CTC GCG CCA TCA -3'

Quantitative PCR was performed on a Roche LightCycler 480 II PCR system with SYBR Green I as the detection dye. A bulk master mix solution was prepared by combining 1 mL of SYBR green, 60 μ L of 10 μ M PCR primer 565 Cla, 60 μ L of 10 μ M PCR primer 454 short, and 680 μ L of H₂O. To 2 μ L of sample was then added 18 μ L of master mix. Samples were subjected to qPCR:

Stage	Temperature/Time	Number of Cycles
HotStart	95 °C / 5 min	1
Amplification	95 °C / 10 sec 55 °C / 15 sec 72 °C / 15 sec	40
Melt	95 °C / 1 sec 70 °C / 1 sec 95 °C	1
Cool	45 °C / 30 sec	1

Samples were then analyzed using the 2nd derivative maximum standard protocol on the instrument to determine how many molecules were present per μ L sample. Samples achieved acceptable consistency across conditions in comparison to the no-light control sample ELT_717, suggesting that the conditions developed are not impacting the amount of amplifiable DNA present in a significant way.

Sample Name	Deviations	Molecules / μ L sample
ELT 714	No deviation from standard conditions	1.13E+13
ELT 715	No DIPEA	8.56E+12
ELT 716	No photocatalyst	8.65E+12
ELT 717	No-light control	9.52E+12

Based on the Agilent TapeStation results following the PCR amplification and purification described above, an aliquot of each sample, representing approximately 1E8 molecules, were prepared for sequencing following the manufacturer's standard protocol with an Illumina MiSeq v3 kit, and sequenced on an Illumina MiSeq. Samples were subjected to 101 cycles for Read 1 and 9 cycles for Index 1. The resulting sequences were aligned to the 71 base reference sequence (below). The number of single base differences were counted and reported as a percentage of the total sequence count.

71 base sequence

5' – GTA GAC CGG GCA TCG TAA CGA CCT TTC TCC GCT TAC CAG GCT TCT TGC GGA
ACA CAT CGA TTT GGG AGT CA – 3'

Minisci Arylation: **Standard conditions** (ELT 714)

# of matched bases (out of 71)	% of total sequences (n = 2730559)
71	85.68
70	11.84
69	1.49
68	0.37
67	0.17
66	0.10
65	0.07
64	0.07
63	0.05
62	0.04
61	0.02
60	0.02
59	0.02
55	0.01
56	0.01
57	0.01
58	0.01
54	0.01
53	< 0.01
51	< 0.01
52	< 0.01
50	< 0.01
49	< 0.01
48	< 0.01
47	< 0.01
46	< 0.01
45	< 0.01
44	< 0.01
43	< 0.01
42	< 0.01
34	< 0.01

71 base sequence

5' – GTA GAC CGG GCA TCG TAA CGA CCT TTC TCC GCT TAC CAG GCT TCT TGC GGA
ACA CAT CGA TTT GGG AGT CA – 3'

Minisci Arylation: **No DIPEA** (ELT 715)

# of matched bases (out of 71)	% of total sequences (n = 2562964)
71	85.31
70	12.20
69	1.53
68	0.36
67	0.16
66	0.11
65	0.08
64	0.06
63	0.04
62	0.03
61	0.02
56	0.02
57	0.01
60	0.01
58	0.01
59	0.01
55	0.01
54	0.01
52	< 0.01
53	< 0.01
51	< 0.01
42	< 0.01
43	< 0.01
41	< 0.01
50	< 0.01
46	< 0.01
48	< 0.01
47	< 0.01
49	< 0.01
40	< 0.01
45	< 0.01
44	< 0.01
38	< 0.01
39	< 0.01
36	< 0.01
34	< 0.01
33	< 0.01
27	< 0.01

71 base sequence

5' – GTA GAC CGG GCA TCG TAA CGA CCT TTC TCC GCT TAC CAG GCT TCT TGC GGA
ACA CAT CGA TTT GGG AGT CA – 3'

Minisci Arylation: **No photocatalyst** (ELT 716)

# of matched bases (out of 71)	% of total sequences (n = 2516811)
71	85.40
70	12.13
69	1.53
68	0.37
67	0.16
66	0.12
65	0.07
64	0.05
63	0.04
62	0.03
61	0.02
57	0.01
60	0.01
58	0.01
56	0.01
59	0.01
55	0.01
54	0.01
53	< 0.01
52	< 0.01
50	< 0.01
51	< 0.01
47	< 0.01
46	< 0.01
49	< 0.01
48	< 0.01
44	< 0.01
45	< 0.01
24	< 0.01

71 base sequence

5' – GTA GAC CGG GCA TCG TAA CGA CCT TTC TCC GCT TAC CAG GCT TCT TGC GGA
ACA CAT CGA TTT GGG AGT CA – 3'

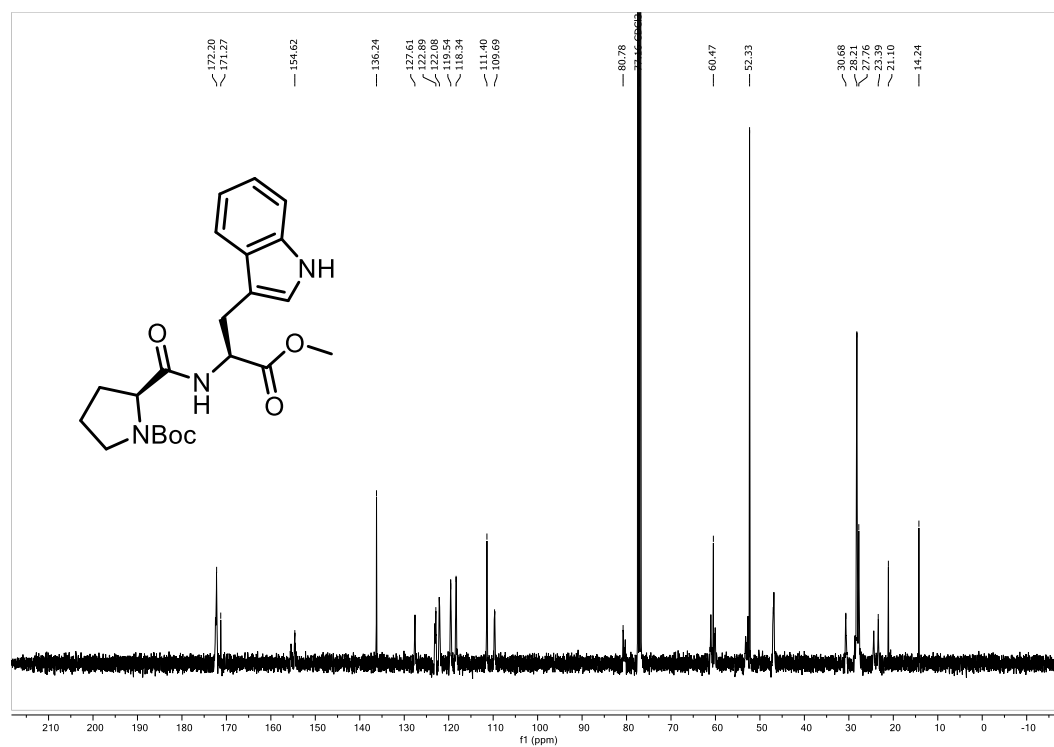
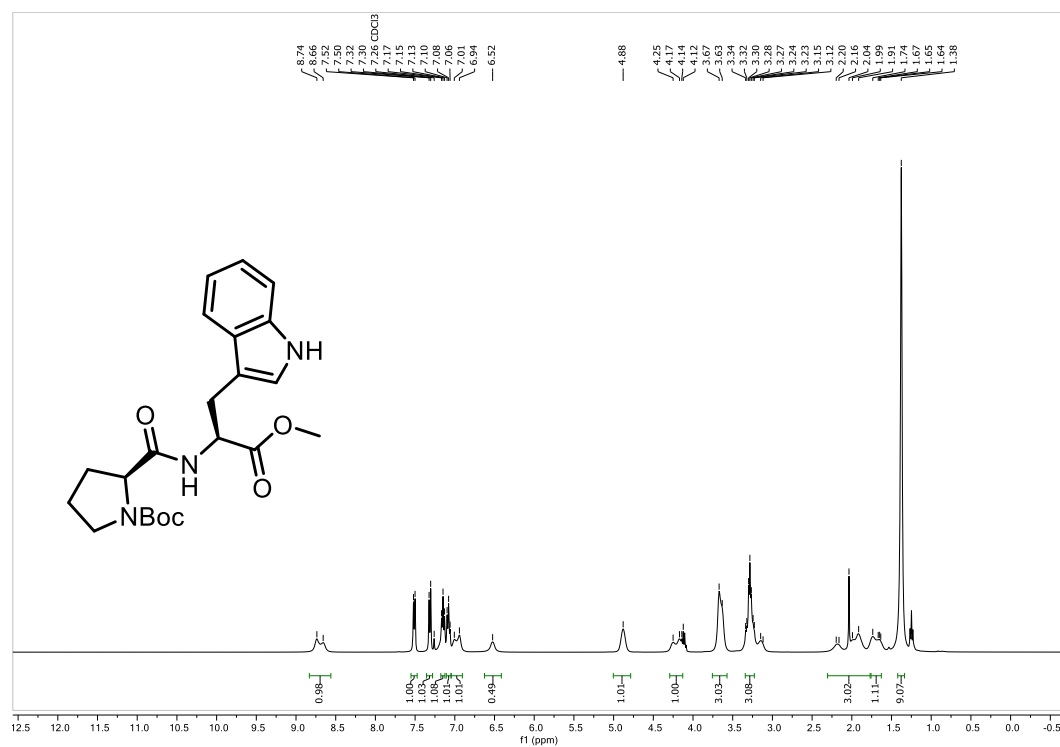
Minisci Arylation: **No-light control** (ELT 717)

# of matched bases (out of 71)	% of total sequences (n = 2641537)
71	85.42
70	12.15
69	1.50
68	0.36
67	0.16
66	0.11
65	0.08
64	0.05
63	0.04
62	0.03
61	0.02
60	0.02
56	0.01
59	0.01
55	0.01
57	0.01
58	0.01
54	0.01
53	< 0.01
52	< 0.01
51	< 0.01
50	< 0.01
47	< 0.01
49	< 0.01
46	< 0.01
45	< 0.01
44	< 0.01
43	< 0.01
42	< 0.01
40	< 0.01
34	< 0.01

7. References

1. L. A. Carpino, *J. Am. Chem. Soc.*, 1993, **115**, 4397–4398.

8. NMR Spectra

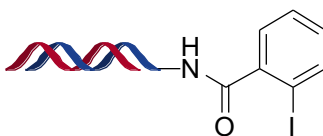


9. UPLC/MS Spectra

Functionalized DNA headpieces

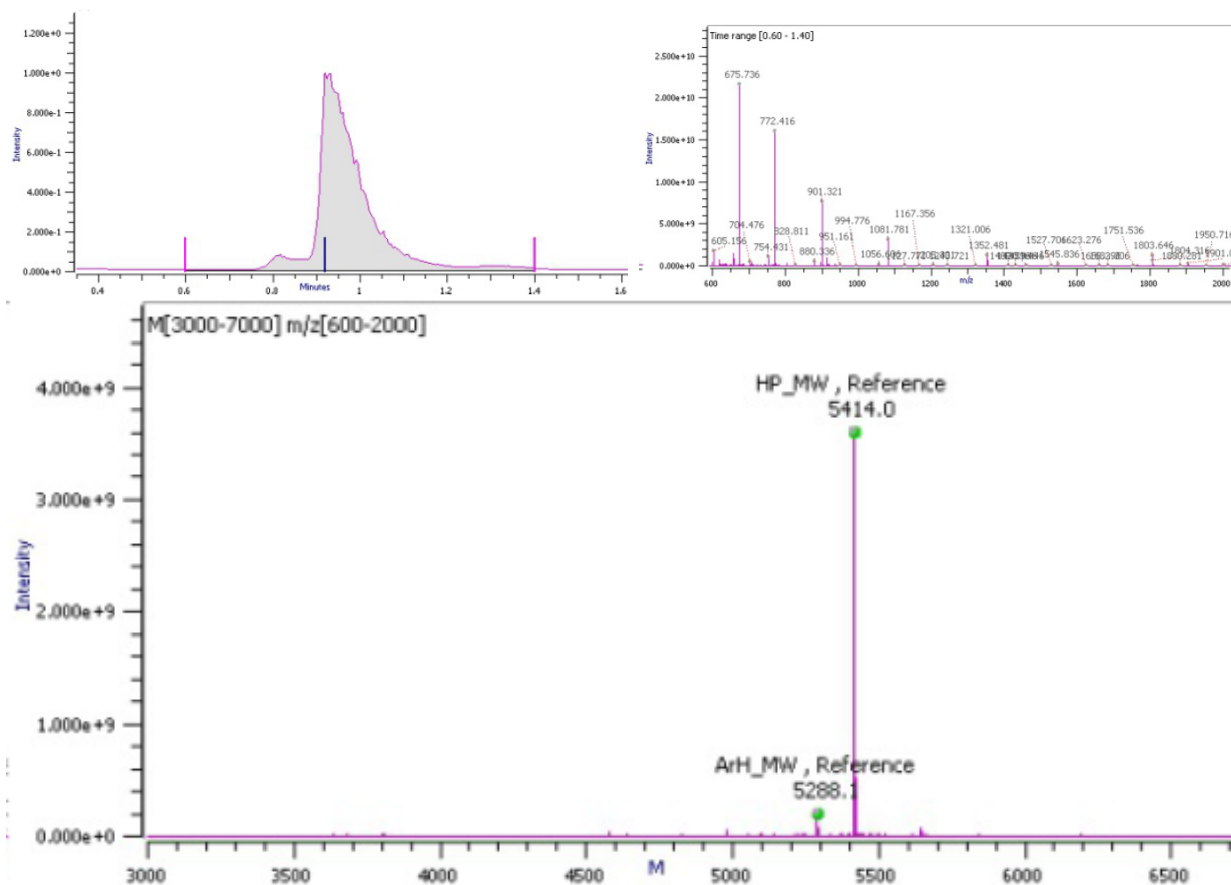
The synthesis of on-DNA aryl halides **1A-L** was previously reported in *J. Am. Chem. Soc.*, 2019, **141**, 3723–3732; *Org. Lett.*, 2020, **22**, 1046–105; and S. O. Badir and G. A. Molander et al., *Chem. Sci.*, 2021, **12**, 12036–12045.

Headpiece 1D

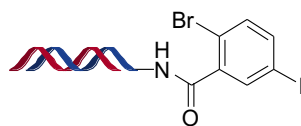


Molecular Weight: 5414.53

ELTM_423, TW-N78441-9-423 - (Plot Elution Peak - Plot MS1 - Plot Deconvoluted Mass spectrum)

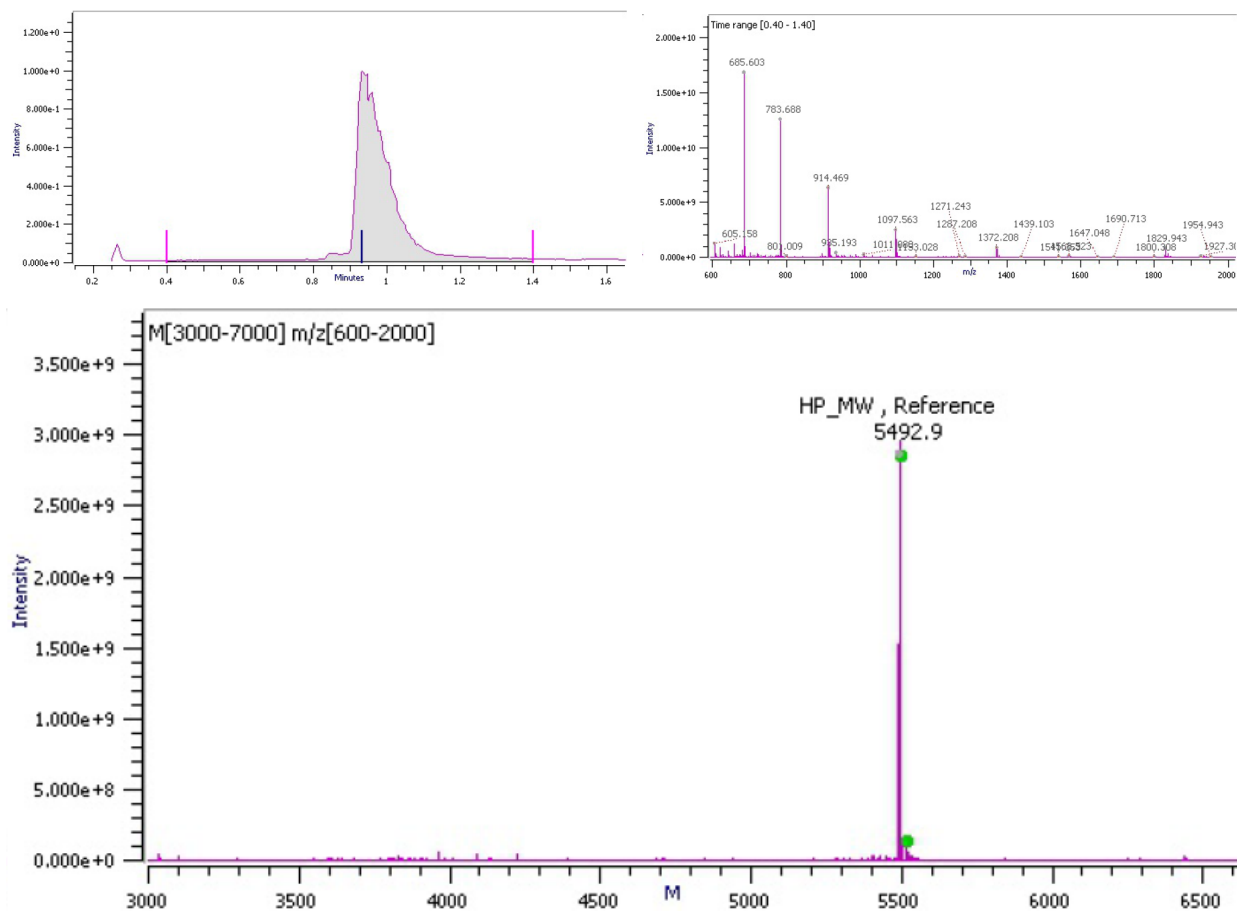


Headpiece 1J



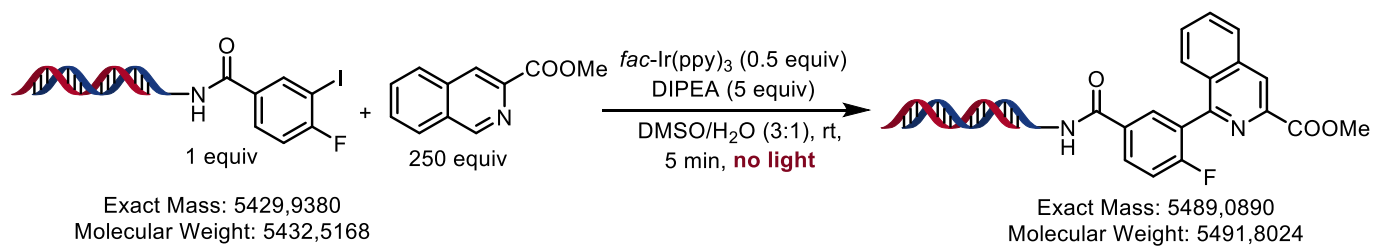
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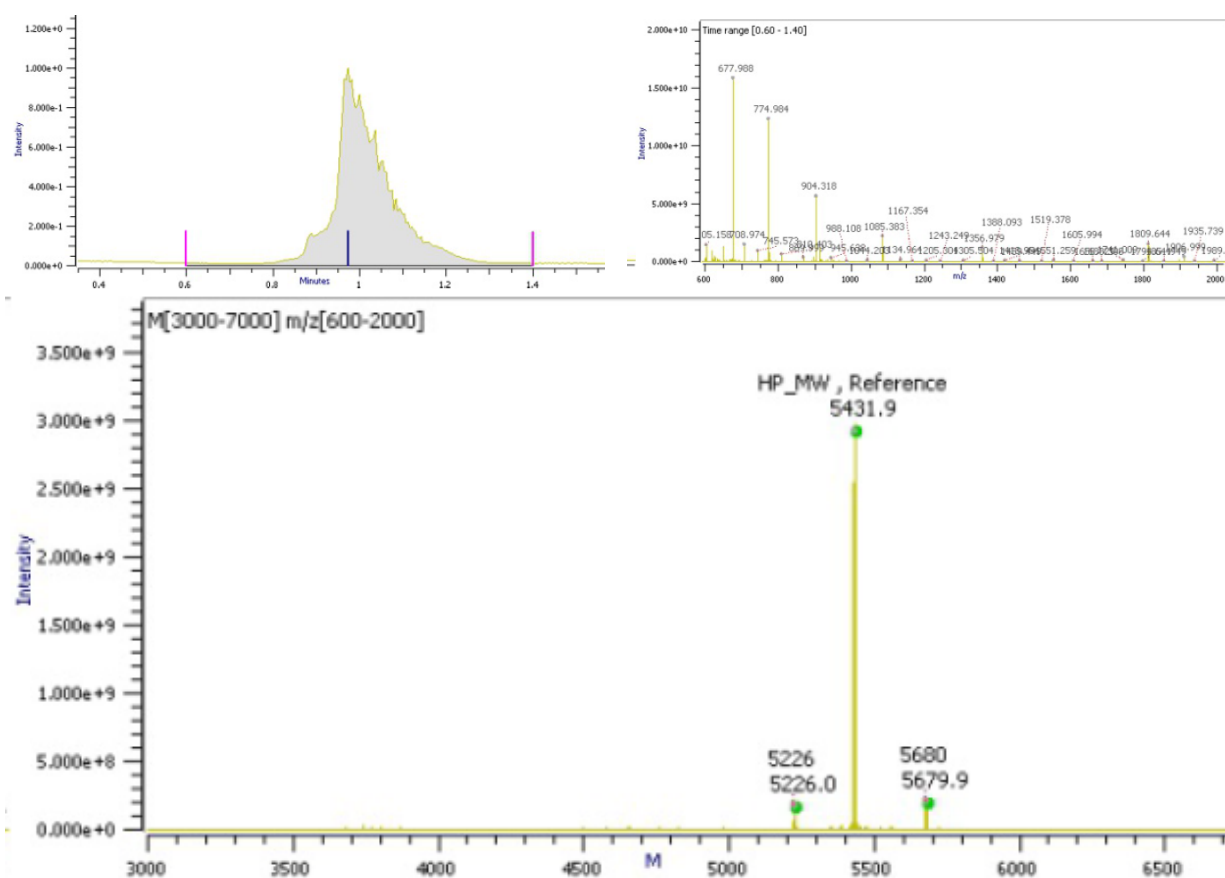


Control experiments for On-DNA reactions

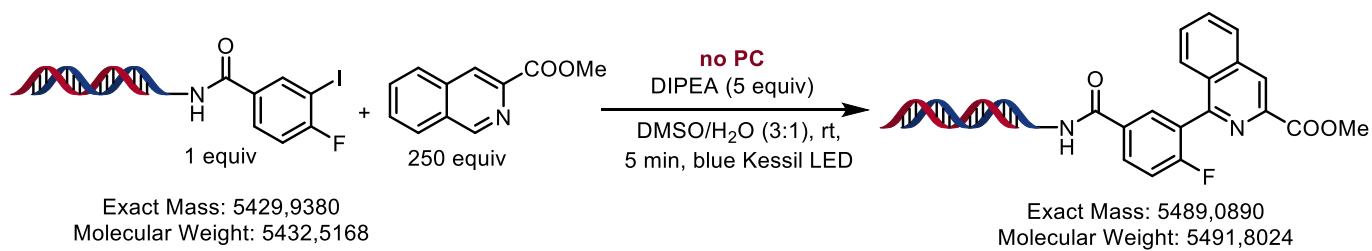
No light: No product formation (**4a**) is detected



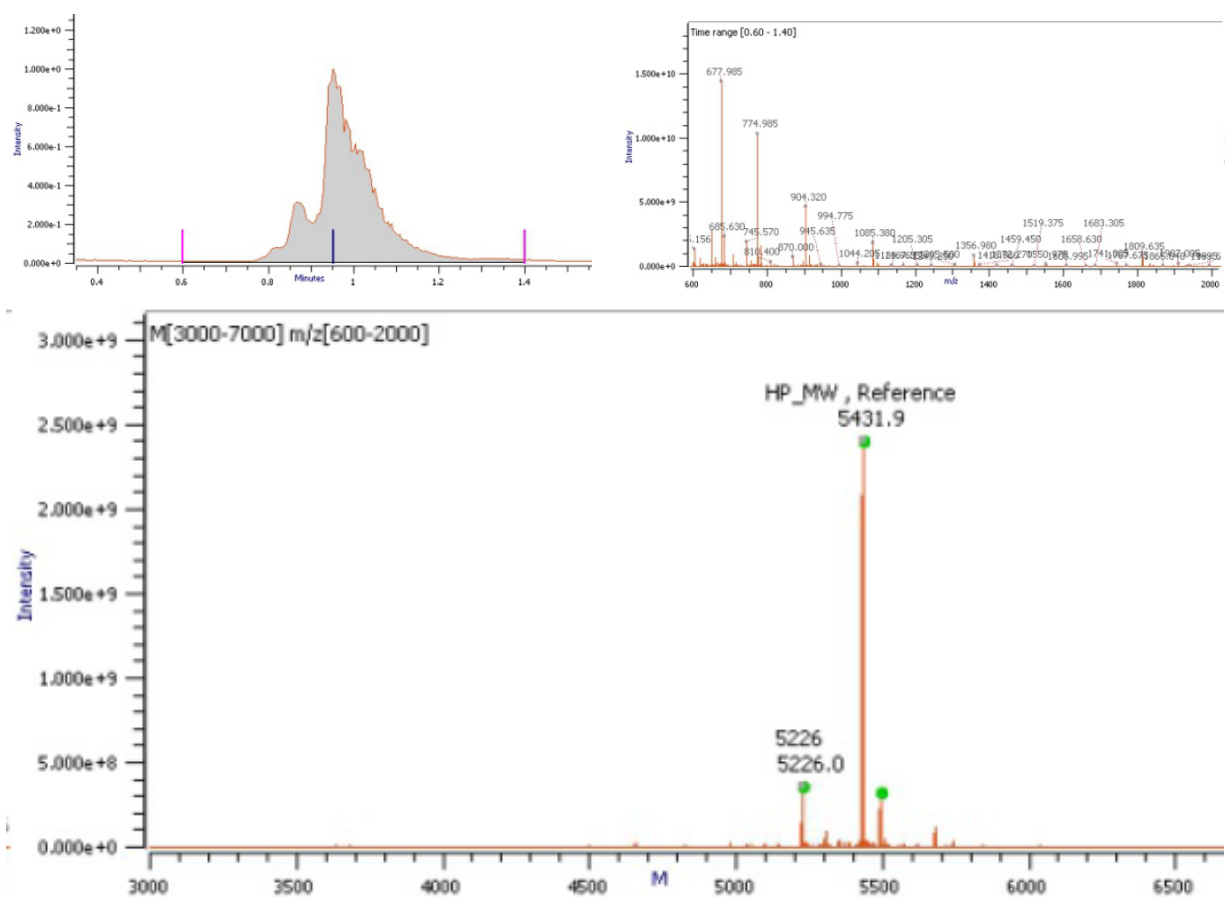
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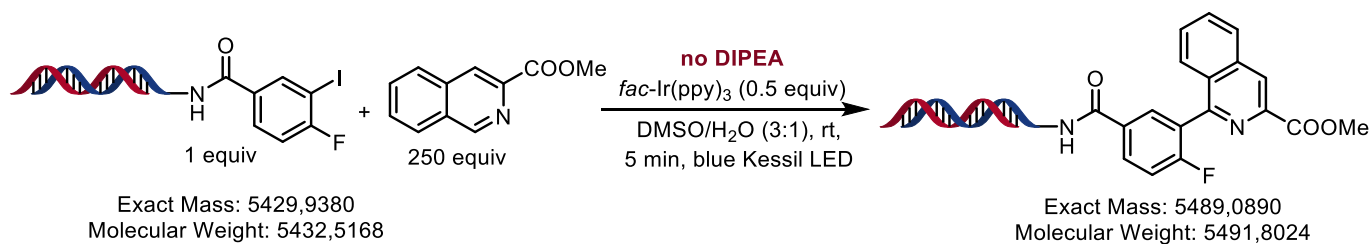
No *fac*-Ir(ppy)₃: No product formation (**4a**) is detected



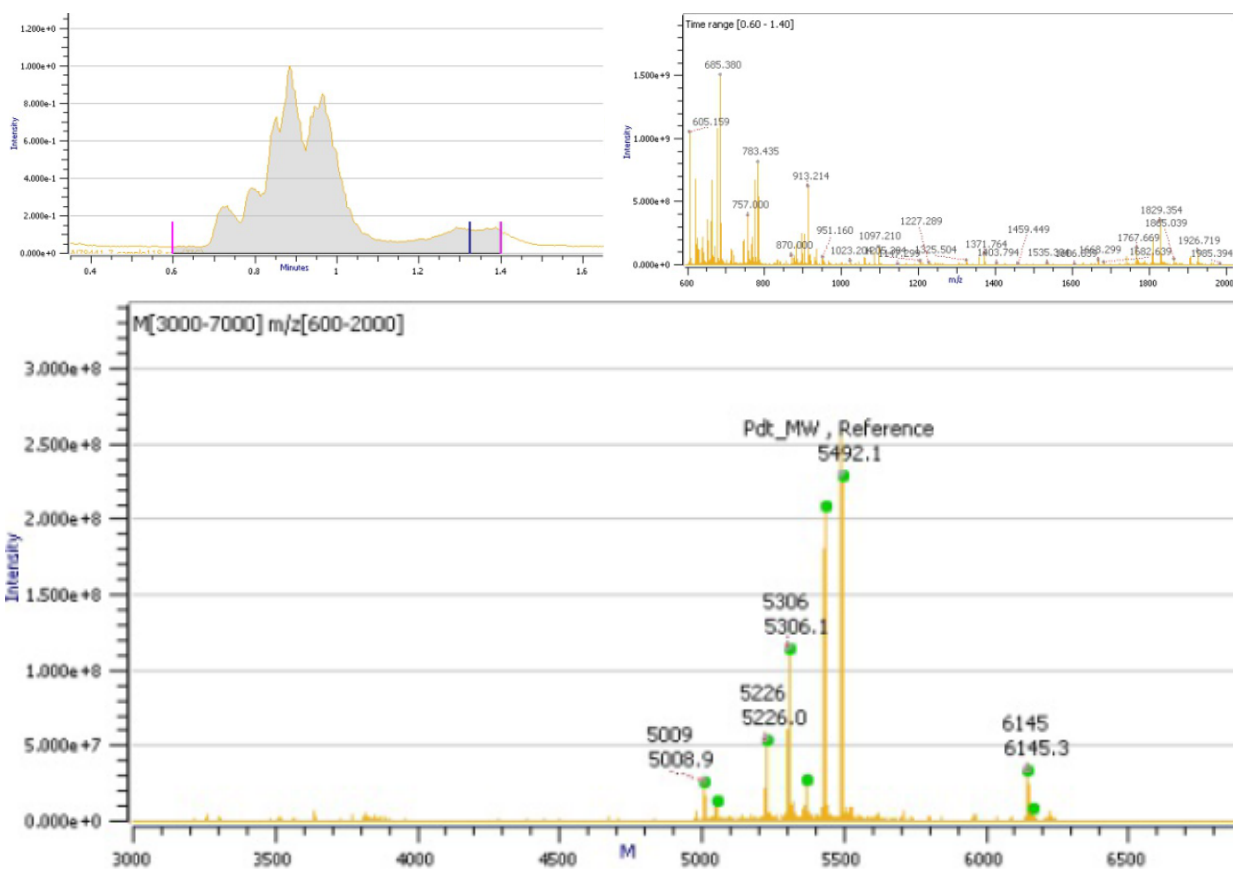
ELTM_414, TW-N78441-9-414 (Plot Elution Peak - Plot MS1 - Plot Deconvoluted Mass spectrum)



No DIPEA: Product **4a**, 34% yield

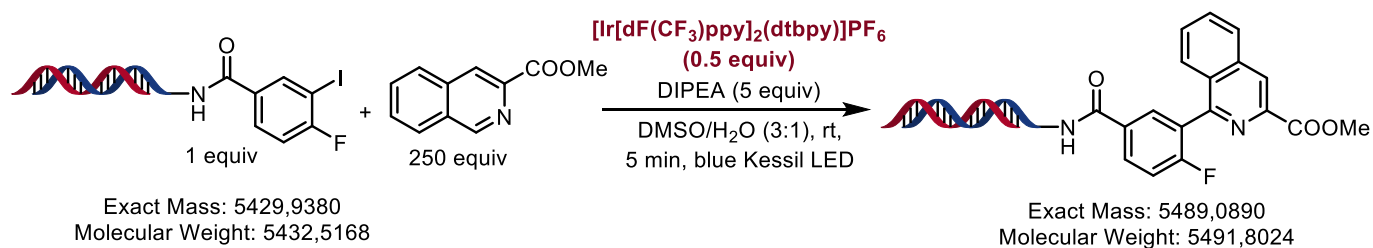


ELTM_118, N78441-7-118 (Plot Elution Peak - Plot MS1 - Plot Deconvoluted Mass spectrum)

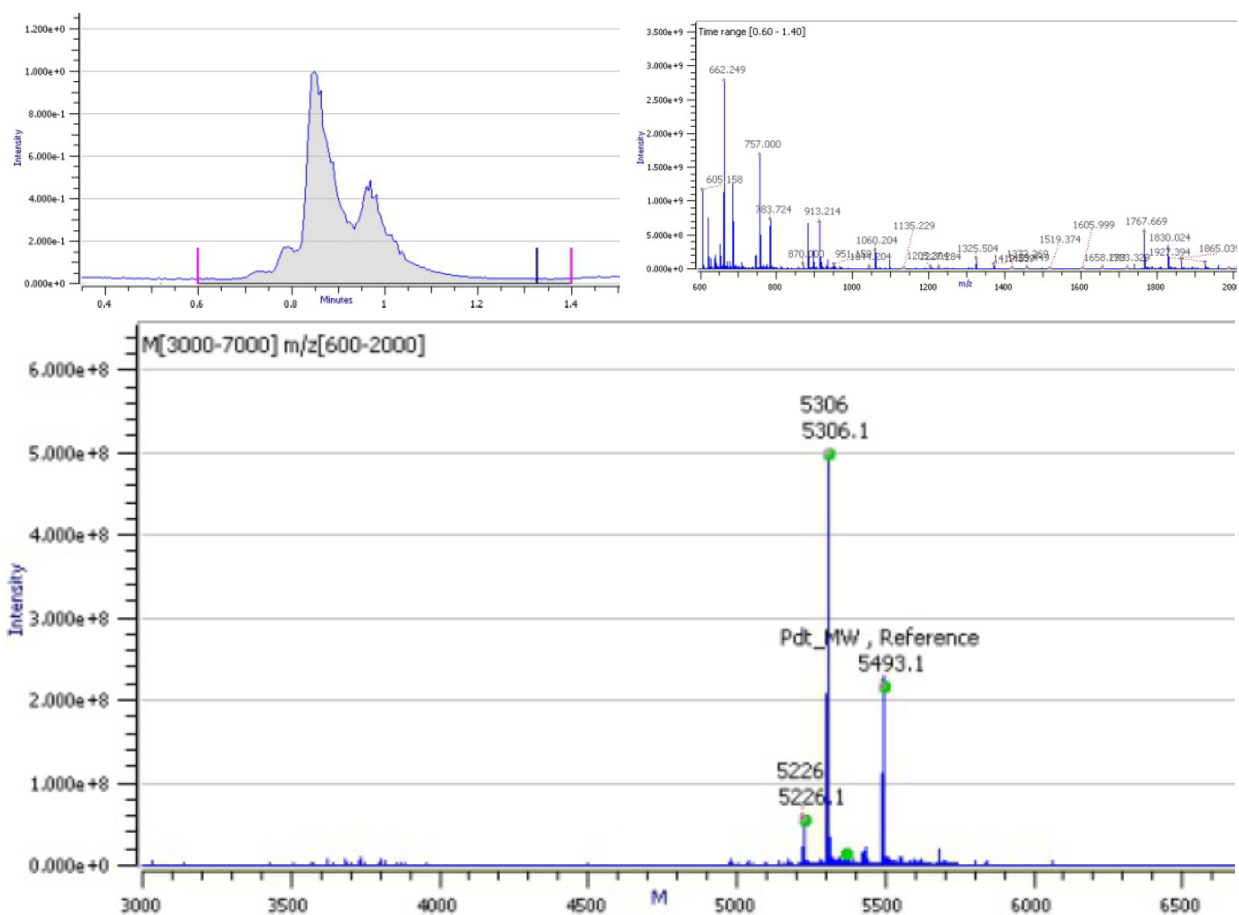


Optimization studies: Catalyst screen

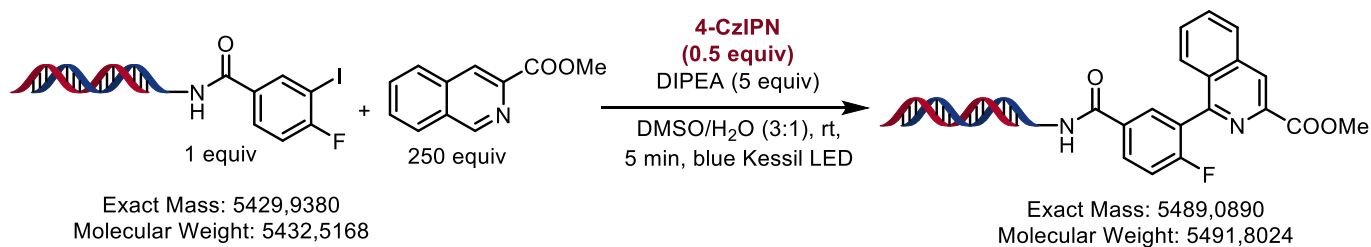
$[\text{Ir}[\text{dF}(\text{CF}_3)\text{ppy}]_2(\text{dtbpy})]\text{PF}_6$: Product **4a**, 30%



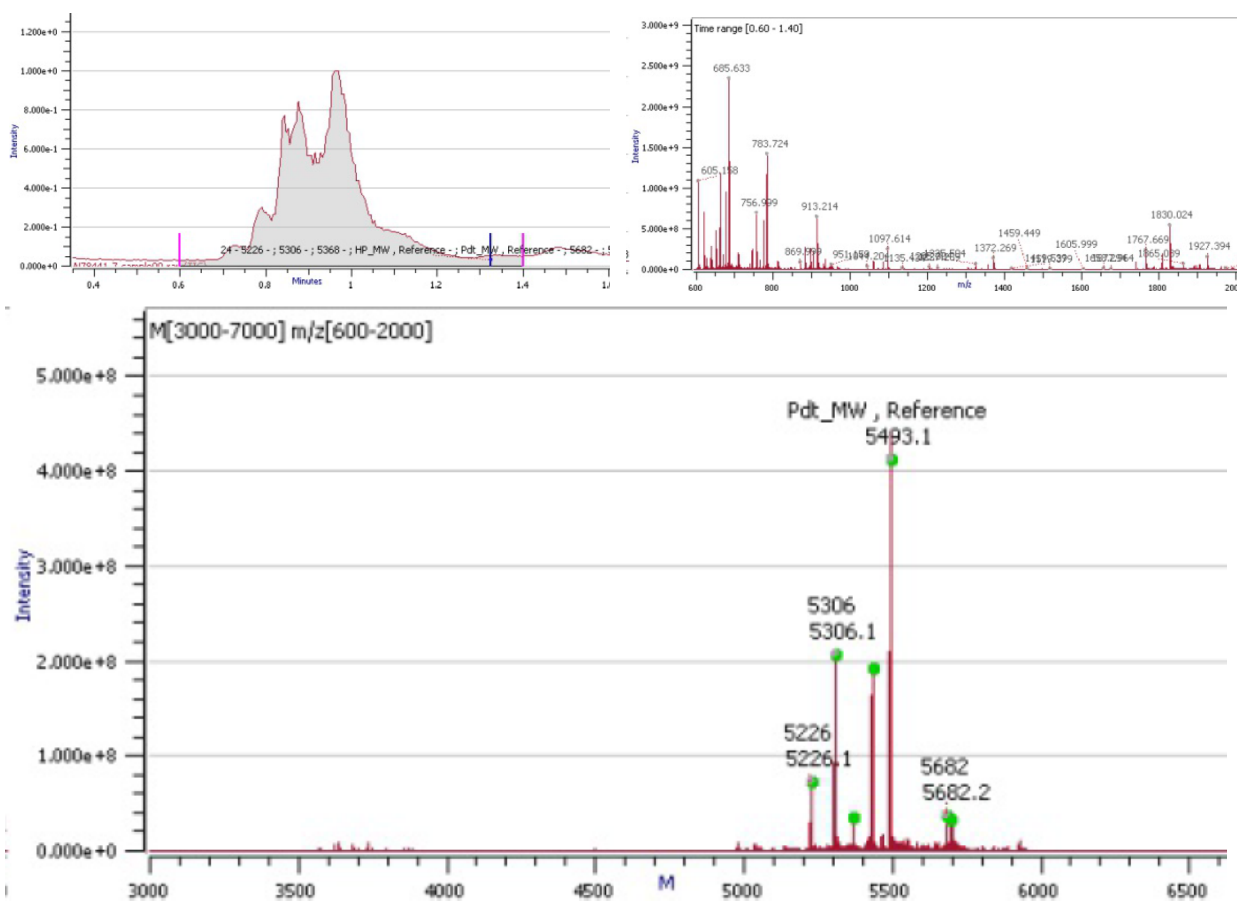
ELTM_98, TW-N78441-7-98 (Plot Elution Peak - Plot MS1 - Plot Deconvoluted Mass spectrum)



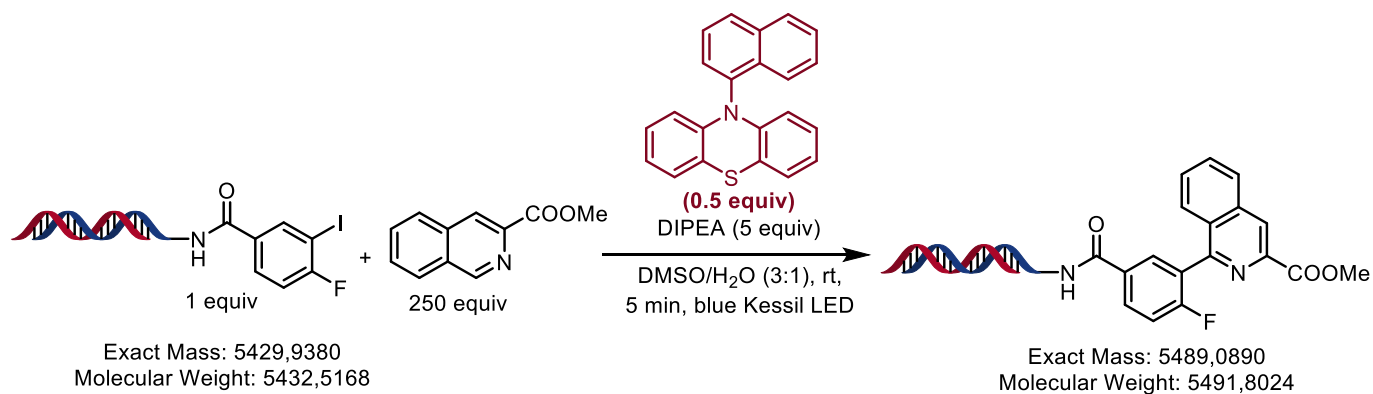
4-CzIPN: Product 4a, 45%



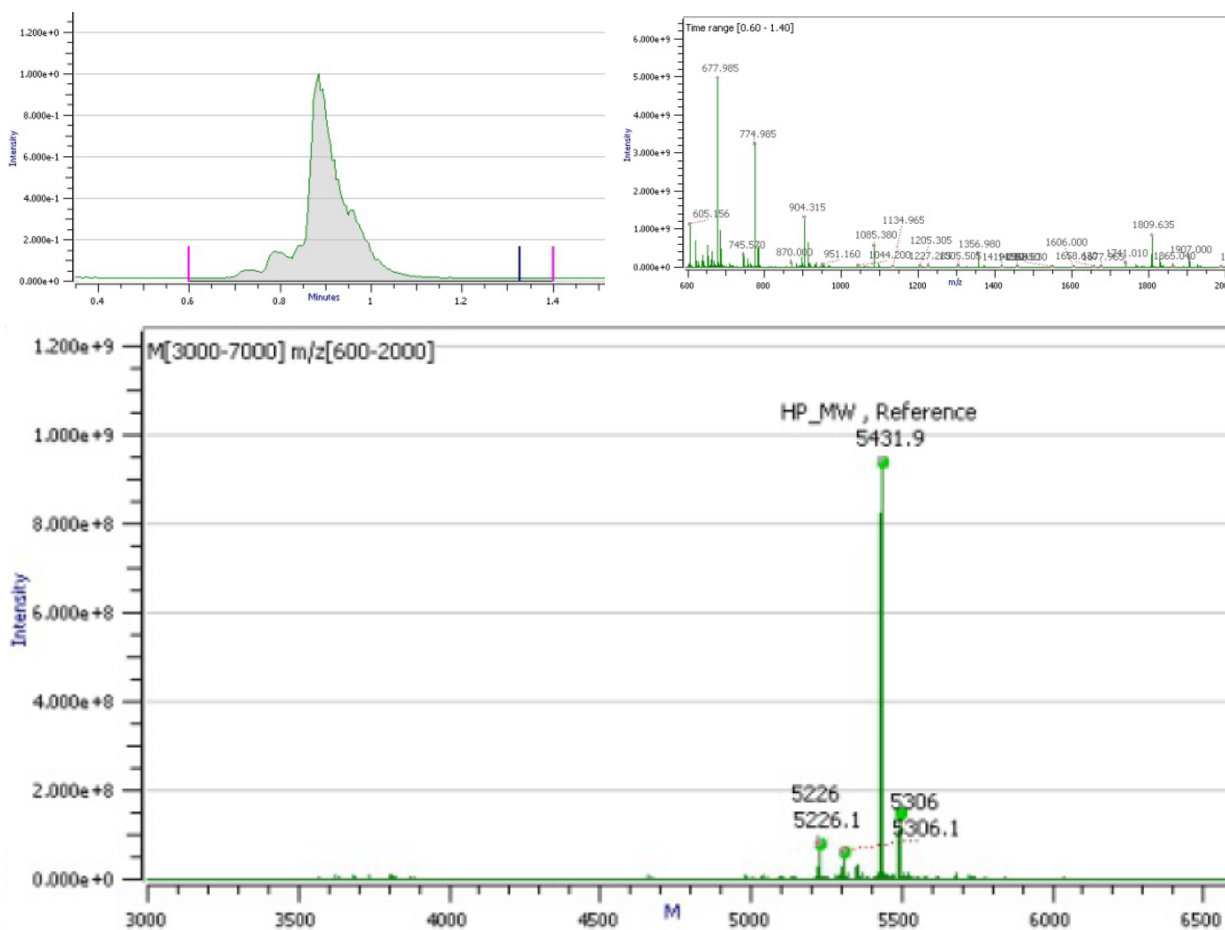
ELTM_99, TW-N78441-7-99 (Plot Elution Peak - Plot MS1 - Plot Deconvoluted Mass spectrum)



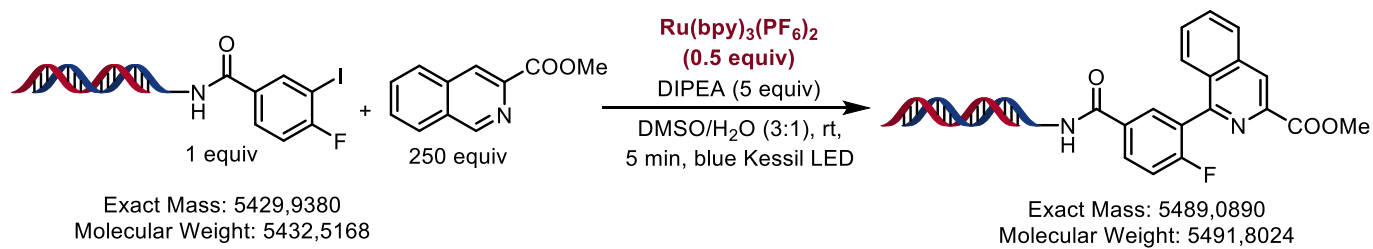
Naphthyl-phenothiazine: Product 4a, 13%



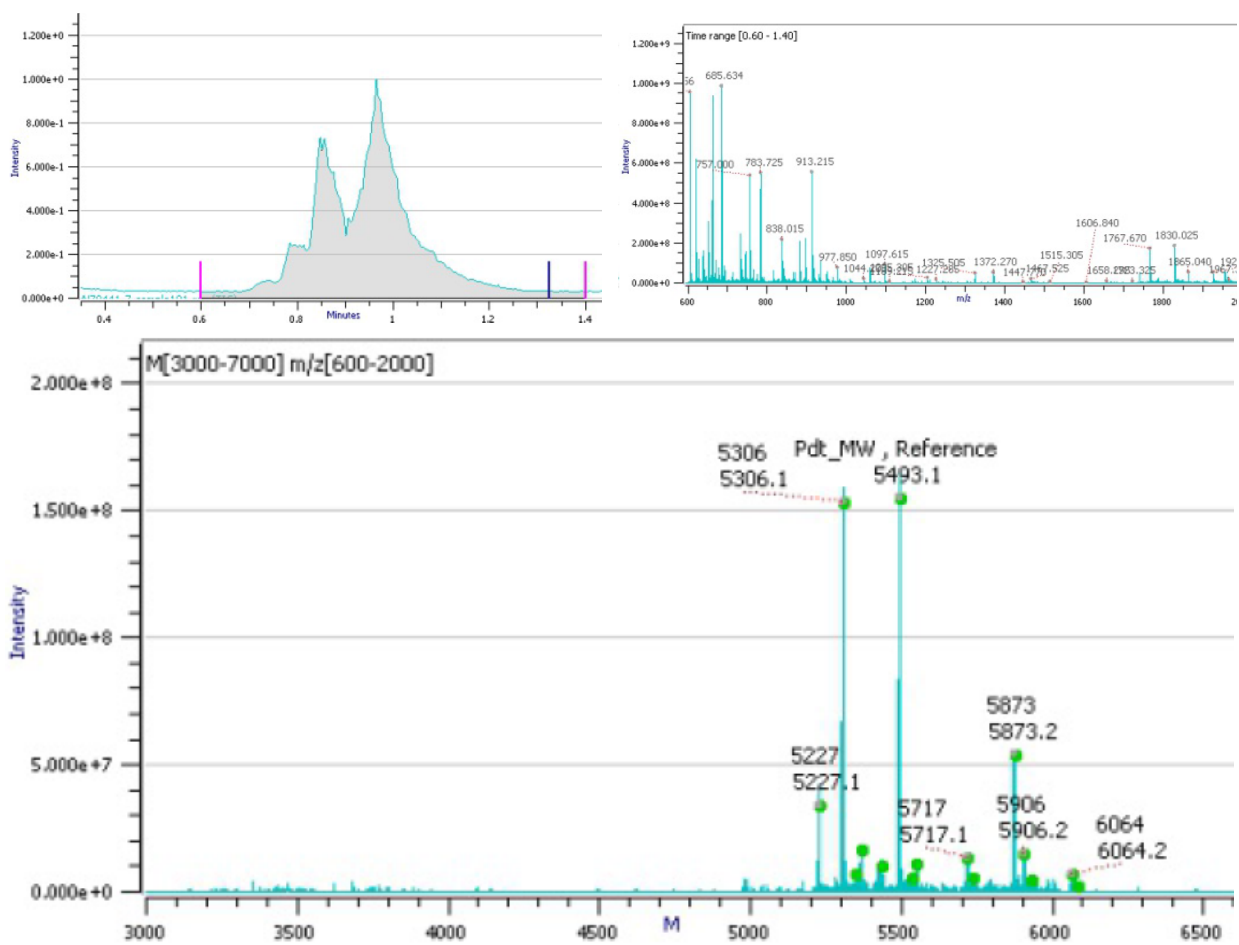
ELTM_100, TW-N78441-7-100 (Plot Elution Peak - Plot MS1 - Plot Deconvoluted Mass spectrum)



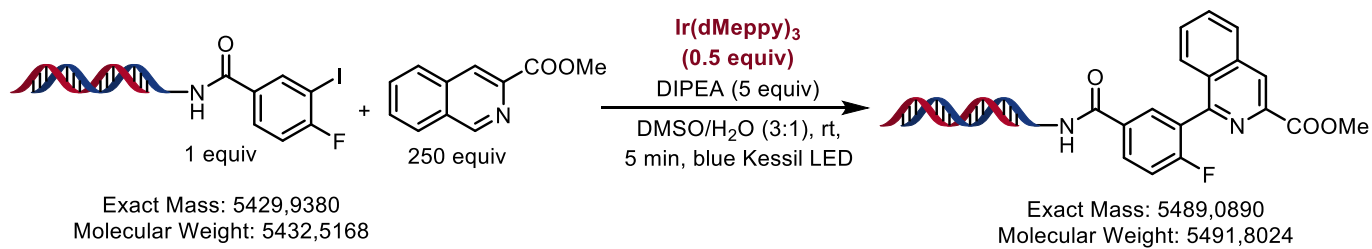
Ru(bpy)₃(PF₆)₂: Product 4a, 34%



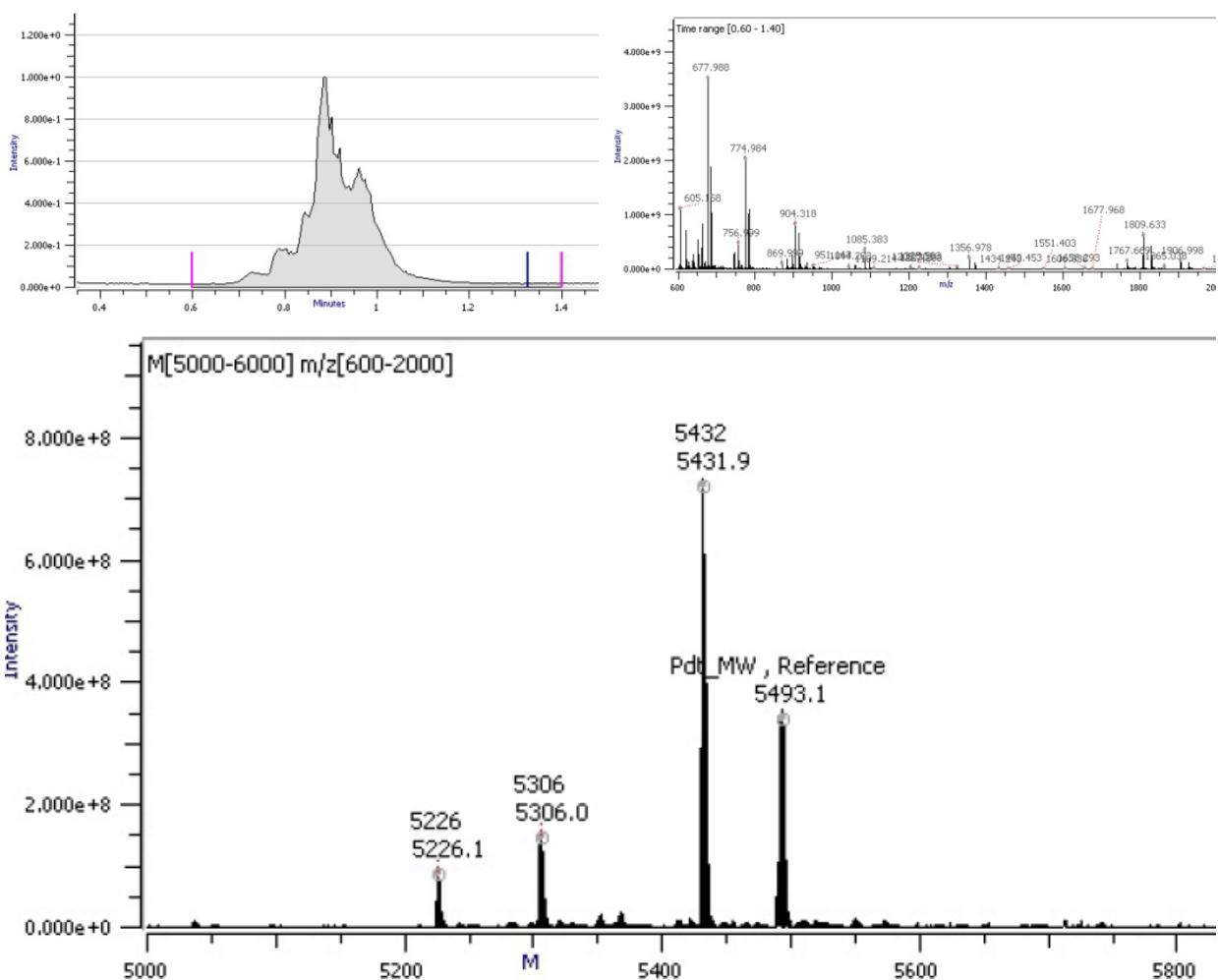
ELTM_101, TW-N78441-7-101 (Plot Elution Peak - Plot MS1 - Plot Deconvoluted Mass spectrum)



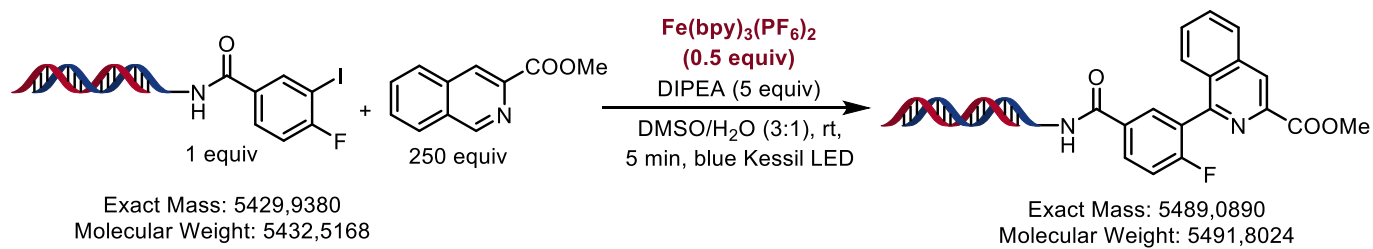
Ir(dMeppy)₃: Product 4a, 28%



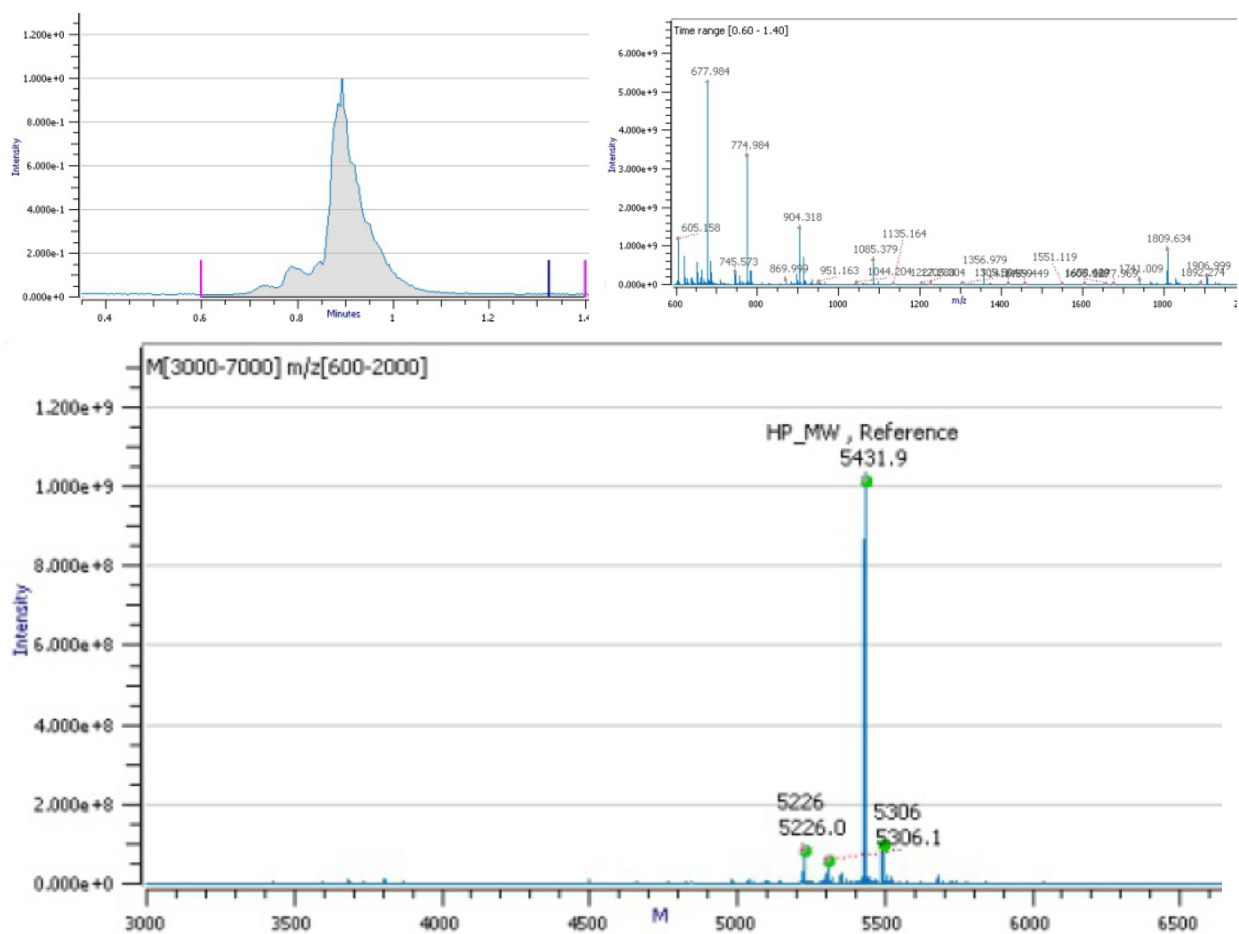
ELTM_102, TW-N78441-7-102 (Plot Elution Peak - Plot MS1 - Plot Deconvoluted Mass spectrum)



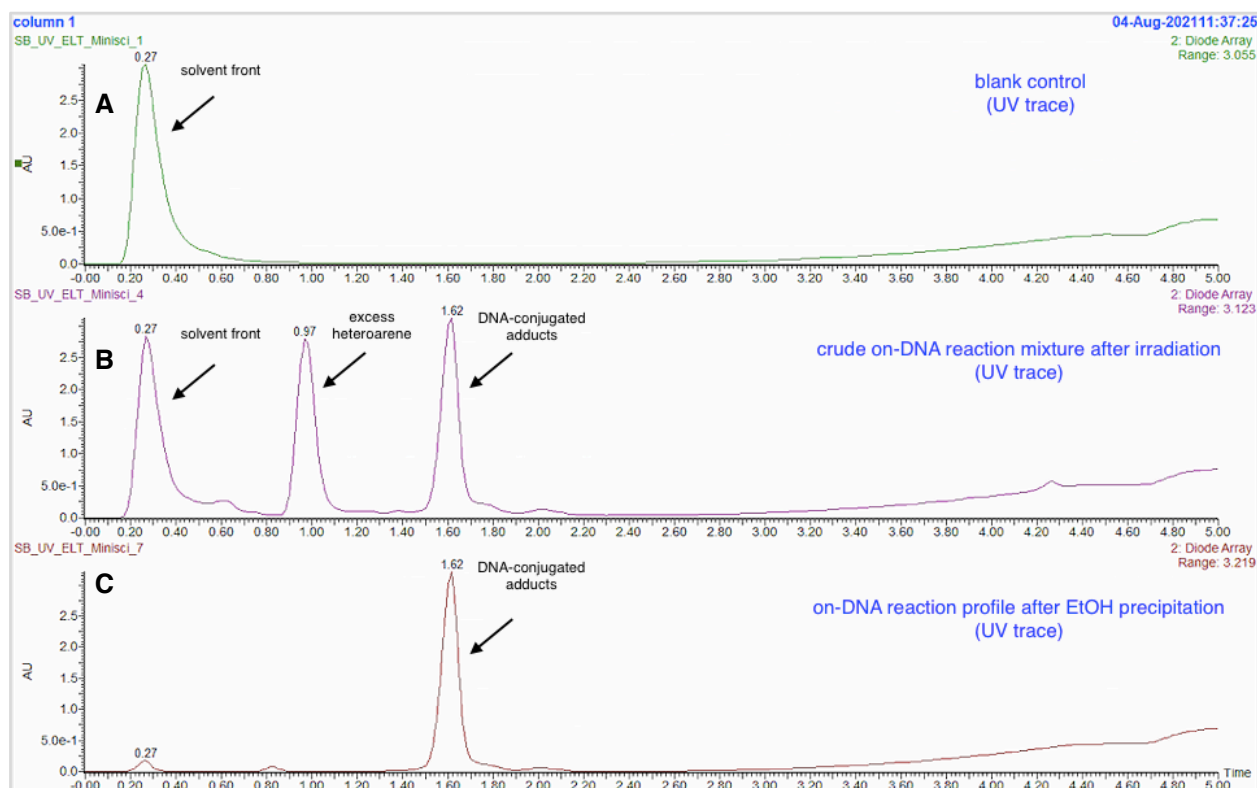
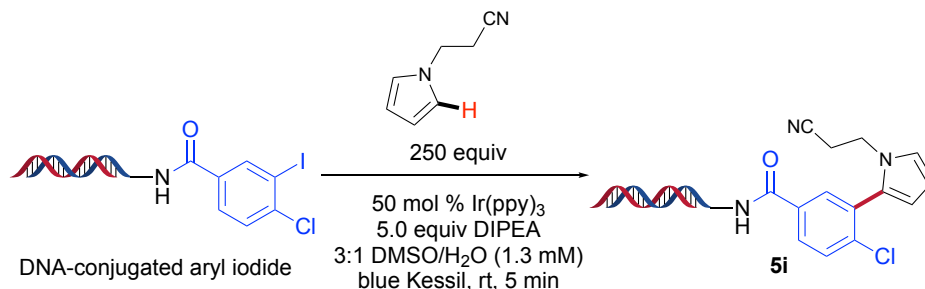
Fe(bpy)₃(PF₆)₂: Product 4a, 8%



ELTM_103, TW-N78441-7-103 (Plot Elution Peak - Plot MS1 - Plot Deconvoluted Mass spectrum)



*UV trace profile for exemplary substrate **5i** before and after ethanol precipitation:*

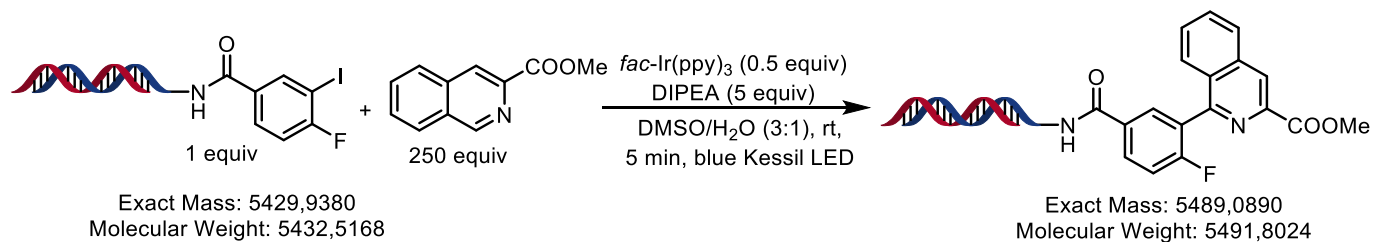


As demonstrated from UV traces **B** & **C** for exemplary substrate **5i**, the organic byproducts can be removed by standard DEL purification procedures (following the ethanol precipitation protocol described in Section 2.2). Furthermore, the exemplary sample submitted to EtOH precipitation has a UV chromatogram that is consonant with that of the DNA-adducts post purification.

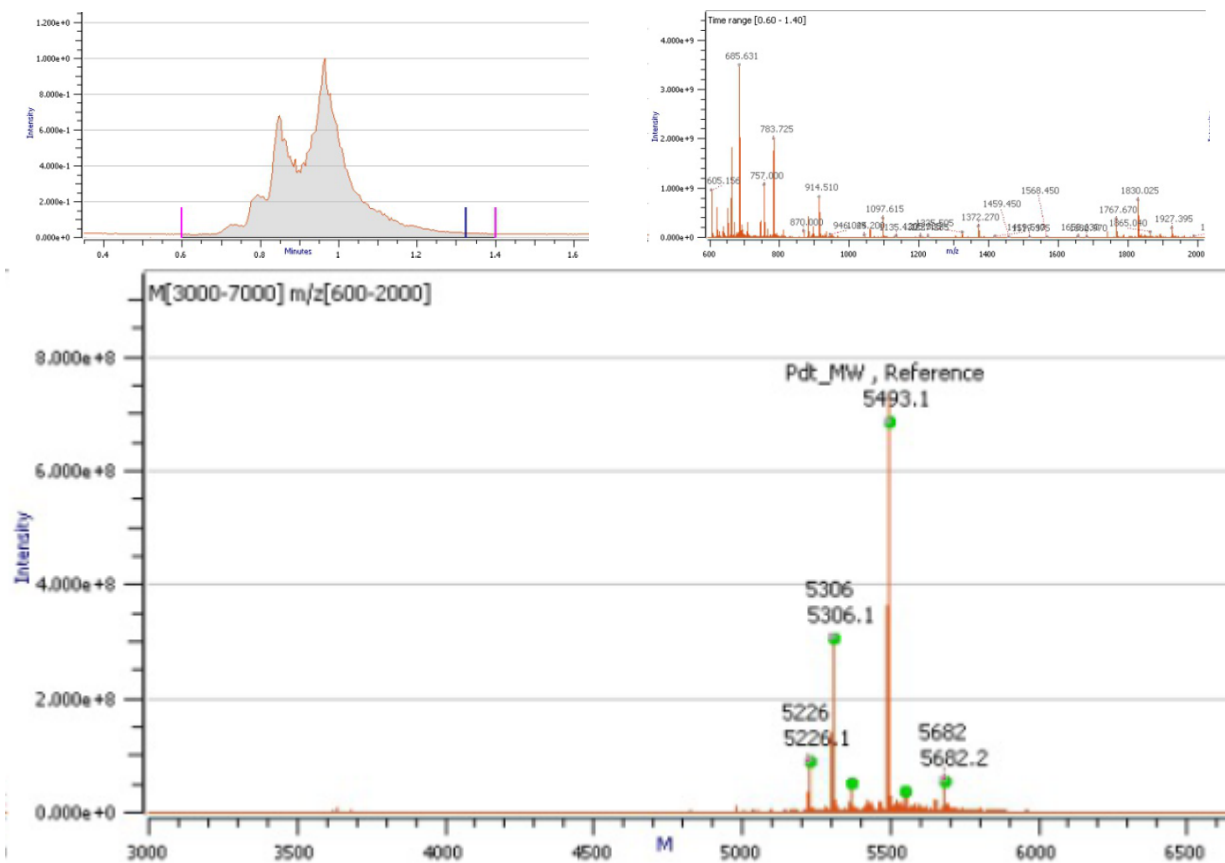
Determination of yields for On-DNA reactions

Variation of heteroarenes

Product **4a**, 60% yield



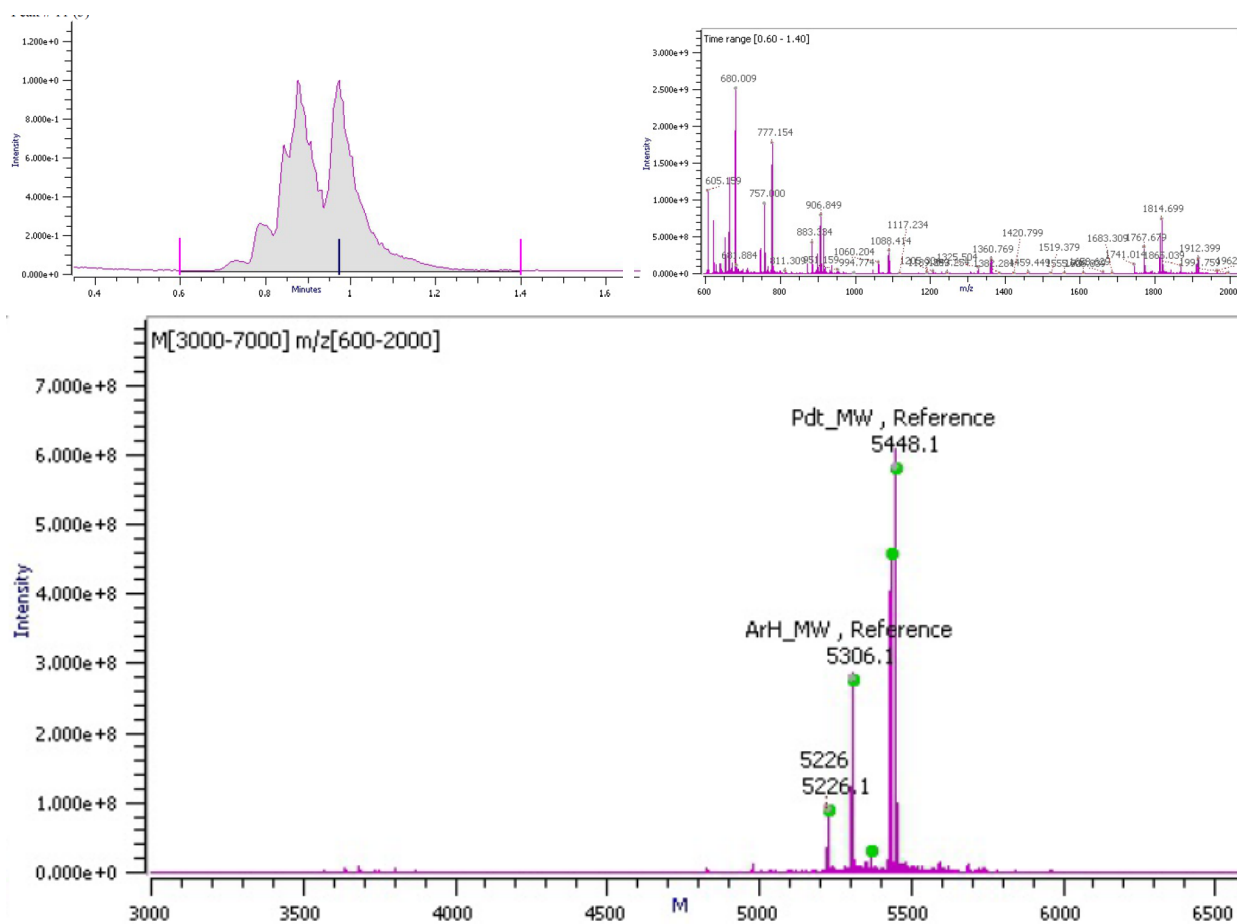
ELTM_117, TW-N78441-7-117.raw (Plot Elution Peak - Plot MS1 - Plot Deconvoluted Mass spectrum)



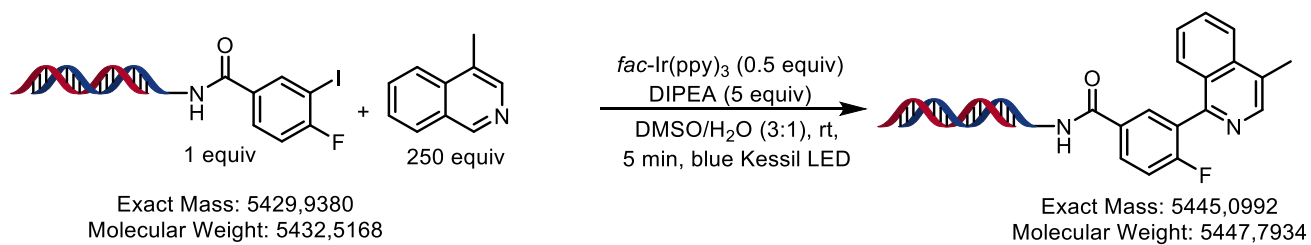
Product **4b**, 44% yield



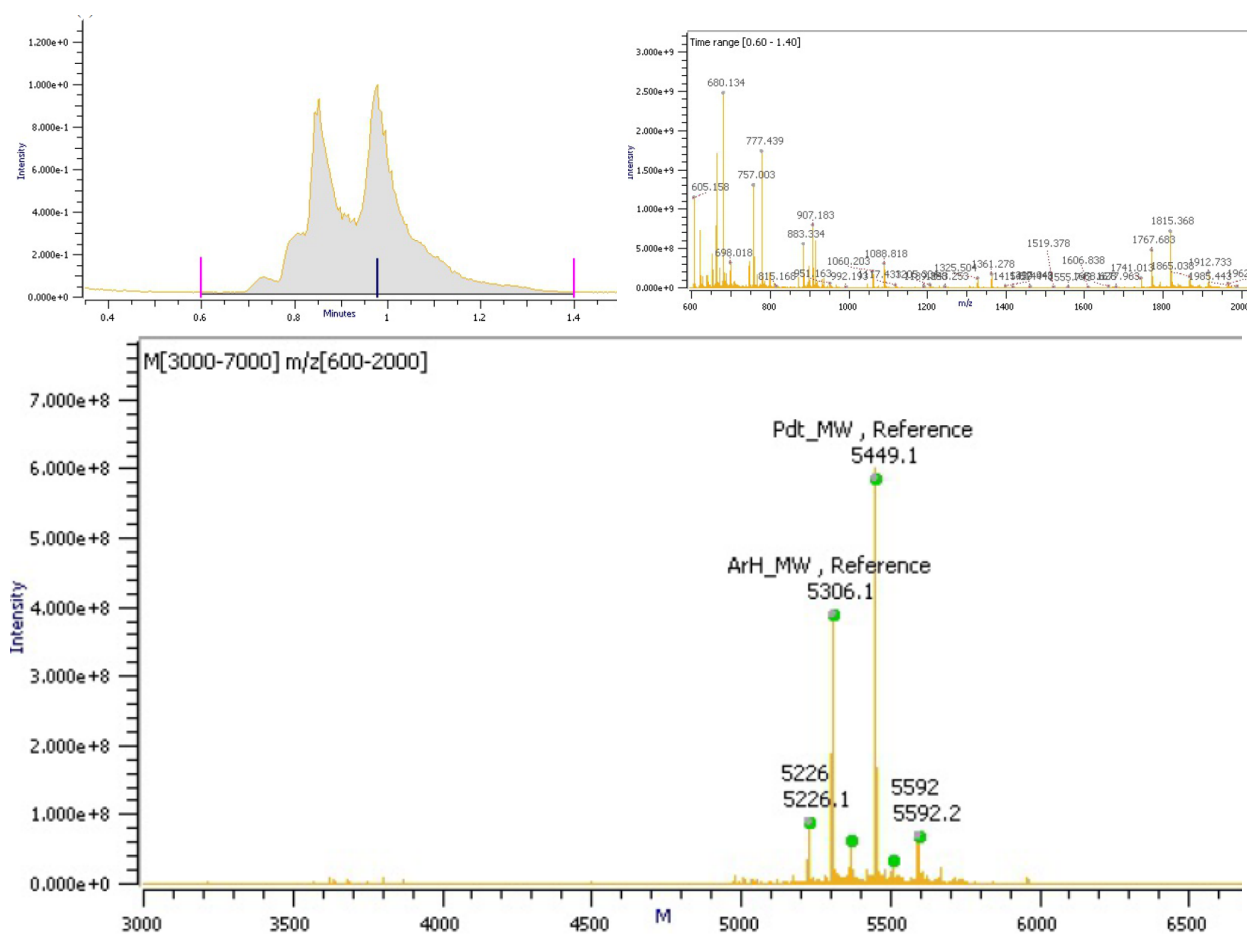
ELTM_206, TW-N78441-8-206.raw (Plot Elution Peak - Plot MS1 - Plot Deconvoluted Mass spectrum)



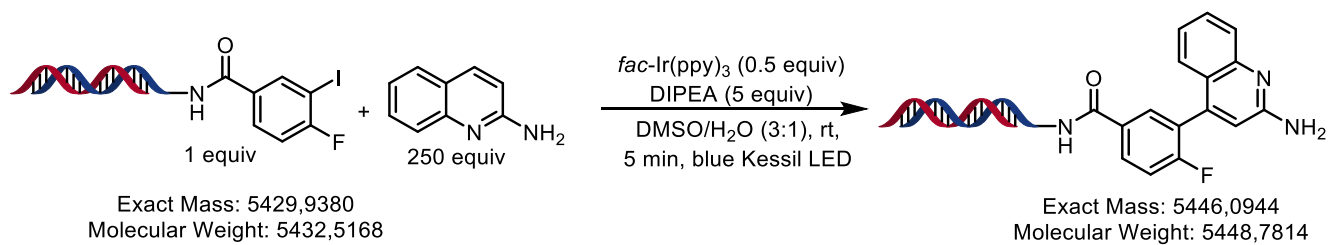
Product **4c**, 52% yield



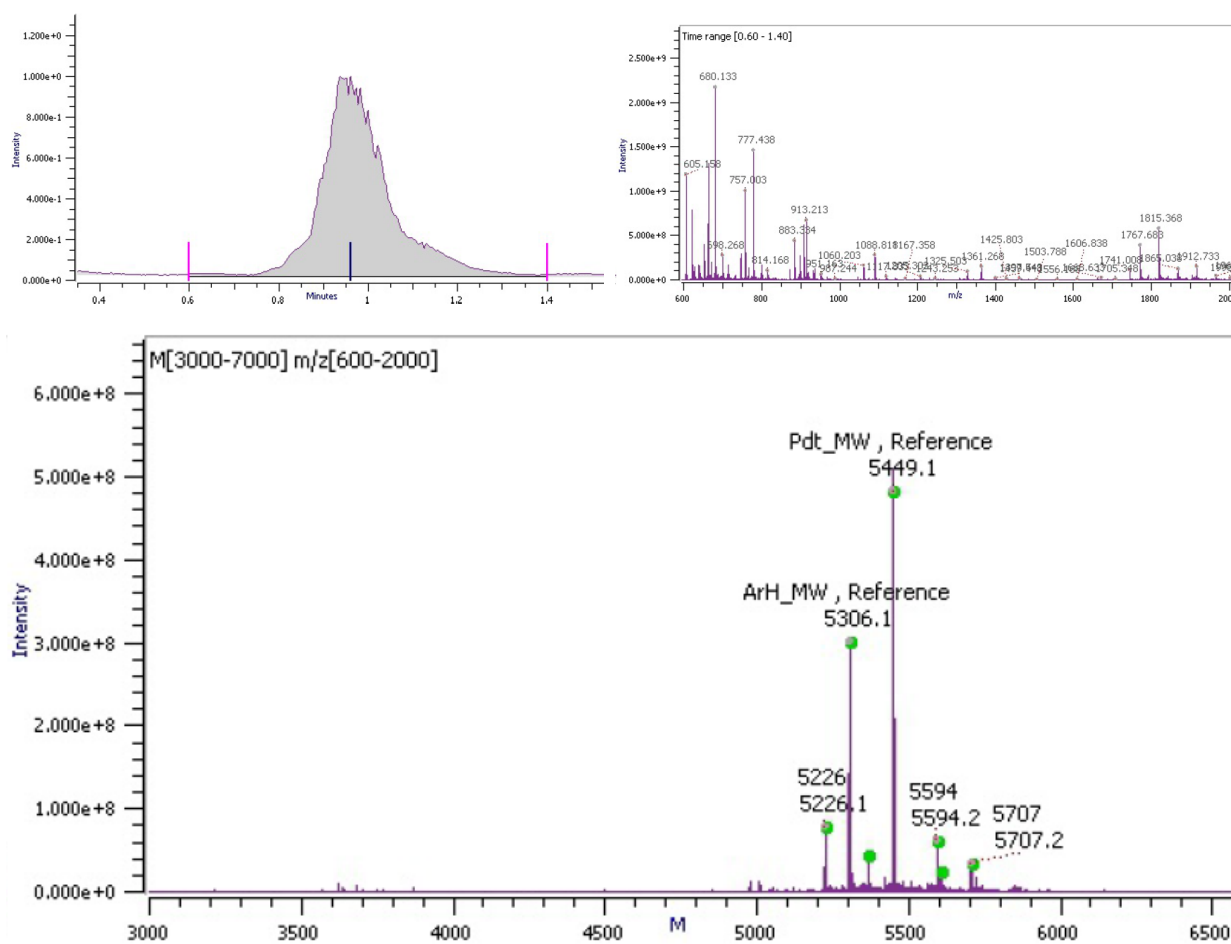
ELTM_167, TW-N78441-8-167.raw (Plot Elution Peak - Plot MS1 - Plot Deconvoluted Mass spectrum)



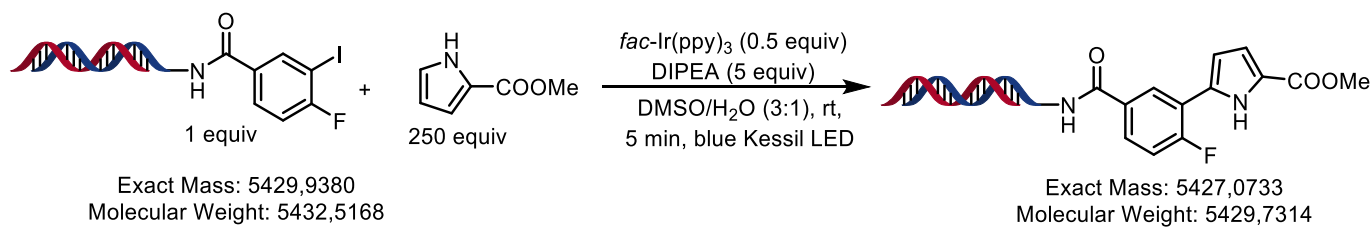
Product **4d**, 52% yield



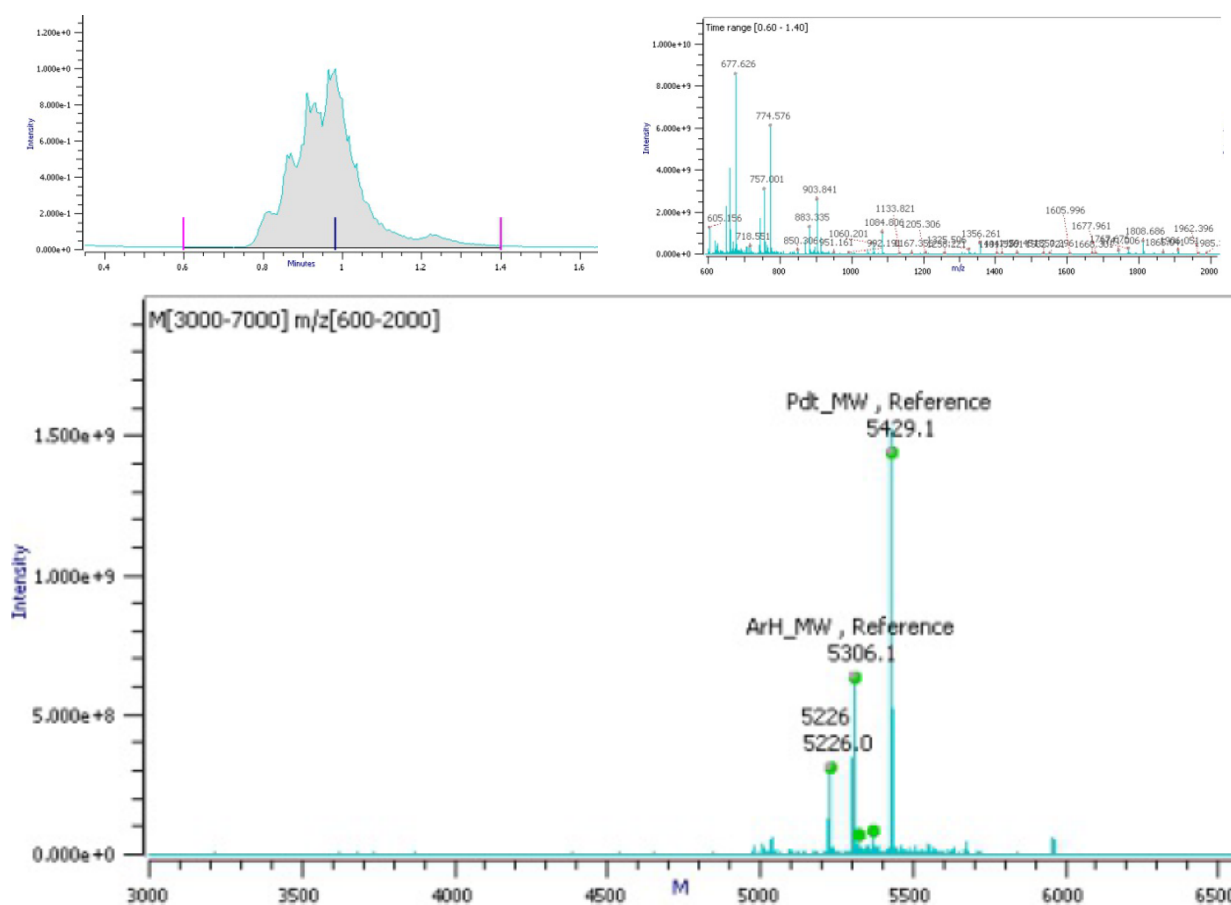
ELTM_171, TW-N78441-8-171.raw (Plot Elution Peak - Plot MS1 - Plot Deconvoluted Mass spectrum)



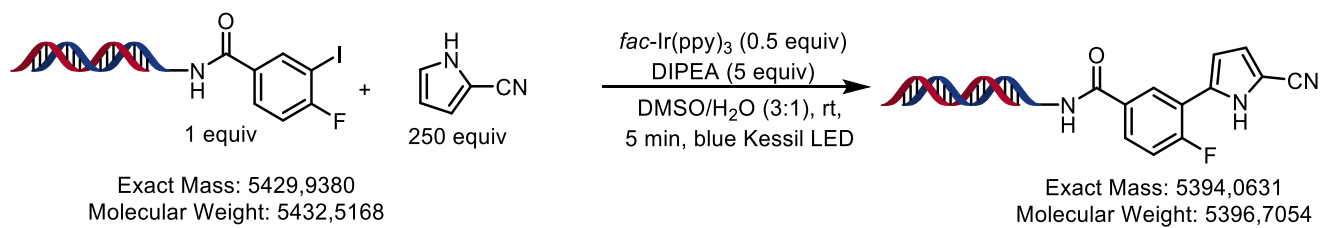
Product **4e**, 67% yield



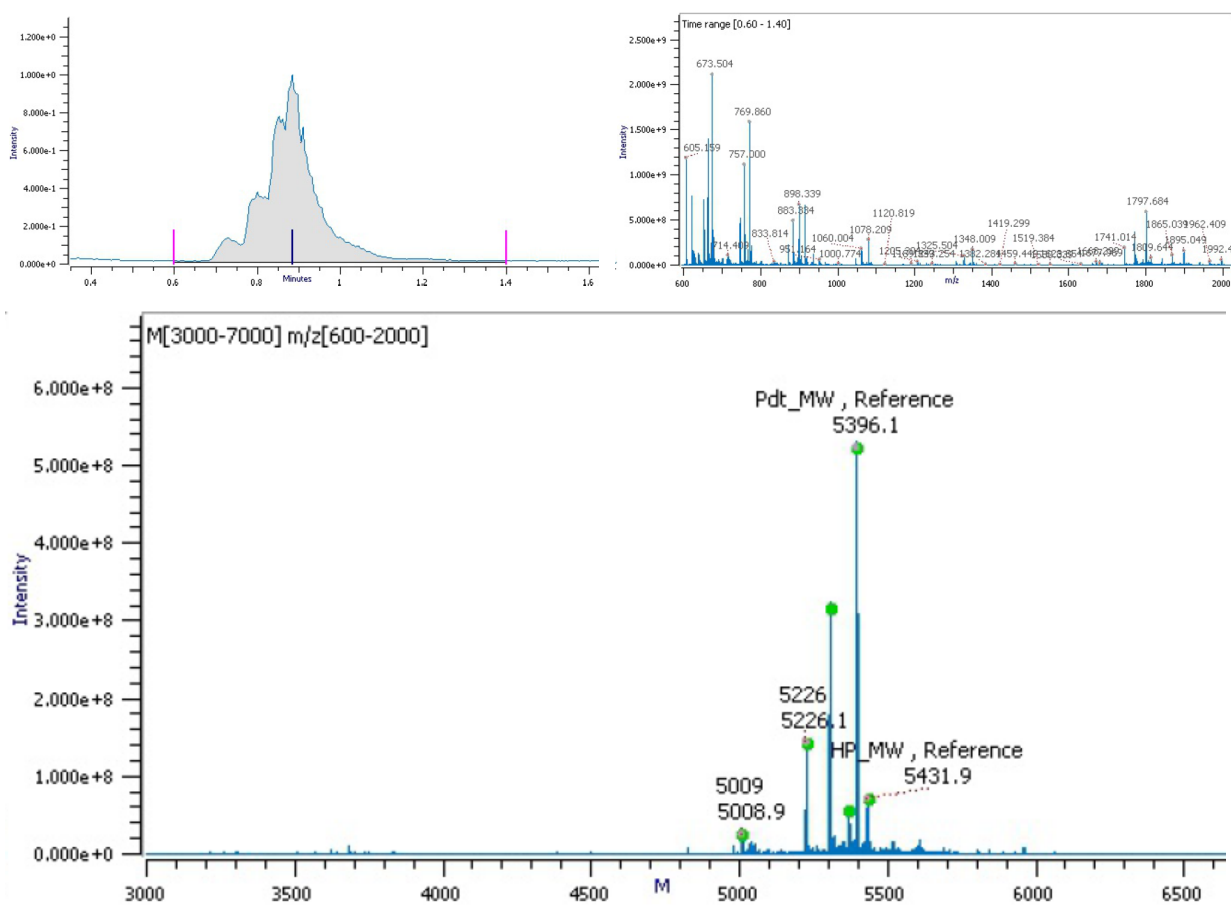
ELTM_370, TW-N78441-9-370.raw (Plot Elution Peak - Plot MS1 - Plot Deconvoluted Mass spectrum)



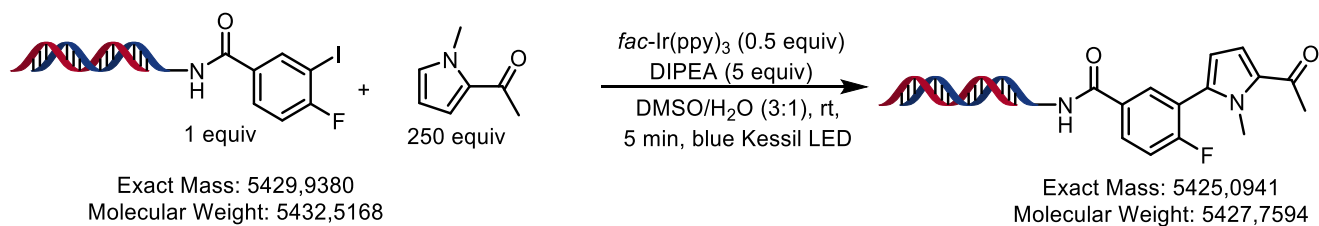
Product **4f**, 51% yield



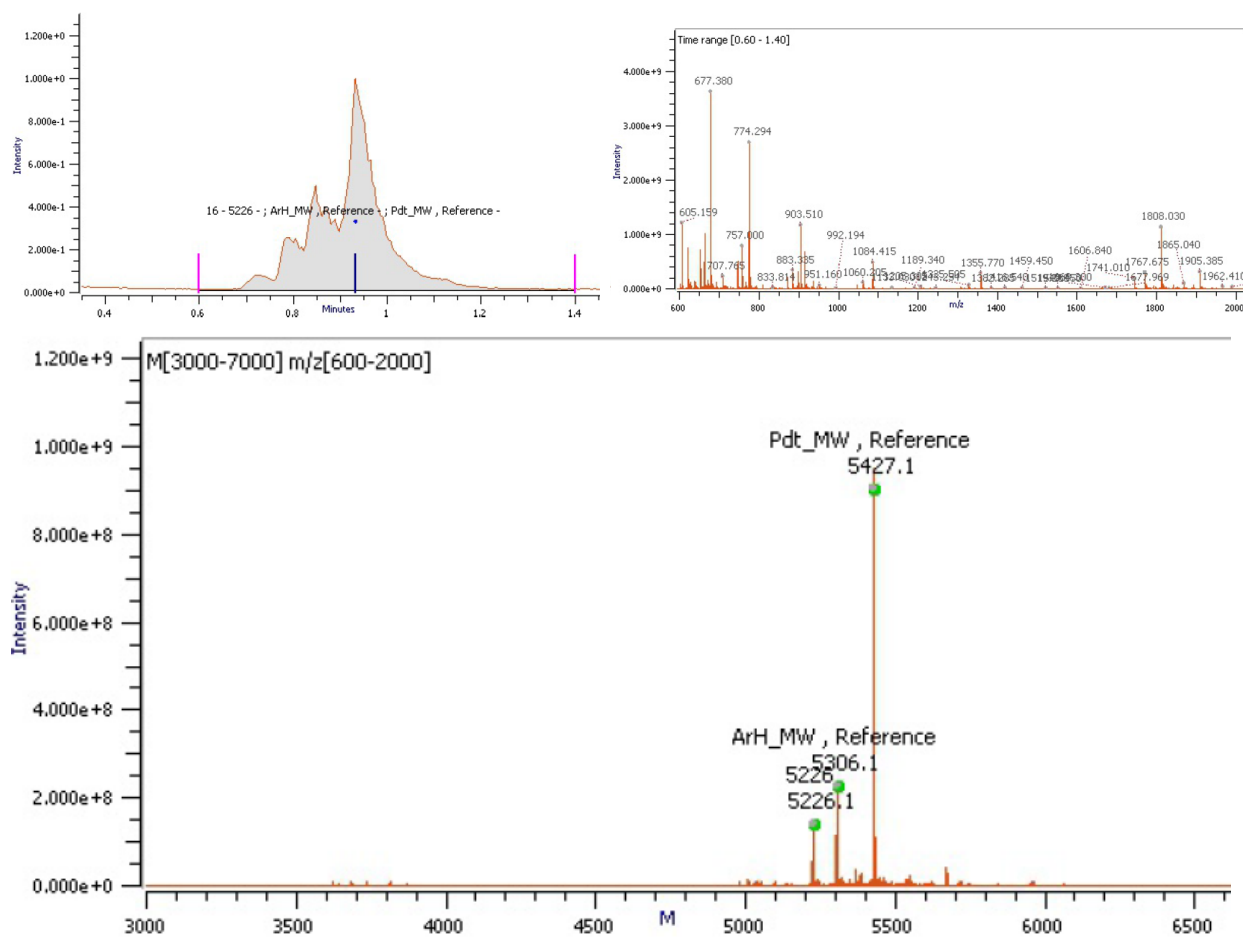
ELTM_224, TW-N78441-8-224.raw (Plot Elution Peak - Plot MS1 - Plot Deconvoluted Mass spectrum)



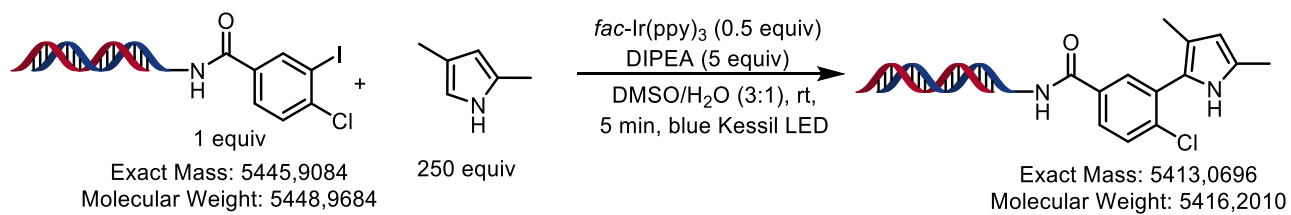
Product **4g**, 78% yield



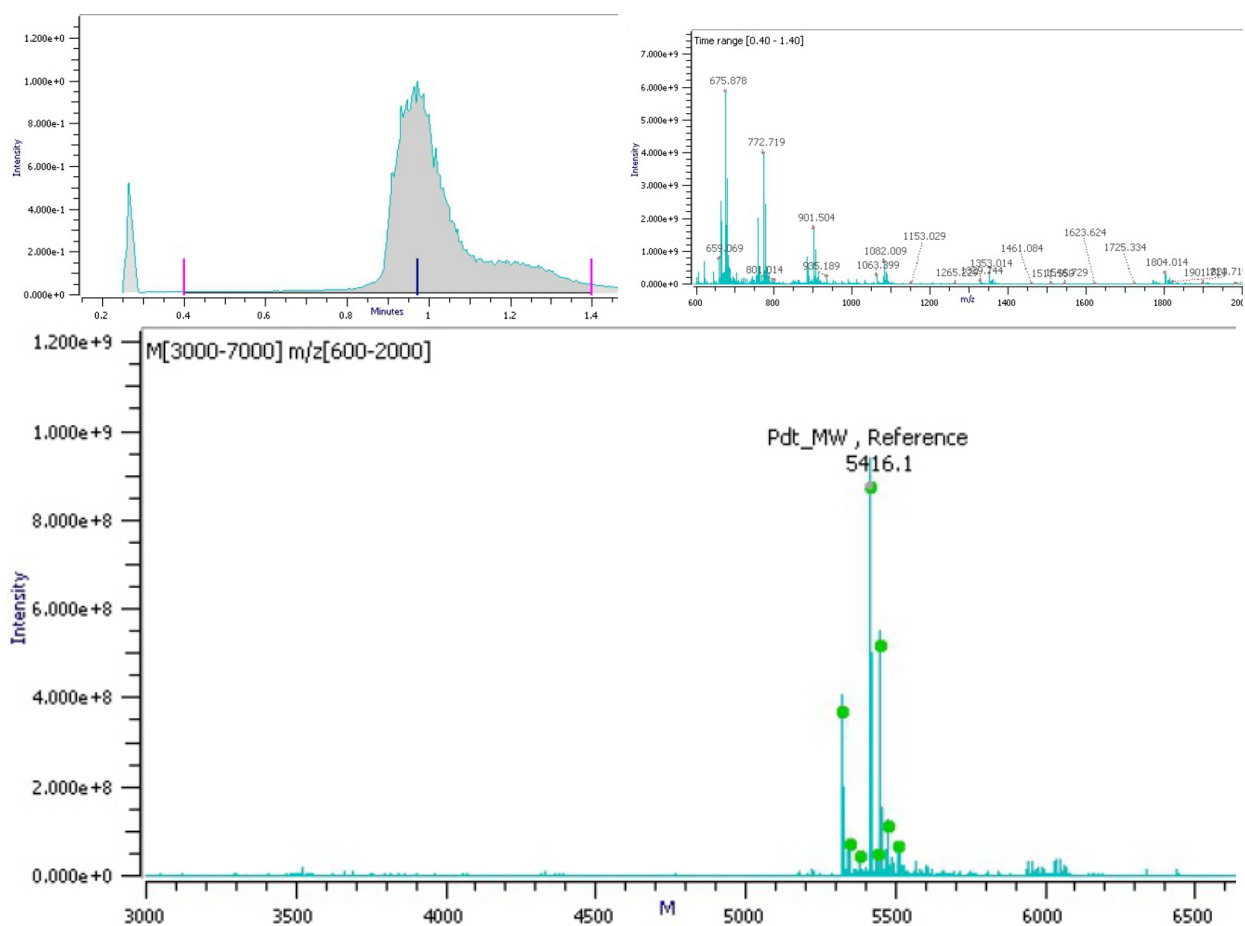
ELTM_228, TW-N78441-8-228.raw - (Plot Elution Peak - Plot MS1 - Plot Deconvoluted Mass spectrum)



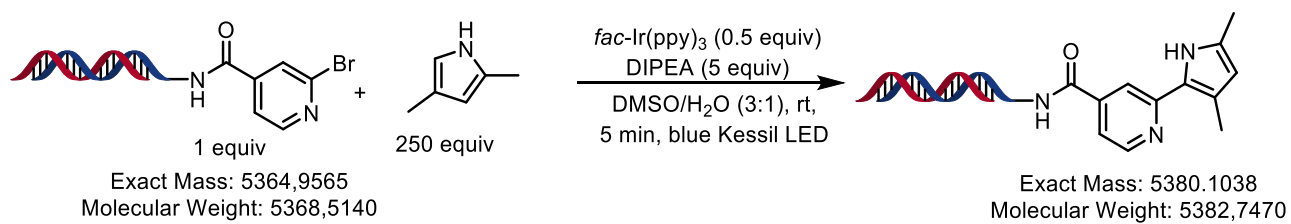
Product **5h** 48% yield



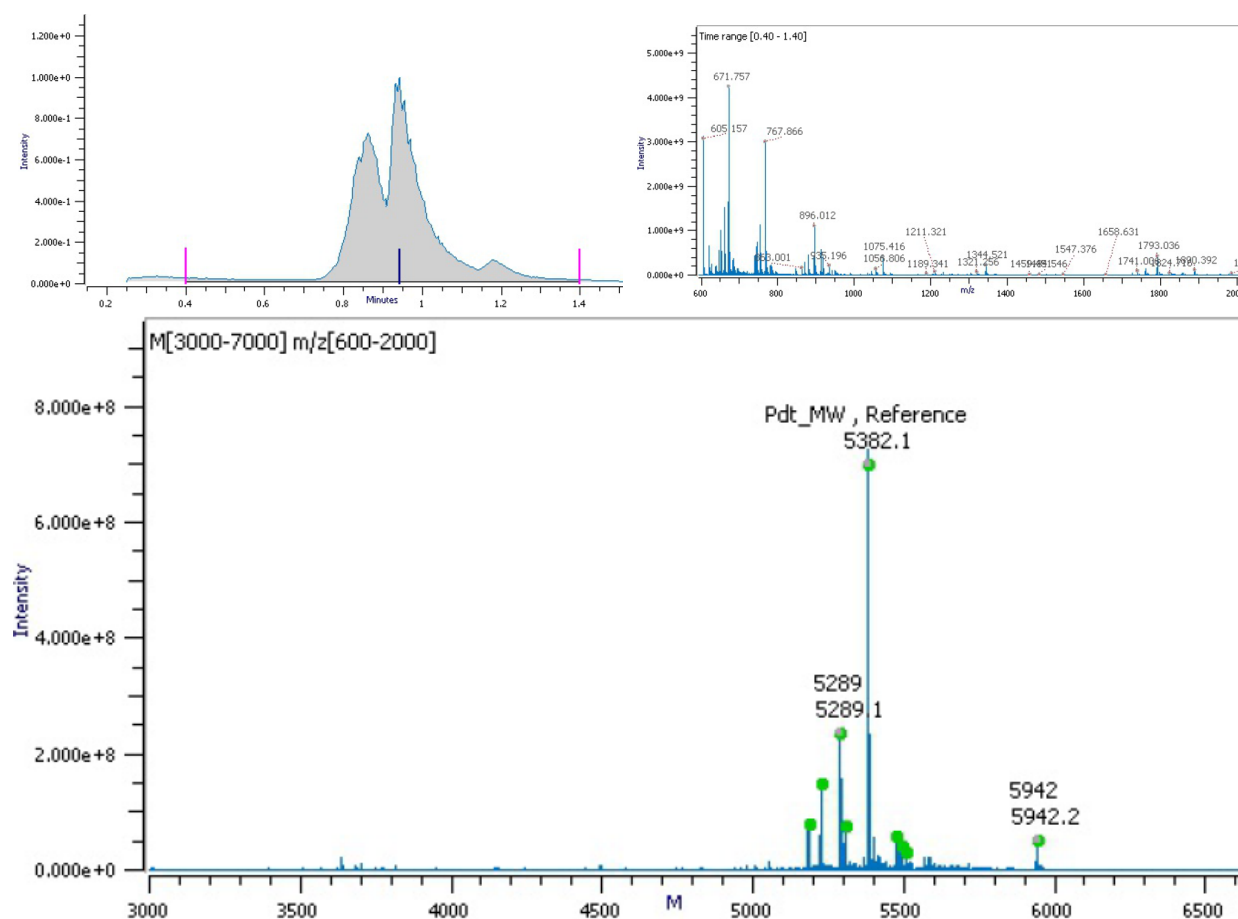
ELTM_544, TW-N78441-10-544.raw (Plot Elution Peak - Plot MS1 - Plot Deconvoluted Mass spectrum)



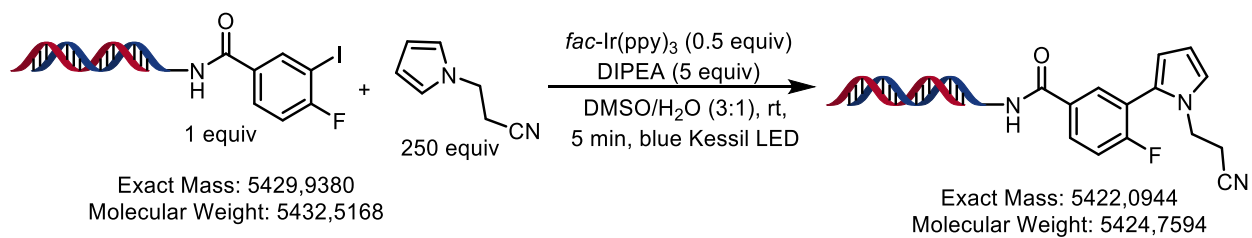
Product **6h**, 67% yield



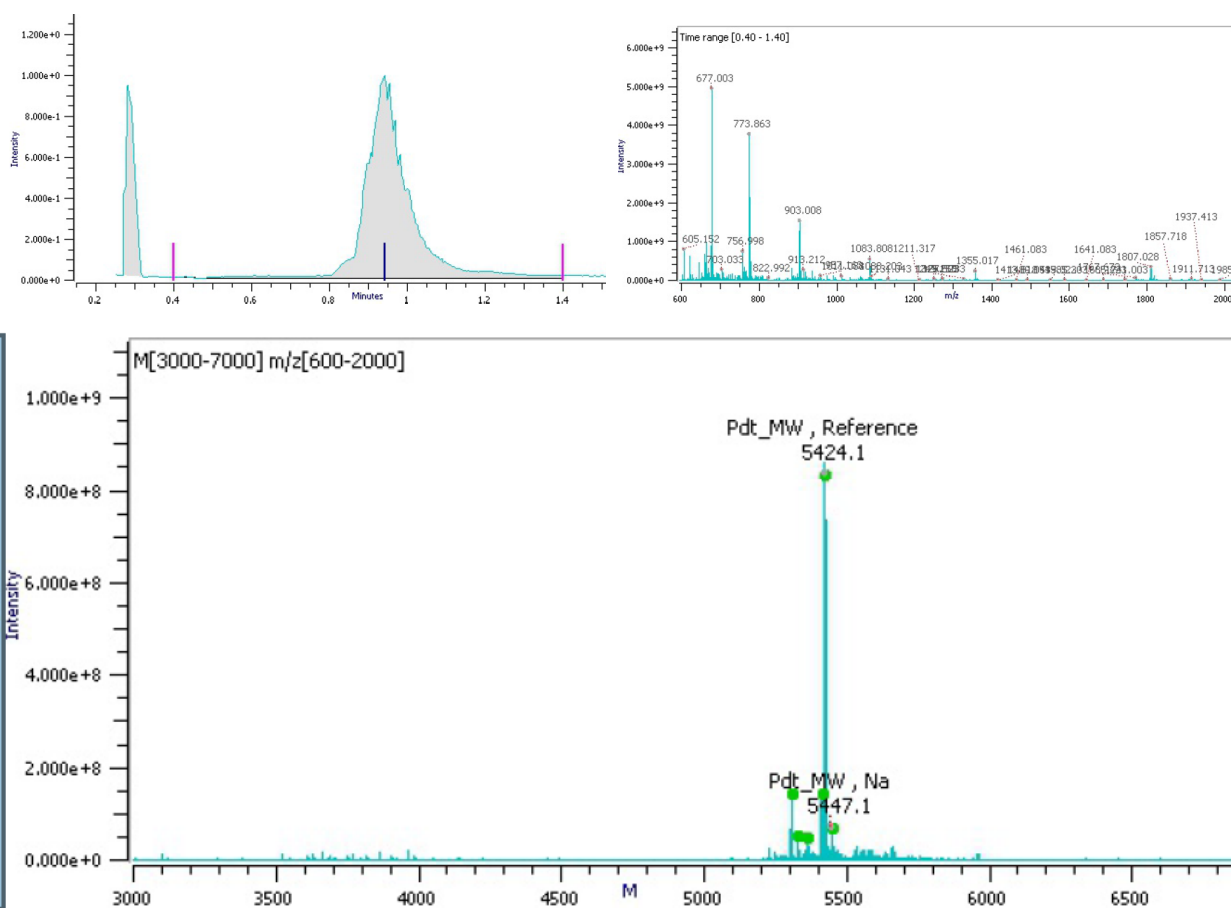
ELTM_481, TW-N78441-10-481.raw (Plot Elution Peak - Plot MS1 - Plot Deconvoluted Mass spectrum)



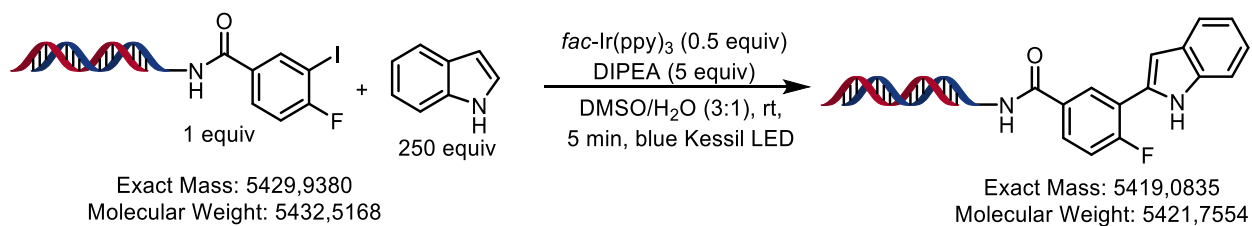
Product **4i**, 76% yield



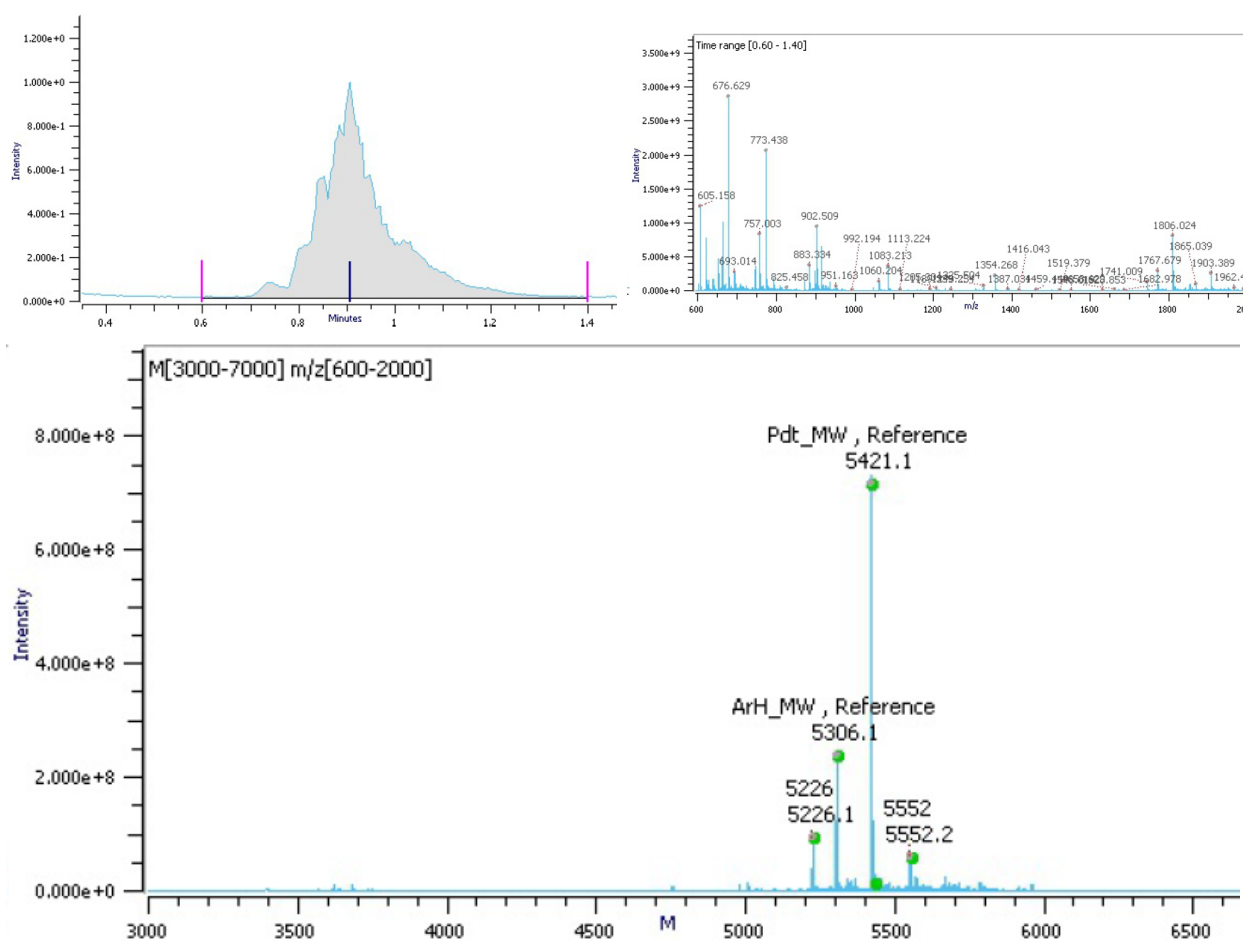
ELTM_648, TW-N78441-14-648.raw - (Plot Elution Peak - Plot MS1 - Plot Deconvoluted Mas spectrum)



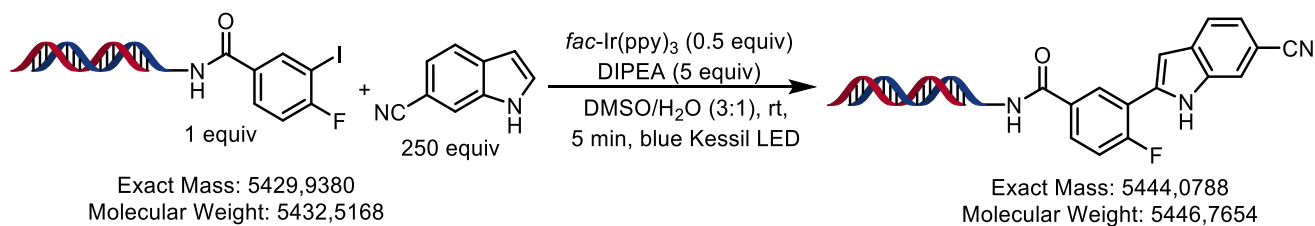
Product **4j**, 70% yield



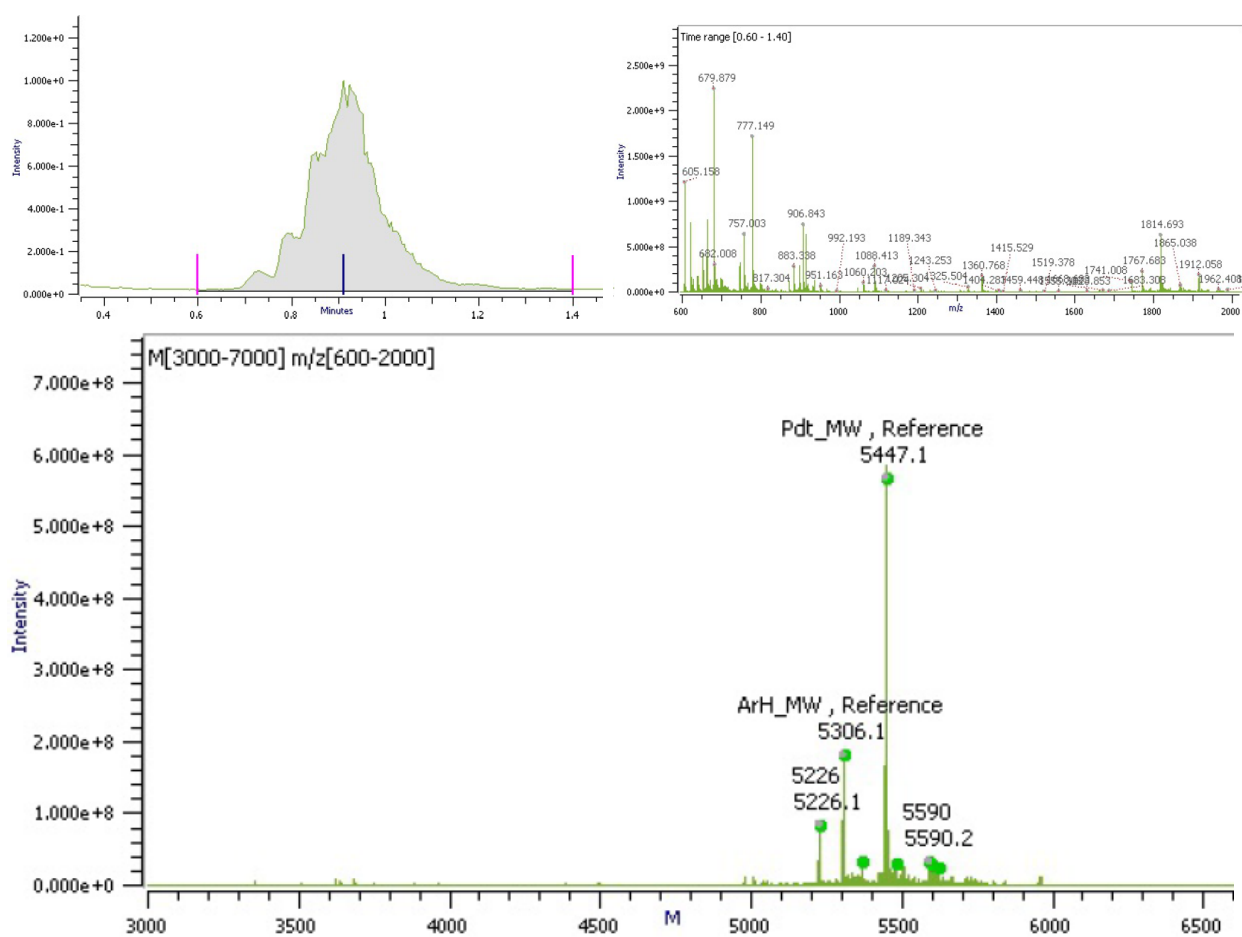
ELTM_179, TW-N78441-8-179.raw - (Plot Elution Peak - Plot MS1 - Plot Deconvoluted Mass spectrum)



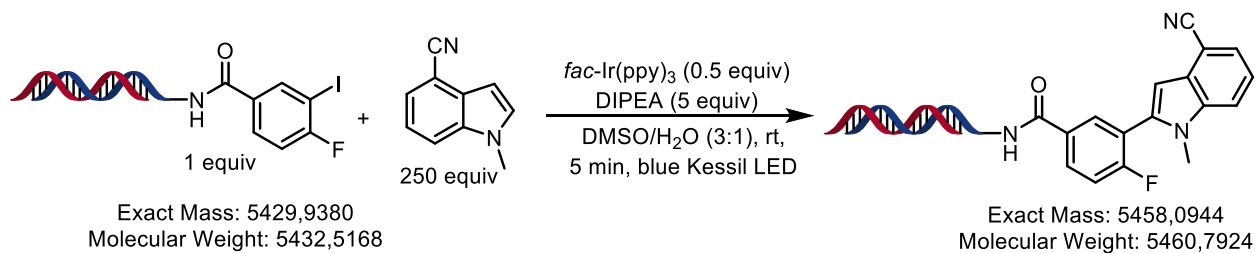
Product **4k**, 63% yield



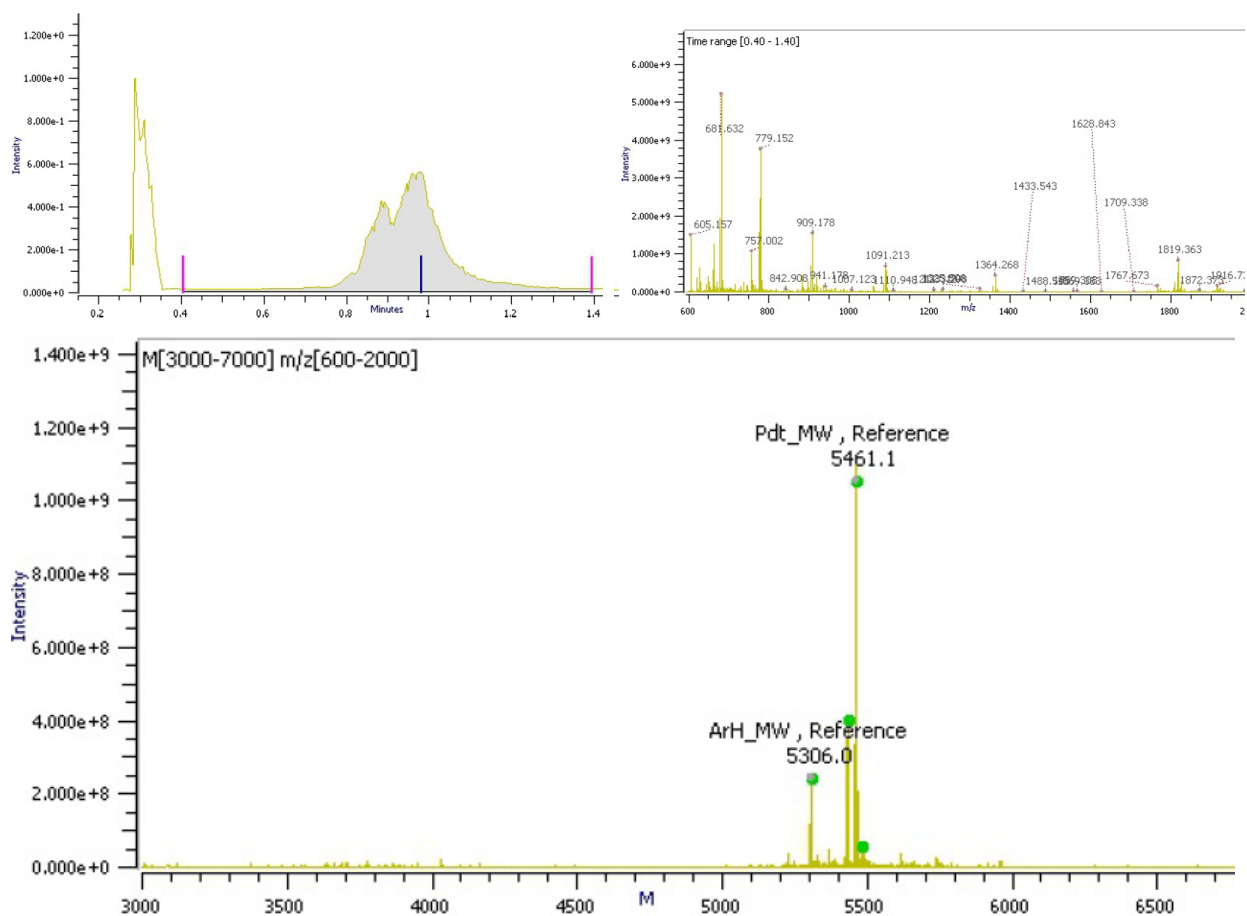
ELTM_176, TW-N78441-8-176.raw (Plot Elution Peak - Plot MS1 - Plot Deconvoluted Mass spectrum)



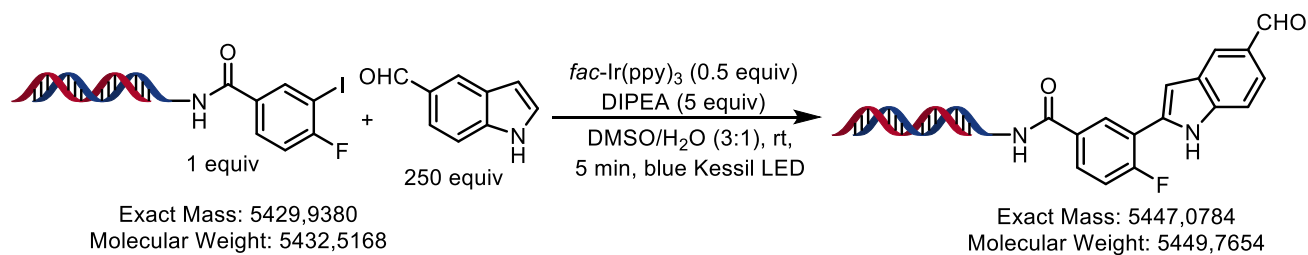
Product **4l**, 72% yield



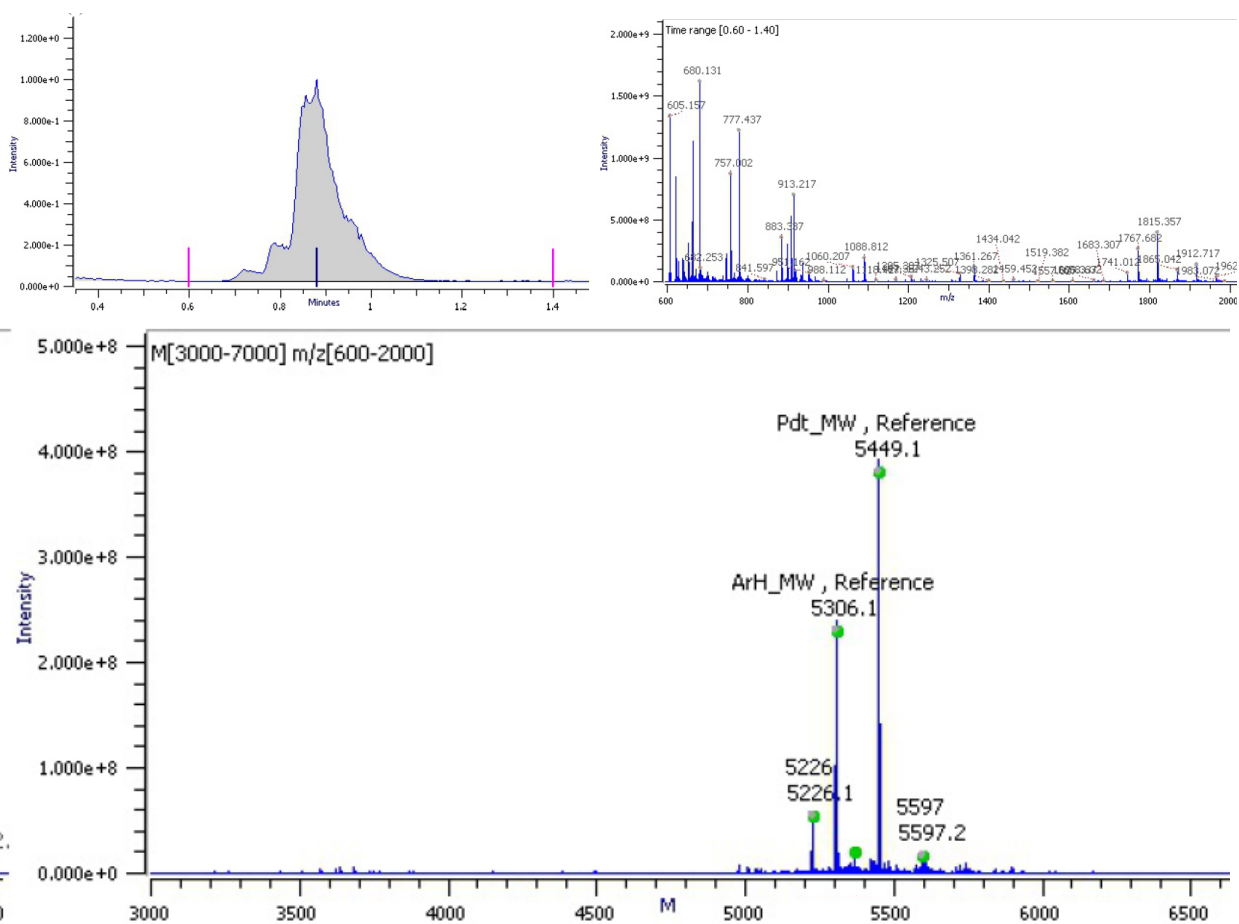
ELTM_660, TW-N78441-15-660.raw (Plot Elution Peak - Plot MS1 - Plot Deconvoluted Mass spectrum)



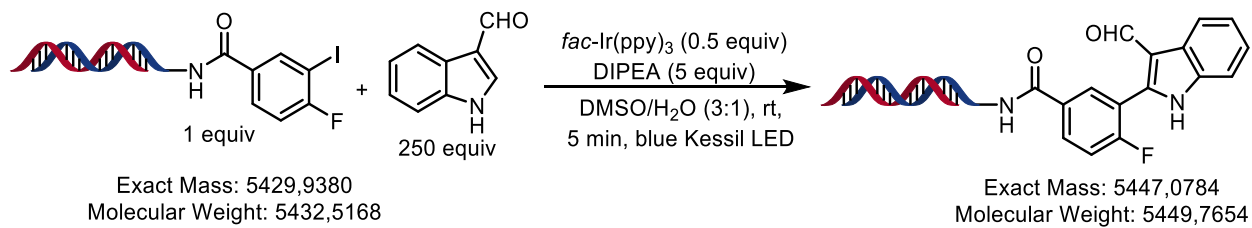
Product **4m**, 60% yield



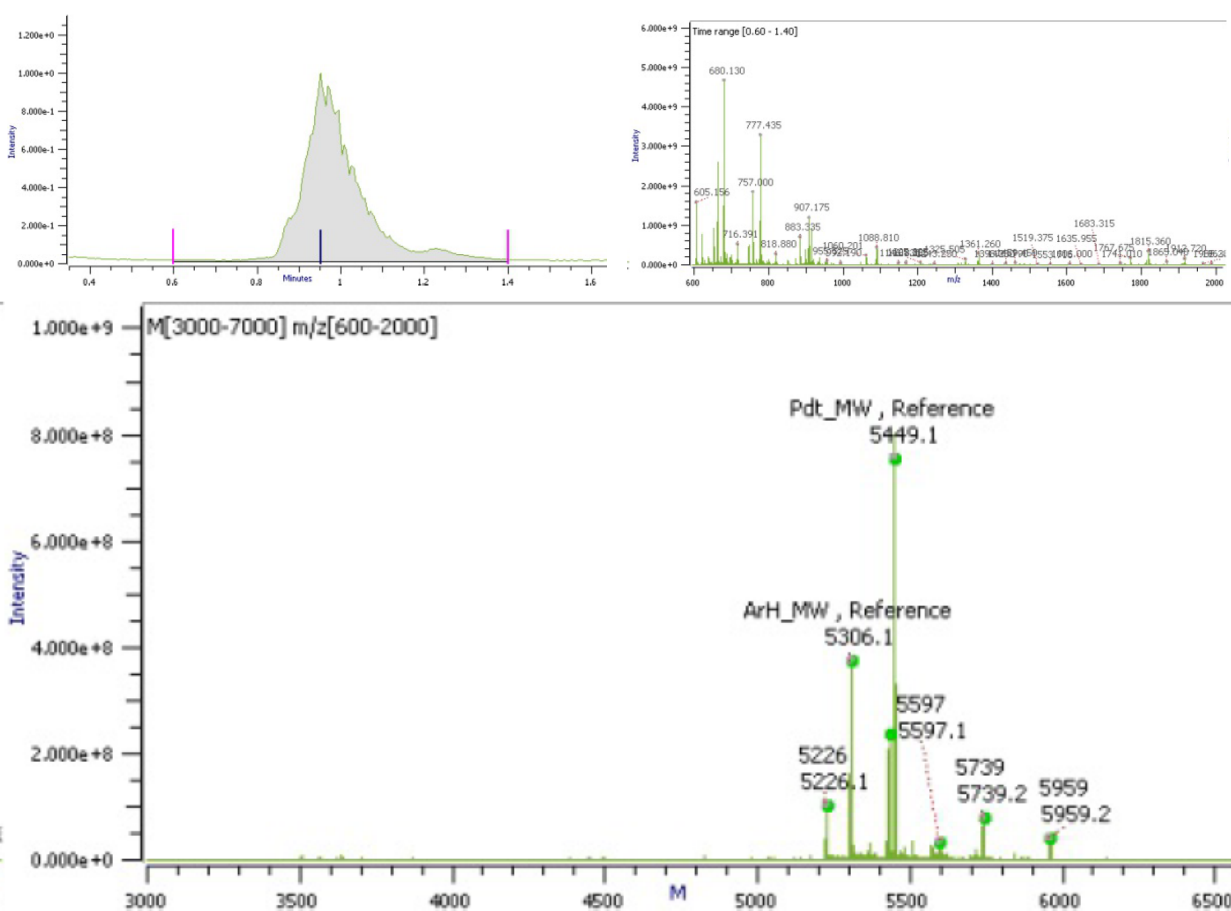
ELTM_180, TW-N78441-8-180.raw (Plot Elution Peak - Plot MS1 - Plot Deconvoluted Mass spectrum)



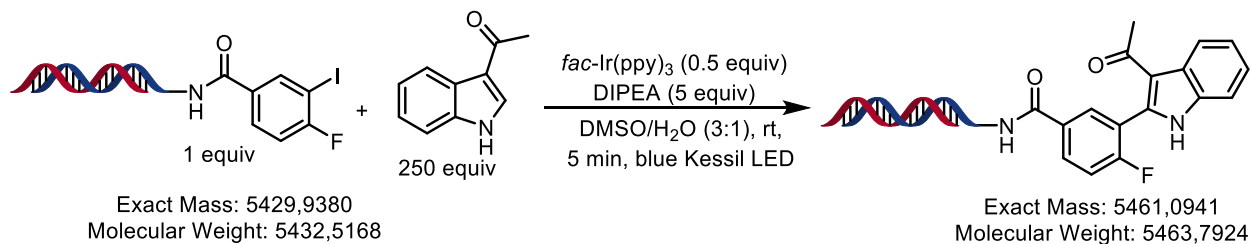
Product **4n**, 55% yield



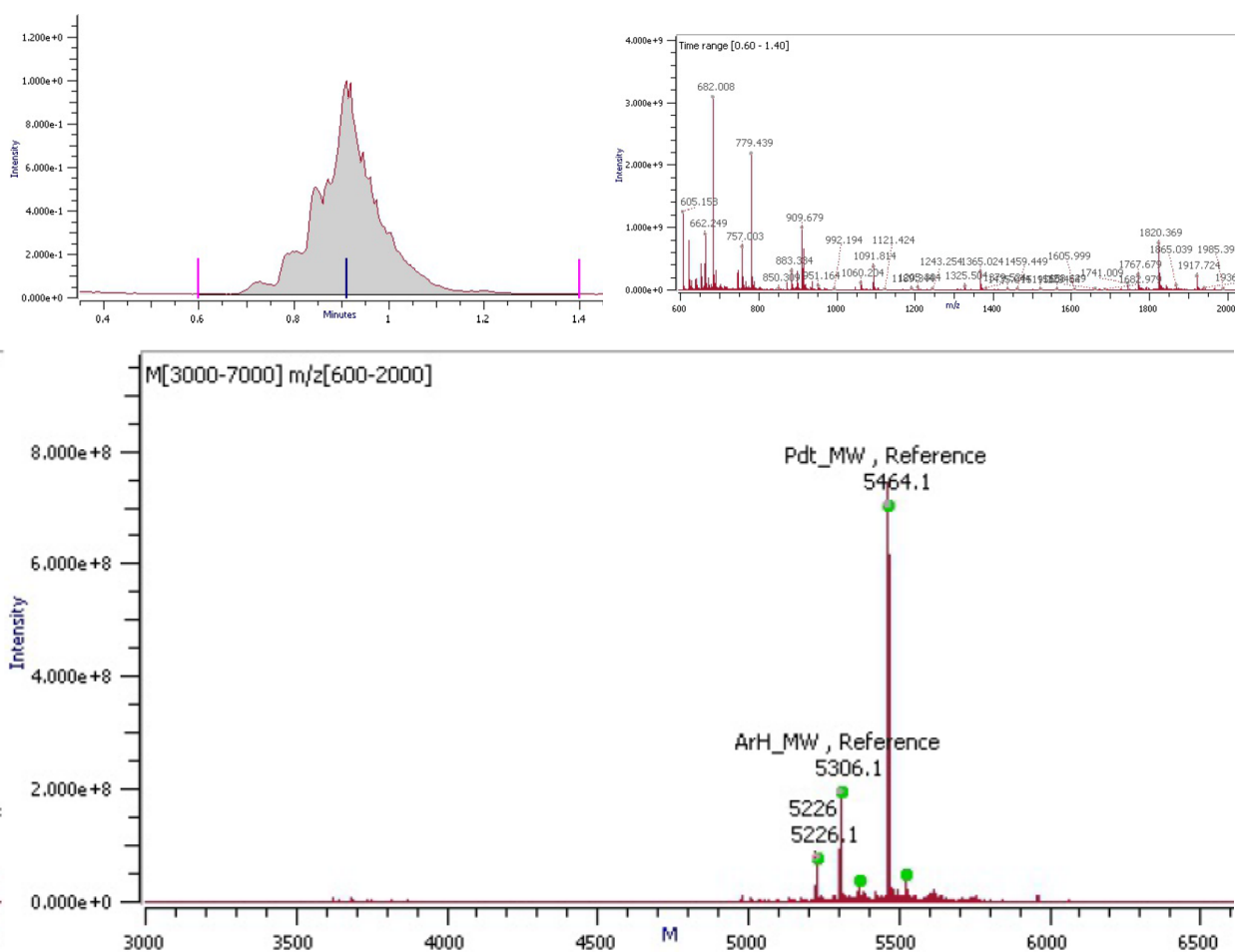
ELTM_346, TW-N78441-9-346.raw (Plot Elution Peak - Plot MS1 - Plot Deconvoluted Mass spectrum)



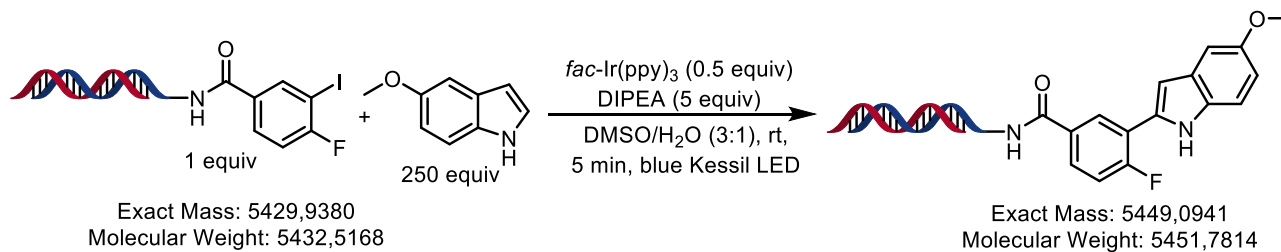
Product **4o**, 73% yield



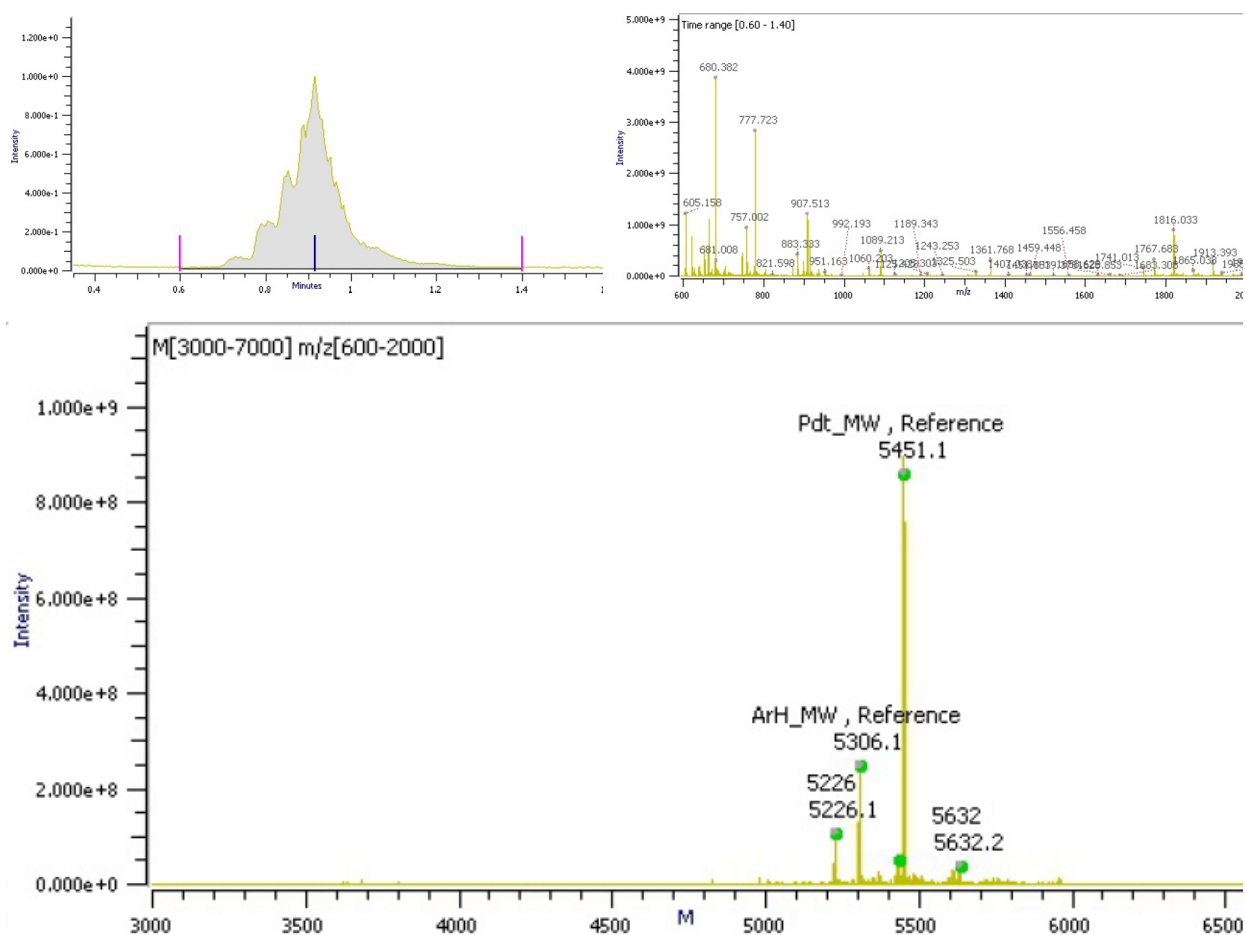
ELTM_181, TW-N78441-8-181.raw (Plot Elution Peak - Plot MS1 - Plot Deconvoluted Mass spectrum)



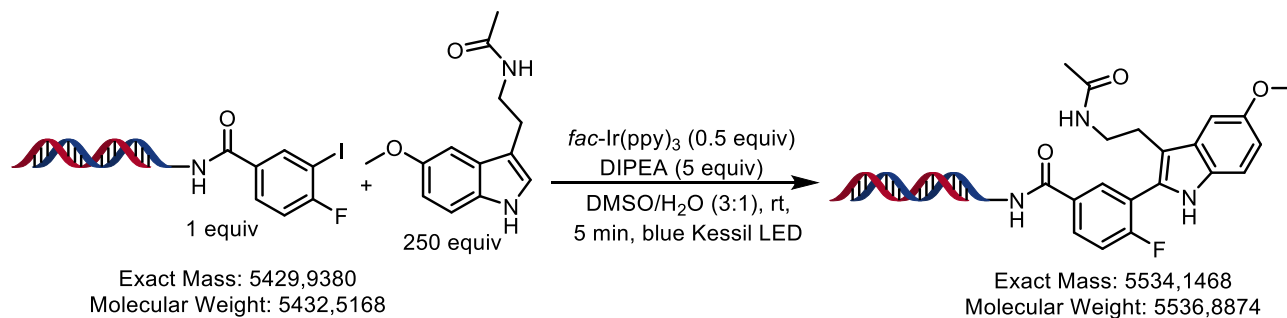
Product **4p**, 72% yield



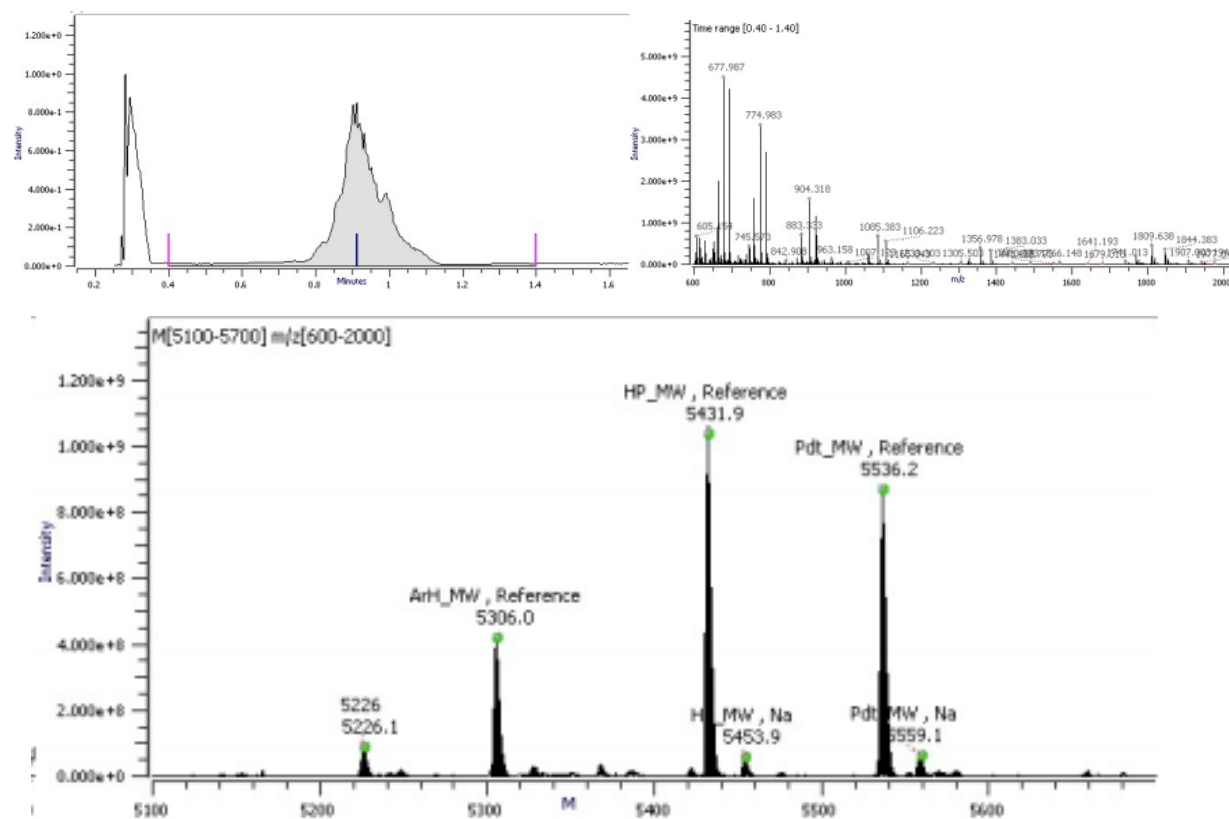
ELTM_182, TW-N78441-8-182.raw (Plot Elution Peak - Plot MS1 - Plot Deconvoluted Mass spectrum)



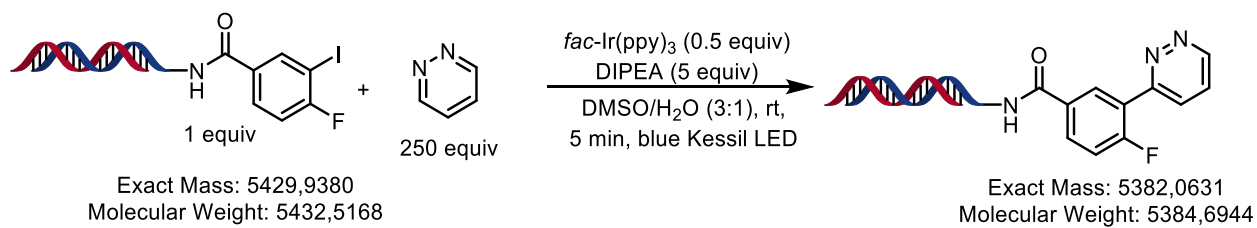
Product **4q**, 37% yield



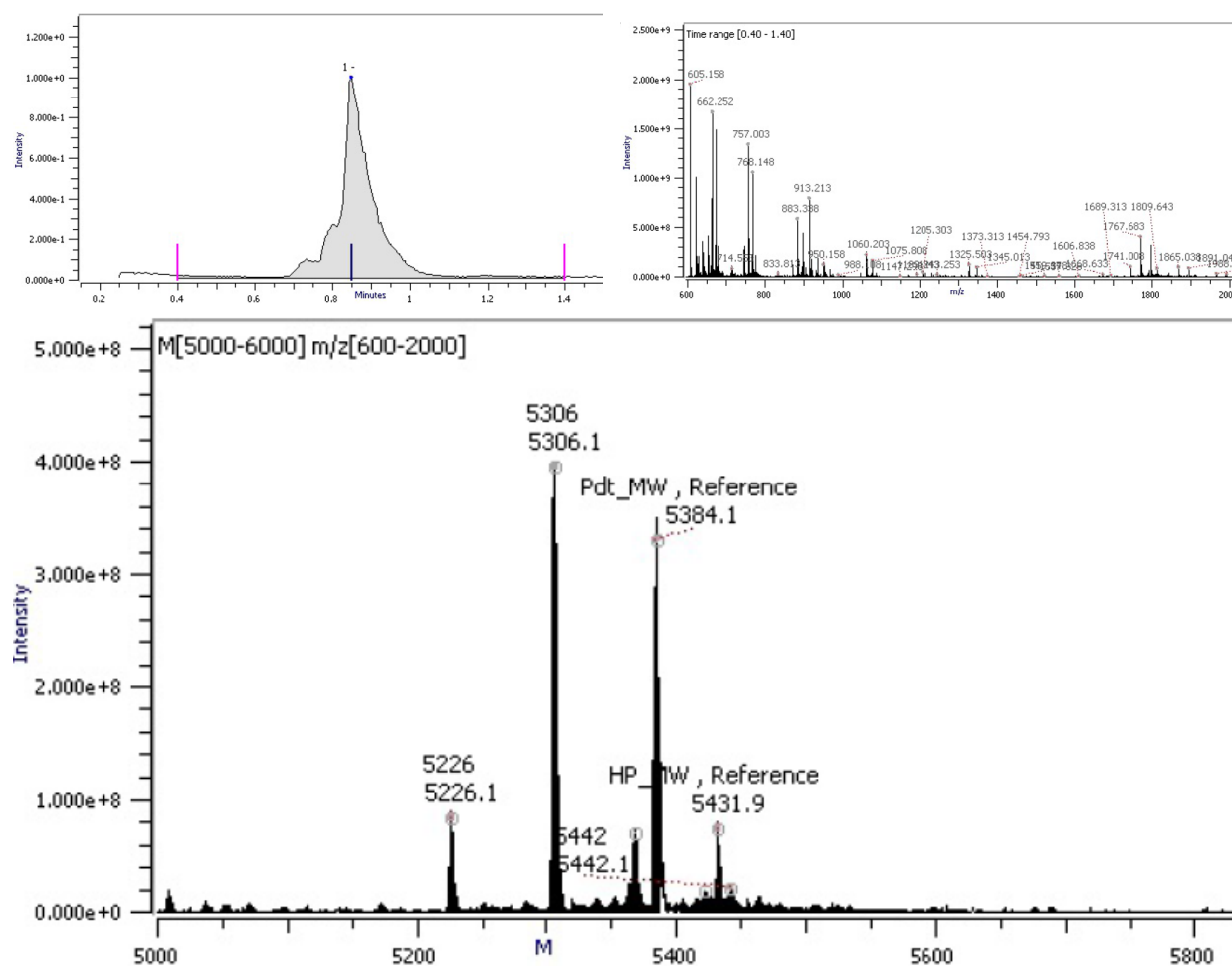
TW-N78441-15-651 - (Plot Elution Peak - Plot MS1 - Plot Deconvoluted Mass spectrum)



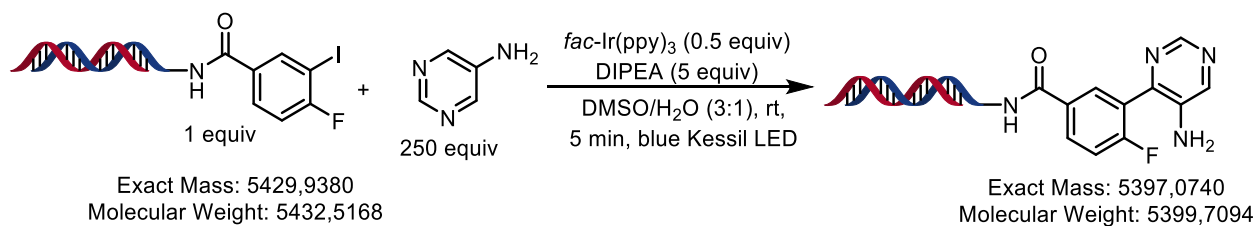
Product **4r**, 37% yield



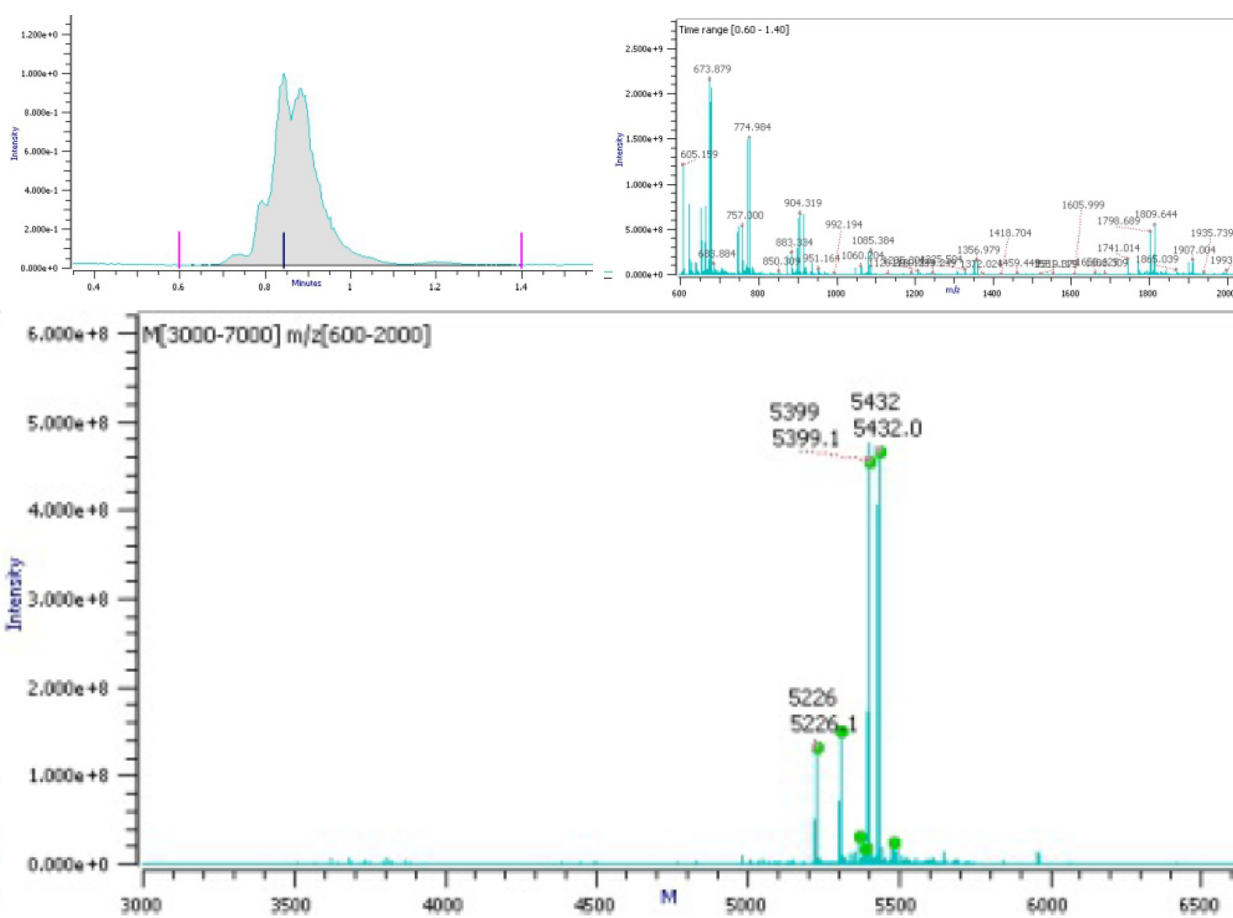
ELTM_146, TW-N78441-8-146.raw (Plot Elution Peak - Plot MS1 - Plot Deconvoluted Mass spectrum)



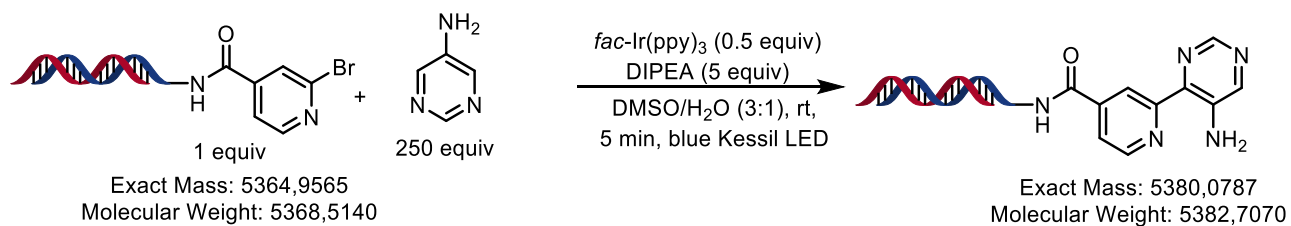
Product **4s**, 40% yield



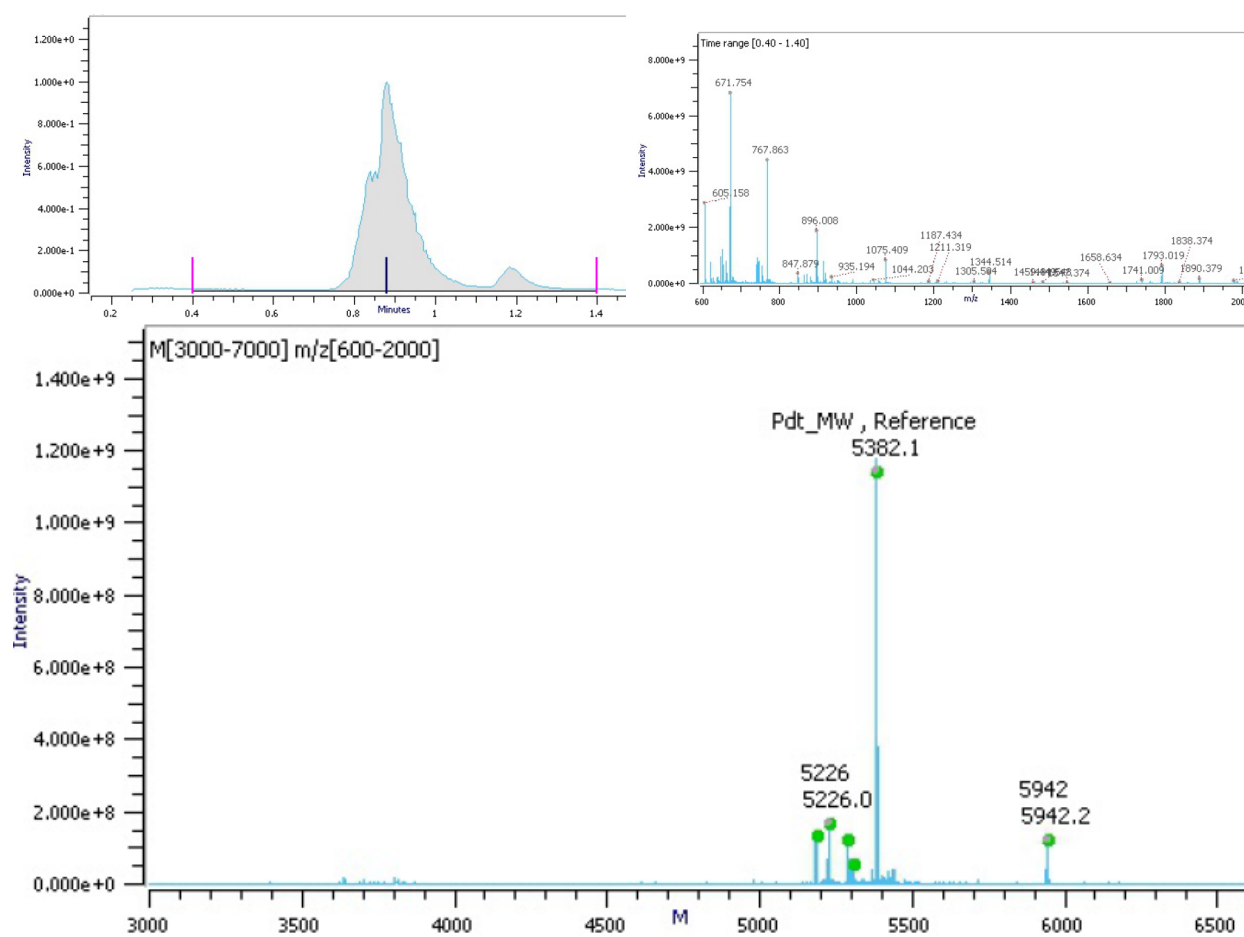
ELTM_225, TW-N78441-8-225.raw (Plot Elution Peak - Plot MS1 - Plot Deconvoluted Mass spectrum)



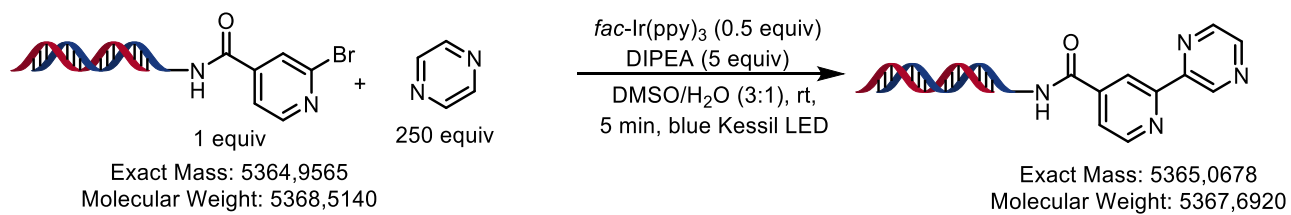
Product **6s**, 89% yield



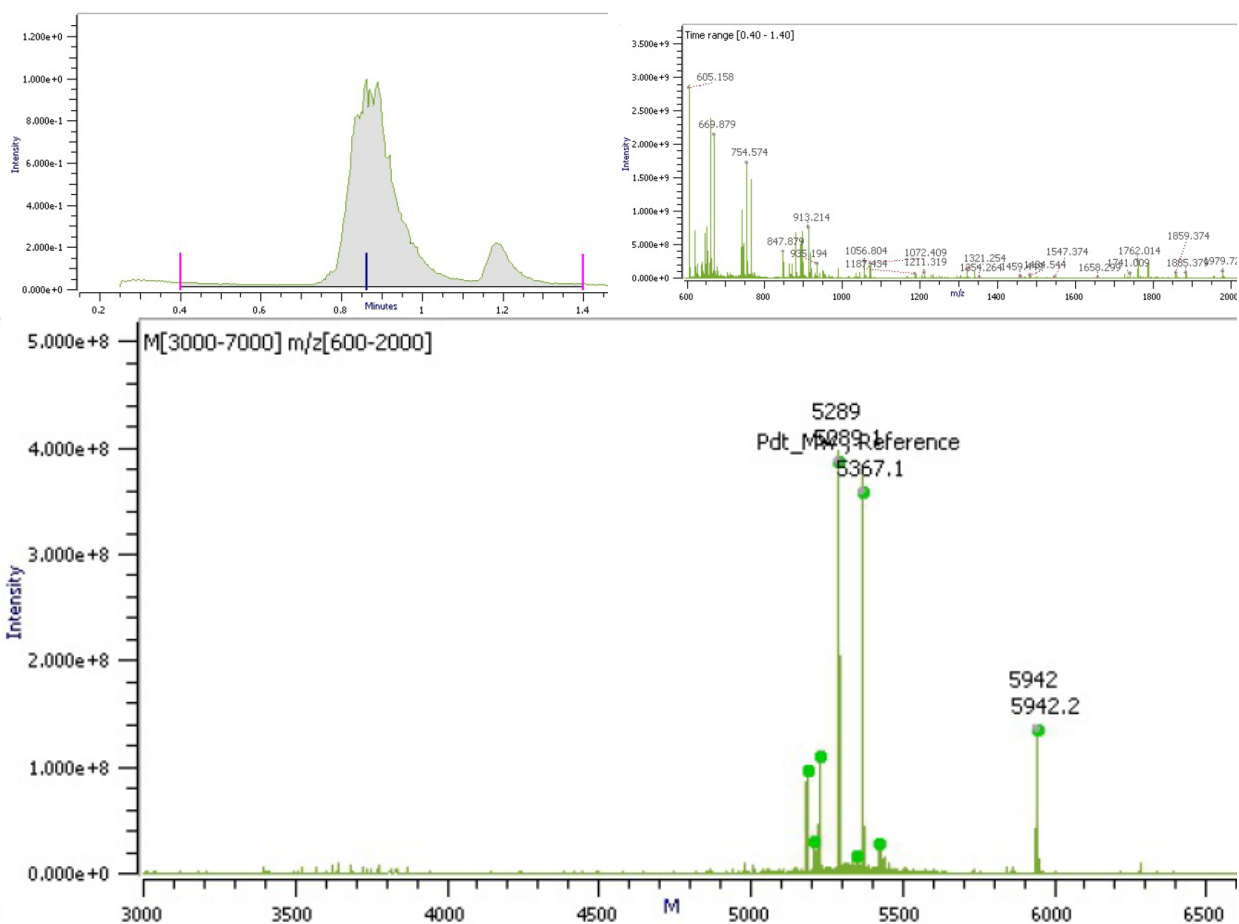
ELTM_447, TW-N78441-10-447.raw (Plot Elution Peak - Plot MS1 - Plot Deconvoluted Mass spectrum)



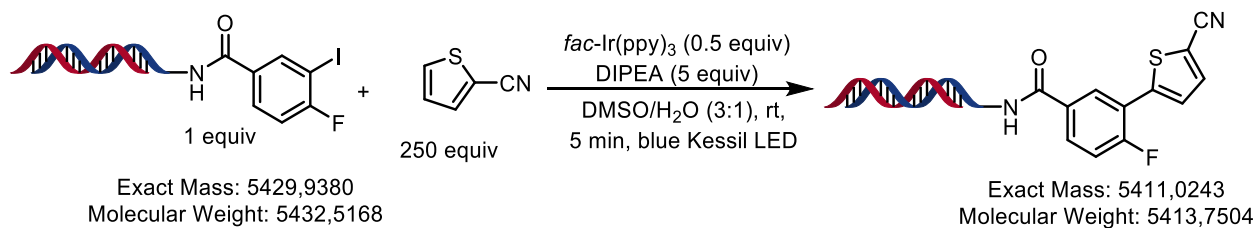
Product **6t**, 42% yield



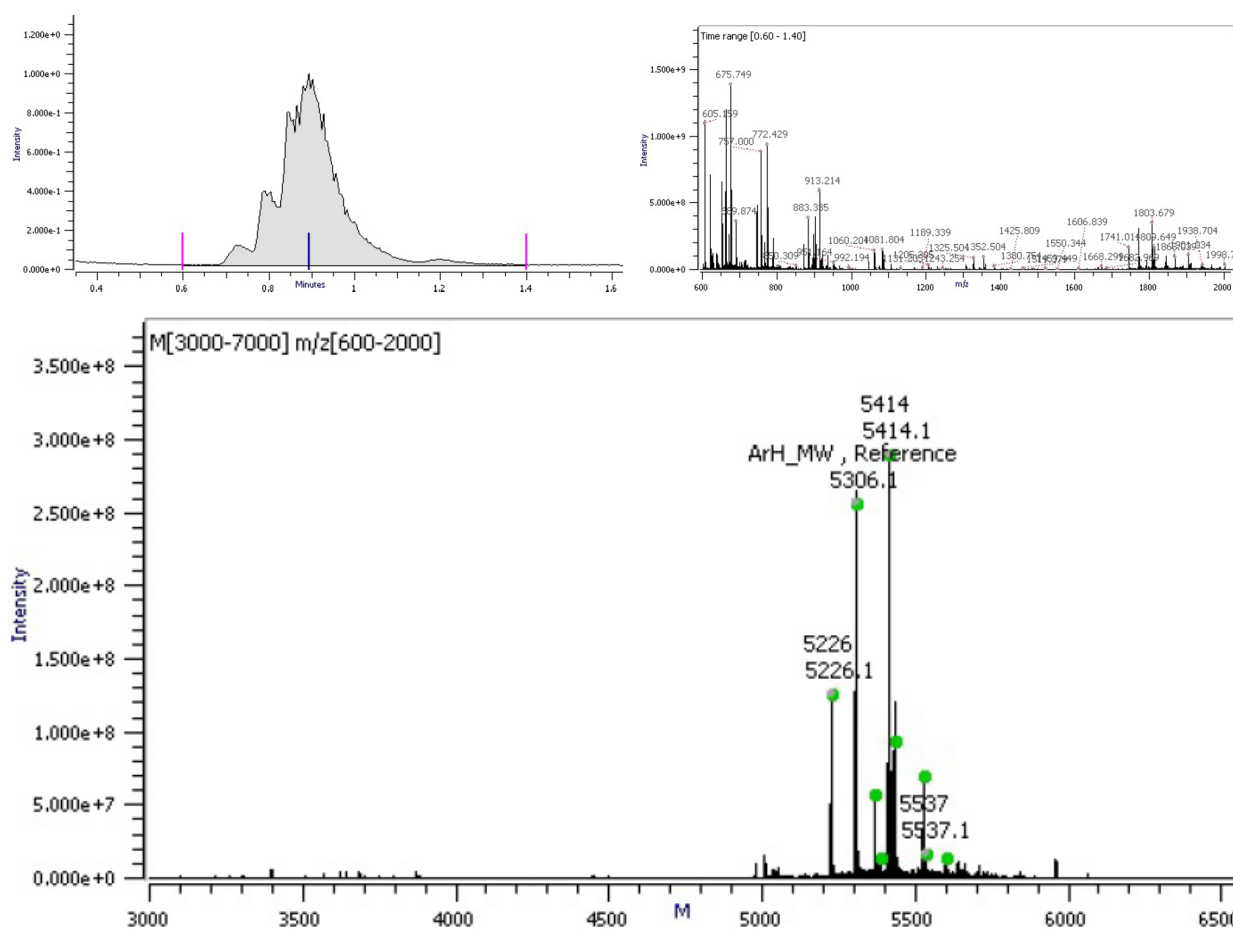
ELTM_446, TW-N78441-10-446.raw (Plot Elution Peak - Plot MS1 - Plot Deconvoluted Mass spectrum)



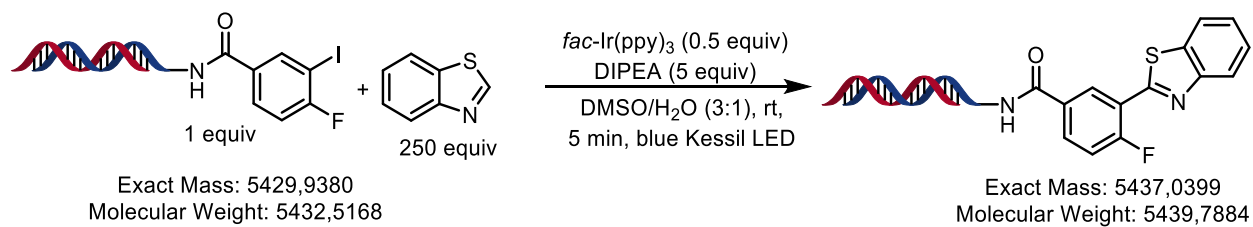
Product **4u**, 34% yield



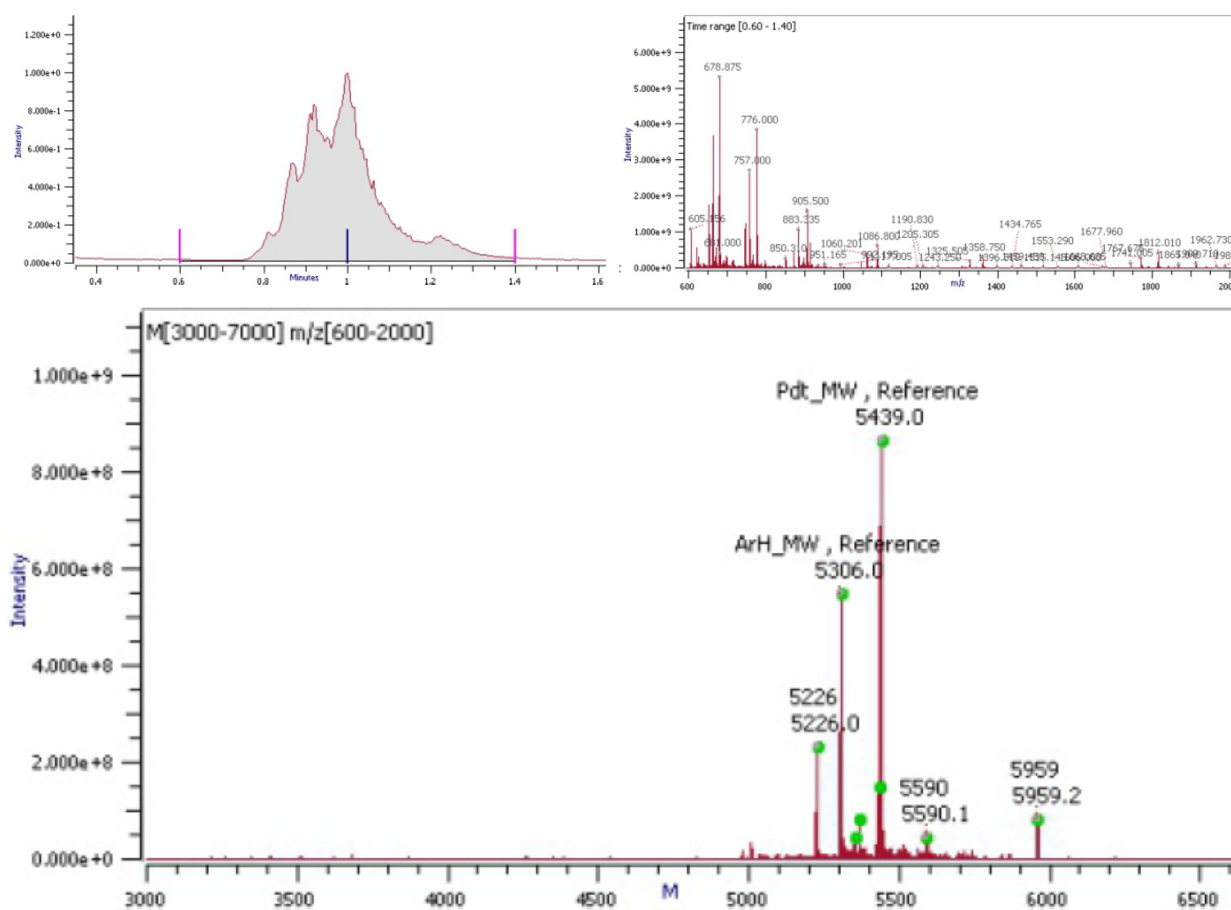
ELTM_223, TW-N78441-8-223.raw (Plot Elution Peak - Plot MS1 - Plot Deconvoluted Mass spectrum)



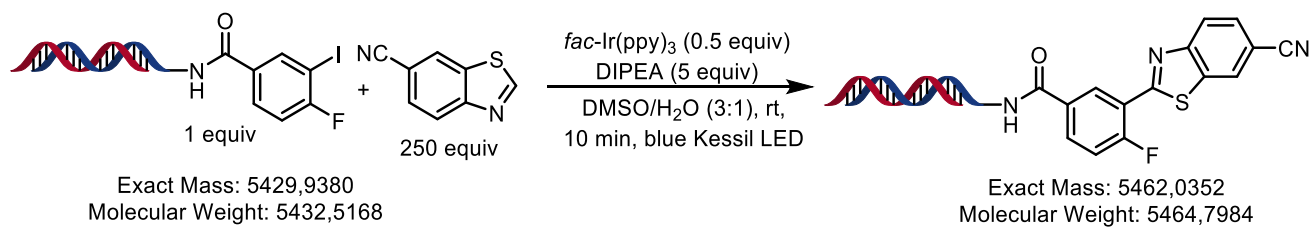
Product **4v**, 50% yield



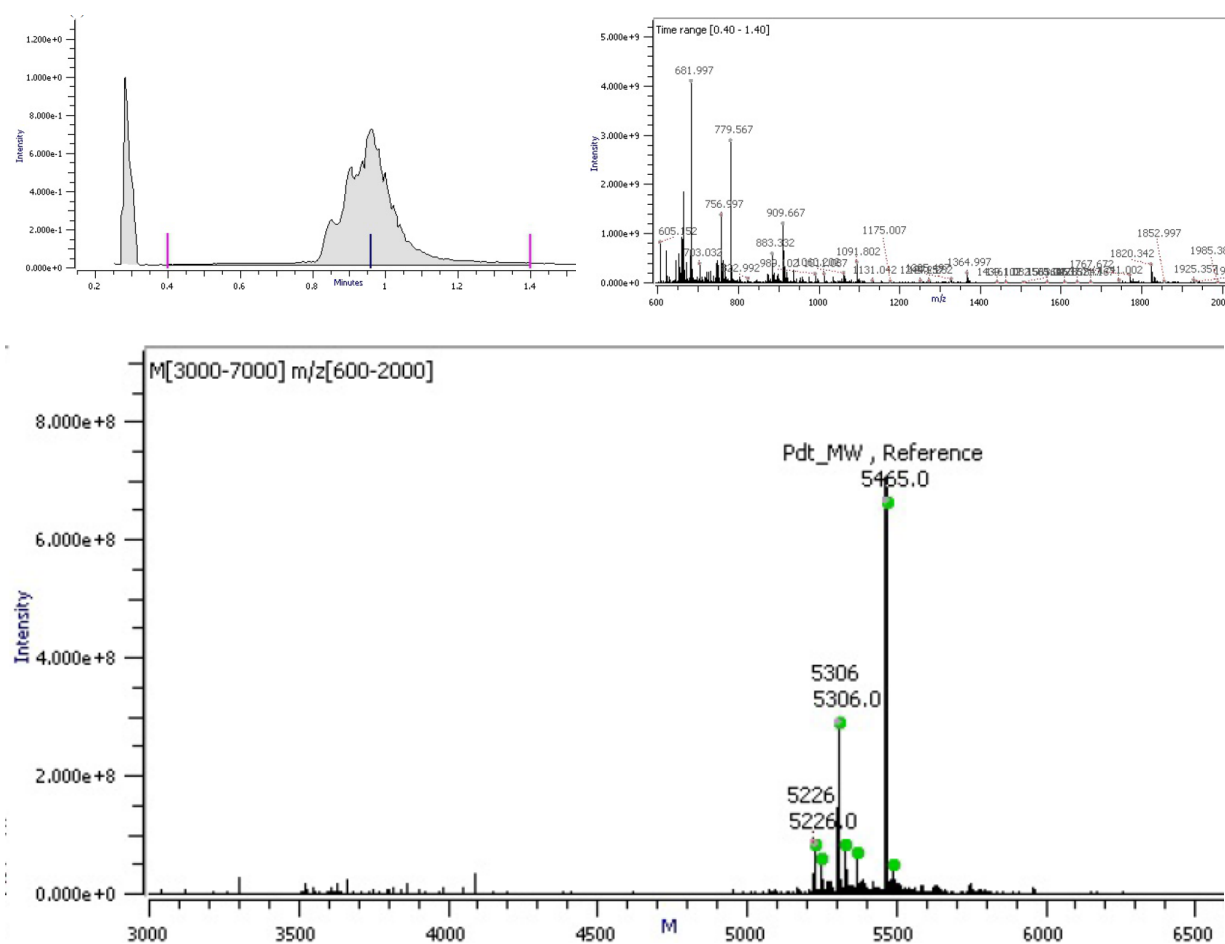
ELTM_390, TW-N78441-9-390.raw (Plot Elution Peak - Plot MS1 - Plot Deconvoluted Mass spectrum)



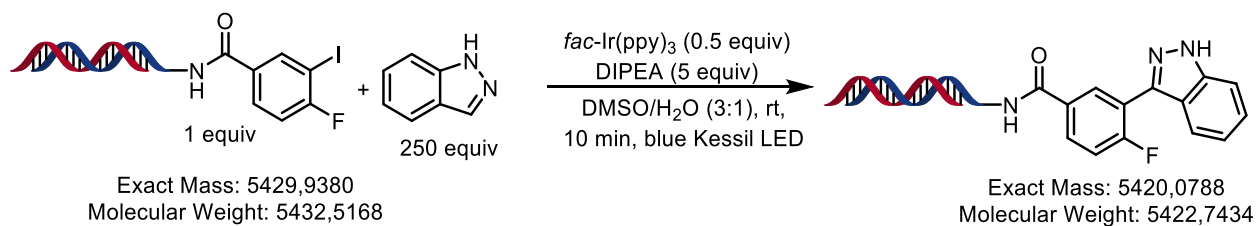
Product **4w**, 61% yield



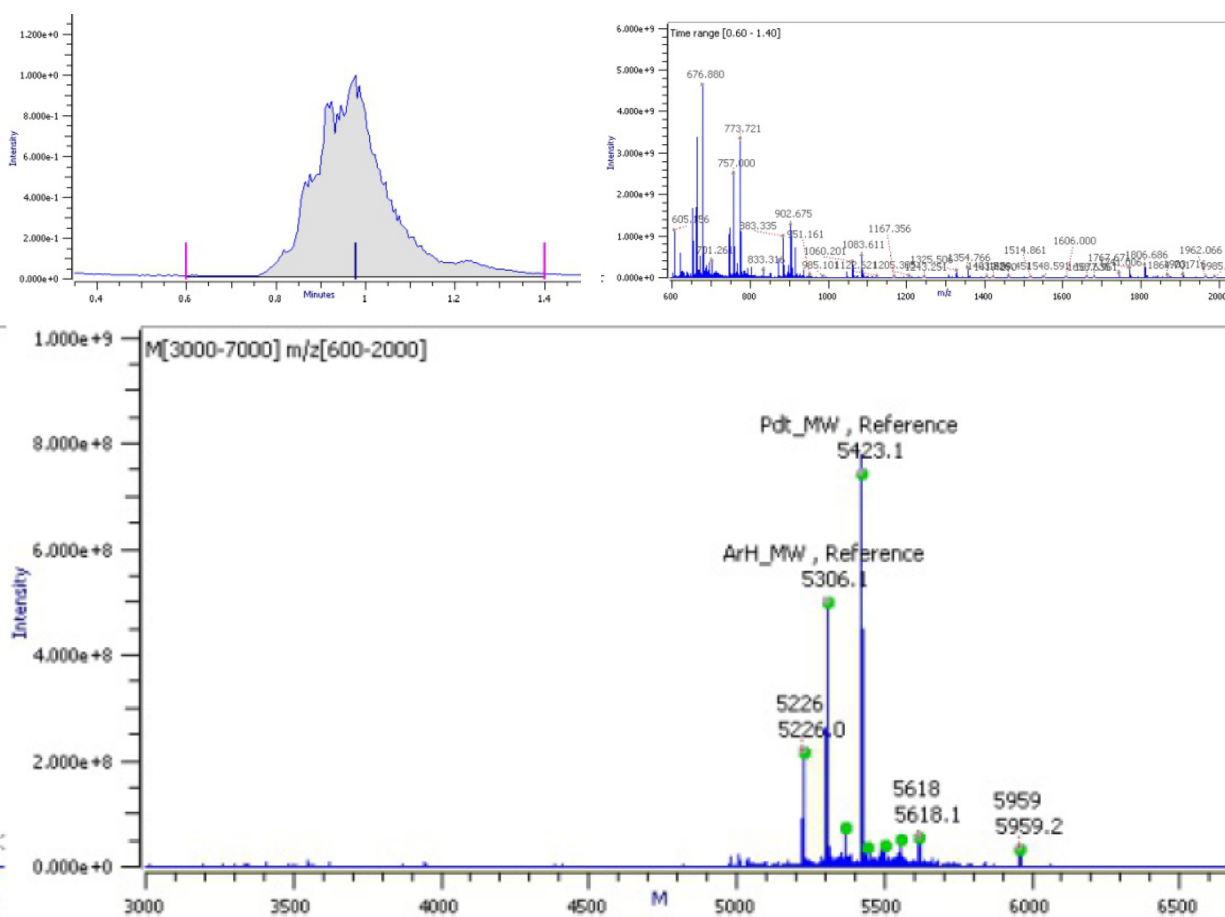
ELTM_636, TW-N78441-14-636.raw (Plot Elution Peak - Plot MS1 - Plot Deconvoluted Mass spectrum)



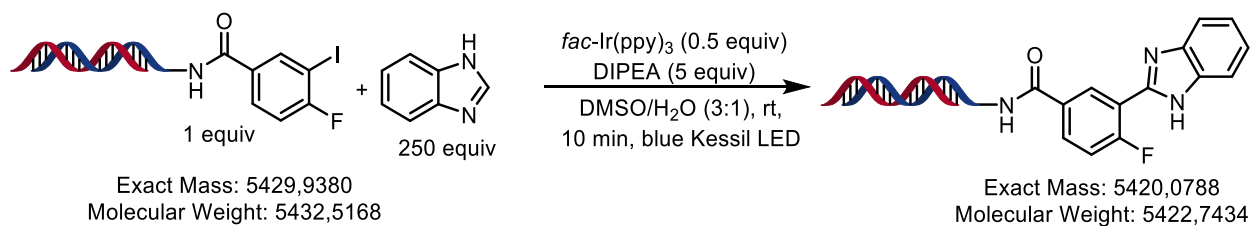
Product **4x**, 51% yield



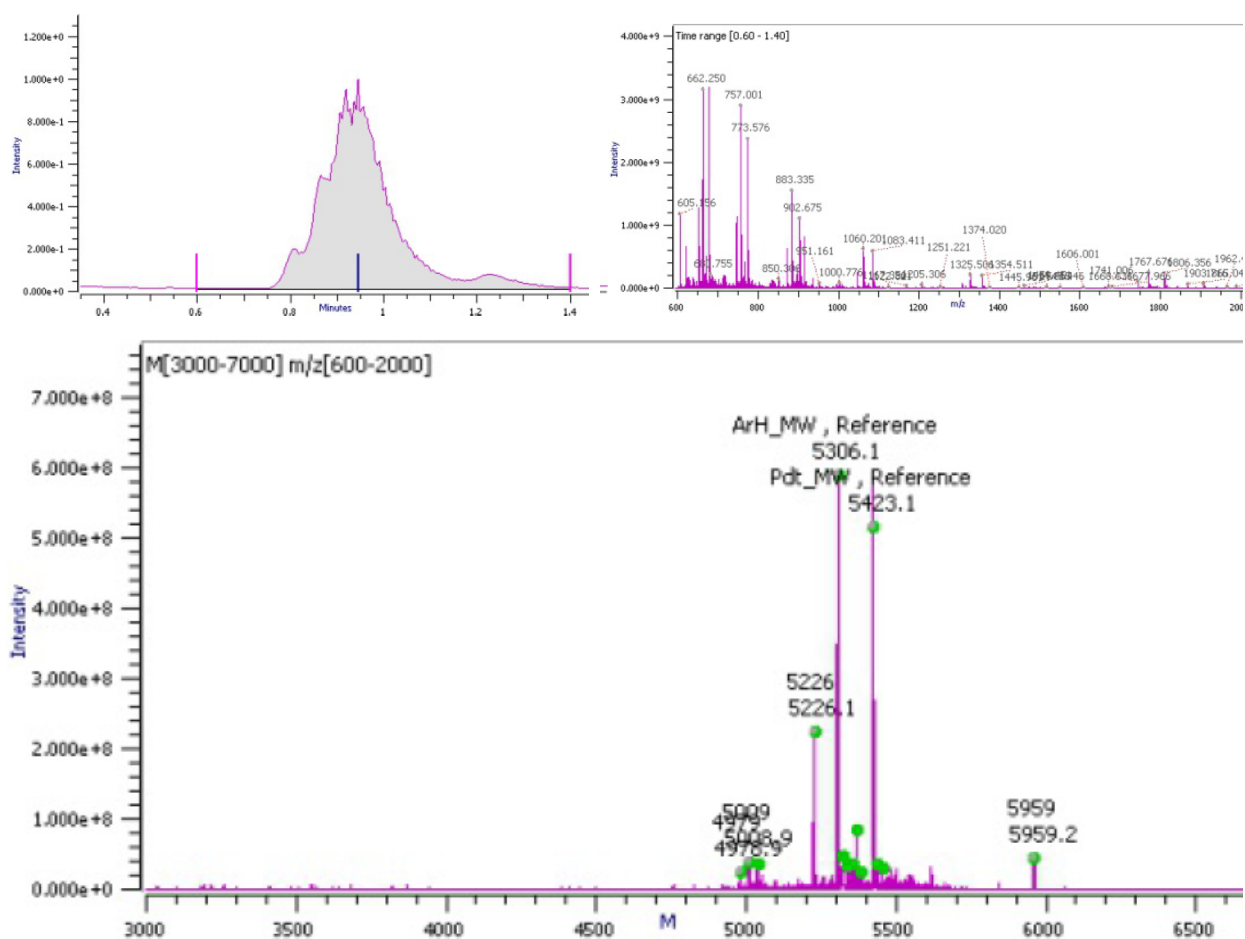
ELTM_355, TW-N78441-9-355.raw (Plot Elution Peak - Plot MS1 - Plot Deconvoluted Mass spectrum)



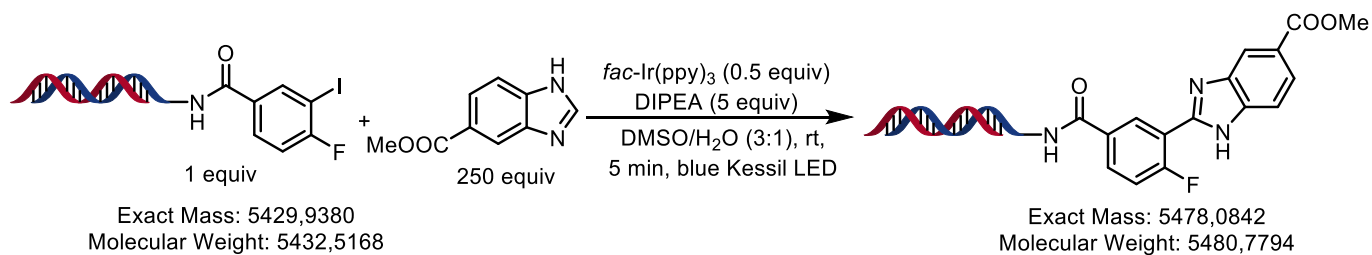
Product **4y**, 35% yield



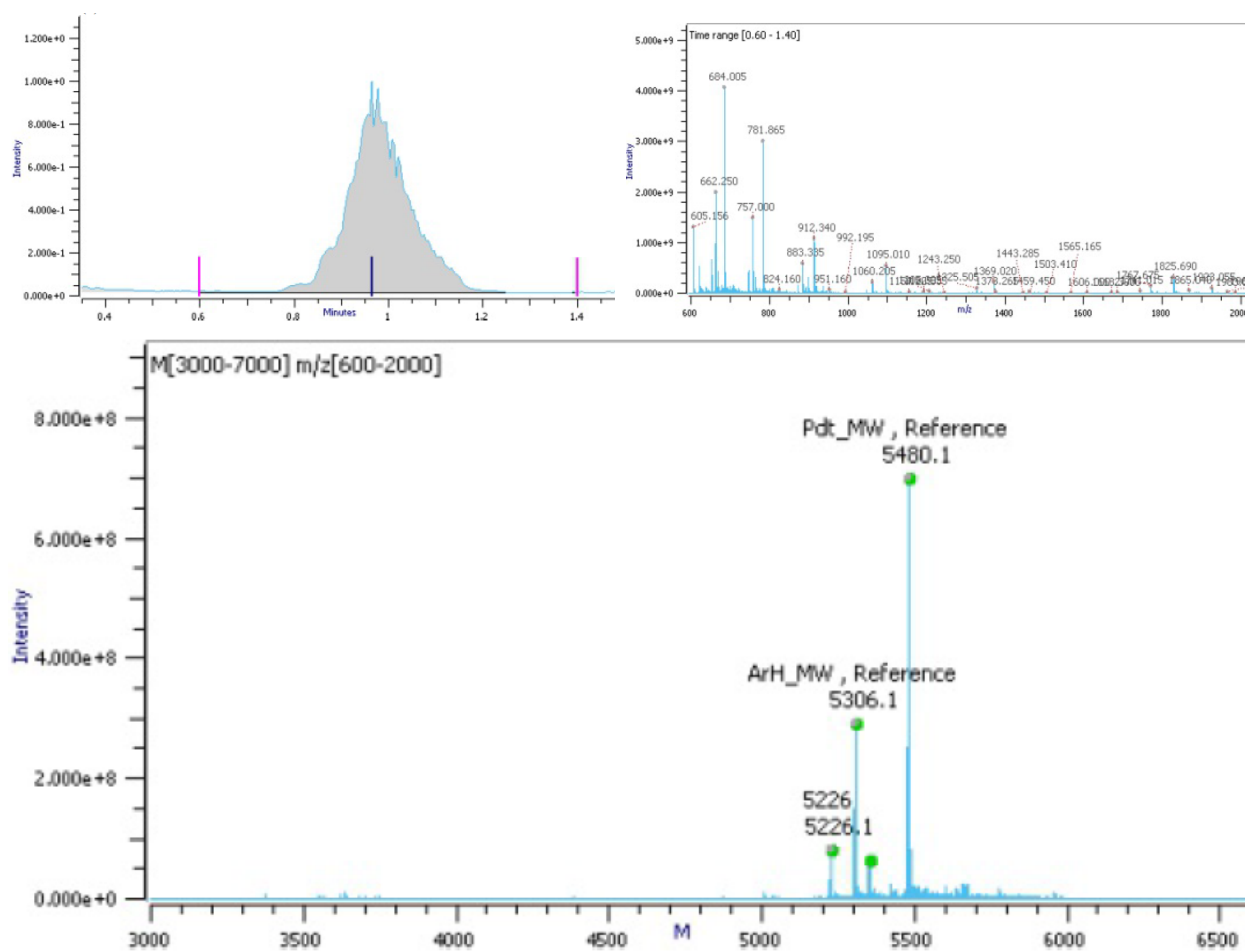
ELTM_364, TW-N78441-9-364.raw (Plot Elution Peak - Plot MS1 - Plot Deconvoluted Mass spectrum)



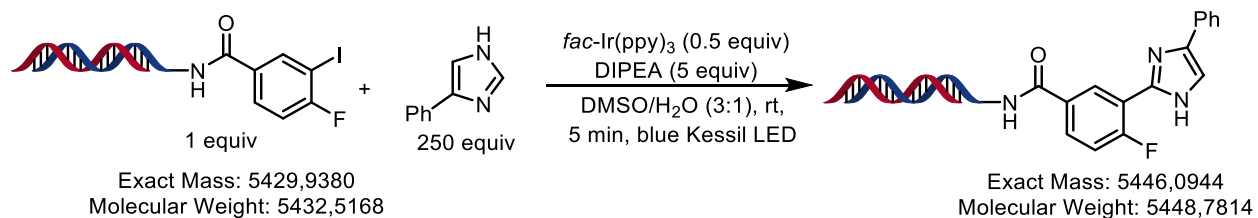
Product **4z**, 73% yield



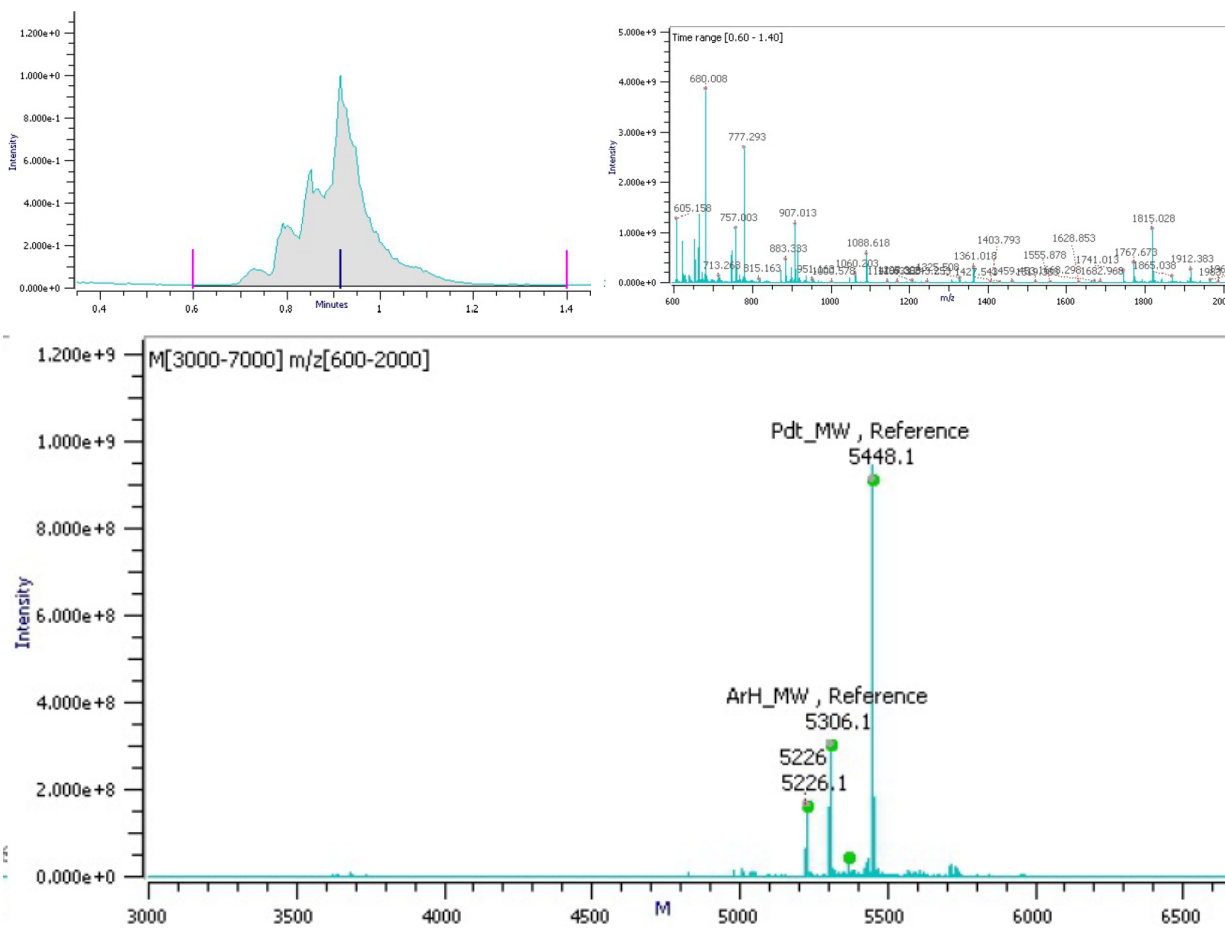
ELTM_349, TW-N78441-9-349.raw (Plot Elution Peak - Plot MS1 - Plot Deconvoluted Mass spectrum)



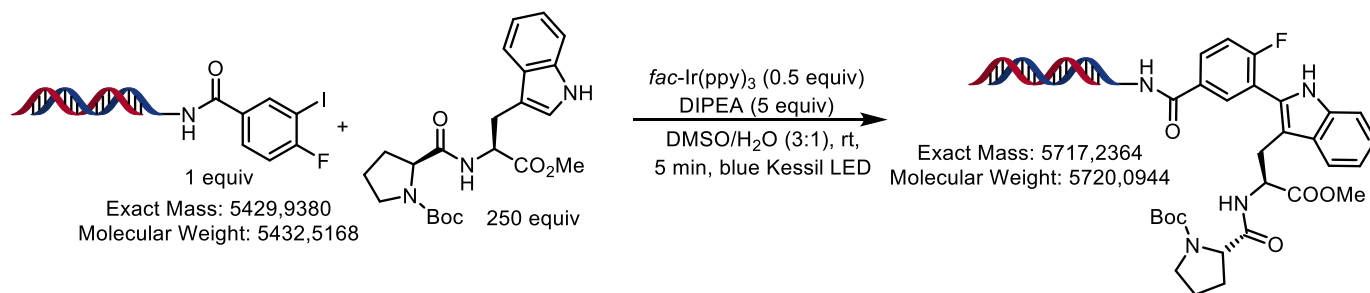
Product **4aa**, 70% yield



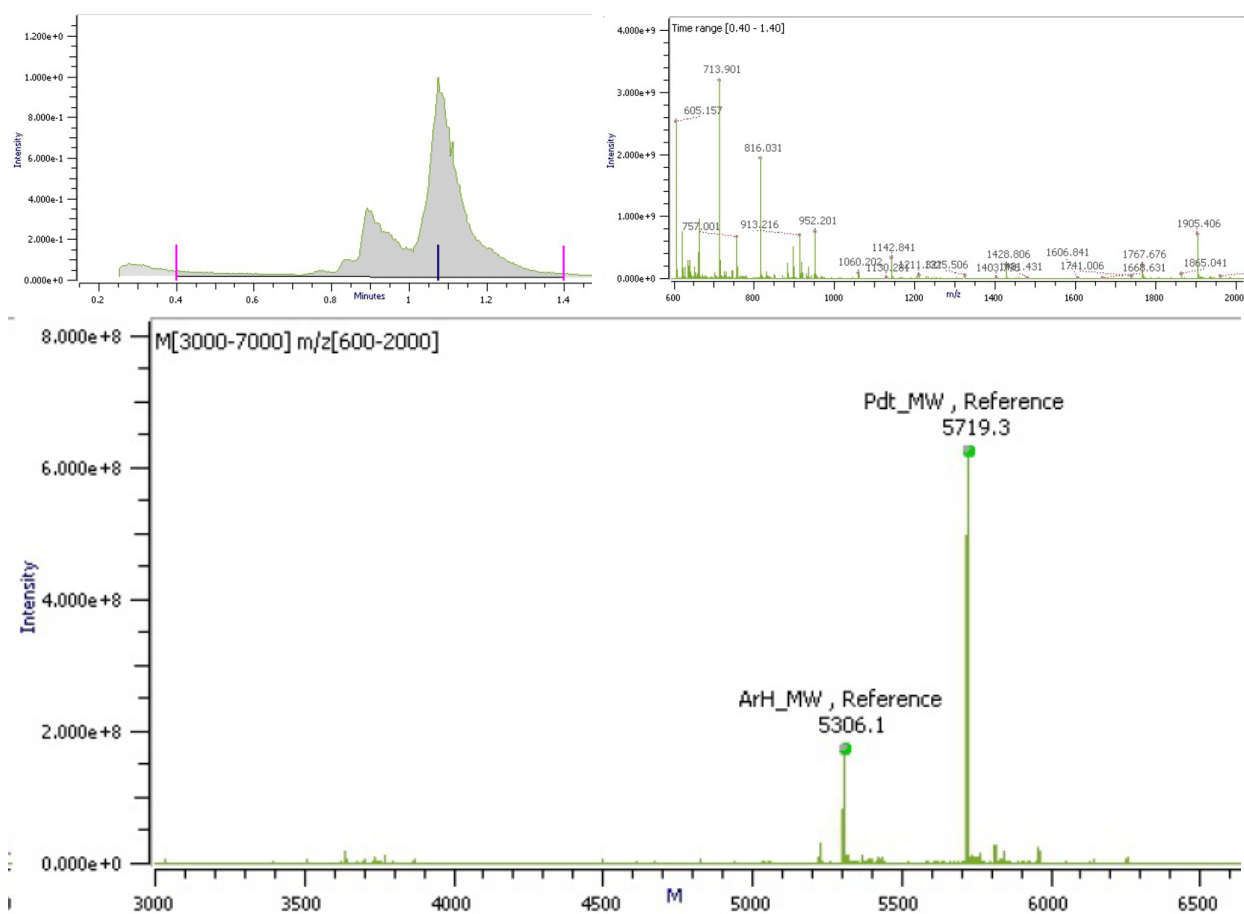
ELTM_222, TW-N78441-8-222.raw (Plot Elution Peak - Plot MS1 - Plot Deconvoluted Mass spectrum)



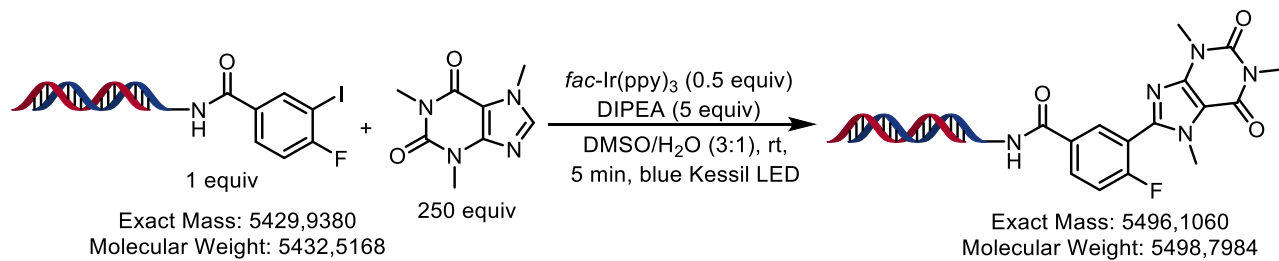
Product **4ab**, 93% yield



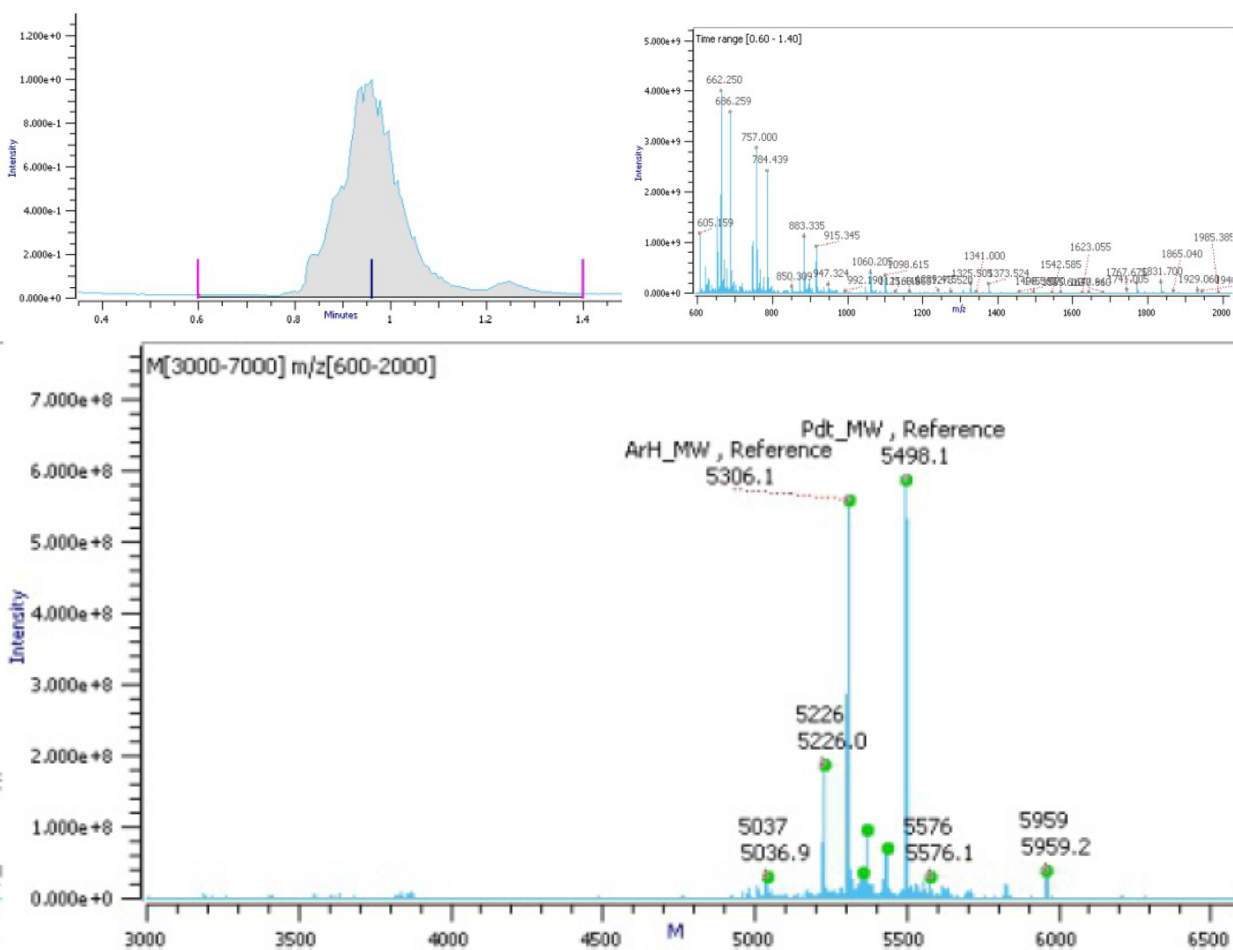
ELTM_433, TW-N78441-10-433.raw (Plot Elution Peak - Plot MS1 - Plot Deconvoluted Mass spectrum)



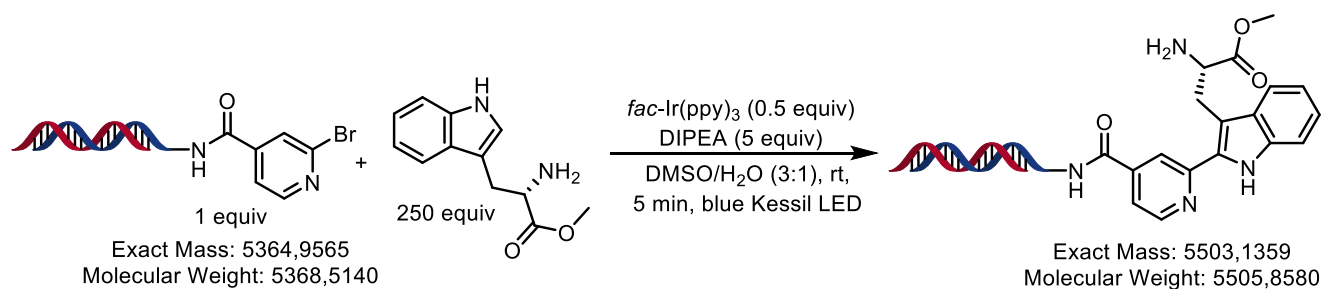
Product **4ac**, 43% yield



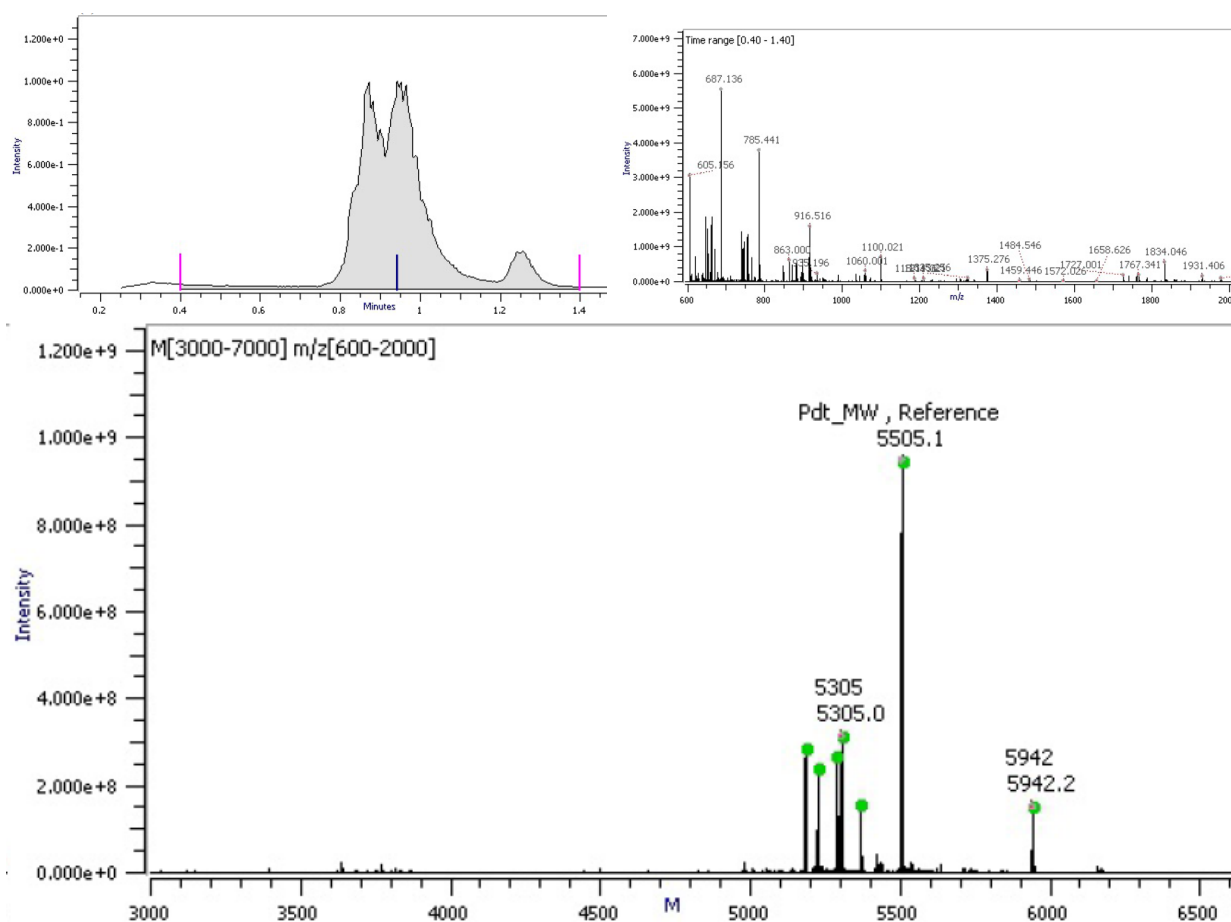
ELTM_388, TW-N78441-9-388.raw (Plot Elution Peak - Plot MS1 - Plot Deconvoluted Mass spectrum)



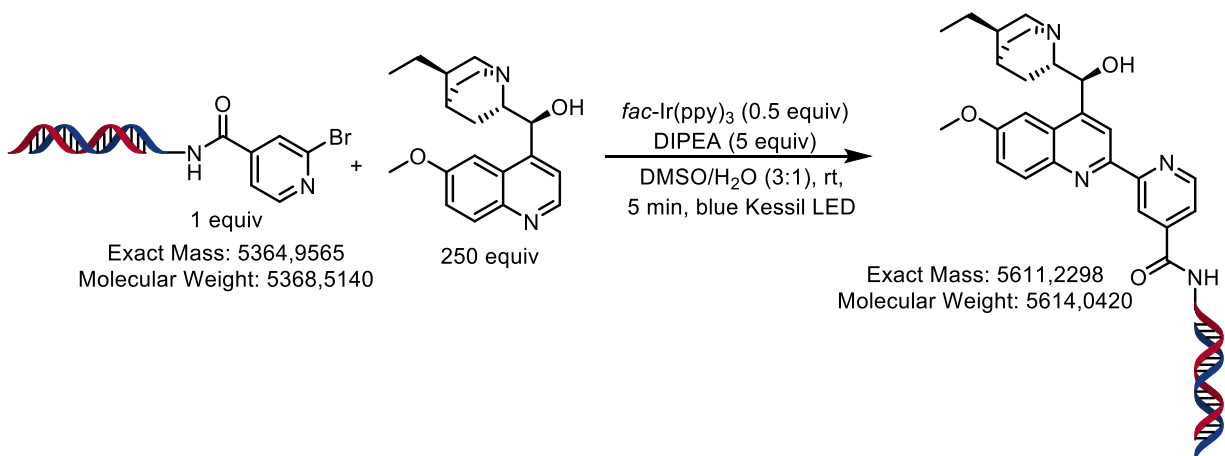
Product **6ad**, 54% yield



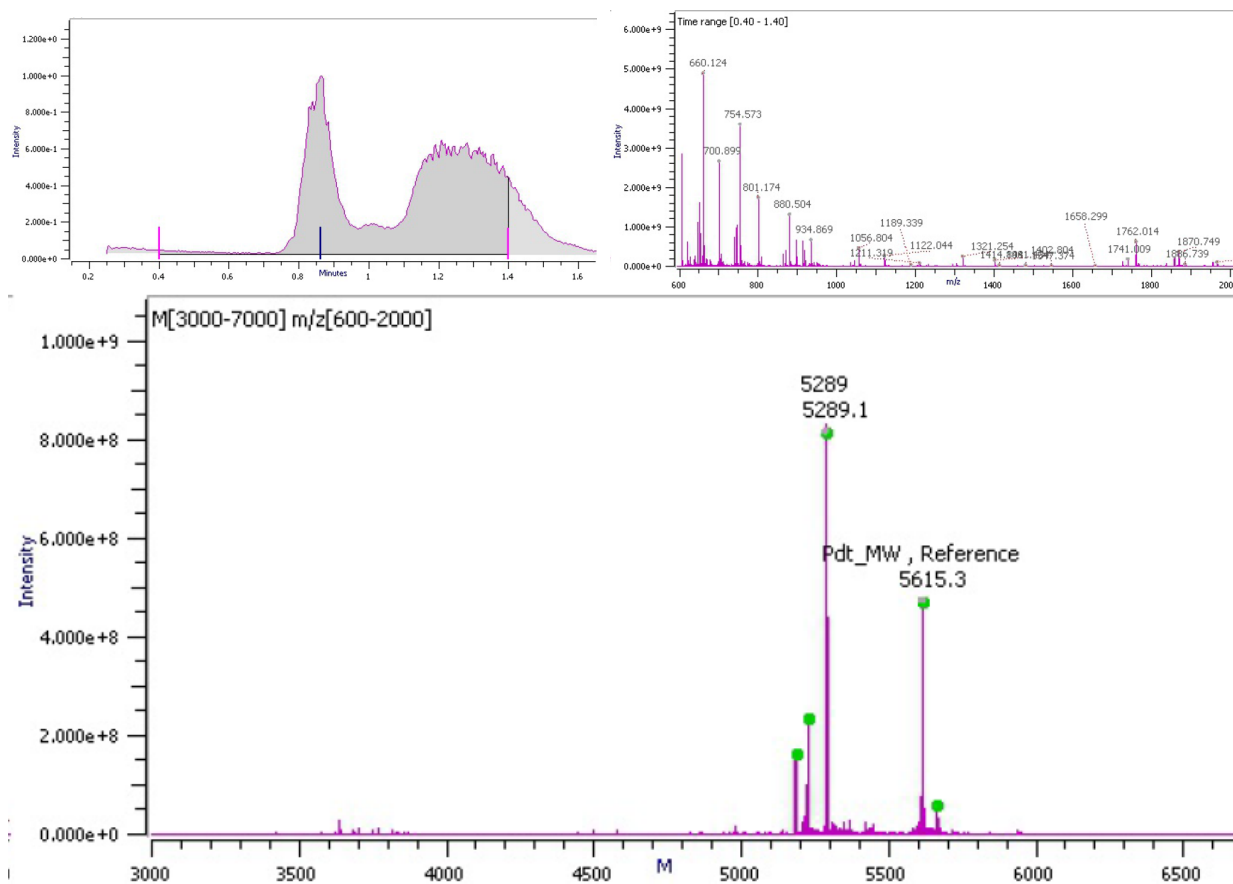
ELTM_480, TW-N78441-10-480.raw (Plot Elution Peak - Plot MS1 - Plot Deconvoluted Mass spectrum)



Product **6ae**, 37% yield

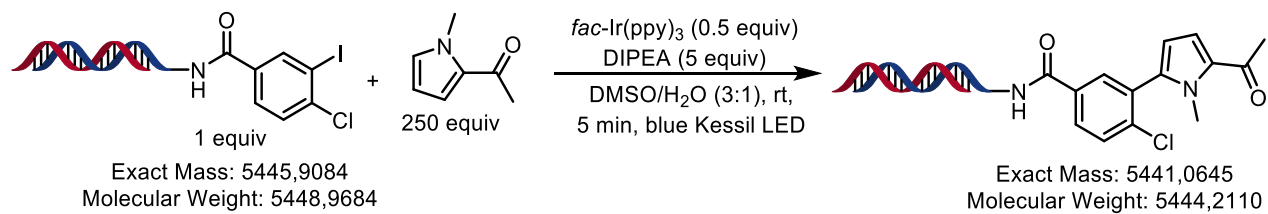


ELTM_464, TW-N78441-10-464.raw (Plot Elution Peak - Plot MS1 - Plot Deconvoluted Mass spectrum)

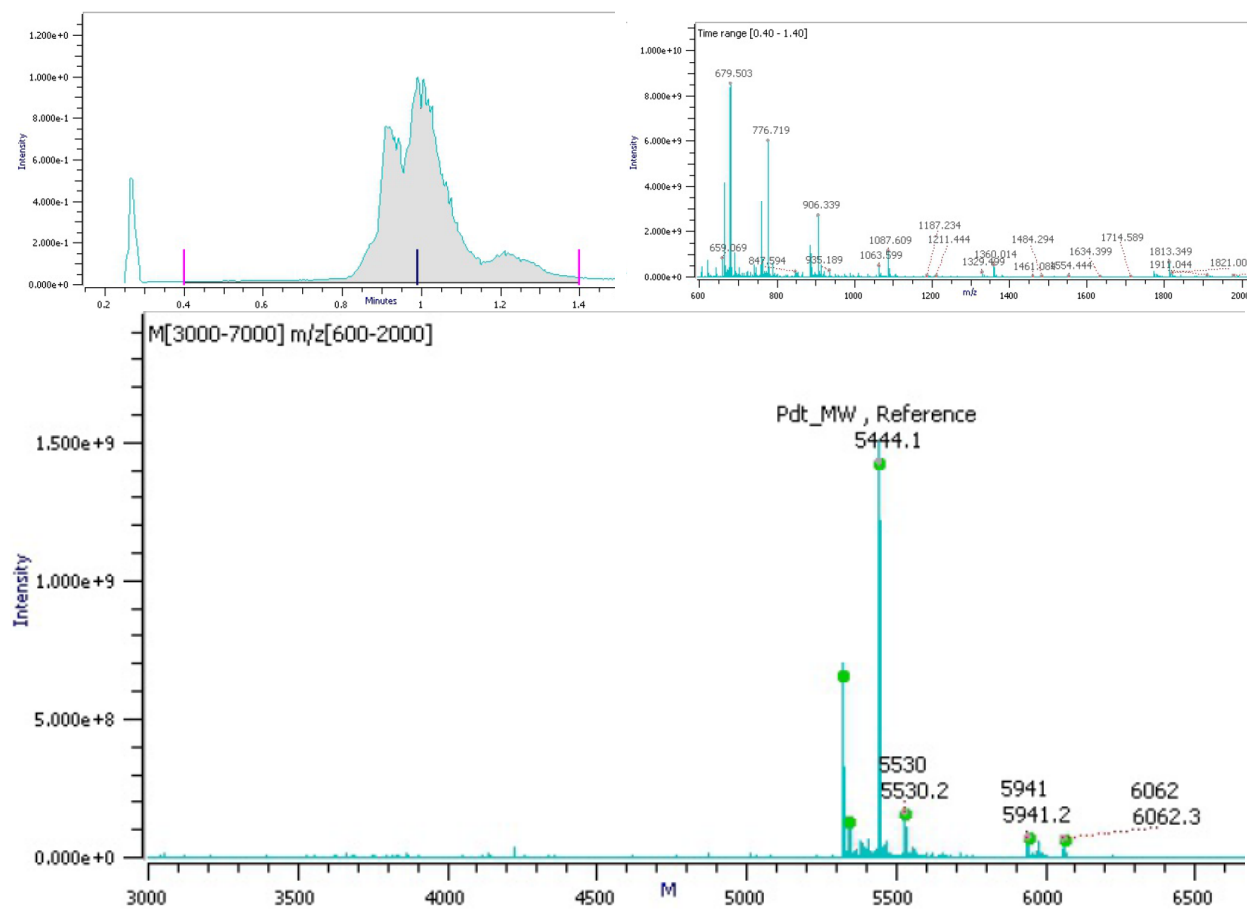


Variation of headpiece

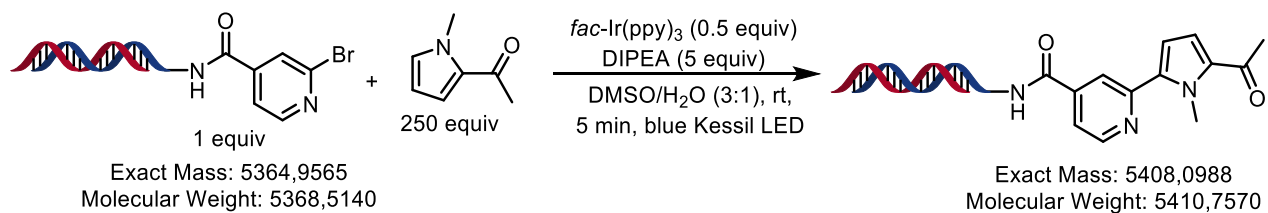
Product **5g**, 67% yield



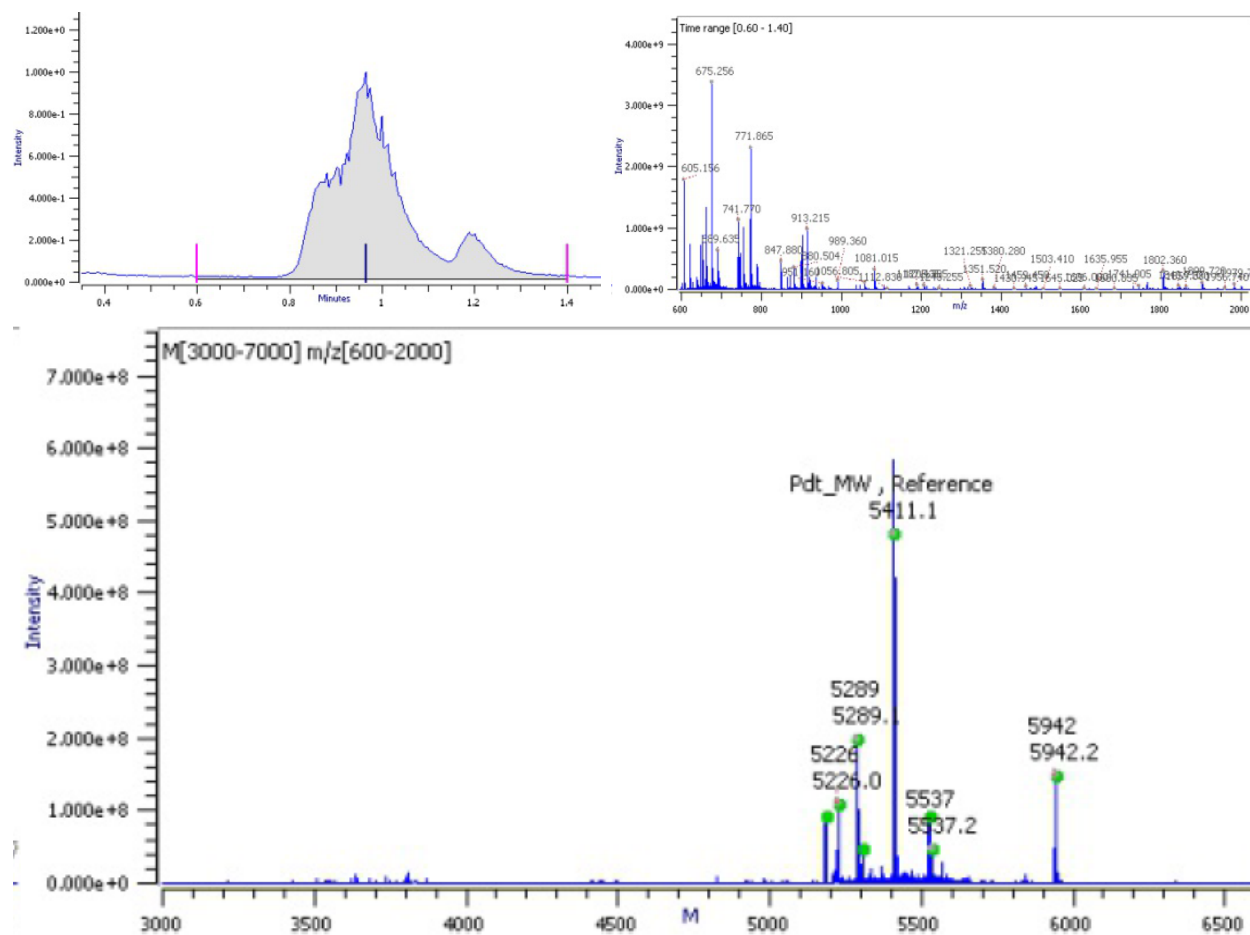
ELTM_570, TW-N78441-10-570.raw (Plot Elution Peak - Plot MS1 - Plot Deconvoluted Mass spectrum)



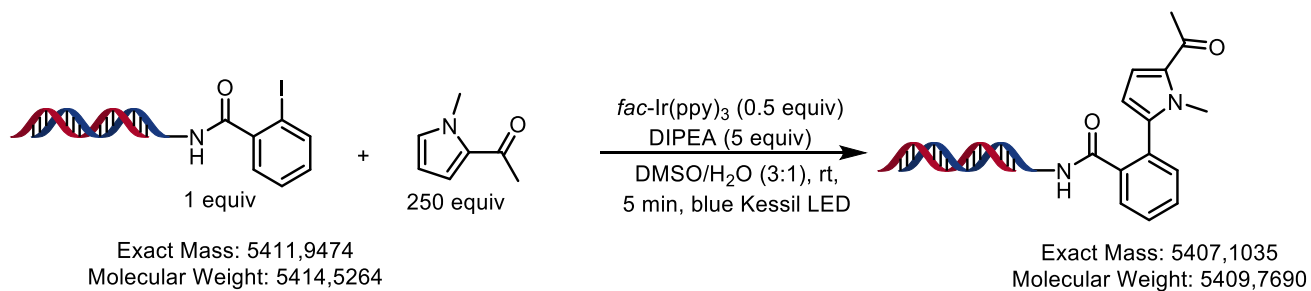
Product **6g**, 54% yield



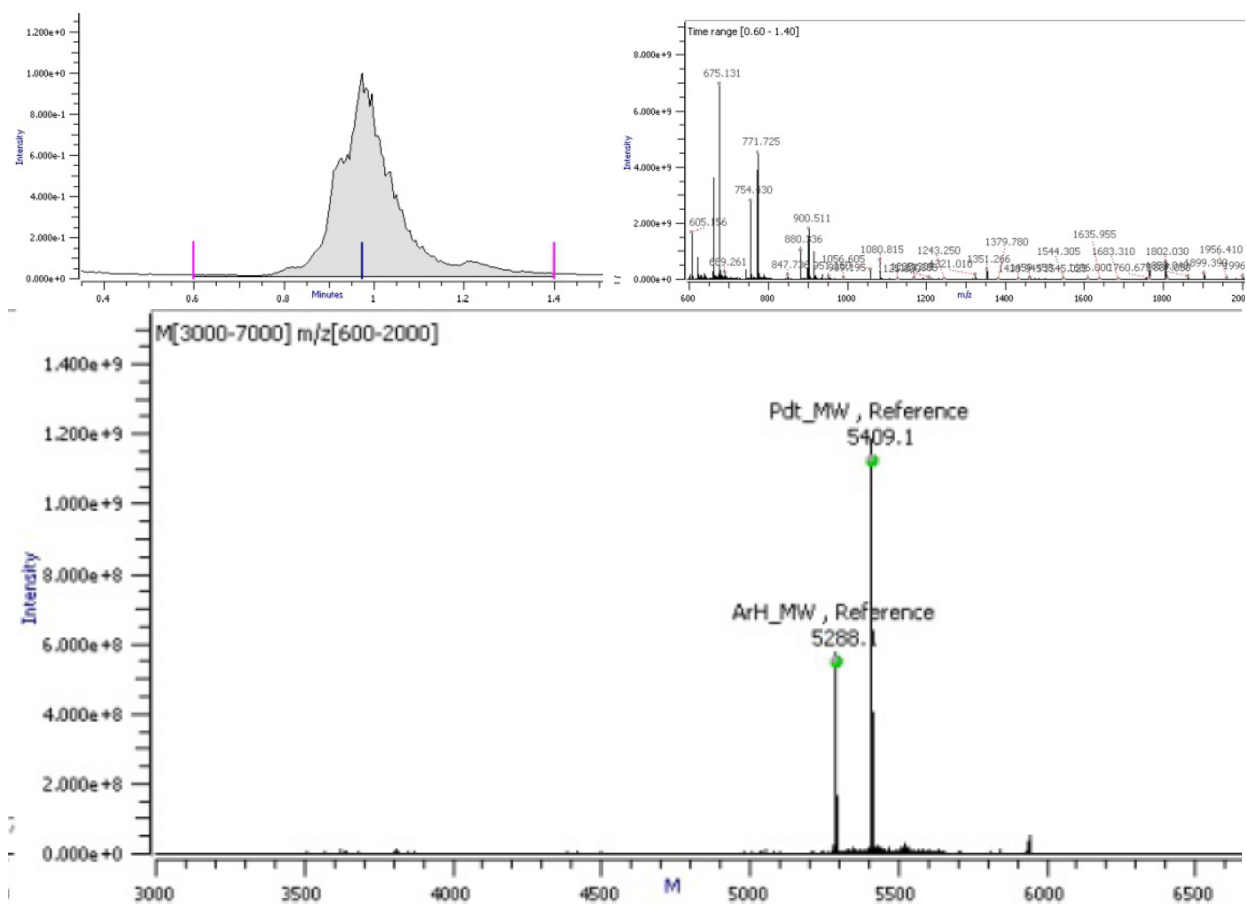
ELTM_420, TW-N78441-9-420.raw (Plot Elution Peak - Plot MS1 - Plot Deconvoluted Mass spectrum)



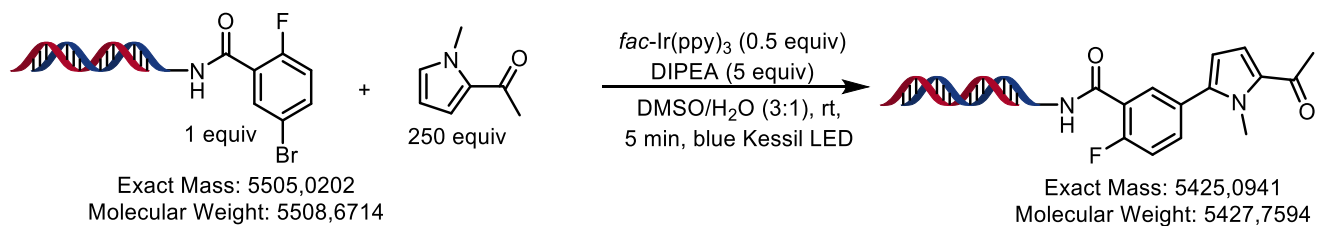
Product **7g**, 71% yield



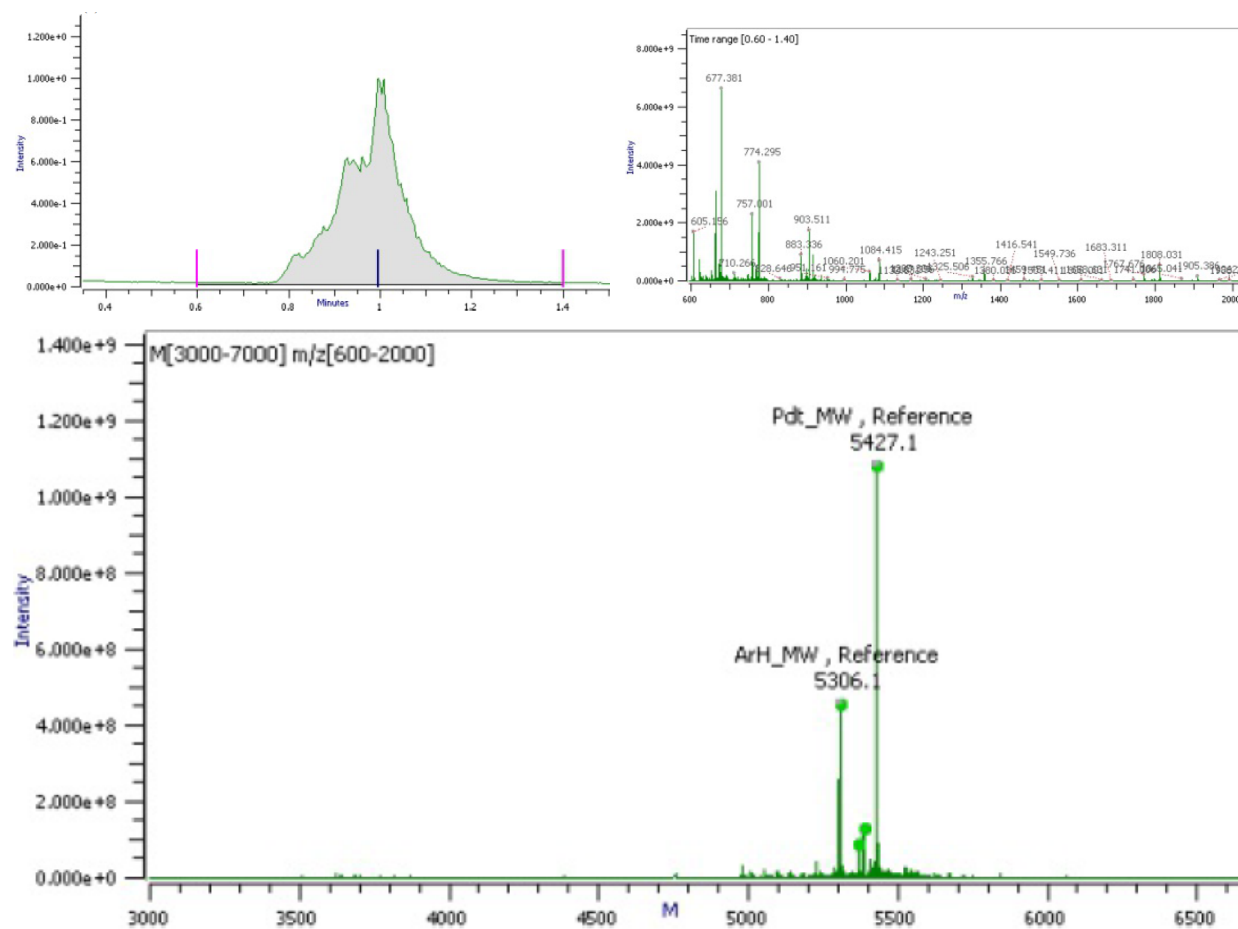
ELTM_426, TW-N78441-9-426.raw (Plot Elution Peak - Plot MS1 - Plot Deconvoluted Mass spectrum)



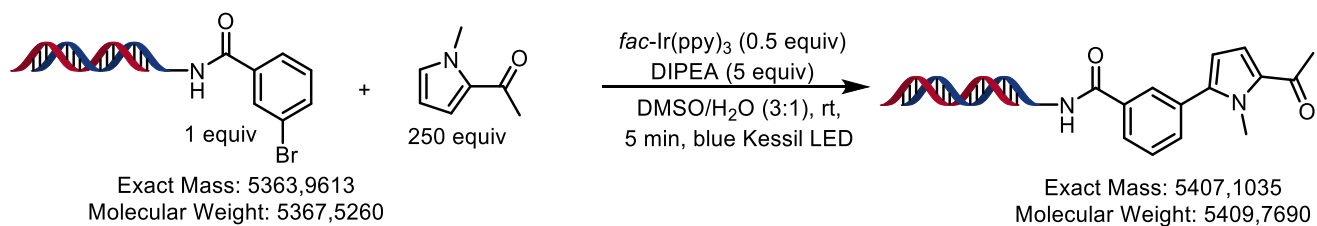
Product **8g**, 61% yield



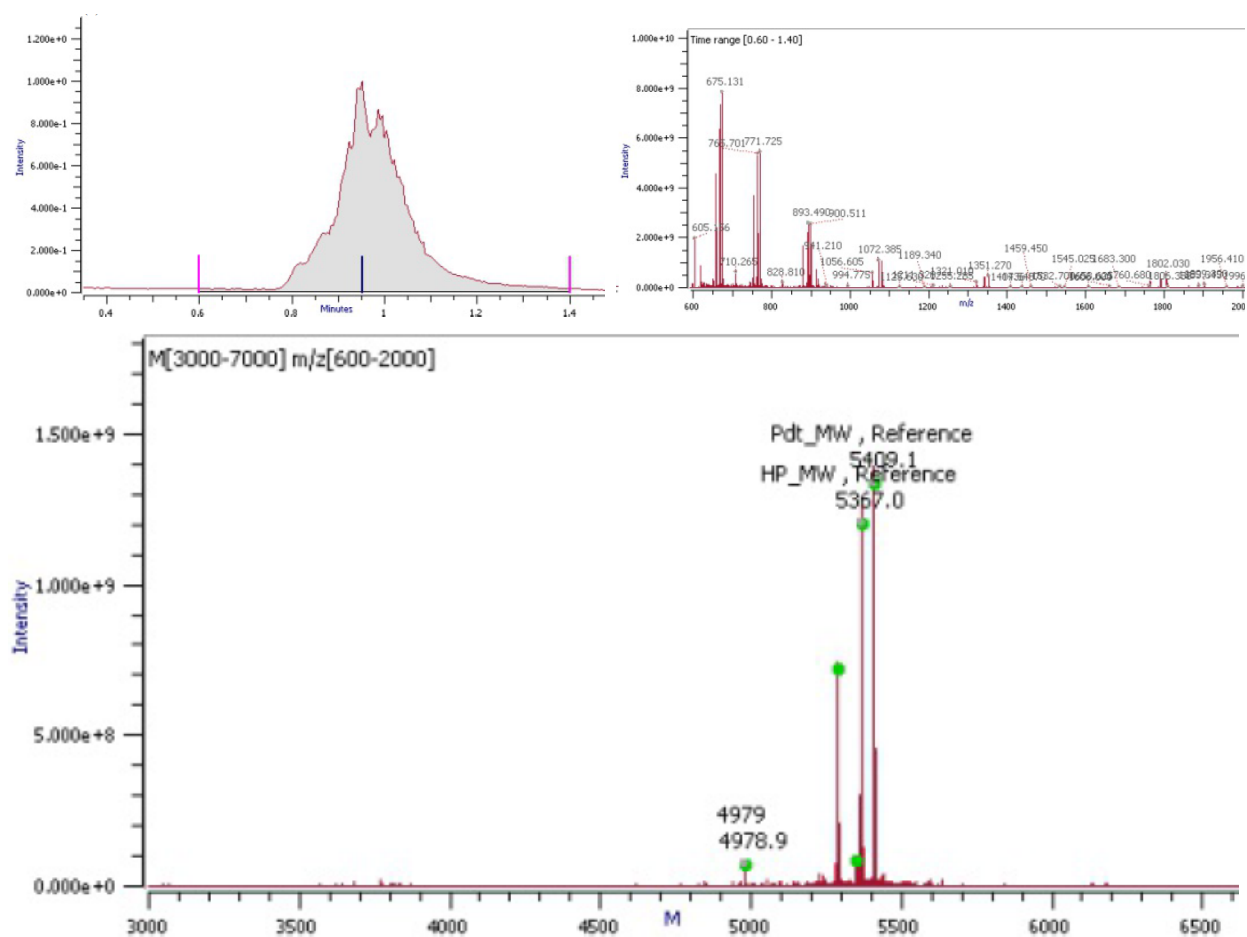
ELTM_326, TW-N78441-9-326.raw (Plot Elution Peak - Plot MS1 - Plot Deconvoluted Mass spectrum)



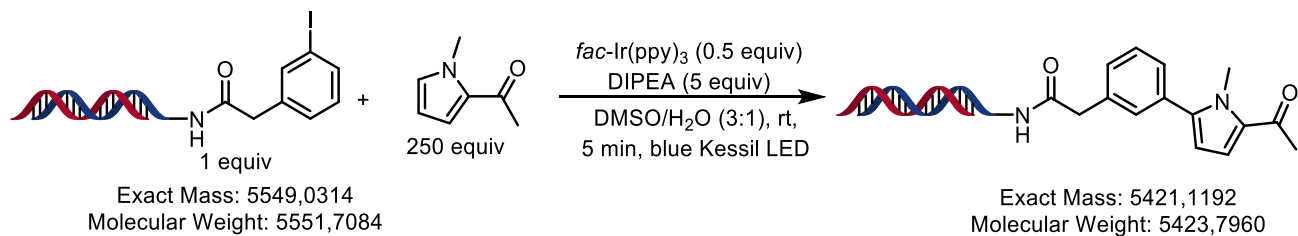
Product **9g**, 41% yield



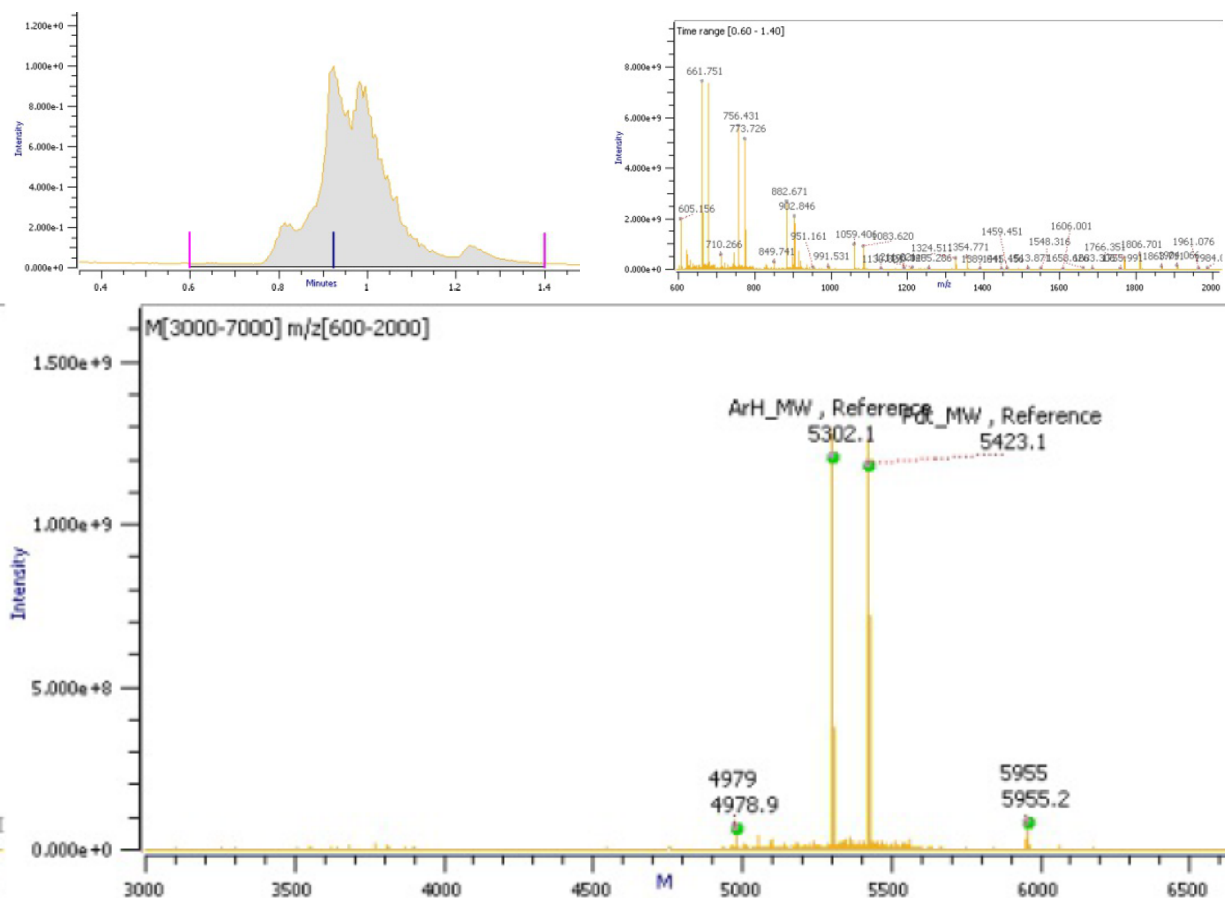
ELTM_323, TW-N78441-9-323.raw (Plot Elution Peak - Plot MS1 - Plot Deconvoluted Mass spectrum)



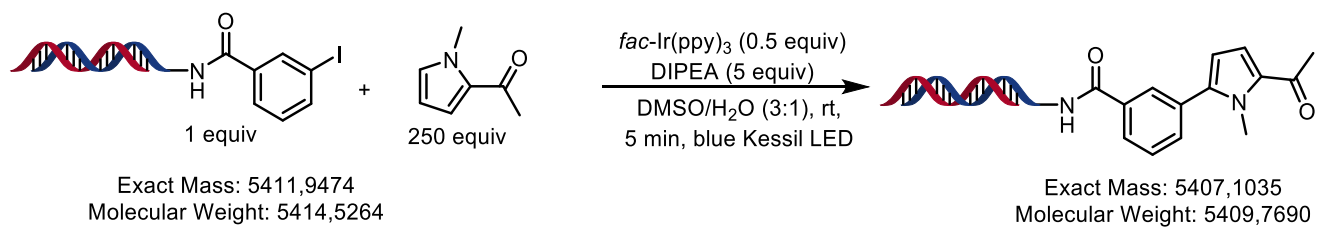
Product **10g**, 51% yield



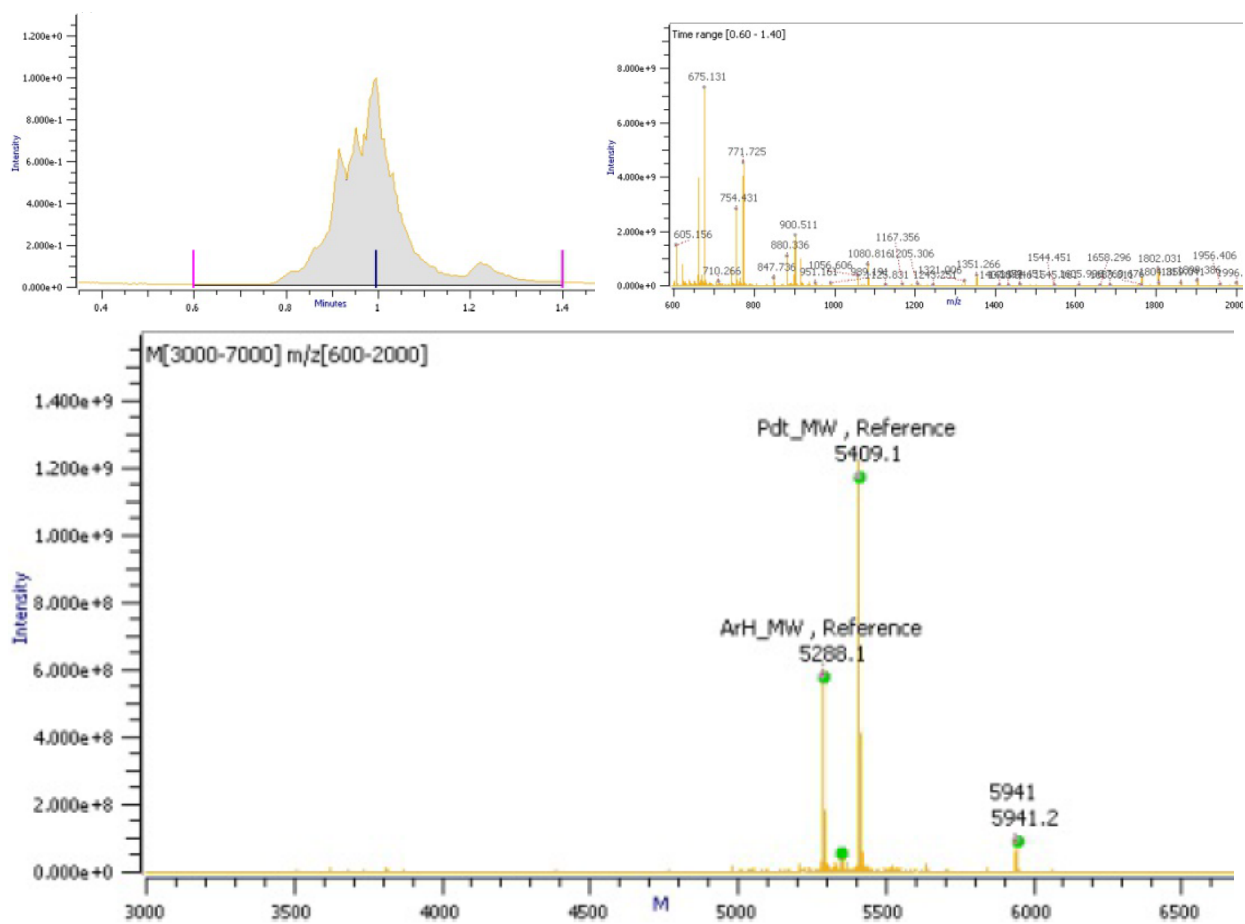
ELTM_344, TW-N78441-9-344.raw (Plot Elution Peak - Plot MS1 - Plot Deconvoluted Mass spectrum)



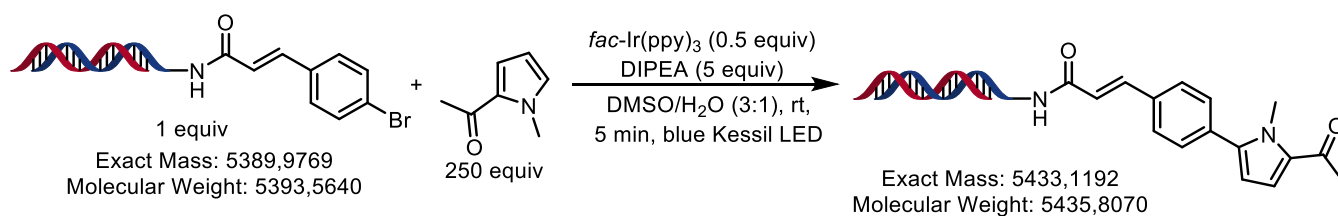
Product **11g**, 68% yield



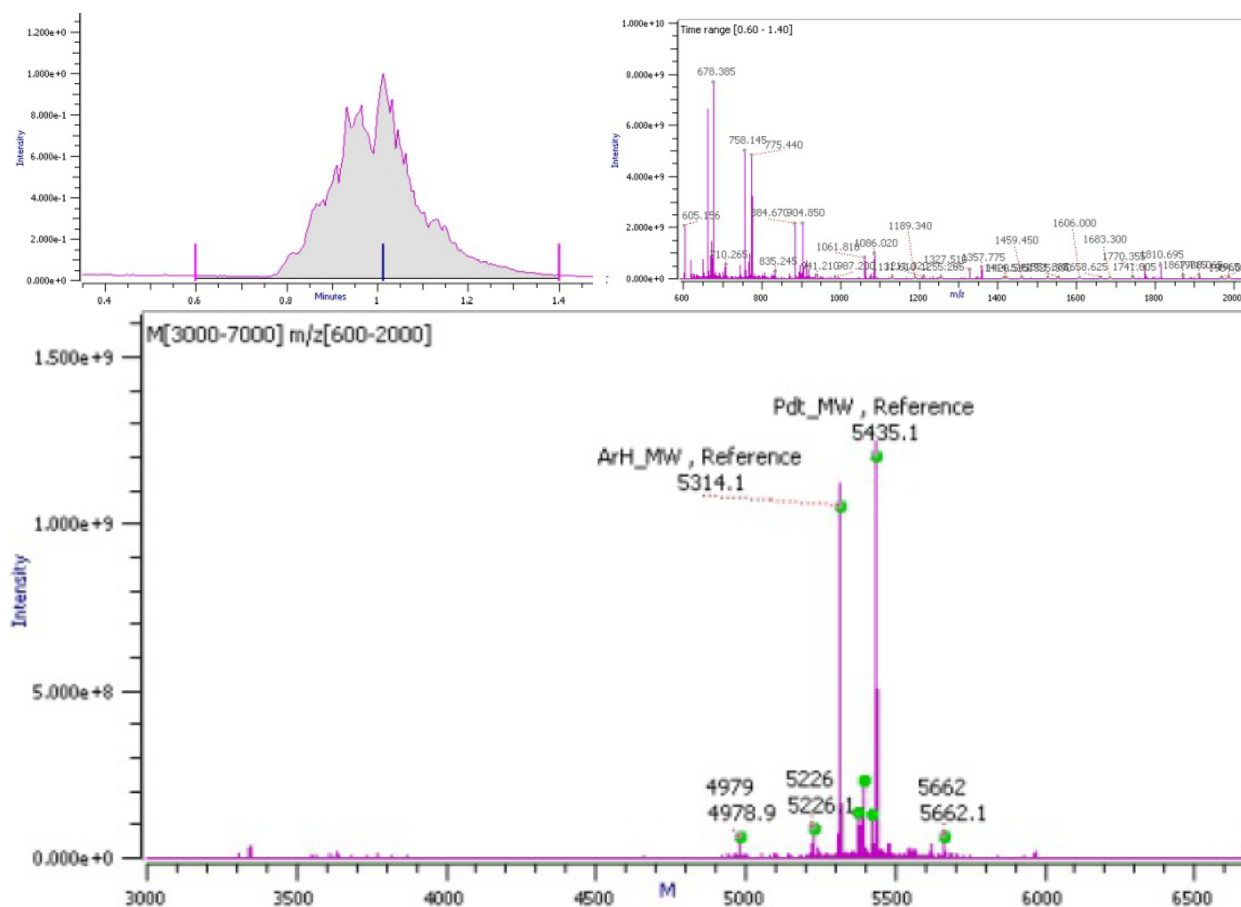
ELTM_301, TW-N78441-9-301.raw (Plot Elution Peak - Plot MS1 - Plot Deconvoluted Mass spectrum)



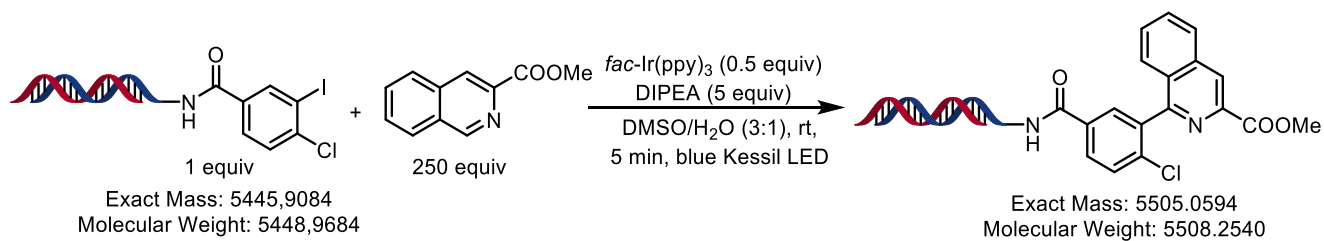
Product **12g**, 47% yield



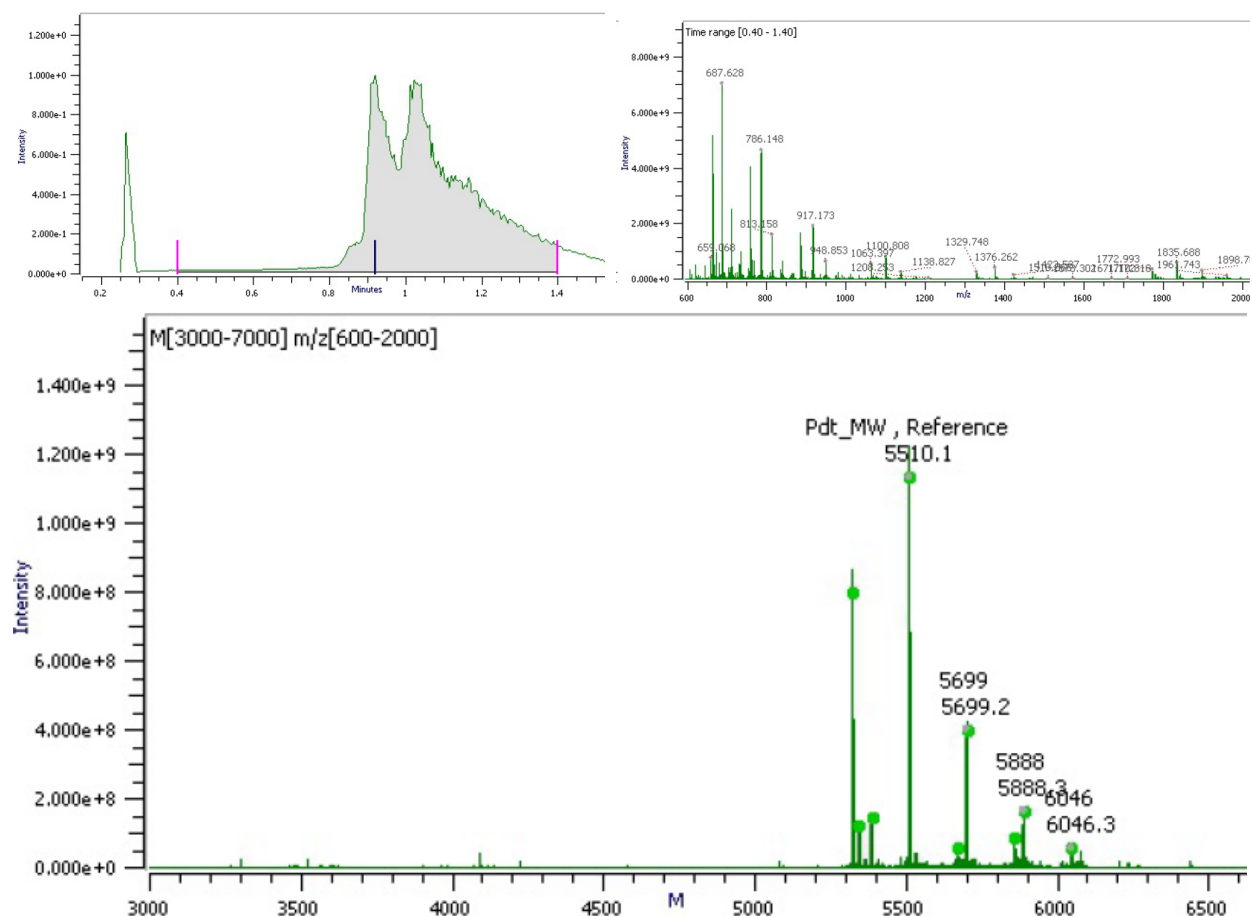
ELTM_286, TW-N78441-9-286.raw (Plot Elution Peak - Plot MS1 - Plot Deconvoluted Mass spectrum)



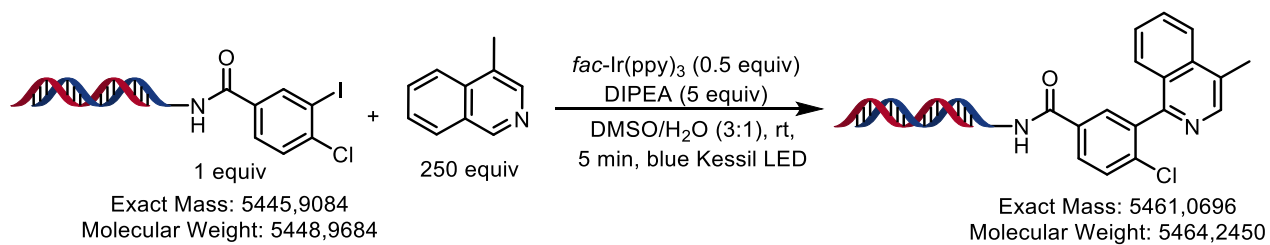
Product **5a**, 45% yield



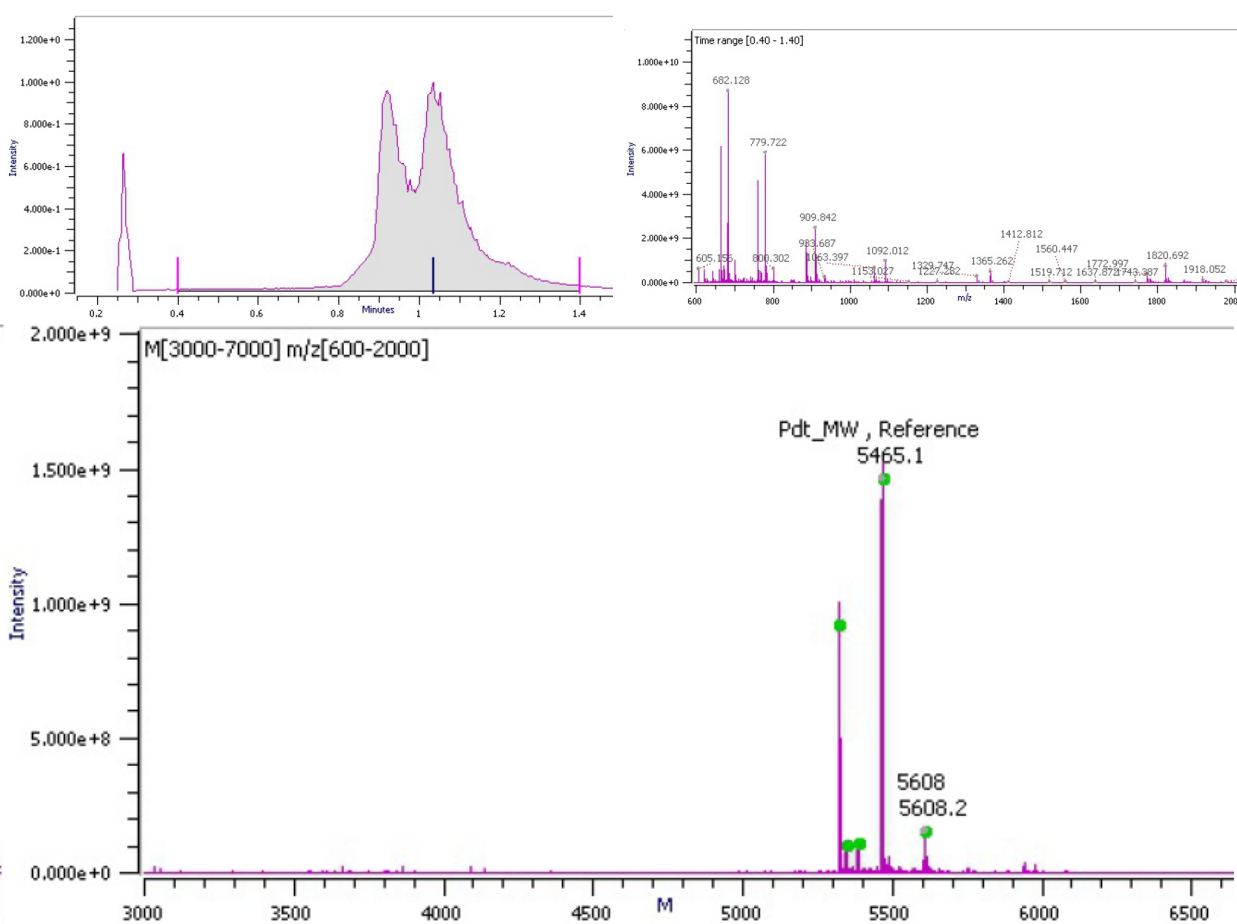
ELTM_569, TW-N78441-10-569.raw (Plot Elution Peak - Plot MS1 - Plot Deconvoluted Mass spectrum)



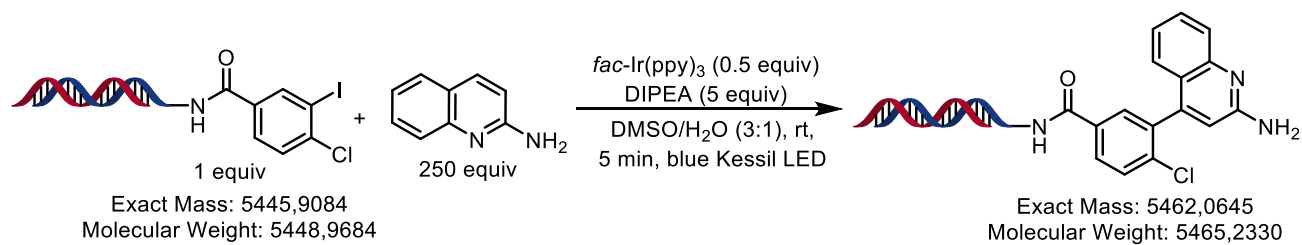
Product **5c**, 63% yield



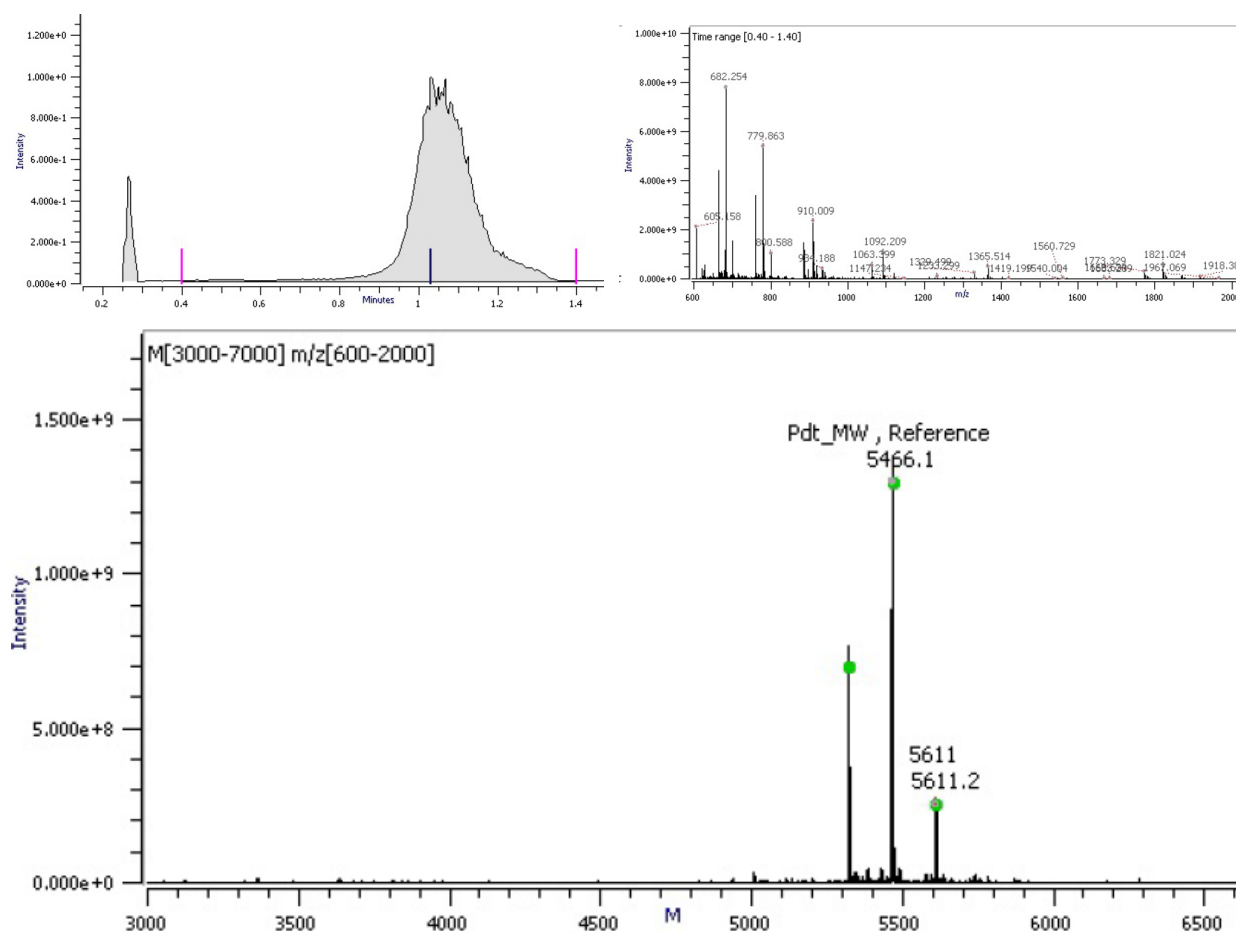
ELTM_529, TW-N78441-10-529.raw (Plot Elution Peak - Plot MS1 - Plot Deconvoluted Mass spectrum)



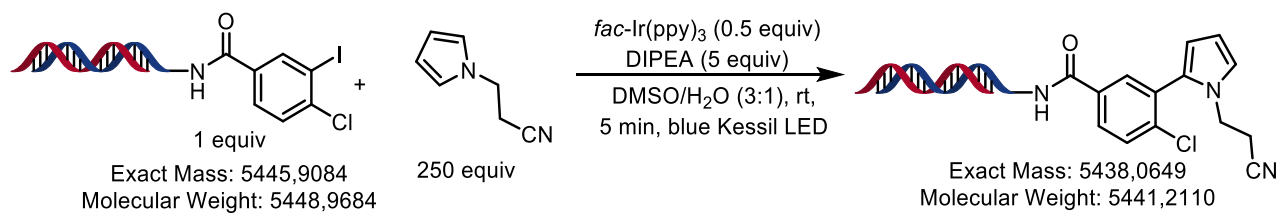
Product **5d**, 68% yield



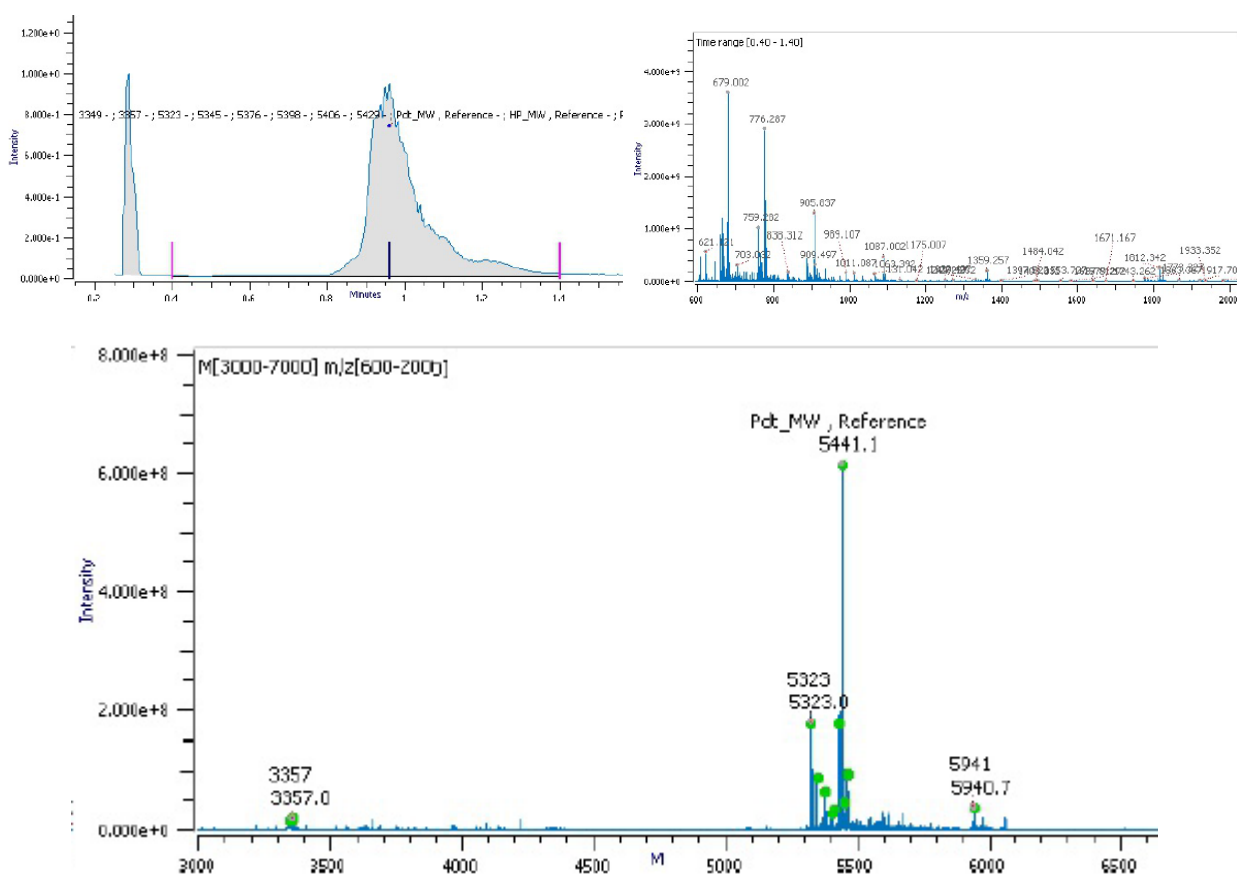
ELTM_532, TW-N78441-10-532.raw (Plot Elution Peak - Plot MS1 - Plot Deconvoluted Mass spectrum)



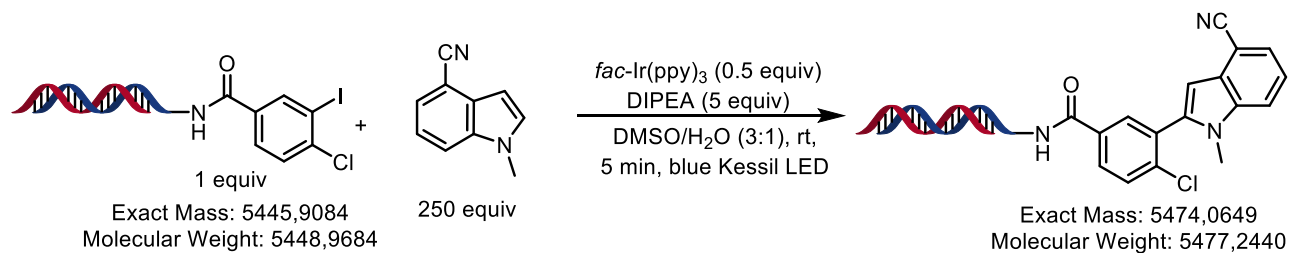
Product **5i**, 43% yield



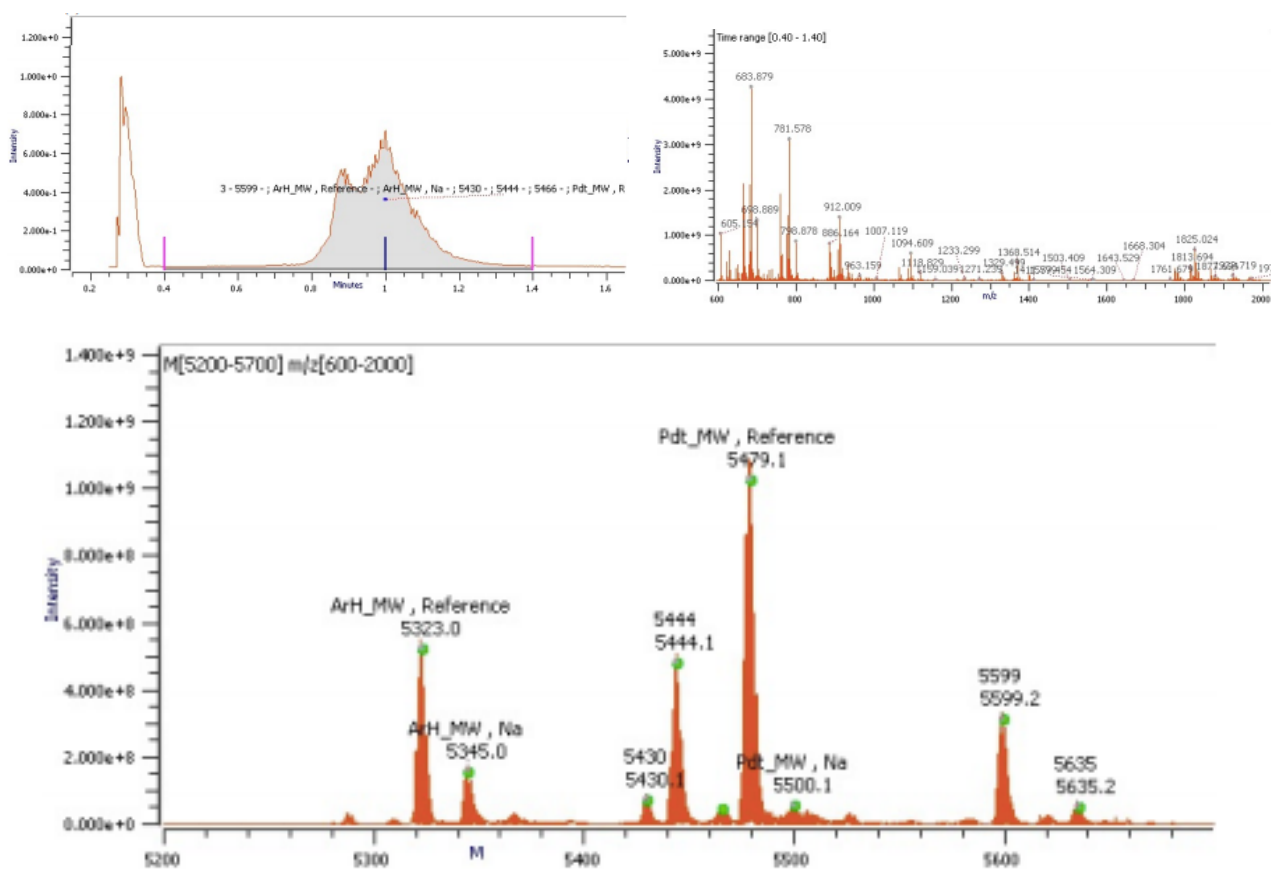
ELTM_650, TW-N78441-14-650.raw (Plot Elution Peak - Plot MS1 - Plot Deconvoluted Mass spectrum)



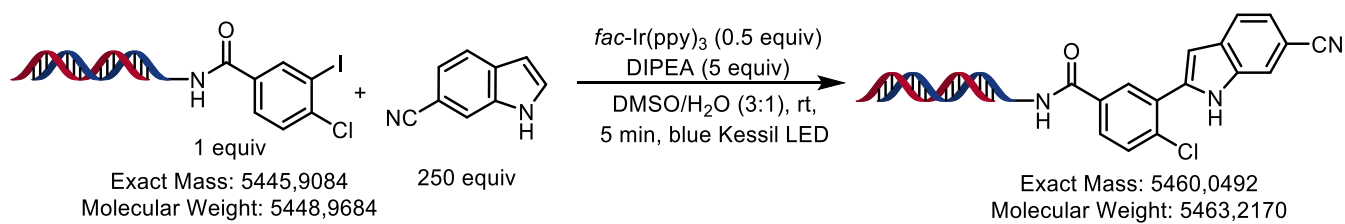
Product **5k**, 40% yield



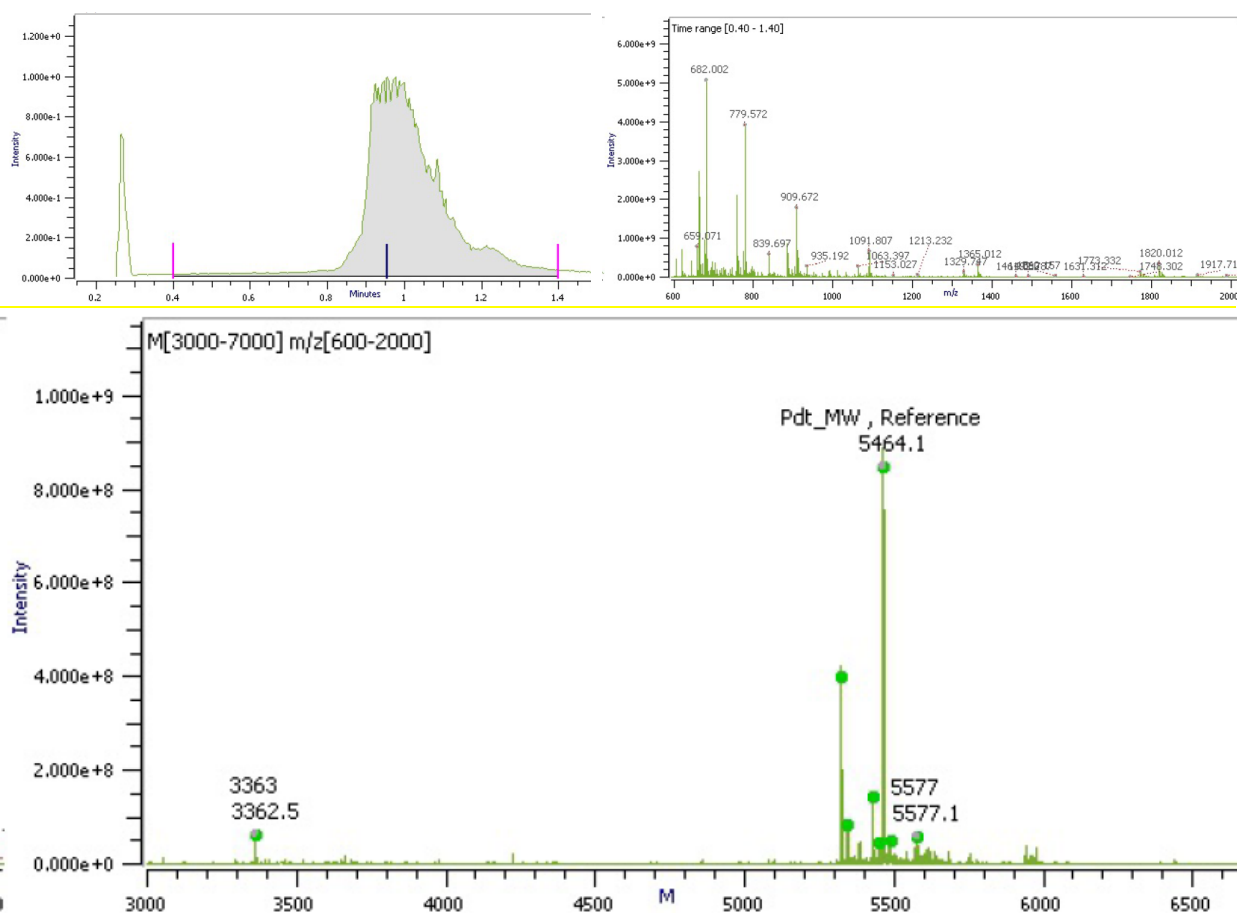
TW-N78441-15-702 - (Plot Elution Peak - Plot MS1 - Plot Deconvoluted Mass spectrum)



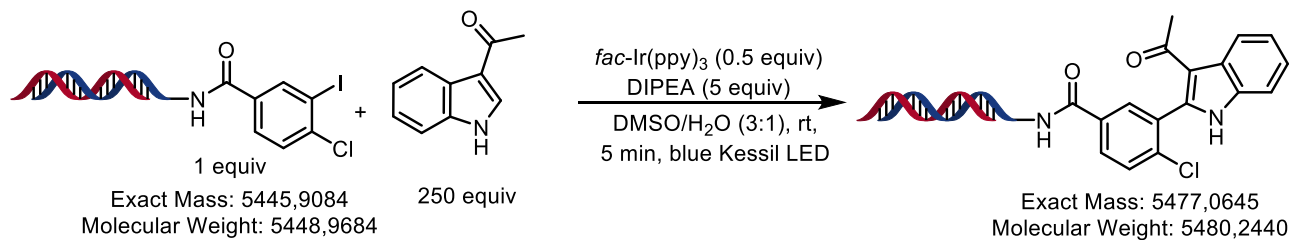
Product **5I**, 60% yield



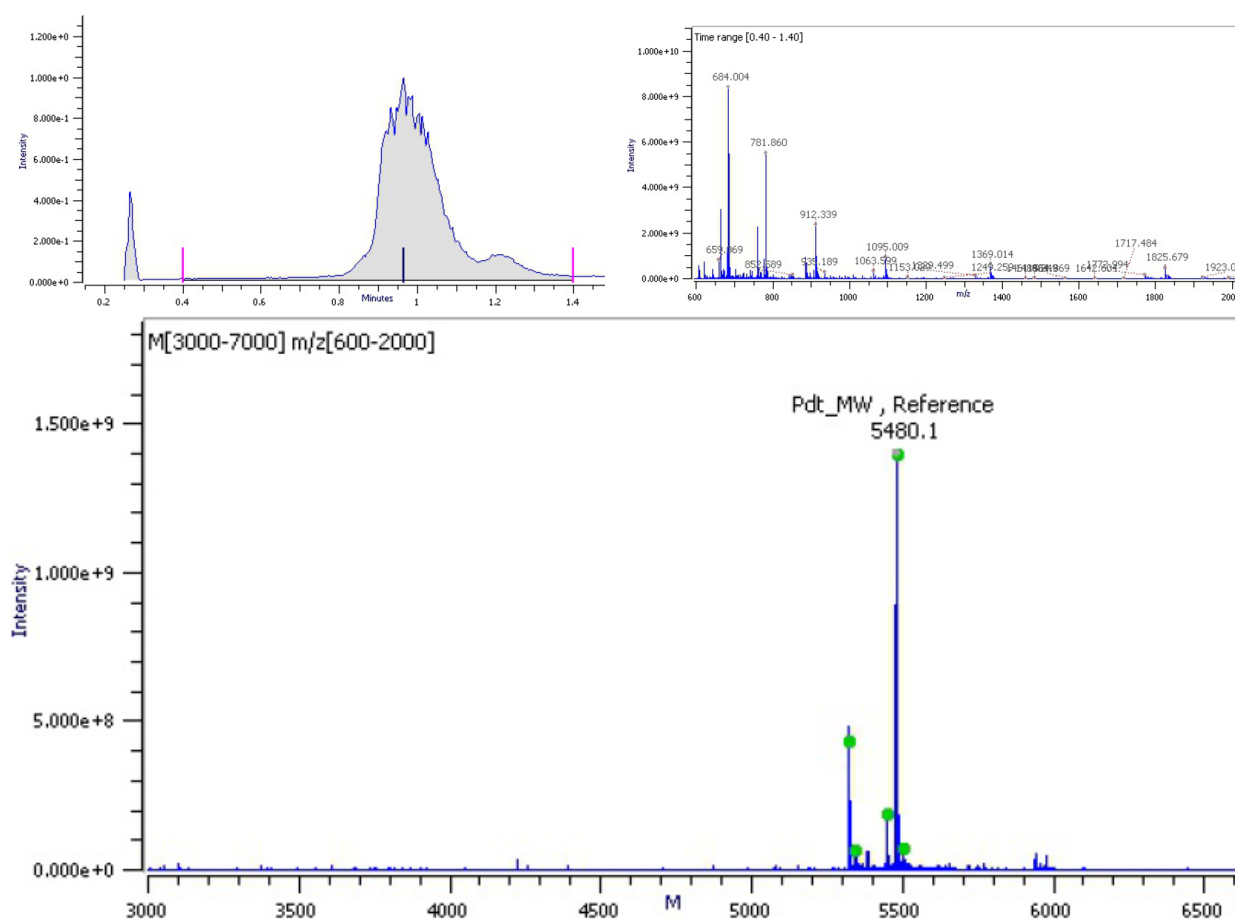
ELTM_537, TW-N78441-10-537.raw (Plot Elution Peak - Plot MS1 - Plot Deconvoluted Mass spectrum)



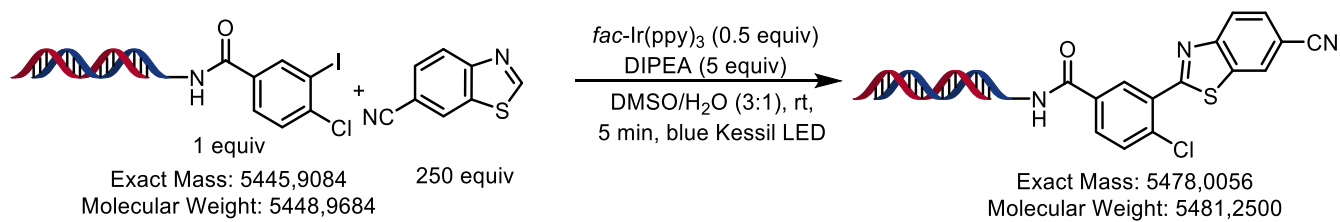
Product **5o**, 77% yield



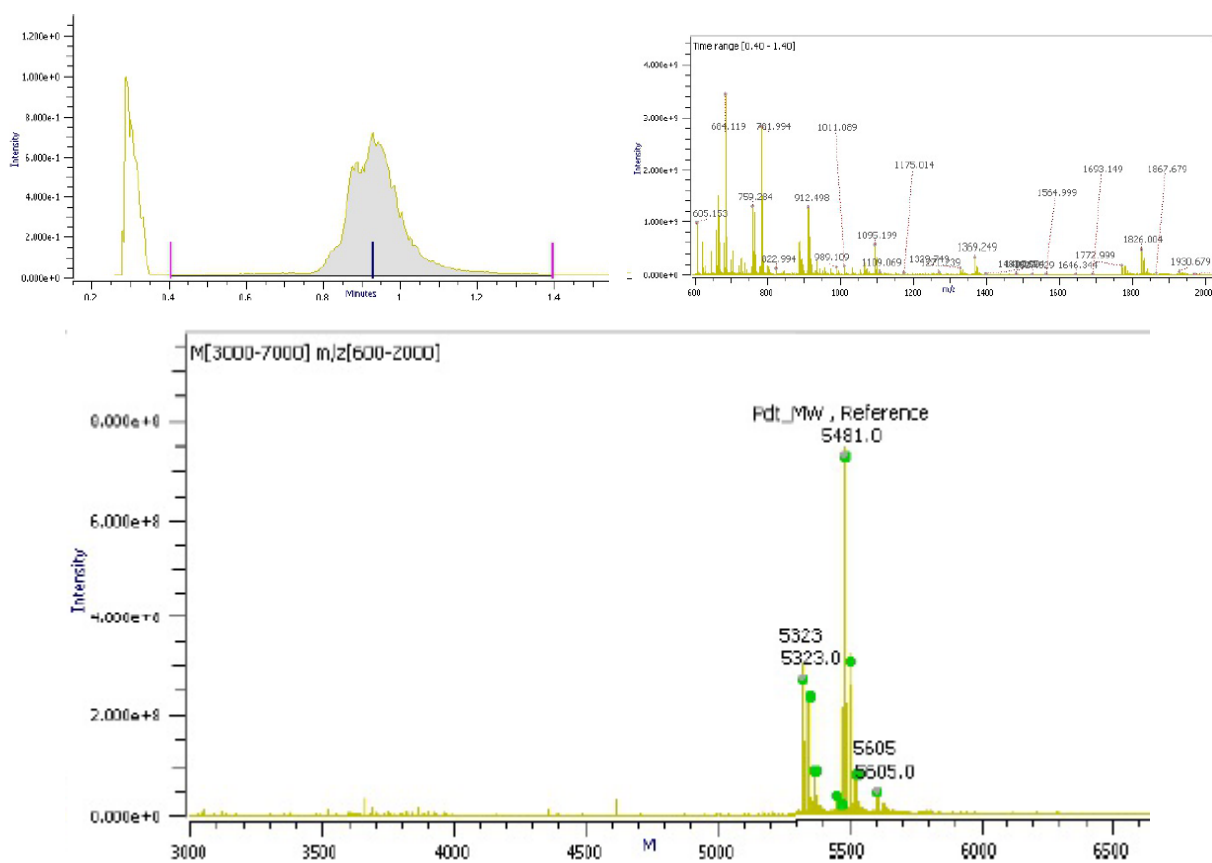
ELTM_539, TW-N78441-10-539.raw (Plot Elution Peak - Plot MS1 - Plot Deconvoluted Mass spectrum)



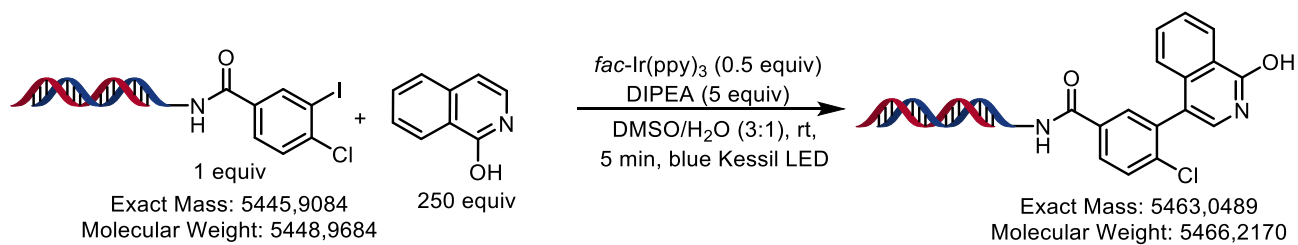
Product **5w**, 40% yield



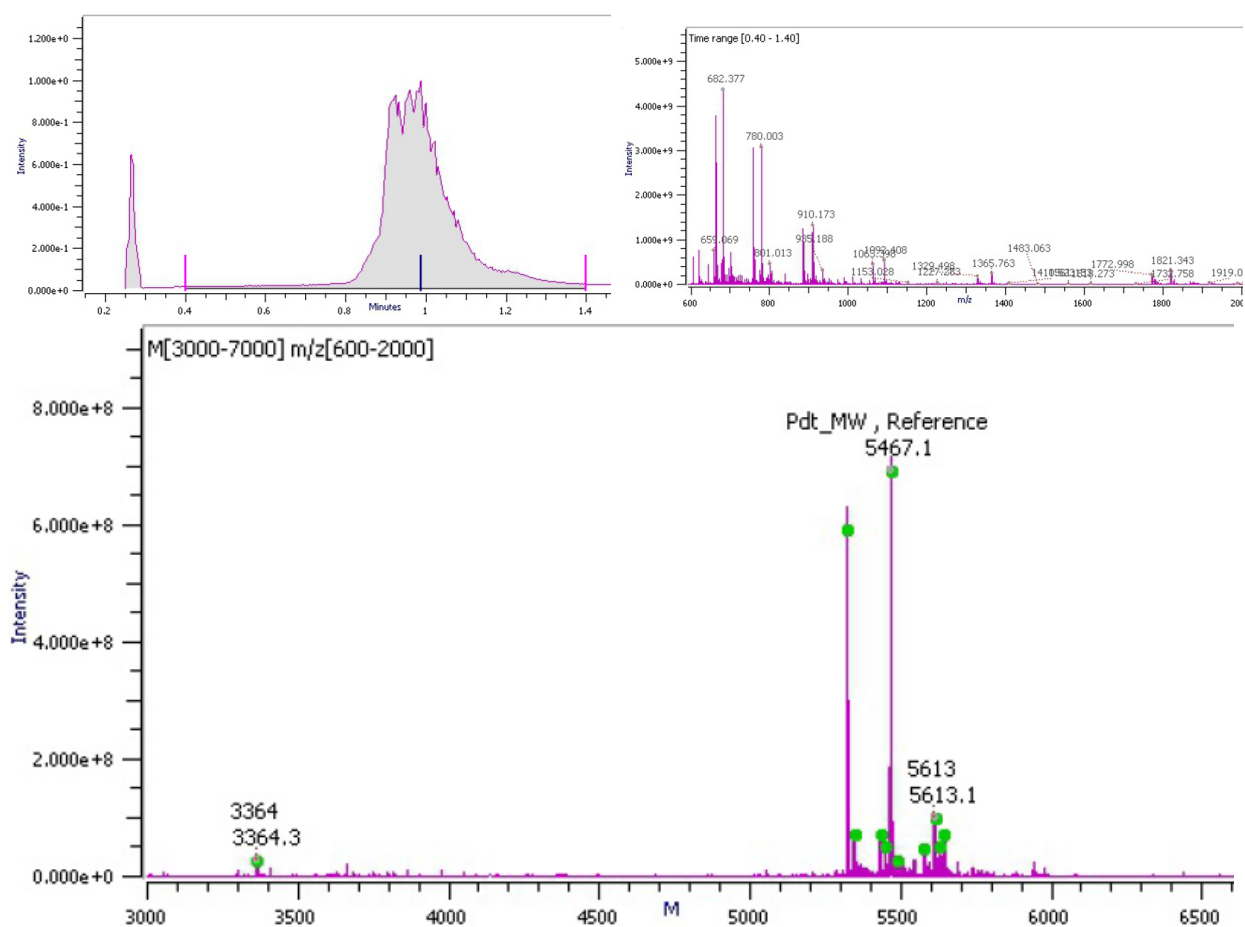
ELTM_712, TW-N78441-15-712.raw (Plot Elution Peak - Plot MS1 - Plot Deconvoluted Mass spectrum)



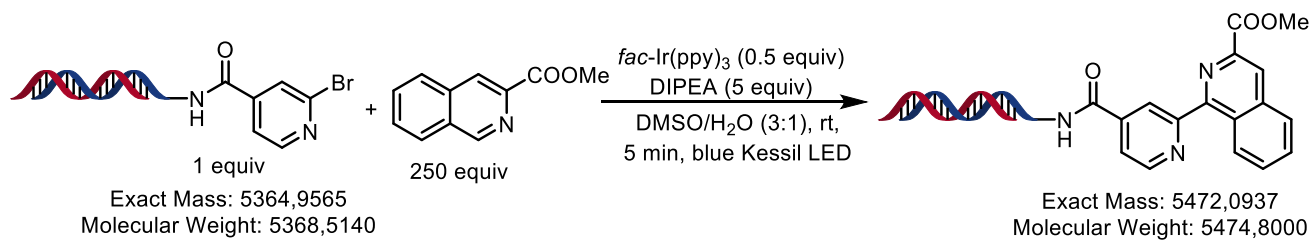
Product **5af**, 45% yield



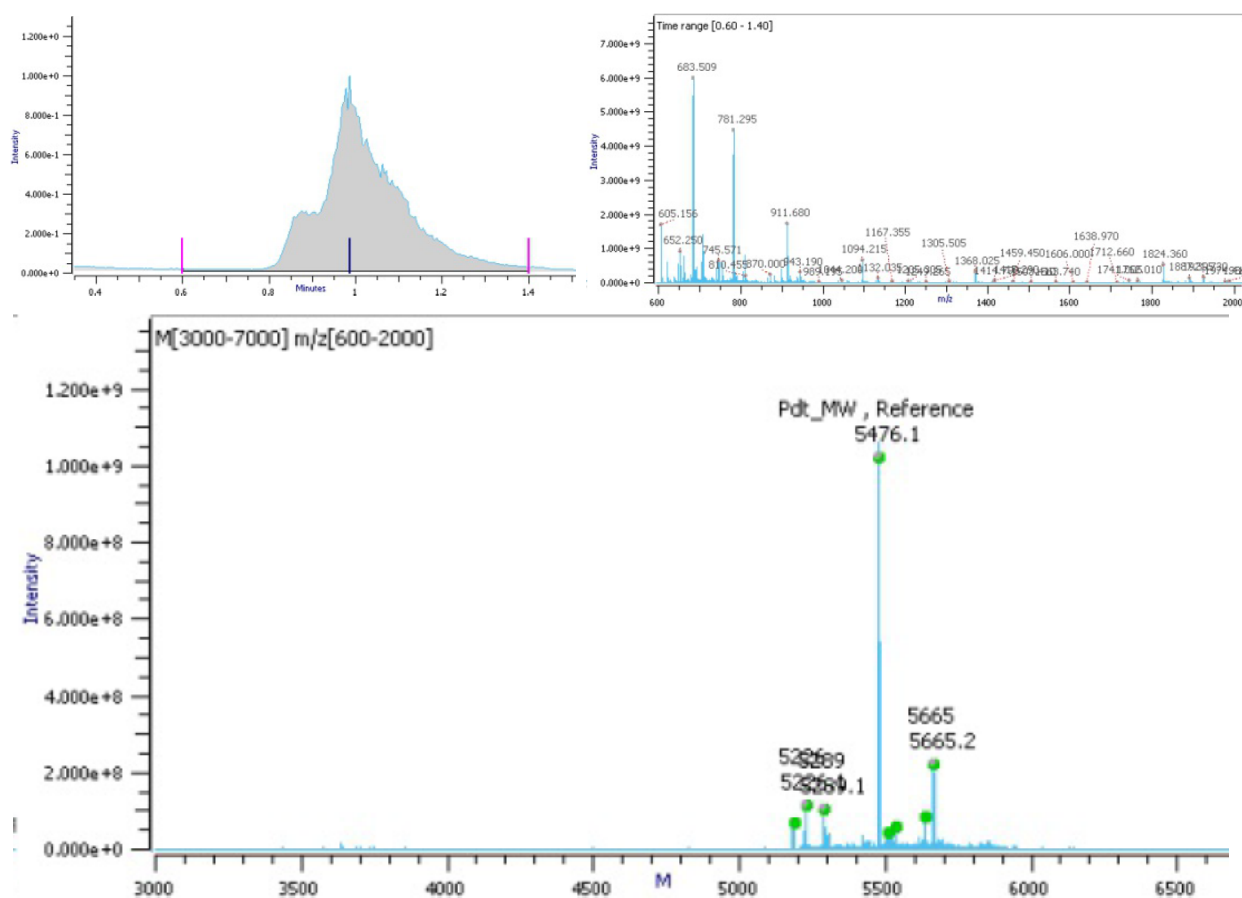
ELTM_542, TW-N78441-10-542.raw (Plot Elution Peak - Plot MS1 - Plot Deconvoluted Mass spectrum)



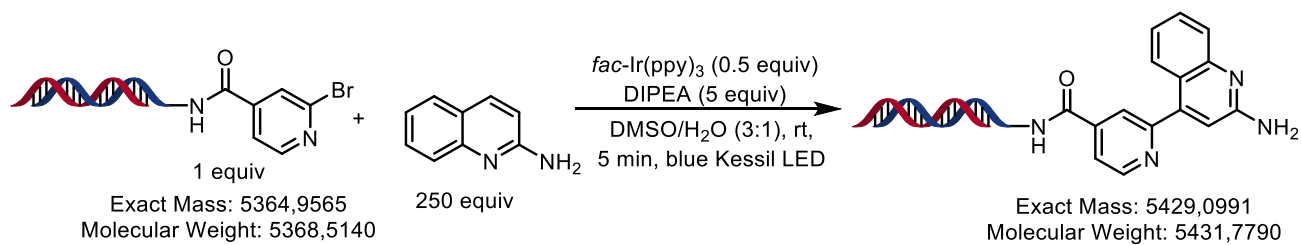
Product **6a**, 81% yield



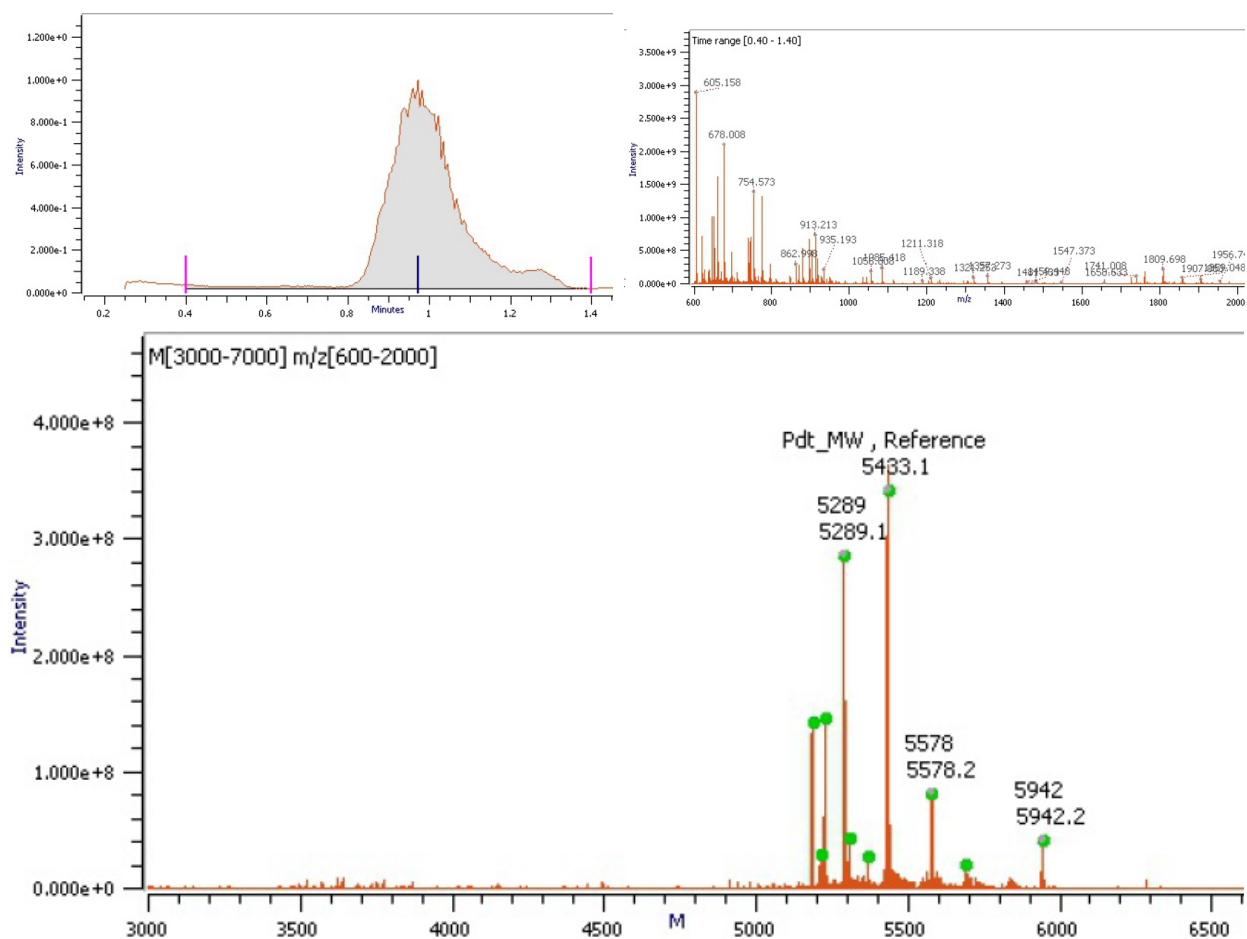
ELTM_419, TW-N78441-9-419.raw (Plot Elution Peak - Plot MS1 - Plot Deconvoluted Mass spectrum)



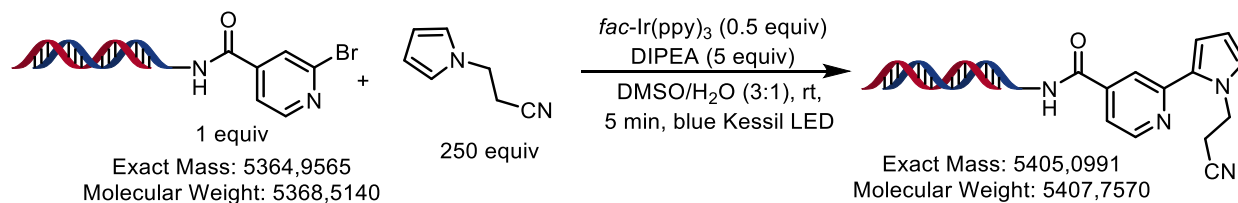
Product **6d**, 40% yield



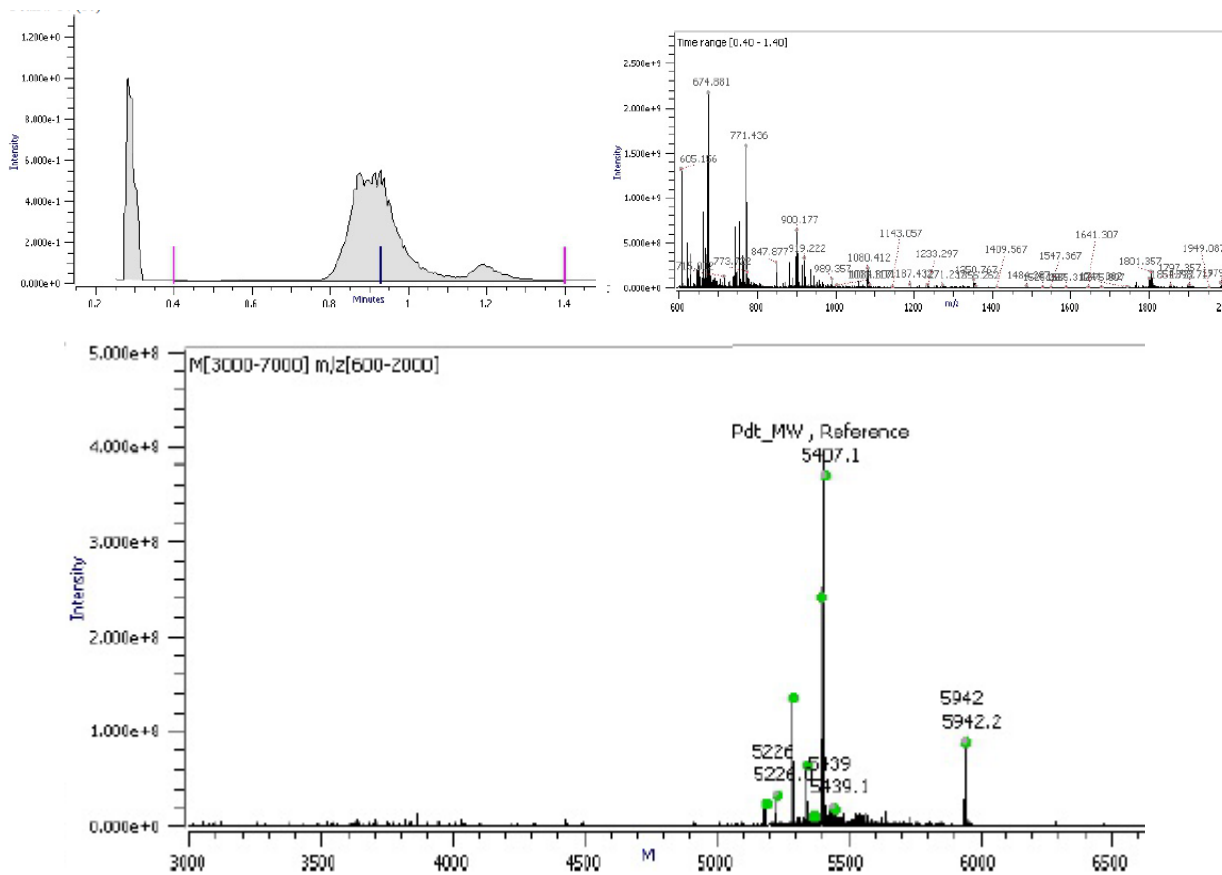
ELTM_469, TW-N78441-10-469.raw (Plot Elution Peak - Plot MS1 - Plot Deconvoluted Mass spectrum)



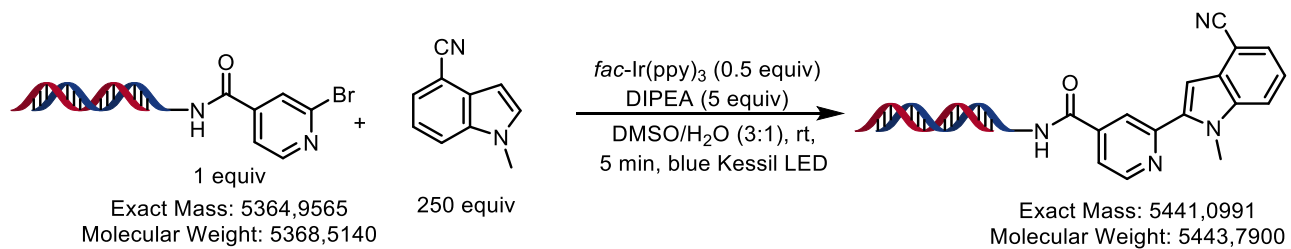
Product **6i**, 46% yield



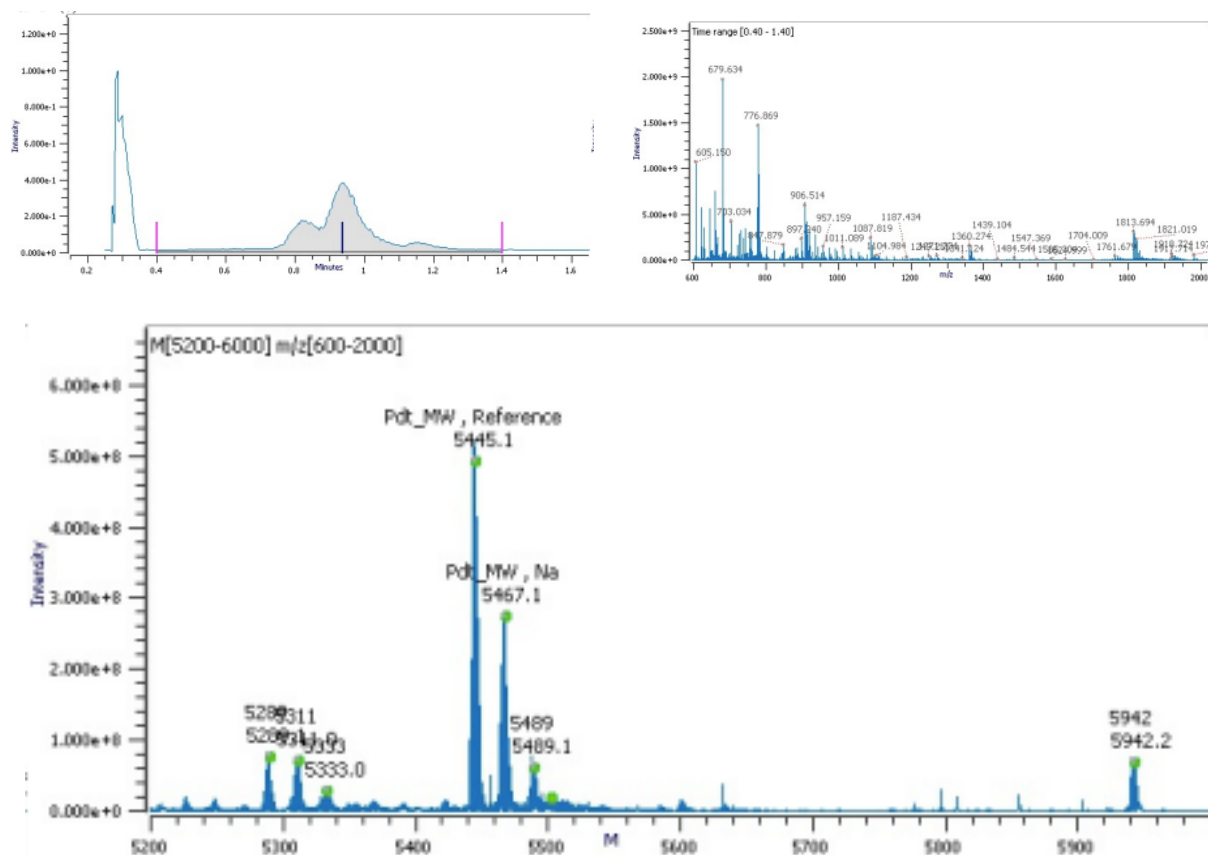
ELTM_649, TW-N78441-14-649.raw (Plot Elution Peak - Plot MS1 - Plot Deconvoluted Mass spectrum)



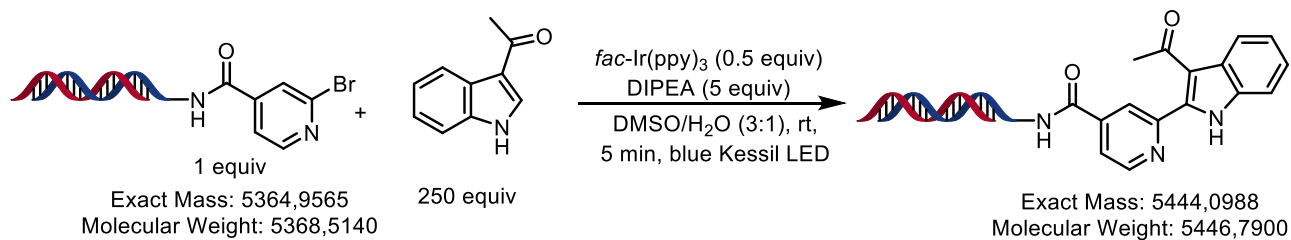
Product **6k**, 70% yield



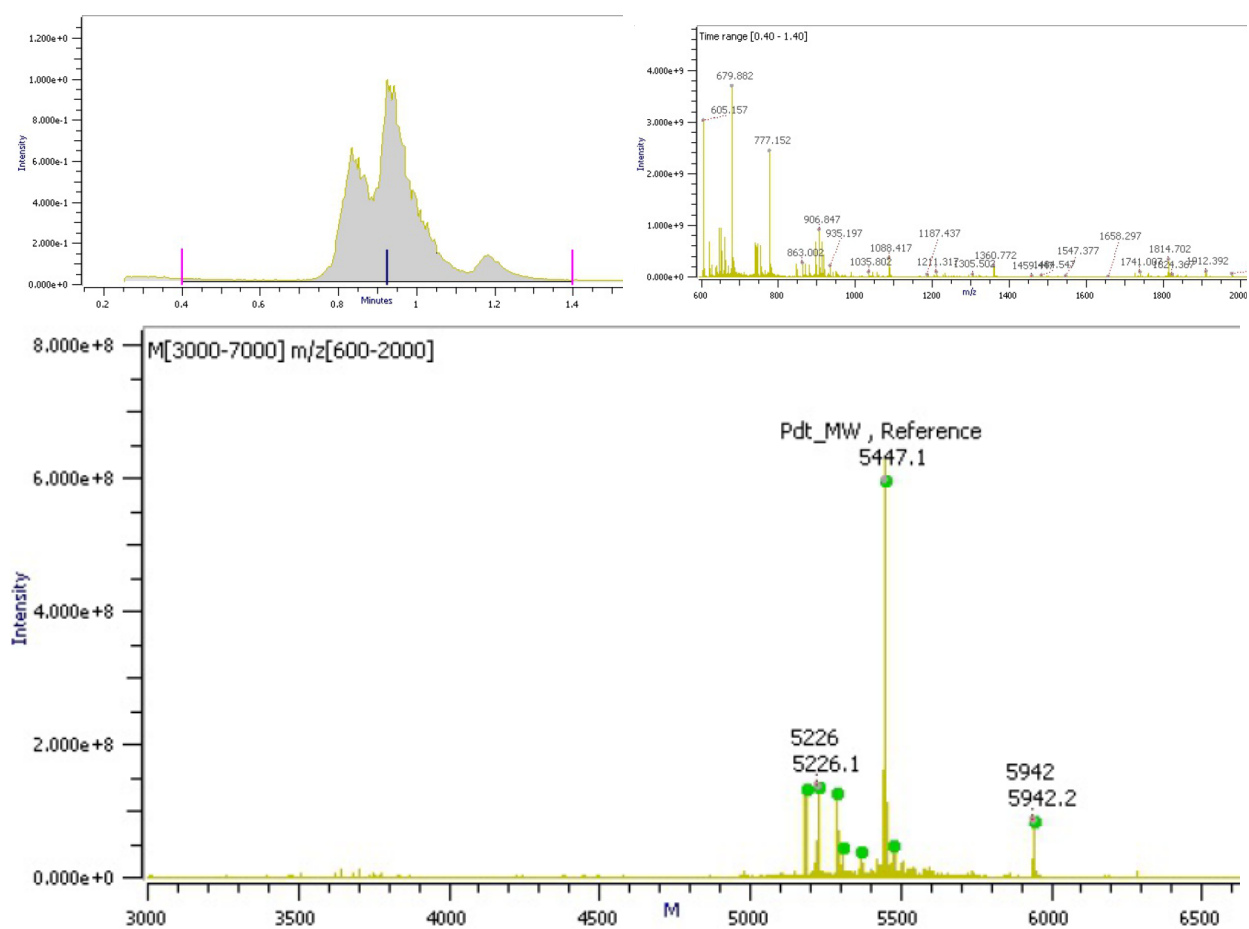
TW-N78441-15-681 - (Plot Elution Peak - Plot MS1 - Plot Deconvoluted Mass spectrum)



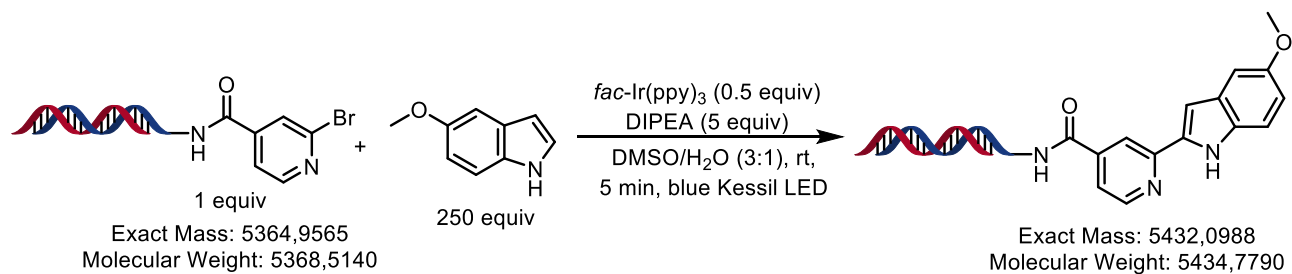
Product **60**, 67% yield



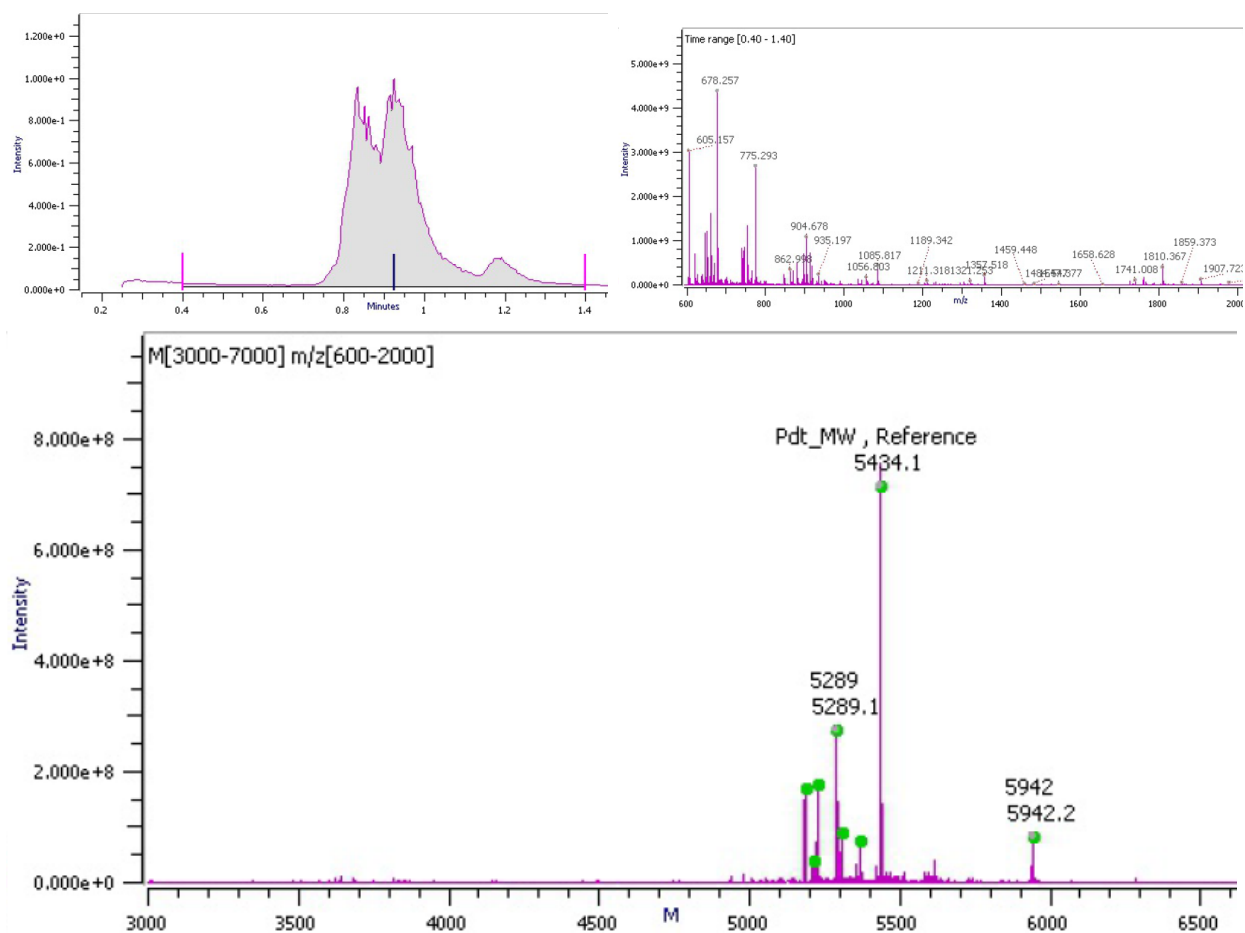
ELTM_476, TW-N78441-10-476.raw (Plot Elution Peak - Plot MS1 - Plot Deconvoluted Mass spectrum)



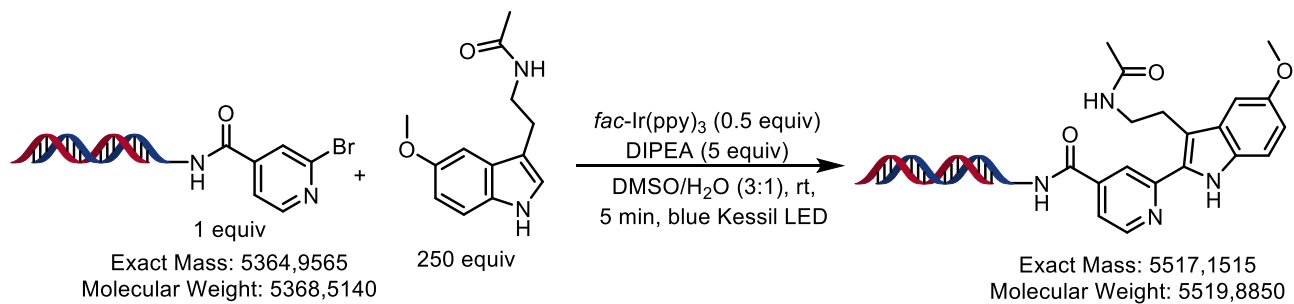
Product **6p**, 60% yield



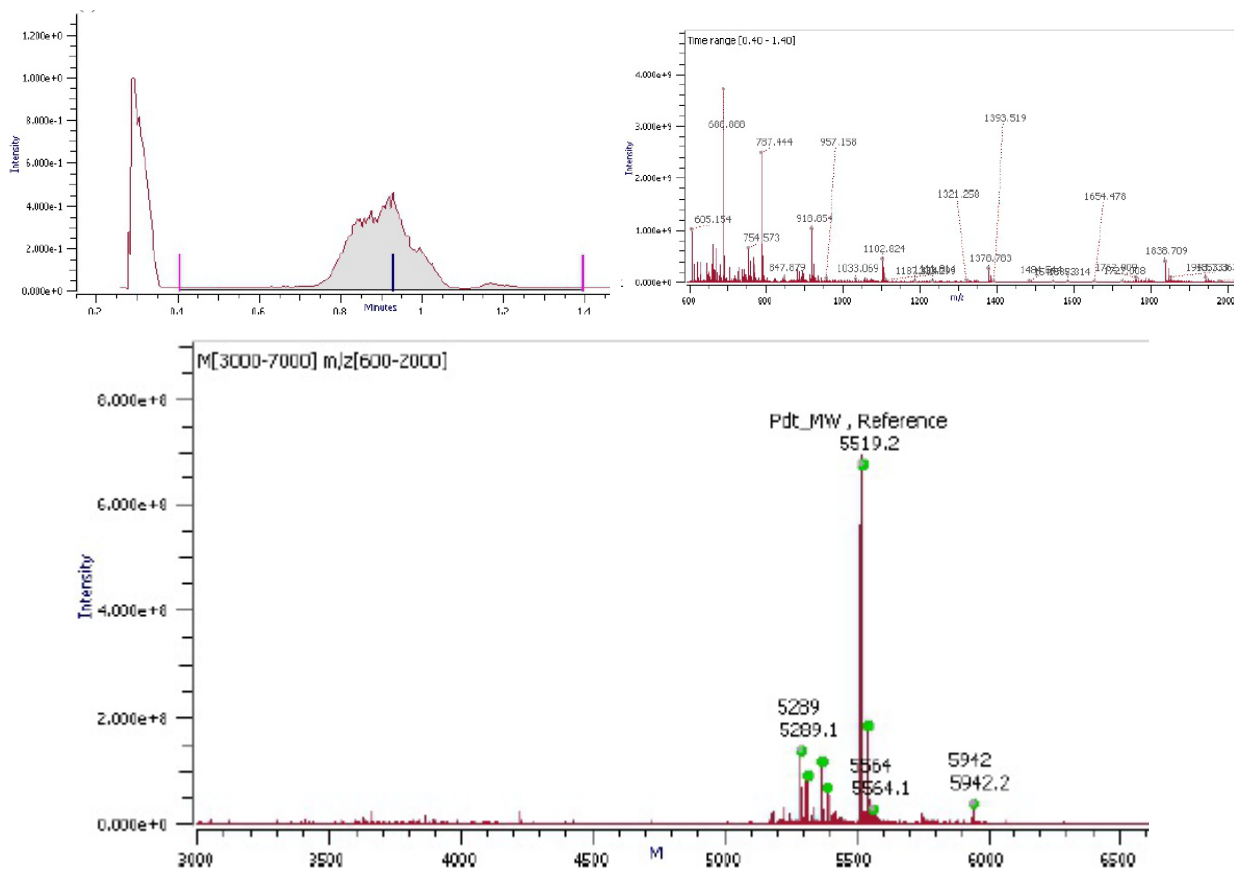
ELTM_477, TW-N78441-10-477.raw (Plot Elution Peak - Plot MS1 - Plot Deconvoluted Mass spectrum)



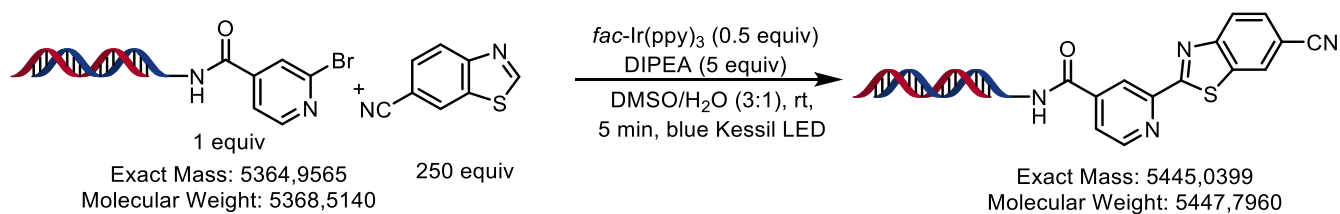
Product **6q**, 50% yield



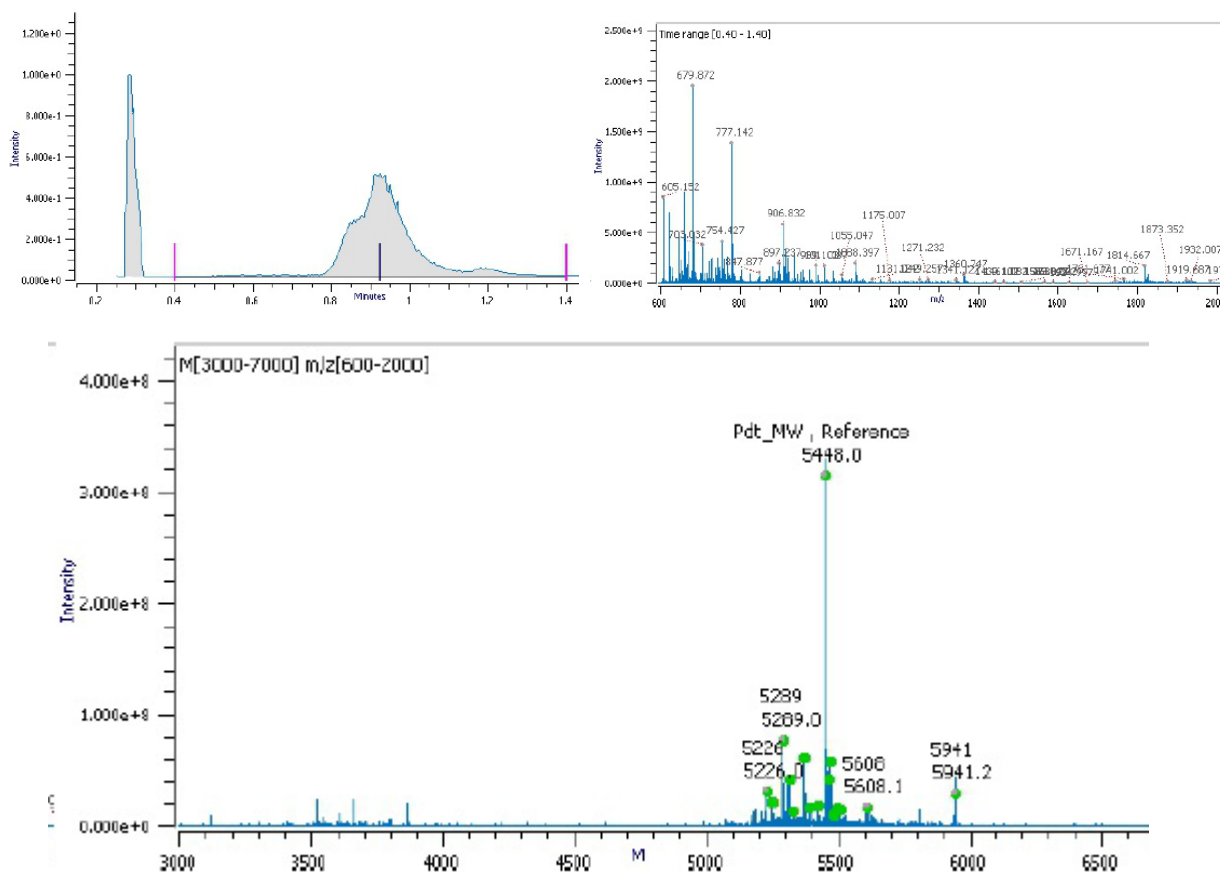
ELTM_672, TW-N78441-15-672.raw (Plot Elution Peak - Plot MS1 - Plot Deconvoluted Mass spectrum)



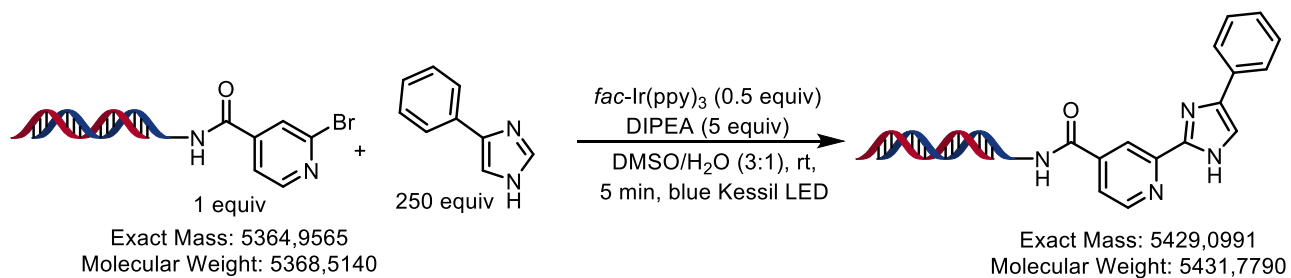
Product **6w**, 54% yield



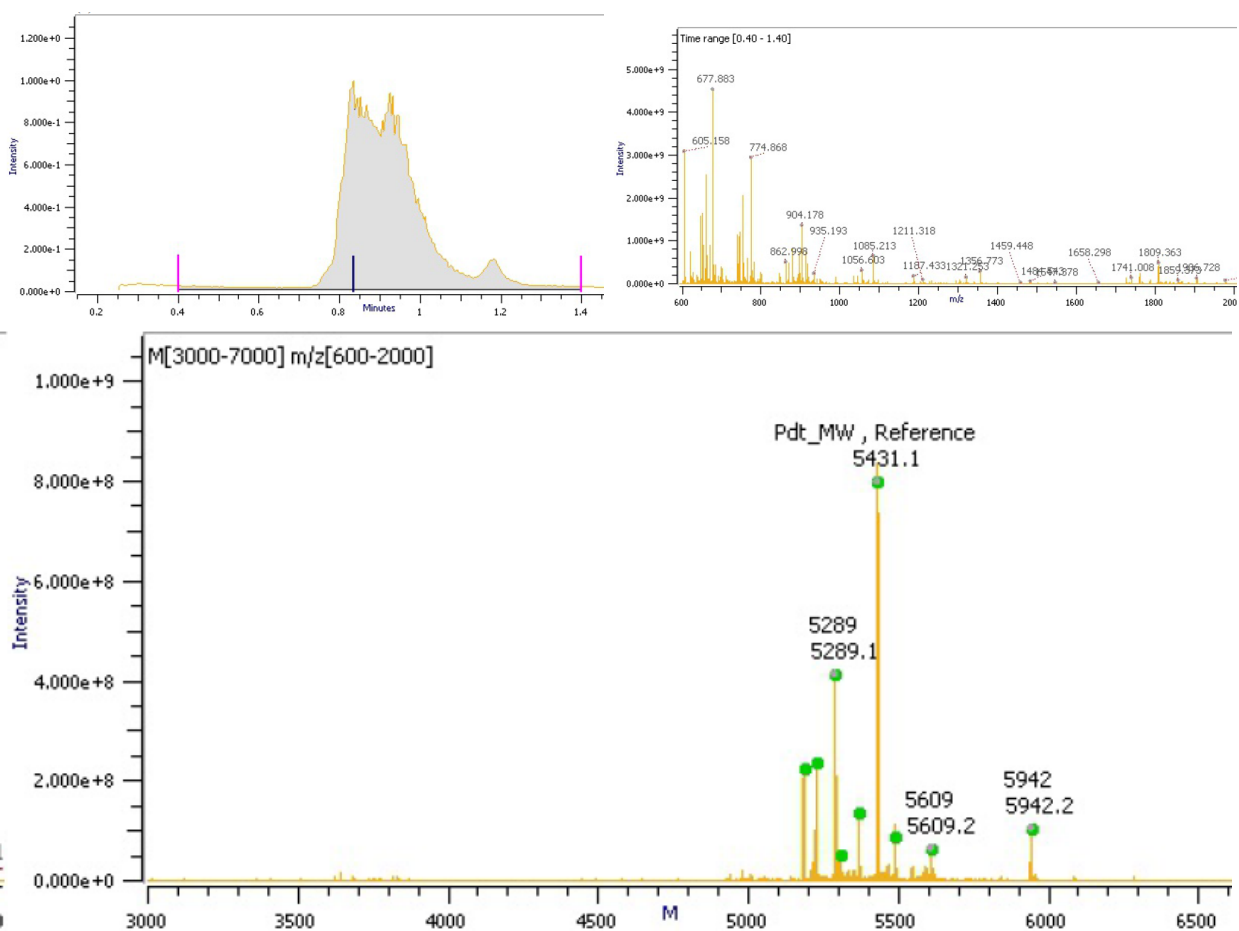
ELTM_637, TW-N78441-14-637.raw (Plot Elution Peak - Plot MS1 - Plot Deconvoluted Mass spectrum)



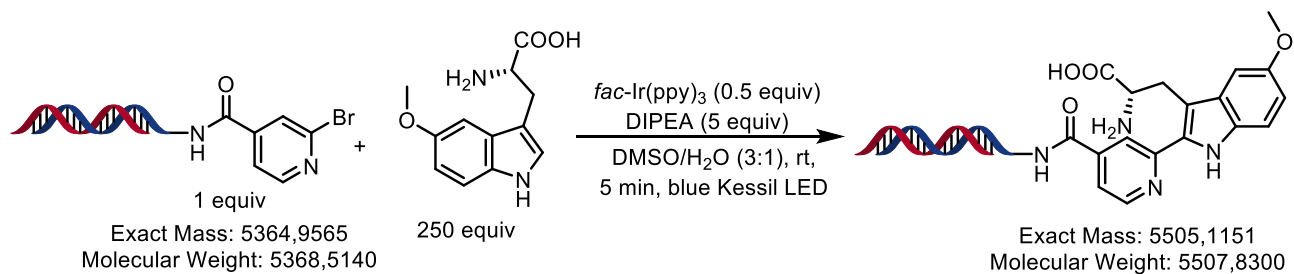
Product **6aa**, 51% yield



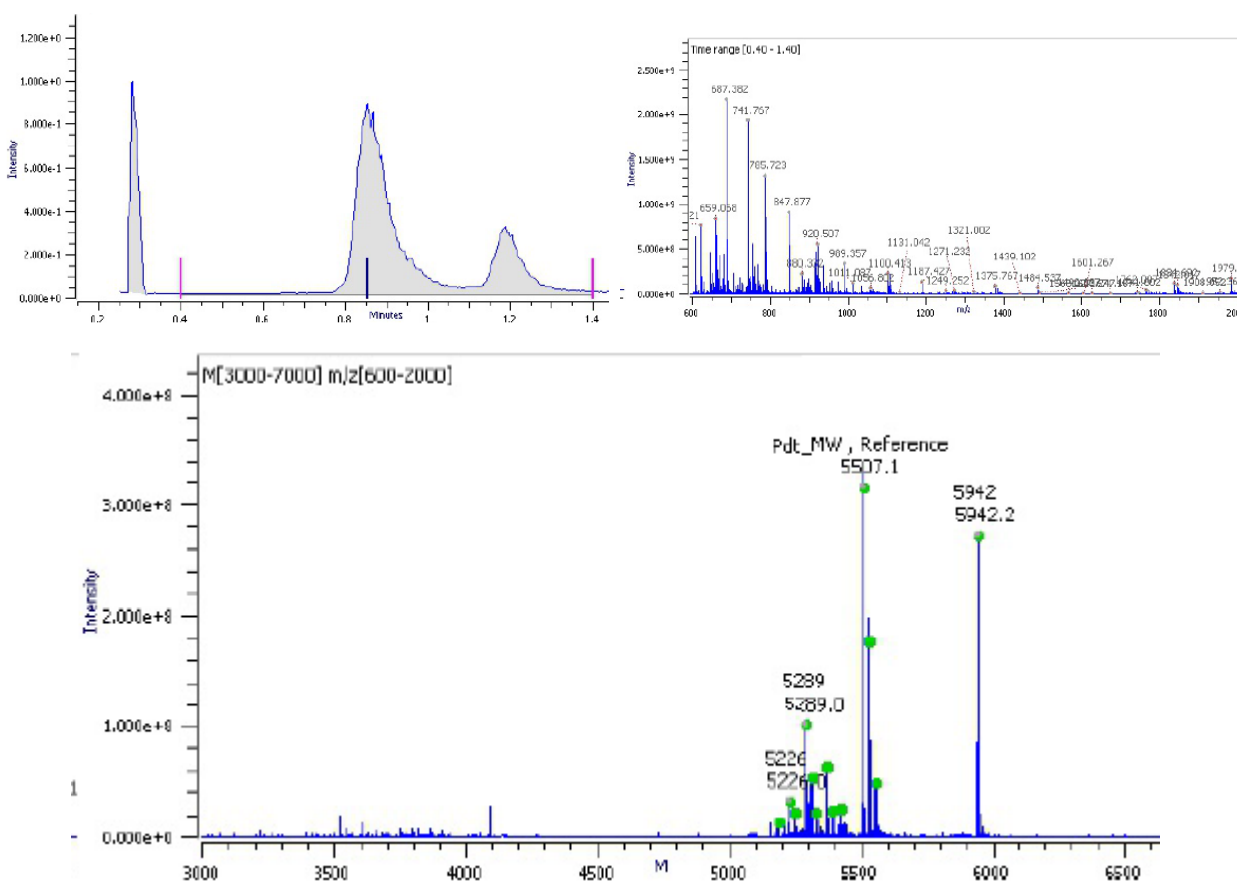
ELTM_483, TW-N78441-10-483.raw (Plot Elution Peak - Plot MS1 - Plot Deconvoluted Mass spectrum)



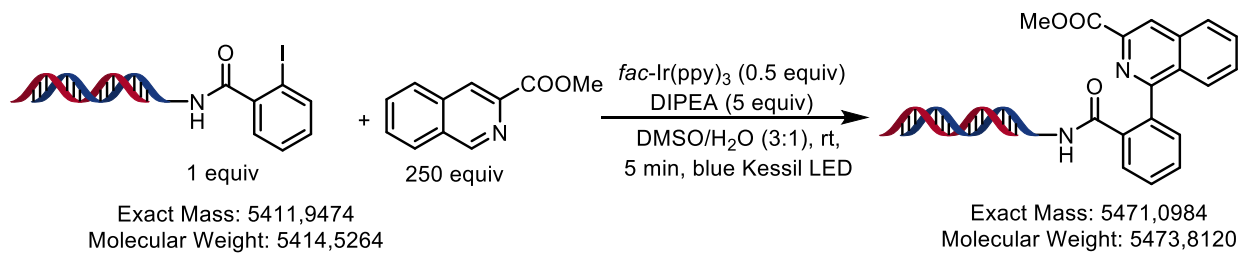
Product **6ag**, 37% yield



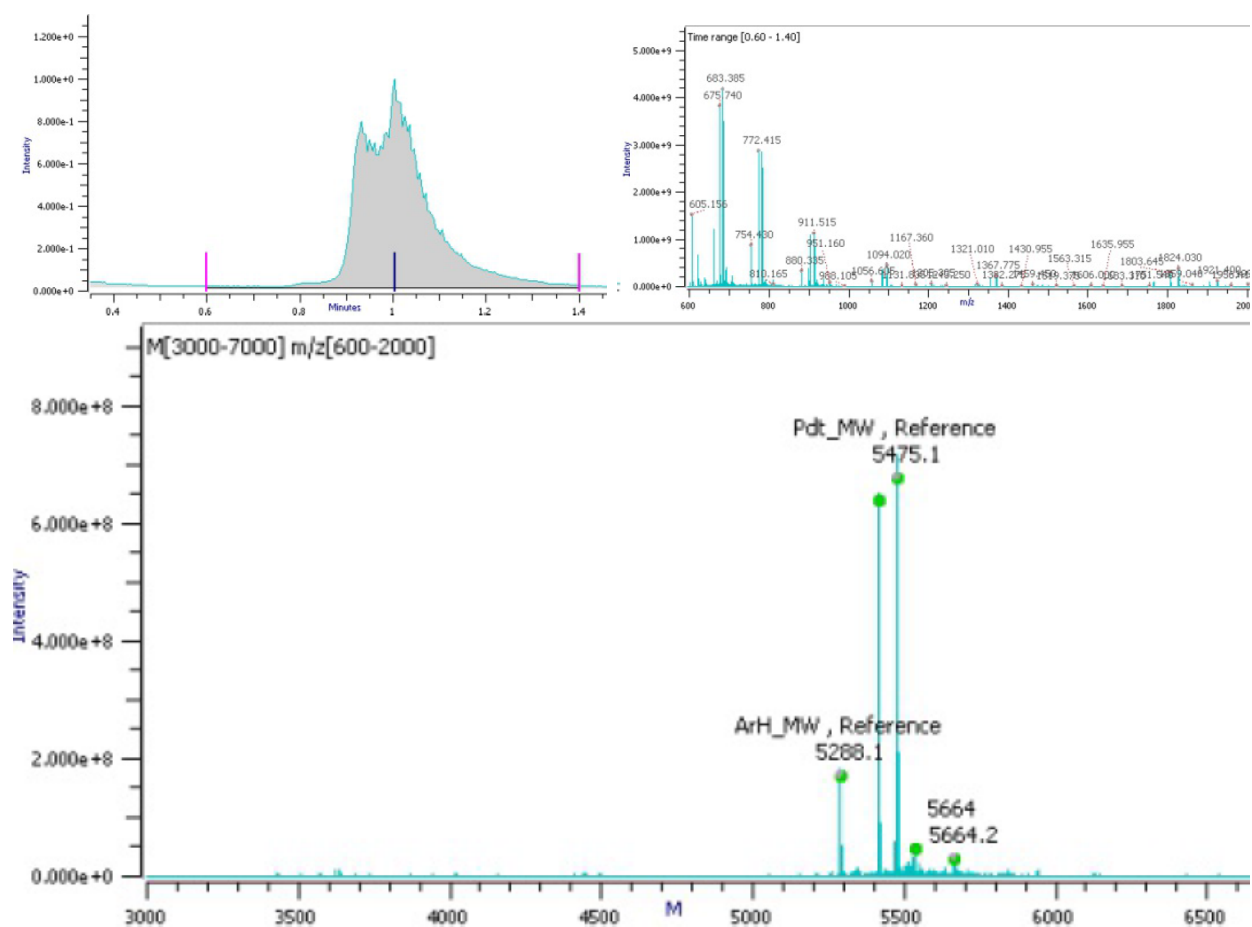
ELTM_643, TW-N78441-14-643.raw (Plot Elution Peak - Plot MS1 - Plot Deconvoluted Mass spectrum)



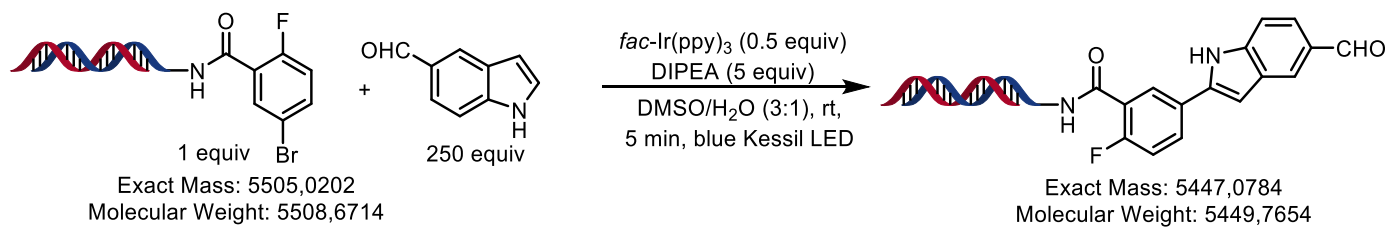
Product **7a**, 46% yield



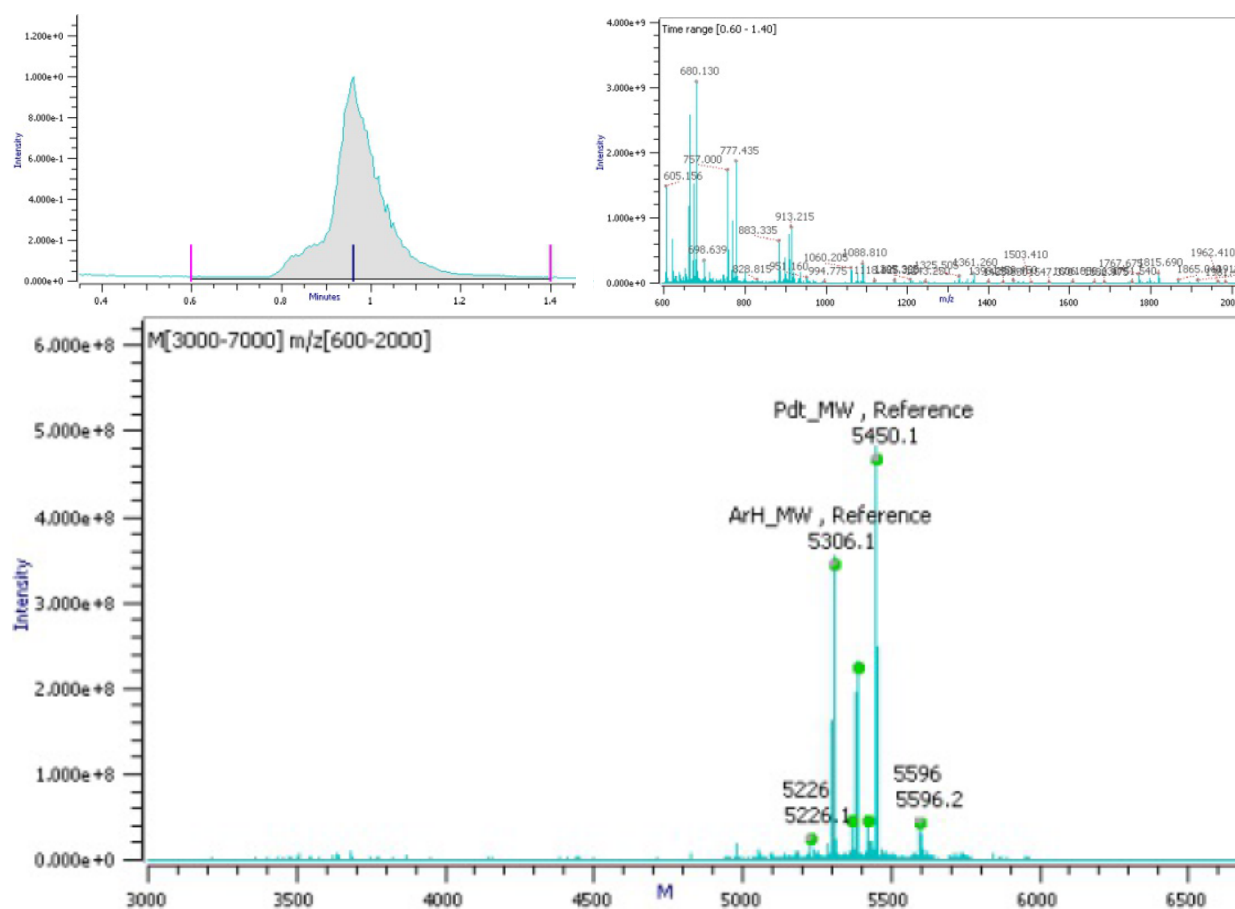
ELTM_425, TW-N78441-9-425.raw (Plot Elution Peak - Plot MS1 - Plot Deconvoluted Mass spectrum)



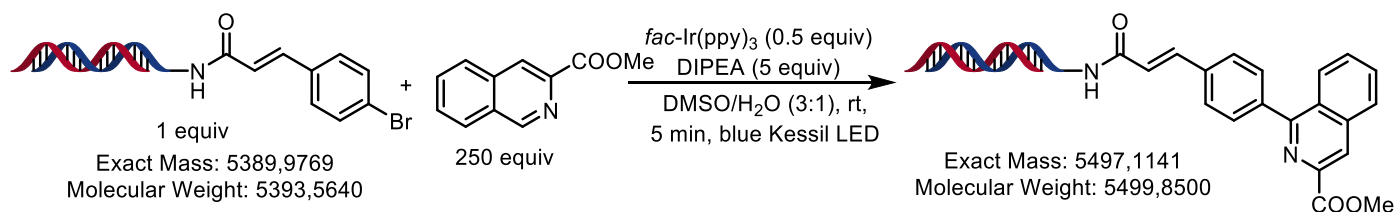
Product **8m**, 39% yield



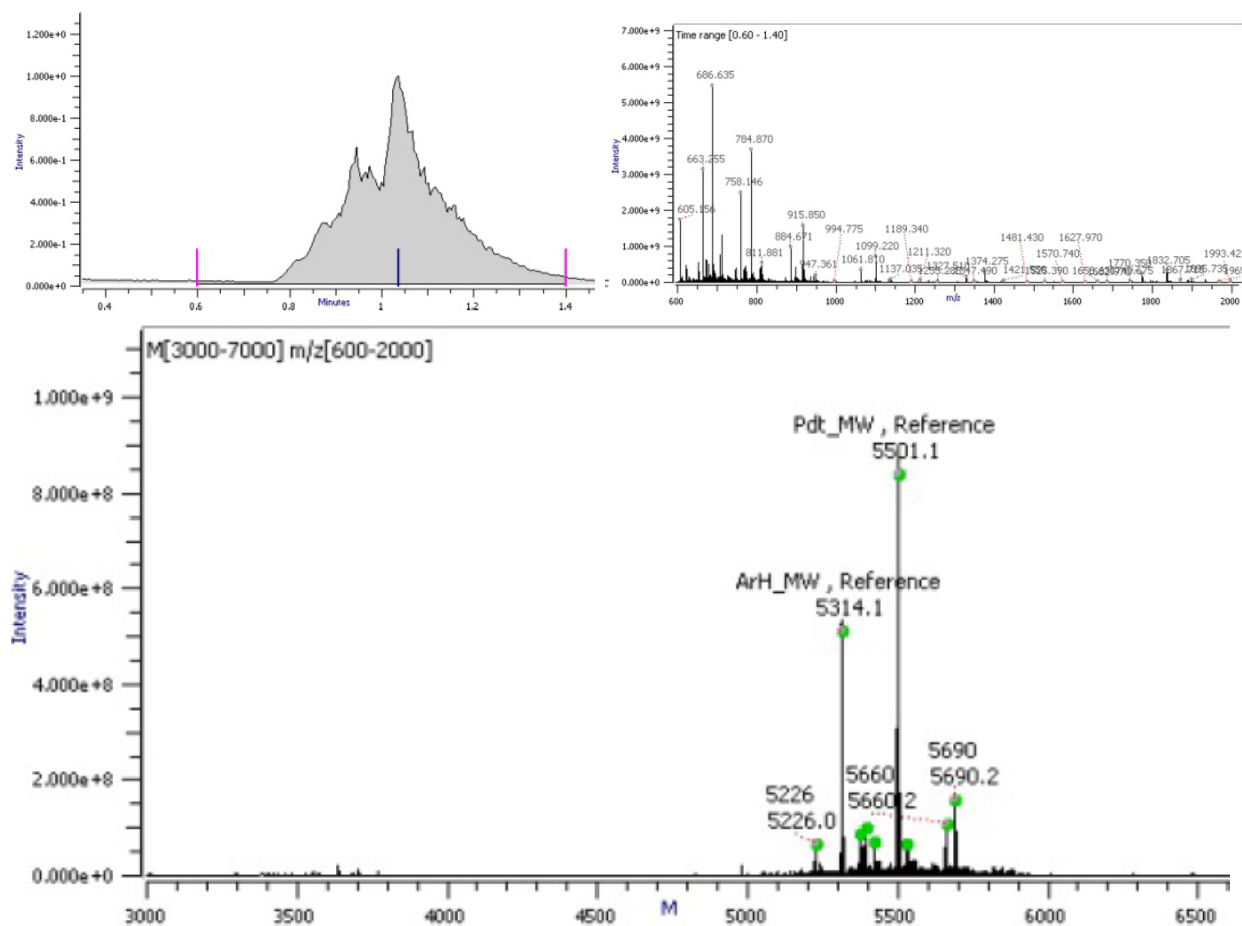
ELTM_327, TW-N78441-9-327.raw (Plot Elution Peak - Plot MS1 - Plot Deconvoluted Mass spectrum)



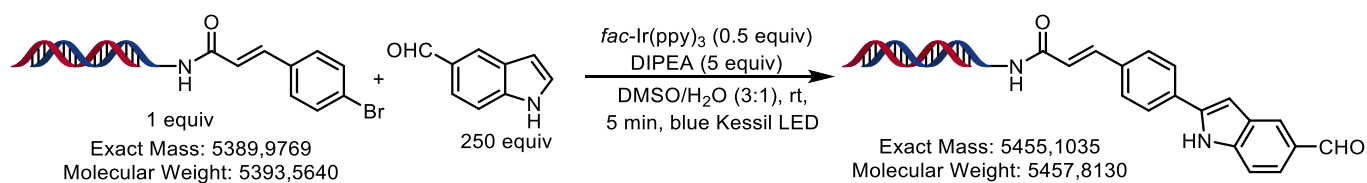
Product **12a**, 50% yield



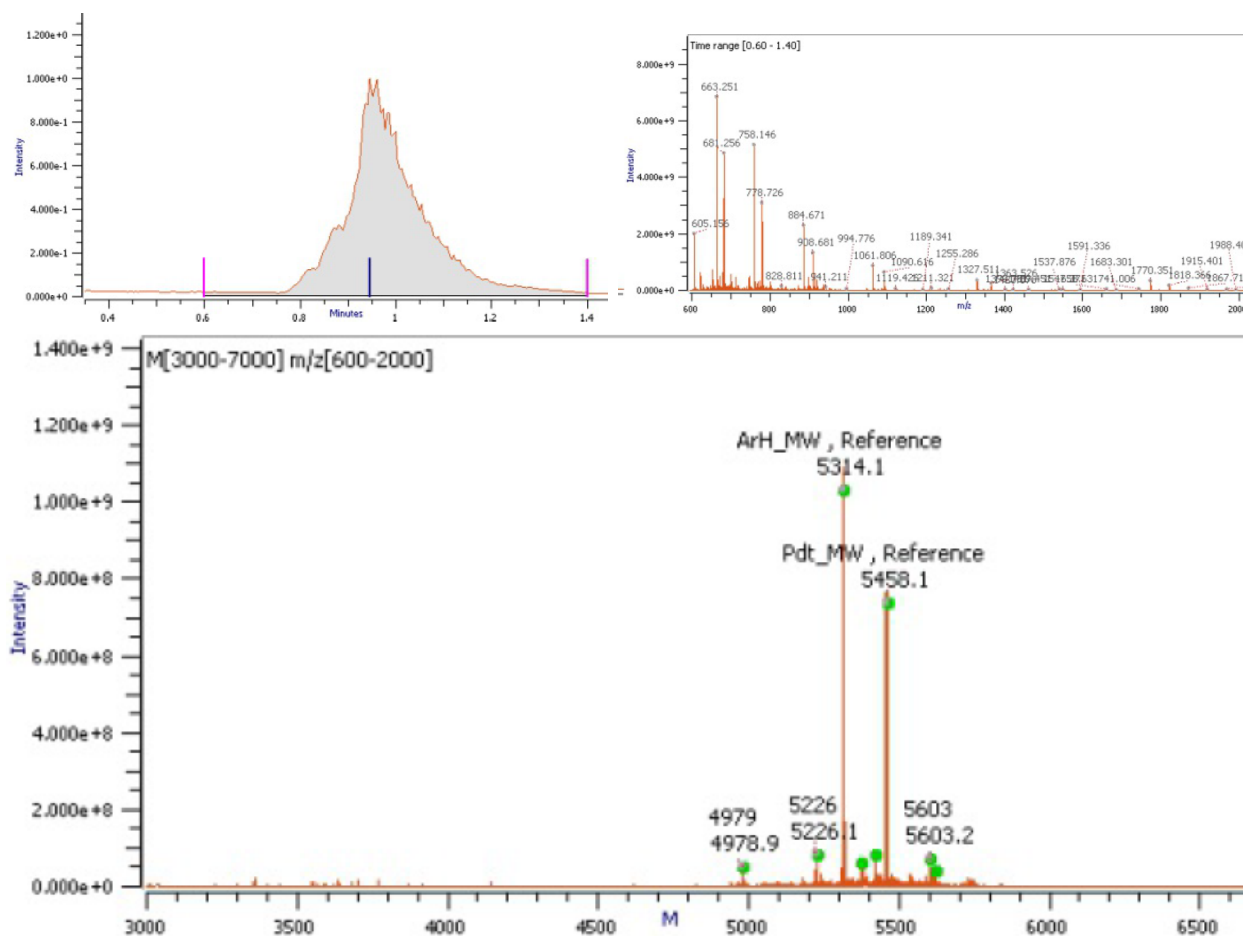
ELTM_328, TW-N78441-9-328.raw (Plot Elution Peak - Plot MS1 - Plot Deconvoluted Mass spectrum)



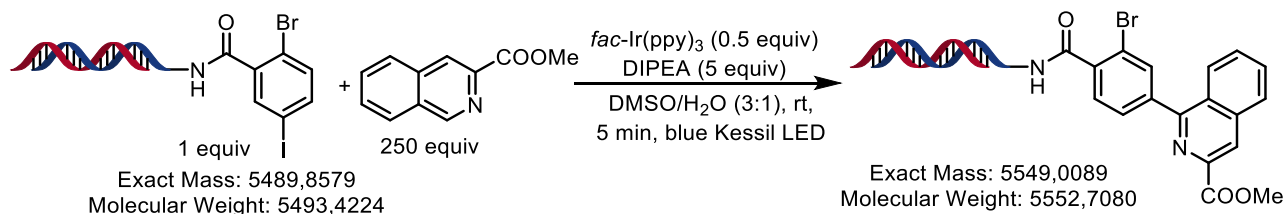
Product **12m**, 40% yield



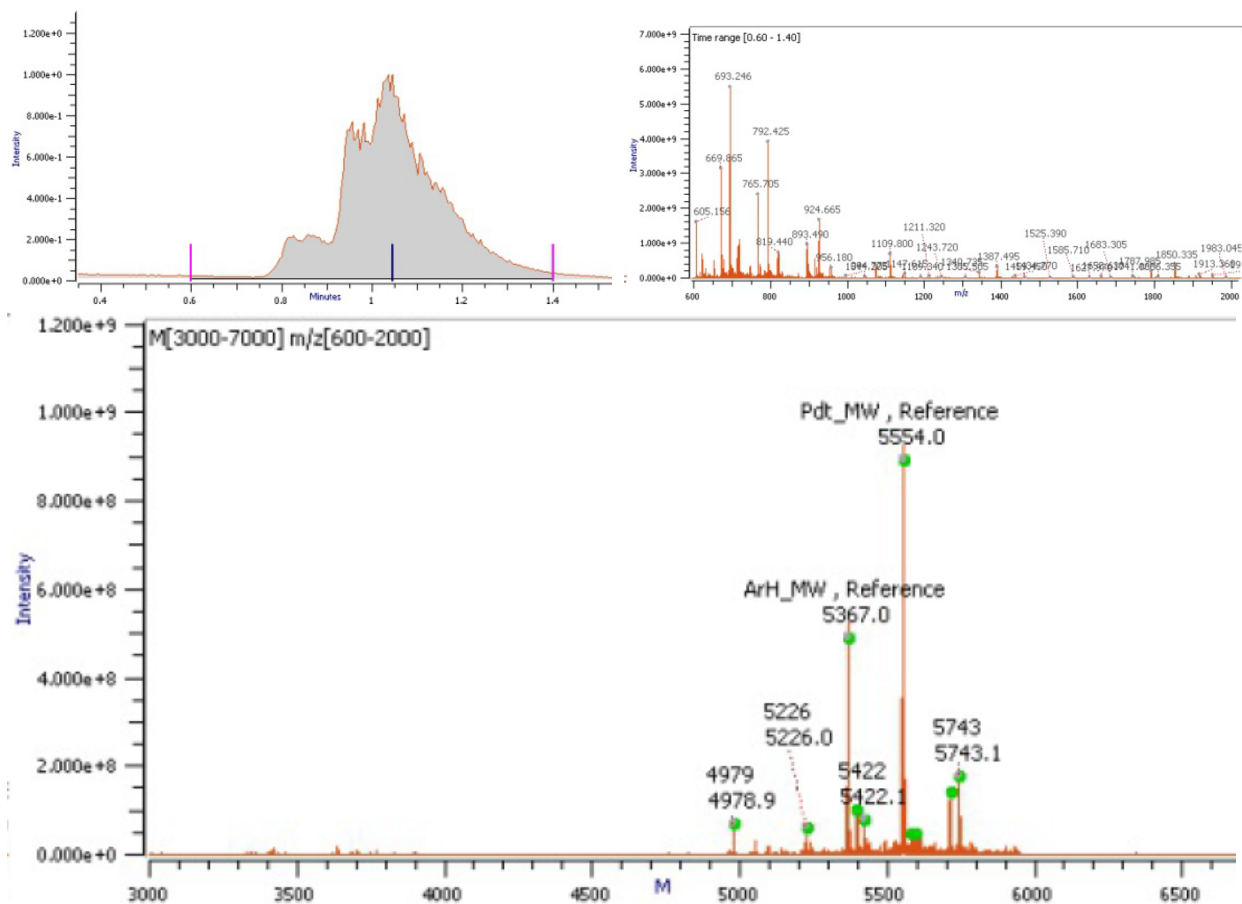
ELTM_330, TW-N78441-9-330.raw (Plot Elution Peak - Plot MS1 - Plot Deconvoluted Mass spectrum)

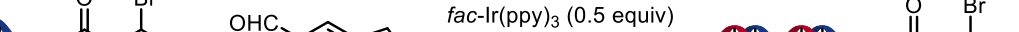


Product **13a**, 44% yield



ELTM_240, TW-N78441-9-240.raw (Plot Elution Peak - Plot MS1 - Plot Deconvoluted Mass spectrum)





Exact Mass: 5489,8579
 Molecular Weight: 5493,4224

Exact Mass: 5506,9984
 Molecular Weight: 5510,6710

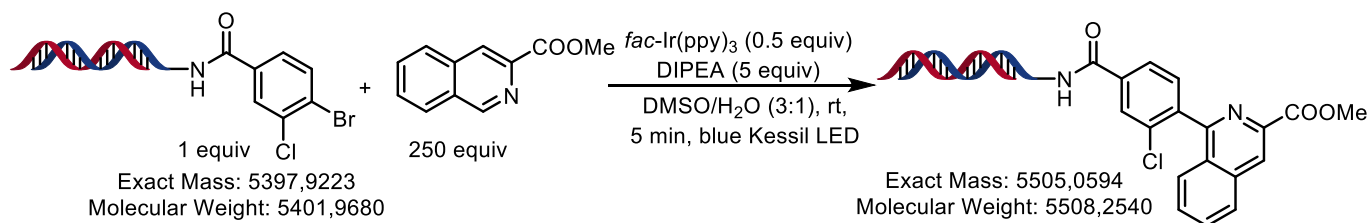
The figure displays three mass spectrometry plots related to the analysis of a sample.

Top Left Plot: A Total Ion Chromatogram (TIC) showing Intensity (Y-axis, 0.000e+0 to 1.200e+0) versus Time (X-axis, 0.4 to 1.4 Minutes). A major peak is observed at approximately 1.0 minute, marked with a blue vertical line.

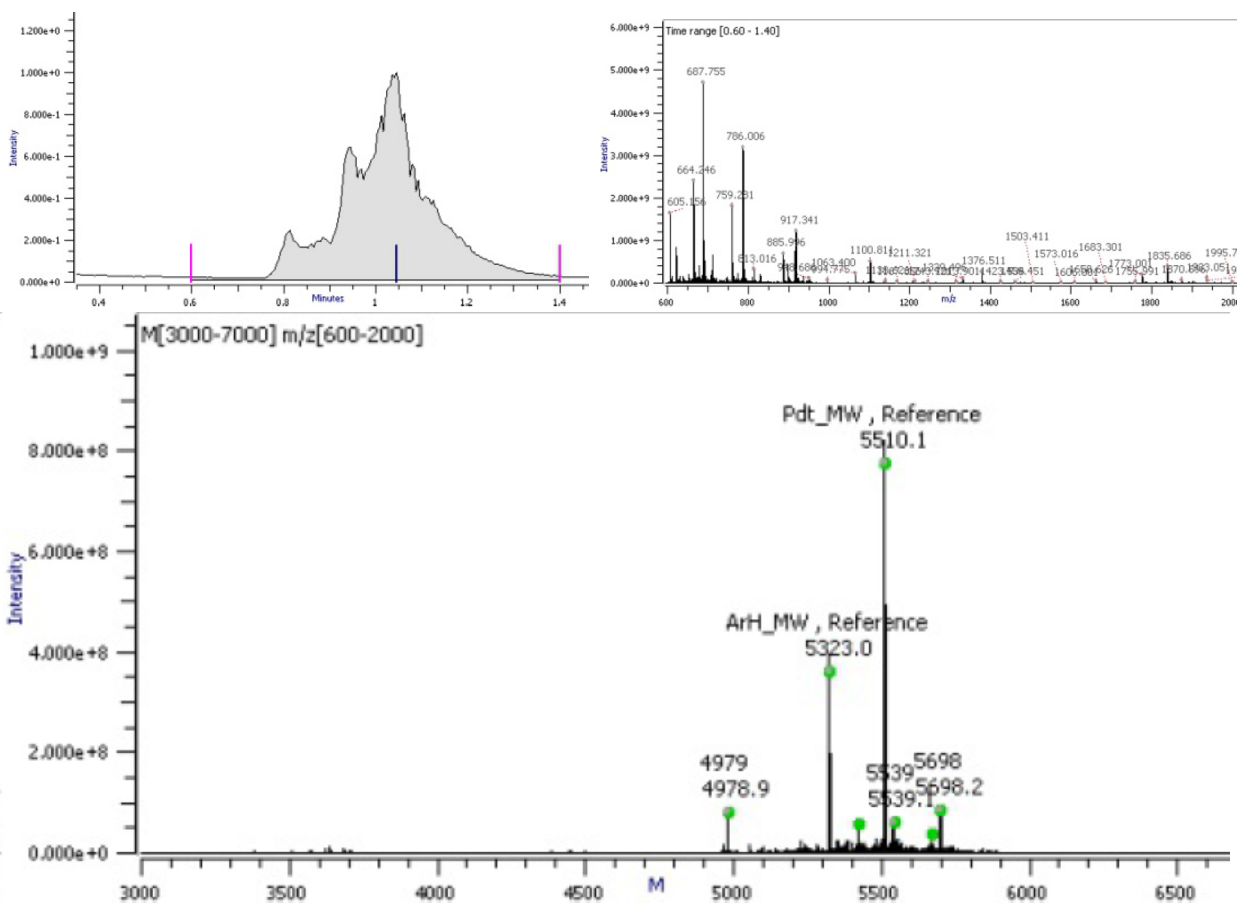
Top Right Plot: A mass spectrum showing Intensity (Y-axis, 0.000e+0 to 4.000e+9) versus m/z (X-axis, 600 to 2000). The spectrum is labeled "Time range [0.60 - 1.40]". Numerous peaks are visible, with the base peak at m/z 669.866. Other labeled peaks include 605.156, 687.870, 765.705, 786.281, 828.811, 893.490, 913.215, 1044.201, 1072.386, 1167.356, 1243.721, 1340.736, 1375.748, 1440.529, 1503.411, 1569.520, 1606.001, 1787.981, 1836.001, 1924.821, and 1938.821.

Bottom Plot: A zoomed-in mass spectrum showing Intensity (Y-axis, 0.000e+0 to 6.000e+8) versus m/z (X-axis, 3000 to 6500). The plot is labeled "M[3000-7000] m/z[600-2000]". Two prominent peaks are identified: "ArH_MW, Reference" at m/z 5367.0 and "Pdt_MW, Reference" at m/z 5511.0. Other labeled peaks include 4979, 4978.9, 5053, 5052.9, 5051.0, 5210.0, 5575, and 5575.1.

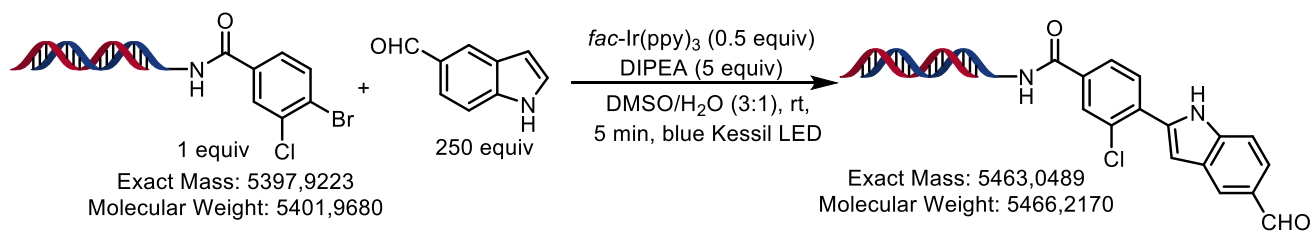
Product **14a**, 56% yield



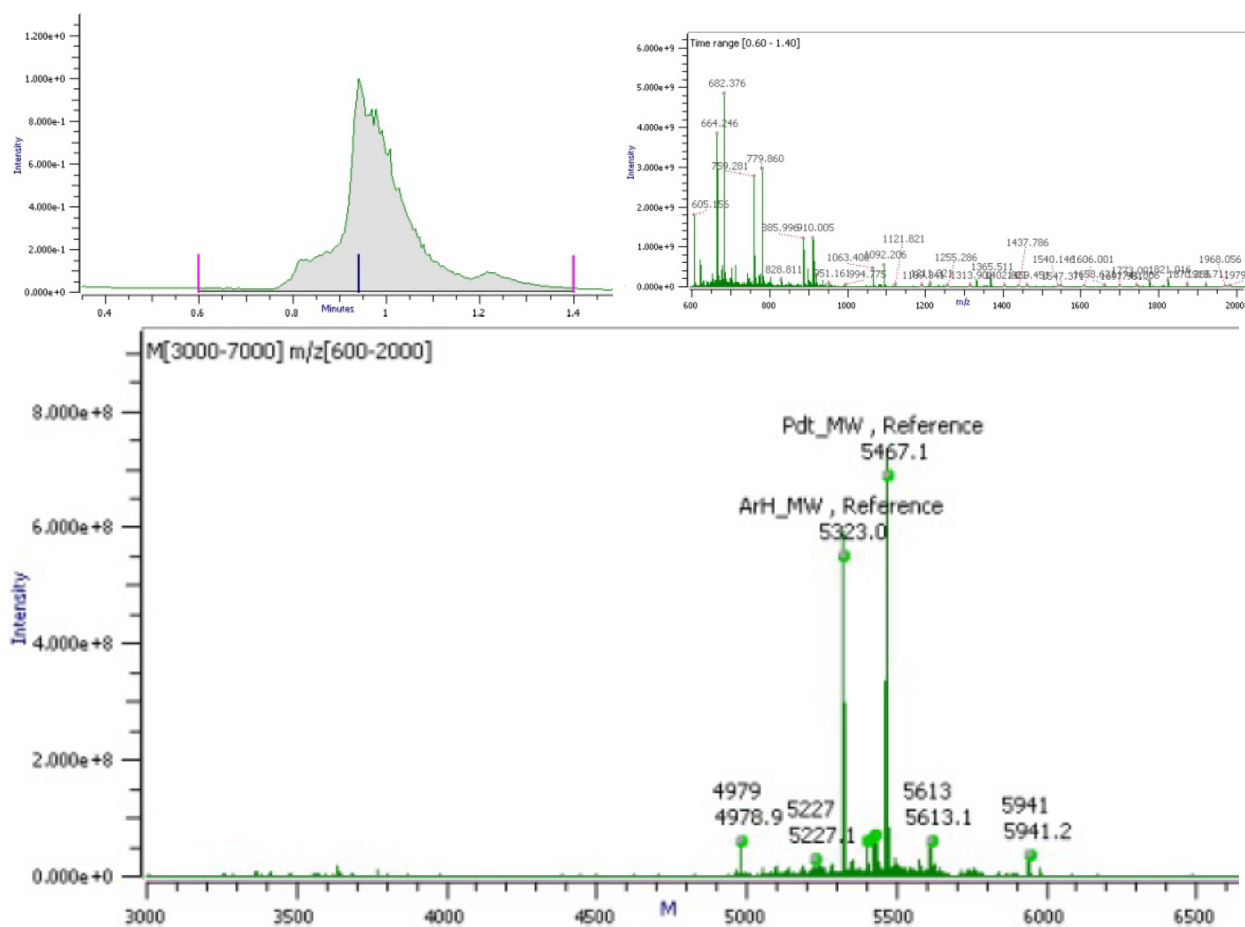
ELTM_297, TW-N78441-9-297.raw (Plot Elution Peak - Plot MS1 - Plot Deconvoluted Mass spectrum)



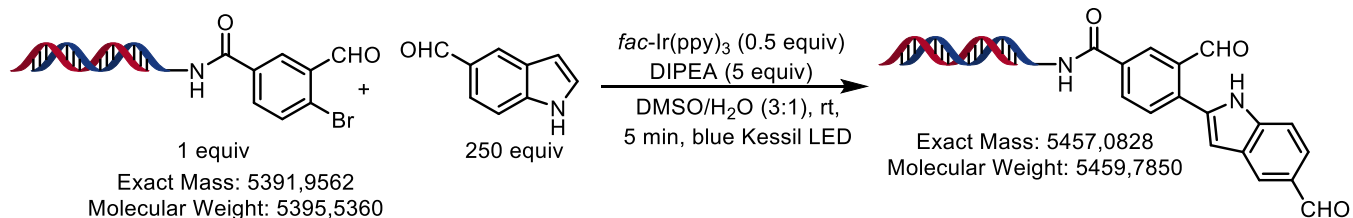
Product **14m**, 44% yield



ELTM_339, TW-N78441-9-339.raw (Plot Elution Peak - Plot MS1 - Plot Deconvoluted Mass spectrum)



Product **15m**, 50% yield



ELTM_239, TW-N78441-9-239.raw (Plot Elution Peak - Plot MS1 - Plot Deconvoluted Mass spectrum)

