

**Asymmetric synthesis of primary amines catalyzed by thermotolerant fungal  
reductive aminases**

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**ELECTRONIC SUPPLEMENTARY INFORMATION (ESI)**

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## **Section S1. General**

Solvents used were of HPLC grade and, when necessary, they were further dried over molecular sieves. Column chromatography was performed on silica gel (Fluka (Buchs, Switzerland), 220-440 mesh). Spectra from  $^1\text{H}$  and  $^{13}\text{C}$  NMR runs were recorded on a Bruker Avance 400 instrument (400 MHz for  $^1\text{H}$  and 100 MHz for  $^{13}\text{C}$ ) in  $\text{CDCl}_3$  or  $\text{CD}_3\text{OD}$  using residual protic solvent as an internal standard. Reported chemical shifts ( $\delta$ ) (in parts per million (ppm)) are relative to the residual protic solvent signal ( $\text{CHCl}_3$  in  $\text{CDCl}_3$ ,  $^1\text{H}$  = 7.26;  $\text{CDCl}_3$ ,  $^{13}\text{C}$  = 77.0;  $\text{CHD}_2\text{OD}$  in  $\text{CD}_3\text{OD}$ ,  $^1\text{H}$  = 3.31;  $\text{CD}_3\text{OD}$ ,  $^{13}\text{C}$  = 49.0).

High-resolution mass spectrometry (HRMS) was recorded using a Waters LCT time-of-flight mass spectrometer, connected to a Waters Alliance LC (Waters, Milford, MA, USA). Data were processed with Waters Masslynx software. Samples for IR spectroscopy were run on a Nicolet 5700 FT-IR (Thermo Electron, Madison, WI, USA) using a Smart Orbit Diamond accessory.

Chiral normal phase HPLC was performed on an Agilent system (Santa Clara, CA, USA) equipped with a G1379A degasser, G1312A binary pump, a G1367A well plate autosampler unit, a G1316A temperature controlled column compartment and a G1315C diode array detector. CHIRALCEL<sup>®</sup>OD-H Analytical (Daicel (Osaka, Japan), 250 mm length, 4.6 mm diameter, 5  $\mu\text{m}$  particle size) columns was used. The typical injection volume was 10  $\mu\text{L}$  and chromatograms were monitored at 265 nm. All solvent mixtures are given in (v/v) ratios.

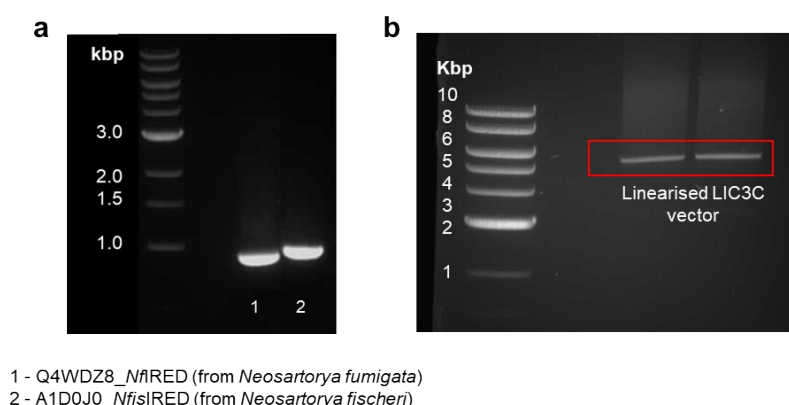
GC analysis was performed on a Agilent 6850 GC (Agilent, Santa Clara, CA, USA) with a flame ionization detector (FID) and autosampler equipped with a 25 m CP-Chirasil-DEX CB column with 0.25 mm inner diameter and 0.25  $\mu\text{m}$  film thickness (Agilent, Santa Clara, CA, USA), BetaDex-325 and BetaDex-120 column (30 m x 0.25 mm x 0.25  $\mu\text{m}$ ) from Supelco (Bellefonte, PA, USA) and a 30 m HP-1 column with 0.32 mm inner diameter and 0.25  $\mu\text{m}$  film thickness (Agilent, Santa Clara, CA, USA). Where necessary, samples were derivatised using acetic anhydride with an excess of triethylamine at room temperature prior to analysis on the GC-FID.

## Section S2. Target Selection, Cloning and Expression

Based on the sequence and structure of AspRedAm, a BLAST<sup>1</sup> search of the databases was performed to select new RedAm targets containing residues D169, N93, Y177 and Q240 (AspRedAm numbering) that were previously shown to be important for catalysis. The sequences of the RedAm targets, from *Neosartorya fumigata* (*Nf*RedAm), and *Neosartorya fischeri* (*Nfis*RedAm) both have 58% overall sequence homology with AspRedAm. Codon-optimized genes for the recombinant expression of each in *E. coli* were synthesized by GeneArt (Life technologies) and cloned into a locally engineered pET-YSBLIC3C vector<sup>2</sup> using the In-Fusion® HD Cloning kit (Clontech Laboratories, Inc.). The gene of interest was amplified by PCR reaction using relevant primers (Table S1) and purified using a QIAquick® Gel Extraction Kit. The In-Fusion reaction was performed using linearized YSBLIC3C vector and purified genes according to manufacturer's protocol. Insertion of target genes into the final constructs was verified by DNA sequencing.

Target gene	Primer ID	Base Sequence 5' to 3'
<i>Nfis</i> RedAm	fwd	<u>TTCCAGGGACCAGCAATGAGCAGCGTTAGCATTTTTGGTCTG</u>
	rev	<u>CATGCTAGCCATATGTTAGGCGCTTTTCACAAAATCAATCAGGC</u>
<i>Nf</i> RedAm	fwd	<u>TTCCAGGGACCAGCAATGAGCAGCGTTAGCATTTTTGGTCTGG</u>
	rev	<u>CATGCTAGCCATATGTTAGGTGCTTTTCACAAAATCAATCAGGC</u>

**Supplementary Table S1.** Primers used for Infusion Cloning of RedAm genes into pET-YSBLIC-3C.



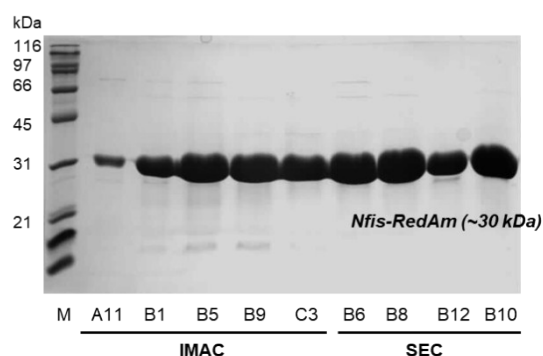
**Supplementary Figure S1.** a. DNA gel visualization of PCR products of the corresponding genes for *Neosartorya* homologues. b. DNA visualization of linearized YSBLIC3C vector used for In-Fusion reaction

The plasmids containing the genes for target enzymes were used to transform *E. coli* BL21(DE3) competent cells for gene expression. Pre-cultures were grown in LB-medium (5 mL) containing 30 µg mL<sup>-1</sup> kanamycin for 18 h at 37 °C with shaking at 180 r.p.m. 1 L

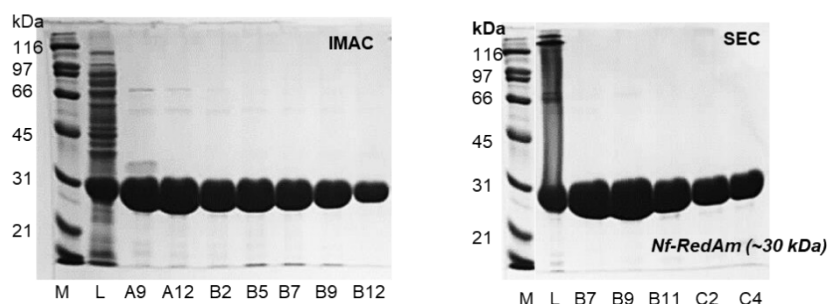
volume cultures were inoculated with the pre-culture (5 mL) and incubated at 37°C, with shaking at 180 r.p.m. until an OD<sub>600</sub> of 0.6-0.8 was reached. Gene expression was induced by addition of IPTG (1 mM) and shaking was continued overnight at 18°C with shaking at 180 r.p.m. The cells were then harvested by centrifugation at 5000 g for 20 min and resuspended in 50 mM Tris-HCl buffer pH 7.5, containing 300 mM NaCl. Cells were disrupted by ultrasonication for 3 x 5 min, 30 s on, 30 s off cycles, and the suspension was centrifuged at 50,000 g for 30 min to yield a clear lysate.

The N-terminal His<sub>6</sub>-tagged proteins were purified using immobilised-metal affinity chromatography (IMAC) using Ni-NTA column, followed by size exclusion chromatography (SEC) (Figure 3a-d). In each case, the lysate was loaded onto a pre-equilibrated Ni-NTA column, followed by washing with a load buffer (50 mM Tris-HCl, 300 mM NaCl, 20 mM imidazole pH 7.5). The bound protein was eluted using a linear gradient with buffer containing 500 mM imidazole. RedAm fractions were pooled, concentrated and loaded onto a HiLoad 16/600 Superdex 75 gel filtration column pre-equilibrated with 50 mM Tris-HCl, 300 mM NaCl pH 7.5 buffer. The concentrated protein sample after gel filtration was used for crystallization screening and biotransformation reactions.

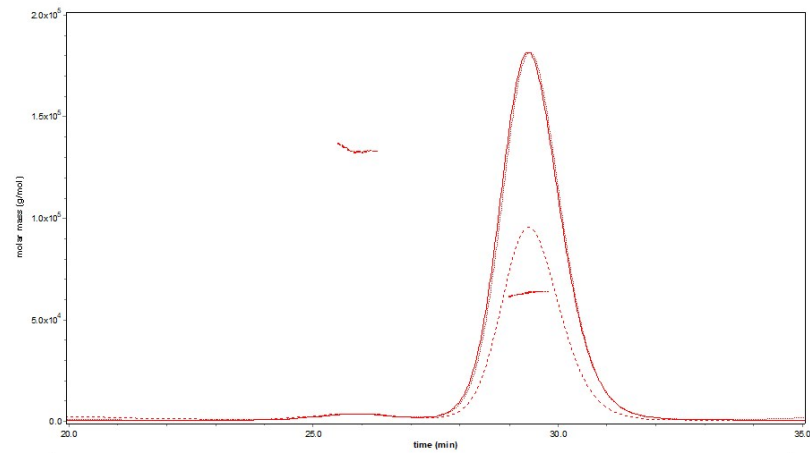
**a. NfisRedAm (from *Neosartorya fisheri*)**



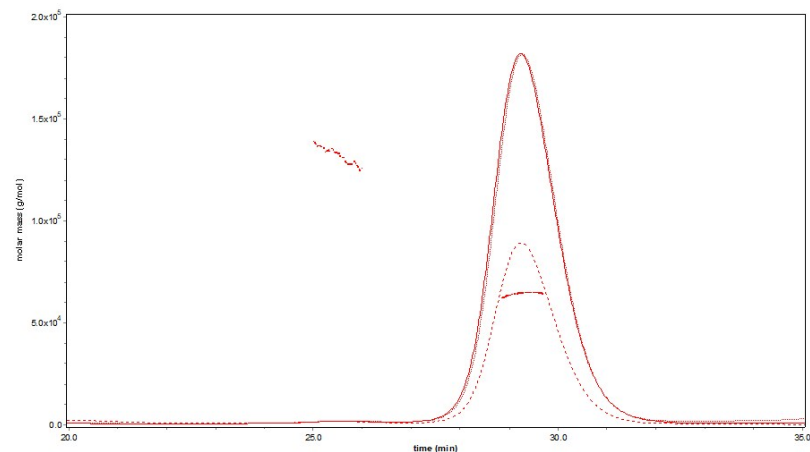
**b. NfRedAm (from *Neosartorya fumigata*)**



**Supplementary Figure S2.** Purification of *Neosartorya* RedAms. SDS-PAGE analysis of the IMAC purification using Ni-NTA column (left) and size exclusion chromatography (right) are presented.

**A****Molar Mass vs. elution time: NfRedAm**

Peak	from	to (min)	Amount (μg)	MW kDa
Major Peak	27.14	32.00	385	63.15
Minor Peak	24.00	26.30	9.4	133.7

**B****Molar Mass vs. elution time: NfisRedAm**

Peak	from	to (min)	Amount (μg)	MW kDa
Major Peak	26.80	32.00	293	64.24
Minor Peak	24.00	25.80	3.7	132.0

**Supplementary Figure S3.** SEC-MALS analysis reveals that *NfRedAm* and *NfisRedAm* exist as dimers in solution. UV-trace and an average molecular weight trace (red), calculated from the refractive index and light scattering signal giving mass estimation of 63 kDa which corresponds to a dimer. A minor peak corresponding to larger oligomer (tetramer) was observed in a ratio of 40 to 1 for *NfRedAm* and 80 to 1 for *NfisRedAm* when compared with the dimer.

## Protein sequences of the Reductive aminases from *Neosartorya* spp.

Reductive aminase from *Neosartorya fumigata* (*Nf*RedAm)

MSSVSIFGLGAMGTALASRFLEEKYKVAVWNRSPKASSLLGKGATLSHTAVDGINASDLIIICLLDNA  
AVEATLAGALDHLHGKTIINLTNGTPDQARKLSDFVSHGARYVHGGIMATPSMIGSPYALVLYSGSP  
DAFKAAEGDLSVLAKCVFLGEDAGTASLHDLALLSGMYGLFSGFLHATALVRSSTPAVKFMDLLVPW  
LGAMTEYTKGMAKQIDEGKYTSEGSNLAMQLVGIQNIIDASEAQQVSAEFIRPMKEFMQKAVAAGHG  
GDDISSLIDFVKST

Reductive aminase from *Neosartorya fischeri* (*Nfis*RedAm)

MSSVSIFGLGAMGTALASRFLEEKYKVAVWNRSPKASSLLEKGATLSYTAVDGINASDLIIICLLDNAA  
VEATLAGALDHLHGKTIINLTNGTPDQARRLSDFVSHGARYVHGGIMATPSMIGSPHALVLYSGSPD  
AFKAAEADLSVLAKCVFLGEDAGSASLHDLALLSGMYGLFSGFLHATALVRSSTPAVKFVDLLVPWLG  
AMTEYTKGMARQIDEGNYASEGSNLGMQLVAIQNIIDASAAQKVSADFIIRPMKEFMGEAVAAGHGGD  
DISSLIDFVKSA

## Thermal Denaturation Studies

CD thermal unfolding measurements were performed using a Jasco J810 CD Spectrophotometer fitted with a computer-controlled Peltier temperature control unit, using protein solutions at 0.25 mg mL<sup>-1</sup> in 100 mM NaPi pH7.8 containing 1 mM NADPH cofactor. The protein solution was heated through a 5 °C ramp with a 5 min relaxation time between the recording of CD spectra at different temperatures from 20-90 °C. The unfolding curves were built by using the CD signal at 220 nm to obtain melting temperature values ( $T_m$ ). The results are shown in **Figure S4**. Unfolding of fungal homologues was studied by recording CD<sub>222</sub> at different temperatures (20-85 °C) as a measure of thermodynamic stability in comparison to previously reported *Asp*RedAm.

## Section S3. Protein Crystallisation; Data Collection and Refinement.

### Protein crystallisation

Initial screening of crystallization conditions was performed using commercially available INDEX (Hampton Research), PACT premier and CSSI/II (Molecular Dimensions) screens in 96-well sitting drop trays. Further optimization was carried out in a 24-well hanging-drop format to obtain optimised crystals for X-ray diffraction. Crystals of *Nf*RedAm-apo were grown using *Nf*RedAm at 40 mg mL<sup>-1</sup> in 50 mM Tris pH 7.5, 300 mM NaCl in a drop with 1 µL protein; 2 µL mother liquor containing 3 M NaCl, 0.1 M Tris pH 8.5 and 0.5% glycerol as additive. For co-crystallization experiments, 0.2 M stock solutions of cofactor NADP<sup>+</sup> was prepared in water. 1 M stock solutions of carbonyl **2** (in DMSO) and 1 M propargylamine was prepared in 100 mM Tris pH 8.5. *Nf*RedAm- NADP<sup>+</sup> crystals were grown with *Nf*RedAm at

40 mg mL<sup>-1</sup> in 50 mM Tris pH 7.5, 300 mM NaCl using a drop containing 0.15  $\mu$ L protein: 0.15  $\mu$ L mother liquor, the latter comprising 20% PEG (polyethylene glycol) 6000 (w/v), 0.2 M CaCl<sub>2</sub>·2H<sub>2</sub>O, 0.1 M HEPES pH 7 along with ligands 2 mM NADP<sup>+</sup>, 5 mM substrate **2** and **a** each, but density for the substrates was not observed in the structure obtained.

### Data collection, structure solution and refinement

Crystals of *Nf*RedAm were transferred into a cryoprotectant solution of 10% (w/v) glycerol in the mother liquor using nylon CryoLoops™ (Hampton Research) before flash-cooling with liquid nitrogen. The datasets described in this report were collected at the Diamond Light Source, Didcot, Oxfordshire, U.K. on beamlines I04-1 (*apo*-) and I03 (NADP<sup>+</sup> complex). Data were processed and integrated using XDS <sup>3</sup> and scaled using SCALA <sup>4</sup> included in the Xia2 processing system <sup>5</sup>. Data collection statistics are provided in **Table S2**. Crystals of *apo*-*Nf*RedAm were obtained in space group *P*3<sub>2</sub>2<sub>1</sub>, with one molecule in the asymmetric unit; crystals of the NADP<sup>+</sup> complex were in space group *P*1. The solvent content in the crystals was 67% and 47%. The structure of the *apo*-*Nf*RedAm was solved by molecular replacement using MOLREP <sup>6</sup> with the monomer of *At*RedAm (PDB Code 6EOD) <sup>7</sup> as the model. The structure was built and refined using iterative cycles in Coot <sup>8</sup> and REFMAC,<sup>9</sup> employing local NCS restraints in the refinement cycles. The structure of *apo*-*Nf*RedAm was then used to solve the structure of the NADP<sup>+</sup> complex. Following building and refinement of the protein and water molecules in this complex, residual density was observed in the omit maps at the dimer interfaces, which could be clearly modelled as NADP<sup>+</sup>. The final structures exhibited %  $R_{\text{cryst}}/R_{\text{free}}$  values of 20.0/23.5 and 28.6/35.7 respectively. Refinement statistics for the structures are presented in **Table S1**. The Ramachandran plot for the *apo*-*Nf*RedAm showed 94.6% of residues to be situated in the most favoured regions, 4.0% in additional allowed and 1.4% residues in outlier regions. The values for the NAD complex were 86.5%, 9.7% and 3.8% respectively. The structures have been deposited in the Protein Databank (PDB) with accession codes **6SKX** (*apo*-*Nf*RedAm) and **6SLE** (NADP<sup>+</sup>) complex.

	<i>NfRedAm-apo</i>	<i>NfRedAm- NADP<sup>+</sup></i>
Beamline	I04-1	I03
Wavelength (Å)	0.92819	0.97631
Resolution (Å)	98.73-2.25 (2.32-2.25)	48.28-2.77 (2.85-2.77)
Space Group	<i>P3<sub>2</sub>2<sub>1</sub></i>	<i>P1</i>
Unit cell (Å)	a = b = 114.0; c = 60.0 $\alpha = \beta = 120.0^\circ$ ; $\gamma = 90.0^\circ$	a = b = 66.4; b = 89.3; c = 97.9 $\alpha = 105.6$ ; $\beta = 90.0^\circ$ ; $\gamma = 94.00^\circ$
No. of molecules in the asymmetric unit	1	8
Unique reflections	21645 (1994)	53924 (4393)
Completeness (%)	100.0 (100.0)	98.1 (98.2)
<i>R</i> <sub>merge</sub> (%)	0.05 (0.76)	0.14 (0.90)
<i>R</i> <sub>p.i.m.</sub>	0.03 (0.37)	0.14 (0.90)
Multiplicity	9.7 (10.1)	3.4 (3.6)
$\langle I/\sigma(I) \rangle$	17.4 (3.0)	5.2 (1.3)
Overall <i>B</i> factor from Wilson plot (Å <sup>2</sup> )	47	36
CC <sub>1/2</sub>	1.00 (0.96)	0.99 (0.56)
<i>R</i> <sub>crysf</sub> / <i>R</i> <sub>free</sub> (%)	20.0/23.5	28.6/35.7
r.m.s.d 1-2 bonds (Å)	0.009	0.008
r.m.s.d 1-3 angles (°)	1.63	1.67
Avg main chain B (Å <sup>2</sup> )	61	63
Avg side chain B (Å <sup>2</sup> )	66	60
NADP <sup>+</sup> B (Å <sup>2</sup> )	-	46
Avg water B (Å <sup>2</sup> )	54	23

**Supplementary Table S2.** Data Collection and Refinement Statistics for *NfRedAm*. Numbers in brackets refer to data for highest resolution shells.

**Section S3. Determination of kinetic constants of the fungal RedAms from *Neosartorya* spp.**

Kinetic assays were performed using a modified method to that previously reported in Aleku et al.<sup>[3]</sup> For the determination of kinetic constants of fungal RedAms for ketones, a typical reaction mixture contained 0.2-60 mM of the corresponding ketone, 60 or 100 mM allylamine **b** from buffer stock adjusted to pH 9, 0.4 mM NADPH, 1 % (v/v) dimethylsulfoxide and 5–100 µg of purified RedAm in a total volume of 200 µl (100 mM Tris-HCl, pH 9). Activity measurements were performed in triplicate at 340 nm ( $\epsilon = 6.22 \text{ mM}^{-1} \text{ cm}^{-1}$ ) or 370 nm ( $\epsilon = 2.216 \text{ mM}^{-1} \text{ cm}^{-1}$ ) using a Tecan infinite M200 microplate reader (Tecan Group, Switzerland). A similar set-up was used for the determination of kinetic constants of fungal RedAms for allylamine **b** where a typical reaction mixture contained 0.2-80 mM amine, 10 mM cyclohexanone **4**, 0.4 mM NADPH, 1 % (v/v) dimethylsulfoxide and 5–100 µg of purified RedAm in a total volume of 200 µL (100 mM Tris-HCl, pH 9). Kinetic constants were determined through non-linear regression based on Michaelis-Menten kinetics using Prism7 software.

RedAm	$K_M$ (mM)	$k_{cat}$ ( $\text{s}^{-1}$ )	$k_{cat}/K_M$ ( $\text{s}^{-1} \text{ mM}^{-1}$ )
<b>NfRedAm</b>	$4.13 \pm 0.26$	$2.48 \pm 0.32$	0.60
<b>NfisRedAm</b>	$0.91 \pm 0.45$	$0.14 \pm 0.02$	0.15

Conditions: 0.2-60 mM cyclohexanone **3** concentration, 60 mM allylamine **b**, 0.4 mM NADPH, 1 % (v/v) dimethylsulfoxide and 5–100 µg of purified RedAm in 100 mM Tris-HCl pH 9 buffer.

**Supplementary Table S3.** Kinetic parameters for cyclohexanone **3** in the RedAm-catalysed reductive amination of cyclohexanone **3** and allylamine **b**.

RedAm	$K_M$ (mM)	$k_{cat}$ ( $\text{s}^{-1}$ )	$k_{cat}/K_M$ ( $\text{s}^{-1} \text{ mM}^{-1}$ )
<b>NfRedAm</b>	$1.52 \pm 0.07$	$0.06 \pm 0.04$	$3.9 \times 10^{-2}$
<b>NfisRedAm</b>	$0.003 \pm 0.001$	$0.03 \pm 0.01$	8.6

Conditions: 0.2-60 mM 4-phenyl-2-butanone **5** concentration, 60 mM allylamine **b**, 0.4 mM NADPH, 1 % (v/v) dimethylsulfoxide and 5–100 µg of purified RedAm in 100 mM Tris-HCl pH 9 buffer

**Supplementary Table S4.** Kinetic parameters for 4-phenyl-2-butanone **5** in the RedAm-catalysed reductive amination of 4-phenyl-2-butanone **5** and allylamine **b**.

## Section S4. Chemicals: Synthesis of Substrates and Product Standards.

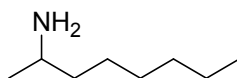
### Procedure for the preparation of amine product standards and spectroscopic characterisation.

Compounds **3-20**, **3f**, **4f**, (*S*)-**4f**, **5f**, (*S*)-**5f**, **6f**, (*S*)-**6f**, **8f**, (*R*)-**8f**, **10f**, (*S*)-**10f**, **11f**, (*S*)-**11f**, **13f**, **14f**, (*R*)-**14f**, **16f**, (*S*)-**16f**, **17f** and (*R*)-**17f** were purchased from commercial suppliers. Preparation and spectroscopic characterisation for compounds **1a-c**, **2a-b**, **3a-e**, **4a-e**, **5a-e**, **6b** and **7b** are reported in Aleku *et al.*<sup>10</sup> and Sharma *et al.*<sup>7</sup>

### Synthesis of Amines **6f**, **7f** and **20f** by Reductive Amination

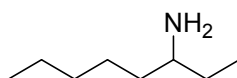
To a solution of ketone (4.0 mmol) in methanol (35 mL) were added ammonium acetate (3.08 g, 40.0 mmol) and sodium cyanoborohydride (754 mg, 12 mmol). The reaction was stirred overnight and then concentrated to 5 mL by rotary evaporation. The reaction was then quenched through the addition of 1 M aqueous NaOH (40 mL) and the crude product was extracted with EtOAc (2 x 20 mL). The combined organic layers were then acidified and extracted with 1 M aqueous HCl (3 x 15 mL) and the aqueous phase was basified to pH = 12 through the addition of 5M aqueous NaOH. The final product was then extracted with EtOAc (2 x 20 mL) before drying over anhydrous magnesium sulfate. The solvent was then removed under reduced pressure to afford the final amine product.

#### 2-Aminooctane (**6f**)



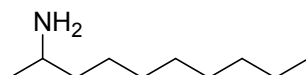
**<sup>1</sup>H NMR** (400 MHz, Chloroform-*d*)  $\delta$  2.93 – 2.78 (m, 1H), 1.55 (s, 2H), 1.29 (dt, *J* = 14.3, 3.9 Hz, 10H), 1.05 (d, *J* = 6.3 Hz, 3H), 0.95 – 0.77 (m, 3H). **<sup>13</sup>C NMR** (101 MHz, Chloroform-*d*)  $\delta$  47.10, 40.23, 31.99, 29.53, 26.52, 23.97, 22.75, 14.22. **HRMS** calcd. for C<sub>8</sub>H<sub>20</sub>N<sup>+</sup> 130.1551 [M+H]<sup>+</sup>, found 130.1590.

#### 3-Aminooctane (**20f**)



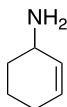
**<sup>1</sup>H NMR** (500 MHz, Chloroform-*d*)  $\delta$  2.59 (tt, *J* = 7.2, 4.6 Hz, 1H), 1.49 – 1.32 (m, 4H), 1.30 – 1.23 (m, 7H), 0.88 (dt, *J* = 10.5, 7.3 Hz, 6H). **<sup>13</sup>C NMR** (126 MHz, Chloroform-*d*)  $\delta$  52.82, 37.71, 32.17, 30.81, 26.01, 22.80, 14.19, 10.53. **HRMS** calcd. for C<sub>8</sub>H<sub>20</sub>N<sup>+</sup> 130.1551 [M+H]<sup>+</sup>, found 130.1590.

#### 2-Aminodecane (**7f**)



**<sup>1</sup>H NMR** (400 MHz, Chloroform-*d*)  $\delta$  2.86 (h,  $J$  = 5.8 Hz, 1H), 1.45 (m, 2H), 1.28 (d,  $J$  = 11.4 Hz, 12H), 1.05 (d,  $J$  = 6.3 Hz, 3H), 0.87 (t,  $J$  = 6.7 Hz, 3H). **<sup>13</sup>C NMR** (126 MHz, Chloroform-*d*)  $\delta$  47.10, 40.36, 32.03, 29.90, 29.75, 29.43, 26.59, 24.10, 22.81, 14.24. **HRMS** calcd. for C<sub>10</sub>H<sub>24</sub>N<sup>+</sup> 158.1864 [M+H]<sup>+</sup>, found 158.1896.

### Synthesis of amine 19f via Mitsunobu Reaction



Following a procedure by Mangas-Sanchez *et al.*,<sup>11</sup> to a stirred solution of 2-cyclohexen-1-ol (500 mg, 5.09 mmol, 1 eq.) in anhydrous THF (25 mL) under an atmosphere of N<sub>2</sub> at 0 °C was added PPh<sub>3</sub> (1.61 g, 6.12 mmol, 1.2 eq.), phthalimide (900 mg, 6.12 mmol, 1.2 eq.) and diisopropyl azodicarboxylate (1.20 mL, 6.12 mmol, 1.2 eq.). The reaction mixture was allowed to warm to rt and stirred for 3 hours, after which a further portion of THF (25 mL) and EtOH (10 mL) were added, followed by the addition of hydrazine monohydrate (50 wt%, 3.67 mL, 38.2 mmol, 7.5 eq.). The reaction mixture was heated to reflux for 2 h, then cooled to rt and filtered through a pad of Celite. The Celite was washed with THF (100 mL), then the filtrate was collected and concentrated *in vacuo*. The residue was taken up in 3 M HCl (25 mL) and washed with DCM (3 x 20 mL). The aqueous phase pH was then adjusted to pH 12 with 5 M NaOH, and extracted with DCM (3 x 20 mL). The combined organic extracts were washed with saturated brine solution (30 mL), dried over MgSO<sub>4</sub> and concentrated *in vacuo* to afford the crude product which was used without further purification. The signals in the <sup>1</sup>H NMR spectrum matched those previously reported in the literature.<sup>12</sup>

### General procedure for transaminase reductive amination.

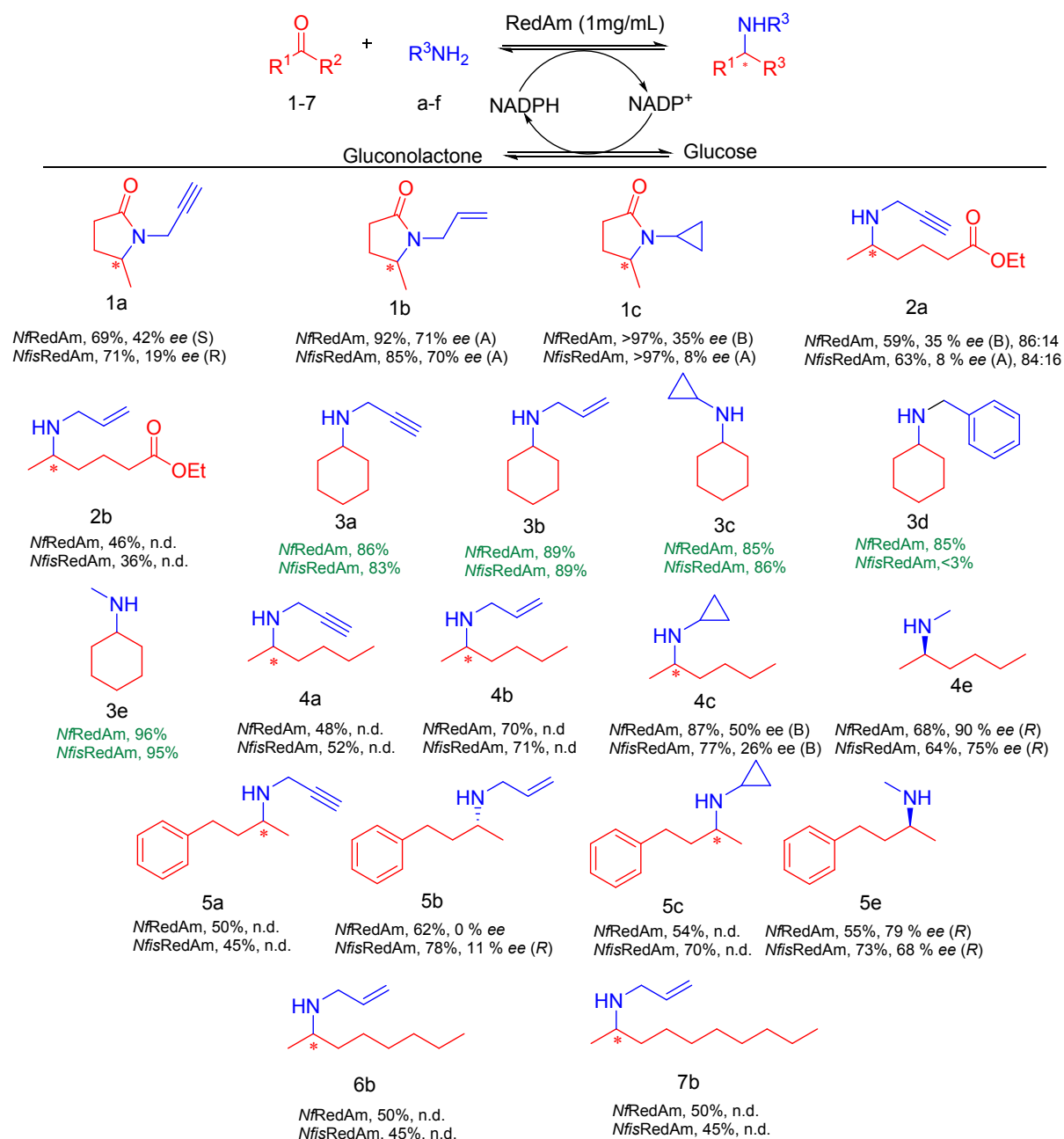
To a solution of the corresponding ketone **7** or **20** (10 mM) in 100 mM NaPi buffer pH 8 containing isopropylamine (1M) and PLP (1 mM), ATA-113 (2.5 mg mL<sup>-1</sup>) was added in 500  $\mu$ L total reaction volume. Reactions incubated at 30°C, 250 rpm, 24 h. Reactions basified to pH 12 with 10 M NaOH, extracted into MTBE (1 mL), dried over MgSO<sub>4</sub> and analysed by GC-FID.

## Section S5. Biotransformations of ketone-amine partners by RedAms.

### Typical procedure for RedAm-catalysed reductive amination.

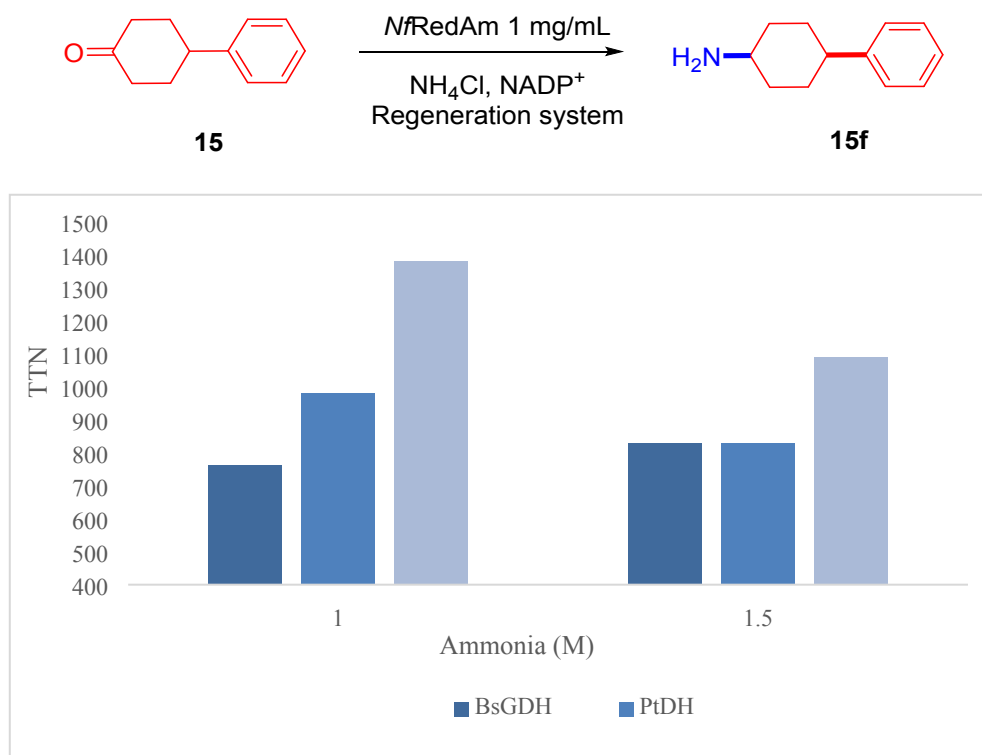
A 500  $\mu$ L reaction mixture contained 20 mM D-glucose, 0.5 mg mL<sup>-1</sup> GDH (Codexis, CDX-901), 0.5 mM NADP<sup>+</sup>, 1 mg mL<sup>-1</sup> purified RedAm, 5 mM ketone, the appropriate ratio of amine nucleophile (in Tris-HCl buffer adjusted to pH 9) and 2 % v/v DMSO. Reactions were incubated at 30 °C with 250 r.p.m. shaking for 24 h, after which they were quenched by the addition of 30  $\mu$ L of 10M NaOH and extracted twice with 500  $\mu$ L *tert*-butyl methyl ether. The organic fractions were combined and dried

over anhydrous  $\text{MgSO}_4$  and analysed by HPLC or GC-FID on a chiral stationary phase.

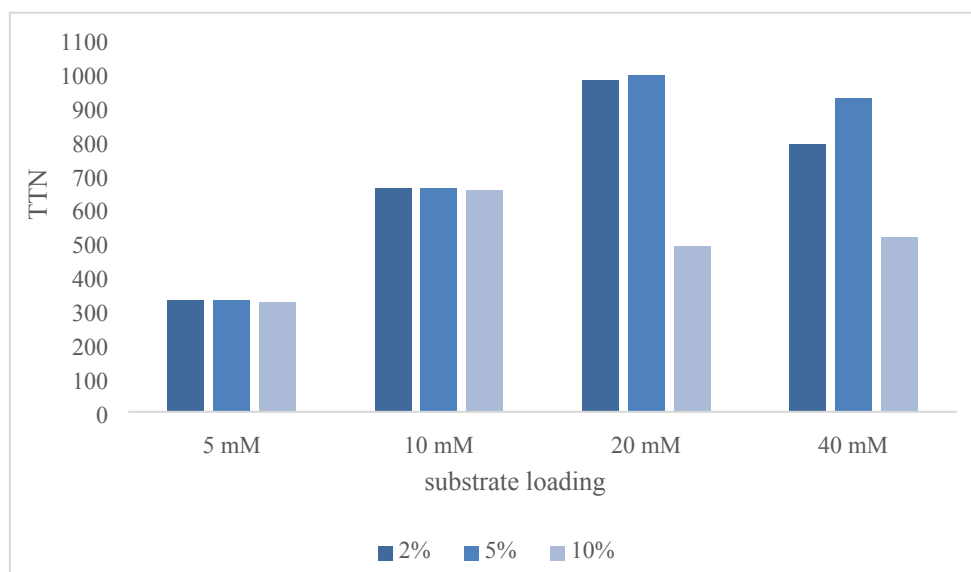
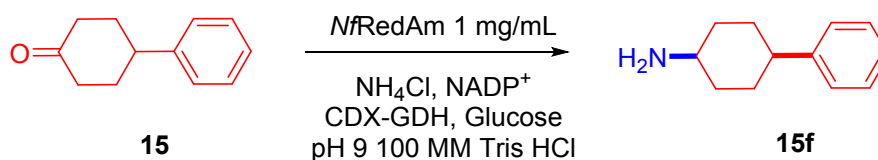


**Supplementary Figure S4.** GC conversions after 24h in the bioreductive amination of a series of carbonyl compounds with primary amines catalysed by the Redams from *N. fumigata* and *N. fischeri*. Conditions: RedAm 1 mg mL<sup>-1</sup>, 5 mM substrate, 5 mM amine (green) or 25 mM amine (black) concentration in pH 7 100 mM Tris-HCl. Conversions based on the areas of substrate and product determined by GC-FID.

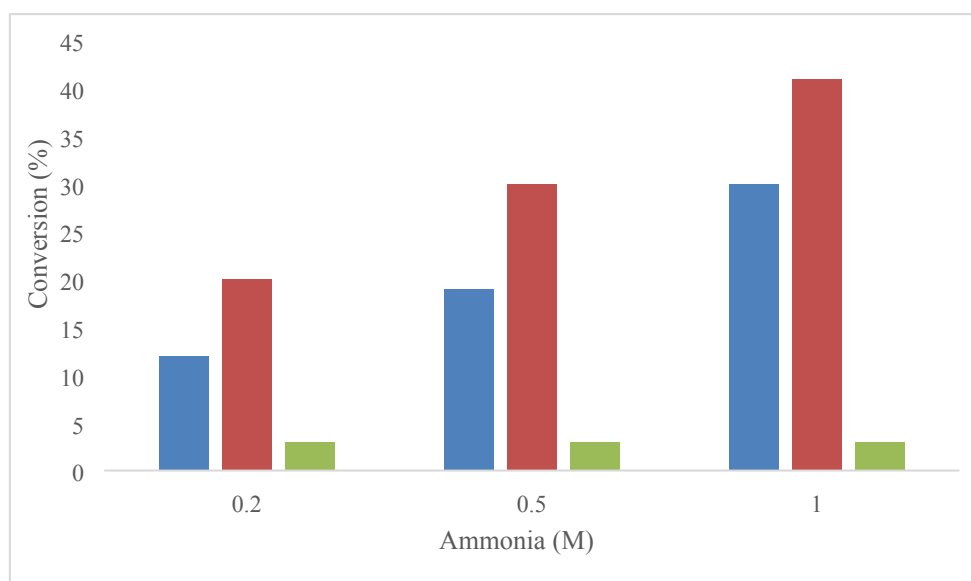
**Study of different regeneration systems and DMSO concentration.**



**Supplementary Figure S5.** Turnover numbers (TN) obtained with different regeneration systems at different ammonia concentrations in the bio-reductive amination of **15** and ammonia catalysed by *Nf*RedAm.

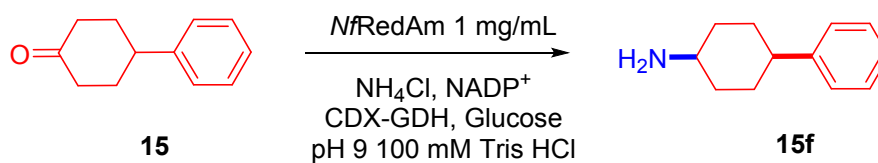


**Supplementary Figure S6.** Turnover numbers (TN) obtained at different DMSO and substrate concentrations in the bio-reductive amination of **15** and ammonia catalysed by *NfRedAm*.



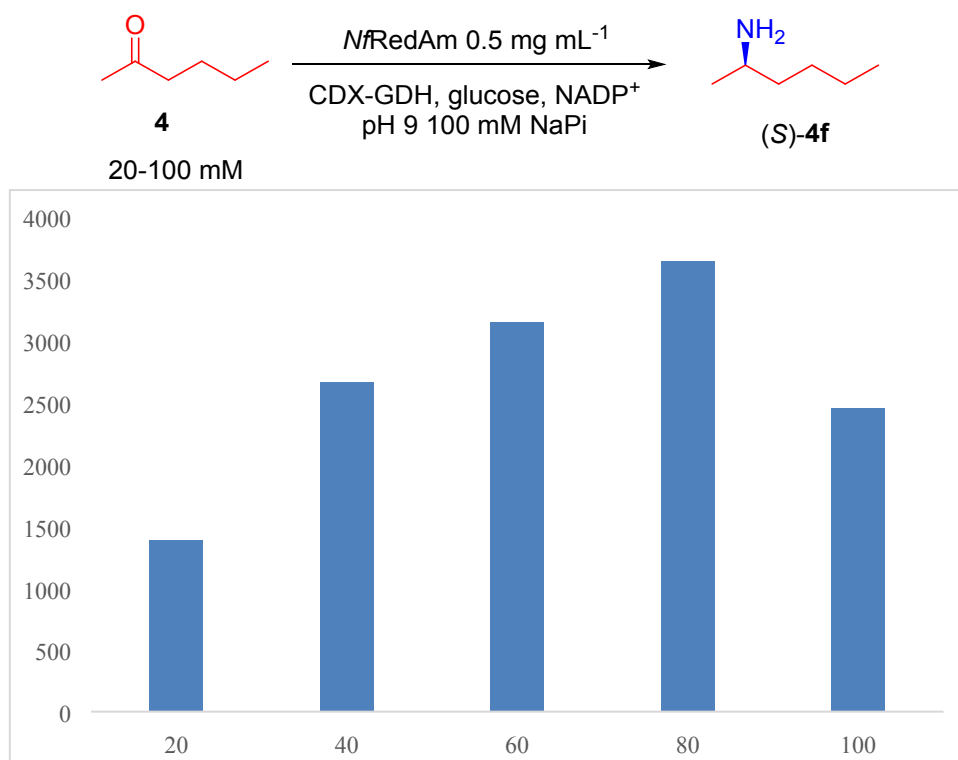
**Supplementary Figure S7.** Conversions after 24 h in the bio-reductive amination of **5** with different ammonia sources. Ammonium hydroxide (NH<sub>4</sub>OH, blue bar), ammonium chloride (NH<sub>4</sub>Cl, red bar) and ammonium sulphate (NH<sub>4</sub>SO<sub>4</sub>, green bar). Conversions based on the areas of substrate and product determined by GC-FID.

Reactions at high substrate loadings.



DMSO (%)	Substrate (mM)	NH <sub>4</sub> Cl (M)	TN	Conversion (%)
4	20	1	>577	>97
4	20	1.5	>577	>97
8	40	1	1149	97
8	40	1.5	933	80
12	60	1	1206	69
12	60	1.5	140	8

**Supplementary Figure S8.** Bioreductive amination of 4-phenyl-cyclohexanone **15** and ammonia **f** at high substrate loadings. Conversions after 24 h. determined by GC-FID based on the areas of substrate and product. Turnover numbers (TN) calculated using conversions after 24 h.



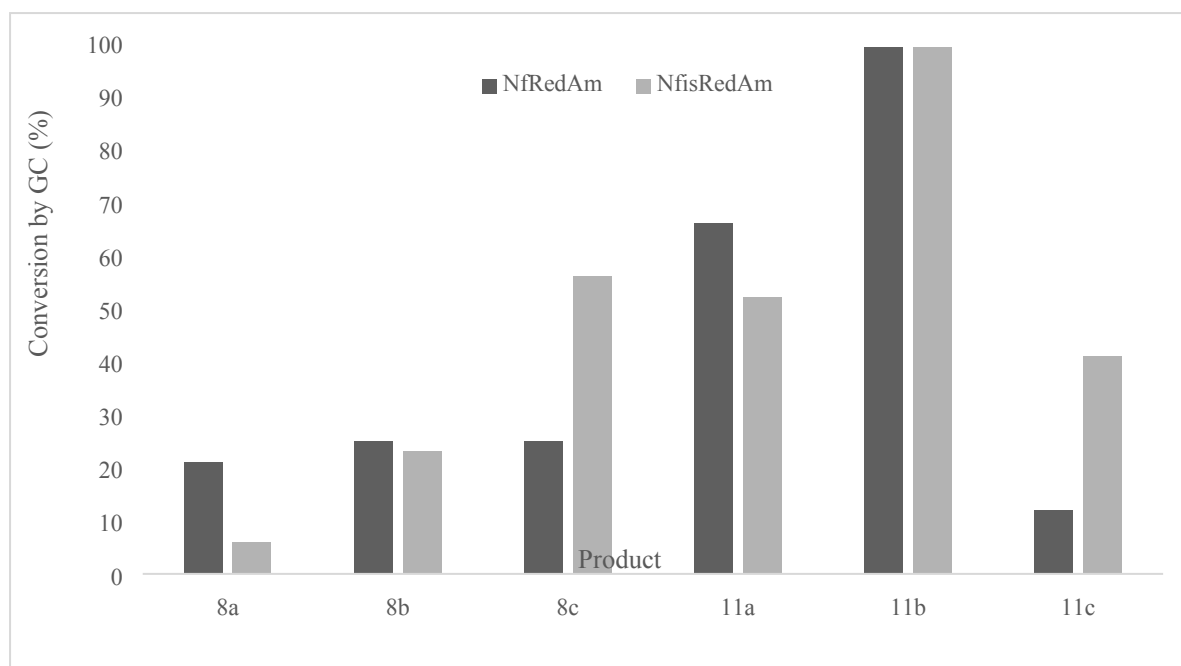
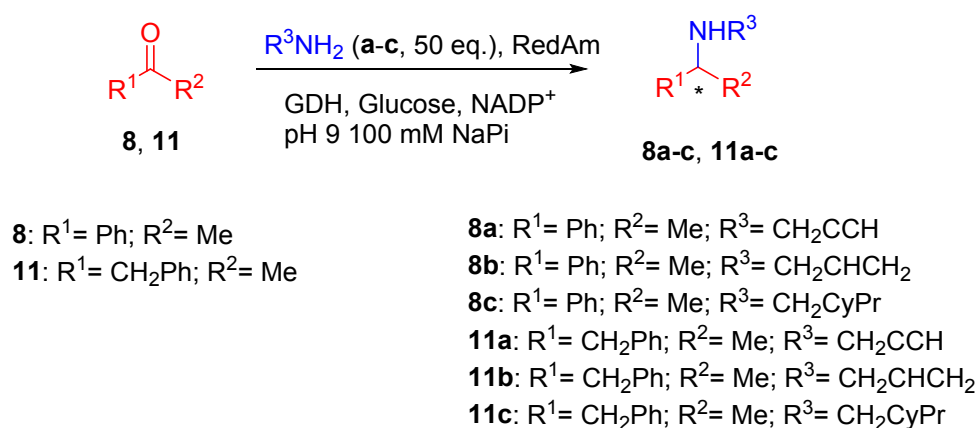
**Supplementary Figure S9.** Bioreductive amination of 2-hexanone (**4**) and ammonia (**f**) at high substrate loadings. Turnover numbers (TN) calculated using conversions after 24 h. determined by GC-FID based on the areas of substrate and product.

#### Biotransformations at high substrate loadings employing primary amines

Entry	Ketone	Ketone concentration (mM)	Amine	Amine equivalents	Conversion (%)	TTN
1	<b>3</b>	100	<b>b</b>	1	93	3255
2	<b>3</b>	100	<b>b</b>	1	90	6300
3	<b>3</b>	100	<b>b</b>	1	95	2217
4	<b>3</b>	200	<b>b</b>	1	85	5950
5	<b>3</b>	200	<b>b</b>	1	82	11480
6	<b>3</b>	200	<b>b</b>	1	88	4107
7	<b>3</b>	300	<b>b</b>	1	82	8610
8	<b>3</b>	300	<b>b</b>	1	66	13860
9	<b>3</b>	300	<b>b</b>	1	69	4830
10	<b>3</b>	100	<b>e</b>	2	83	2905
11	<b>4</b>	100	<b>c</b>	5	97	3395
12	<b>4</b>	200	<b>c</b>	2	97	6790
13	<b>5</b>	100	<b>c</b>	5	62	2170

**Supplementary Table S5.** Bioreductive amination of a series of carbonyl compounds with primary amines at high substrate loadings. Conversions after 24 h. determined by GC-FID based on the areas of substrate and product. Turnover numbers (TN) calculated using conversions after 24 h.

**Bioreductive amination of acetophenone **8** and 4-fluorophenyl acetone **11** with different amine partners a-c using 50 amine equivalents.**



**Supplementary Figure S10.** Bioreductive amination of acetophenone (**8**) and 4-fluorophenyl acetone (**11**) with different amine partners **a-c**. Conversions based on the areas of substrate and product determined by GC-FID after 24. **8a-c** *ee* from 91% to >97% (absolute configuration not determined). **11a** obtained in 90% *ee* (*R*) *Nf*RedAm and >97% *ee* (*R*) *Nfis*RedAm. Optical purity for **11b-c** not determined.

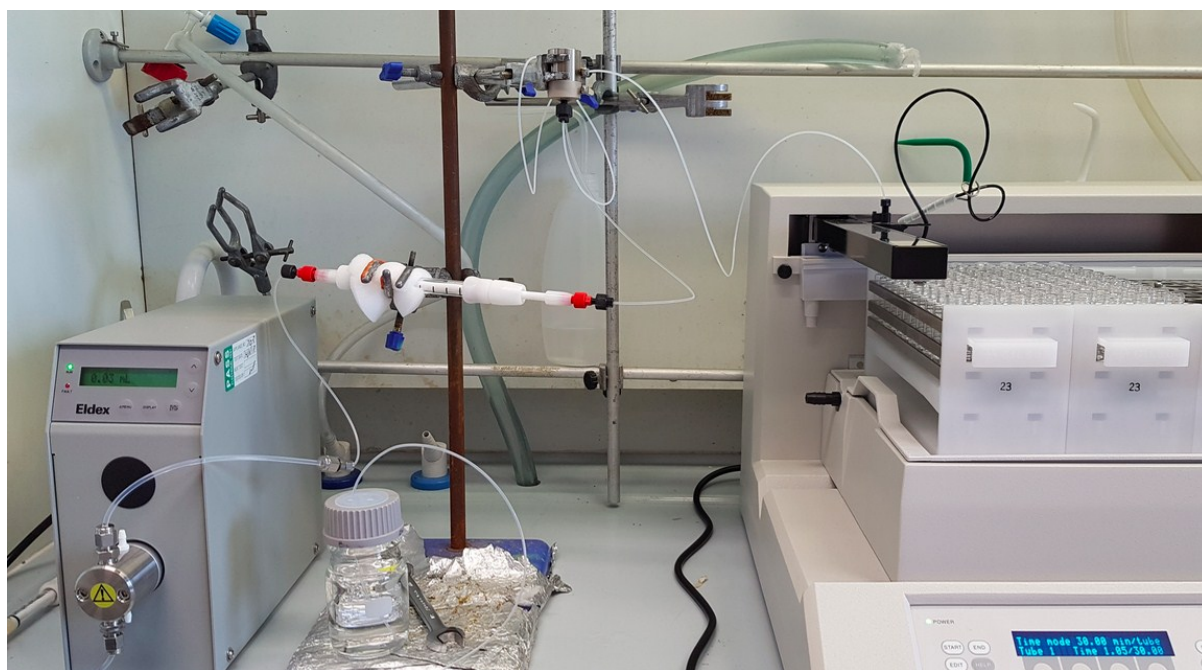
## Section S6. Flow reactions

### *General flow experimental*

Continuous flow reactions were performed using the following equipment: Eldex Optos series pumps model 2SM (flow rate 0.003–5.000 mL min<sup>-1</sup>), Kinesis Omnifit glass columns (I.D 0.68 mm) and PTFE tubing (I.D 1/16") were purchased from Cole-Parmer (Cambridge, UK). Stainless steel and PEEK fittings were purchased from Swagelok (Manchester, UK). A Gilson FC204 110/220V fraction collector was purchased from Gilson (Dunstable, UK). An SSI flow-through back-pressure regulator (5–75 psi) was purchased from Sigma-Aldrich (Gillingham, UK). EziG was purchased from EnginZyme (Stockholm, Sweden).

### *Flow experiments*

Flow experiments were carried out using the set-up show in Supplementary Figure S11.



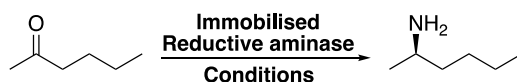
**Supplementary Figure S11.** Flow reactions set-up

### *Immobilisation procedure*

EziG was weighed out to give 10 wt% with respect to the biocatalyst. It was found that EziG<sup>2</sup> was the best support for *NfRedAm*. To immobilise *NfRedAm* (25 mg), EziG<sup>2</sup> (225 mg) was suspended in Tris-HCl (20 mM, 300 mM NaCl, pH 8) and the biocatalyst solution was added to give a final total volume of 5 mL. This was stirred using orbital rotation at 12 rpm for 30 minutes, after which the solution was centrifuged and the supernatant biocatalyst concentration recorded using a Nanodrop. When the concentration was <0.1 mg mL<sup>-1</sup>, the supernatant was discarded and the immobilised enzyme preparation washed with the same Tris-HCl buffer (x 3). This was combined with immobilised *BsGDH*-EziG<sup>3</sup> (10 wt% w.r.t GDH, 75 mg total mass) and stirred for 5 minutes to ensure efficient mixing. The combined enzyme preparation was then packed into a column, and the final volume of the packed bed calculated as according to the manufacturer's instructions. The combined mass of 325 mg typically gave a column volume of ~1 mL.

## Flow Reactions

The column was attached to the pump, and after the column a back-pressure regulator was placed and calibrated to 60 psi. A total of 10 column volumes of Tris-HCl buffer (100 mM, pH 8) was passed through the reactor at 500  $\mu\text{L min}^{-1}$  and discarded, after which the column was primed with reaction buffer (see table), which also contained substrate, co-factor and glucose. After being primed, the reactions were slowed to the appropriate time to give a 30 minute residence time. For example, a column with a volume of 1 mL would require a 33  $\mu\text{L min}^{-1}$  flow rate. The effluent was collected using a fraction collector, and the fractions were analysed individually by gas chromatography.



Entry <sup>a</sup>	RedAm	EziG <sup>b</sup>	Buffer	Conc	RV conv loss <sup>c</sup>
1	<i>Nf</i> RedAm	3	NH <sub>4</sub> Cl	1 M	10 (23%)
2	<i>Nf</i> RedAm	3	NH <sub>4</sub> Cl	0.5 M	20 (77%)
3	<i>Nf</i> RedAm	3	NH <sub>4</sub> OH	0.5 M	20 (70%)
4	<i>Nf</i> RedAm	3	NH <sub>4</sub> CO <sub>2</sub> H	0.5 M	15 (52%)
5	<i>Nf</i> RedAm	2	NH <sub>4</sub> Cl	0.5 M	25 (68%)
6	<i>Nf</i> RedAm	2 <sup>d</sup>	NH <sub>4</sub> Cl	0.5 M	25 (77%)
7	<i>Ad</i> RedAm	3	NH <sub>4</sub> Cl	0.5 M	26 (68%)
8	<i>Nf</i> RedAm	2	NH <sub>4</sub> Cl	0.25 M	20 (92%) <sup>e</sup>

**Supplementary Figure S12.** Flow reactions. <sup>a</sup>Conditions: 2:1 RedAm:*Bs*GDH (10 wt% Enzyme), 2-hexanone (40 mM), NADP<sup>+</sup> (1 mM), glucose (200 mM), DMSO (5%),  $t_{res}$ : 0.5 h, 35 °C; <sup>b</sup>*Bs*GDH always immobilised on EziG<sup>3</sup>; <sup>c</sup>First reactor volume where conversion is not >95%; <sup>d</sup>Soluble CDX GDH-901 used instead of immobilised *Bs*GDH; <sup>e</sup>Conversion had dropped to 26% by RV30;

## Section S7. Analytical Procedures

### GC analysis

Analytical procedures for compounds **1a-c**, **2a-b**, **3a-e**, **4a-e**, **5a-e**, **6b** and **7b** are reported in Aleku *et al.*<sup>10</sup> and Sharma *et al.*<sup>7</sup>

Entry	Ketone	Ketone retention time (min)	Amine	Amine retention time (min)
1	<b>3</b>	7.7 <sup>a</sup>	<b>3f</b>	6.8 <sup>a</sup>
2	<b>4</b>	3.9 <sup>b</sup>	<b>4f</b>	3.8
3	<b>6</b>	13.4 <sup>a</sup>	<b>6f</b>	13.2 <sup>a</sup>
4	<b>9</b>	21.0 <sup>a</sup>	<b>9f</b>	21.9 <sup>a</sup>
5	<b>13</b>	14.0 <sup>a</sup>	<b>13f</b>	15.1 <sup>a</sup>
6	<b>15</b>	22.7 <sup>a</sup>	<b>15f</b>	22.4 and 22.5 <sup>a</sup>
7	<b>16</b>	17.1 <sup>a</sup>	<b>16f</b>	16.7 <sup>a</sup>
8	<b>18</b>	13.3 <sup>a</sup>	<b>18f</b>	13.1 <sup>a</sup>
9	<b>19</b>	8.7 <sup>b</sup>	<b>19f</b>	7.1 <sup>b</sup>

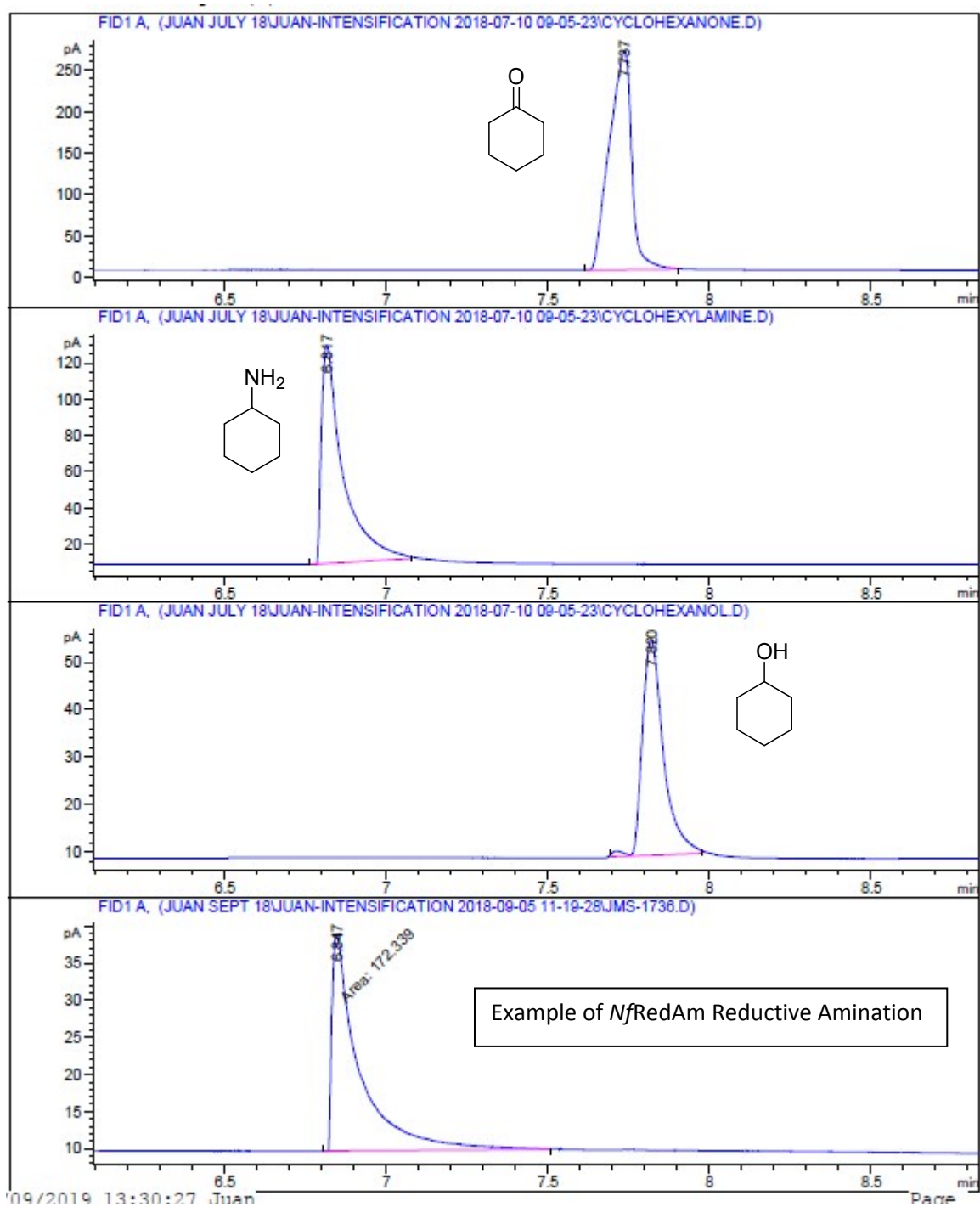
**Supplementary table S6.** GC analysis: methods and retention times of ketone substrates and amine products from biotransformations. Column: HP-1, <sup>a</sup> temperature program: 50 °C for 0 min then 5 °C min<sup>-1</sup> until 200 °C, then hold for 2 min. Injector temperature 200 °C, detector temperature 250 °C, helium flow: 1.2 mL min<sup>-1</sup>. <sup>b</sup>. Column: HP-1 temperature program: 40 °C for 1 min then 3 °C min<sup>-1</sup>

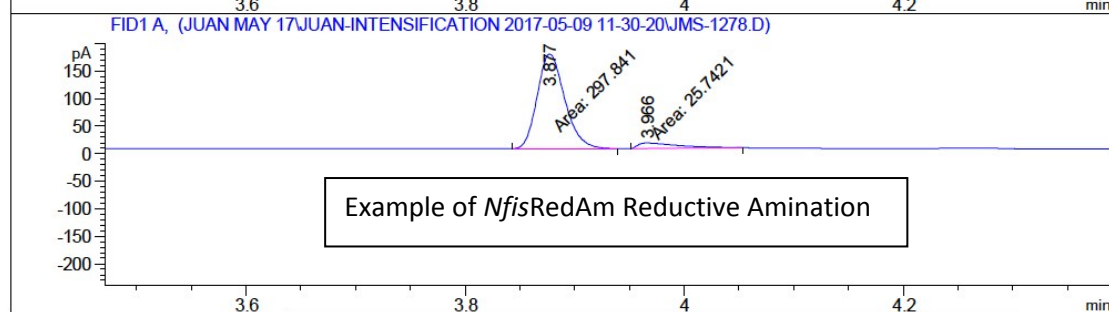
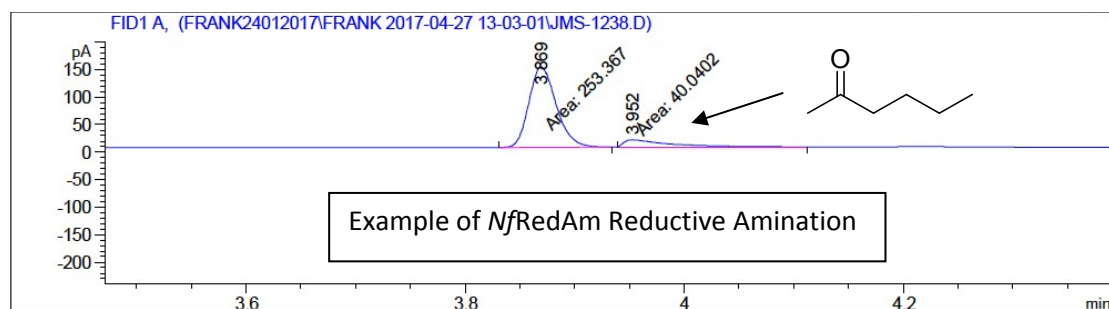
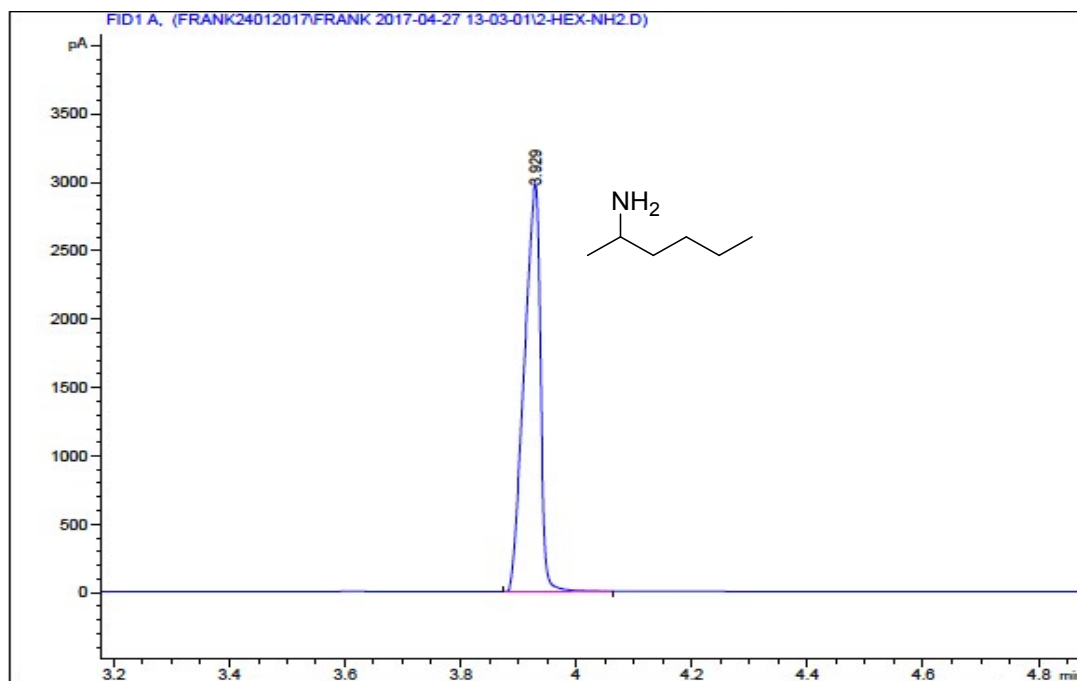
until 120 °C, then 3 °C min<sup>-1</sup> until 200 °C and then hold for 2 min. Injector temperature 200 °C, detector temperature 250 °C, helium flow: 1.2 mL min<sup>-1</sup>.

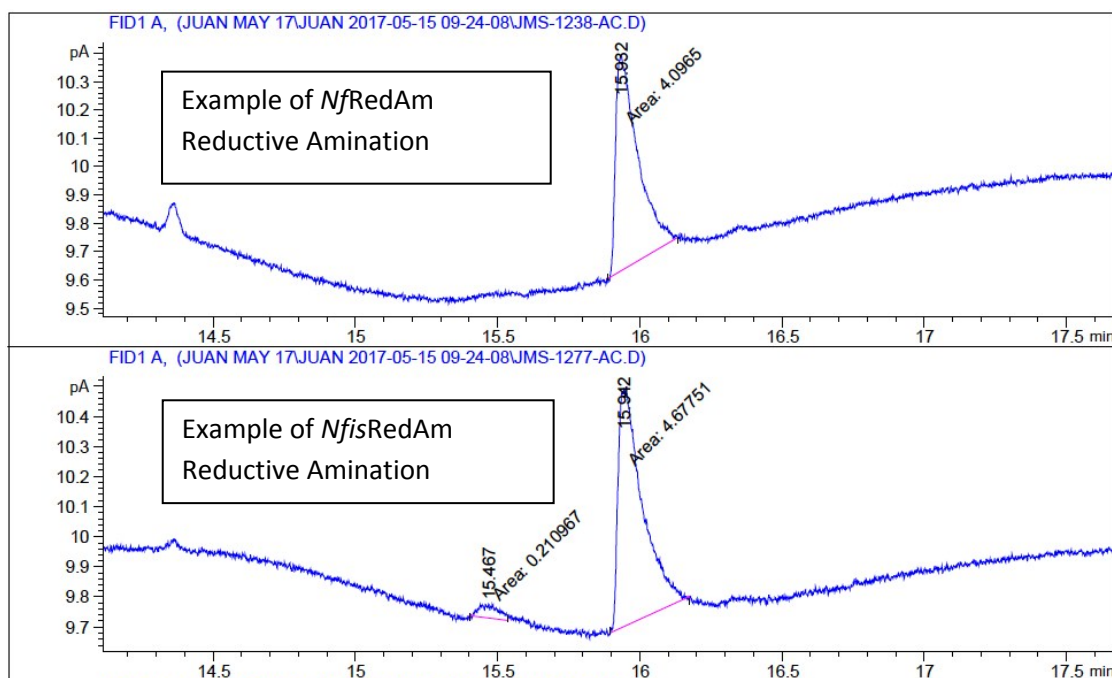
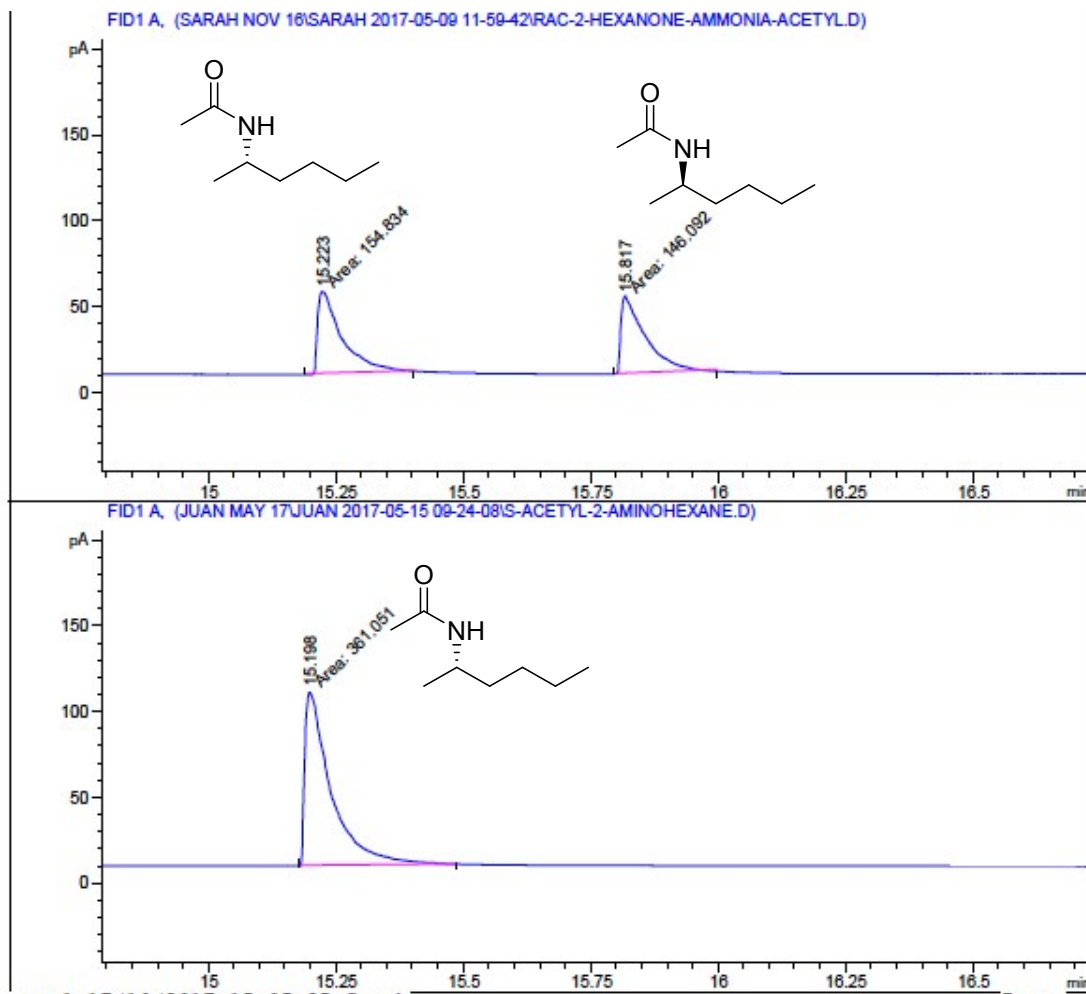
Entry	Ketone	Ketone retention time (min)	Amine	Amine retention time (min)	
1	<b>4</b>	---	<b>4f</b>	15.2 ( <i>S</i> )	15.8 ( <i>R</i> )
2	<b>5</b>	16.7	<b>5f</b>	25.7 ( <i>S</i> )	25.9 ( <i>R</i> )
3	<b>7</b>	14.2	<b>7f</b>	23.4 ( <i>R</i> )	23.6 ( <i>S</i> )
4	<b>8</b>	12.2	<b>8f</b>	21.8 ( <i>S</i> )	22.4 ( <i>R</i> )
5	<b>10</b>	20.1	<b>10f</b>	28.0 ( <i>S</i> )	28.4 ( <i>R</i> )
6	<b>11</b>	15.0	<b>11f</b>	22.8 ( <i>S</i> )	23.1 ( <i>R</i> )
7	<b>14</b>	17.9	<b>14f</b>	26.0 ( <i>S</i> )	26.4 ( <i>R</i> )
8	<b>17</b>	12.0	<b>17f</b>	21.0 ( <i>S</i> )	21.5 ( <i>R</i> )
9	<b>20</b>	6.8	<b>20f</b>	18.3 ( <i>R</i> )	18.6 ( <i>S</i> )

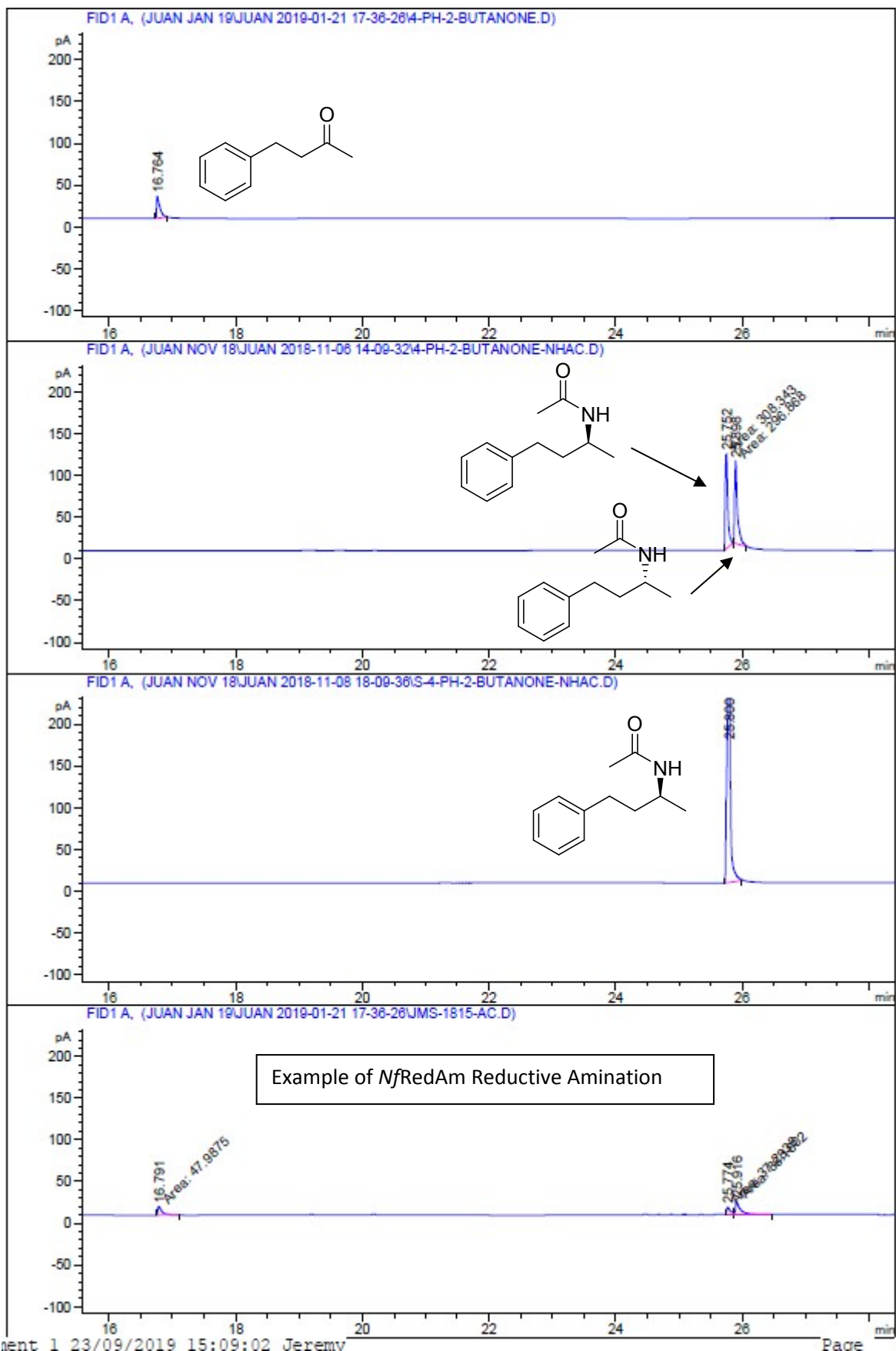
**Supplementary table S7.** GC analysis: methods and retention times of ketone substrates and amine products from biotransformations. Column: CP-ChiralSil-DEX CB, temperature program: 50 °C for 0 min then 5 °C min<sup>-1</sup> until 200 °C, then hold for 2 min. Injector temperature 200 °C, detector temperature 250 °C, helium flow: 1.2 mL min<sup>-1</sup>. Reactions were acetylated using acetic anhydride and 4-(dimethylamino)pyridine prior to analysis. Absolute configurations were determined either via commercial standards or by comparison with ATA-113 transamination.

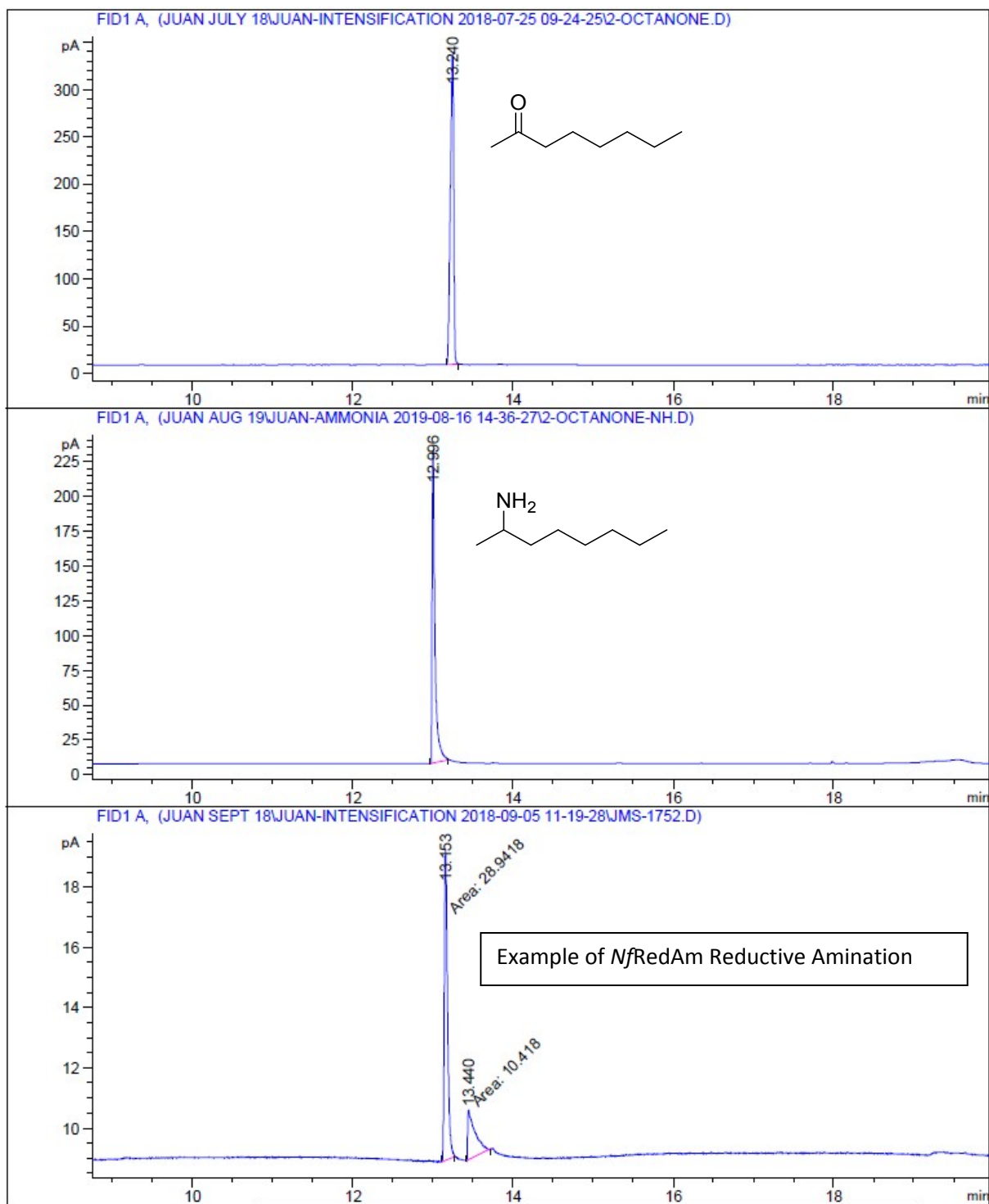
## Section S8. Selected Chromatograms

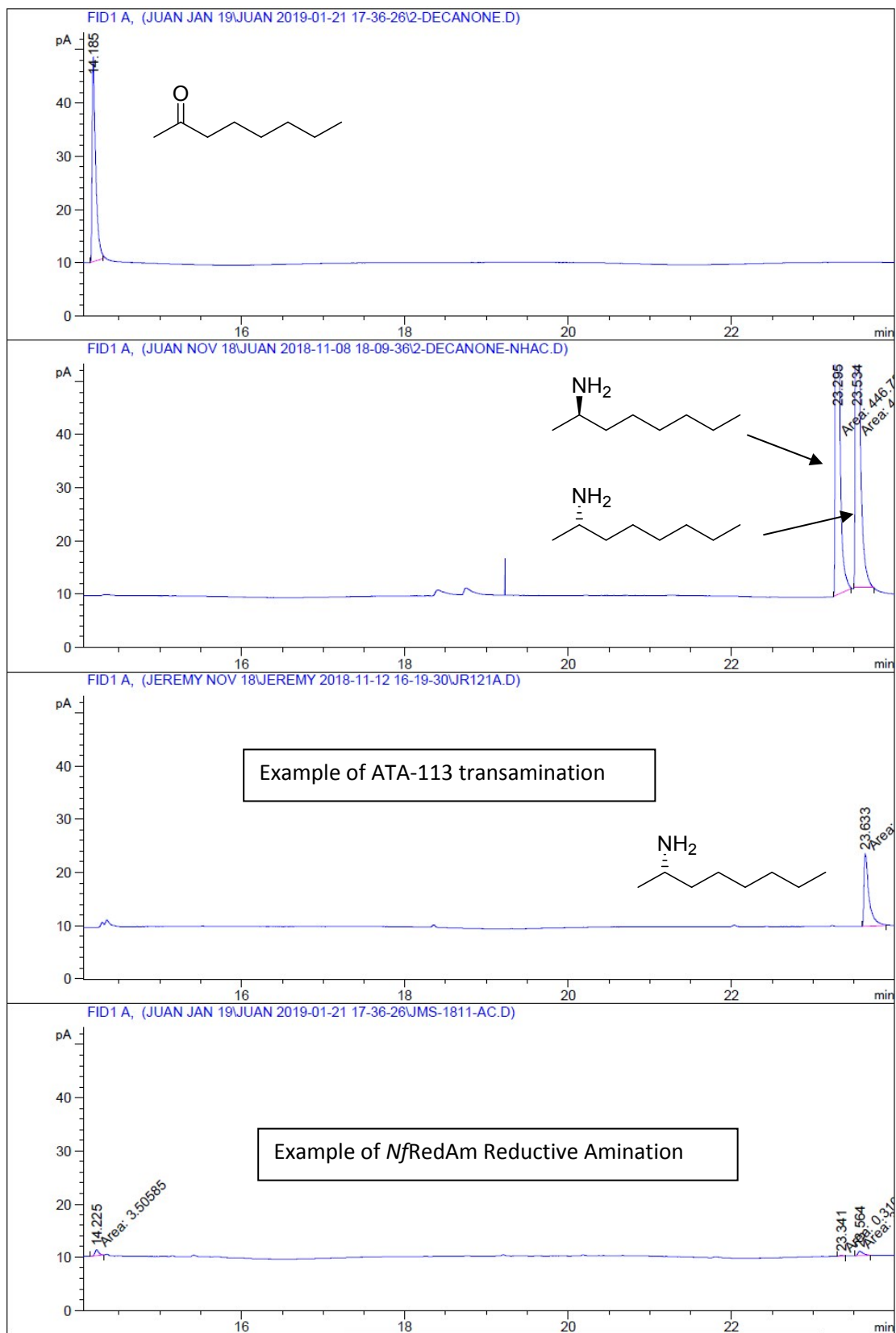




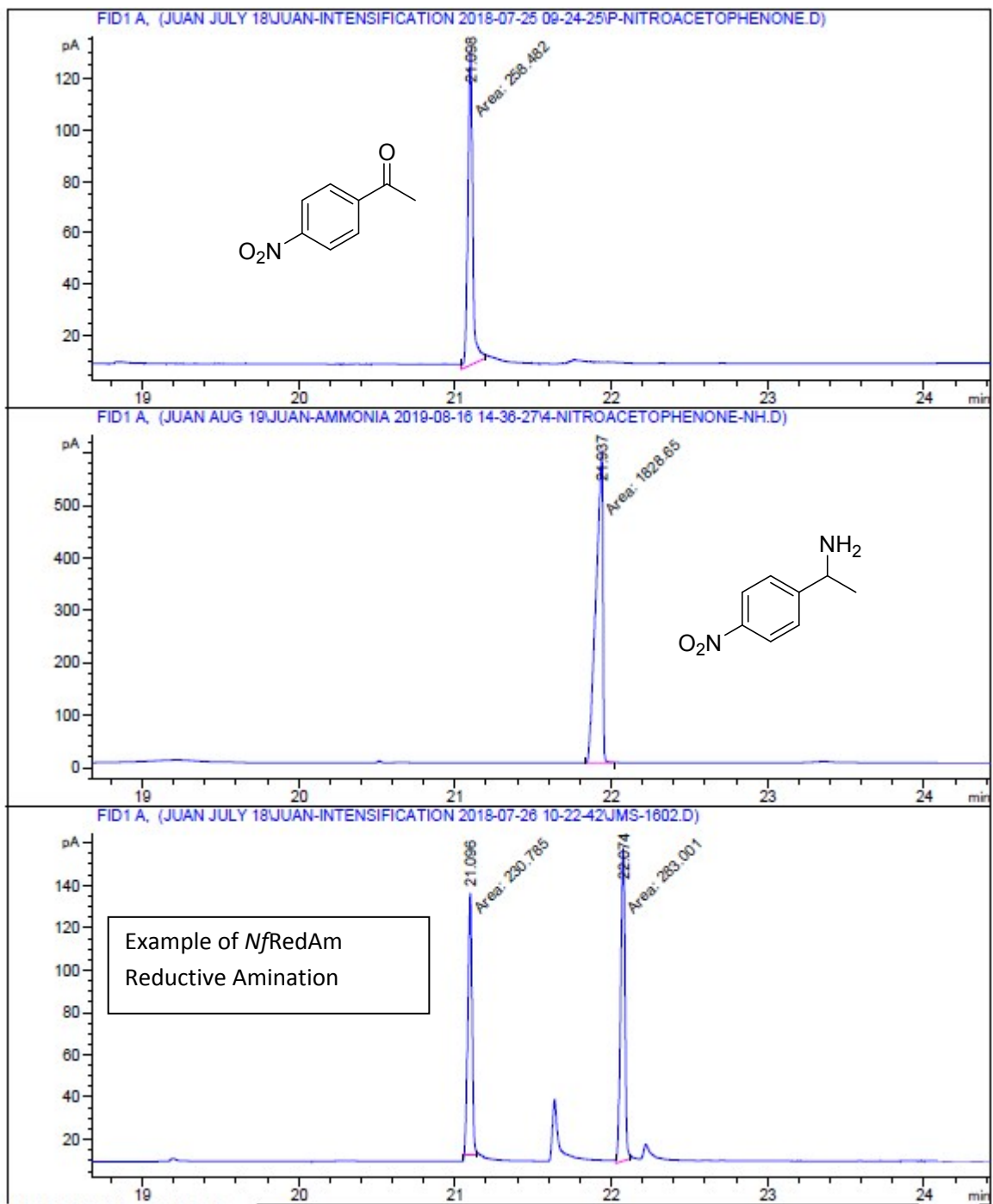


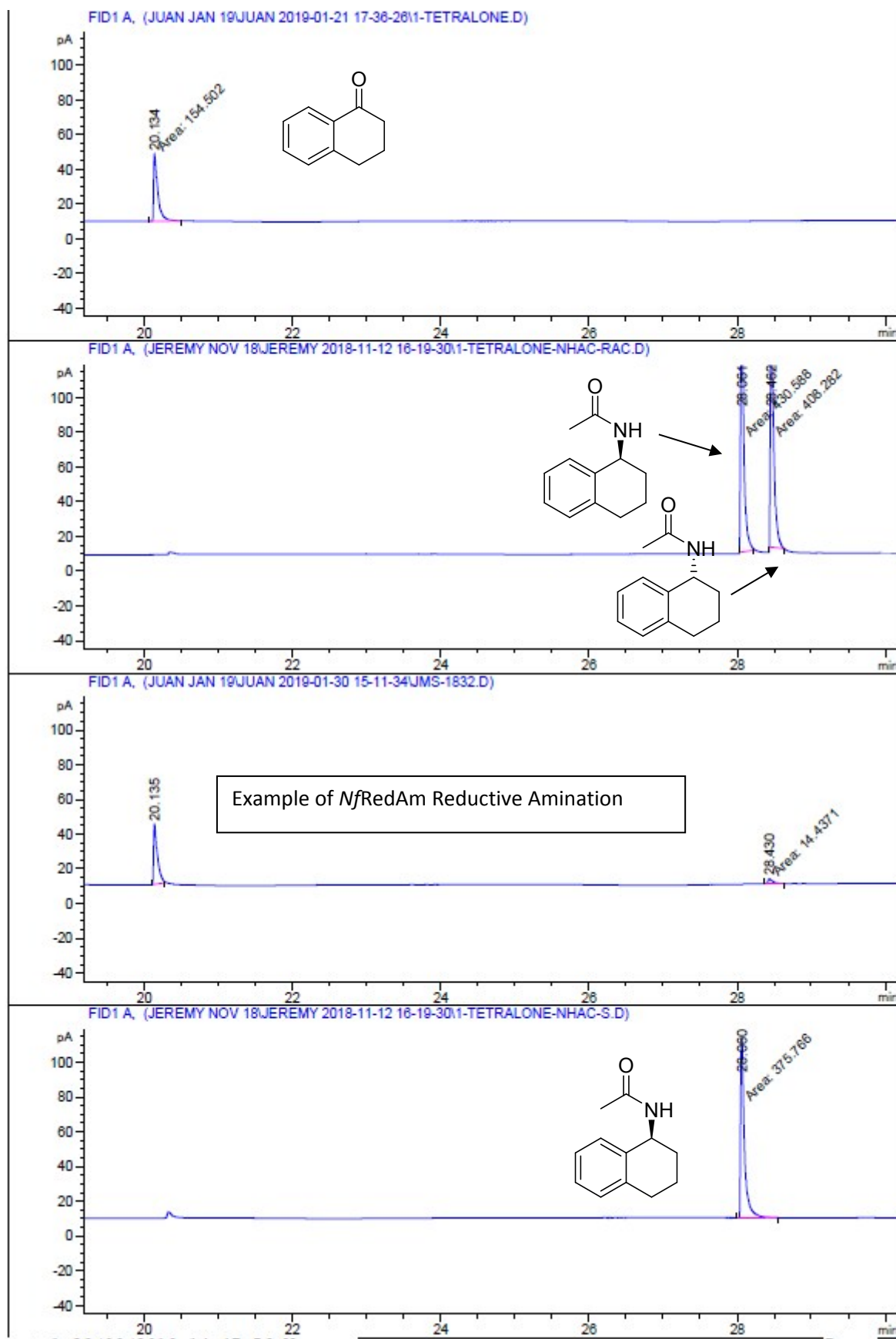


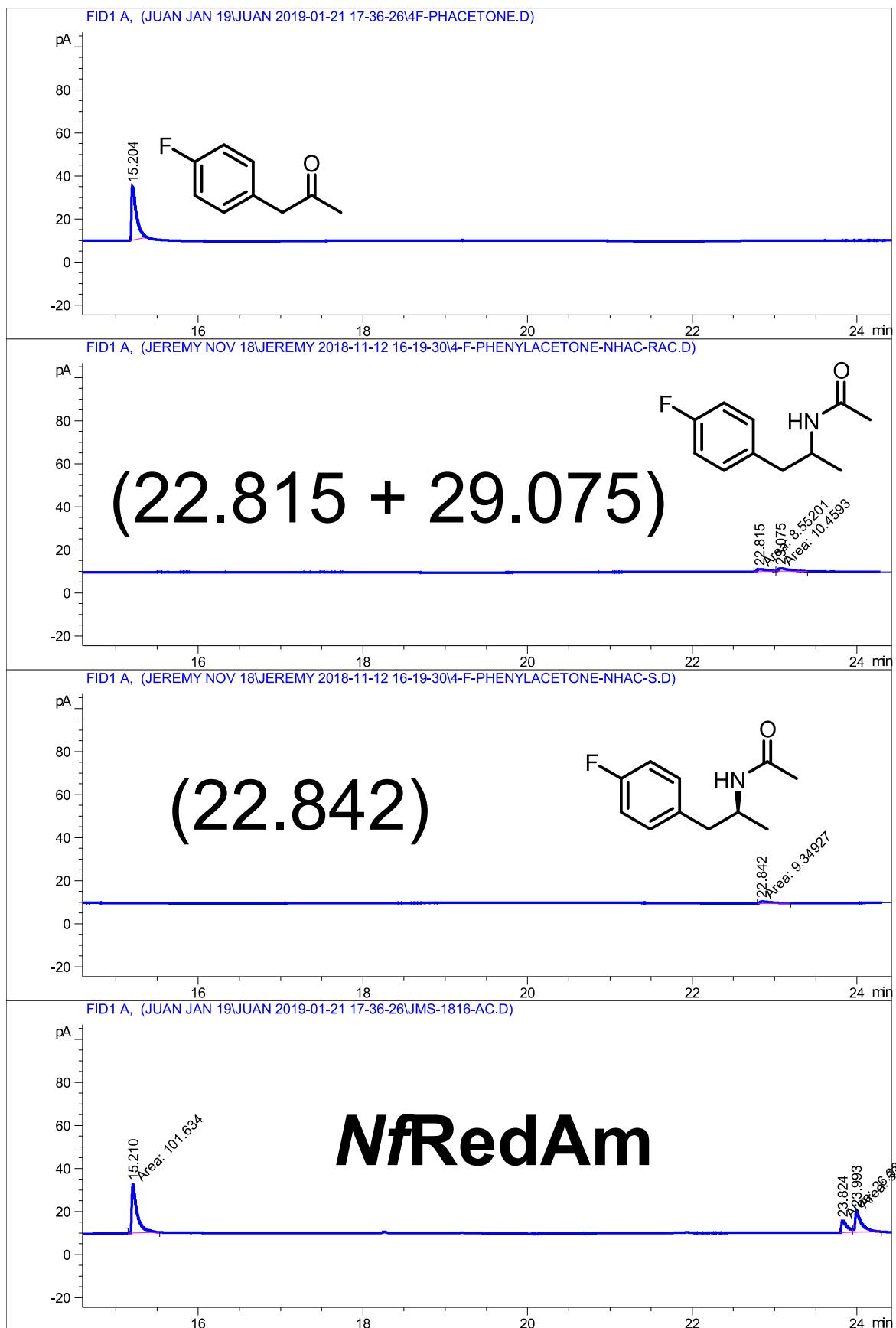


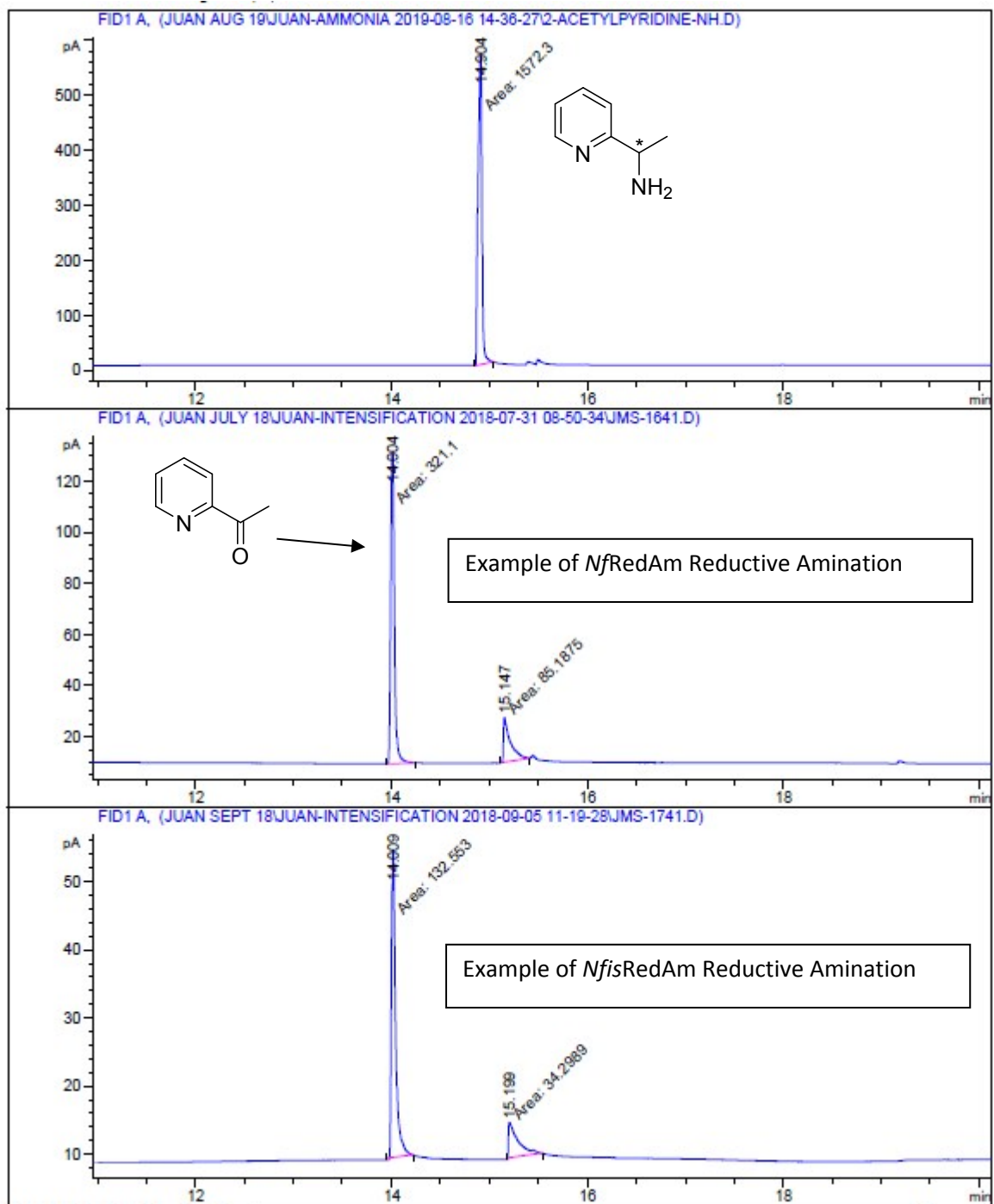


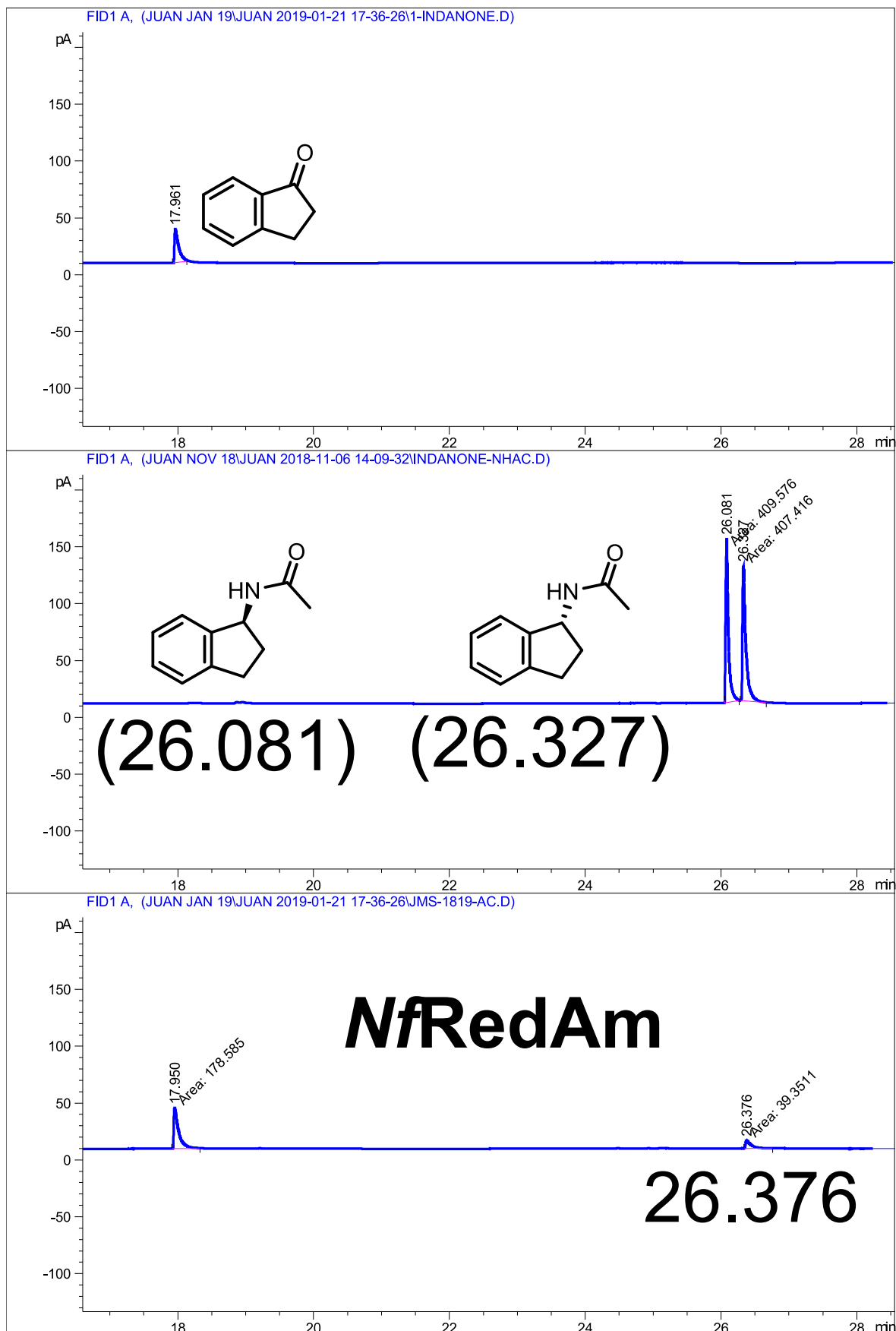


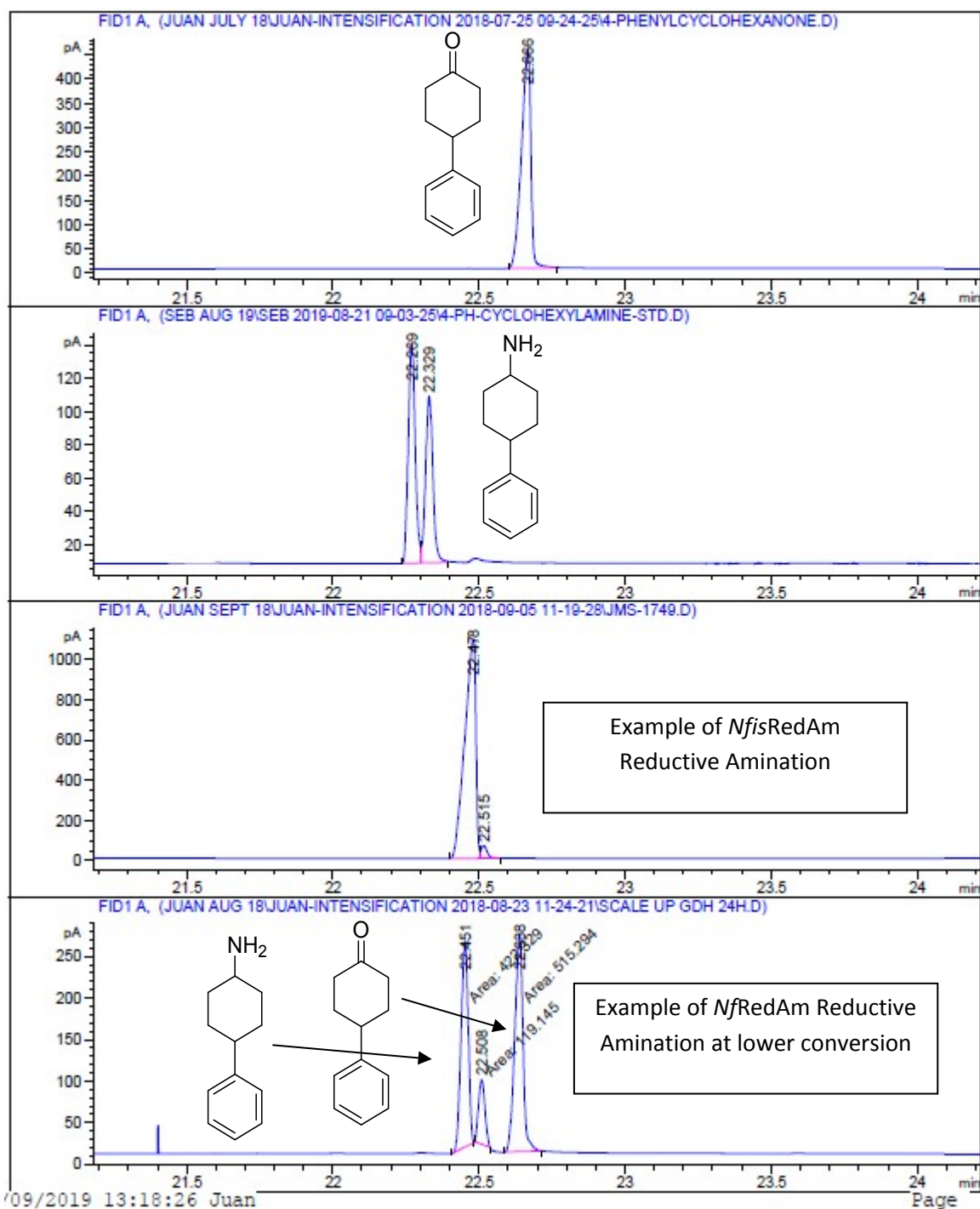


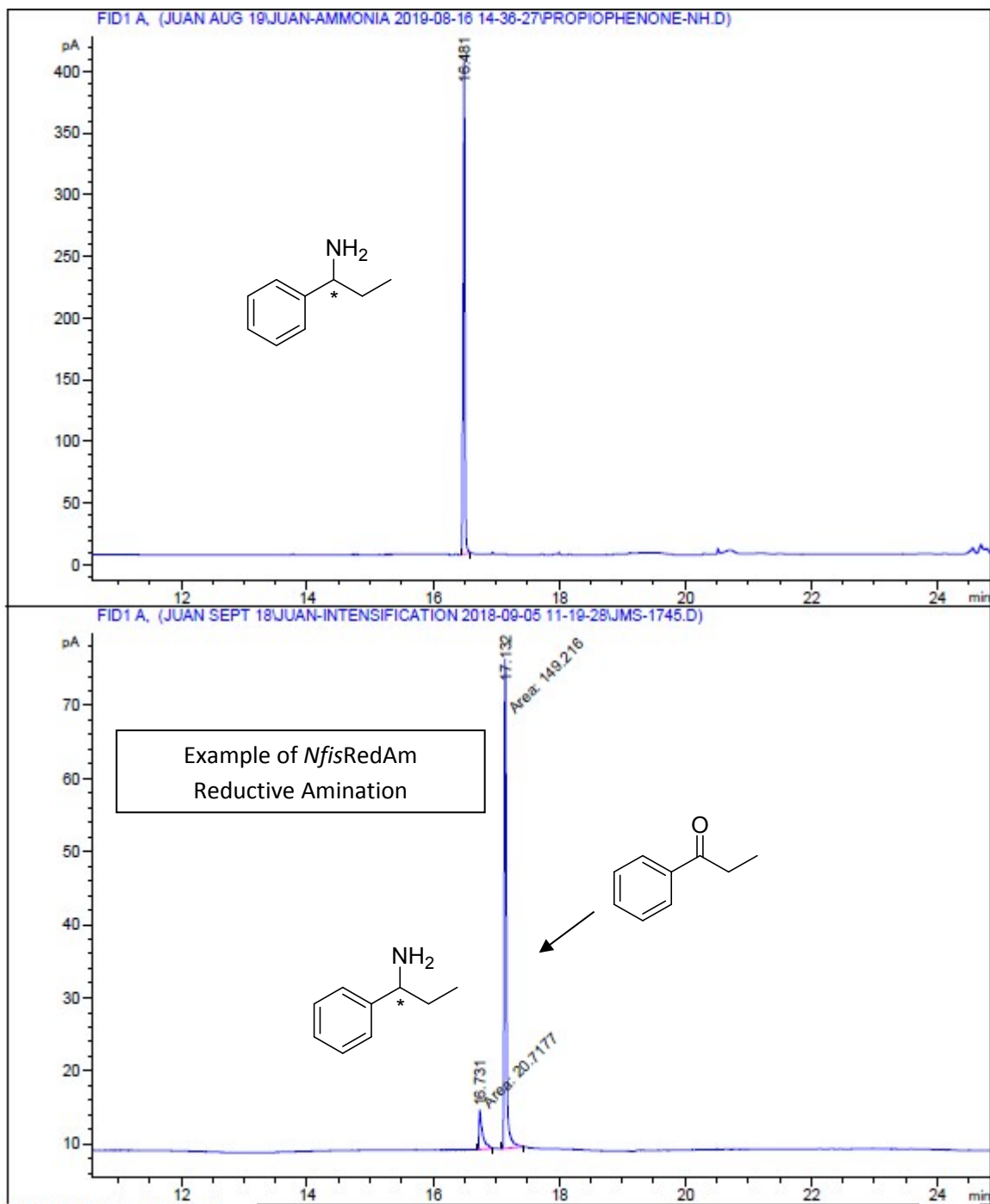


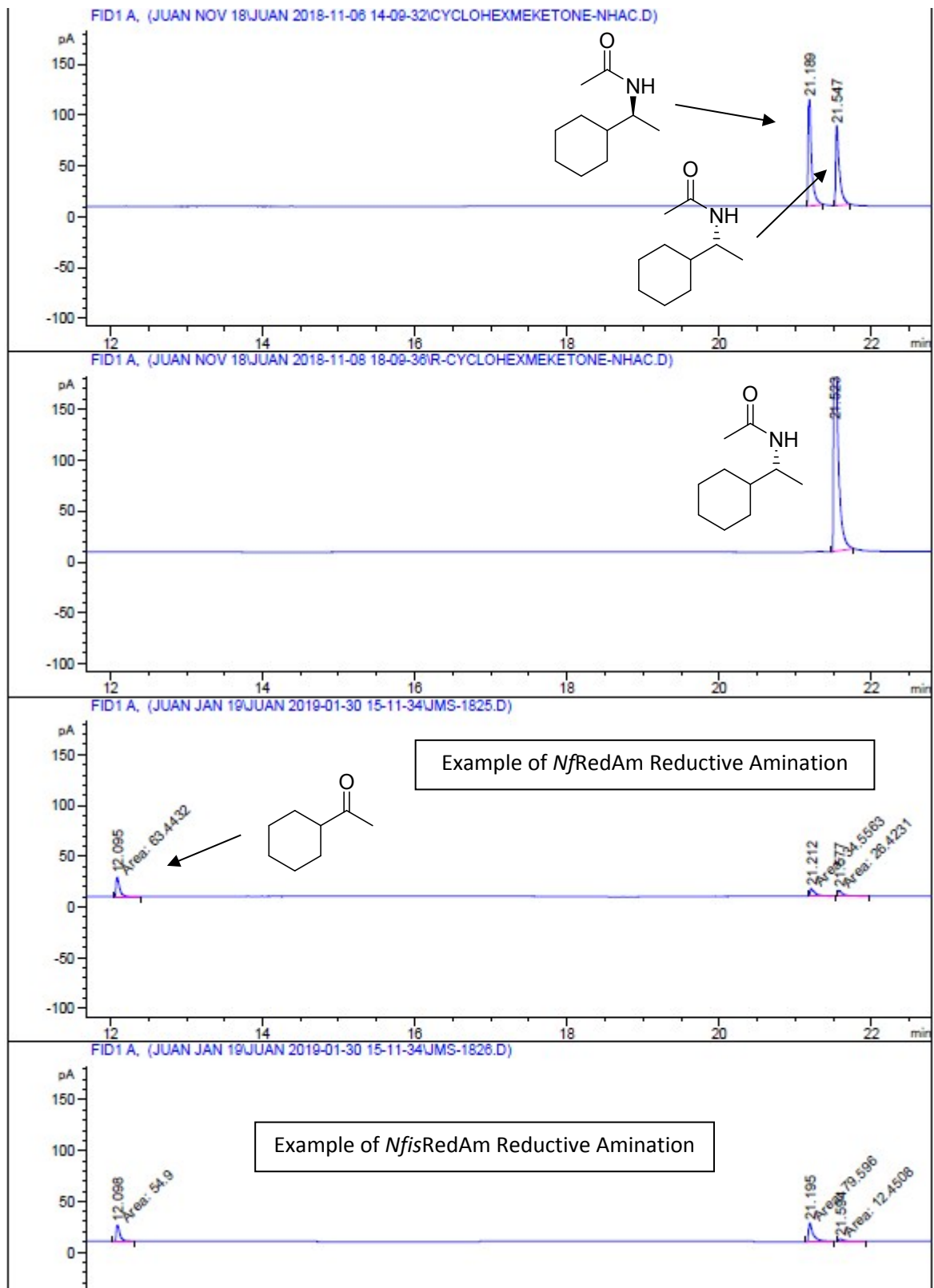


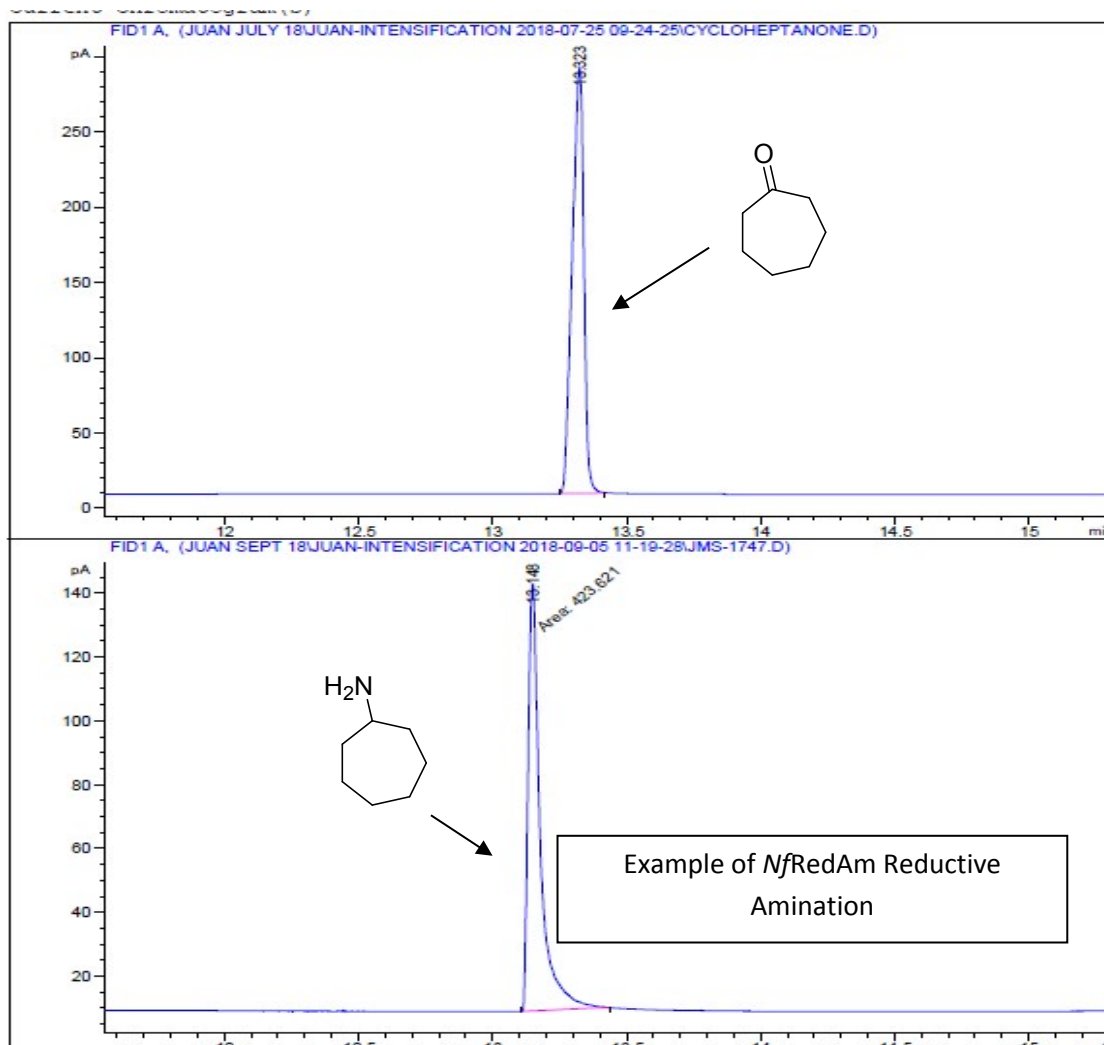




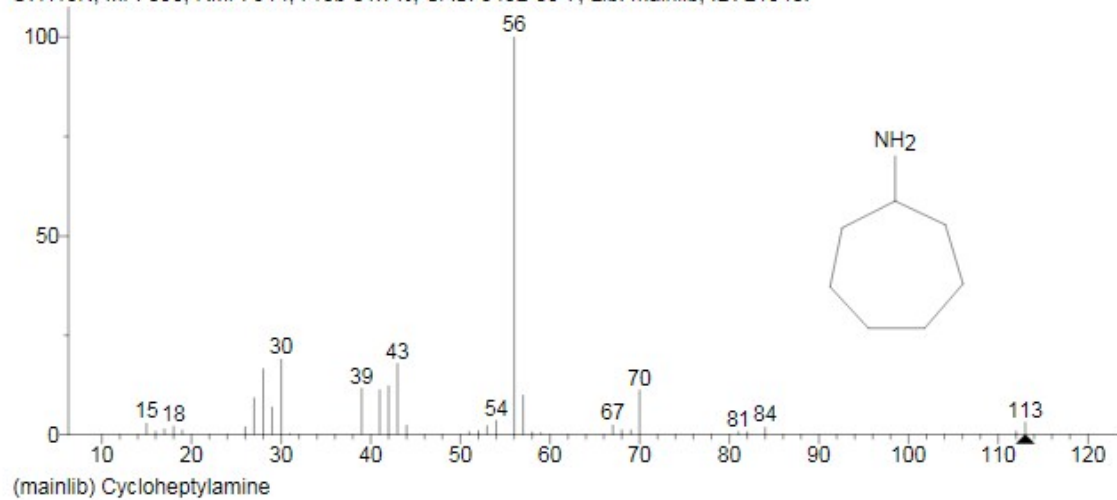


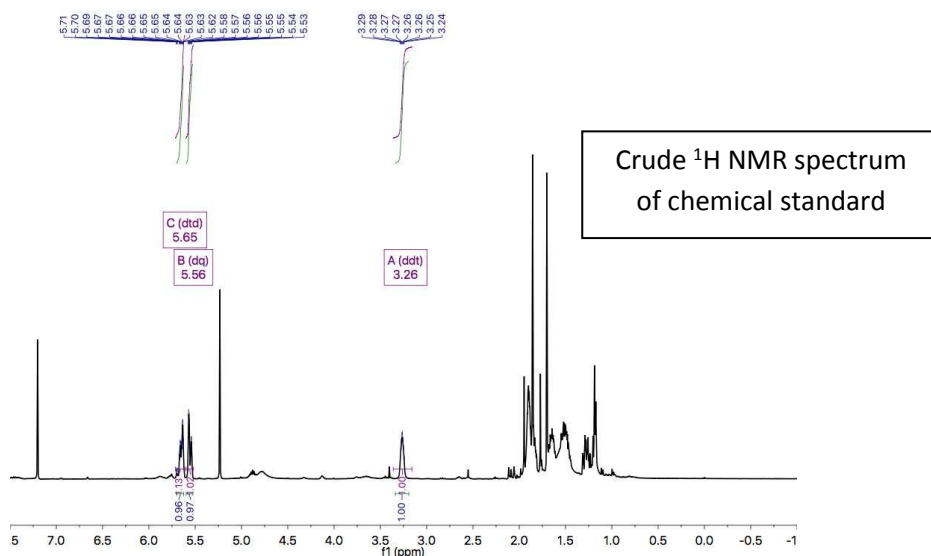
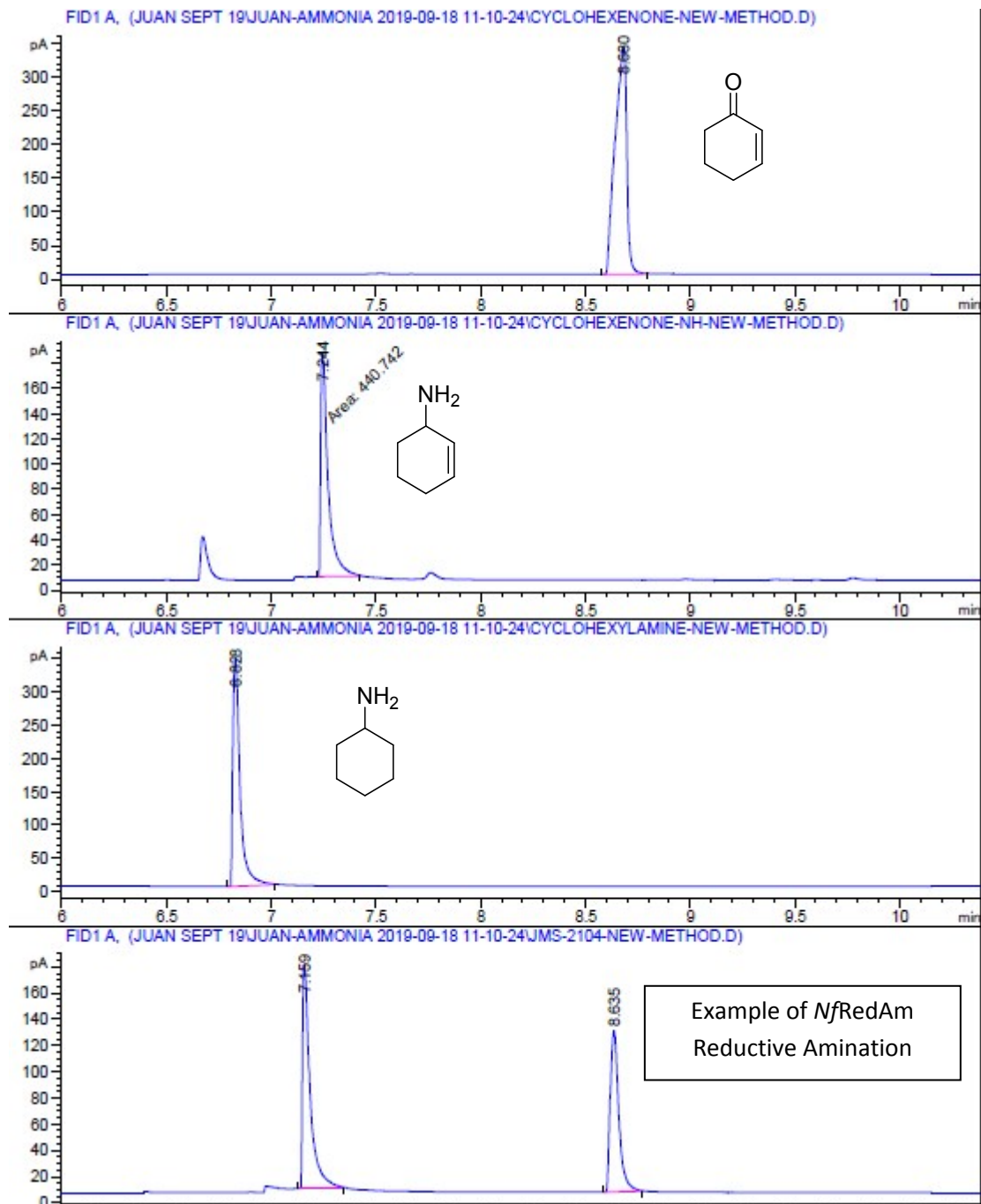


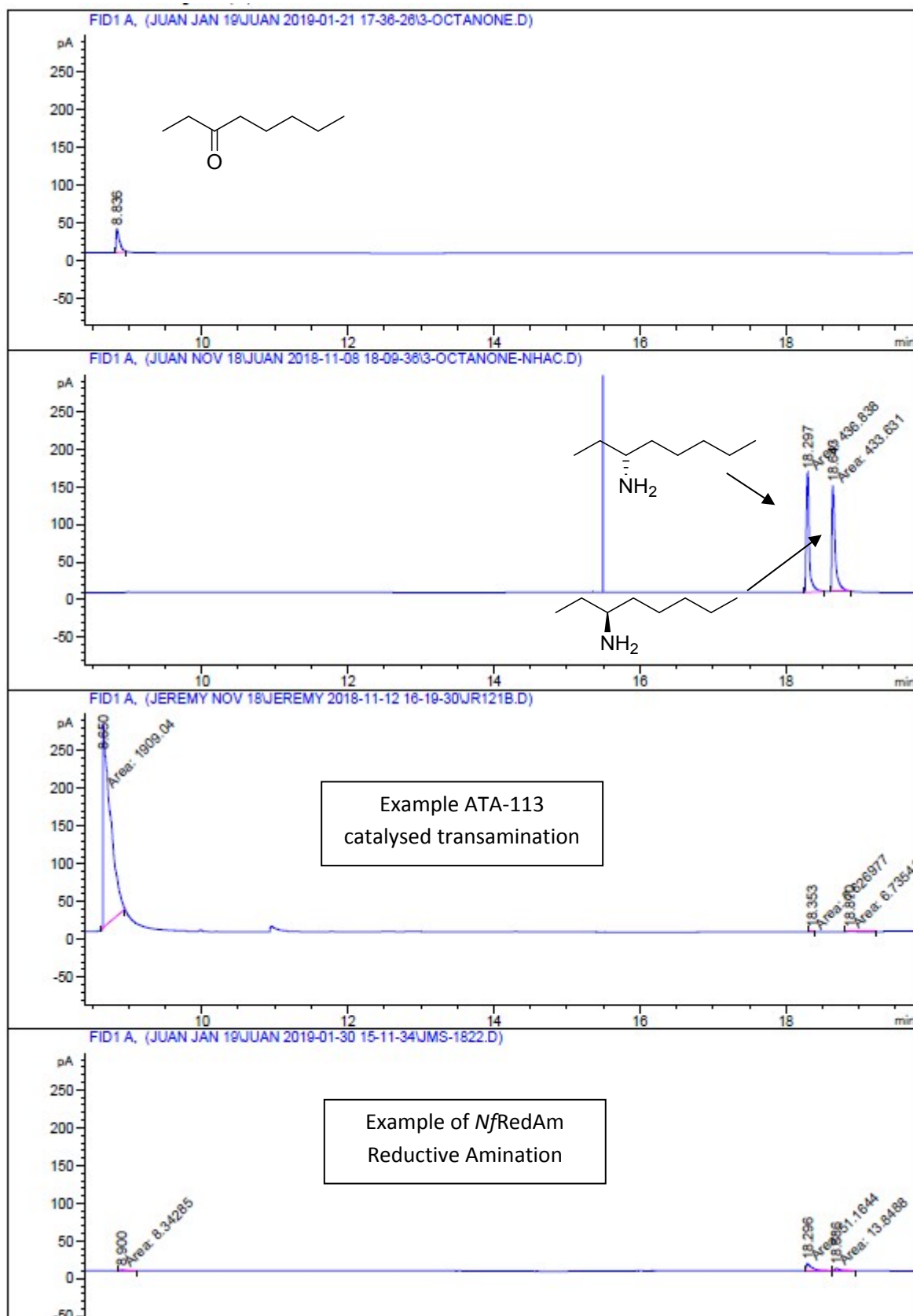


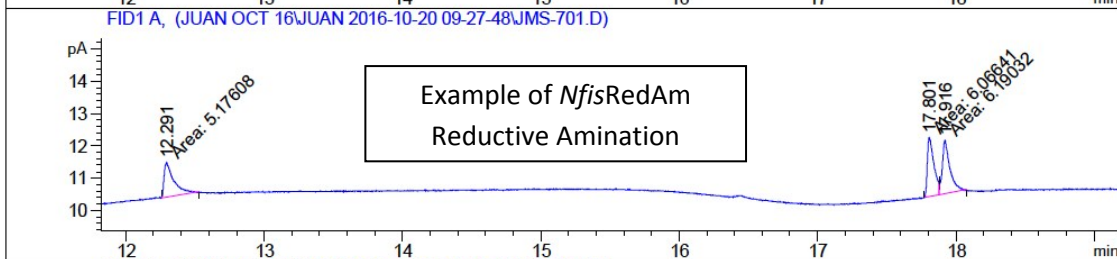
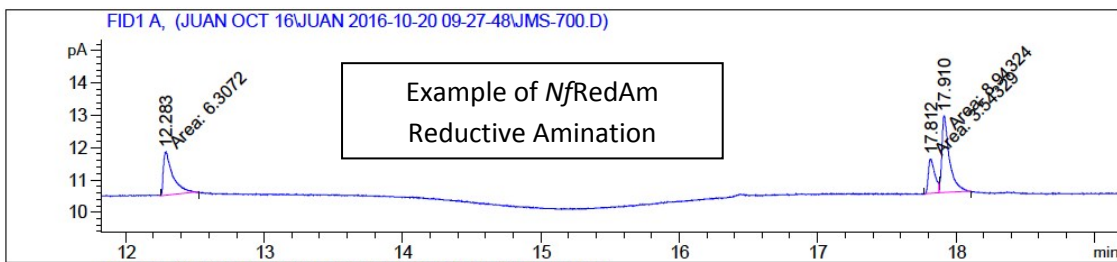
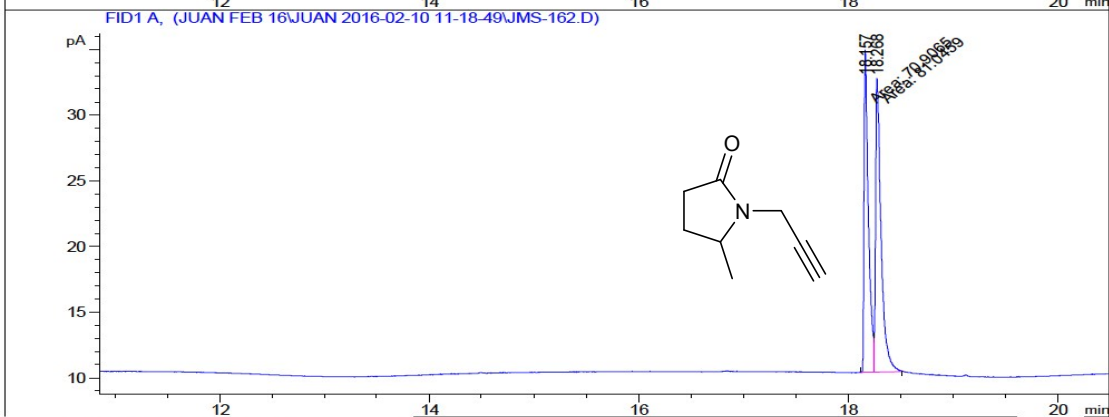
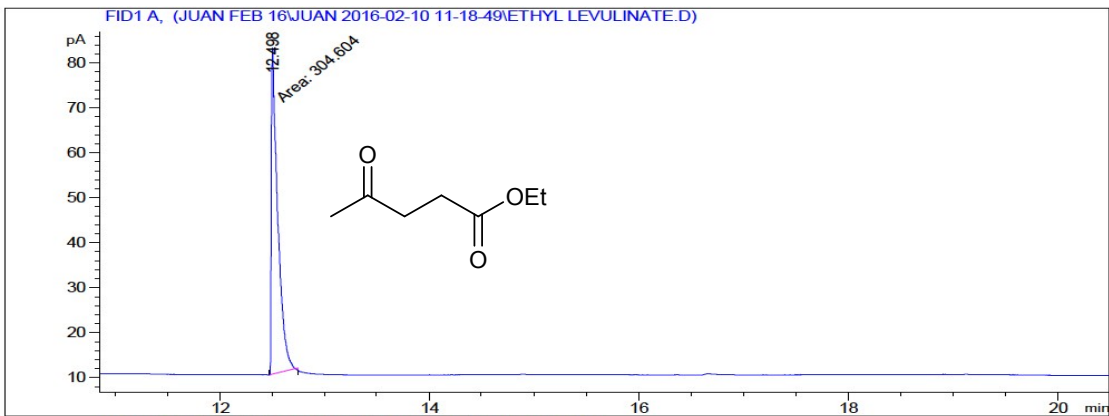


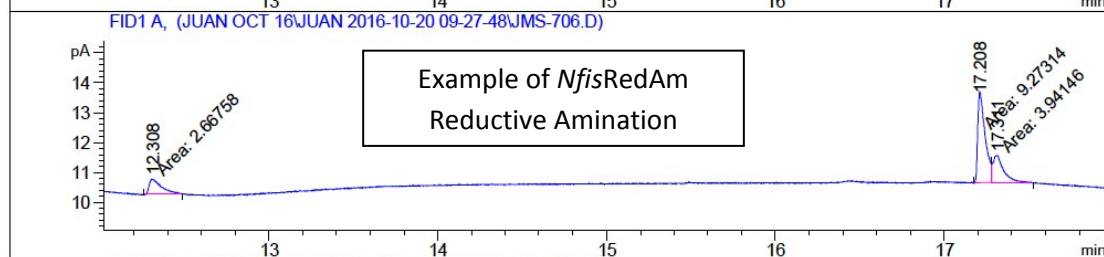
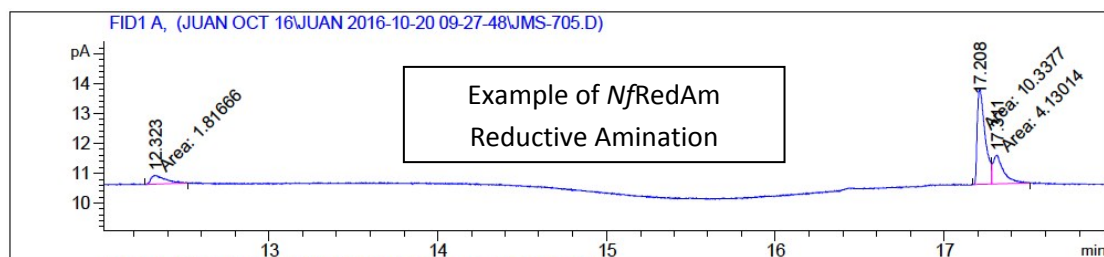
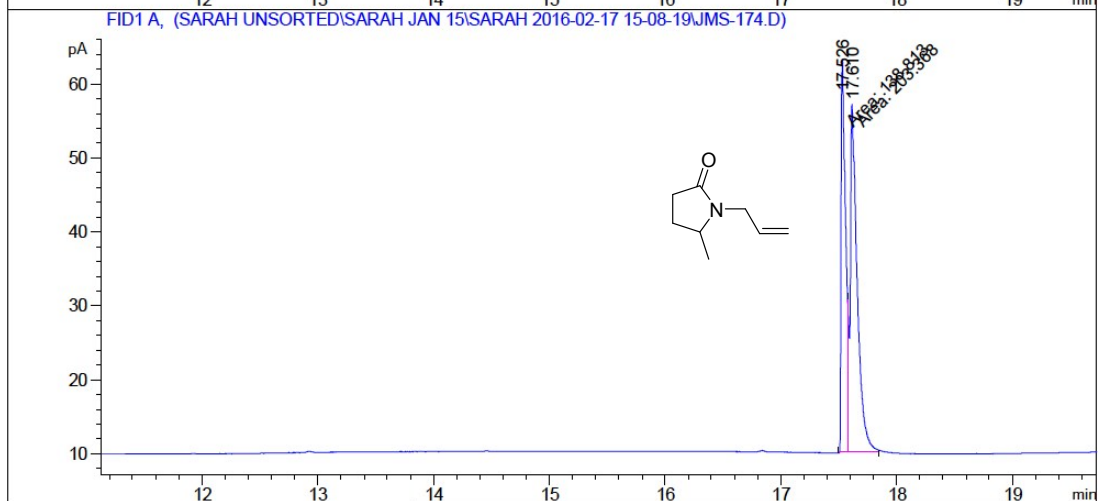
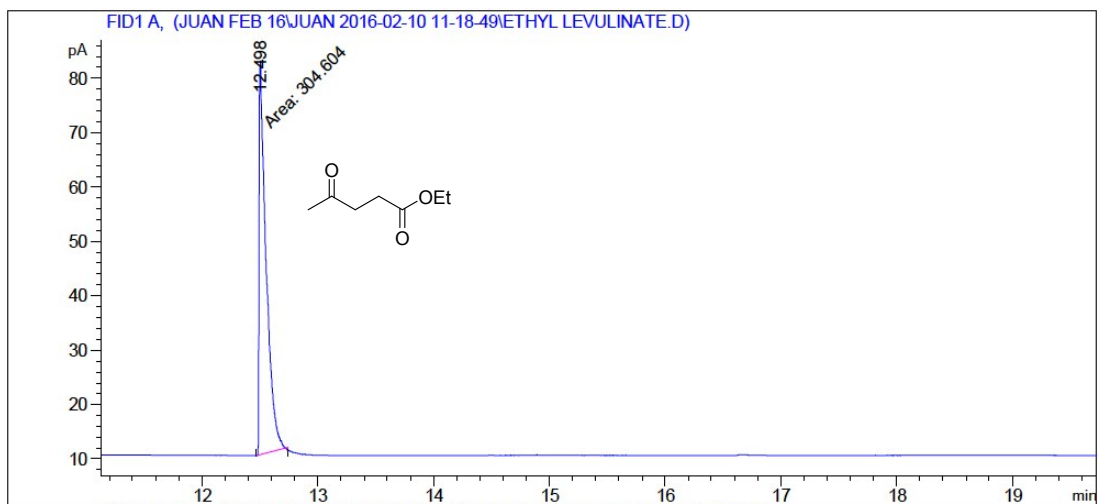
Hit 1 : Cycloheptylamine  
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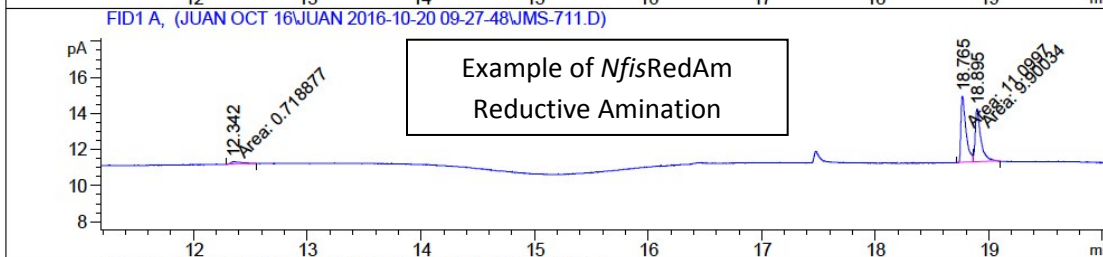
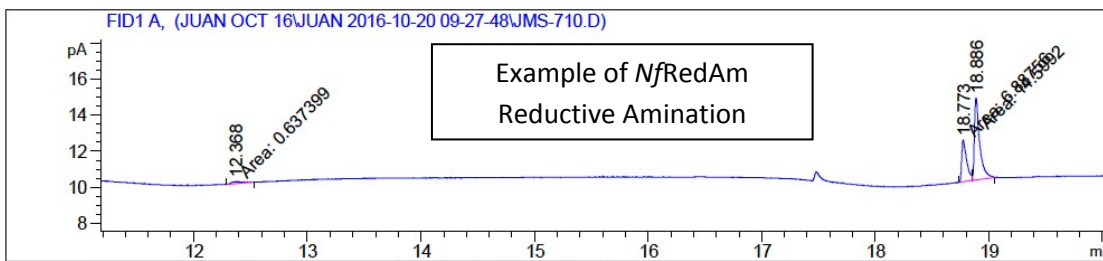
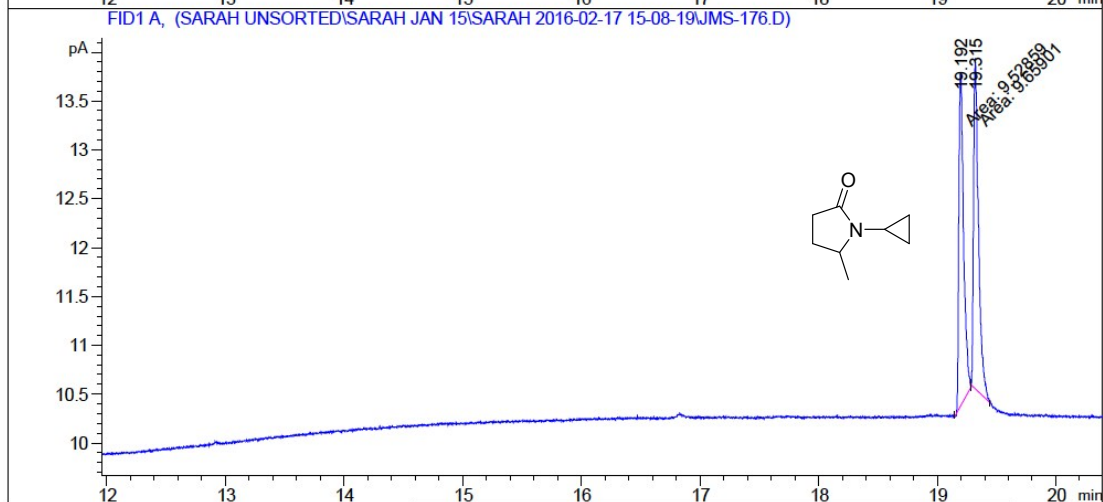
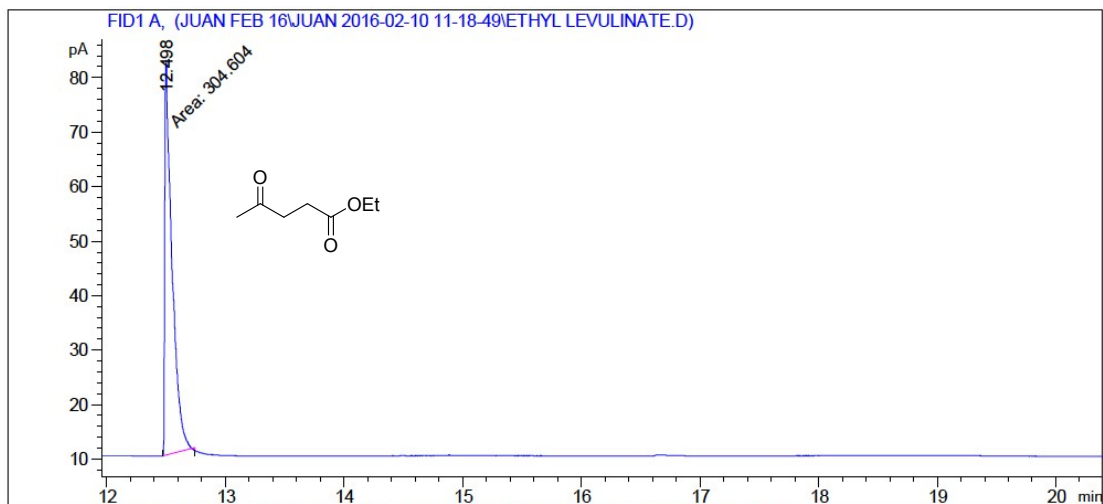


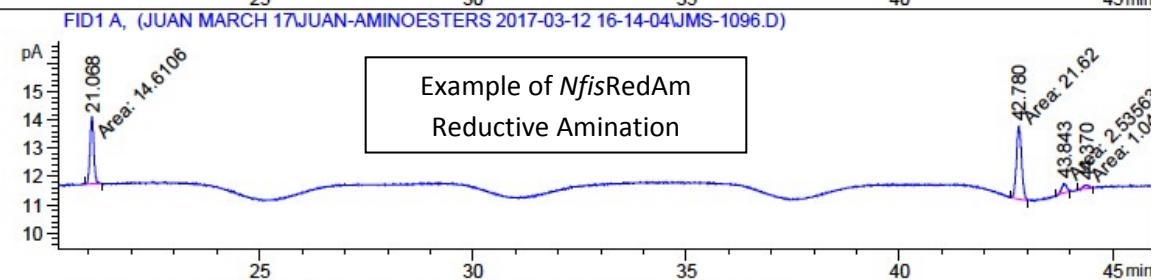
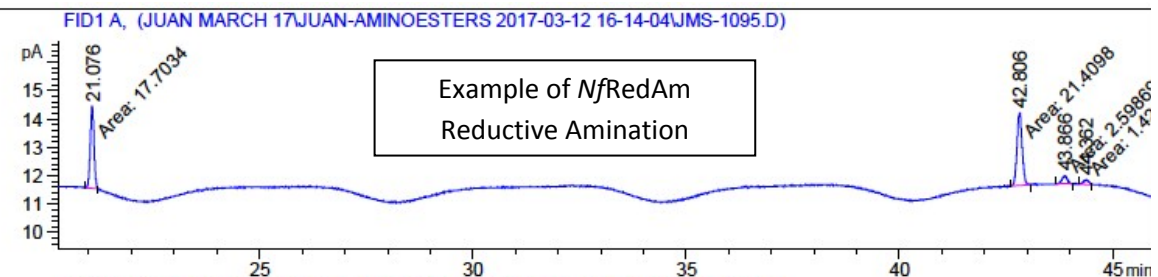
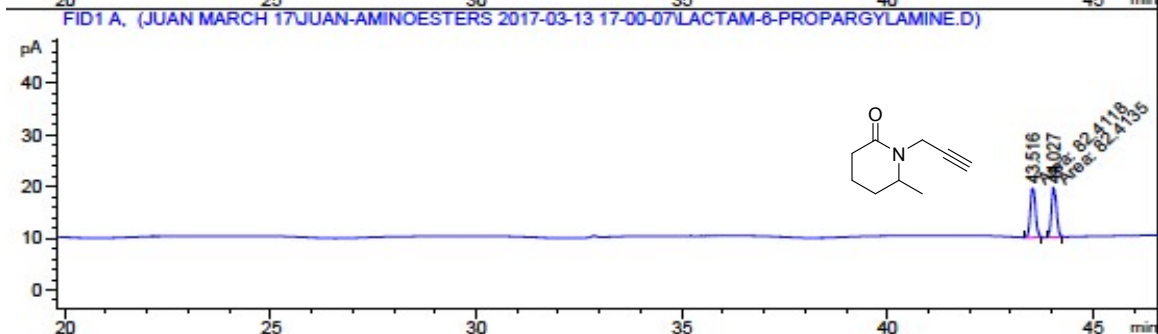
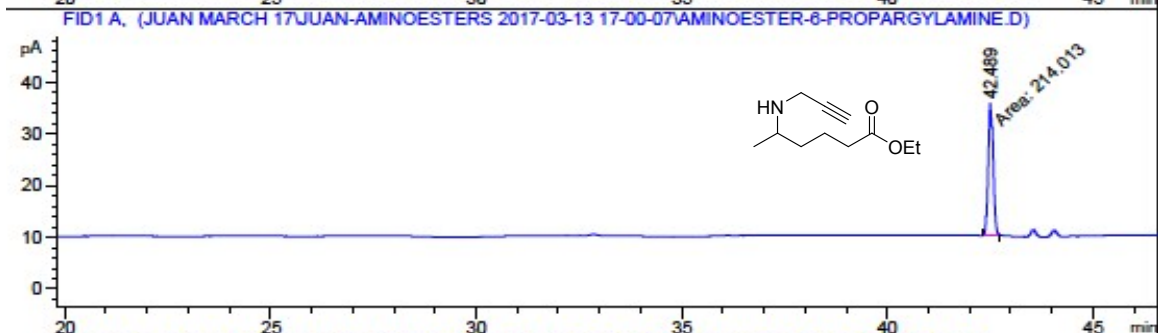
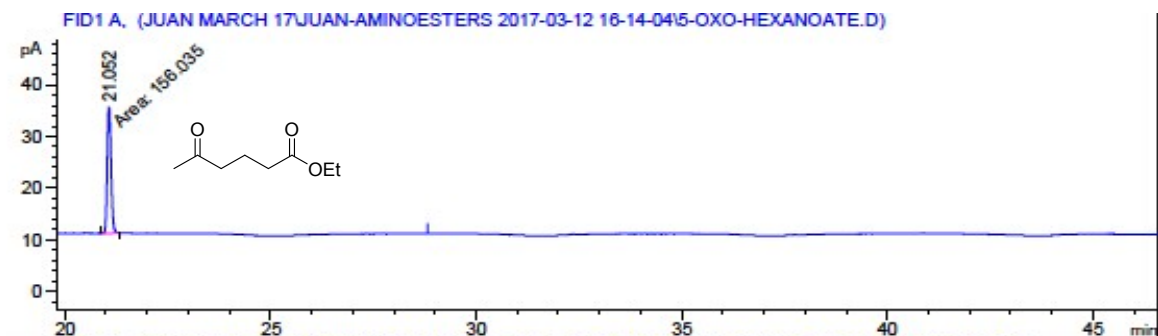


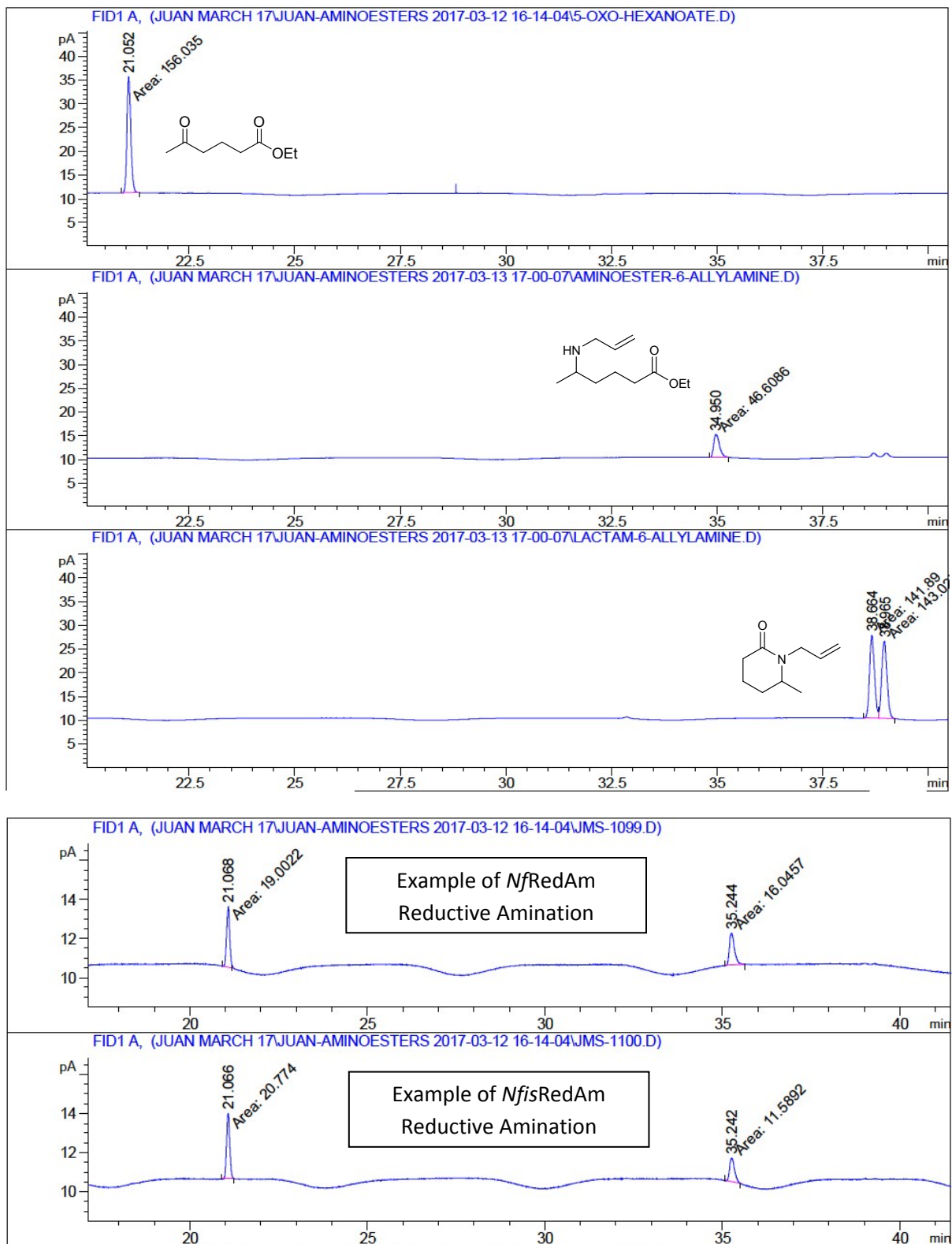


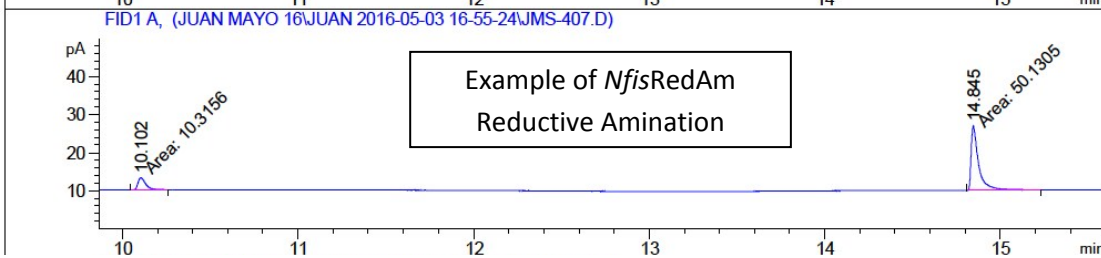
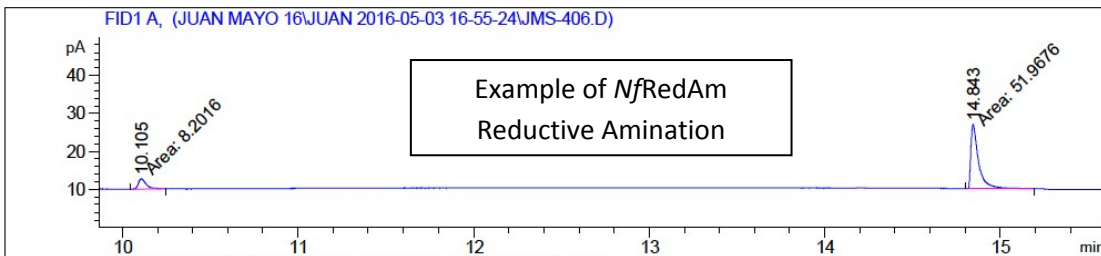
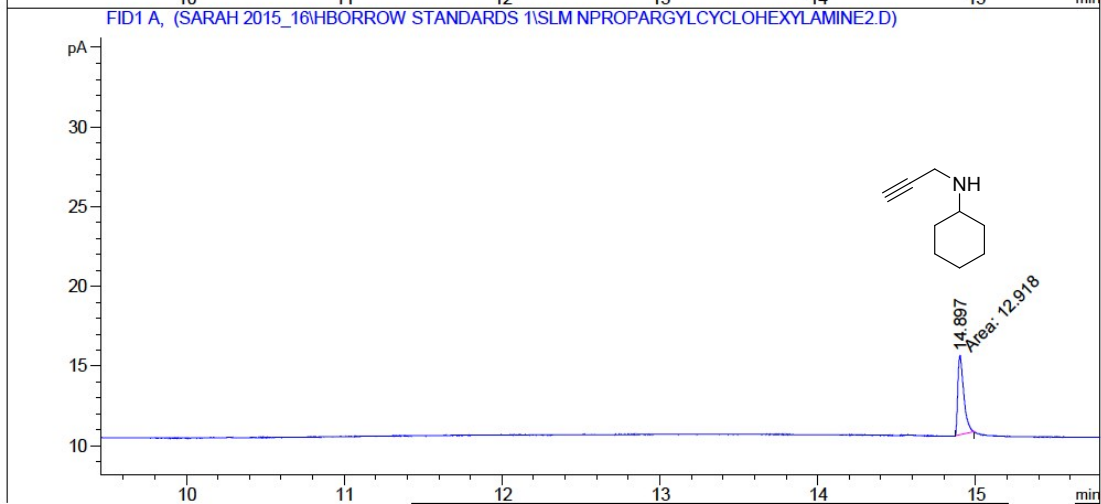
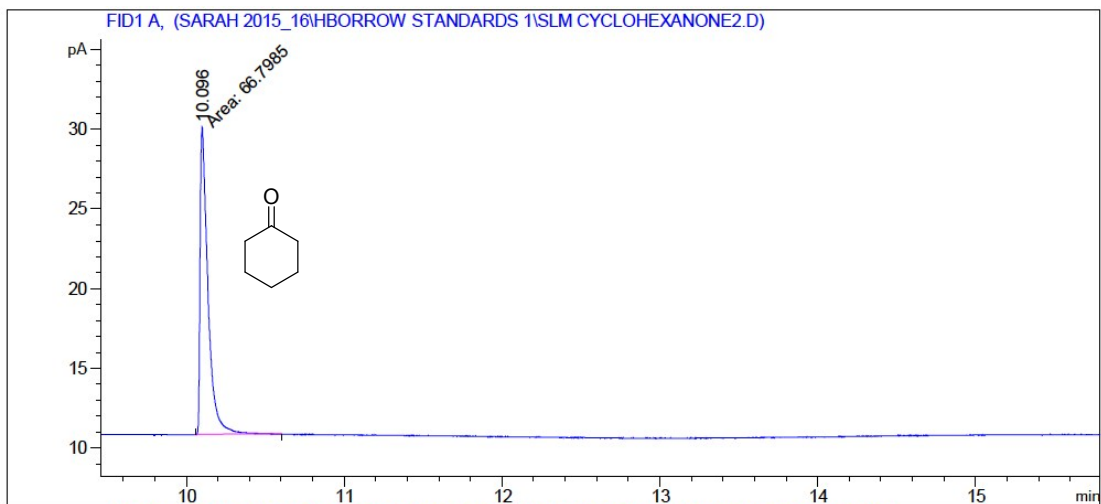


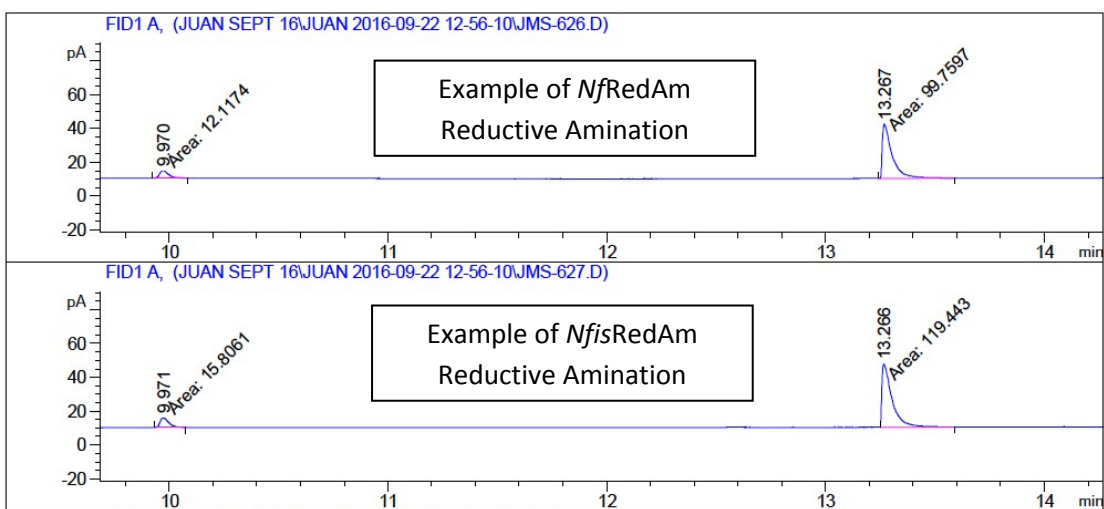
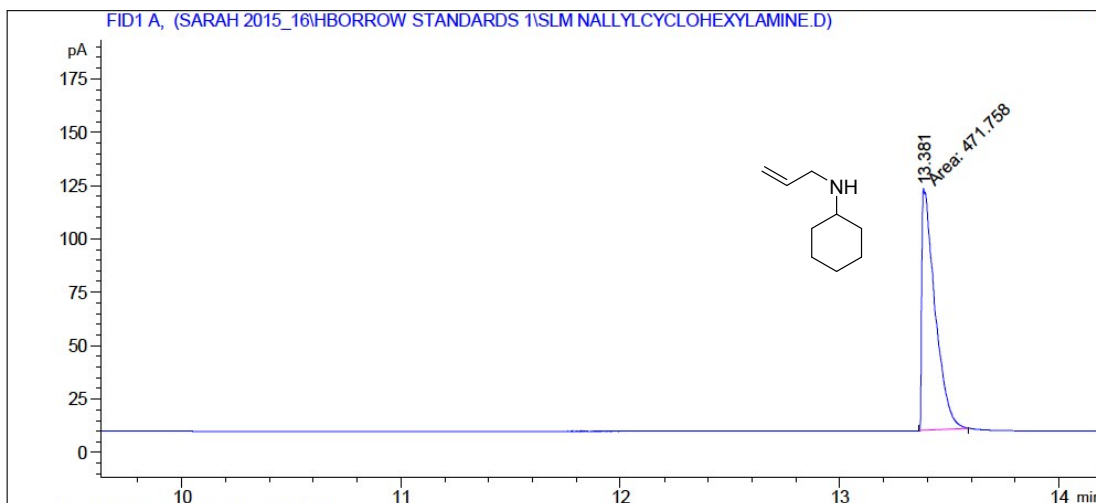


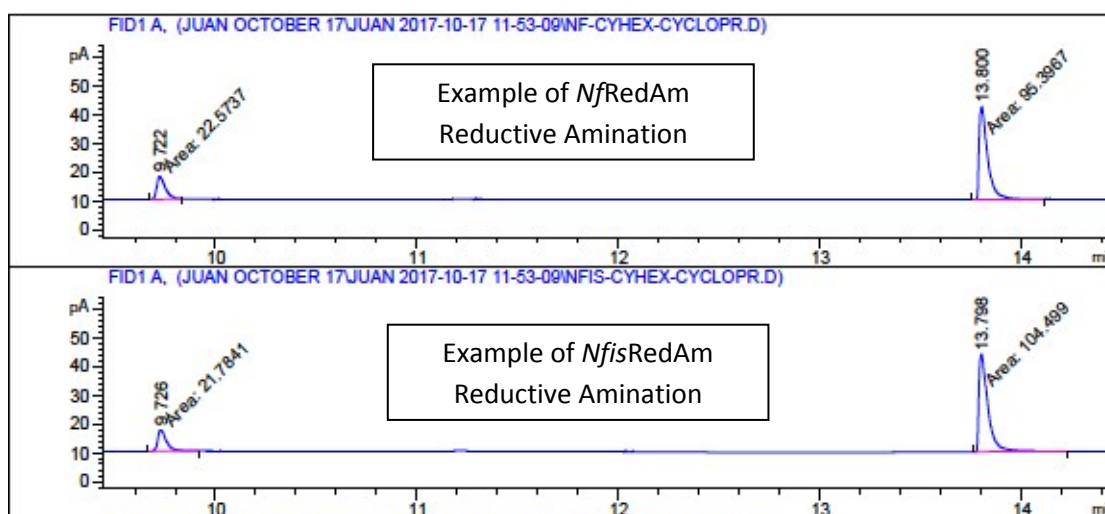
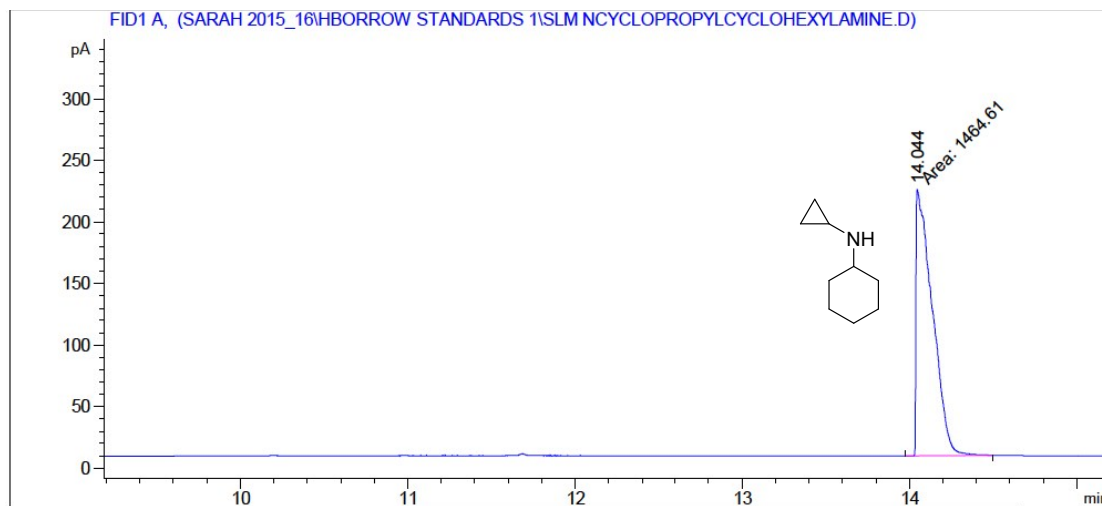


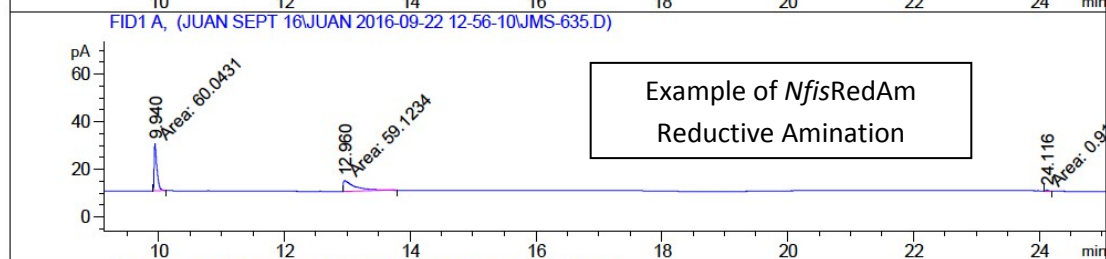
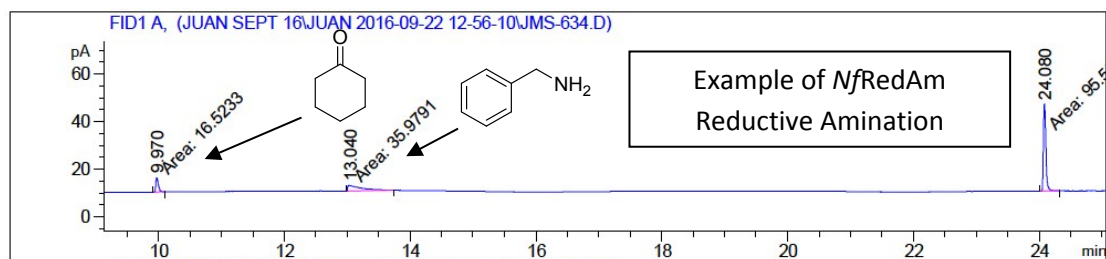
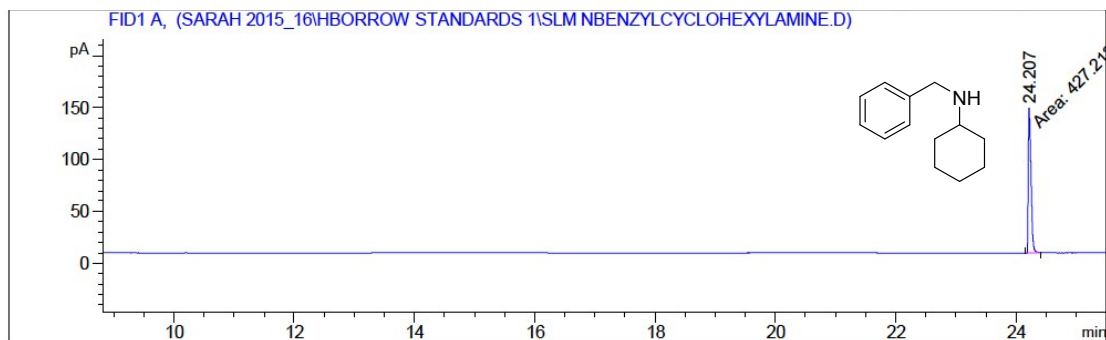


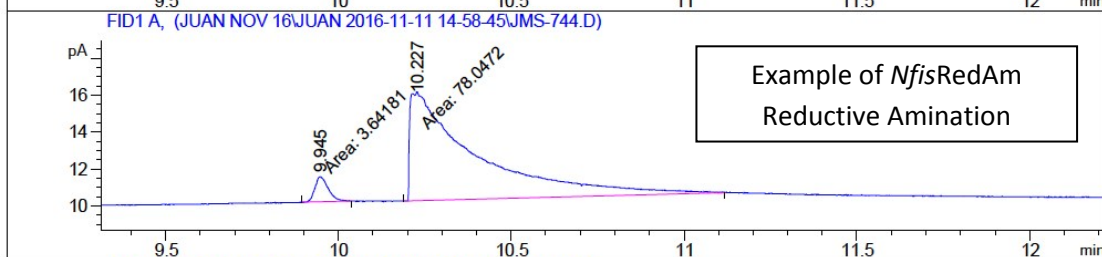
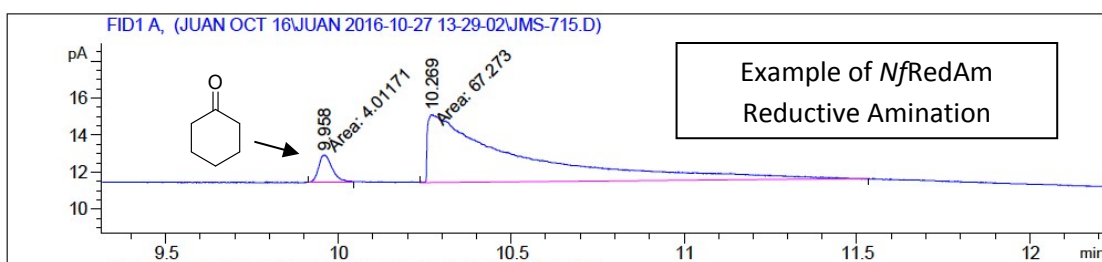
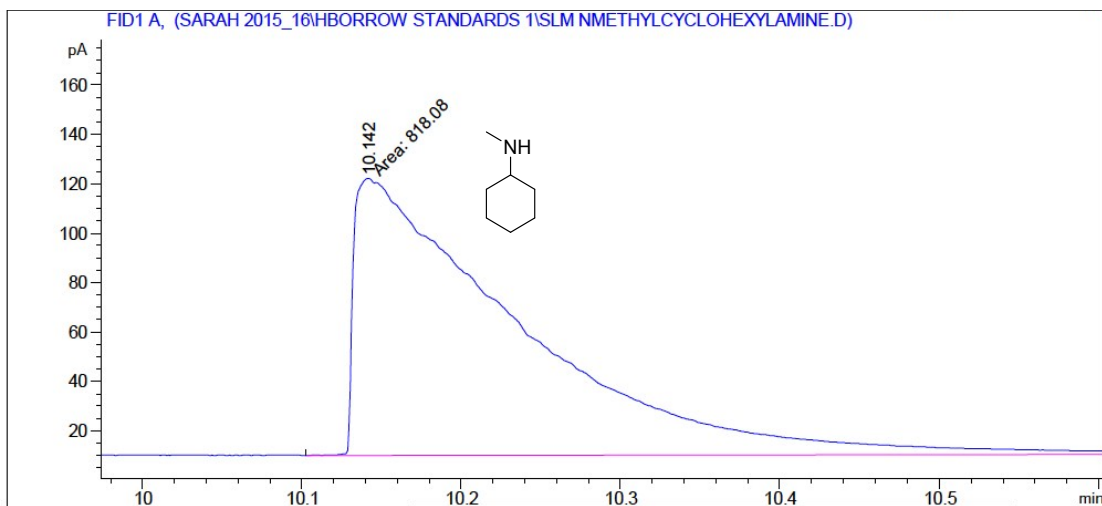


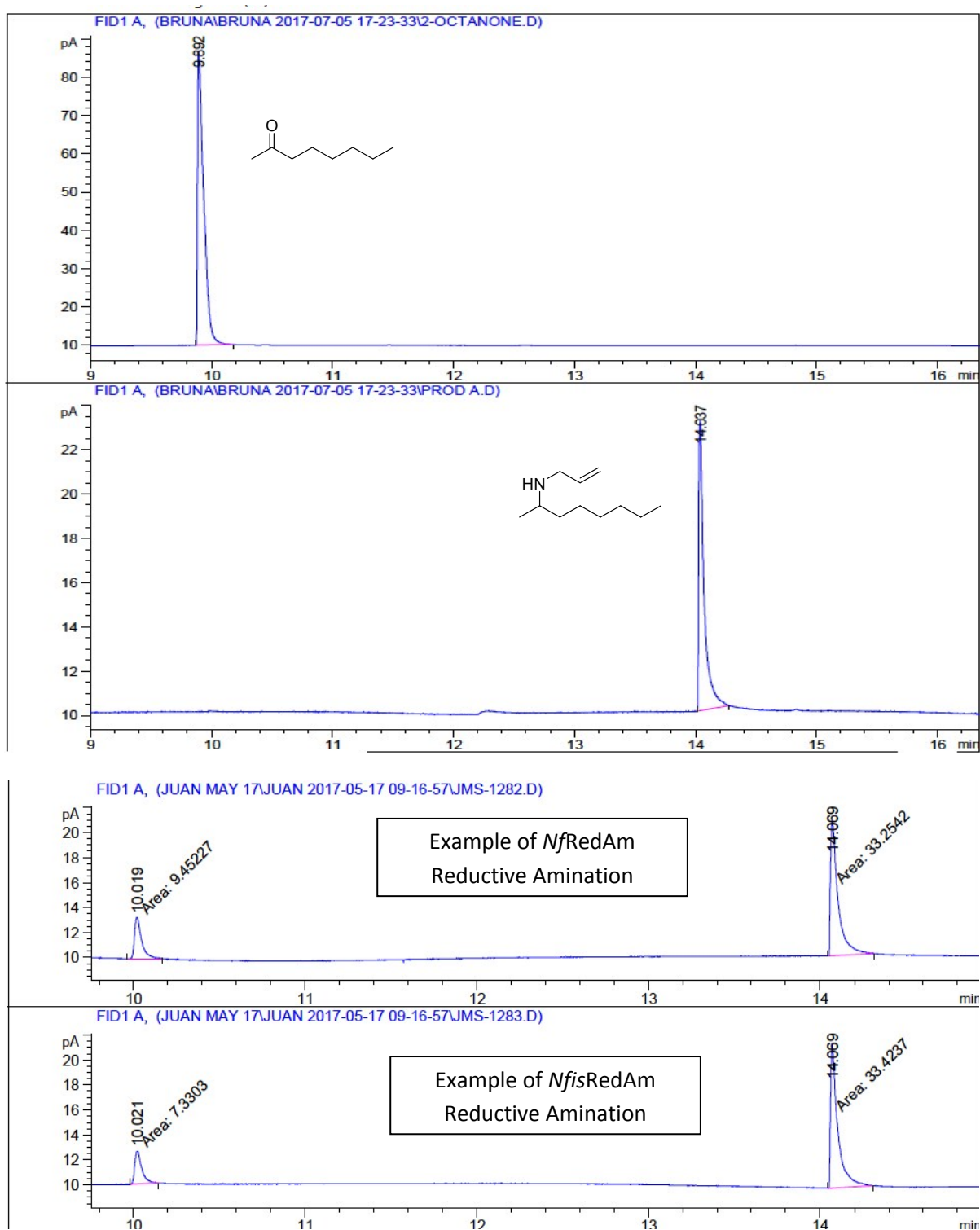




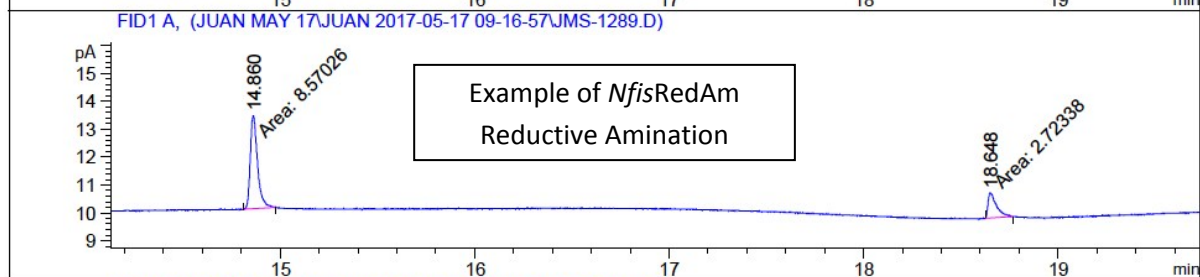
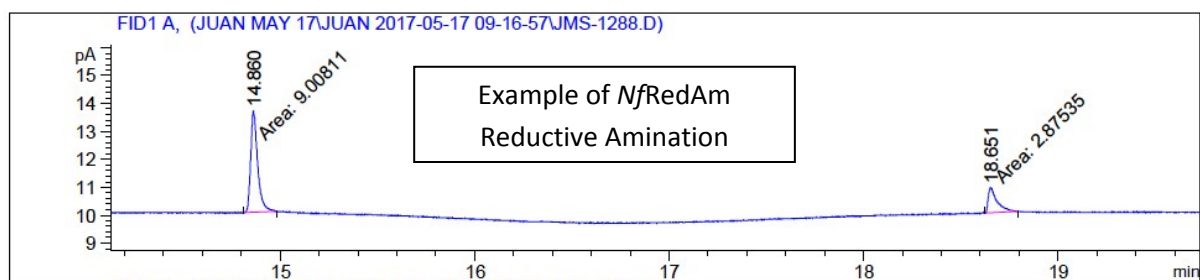
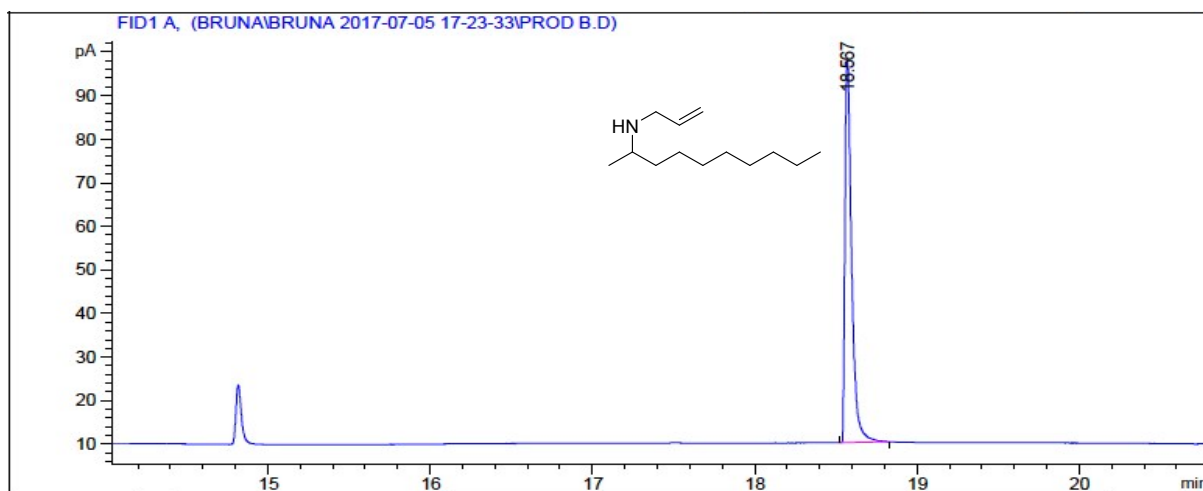


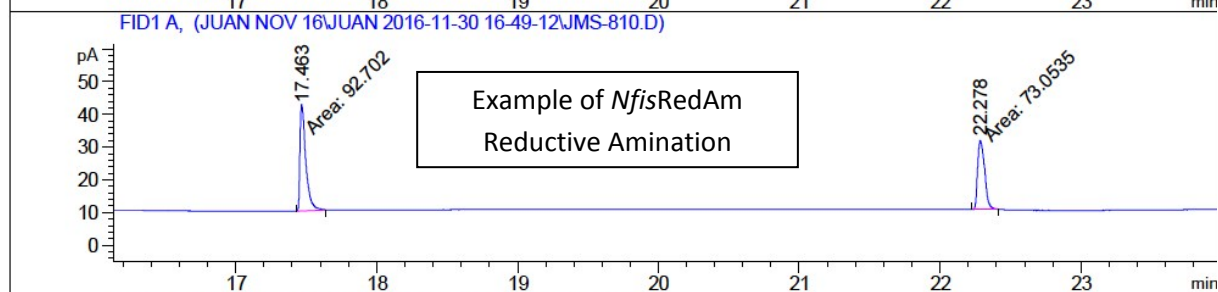
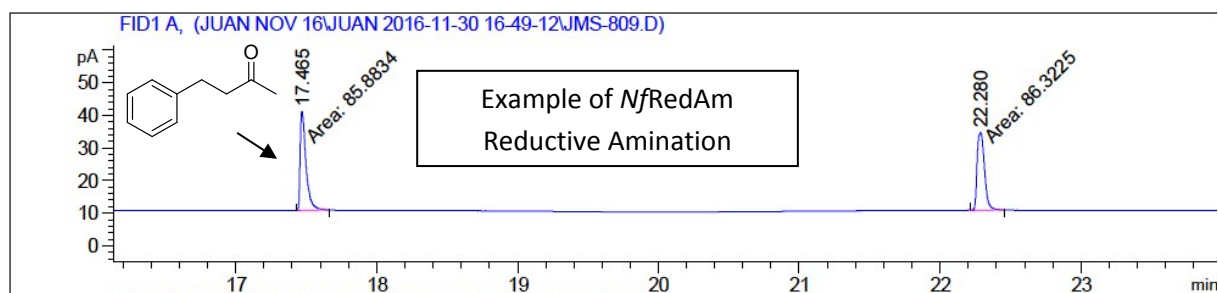
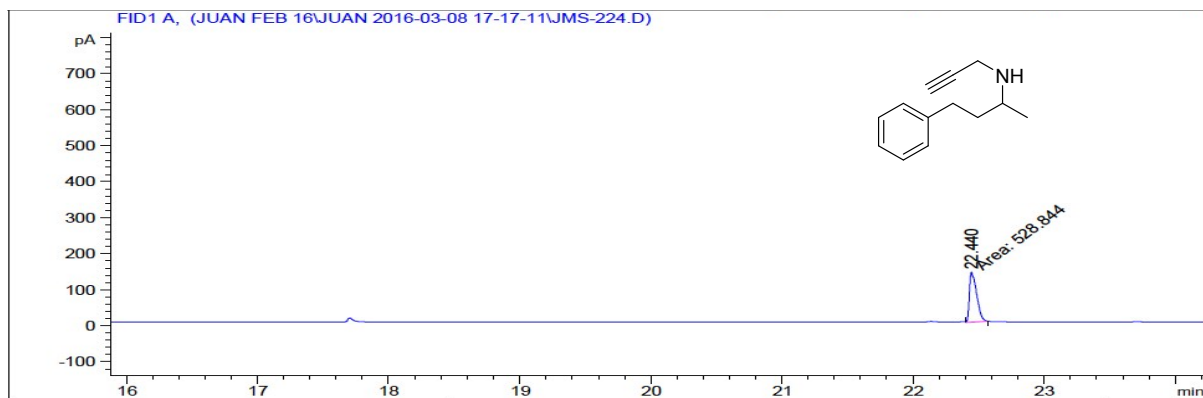


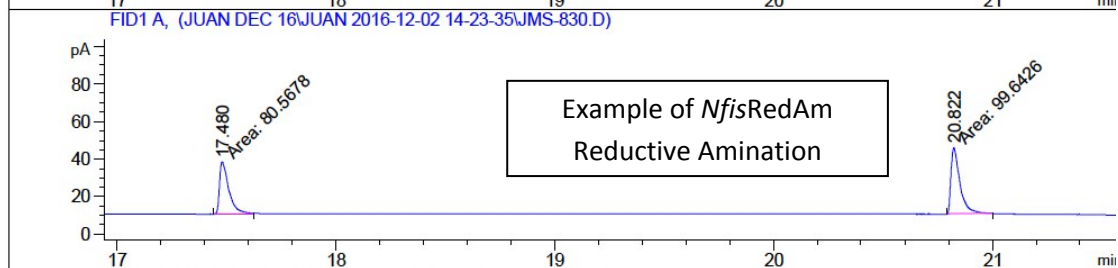
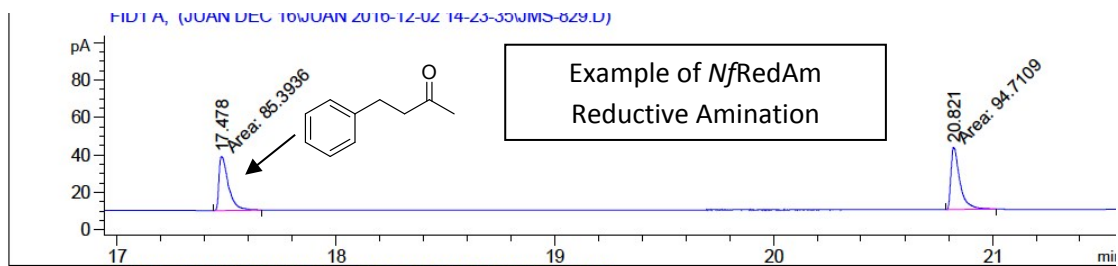
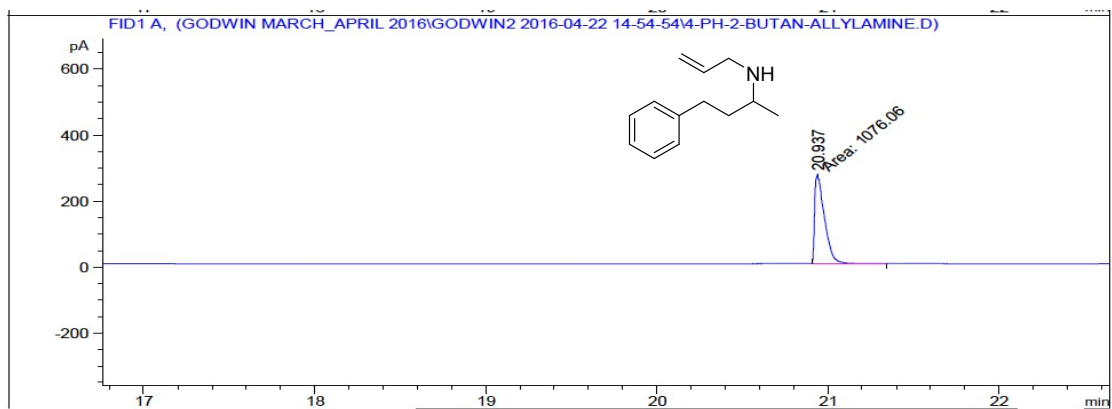


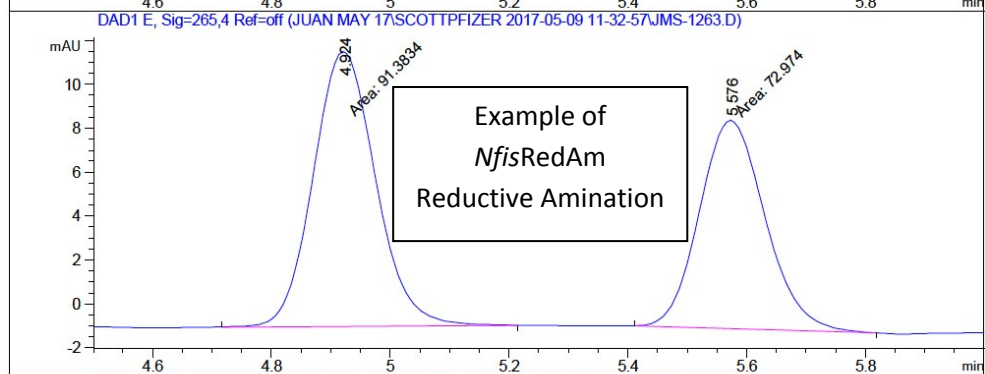
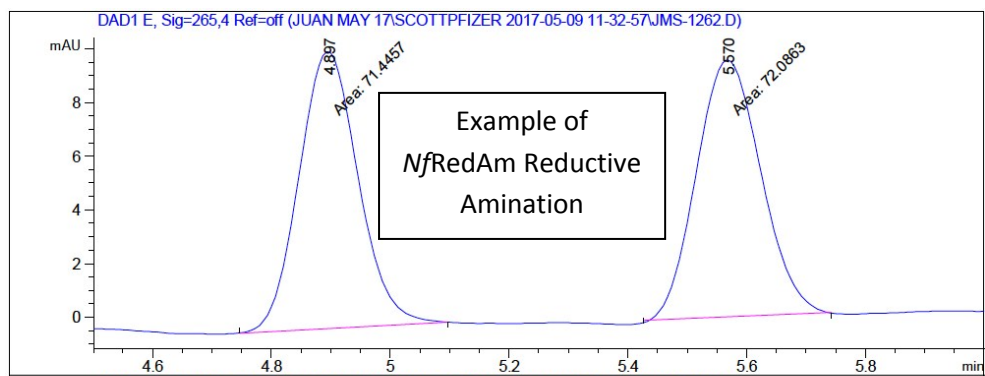
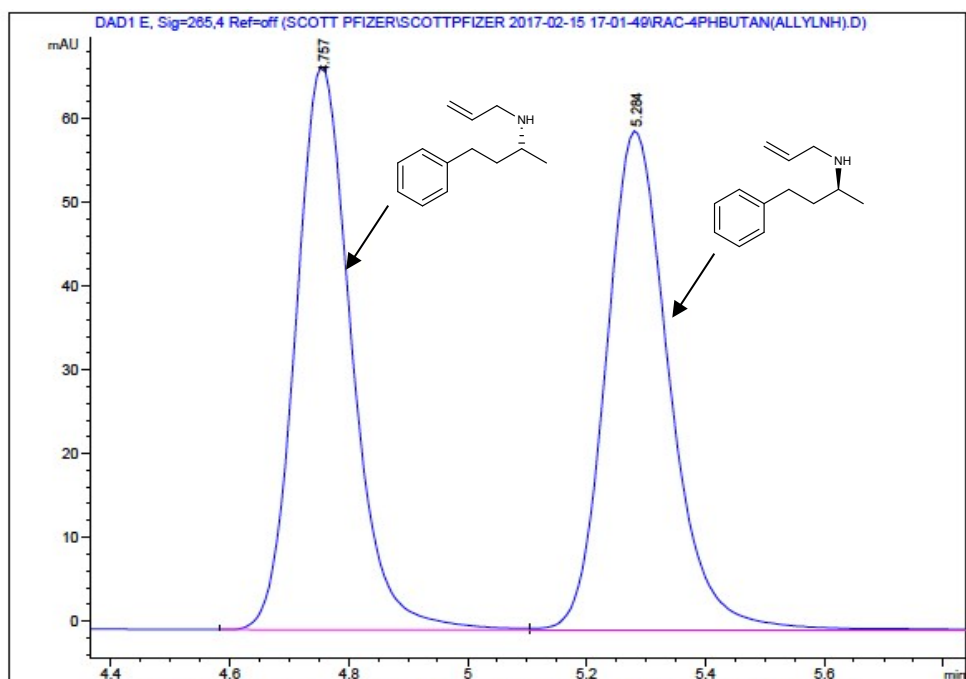


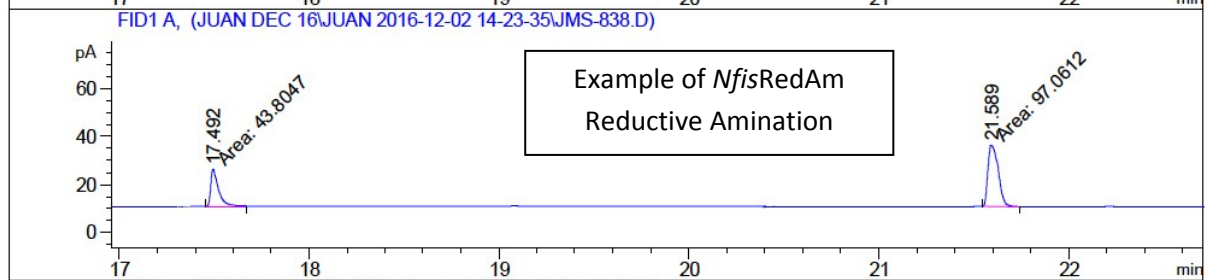
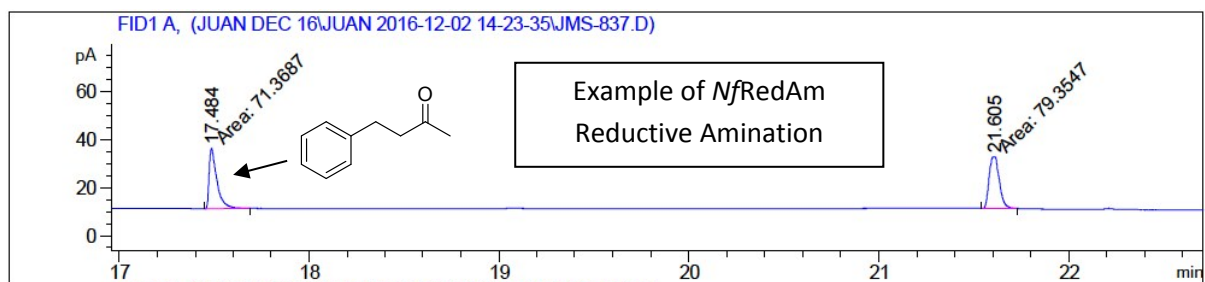
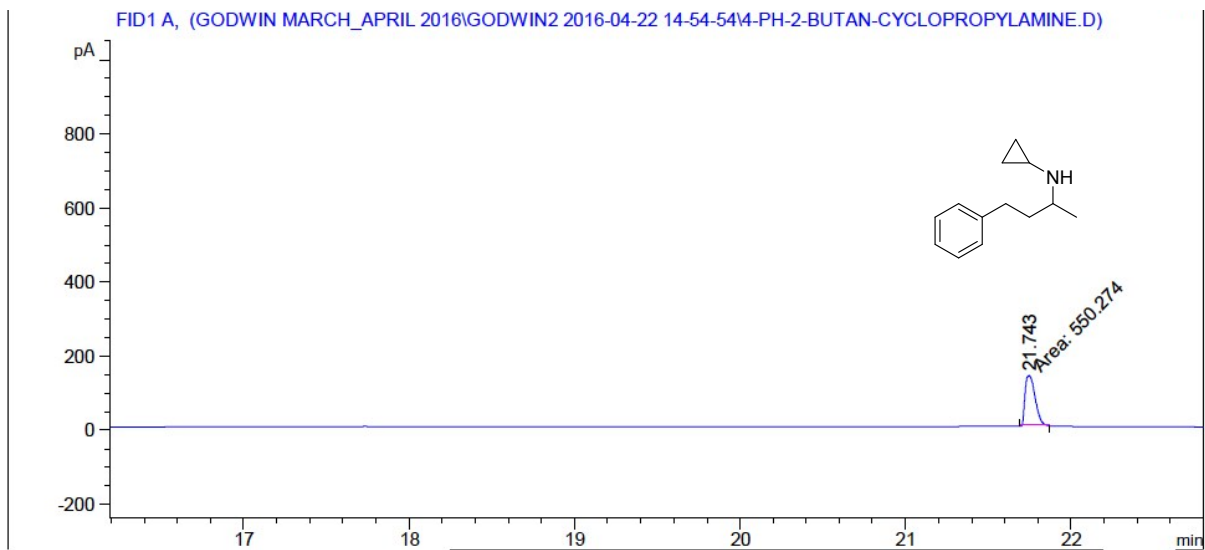
**Supplementary Figure S33.** GC-FID analysis: RedAm-catalysed reductive amination of 2-octanone **5** with allylamine **b** (5 equivalents) showing *NfRedAm* (top) and *NfisRedAm* (bottom).

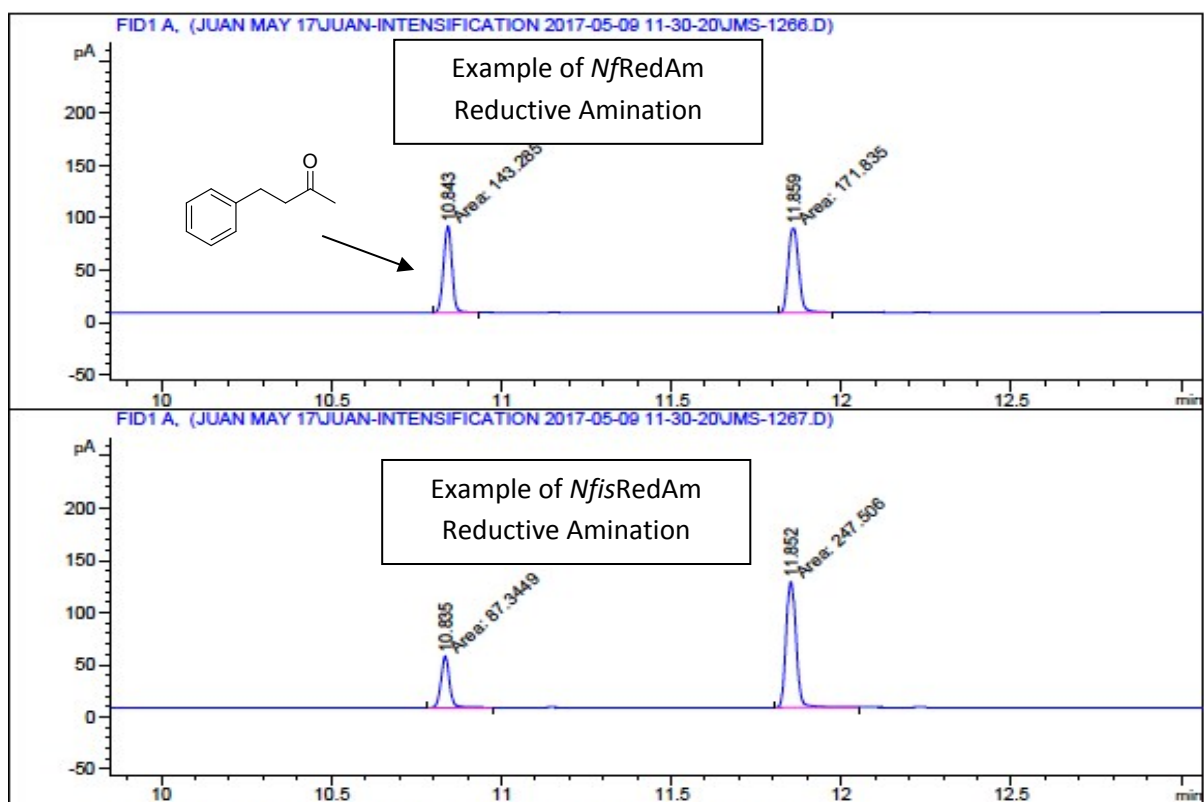
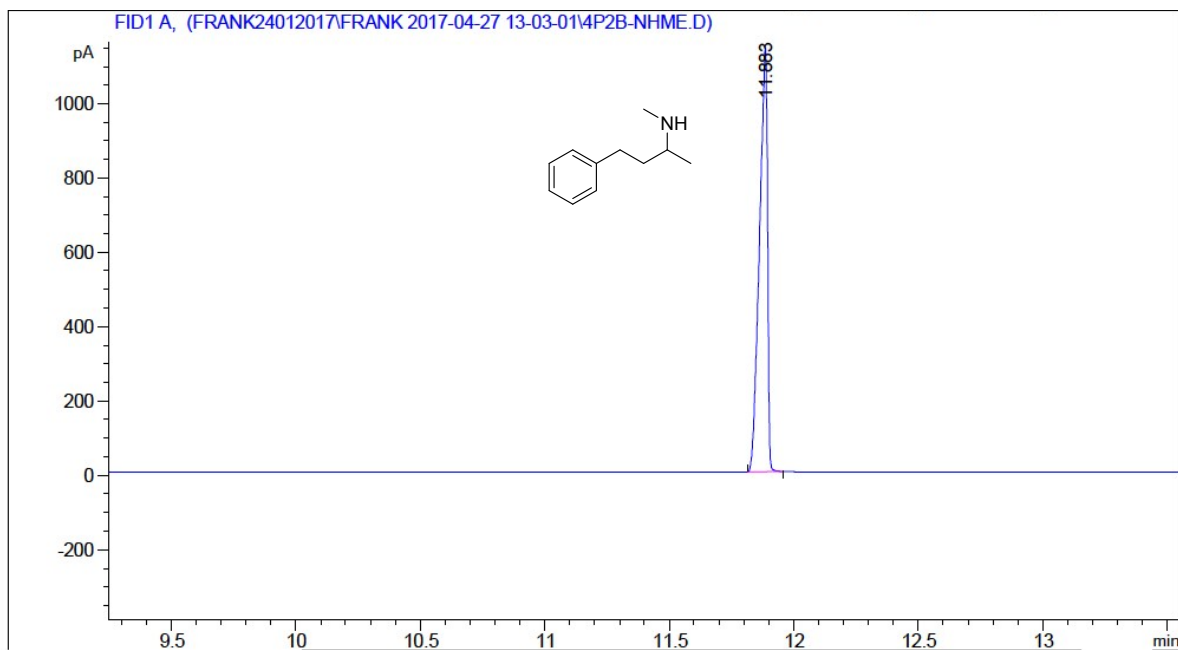


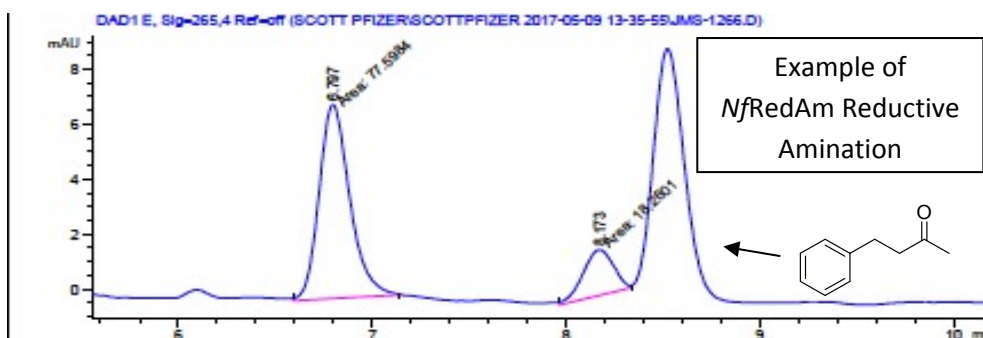
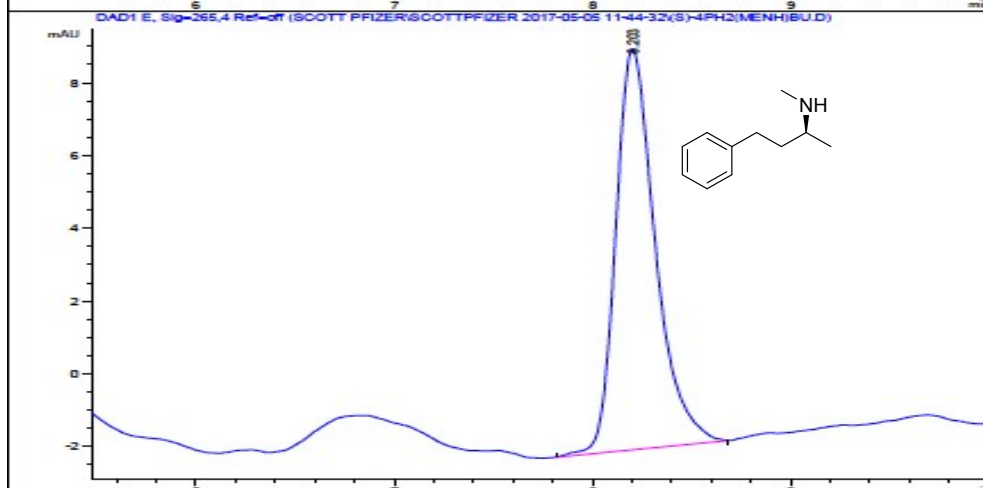
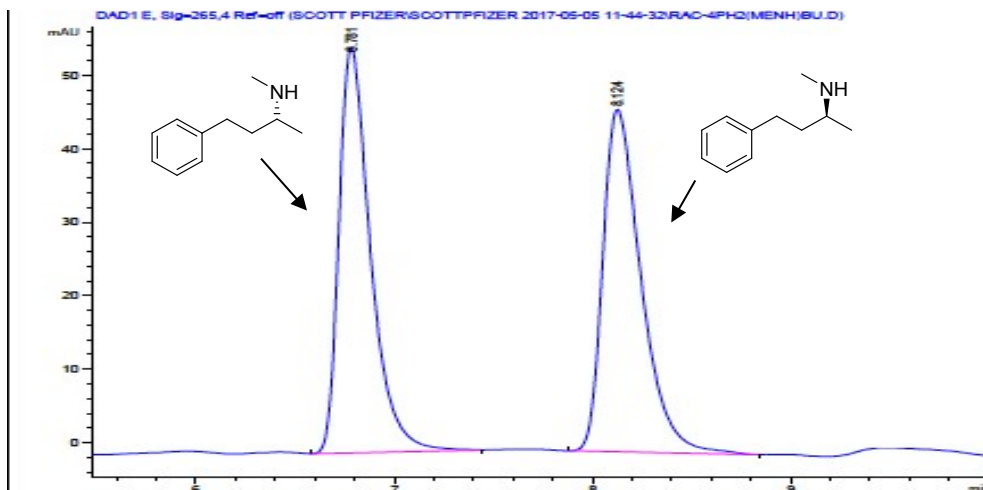




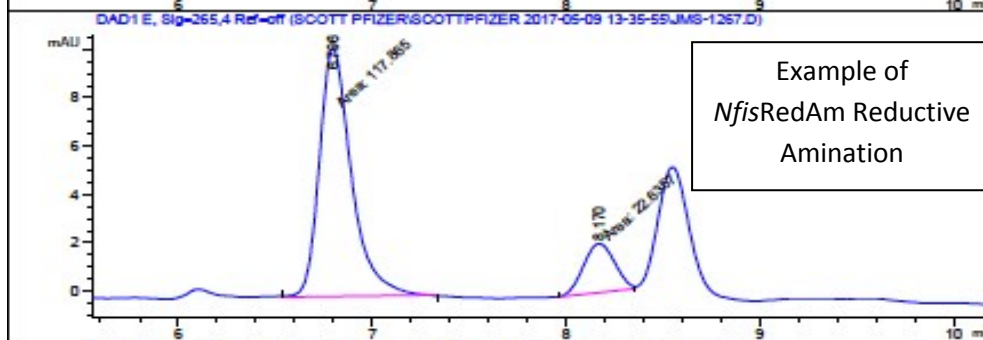




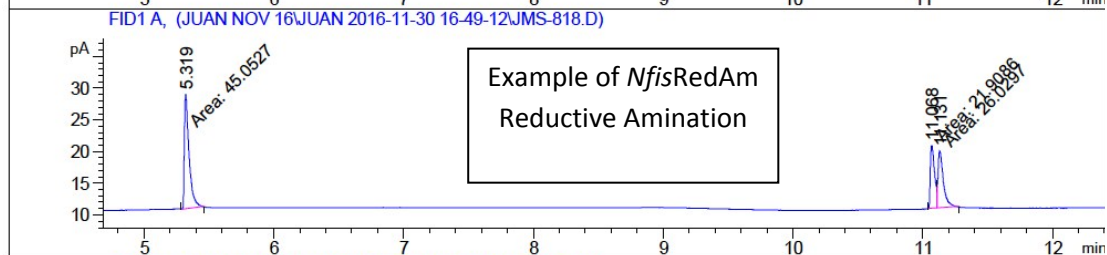
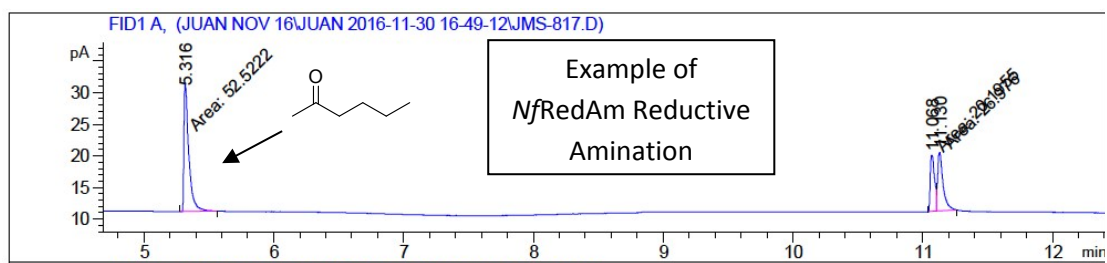
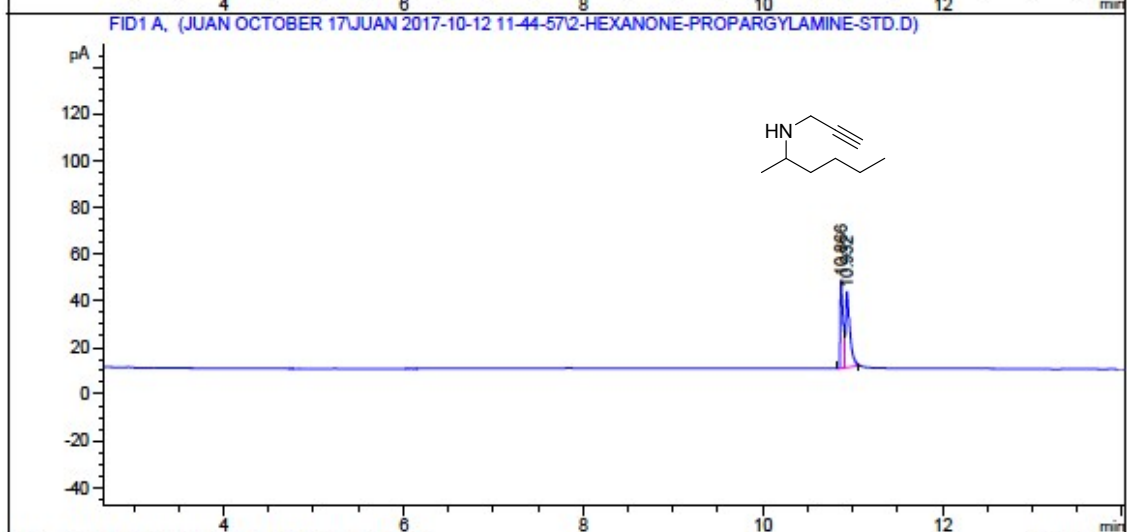
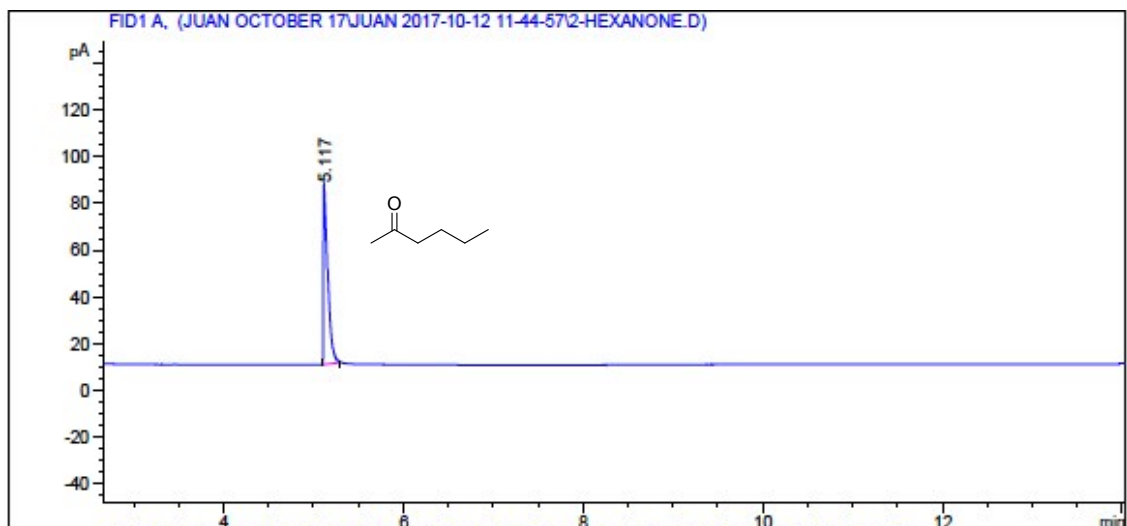


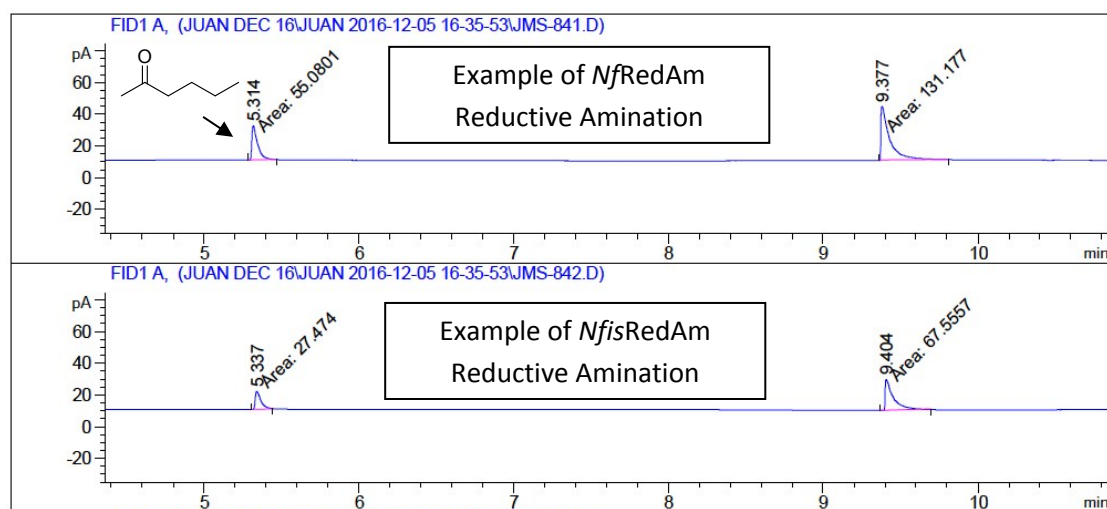
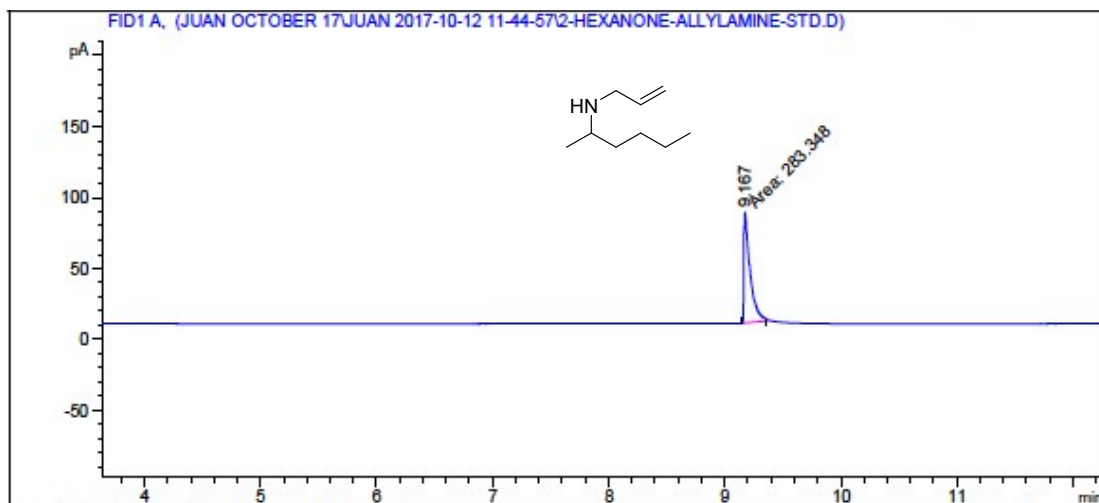


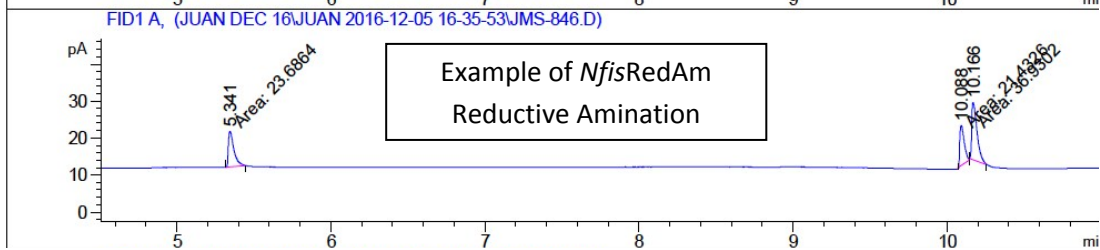
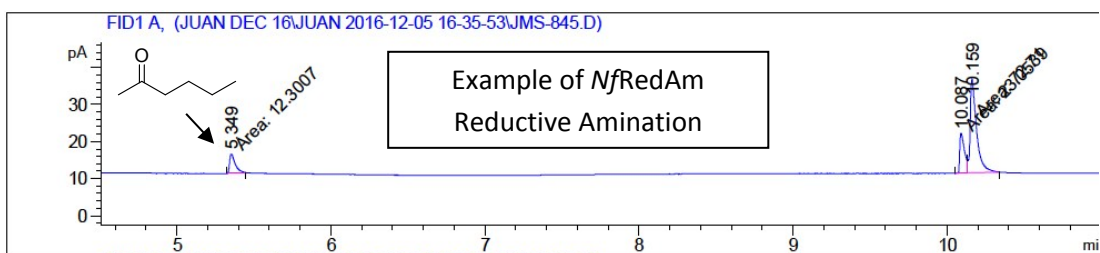
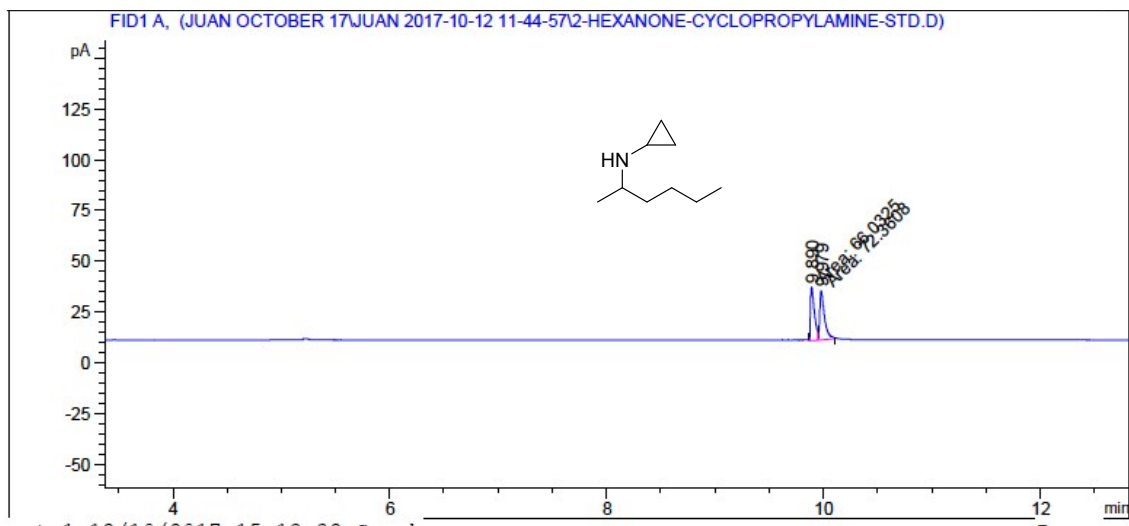
Example of  
*Nf*RedAm Reductive  
Amination

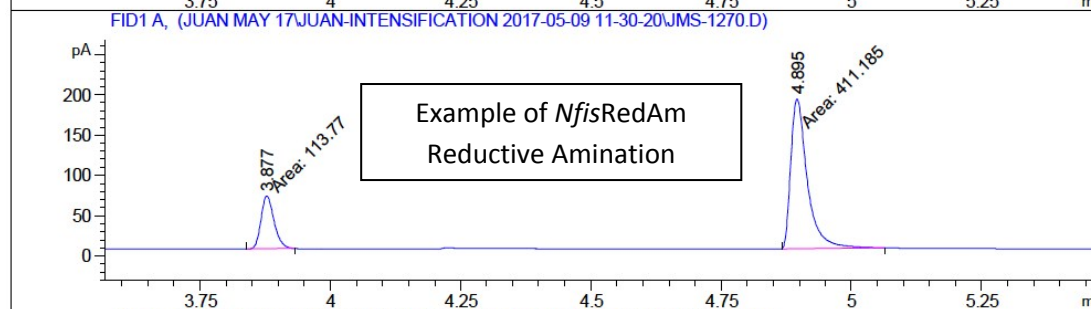
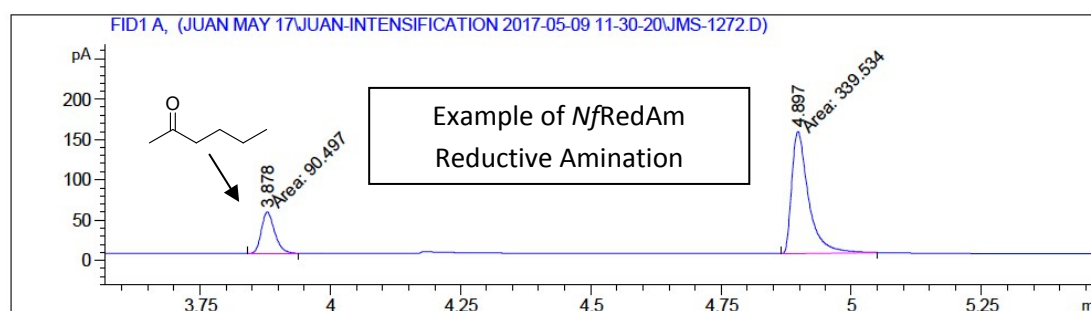
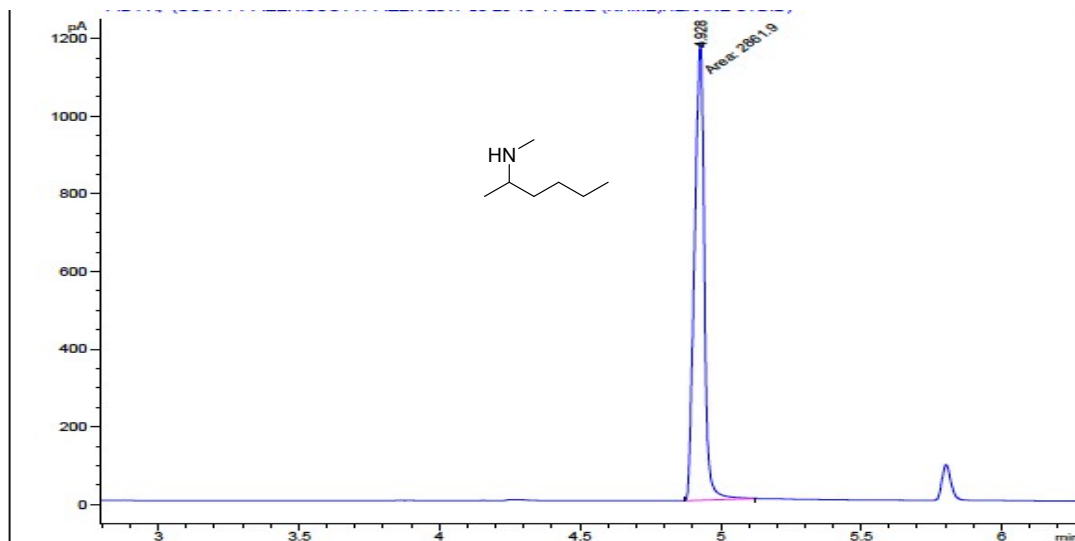


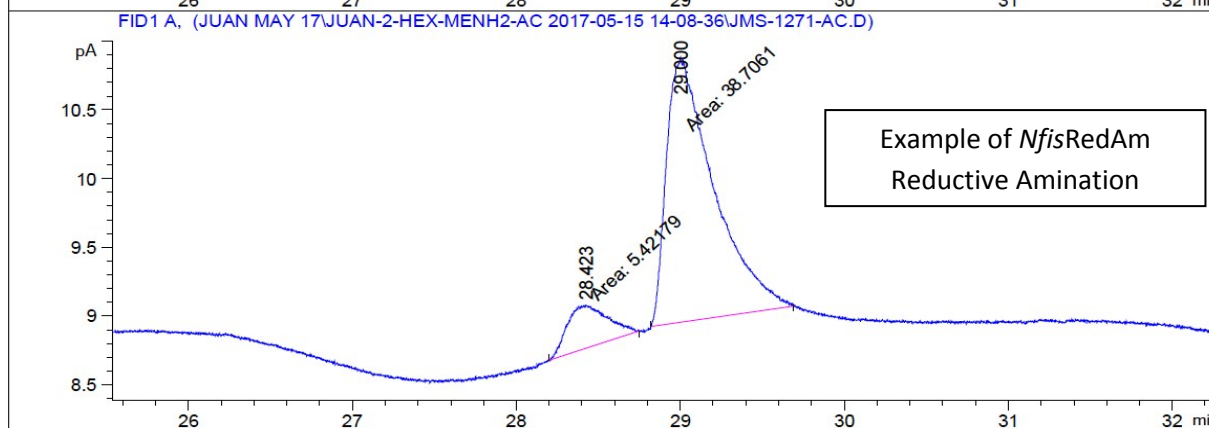
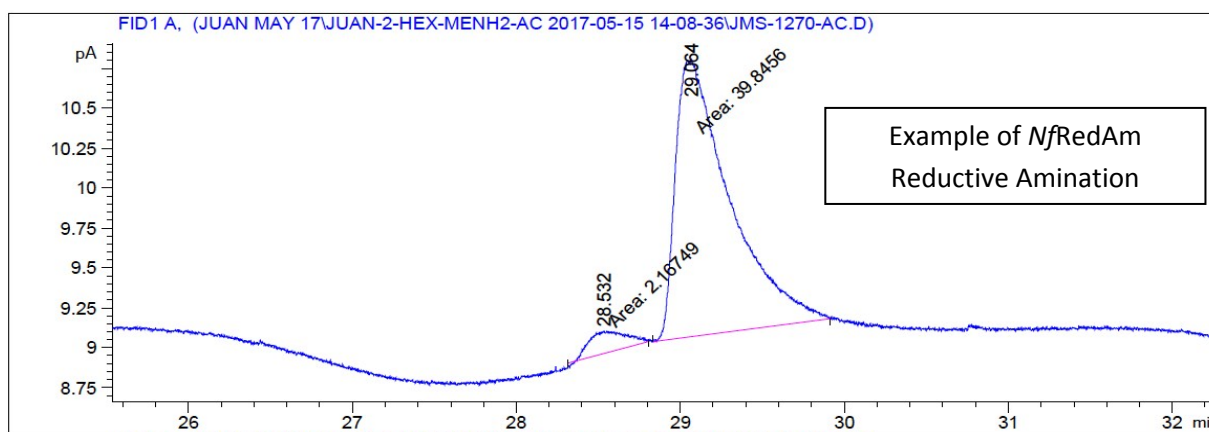
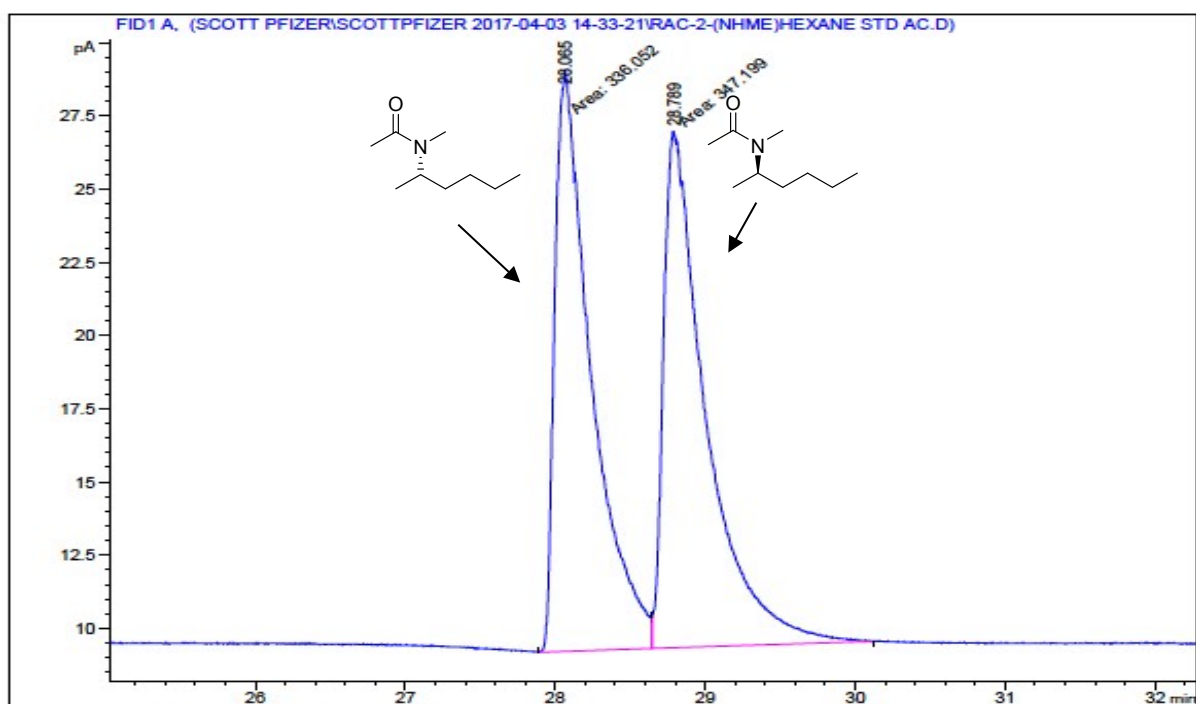
Example of  
*Nfis*RedAm Reductive  
Amination











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