

Supplementary Materials for:
Dihydrooxazine Byproduct of a McMurry-Melton Reaction
En Route to a Synthetic Bacteriochlorin

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(1) X-ray crystal data**Table S1.** Crystallographic data of **5b** and **5a**

Identification code	5a	5b
CCDC number	2176728	2176729
Empirical formula	C ₂₂ H ₂₆ N ₂ O ₄	C ₂₂ H ₂₈ N ₂ O ₆
Formula weight	382.45	416.46
Temperature/K	100.0	100.00
Crystal system	monoclinic	monoclinic
Space group	P2 ₁	P2 ₁ /c
a/Å	6.1873(4)	11.9124(9)
b/Å	26.3380(17)	12.6552(9)
c/Å	12.1924(8)	13.9689(10)
α /°	90	90
β /°	102.960(3)	91.409(3)
γ /°	90	90
Volume/Å ³	1936.3(2)	2105.2(3)
Z	4	4
ρ_{calc} g/cm ³	1.312	1.314
μ /mm ⁻¹	0.091	0.096
F(000)	816.0	888.0
Crystal size/mm ³	0.48 × 0.24 × 0.12	0.22 × 0.16 × 0.12
Radiation	MoK α (λ = 0.71073)	MoK α (λ = 0.71073)
2 θ range for data collection/°	4.618 to 54.204	4.344 to 54.968
Index ranges	-7 ≤ h ≤ 7, -33 ≤ k ≤ 33, -15 ≤ l ≤ 15	-15 ≤ h ≤ 15, -16 ≤ k ≤ 16, -18 ≤ l ≤ 18
Reflections collected	26402	62423
Independent reflections	8506 [R _{int} = 0.0423, R _{sigma} = 0.0483]	4831 [R _{int} = 0.0659, R _{sigma} = 0.0261]
Data/restraints/parameters	8506/1/521	4831/0/313
Goodness-of-fit on F ²	1.009	1.042
Final R indexes [I >= 2 σ (I)]	R ₁ = 0.0396, wR ₂ = 0.0901	R ₁ = 0.0439, wR ₂ = 0.1112
Final R indexes [all data]	R ₁ = 0.0515, wR ₂ = 0.0950	R ₁ = 0.0569, wR ₂ = 0.1188
Largest diff. peak/hole / e Å ⁻³	0.19/-0.26	0.65/-0.33
Flack parameter	0.1(4)	–

(2) pH Simulation

The pH simulations were computed using the following Python script:

```
import math
from scipy.optimize import fsolve
import matplotlib.pyplot as plt

pka = 9.25 # pKa of NH4
pkb = 9.25 # pKb of OAc-
kw = 1e-14 # constant
ka = 10 ** (-1 * pka) # Ka
kb = 10 ** (-1 * pkb) # Kb
equiv = 0.01 # [R-NO2] = 1 equiv = 0.01 M = 10 mM
# Assuming initial [HCl] = a M in [NH4OAc] = s M solution
# [H+] = x, [OH-] = y

def equations(p):
    x, y = p
    return (x*s/(ka + x) + x - y*s/(kb + y) - y - a, kw - x*y)

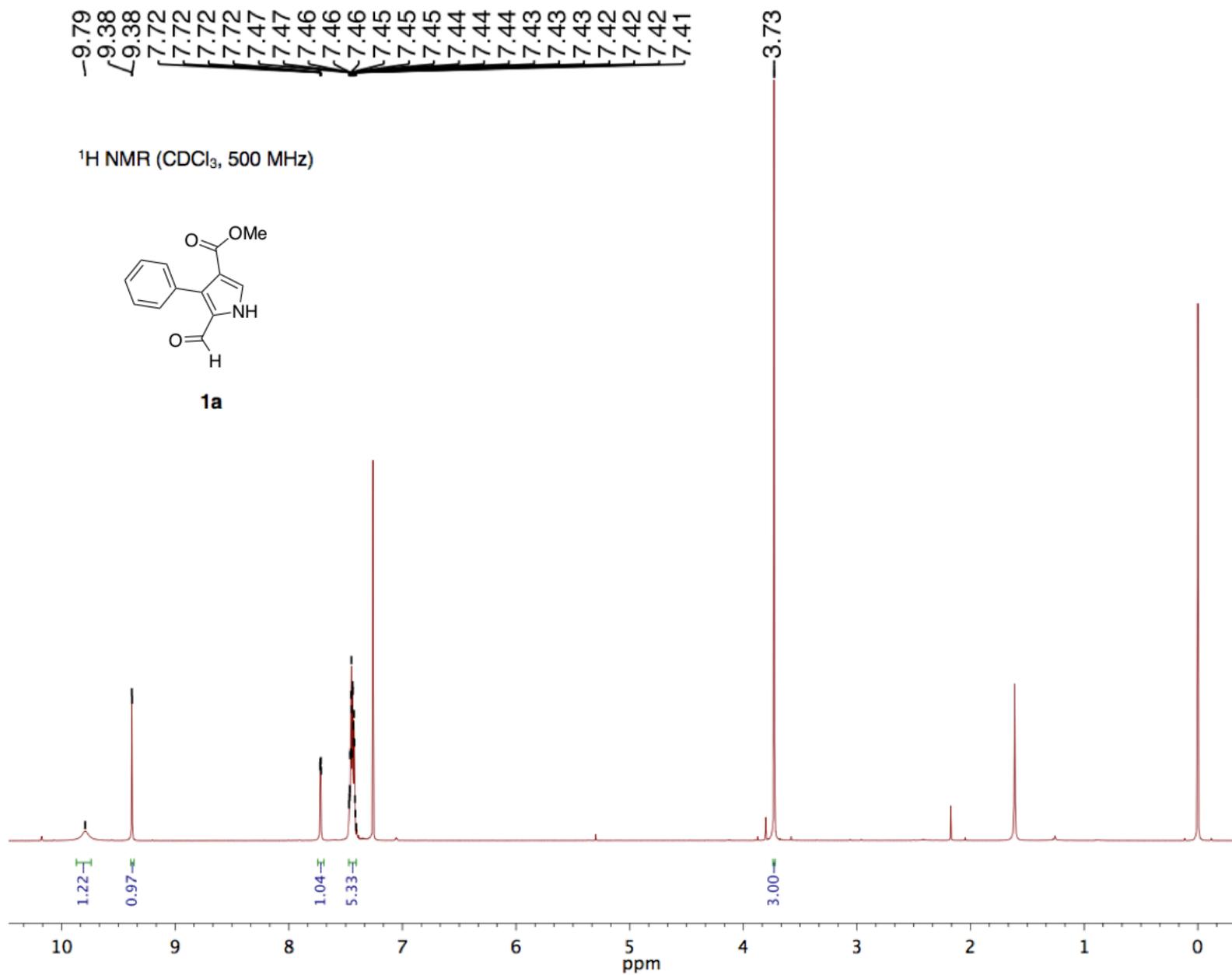
s_set = [1000, 400, 160, 64, 25.6]# [NH4OAc] (equiv)

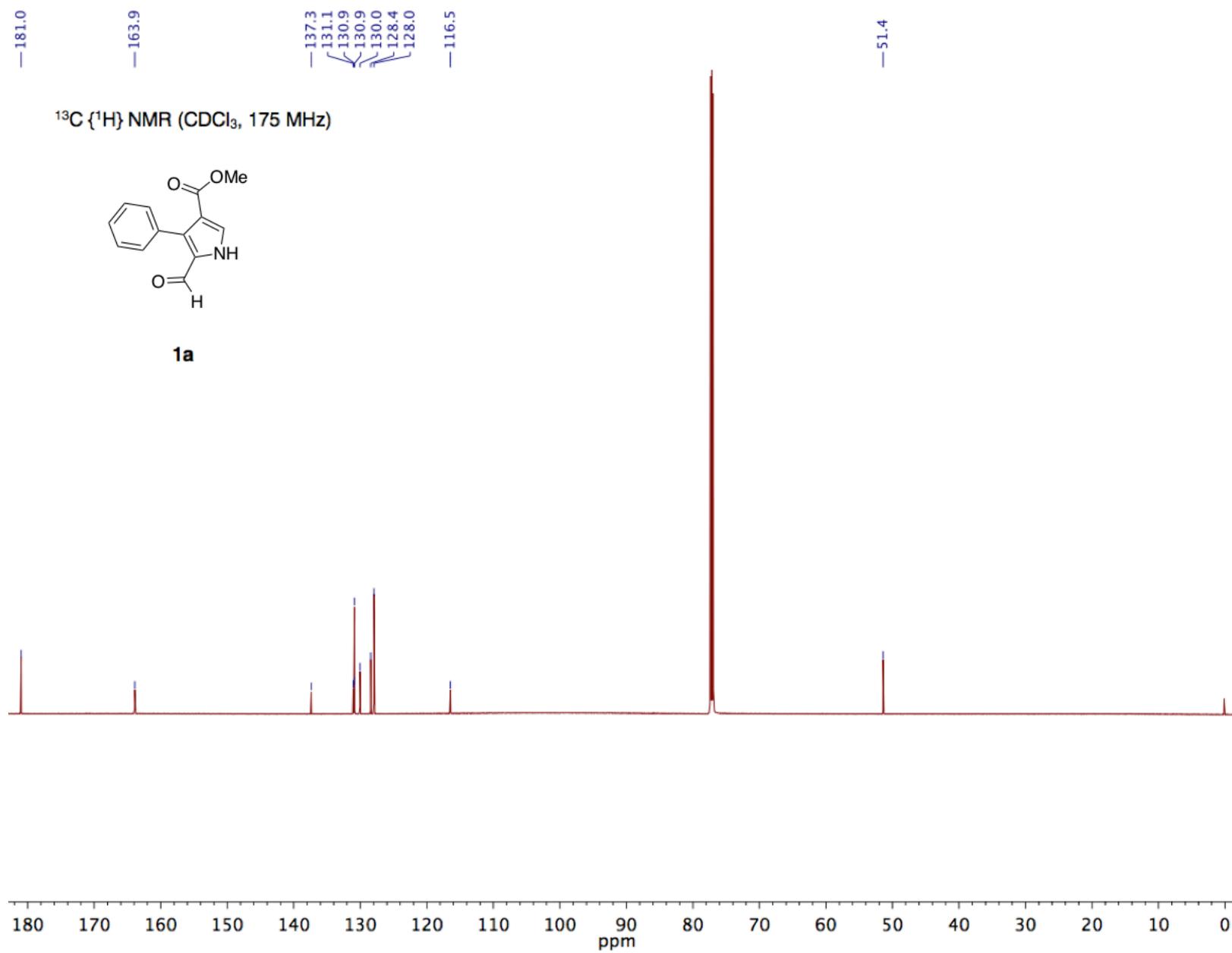
# calculation and plot
fig, ax = plt.subplots(figsize=(6, 4))
for se in s_set:
    s = se * equiv
    pHs = []
    x, y = 1e-7, 1e-7 # initial guessing solutions
    for ae in range(120): # [HCl] (equiv)
        a = ae * equiv
        x, y = fsolve(equations, (x, y), factor=1, xtol=1e-24)
        pH = -1 * math.log10(x)
        pHs.append(pH)
        print(se, ae, pH, x, y, equations((x, y)))
    ax.plot(range(120), pHs, label='{} equiv'.format(se))

ax.set_ylabel('pH')
ax.set_xlabel('[HCl] equiv')
ax.minorticks_on()
ax.grid(True, which='both')
ax.legend()
```

The script provides for successive iteration given an initial estimate to arrive at a calculated value. The features *factor* and *xtol* make the respective initial iteration step and error tolerance small. A root expected here is as small as 10^{-7} (pH = 7). The error was assessed by putting the calculated roots back into the acid-base equation. The maximum error was 1.78×10^{-15} . The resulting pH estimates are in excellent agreement with expected values. For example, with no HCl the calculated pH is 7.0, in agreement with expectation.

(3) NMR data

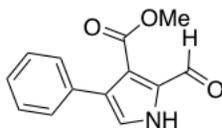




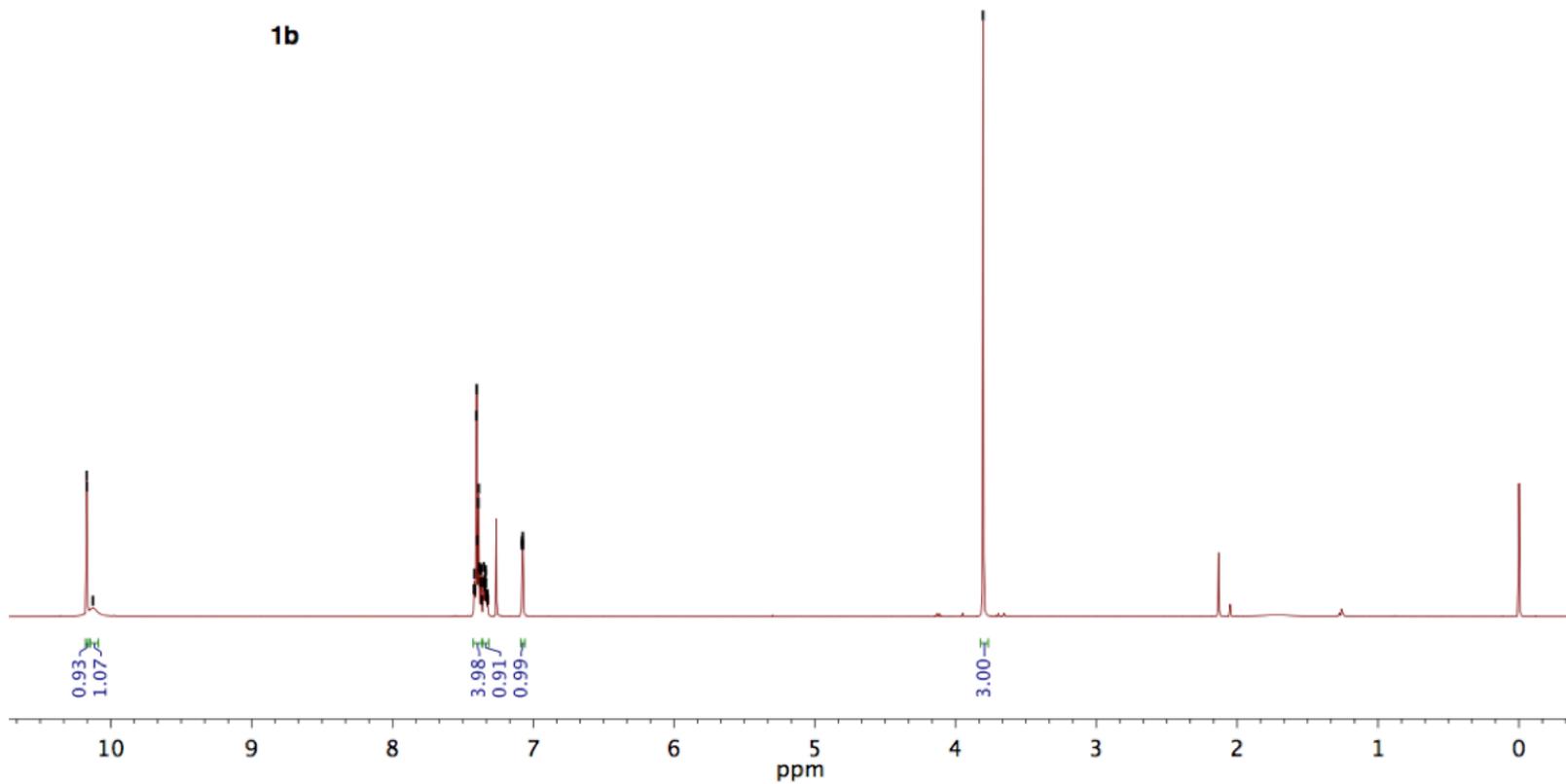
10.17
10.17
10.13

7.42
7.42
7.41
7.40
7.40
7.40
7.39
7.39
7.38
7.38
7.37
7.37
7.37
7.36
7.35
7.35
7.34
7.34
7.34
7.34
7.33
7.33
7.33
7.32
7.08
7.08
7.07
7.07
3.80

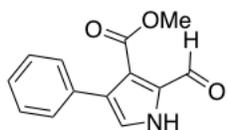
¹H NMR (CDCl₃, 500 MHz)



1b



^{13}C $\{^1\text{H}\}$ NMR (CDCl_3 , 175 MHz)



1b

