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THE EFFECT OF AMINO ACIDS AND MOLAR PEROXIDE RATIO ON THE OXIDATION OF 2,4 DINITROANISOLE IN AN ULTRAVIOLET LIGHT EMITTING DIODE/H2O2 ADVANCED OXIDATION PROCESS

THESIS

Jeffry P. Hart, Major, USMC

AFIT-ENV-MS-21-M-232

DEPARTMENT OF THE AIR FORCE AIR UNIVERSITY

AIR FORCE INSTITUTE OF TECHNOLOGY

Wright-Patterson Air Force Base, Ohio

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THESIS

Presented to the Faculty

Department of Systems Engineering & Management

Graduate School of Engineering and Management

Air Force Institute of Technology

Air University

Air Education and Training Command

In Partial Fulfillment of the Requirements for the

Degree of Master of Science

Jeffry P. Hart, BS

Major, USMC

March 2021

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Abstract

2,4 Dinitroanisole (DNAN) is an organic insensitive munition that is a likely candidate to replace trinitrotoluene (TNT) for a variety of purposes. The manufacturing and use of DNAN poses several environmental hazards that may cause human and environmental health problems. Safe and efficient treatment of wastewater and drinking water is required for water for military and civilian operations. Advanced Oxidation Processes (AOPs) are a promising method that have the potential to reduce a variety of persistent chemicals, however, the performance of these systems may be degraded by cocontaminants in the influent. In this contribution, DNAN, with casamino acids as a cocontaminant, was oxidized with Ultraviolet (UV) Light Emitting Diodes (LEDs) with hydrogen peroxide (H₂O₂) in an AOP in a laboratory.

The UV/H₂O₂ AOP was capable of degrading DNAN with casamino acids present, from a relative concentration (C/C₀) of 1.0 - 0.63 over a molar peroxide ratio (H₂O₂:DNAN) range of 50:1 to 1000:1. An increase in the degradation rate of DNAN was observed with increased concentrations of H₂O₂. The pseudo first order rate constant for DNAN removal was typically greatest at 250:1 and 500:1. The presence of casamino acids had minimal effects on the effectiveness of the AOP, possibly due to light screening.

Potential byproducts were identified using mass spectrometry chromatograms and Nitrobenzene +CN is a potential byproduct of DNAN degradation.



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Acknowledgments

I would like to express my sincere appreciation to my thesis advisor, Dr. Willie Harper Jr., for his guidance and support throughout the course of this thesis effort. I would also like to thank Dr. Daniel Felker and Dr. Adam Burdsall for their guidance and wisdom in navigating the complexities of this work inside the laboratory. Finally, I would like to thank my wife and children for their unwavering support throughout this endeavor.

Jeffry P. Hart



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I. Introduction

1.1 Chapter Overview

This chapter identifies the problem, background, and investigative questions for using an UV LED AOP in a water treatment process. Additionally, it includes a brief discussion of the methodology for the experiments. Finally, this section defines the assumptions and limitations of this study.

1.2 General Issue

The purpose of this thesis is to increase understanding for using UV LEDs in a water treatment system utilizing an AOP. This research attempts to optimize the molar peroxide ratio for the AOP of DNAN with casamino acid as a co-contaminant in an UV LED reactor as well as suggest possible byproduct structures.

Treating water has long been a task the military has undertaken to ensure clean and safe water is available for use (Mitchell & Ensley, 2019). The military needs water treatment capabilities that can operate in austere environments and that are capable of removing traditional pollutants, as well as pollutants found on a battlefield such as munitions constituents and chemical weapon byproducts (Duckworth et al., 2015). The Department of Defense (DoD) has a responsibility to meet National Pollutant Discharge Elimination System (NPDES) permit requirements at its wastewater treatment plants (US EPA, 2010). Wastewater treatment standards may become more stringent over time. As



such, munitions constituents and other chemicals in wastewater may require advanced treatment methods in order to ensure effluents are safe for discharge.

This research used use a UV LED/H₂O₂ based AOP. There are several scholarly works using UV LED AOPs, however, the overall research conducted is still limited and warrants further investigation (Duckworth et al., 2015; Scott et al., 2017; Stubbs, 2017). Additionally, there is little research that targets the effects of co-contaminants, such as casamino acids, in the treatment process. Specifically, research has shown that background chemicals such as nitrates and carbonates may interfere with the destruction of the target contaminant (Stocking, Rodriguez, & Browne, 2000). These background chemicals and other co-contaminants that are not the primary target of AOPs have the potential to create regulated byproducts that may be as toxic or more toxic than those present before treatment started (Munter, 2001; Stocking et al., 2000). Thus, it is important to understand and predict byproducts created by the AOP.

UV/H₂O₂-based AOPs expose H₂O₂ to UV LED light inside a reactor which transforms into hydroxyl radicals that can quickly and non-selectively react with any organic pollutants and their byproducts (Crittenden, Trussell, Hand, Howe, & Tchobanoglous, 2014; Scott et al., 2017). These hydroxyl radicals can attack organic pollutants by: (1) hydrogen abstraction (i.e. removal of a hydrogen atom from a saturated hydrocarbon), (2) hydroxylation (i.e. adding the hydroxyl group to an unsaturated hydrocarbon), or (3) oxidation without transfer of atoms (Buxton, Greenstock, Helman, W, & Ross, 1988; Scott et al., 2017; Stubbs, 2017).



1.3 Problem Statement

The Air Force Institute of Technology (AFIT), in collaboration with the Environmental Protection Agency (EPA), is studying the use of UV LEDs for improving water treatment procedures. UV LED AOPs are relatively new, however, they provide many benefits over traditional mercury lamp-based AOPs and have demonstrated efficient and reliable operation in several experiments (Duckworth et al., 2015; Scott et al., 2017; Stewart, 2016; Stubbs, 2017). While promising, further study and analysis is warranted to fully understand the operational limits and conditions required for properly treating water.

1.4 Research Objectives/Questions

This research has two main questions: 1.) What molar peroxide ratios best effect the degradation of DNAN in a UV LED/H₂O₂ AOP? 2.) What effect do casamino acids have on the degradation of DNAN in a UV LED/H₂O₂ AOP?

- Determine the effect of amino acids and molar peroxide ratios on the oxidation of DNAN in an UV LED/H₂O₂ AOP.
- Propose associated byproducts from oxidation of DNAN in an UV LED/H₂O₂ AOP.

1.5 Investigative Questions

How do molar peroxide ratios affect the reaction? Several studies have shown there is a relationship between molar stoichiometry and associated degradation of contaminants (Scott et al., 2017; Stewart, Miller, Kempisty, Stubbs, & Harper, 2018; Stubbs, 2017; Su et al., 2019). Literature suggests increasing H₂O₂ may improve



degradation rates, however, too much H_2O_2 can reduce degradation rates because it will act as a scavenger for OH· (Su et al., 2019; Yang et al., 2018). Additionally, the hypothesis for this research question is that molar peroxide ratio has a has a significant effect on the degradation of DNAN.

How does the presence of casamino acids effect the degradation of DNAN? Previous research by Hoigne (1998) demonstrated that nearly all dissolved organic compounds in water create a detrimental effect on the degradation of target compounds by removing •OH. Thus, it is prudent to suggest that casamino acids will impact the degradation process. The hypothesis for this research question is that casamino acids have a detrimental effect on the degradation of DNAN in an UV LED/H₂O₂ AOP.

1.6 Methodology

To answer the investigative questions, a series of AOP experiments were conducted at AFIT. The AOP experiment consisted of five different molar ratios of DNAN and H₂O₂ while the duty cycle (DC) remained constant at 100% and powered by 12.50v and 0.10 amperes. Casamino acid was added as a co-contaminant to determine what effect, if any, it had on DNAN removal. For each experiment, a solution of DNAN casamino acid, and H₂O₂ flowed from the source flask, through biocompatible tubing, through a reactor where it was exposed to UV LEDs, and then flowed out of the reactor where samples were collected. Effluent that was not collected for sampling flowed into a waste beaker for disposal.

Reactor effluent samples were collected, filtered, well mixed, and processed in a High-Performance Liquid Chromatography (HPLC) to produce chromatograms.



Chromatograms were used to analyze the effect of H₂O₂:DNAN molar peroxide ratios on DNAN degradation. Mass spectrophotometry (MS) was also conducted and used for proposing potential effluent byproduct structures.

Two control experiments were conducted for this research. The first control was conducted without H_2O_2 , which prevented a complete AOP from occurring and resulted in negligible DNAN degradation. A second control was conducted, also without H_2O_2 but with casamino acids well mixed into the solution to determine if the casamino acids and DNAN interact.

Results were statistically analyzed with Anaconda ® and JMP ® software to conduct a one-way Analysis of Variance (ANOVA) and *t*-Test. MathWorks ® MATLAB 2020 software was used for curve fitting of the data.

1.7 Assumptions/Limitations

The limitations of this research are:

1. The dual LED method and low flow rates used in this experiment is not likely to be replicated on a full-sized water treatment system due to scaling issues. While appropriate at the experimental level, methods will likely need to be up-scaled and modified in order to replicate effects on a high-volume system.

2. Casamino acid levels in the laboratory setting are assumed to remain consistent because it was well mixed in the solution beaker. If future water treatment system tests are to occur at a larger scale it is important to understand the effects and likely concentrations of co-contaminants and understand that they may change throughout the treatment process, potentially altering degradation efficiency.



II. Literature Review

2.1 Chapter Overview

This chapter reviews relevant literature and its application to the AOP process. Specifically, the literature is used to analyze operating parameters in a UV LED H_2O_2 AOP. Relevant areas of research include UV light, AOPs, and previous work with DNAN and co-contaminants.

2.2 Background

The DoD has a non-negotiable requirement for access to clean and safe water for all its operations (Mitchell & Ensley, 2019). The DoD is responsible for the manufacturing and use of insensitive munitions which have the potential to cause contamination to wastewater and drinking water systems. As such, the DoD and civilian systems must be prepared to protect against and treat a variety of contaminants that may enter wastewater and drinking water systems.

2.3 Advanced Oxidation Processes

AOPs were first proposed in the 1980s and use strong hydroxyl (OH·) or sulfate radicals (SO₄· $^-$) as major oxidizers to treat wastewater (Deng & Zhao, 2015). AOPs form strong oxidants and these react with organic contaminants in water (Stocking et al., 2000). These methods were further used to treat several types of wastewaters because the strong oxidants were capable of removing recalcitrant organic pollutants as well as certain inorganic pollutants, or to increase the biodegradability of wastewater as a pretreatment prior to being subject to a follow-on biological treatment (Deng & Zhao, 2015). AOPs are not commonly employed for inactivation of pathogens because the



radical half-life is too short and the detention times are prohibitive (Deng & Zhao, 2015). OH· is non-selective and will rapidly react with numerous species at rate constants of $10^8 - 10^{10}$ M⁻¹ s⁻¹ (Deng & Zhao, 2015). Since the OH· has such a short lifetime, they are produced *in situ* through different methods, including irradiation with an UV light (Deng & Zhao, 2015; Huang, Dong, & Tang, 1993).

Scott et al. (2017) researched the effect of UV LEDs and H₂O₂ in an AOP to degrade Brilliant Blue dye and tartrazine. Their research demonstrated the potential of using UV LED AOP treatment methods for contaminated water and identified several factors that may influence their performance, including mixing, DC, and operating time (Scott et al., 2017). Their research highlights the need for further understanding AOPs because they are effective at destroying toxic pollutants in water. Specifically, their study chose UV light for the AOP process in place of the larger mercury-based fluorescent lamps. While mercury-based fluorescent lamps were the leading source of UV light for water treatment, they are large, fragile, and potentially hazardous due to high voltage and mercury contained in the system (Scott et al., 2017). UV LEDs offer many benefits over conventional mercury lamps because of their small size, durability, and lack of hazardous materials (Scott et al., 2017). Scott et al. (2017) notes, however, that UV LEDs have yet to prove themselves as a full replacement for conventional mercury lamps and require further testing and evaluation. Additionally, Scott et al. (2017) also researched the effect of DC, which periodically pulsed the UV LED, in order to determine optimum conditions for reducing brilliant blue dye and tartrazine. A flow through reactor with 250 nm LEDs was utilized, with a peak output at 247 nm because peroxide absorbs light energy well within this range (Beers & Sizer, 1951; Scott et al., 2017). DCs of 5, 10, 20, 30 and 100%



were used and those with higher DCs, particularly those at 100%, yielded higher reduction of brilliant blue, whereas lower DCs, removed only very small amounts of the brilliant blue (Scott et al., 2017). Tartrazine removal was conducted using similar DCs of 5, 10, 20, 30, 50, 70, and 100%. Conversely, tartrazine was only reduced by 17% at 100% DC for over 300 minutes, 13% at 70% DC, and continually decreased with lower DC (Scott et al., 2017). Tartrazine and brilliant blue experiments were conducted in duplicate, and showed that brilliant blue is more receptive to UV AOP than tartrazine (Scott et al., 2017).

During this study the data points for degradation of tartrazine and brilliant blue oscillated above and below the R² value best fit lines (Scott et al., 2017). These oscillations can be attributed to non-ideal mixing conditions, multiple flow paths within a reactor, as well as variations in the radiation intensity (Scott et al., 2017; Wols, Hofman, Uijttewaal, Rietveld, & van Dijk, 2010). If the continuously stirred tank reactor (CSTR) conditions are not ideal, each particle may receive greatly different UV doses, and lead to instability in the effluent concentration (Scott et al., 2017). Tartrazine experiments were repeated while mechanically stirring the UV LED reactor which showed an 8% improvement in TAR removal at 300 minutes and 100% DC. The methods researched by Scott et al. (2017) are of importance to future AOP processes, particularly the effect of DC and mixing within the reactor.

Scott et al. (2017) also observed the effect of staining and found it had a minimal impact because tartrazine and brilliant blue are anionic dyes and were not expected to adsorb to the negatively charged quartz LED lenses. These results differed from Duckworth et al. (2015), who used methylene blue in their study and observed LED



power degradation due to staining (Scott et al., 2017). Interestingly, Scott et al. (2017) observed steadily declining normalized apparent first-order rate constants and attributed this behavior to heat buildup in the LEDs which led to their degradation. This can be attributed to both the heat during the "on" condition as well as cycling the LED on and off (Scott et al., 2017). DC was positively correlated with first-order rate constants for tartrazine and brilliant blue, but was negatively correlated with the normalized first-order rate constants k_s /DC which demonstrates pollutant removal was more efficient at lower DCs (Scott et al., 2017). Scott et al. (2017) demonstrated the potential to treat contaminated water with UV LEDs and highlight the need for more research of mixing DC, operating time, as well as understanding the impacts of staining and chemical structure of contaminants on the AOP.

Duckworth et al. (2015) used an UV LED H₂O₂ AOP to degrade methylene blue. Radical production is hypothesized to be proportional to optical power of the LEDs, regardless of pulse rate (Duckworth et al., 2015). McDonald et al. (2000), however, offer that optical power may not be proportional to the inactivation of organisms in the presence of an oxidizing agent. In the experiment conducted by Duckworth et al. (2015), they investigated the rate of radical production from hydrogen peroxide, as indicated by the degradation of methylene blue, as a function of DC with pulsed UV LEDs. The UV LED AOP used a flow through electro-polished 316 L stainless steel reactor with 240 nm LEDs was used in which 5 mM hydrogen peroxide and 0.01 mM methylene blue were exposed to UV light, permitting the creation of hydroxyl radicals to destroy target contaminants (Duckworth et al., 2015). Experiments were conducted using various DCs and their results showed first-order degradation kinetics for methylene blue at all DCs



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(Duckworth et al., 2015). Interestingly, the adjusted first-order degradation rate constant for methylene blue was significantly higher for the 5 and 10% DCs (Duckworth et al., 2015). Duckworth et al. (2015) state this increased degradation could be because the short UV pulses more effectively produce hydroxyl radicals, however, they could also be caused by peroxide limitations or scavenging of hydroxyl radicals by MB byproducts. Hydroxyl radical production may also not be accurately measured if the hydroxyl radicals are scavenged by the methylene blue byproducts (Duckworth et al., 2015). Additionally, LED surfaces were fouled during the experiment by methylene blue adsorption which complicated the data analysis process (Duckworth et al., 2015). The adsorption of chemicals onto LED surfaces must be dealt with in large scale applications, as it creates the likelihood of decreased degradation that may require additional chemicals or increased exposure time within a reactor, both of which will cause delays and may increase costs associated with water treatment.

Stewart et al. (2018) researched the effects of UV LEDs in a H₂O₂ AOP reactor to reduce tartrazine under different pH and DC conditions. The objective of their work was to determine what effect pH and DC had on the oxidation of tartrazine in a UV/H₂O₂-based AOP. Alternative water treatment methods such as AOPs have the potential to remove harmful contaminants from water because AOPs use radicals to rapidly and non-selectively oxidize several electron-rich organic pollutants (Crittenden et al., 2014; Scott et al., 2017). Stewart et al. (2018) also used pulsing UV LEDs to extend the life of the UV LED, and found that DC was positively correlated with oxidation efficiency and pH was negatively correlated with oxidation efficiency and was typically greatest at pH 6.



Stewart et al. (2018) expanded upon previous research of Scott (2017), and sought to identify byproducts associated with UV LED AOPs. After processed through the AOP, byproducts in the effluent were analyzed using High Performance Liquid Chromatography Mass Spectrometry (HPLC-MS) (Stewart et al., 2018). Additionally, first order rate constants were determined from the non-steady state solution for the effluent tartrazine concentration (Stewart et al., 2018). Each experiment was conducted with approximately 25 mM H_2O_2 and .05 mM tartrazine processed in a stainless steel cylindrical reactor with seven 245 nm LEDs in the end plate of the reactor (Stewart et al., 2018). The UV LED DC was controlled via computer at rates of 5, 10, 20, 30, 50, 70, and 100% (Stewart et al., 2018). The LEDs made physical contact with the solution in the reactor and the tartrazine and H_2O_2 solution was pumped through the reactor at approximately 0.7 mL per minute (Stewart et al., 2018). Improving on the method of Scott et al. (2017), Stewart (2018) mechanically mixed the solution within the reactor with a magnetic stir bar. For pH 6 and 7, tartrazine degradation increased as DC increased from 0 to 100% (Stewart et al., 2018). There was a notable exception at pH 7, where the 50% DC narrowly exceeded the degradation of the 70% DC (Stewart et al., 2018). Lower levels of tartrazine degradation occurred for pH of 8 and 9, and both exhibited their highest relative degradation levels at the 50% DC instead of the 100% DC (Stewart et al., 2018). Interestingly, while increasing pH negatively impacted tartrazine oxidation, the computational data showed that tartrazine reactivity did not increase with pH (Stewart et al., 2018). This may be attributed to hydroxyl radicals being scavenged by bicarbonate ions (Buxton et al., 1988; Stewart et al., 2018).



Additionally, Stewart et al. (2018) found that while the relative contribution of DC to tartrazine degradation was 57%, and pH was 19%, the interaction of DC and pH resulted in a 24% contribution to degradation. Stewart et al. (2018) found that it was difficult to degrade tartrazine in a UV/H₂O₂ AOP, and assert this is due to the strong absorbance of tartrazine in the UV spectrum, resulting in nondestructive radiative transfer and fluorescence which reduces the available UV energy for cleaving the O-O bond and produce hydroxyl radicals. Four byproduct structures were proposed, including two that demonstrate tartrazine rings were cleaved (Stewart et al., 2018). Stewart et al. (2018) suggested future studies use stronger LEDs and focus on improving reactor mechanics including materials (stainless steel vs. Teflon), UV arrangement, and hydraulic residence time distribution.

Tran et al. (2014) used pulsed LEDs in the UV range to inactivate *Bacillus globigii*. This was done using pulsed UV LEDs instead of continuous UV LEDs to reduce the power consumption and increase LED bulb operational life (Tran et al., 2014). LED bulbs are more capable of conducting pulsed operations because they don't require a warm-up time which allows them to be rapidly turned on and off (Tran et al., 2014). While the research conducted was not specific to AOPs, its findings are applicable to future work with AOPs. Specifically, it was found that kinetic profiles for continuous UV LEDs reached 6-log inactivation than pulsed UV LED, however the pulsed required less fluence (Tran et al., 2014). Additionally, pulsed UV LED inactivation rate constants were higher than continuous UV LEDs, indicating that the high energy bursts associated with pulsing UV LEDs were more effective at causing cellular damage (Tran et al., 2014). LED bulb life is increased by pulsing in part because bulbs do not reach critical



temperature thresholds (Lenk & Lenk, 2017; Tran et al., 2014). The disinfection apparatus was mounted atop a shaker table with a n orbital motion of 115-120 rpm (Tran et al., 2014). It is worth considering the results of using a shaker table compared to a CSTR, and how each may be scaled up to meet future water treatment systems. Specifically, Tran et al. (2014) noticed tailing in *Bacillus globigii* spore disinfection over time and partially attributed this to crevices in the test apparatus. This observation should directly translate to UV H₂O₂ AOPs as it also requires influent to be exposed to UV LED and any crevices may cause improper mixing and exposure to UV LEDs. By running UV LEDs in a pulsing configuration, there is potential to increase operational life of the bulbs, thus reducing maintenance or increasing replacement intervals in future water treatment systems.

Stubbs (2017) conducted a study to "evaluate the effect of reaction stoichiometry, molecular structure, and optical output power on the UV LED/H₂O₂ process". His work used a bench-scale UV LED H₂O₂ AOP to degrade 6 dye and 5 achromatic organic compounds (Stubbs, 2017). His research found a linear relationship between input drive current, optical output power, and the apparent first order degradation rate constant (Stubbs, 2017). Additionally, the drive current and degradation exhibited a linear relationship (Stubbs, 2017). He found that the ideal ratio for moles peroxide to moles of a test compound were at or near 500:1 for the majority of the dyes (Stubbs, 2017). Interestingly, erythrosine B exhibited the best results in the 2500:1-3000:1 range and this is most likely attributed to its relatively high molar absorptivity ratio (Stubbs, 2017).

Additionally, Stubbs (2017) highlights further benefits of using UV LEDs in an AOP as compared to traditional mercury lamps. Specifically, while UV LEDs may have



output power in the milliwatt (mW) range, they can be arranged more effectively and be adjusted to output specific wavelengths, whereas the large and more powerful mercury lamps can reach significantly higher outputs in the kilowatt (kW) range (Stubbs, 2017). Furthermore, UV LEDs may have other benefits beyond more flexible arrangements, they offer selective output wavelengths, while low pressure lamps are limited to a single 254 nm wavelength and medium pressure lamps emit between 200 and 320 nm (Stubbs, 2017). The comparison of mercury lamps to LED is important as the reactor must provide adequate exposure to UV light to cleave the O-O bond in the H_2O_2 molecule (Stubbs, 2017). Because the UV LEDs produce significantly less optical output power than their mercury-based equivalent, design of a UV LED AOP reactor needs careful consideration in order to reach the desired energy per unit time of the UV LEDs as well as the solution's residence time in the reactor. Proper mixing and UV fluence are also critical to the effectiveness of hydroxyl radicals as oxidants (Stubbs, 2017; US EPA, 1999). His work also emphasizes the importance of selecting the correct starting molar ratios of H_2O_2 to dyes, as too low a level of H_2O_2 may limit the generation of hydroxyl radicals, whereas too much H_2O_2 appears to scavenge hydroxyl radicals (Muruganandham & Swaminathan, 2004; Oancea & Meltzer, 2014; Sharma, 2015; Stubbs, 2017). Stubbs' (2017) work is applicable to future research as well as water treatment systems. Specifically, his study of the effect of different dyes and achromatic compounds and their degradation in a UV LED AOP emphasize the importance of design and the ability of a large-scale UV LED AOP to reduce a variety of chemicals in a water treatment train.

UV AOPs can leave a variety of byproducts compounds in the effluent after treatment (Stewart et al., 2018). Chang and Young (2000) studied Methyl *tert*-butyl ether



(MTBE) degradation kinetics in UV/H₂O₂ AOP with H₂O₂:MTBE molar ratios of 15:1, 7:1, and 4:1. Over 99.9% of MTBE was removed after 75 minutes at each peroxide (Chang & Young, 2000). Of interest, the AOP process resulted in a *tert*-butyl formate (TBF) byproduct (Chang & Young, 2000). After 1-hour of treatment, there was 35 times as much TBF as the remaining MTBE (Chang & Young, 2000). Chang and Young (2000) suggest that other byproducts, such as formaldehyde or acetone, were likely formed, however they may have gone undetected because they were not purgeable or they were too small or volatile to appear in the analytical results. The resulting byproducts reported by Stewart (2016), Stubbs (2017), and Chang and Young (2000) are important to future water treatment processes, as some byproducts have the potential to be damaging to human health and may require further treatment prior to being safe to enter wastewater effluent.

Terracciano et al. (2018) used a UV/H2O2 AOP to treat water contaminated with the insensitive munition 3-nitro-1,2,4-trizole-5-one (NTO). The reactor was able to successfully remove NTO, sourced either from actual chemical plants or created synthetically, from the water (pH= 3.0 ± 0.1) when using a hydrogen peroxide concentration of at least 1500 mg L⁻¹ (Terracciano et al., 2018). The organic carbon in the NTO ring was completely converted to inorganic carbon (CO₂) and produced nitrate and ammonium ions as the primary byproducts (Terracciano et al., 2018).

Furthermore, implementing AOPs can be a difficult process, as their mechanisms are not as well understood when compared to air stripping and sorption because of the complex physical and chemical reactions that are occurring in oxidation processes (Stocking et al., 2000). Additionally, because their effectiveness is mainly determined by



the quality of the contaminated water, they may not be practical or affordable in many cases (Stocking et al., 2000). Because oxidation processes react non-selectively and are prone to interference, they may result in increased costs due to extra chemicals or power required to properly degrade target contaminants. Background chemicals that are not the primary target of AOPs can result in other regulated by-products that essentially cause water to become worse off than when treatment started (Stocking et al., 2000). Other background chemicals such as nitrates and carbonates may interfere with the destruction of the target contaminant (Stocking et al., 2000). Thus, it is important for future research and water treatment applications to ensure that not only is the AOP process understood for the target pollutant, but to know how a variety of other co-contaminants and background chemicals will impact the process.

2.4 2,4-dinitroanisole

Nitroaromatic compounds are associated with industrial chemical processes, including explosives production (Li, Shea, & Comfort, 1998). Production of TNT and dinitrotoluene (DNT) may produce over 30 nitroaromatic compounds (Levsen, Preiss, & Berger-Preiss, 1995; Li et al., 1998). Li et al. (1998) found that more than 95% of TNT in aqueous extracts of contaminated soil was mineralized when exposed to UV/Fenton oxidation. Furthermore, Li et al. (1998) highlight that AOPs using highly reactive intermediates, such as hydroxyl radicals, have shown promising results for remediating wastewater contaminated with aromatic compounds (Ho, 1986; Li, Comfort, & Shea, 1997). Because TNT and DNAN are both nitroaromatic compounds and share similar



chemical structures, AOPs with hydroxyl radicals are a promising source for their chemical remediation in wastewater

DNAN is a potential replacement for TNT. DNAN is less sensitive to inadvertent detonation than TNT, has an increased detonation temperature, yet still provides similar desirable properties to TNT which makes for an easier manufacturing process (Hawari et al., 2015; Platten III, 2011). While DNAN has been manufactured since at least the 1950s, it has not been widely produced (Platten III, 2011). The U.S. Army is currently evaluating the use of DNAN, and if accepted as an alternative to TNT, its manufacturing rate will likely increase dramatically and may end up in waste streams at the Load, Assemble, and Pack (LAP) plants (Platten III, 2011). Additionally, if DNAN replaces TNT, it will likely be used worldwide for training and combat purposes. TNT detonation often leaves chemical residue around the blast site which has the potential to leach into the ground and water. Without proper treatment, DNAN has the potential to pass through water treatment trains intact. DNAN, given similar properties to TNT, may have similar negative effects on the environment. Studies have indicated that DNAN has deleterious effects on organisms such as bacteria, algae, earthworms, and plants (Dodard et al., 2013; Yang et al., 2018). DNAN's known toxic effects, future mass production, and its potential for introduction into associated waste streams and training environments create a need for an increased understanding of the environmental fate and transport as well as potential remediation techniques.



2.4.1 Advanced Oxidation of 2,4-dinitroanisole

Environmental transformation of DNAN can occur naturally by photolysis, although these processes generally exhibit slow rates of degradation of DNAN (Yang et al., 2018). These degradation rates, while slow, have the potential to be combined with advanced processes to further reduce DNAN. Because DNAN slowly transforms, and has a high potential to end up in waste streams at LAP plants, degradation methods using an AOP have a strong potential to appreciably reduce DNAN in wastewater.

Noss and Chyrek (1984) studied the effects of UV radiation and H_2O_2 on TNT and a variety of other chemicals commonly found in manufacturing plants. Their study found that pH had a minimal effect on the degradation of chemicals (Noss & Chyrek, 1984). It was noted that UV alone, at 253.7 nm, effectively degraded all compounds, including TNT, RDX, and HMX, when they were treated together (Noss & Chyrek, 1984). Interestingly, among all the munitions tested in the presence of UV radiation alone, only TNT persisted when treated individually (Noss & Chyrek, 1984). This is important, as understanding waste plant effluent composition may impact treatment plans. When TNT absorbs UV light, it inhibits the radical production necessary for its degradation (Noss & Chyrek, 1984). Noss and Chyrek (1984) found ideal concentrations of H_2O_2 to be less than 0.1% when combined with UV radiation which produced firstorder reaction rate constants of 0.038 - k_{min}^{-1} with 0.01% H_2O_2 .

Yang et al. (2018) investigated the degradation of DNAN in water by UV-based AOPs, including UV/H_2O_2 and UV/persulfate (UV/PS). The UV/H_2O_2 reactor used low pressure mercury lamps which predominantly emitted light at 254 nm (Yang et al., 2018). Both methods were able to degrade DNAN, however, UV/PS appeared to be a more



efficient process than UV/H_2O_2 , particularly when high levels of peroxide were applied (Yang et al., 2018). Additionally, Yang et al. (2018) tested pH levels of 3.03, 7.10, and 10.08 found that it had a negligible impact on DNAN degradation. The data from the UV/H_2O_2 AOP process demonstrated an increase in DNAN degradation when H_2O_2 concentration was elevated from 2 to 5 mM but exhibited a detrimental effect at high levels (e.g. 10mM) (Yang et al., 2018). This is likely attributed to the scavenging effect of H_2O_2 and self-recombination of HO (Yang et al., 2018). The rate constants for the UV/H_2O_2 were not available at the time of publishing this report. The UV/PS was also capable of degrading DNAN, but the process did not inhibit DNAN degradation with increased levels of PS (Yang et al., 2018). Specifically, the UV/PS reactor achieved pseudo-first-order rate constants of 0.0014 to 0.0189 min⁻¹, with 10 mM yielding the best performance (Yang et al., 2018). Yang (2018) attributes this to the lower rate of selfrecombination of SO_4^{2-} % and how it reacts with PS. This suggests that UV/PS may be a more efficient system for DNAN degradation when compared to UV/H_2O_2 (Yang et al., 2018). Photolysis of the naturally occurring photoinducer NO_3^- can also create reactive species, including HO, nitrogen dioxide radical (NO2), and peroxynitrite anion (ONOO–), that may react with DNAN and mitigate the photoinducing effects of NO3– and effectively degrade DNAN (Yang et al., 2018).

Su et al. (2019) conducted photocatalyzed H2O2 oxidation experiments to study the effect of initial pH and H2O2 dosage on the kinetics of DNAN decomposition. The results show that DNAN degradation followed zero-order kinetics in a 250 ppm DNAN solution with UV light and 1500-4500 ppm H2O2 and a pH between 4-7 (Su et al., 2019). When H2O2 was increased to 750ppm, DNAN degradation increased to pseudo-first



order kinetics, indicating DNAN is easily reduced by UV/H2O2 treatment (Su et al., 2019). Su et al (2019) concluded that 1500 ppm H2O2 and an initial pH of 7 were optimal conditions for treating 250 ppm of a DNAN solution and resulted in DNAN reduction from 250 to 1 ppm in 3 hours. Total organic carbon (TOC) and total carbon (TC) concentrations were reduced slowly, indicating the formation of other organic compounds during the treatment process (Su et al., 2019). These intermediates were oxidized to CO₂, and they found that most of the DNAN could be oxidized to CO₂ and nitrate (Su et al., 2019). While Su et al. (2019) found that the H₂O₂ AOP was a good candidate for DNAN reduction, there is research to be done, specifically on how well this system maintains efficiency over time as well as how it reacts in the presence of co-contaminants, specifically, naturally occurring photoinducers as they have the potential to inhibit system efficiency and degradation of target organisms. Additionally, it is worth considering the application of the system on a large scale and whether the time required for proper degradation is feasible in a conventional water treatment system.

Conventional biological treatment does not effectively treat wastewater containing nitroaromatic compounds such as DNAN (Shen et al., 2013). Shen et al. (2013) used a combined zero-valent iron (ZVI) reduction and Fenton oxidation process to evaluate the pretreatment of 2,4-dinitroanisole (DNAN) in wastewater. The combined process uses ZVI as a reductive stage to convert nitroaromatic compounds in DNAN into chemical species that are more susceptible to the subsequent Fenton oxidation process (Shen et al., 2013). Using this method, nearly all nitroaromatic compounds were removed with an 8-hour empty bed processing time (Shen et al., 2013). Since this treatment process uses a two-stage method, it may be beneficial when treating water with co-



contaminants that may inhibit other AOPs. Because the ZVI can convert nitroaromatic compounds like DNAN to compounds that are more susceptible to the following Fenton oxidation, it may lead to enhanced DNAN degradation during the oxidation process and overall efficiency in the combined system.

Gallucci (2016) studied the effects of different LED designs in a variety of reactor conditions. His work demonstrated that UV LED H2O2 AOP was capable of a 2-Log reduction of *E. coli* (Gallucci, 2016). More importantly, his work optimized conditions with a medium thickness Teflon walled reactor with high power UV LEDs that could be used for future research (Gallucci, 2016). This study uses a reactor designed by Gallucci and used by Stubbs (Gallucci, 2016; Stubbs, 2017). Much of the work in this study is a continuation of the work of Scott, Stewart, and Stubbs (Scott et al., 2017; Stewart, 2016; Stubbs, 2017).

2.5 Soluble Microbial Products and Co-Contaminants

Effluents from wastewater treatment systems are known to contain a variety of soluble organic compounds, including residual degradable and hard-biodegradable influent substrate, as well as complex organic compounds which are categorized as Soluble Microbial Products (SMPs) (Azami, Sarrafzadeh, & Mehrnia, 2012). SMPs have been identified as containing humic acids, proteins, antibiotics, and amino acids (Azami et al., 2012). SMPs in wastewater effluents vary depending on the method of treatment. Utilization-associated products (UAPs) in SMP were found to be carbonaceous compounds with a molecular weight less than 290kDa (Ni, Rittmann, & Yu, 2011). Secondary effluent from three wastewater treatment facilities showed protein



concentrations of less than 10 mg/L (Westgate, 2009). SMPs also have a significant effect on the physico-chemical properties of microbial aggregates in secondary wastewater sludge (Sheng, Yu, & Li, 2010; Zhang et al., 2017). Additionally, SMPs can increase membrane fouling and cause flux decline in wastewater reclamation and reuse systems (Jarusutthirak & Amy, 2006). Specifically, reverse osmosis, nanofiltration, and ultrafiltration fouling is caused by SMPs forming a cake or gel layer due to steric exclusion (Jarusutthirak & Amy, 2006). Because SMPs can cause fouling of filters, it is possible that over time they will foul UV lights in an AOP. More importantly, because the AOP used in this experiment has the potential to be used in wastewater treatment, it is critical to understand the effects of SMPs on the performance of the reactor.

Yang et al. (2018) also researched the effects of naturally occurring photoinducers, including Suwannee River fulvic acid (SRFA) and nitrate (NO3-) in a UV/PS system and found they inhibited the reduction of DNAN. DNAN degradation was likely inhibited because the SRFA caused radical scavenging, light screening effects, and reductive conversion of intermediate radicals (Yang et al., 2018). Additionally, "High concentration of NO3– mitigated the inhibitory effect, presumably due to the reactive nitrogen species (RNS) generated by NO3– photolysis" (Yang et al., 2018). Furthermore, Yang et al. (2018) propose that SRFA's strong absorbance at 254 nm may inhibit PS decomposition upon UV radiation to produce SO4-.

There is a gap in understanding how photoinducing co-contaminants react and influence DNAN degradation in an UV/H2O2 AOP. While Yang et al. (2018) did not research the effects of naturally occurring photoinducers in the UV/ H_2O_2 process, it is likely they have an inhibitory effect, possibly due to blocking UV light within a reactor.



Assuming wastewater from DNAN production and municipal wastewater will have other co-contaminants, further research should be conducted using an UV/H₂O₂ AOP with likely co-contaminants to determine the efficacy of the system when exposed to various concentrations of co-contaminants.

2.6 Wastewater Treatment at DoD facilities in Continental United States

DoD wastewater facilities in the Continental United States (CONUS) must comply with the parameters of National Pollution Discharge Elimination System (NPDES) permits (US EPA, 2010, p. 1–5). Conventional wastewater facilities can be expected to produce effluent that complies with NPDES permits. This effluent, however, may cause complications with subsequent advanced treatment methods, particularly AOPs which may be degraded my naturally occurring photoinducers (Yang et al., 2018).

Barry (2012) characterized domestic wastewater treatment processes at DoD installations located in the Continental United States. Of the 86 military water treatment facilities studied, approximately 63% used an activated sludge process, 17% used advanced treatment, 15% primary treatment only, 6% settling ponds, and 1% used septic tanks (Barry, 2012). Those systems with advanced sludge processes would produce effluent containing SMPs. Because naturally occurring photoinducers can degrade the DNAN in an AOP (Yang et al., 2018), it is important that the DoD understand not only the characterization of its wastewater byproducts, but its selected treatment method in order to produce safe water that meets NPDES permit requirements.


III. Methodology

3.1 General Operating Parameters

AOP experiments were conducted in a Teflon UV LED reactor with an internal volume of approximately 35 ml, a flow rate of 2 ml/min, and a residence time of approximately 17.5 minutes (Stubbs, 2017). Solution flowed through a Masterflex L/S® Model 77200-50 peristaltic pump and Masterflex L/S® PharMed® BPT 14 precision pump tubing (Cole-Parmer Instrument Co, Vernon Hills, Illinois). The pump was set to 7.8 rpm which resulted in a 2 mL/min flow rate for all experiments. A 0.5-inch PTFE coated stir bar was placed inside the reactor to create a CFSTR and the reactor was placed horizontally on a Fisher Scientific 14-511-2 magnetic stir plate (Thermo Fisher Scientific, Waltham, Massachusetts). Figures 1-3 depict the reactor used in this experiment. The BPT tubing entered the reactor where the solution was exposed to light from two UV-CLEAN LEDs (Sensor Electronic Technology Inc, Columbia, South Caroline) emitting at 264 nm, and each light consisting of nine diodes receiving 100mA. The LEDs were powered by a circuit board with 12 LUXdrive[™] model 4006 DynaOhm[™] 20mA semiconductor resistors (LEDdynamics, Randolph, Vermont). The circuit board was controlled by a Keysight E3620A series bench power supply. After passing through the reactor, effluent exited in PTFE tubing and was used for grab sampling or directed into a waste beaker.

3.2 AOP Experiment

In order to answer the first research question, the independent variable, molar peroxide ratio, was adjusted and expected to greatly influence the observed first order



rate constants (k_s). The solutions for the AOP experiments were comprised of DNAN (CAS 119-27-7 Alfa Aesar ®), reverse osmosis, purified, deionized water (DI Water, AFIT ENV Lab), casamino acids (MP Biomedicals Cat No. 3060-012, Solon, OH), and Hydrogen Peroxide (30% in water, Fisher Scientific, Pittsburgh, PA). Molar peroxide ratios H2O2:DNAN were adjusted to 50:1, 100:1, 250:1, 500:1, and 1000:1.

DNAN solutions were prepared three days prior to experiments to ensure thorough mixing. The 250 ml solution consisted of 10mg/L DNAN in a 250ml Type A volumetric flask. DNAN was measured using a Mettler-Toledo XP26 Precision Balance (Mettler-Toledo, LLC, Columbus, Ohio). A 1.0-inch PTFE stir bar was placed inside the volumetric flask, the flask was capped, covered in foil, and placed on a Thermo Scientific Model SP88857100 stir plate (Thermo Fisher Scientific, Waltham, Massachusetts) set to 850 rpm for three days.

On the day of the experiment, a casamino acid solution was prepared, that when added to the DNAN solution, produced a casamino acid concentration of 1 mg/L. To prepare the casamino acid solution, 250 mg of casamino acid powder was mixed with reverse osmosis, purified, deionized water in a 100 ml volumetric flask. A 0.5-inch PTFE stir bar was placed inside the volumetric flask, hand mixed for 20 minutes, then mixed on a Thermo Scientific Model SP88857100 stir plate (Thermo Fisher Scientific, Waltham, Massachusetts) for one-hour. Upon thorough mixing of the casamino acid solution, an appropriate volume was added to the DNAN solution to create a concentration of 1 mg/L of casamino acids in the DNAN solution.

 H_2O_2 was then added (volume dependent on target molar ratio) to the DNAN and casamino acid solution and hand mixed for five minutes, then placed back on the stir



plate for 20 minutes. After thorough mixing, a sample of approximately 8 ml was drawn from the solution in a 10 ml luer lock syringe (Henke Sass Wolf, Tuttlingen, Germany) to be analyzed by a SevinMulti pH Meter (Mettler-Toledo, LLC, Columbus, Ohio). It is important to note the pH of the solution varied throughout the experiments, from 5.18 to 7.09, and was only measured after a complete DNAN-Casamino Acid-H₂O₂ solution was well mixed. The variations in pH are likely due to storage conditions as well as maintenance conducted on the water purification system. Standards were then created for a calibration curve. Standards were made from the prepared DNAN solution and DI water to create a blank, 10, 20, 40, 60, 80, and 100% DNAN solution. DNAN presence was detected and quantified via HPLC chromatogram analysis. DNAN appears at 1.098 min residence time and increased proportionately with increased ratios in standards.

3.2.1 AOP Experiments Description

For each experiment, the reactor was placed on a Fisher Scientific stir plate 14-511-2 magnetic stir plate (Thermo Fisher Scientific, Waltham, Massachusetts) which was started once fluid entered the reactor. Approximately 45 ml of DNAN solution was added to the influent lines, reactor, and effluent lines via a 60 ml Luer-Lok syringe (Becton, Dickinson, Franklin Lakes, New Jersey) in order to remove any air from the system. The pump was started and the DNAN flowed at 2.0 ml/min through the reactor with the UV LEDs turned off for 60 minutes of control sampling. Samples were taken at 10, 20, 30, 40, 50 and 60 minutes. Each 1.5 ml sample was collected in a 10 ml syringe, and filtered with a Millex ® Hydrophobic Flouropore TM PTFE filter with 0.2 um membrane (MilliporeSigma, Burlington, Massachusetts) into a 2.0 ml amber screw top vial (Agilent



Technologies, Santa Clara, California). All samples were well mixed for 30 seconds on a SBV1000 Vortex Mixer (Southwest Science, Hamilton Township, New Jersey). After 60 minutes elapsed, the circuit board was turned on, applying 100mA and 12.50v to the UV LEDs. The DNAN solution was then ran through the reactor for 60 minutes, with samples taken at 5, 10, 15, 20, 25, 35, 45, and 60 minutes. Samples were collected and prepared in the same manner as the previous step, and prepared for analysis in the HPLC.

3.2.2 H₂O₂ Control Experiments

There may be interaction between the DNAN and casamino acids. An experiment was conducted without H_2O_2 but with casamino acids present. A control was conducted for 60 minutes with UV LEDs turned off (samples taken at 0, 10, 20, 30, 40, 50, & 60 min), followed by 60 minutes with UV LEDs turned on (samples taken at 5, 10, 15, 20, 25, 35, 45, & 60 min). The k_s was expected to be near zero. A second control was conducted, in similar fashion to the one previously described, however, casamino acids were not added. The k_s was also expected to be near zero.





Figure 1: AOP Experimental Setup





Figure 2: Internal View of Reactor LED and Stir Bar





Figure 3: AOP Reactor Power Input, Influent and Effluent Lines, and Heat Sinks



3.3 HPLC and Mass Spectroscopy Analysis

Samples were analyzed in an Agilent Technologies 1260 Infinity HPLC coupled with a 6130 Quadrupole LC/MS (Agilent Technologies, Santa Clara, California). Treated DNAN was separated by a 1.8 µm, 2.1x50 mm, C18 column (Model: 82770-902, SN: USWEY 12941, Agilent Technologies, Santa Clara, California). Acetonitrile and water (1% formic acid) constituted the mobile phase. The HPLC quaternary pump flow was set to 0.6 ml/min with a solvent composition of 50% water, 10% formic acid, and 40% acetonitrile. Chromatogram peaks were integrated using Agilent Technologies ChemStation software.

MS spectra was used to suggest possible byproduct structures. After processing each experiment in the HPLC, they were analyzed by mass spectrometry. Chromatogram peaks were integrated using Agilent Technologies ChemStation software. Atomic mass units and retention times were used to propose possible byproduct structures. See Appendix F for chromatograms.

3.4 Statistical Analysis

Data for all experiments was entered into Microsoft Excel to show the change in effluent DNAN concentration (C/C₀) over time as measured by the HPLC. Curve-fitting was conducted with MATLAB R2020 in order to retrieve the observed pseudo first-order rate constants associated with DNAN removal. See Appendix D for MATLAB code. The mathematical basis of the curve fit was non-steady state solution for a CFSTR with first order reaction:



Equation 1: CFSTR with 1st order reaction

 $C(t)/Cin = [(1 + (\tau k)(exp[(1/\tau + k)(-1)t])]/(\tau k + 1))$

Where C(t) is concentration at time t Cin is initial concentration τ is average reactor residence time t is time k is apparent first-order reaction rate constant

3.4.1 Analysis of Variance

A Kruskal-Wallis H-Test was conducted using JMP® and Python ® software to determine if there are statistically significant differences between treatments (k_s values). The Kruskal-Wallis H-Test is a non-parametric technique that compares the means of the groups, categorized here as k_s by molar ratio. Additionally, the Kruskal-Wallis H-Test requires no assumptions about population probability distributions (Sincich, Mcclave, & Benson, 2018). H₀ for this test is that the populations medians are equal. H_a for this test is that at least two of the population medians are not equal. This test will indicate whether the population medians are different, however, it will not indicate which populations medians are different. For that, the Two-Sample *t*-Statistic is used.

3.4.2 Two Sample t-Statistic

In order to determine which treatment is differs at a statistically significant level, a t-test was performed. The t-test is useful when the sampled populations are only approximately normally distributed, which may be the case with only three samples per molar ratio. Additionally, when sample sizes are equal, the assumption of equal population variance can be relaxed and the test statistic will still produce an approximate Student's t-distribution (Sincich et al., 2018, p. 463). The t-test will use approximate



small-sample procedures to compare molar ratios to determine if there is a statistically significant difference. With this test, t is based on 2(n-1) degrees of freedom.

Equation 2: t-Test for Small Samples When $\sigma_1^2 \neq \sigma_2^2$

Confidence Interval:
$$(\bar{x}_1 - \bar{x}_2) \pm t_{\alpha/2} \sqrt{(s_1^2 + s_2^2) / n}$$

Test Statistic for H₀:
$$t = \frac{(\overline{x_1} - \overline{x_2})}{\sqrt{(s_1^2 + s_2^2)/n}}$$

Where \bar{X} is the sample mean $t_{\alpha/2}$ is Student's t-value s_1^2 is the sample variance *n* is number of samples



IV. Analysis and Results

4.1 The Effect of Molar Peroxide Ratio on DNAN Degradation

Figure 4 shows the effect of 50:1 H₂O₂ to DNAN ratio on the relative concentration of DNAN. The x-axis shows time elapsed, and the y-axis shows relative concentration of DNAN (C/C₀). For trial one, over the course of a 60-minute experiment, the relative concentration of DNAN (C/C₀) decreased to 0.899, 0.891, 0.837, 0.828, 0.816, 0.805, 0.812, and 0.814. Trial two decreased to 0.909, 0.870, 0.849, 0.834, 0.826, 0.821, 0.821, and 0.811. Trial three decreased to 0.902, 0.866, 0.848, 0.816, 0.817, 0.807, 0.808, and 0.803. The k_s (min⁻¹) for trials 1-3 were 0.015, 0.015, and 0.016, respectively. The mean k_s (min⁻¹) for 50:1 trials was 0.0153 and is displayed with the other molar ratios in Figure 10. With a low relative concentration of H₂O₂, the overall degradation of DNAN was less than subsequent experiments. A possible explanation for lower performance than subsequent molar ratios may be a lack of hydroxyl radical production due to decreased presence of H₂O₂.





Figure 4: The Effect of 50:1 H2O2 to DNAN on the Removal of DNAN



Figure 5 shows the effect of 100:1 H2O2 to DNAN ratio on the relative concentration of DNAN. The x-axis shows time elapsed, and the y-axis shows relative concentration of DNAN (C/C₀). For trial one, over the course of a 60-minute experiment, the relative concentration of DNAN (C/C0) decreased to 0.894, 0.827, 0.786, 0.775, 0.753, 0.732, 0.732, and 0.719. Trial two decreased 0.920, 0.854, 0.822, 0.791, 0.765, 0.755, 0.750, 0.744. Trial three decreased to 0.919, 0.856, 0.825, 0.804, 0.782, 0.765, 0.759, 0.729. The k_s (min⁻¹) for trials 1-3 were 0.023, 0.02, and 0.02, respectively. The mean k_s (min⁻¹) for 100:1 trials was 0.021 and is displayed with the other molar ratios in Figure 10. The data was as expected, with increased degradation compared to the 50:1 trial.





Figure 5: The Effect of 100:1 H2O2 to DNAN on the Removal of DNAN



Figure 6 shows the effect of 250:1 H₂O₂ to DNAN ratio on the relative concentration of DNAN. The x-axis shows time elapsed, and the y-axis shows relative concentration of DNAN (C/C₀). For trial one, over the course of a 60-minute experiment, the relative concentration of DNAN (C/C0) decreased to 0.846, 0.795, 0.770, 0.731, 0.715, 0.710, 0.701, and 0.686. Trial two decreased to 0.832, 0.786, 0.730, 0.719, 0.709, 0.695, 0.691, and 0.691. Trial three decreased to 0.845, 0.806, 0.763, 0.737, 0.736, 0.728, 0.729, and 0.715. The k_s (min⁻¹) for trials 1-3 were 0.027, 0.029, and 0.025, respectively. The mean k_s (min⁻¹) for 250:1 trials was 0.027 and is displayed with the other molar ratios in Figure 10.





Figure 6. The Effect of 250:1 H2O2 to DNAN on the Removal of DNAN



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Figure 7 shows the effect of 500:1 H₂O₂ to DNAN ratio on the relative concentration of DNAN. The x-axis shows time elapsed, and the y-axis shows relative concentration of DNAN (C/C₀). For trial one, over the course of a 60-minute experiment, the relative concentration of DNAN (C/C0) decreased to 0.861, 0.814, 0.756, 0.743, 0.721, 0.691, 0.685, and 0.629. Trial two decreased to 0.866, 0.767, 0.757, 0.711, 0.706, 0.699, 0.690, and 0.683. Trial three decreased to 0.848, 0.775, 0.754, 0.730, 0.715, 0.714, 0.693, and 0.688. The k_s (min⁻¹) for trials 1-3 were 0.029, 0.029, and 0.028, respectively. The mean k_s (min⁻¹) for 500:1 trials was 0.0287 and is displayed with the other molar ratios in Figure 10.





Figure 7. The Effect of 500:1 H2O2 to DNAN on the Removal of DNAN



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Figure 8 shows the effect of 1000:1 H_2O_2 to DNAN ratio on the relative concentration of DNAN. The x-axis shows time elapsed, and the y-axis shows relative concentration of DNAN (C/C₀). For trial one, over the course of a 60-minute experiment, the relative concentration of DNAN (C/C0) decreased to 0.841, 0.795, 0.751, 0.735, 0.728, 0.713, 0.722, and 0.714. For this trial, the 45-minute sample of 0.722 relative concentration of DNAN (C/C₀) showed less degradation than the sample drawn at 35 minutes. This is likely attributed to the solution reaching maximum residence time in the reactor and the effluent being influenced by mixing performance inside the reactor. Trial two decreased to 0.831, 0.794, 0.769, 0.756, 0.748, 0.721, 0.709, and 0.706. Trial three decreased to 0.764, 0.706, 0.681, 0.668, 0.653, 0.645, 0.639, 0.626. The k_s (min⁻¹) for trials 1-3 were 0.026, 0.026, and 0.038, respectively. The mean k_s (min⁻¹) for 1000:1 trials was 0.030 and is displayed with the other molar ratios in Figure 10.

Trial three displayed significantly more degradation (10.1% and 8.9% respectively) at the five-minute sampling mark than trial one and two. This is statistically significant and may be attributed to several factors. It is possible that this result, although an outlier, is actually a valid result. It is important, however, to speculate why it could be an anomaly. Because the CFSTR is made of Teflon, it is not possible to observe the internal conditions, specifically whether the stir bar is properly spinning within the reactor. It is possible to hear and feel the stir bar spinning, but it cannot be guaranteed where the stir bar is spinning and whether it is spinning properly. It is possible the stir bar, when exposed to a continuous flow, moved inside the reactor and created suboptimal mixing conditions. This is plausible because the 0.5-inch stir bar is spinning in a cylindrical reactor laying on its side, as opposed to a flat surface which would allow the



stir bar to move freely without impacting the sides of the reactor. Although mixing conditions may not have been optimal, this may have produced samples with higher degradation than a trial with proper mixing. This is counterintuitive, but is possible because the effluent is a mixture of fresh influent that has just entered the reactor, and fluid that has been in the reactor close to the maximum residence time. If the stir bar were to improperly operate, it is possible that the effluent was more composed of a solution that had achieved peak residence time instead of a properly mixed solution of untreated and treated fluid with a lower average residence time. If the stir bar were to have a temporary unbalance, this could be noticed as a positive or negative spike on the degradation curve which then recovers back to normal parameters. Additionally, increased degradation could have occurred if pump errors caused either a decreased volume in the reactor or increased residence time. With 1000:1 trial number three, there was no spike, just a significantly larger drop at the first sample. This may be indicative of results with actual increased performance compared to trials one and two, or a reactor that did not stir properly for the entire experiment and only appears to have enhanced degradation.



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Figure 8. The Effect of 1000:1 H2O2 to DNAN on the Removal of DNAN



Figure 9 shows effect of each molar ratio of H_2O_2 to DNAN (averaged) on the relative concentration of DNAN. The x-axis shows time elapsed, and the y-axis shows relative concentration of DNAN (C/C₀). This depicts the average of each molar ratio to best compare them to each other. By visual analysis, based solely on means, it appears that DNAN degradation increased with an increase in H_2O_2 , with 50:1 showing the least overall degradation and 1000:1 with the most degradation. Furthermore, the results show non-linear DNAN reduction under all experimental conditions. This information will be used for further statistical analysis in the next section.

Results depicted in Figure 9 are likely influenced by radical scavengers present in the DNAN solution. The reverse osmosis, purified, deionized water used in the solution limits the types of potential radical scavengers to radical-radical reactions, bicarbonate, and H_2O_2 . Among these, radical-radical reactions are the most thermodynamically favorable, followed by bicarbonate, then H_2O_2 , with activation energy (Ea) of 8, 14, and 21.2 KJ/mol respectively (Buxton et al., 1988).





Figure 9. Average DNAN Removal by Molar Ratio



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4.2 Statistical Analysis of Pseudo-First Order Rate Constants

Figure 10 shows the results of Welch's ANOVA. The F-Ratio of 144.21 indicates that the means between molar ratios is high and that H_0 (means are equal) will likely be rejected. With an F value of < 0.0001, it is extremely unlikely the differences observed are due to random sampling, thus, the H_0 is rejected. This confirms that there is a statistically significant difference between the five molar ratios.

Welch's Test

 Welch Anova testing Means Equal, allowing Std Devs Not Equal

 F Ratio
 DFNum
 DFDen
 Prob > F

 144.2129
 4
 4.6829
 <.0001*</td>

Figure 10: Welch's ANOVA

Table 1 shows the results of a *t*-test that was performed to determine which treatment is different. The results indicate that four ratio comparisons are different. Specifically, 50:1 is different from 100:1, 250:1, and 500:1. 100:1 is also different from 500:1. In order to determine which molar ratio is "optimum," it is important to define what is desired from the experiment. If 100:1 and 250:1 produce results that are not statistically different, it may be best to use the 100:1 for financial purposes, which would require 2.5x less H₂O₂. Conversely, if 100:1 and 500:1 produce statistically significant different results, it may make most sense to use 500:1 and achieve better overall DNAN degradation. It is important to note, however, that the higher k_s from 1000:1 Trial 3 may be an anomaly. If not treated as an anomaly, then it is not statistically different than 50:1, even though, as shown in Figure 10, 1000:1 achieved greater overall degradation. 50:1



and 1000:1 are not statistically different because of the large degree of variance within the three 1000:1 trials. When all trials are analyzed in this manner, an ideal molar ratio can be selected based on desired criteria. If maximum degradation is a priority, 1000:1 may be best, although the large degree of variance may not always produce the desired results. In that case, 250:1 may be the best ratio of those tested. It produced results only slightly inferior to 500:1, but used half the H₂O₂. If this model were scaled to a large water treatment plant with continuous flow, savings on H₂O₂ could be significant. In order to determine if the k_s of 0.038 is truly and outlier, repeat experiments of the 1000:1 ratio should be conducted.

Comparison	Margin of error	Lower Bound	Upper Bound	Significant?
50 - 100	0.005	-0.011	-0.001	Y
50 - 250	0.006	-0.017	-0.006	Y
50 - 500	0.002	-0.016	-0.011	Y
50 - 1000	0.019	-0.034	0.005	N
100 - 250	0.007	-0.013	0.001	N
100 - 500	0.005	-0.013	-0.003	Y
100 - 1000	0.020	-0.029	0.011	N
250 - 500	0.006	-0.007	0.004	N
250 - 1000	0.020	-0.023	0.017	N
500 - 1000	0.019	-0.021	0.018	N

Table	· 1.	t-T	'est.

If the k_s value of 0.038 for 1000:1 Trial 3 is assumed to be an error due to improper mixing or another reason, the data point could be removed and the data reanalyzed with a *t*-test. This can be evaluated using Dixon's Q-Test as shown in Equation 3, which allows for rejection of outliers. Dixon's Q-Test will work with only three data points, however, if two of those data points are the same, this will result in the rejection of the third data point, as long as it is not the same as the previous two. For instance, values of 0.026, 0.026, and 0.027 would indicate the rejection of 0.027, even



though this is very likely an accurate data point. Thus, this test will not work to exclude 0.038 from the data set.

Equation 3: Dixon's Q-Test

$$Q = \frac{Gap}{Ramge} = \frac{x_2 - x_1}{x_n - x_1}$$

Where x_1 is the smallest (suspect) value, x_2 is the second smallest value, x_n is the largest value.

For the purposes of this statistical analysis, the 0.038 data point will be temporarily removed for further analysis. Table 2 shows the results of a *t*-test with 1000:1 k_s of 0.038 removed, leaving only 0.026 and 0.026. When analyzed in this manner, the statistical differences between molar ratios remain similar, except 50:1 now has a statistically significant difference than 1000:1. Once the 0.038 data point is removed from the 1000:1 trials, the average k_s becomes 0.026. Figure 11 shows that when analyzed in MATLAB, 1000:1 achieves less degradation than 250:1 and 500:1, with 500:1 achieving the most degradation, although only slightly greater than 250:1. By this method of analysis, 250:1 would be the optimal of the five molar ratios tested because it uses half the H₂O₂ of 500:1 and achieves similar results.

Comparison	Margin of error	Lower Bound	Upper Bound	Significant?
50 - 100	0.005	-0.011	-0.001	Y
50 - 250	0.006	-0.017	-0.006	Y
50 - 500	0.002	-0.016	-0.011	Y
50 - 1000	0.002	-0.012	-0.009	Y
100 - 250	0.007	-0.013	0.001	Ν
100 - 500	0.005	-0.013	-0.003	Y
100 - 1000	0.005	-0.010	0.000	N
250 - 500	0.006	-0.007	0.004	Ν
250 - 1000	0.006	-0.005	0.007	Ν
500 - 1000	0.002	0.001	0.004	N

Table 2: *t*-Test With *k*_s of .038 Removed as a Data Point





Figure 11: Average DNAN Removal With 1000:1 ks .038 Removed





A regression analysis, as depicted in Figure 12, was conducted using linear and quadratic models. The blue line depicts a linear analysis which does not fit the data well and has an r^2 value of 0.694. This is expected as previous studies have shown that excess H_2O_2 can increase hydroxyl radical scavenging and thus cause degradation to eventually decrease when a threshold concentration is reached (Su et al., 2019; Yang et al., 2018). The red line depicts a quadratic model with the curve forced through the origin in order to best match the results of near 0.0 k_s (min⁻¹) when there is no H₂O₂ present. This model produces a favorable r^2 value of 0.903, however, a visual analysis makes it clear that this model grossly underestimates k_s values when H₂O₂: DNAN ratios are below 250:1 and overestimates when ratios are above 500:1. The green line represents another quadratic model without forcing the curve through the origin. This model produces an r^2 value of 0.701, however a visual analysis shows that it appears to fit the data better than both the linear model and the quadratic model when forced through the origin. This model produces slight underestimations of k_s when H₂O₂: DNAN ratios are below 250:1 and begins to overestimate when above 500:1. None of the regression models that were analyzed provided a good fit to the data which limits the models use for predicting results. Because of this, further work should be conducted in order to identify a better model that lends itself to accurate predictions across a range of H_2O_2 : DNAN ratios.





Figure 12: Linear and Quadratic Regression Analysis



4.3 Results Comparison with Related Works

Searcy (2020) conducted similar experiments, with the main exception that he did not include casamino acids as a co-contaminant. The molar ratios and methodology were nearly identical for his experiments. The k_s for 50:1 H₂O₂: DNAN were 0.019, 0.18, and 0.017. The k_s for 100:1 H₂O₂: DNAN were 0.025, 0.022, and 0.023. The k_s for 250:1 H_2O_2 : DNAN were 0.032, 0.029. and 0.031. The k_s for 500:1 H_2O_2 : DNAN were 0.033, 0.029, and 0.034. The k_s for 1000:1 H₂O₂: DNAN were 0.024, 0.024, and 0.022. The 1000:1 experiment had a trial with a k_s of 0.033 that was rejected. Searcy's average k_s for 50:1, 100:1, 250:1, 500:1, and 1000:1 (after outlier rejection) were 0.018, 0.023, 0.031, 0.032, and 0.023, respectively. The average k_s for Searcy's 50:1, 100:1, 250:1, and 500:1 H₂O₂: DNAN ratios had higher degradation than this experiment. Figure 13 displays Searcy's average DNAN degradation (Searcy, 2020). Searcy's k_s for 1000:1 H₂O₂: DNAN had higher degradation, but only if the 0.038 data point from this experiment is excluded (Searcy, 2020). When analyzed in this manner, the data from Searcy's experiment follows a similar pattern as this study, except Searcy experienced more degradation. The slightly increased degradation reported by Searcy may be attributed to the lack of a co-contaminant in his DNAN solutions. This agrees with previous studies that offer co-contaminants may have an inhibitory effect on UV AOPs (Hoigné, 1998; Yang et al., 2018).





Figure 13: Searcy's Average DNAN Degradation in UV LED AOP (Searcy, 2020)





A statistical comparison of this study and Searcy's work was conducted. The boxplot depicted in Figure 14 indicates that when all experiments are grouped by H₂O₂: DNAN ratios, only one outlier exists, which is the 1000:1 H₂O₂: DNAN ratio experiment from this study with a k_s of 0.038. A simple visual analysis, depicted in Figures 15-18 show that the k_s and C/C₀ values (individual and average) for both studies are similar.



Figure 14: Boxplot of Hart and Searcy k_s Values





Figure 15: Comparison of Hart and Searcy Average ks Values



Figure 16: Comparison of Hart and Searcy k_s Values





Figure 17: Comparison of Hart and Searcy Average Final C/C₀ Values



Figure 18: Comparison of Hart and Searcy Final C/C₀ Values

Further analysis was conducted to determine if the presence of casamino acids from this study caused a statistically significant different effect than the k_s values observed by Searcy. In order to do this, the assumption that both experiments were the same needs to be established. It is possible that slight undetected variations in technique occurred, however, the selected methodology, equipment, and procedures were nearly



identical. Thus, it is assumed the experiments were the same except for the use of casamino acids in this study. A one-way ANOVA was conducted for each molar ratio with researcher (Hart or Searcy) as treatments and k_s as the response at a significance level of 0.05 in order to determine if the presence of casamino acids had an effect on k_s values. Table 3 depicts the one-way ANOVA which indicates that only 50:1 H₂O₂: DNAN differed at a statistically significant level. Thus, it appears casamino acids only had a statistically significant effect at the 50:1 H₂O₂: DNAN level. While the majority of experiments conducted in this study had lower k_s values, only one H₂O₂: DNAN ratio was significant. It is plausible that because there is less H₂O₂ available in the 50:1 experiment, that the casamino acids have an increased inhibitory effect on the degradation of DNAN due to radical scavenging or light screening effects. It is also possible that casamino acids have a slight effect at higher ratios (100:1, 250:1, 500:1, and 1000:1), but the effect is not enough to be of statistical significance, perhaps because of its inability to scavenge enough radicals or screen enough light.

Treatment	sum_sq	dd	F	PF (>F)
C(mr50researcher)	0.000011	1	16	0.01613
Residual	0.00003	4	NaN	NaN
C(mr100researcher)	0.000008	1	3.0625	0.15502
Residual	0.000011	4	NaN	NaN
C(mr250researcher)	0.00002	1	6.36842	0.06511
Residual	0.000013	4	NaN	NaN
C(mr500researcher)	0.000017	1	4.54546	0.09998
Residual	0.000015	4	NaN	NaN
C(mr1000researcher)	0.000067	1	2.7027	0.17552
Residual	0.000099	4	NaN	NaN

Table 3: One-Way ANOVA of Hart and Searcy k_s Values for Each Molar Ratio



Yang et al. (2018) reported increased DNAN degradation in a UV/H2O2 AOP when H₂O₂ was increased from 2 mM to 5 mM (50:1 and 125:1 H₂O₂: DNAN ratio), but saw decreased performance when increased to 10 mM (250:1 H₂O₂: DNAN ratio). This report saw increased degradation from 2 mM to 20 mM, with the best results from 10 mM and 20 mM (250:1 and 500:1 H₂O₂:DNAN ratio). While it is a different system, it is important to compare the results of the AOP in this study to those of the UV/PS used by Yang for selecting optimum conditions for future experiments. The UV/PS used by Yang reactor yielded pseudo first-order rate constants up to 0.0189 min⁻¹ (Yang et al., 2018). This study achieved higher pseudo-first order rate constants of 0.028 min⁻¹.

Su et al. (2019) reported optimal conditions at 70:1 H_2O_2 : DNAN ratio which, when processed in MATLAB ® software, yields a rate constant of .0097 min⁻¹. Su et al. (2019) used a batch reactor vice a CFSTR which may explain the difference in results. Their reactor used an 800 ml solution of DNAN which has significantly higher overall volume than the reactor in this experiment. Additionally, the reactor used by Su et al. (2019) used a single 254 nm LSE Lighting UV Bulb which may account for further differences. It is not known if the bulb used by Su et al. (2019) was an LED or another style.

4.4 Potential Byproducts

Several potential byproducts were detected via mass spectrometry analysis. Mass spectrometry chromatograms (Appendix G) show profiles that were used for potential byproduct identification. Nitrobenzene +CN was a potential byproduct detected during chromatogram analysis for 100:1, 250:1, 500:1, and 1000:1 experiments with a retention


time of 0.371 to 0.382 min and an atomic mass of 146. Potential byproducts with a retention time of 1.164 and an atomic mass of 240 were also detected in 100:1 and 250:1 chromatograms. Potential byproducts with a retention time of 0.376 to 0.377 min and atomic mass of 192 were detected in 250:1 and 1000:1 chromatograms.

4.5 Investigative Questions Answered

The first investigative question asked how molar peroxide ratios affect the degradation of DNAN and the hypothesis proposes that molar peroxide ratio has a has a significant effect on the degradation of DNAN. This hypothesis is supported by the results and analysis of this experiment. Specifically, results show a non-linear removal of DNAN under all experimental conditions with molar peroxide ratios exhibiting a strong influence on reactor performance and degradation of DNAN. This study showed optimal DNAN removal at 250:1 and 500:1 H_2O_2 : DNAN ratio with an average pseudo first-order rate constant (k_s) of 0.027 and 0.0287, respectively.

The second investigative question asks how the presence of casamino acids will affect the degradation of DNAN and the associated hypothesis was that casamino acids will impact the degradation process. As demonstrated by Hoigne (1998), nearly all dissolved organic compounds in water create a detrimental effect on the degradation of target compounds. When compared to Searcy's (2020) work, which is very similar to this work except it lacked a co-contaminant, it suggests that Searcy achieved slightly better overall degradation. The presence of casamino acids appear to have a slight inhibitory effect on the degradation of DNAN in this study, however, it was only statistically significant at the 50:1 H_2O_2 : DNAN ratio.



V. Conclusions and Recommendations

5.1 Chapter Overview

The chapter provides the results of this study and any conclusions that were determined from the research. The broader significance of this research is also analyzed and recommendations for future research and work are presented.

5.2 Conclusions of Research

The relative concentration of DNAN (C/C₀) was reduced from 1.0 to 0.6259 (maximum value) over the range of selected molar peroxide ratios selected for this study with greatest degradation typically between 250:1 and 500:1 H_2O_2 :DNAN ratios. 1000:1 H_2O_2 :DNAN ratio had high levels of variance and its results should be treated as such.

Casamino acids as a co-contaminant had slight impacts on DNAN degradation, albeit they were only significant at the 50:1 H₂O₂:DNAN ratio. When compared to Searcy (2020), this study showed similar patterns, albeit with less overall degradation. The reduced k_s values in this study are likely the results of •OH removal by the casamino acids.

Chemical byproduct analysis suggests that Nitrobenzene +CN was created.

5.3 Significance of Research

This study explains the effect of molar peroxide ratios on the pseudo first-order rate constant of DNAN in an UV LED AOP. This research shows that an ideal molar peroxide ratio can be selected for DNAN degradation. Additionally, the impact of SMPs on DNAN degradation in a UV LED AOP was analyzed. This is significant, because



SMPs are commonly found in wastewater secondary effluent, and can negatively influence treatment plans.

The influence of molar peroxide ratios and co-contaminants such as casamino acids are significant findings. Little research has been conducted on the effect of cocontaminants on the degradation of DNAN in an AOP. Additionally, there is limited research on the reduction of DNAN in a UV LED AOP. By studying AOPs and how they are influenced by influent conditions, ideal conditions and parameters can be developed and applied to future water treatment systems.

AOPs that are used to treat water contaminated with DNAN, and possibly other co-contaminants, have the potential to create effluent that contains toxic compounds (Munter, 2001; Stocking et al., 2000). Understanding the mechanisms of degradation and structures of byproducts is important to future water treatment studies. Water treatment plans may need additional treatment beyond the AOP to create effluent that meets the criteria for its desired use.

5.4 Recommendations for Future Research

Future research should consider conducting further experiments to identify the optimal molar peroxide ratios for DNAN degradation and a model that can be used to predict k_s values. Conducting more trials at each ratio would allow for more confidence when conducting statistical analysis. Furthermore, repeat experiments at the 1000:1 H2O2: DNAN ratio should be conducted to determine if the suspected outlier in this study is actually a valid data point. Additionally, future experiments could explore the impacts of higher concentrations of casamino acids on the degradation of DNAN.



Future studies should also focus on the impacts of other co-contaminants,

particularly SMPs that are likely to react with hydroxyl radicals such as phenolics or high molecular weight organics, in an UV LED AOP. Specifically, solutions of a variety of co-contaminants commonly found in secondary water treatment effluent may have dramatic effects on the degradation of the target contaminant. Additionally, these co-contaminants may have an effect on long term UV LED performance because of staining or scaling and warrant further research. Future research may also benefit from increasing the scale of the experiment to better simulate actual operating conditions expected with wastewater secondary treatment effluent.

5.5 Summary

Wastewater treatment plays an extremely important role in society and is critical to the safe manufacture of a variety of explosives used by the DoD. UV LED AOPs are a promising approach to treating a variety of chemicals that are present in may wastewater systems. This study demonstrated that a UV LED/H₂O₂ AOP of DNAN is significantly affected by altering the molar peroxide ratio of H₂O₂:DNAN. Additionally, the addition of 1 mg/L casamino acids as a co-contaminant had little effect on DNAN degradation, and was only statistically significant at the 50:1 H₂O₂:DNAN ratio. Future research can be conducted to optimize k_s values in the presence of co-contaminants.



Trial #	H2O2:DNAN	Date	Notes
1	0:1	5/29/2020	Control - No Casamino Acid or H ₂ O ₂
2	100:1	6/5/2020	
3	100:1	6/12/2020	
4	100:1	6/19/2020	
5	500:1	6/26/2020	
6	500:1	7/2/2020	
7	500:1	7/16/2020	
8	1000:1	7/16/2020	
9	1000:1	7/23/2020	
10	1000:1	7/23/2020	Conducted immediately after Trial 9
11	0:1	7/30/2020	Control - Casamino Acids, no H2O2
12	250:1	8/6/2020	
13	250:1	8/6/2020	Conducted immediately after Trial 12
14	250:1	8/13/2020	
15	50:1	8/13/2020	Conducted immediately after Trial 14
16	50:1	8/20/2020	
17	50:1	8/20/2020	Conducted immediately after Trial 16

Appendix A: AOP Experiment Schedule



Appendix B: AOP	Experiment Data
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Trial	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17
H ₂ O ₂ :DNAN Ratio	0:1	100:1	100:1	100:1	500:1	500:1	500:1	1000:1	1000:1	1000:1	0:1	250:1	250:1	250:1	50:1	50:1	50:1
Experiment Date	5/29/2020	6/5/2020	6/12/2020	6/19/2020	6/26/2020	7/2/2020	7/2/2020	7/16/2020	7/23/2020	7/23/2020	7/30/2020	8/6/2020	8/6/2020	8/13/2020	8/13/2020	8/20/2020	8/20/2020
DNAN Solution Prepared	5/26/2020	6/2/2020	6/9/2020	6/16/2020	6/23/2020	6/29/2020	6/29/2020	7/13/2020	7/20/2020	7/20/2020	7/27/2020	8/3/2020	8/3/2020	8/10/2020	8/10/2020	8/17/2020	8/17/2020
Calculated DNAN Conc (ppm)	10.009	10.016	10.016	10.011	10.001	10.000	10.011	10.009	10.005	10.007	10.004	10.001	10.004	10.001	10.015	10.003	10.001
рН	6.531	6.198	6.745	6.711	7.094	7.079	6.682	6.932	6.238	6.140	6.248	5.177	5.188	5.365	5.232	5.197	5.232
H ₂ O ₂ Vol (μl)	0	128	128	128	638	638	638	1276	1276	1276	0	319	319	319	64	64	64
Avg C ₀	9.451	9.583	9.358	9.495	9.607	9.189	9.326	9.301	9.558	9.642	9.568	9.598	9.736	9.547	9.546	9.555	9.646
Control Sample Time (min)				•		•		•	PPM			·			•	•	
0	9.431	9.576	8.292	8.721	9.179	8.799	9.015	9.158	9.131	9.406	9.126	9.203	9.689	9.151	9.322	9.260	9.478
10	-	9.678	9.440	9.590	9.606	9.168	9.227	9.489	9.662	9.639	9.675	9.531	9.686	9.491	9.520	9.554	9.639
20	9.508	9.565	9.528	9.636	9.665	9.676	9.375	9.396	9.700	9.658	9.590	9.559	9.745	9.697	9.583	9.643	9.668
30	-	9.610	9.525	9.557	9.672	9.173	9.484	9.322	9.569	9.617	9.778	9.588	9.639	9.677	9.579	9.680	9.706
40	9.407	9.583	9.526	9.609	9.688	9.012	9.332	9.223	9.648	9.703	9.634	9.714	9.879	9.613	9.637	9.625	9.654
50	-	9.493	9.606	9.657	9.684	9.272	9.474	9.179	9.583	9.711	9.579	9.888	9.807	9.563	9.602	9.532	9.688
60	9.456	9.578	9.588	9.692	9.755	9.220	9.378	9.339	9.615	9.759	9.597	9.703	9.709	9.639	9.582	9.593	9.687
Experiment Sample Time (min)									C/C₀								
5	0.993	0.894	0.920	0.919	0.861	0.866	0.848	0.841	0.831	0.764	1.008	0.846	0.832	0.845	0.900	0.909	0.902
10	0.994	0.827	0.854	0.856	0.814	0.767	0.775	0.795	0.794	0.706	1.011	0.795	0.786	0.806	0.891	0.870	0.866
15	0.988	0.786	0.822	0.825	0.756	0.757	0.754	0.751	0.769	0.681	1.006	0.770	0.730	0.763	0.837	0.849	0.848
20	0.996	0.775	0.791	0.804	0.743	0.711	0.730	0.735	0.756	0.668	1.005	0.731	0.719	0.737	0.828	0.834	0.816
25	0.993	0.752	0.765	0.782	0.721	0.706	0.715	0.728	0.748	0.653	1.003	0.715	0.709	0.736	0.816	0.826	0.817
35	0.992	0.732	0.755	0.765	0.691	0.699	0.714	0.713	0.721	0.645	0.998	0.710	0.695	0.728	0.805	0.821	0.807
45	0.985	0.732	0.750	0.759	0.685	0.690	0.693	0.722	0.709	0.639	1.001	0.701	0.691	0.729	0.812	0.821	0.808
60	0.988	0.719	0.744	0.729	0.629	0.683	0.688	0.714	0.706	0.626	1.007	0.686	0.691	0.715	0.814	0.811	0.803

Data File Name				Notes											
DNAN Proported	5/26/2020		This is the first control	ovnorime	ent. Conducted without	-			_						
DIVAN Prepareu	5/20/2020			experime	int. Conducted without				_						
DNAN Conc (mg/L or ppm)	10.0093		H2O2, so we don't exp	ect to see	any degradation. There										
pH	6.531		also weren't any Casar	nino acids	, so we may need to										
H2O2 Vol (µl)	0		conduct another contr	ol later w	ith DNAN, CAS, and no										
CAS weight (g)	0		H2O2												
	0								_						
CAS VOI (µI)	0														
Start Setup	N/A														
Start Control	N/A														
Stop Experiment	N/A														
Ran in HPI C															
						-									
		G	libration Curve			- (Calibra	ation Curve: Conce	ntrati	on (%) v	vs Area	253 n	m		
		Concentration (%)	Concentration (ppm)	RT (min)	Area (meas. @ 253 nm)		cambre			011 (70) 1	/5. / 1 60.	20011			
		0.0000	0.0000		0.0	1	00.0000								
		10.0000	1.0009	1.154	77.5		90.0000						- and		
		20.0000	2 0010	1 151	149.7		80.0000					and the second			
		20.0000	2.0015	4.454	145.7	-	60.0000				a service	100			
		40.0000	4.0037	1.151	299.9	DNAN Concentration	50.0000				100 C		y = 0.1	.34\$x - 0.0	992
		60.0000	6.0056	1.151	441.2	(%)	40.0000			and the second second			R	· = 0.9999	
		80.0000	8.0074	1.153	594.1		30.0000		and the second second						
		100.0000	10.0093	1.15	747.9		20.0000								
						1	10.0000	and the second sec							
		Slone	0.1245				0.0000	∳ann.							
		Siope	0.1545			-		0.0 100.0 200.0	30	0.0 40	JO.O 500	0.0	i00.0	700.0	800.0
		y-intercept	-0.0992			-				Area @	253 nm				
		Control # :	: No H2O2, No UV Ligh	ıt											
HPLC Type	Sample Time (min)	Concentration (%)	Concentration (pnm)	RT (min)	Area (meas, @ 253 nm)	C o = Avg Ctrl Conc. ((mag								
C1	0	94 2257	9 4212	1 150	701.2	0 4505									
	0	54.2257	5.4515	1.150	701.5	5.4505			_						
	20	94.9923	9.5081	1.151	707.0										
C3	40	93.9836	9.4071	1.148	699.5										
C4	60	94.4678	9.4556	1.151	703.1										
		Experiment: No	H2O2 With UV Light a	nnlied											
		Experiment. No	Datasi	ppneu											
			DNAN	em (1)		B ())	syproa	lucts							
HPLC Type	Sample Time (min)	Concentration (%)	Concentration (ppm)	RT (min)	Area (meas. @ 253 nm)	RT (min)		Area (meas. @ 253 r	im)	Mass Rat	cio (C_n /	C_0)			
C_o (starting Conc)	0		9.4505							1	1.0000				
R1	5	93.7146	9.3802	1.151	697.5					0).9926				
R2	10	93 8894	9 3977	1 151	698.8					0	9944				
02	10	02 2572	0.3344	1 152	604.1				_	0	0.0077				
no i	15	35.2375	9.5544	1.155	094.1				_	0	1.36//				
R4	20	94.0105	9.4098	1.151	699.7					0).9957				
R5	25	93.7953	9.3882	1.150	698.1					0	J.9934				
R6	35	93.6877	9.3775	1.153	697.3					0	1.9923				
R7	45	92,9883	9,3075	1.150	692.1					0	0.9849				
RS					604.2						0000				
110	60	93 2842	9 3371	1 150	11714 3					0	LASSI				
	60	93.2842	9.3371	1.150	034.5					0	1.9880				
	60	93.2842	9.3371	1.150	094.5					0	J.9880				
	60	93.2842	9.3371	1.150	054.5					0	0.9880				
	60	93.2842	9.3371	1.150	054.5			DNAN Degrad	ation:	0 Mass P	atio vs 1	Time			
	60	93.2842 DNAN Degradati	9.3371 on: Concentration v	s. Time	C.+EU			DNAN Degrad	ation:	0 Mass R	atio vs. 1	Time			
	60	93.2842 DNAN Degradati	9.3371 on: Concentration v	s. Time		1.1		DNAN Degrad	ation:	0 Mass R	atio vs. 1	Time			
	1	93.2842 DNAN Degradati	9.3371 on: Concentration v	s. Time	034.3	11		DNAN Degrad	ation:	0 Mass R	atio vs. 1	Time			
	60 ي	93.2842 DNAN Degradati	9.3371 on: Concentration v	rs. Time	054.5	1.1	•	DNAN Degrad	ation:	0 Mass R	atio vs. 1	Time	•		
	<u>60</u> ۱	93.2842 DNAN Degradati	9.3371 on: Concentration v	•	034.3	1.1 1.0 0.9		DNAN Degrad	ation:	Mass R	atio vs. 1	Time	•		-
	60 ۱۰	93.2842	9.3371 on: Concentration v	s. Time	054.5	11 10 09		DNAN Degrad	ation:	Mass R	atio vs. 1	Time	•		•
		93.2842	9.3371	s. Time	•	1.1 1.0 0.9 0.8		DNAN Degrad	ation:	Mass R	atio vs. 1	Time	•		
	60 	93.2842	9.3371	•	•	11 10 09 0.8 0.7		DNAN Degrad	ation:	Mass R	atio vs. 1	Time	•		
	1	93.2842	9.3371	s. Time	•	1.1 1.0 0.9 0.8 0.7		DNAN Degrad	ation:	Mass R	atio vs. 1	Time	•		
	60	93.2842	9.3371	s. Time	•	1.1 1.0 0.9 0.8 0.7 Mass 0.7		DNAN Degrad	ation:	Mass R	atio vs. 1	Time	•		
	60	93.2842	9.3371	rs. Time	094.3	1.1 1.0 0.9 0.8 0.7 Mass Ratio 0.6 (C_n / C_0) 0.5		DNAN Degrad	ation:	Mass R	atio vs. 1	Time	•		
	60	93.2842	9.3371	s. Time	•	1.1 1.0 0.9 0.8 0.7 Mass Ratio 0.6 (C_n / C_0) 0.5		DNAN Degrad	ation:	Mass R	atio vs. 1	Time			
	60	93.2842	9.3371	rs. Time	•	1.1 1.0 0.9 0.8 0.0 Mass Ratio 0.6 (C_n / C_0) 0.5 0.4		DNAN Degrad	ation:	Mass R	tatio vs.	Time			
	60 2 Concentration (ppm)	93.2842	9.3371	•	•	1.1 1.0 0.9 0.8 0.7 Mass Ratio 0.6 (C_n / C_0) 0.4 0.3		DNAN Degrad	ation:	Mass R	tatio vs.	Time			
	60	93.2842	9.3371	rs. Time	•	1.1 1.0 0.9 0.8 0.0 0.8 0.0 0.9 0.8 0.0 0.9 0.8 0.0 0.9 0.0 0.9 0.0 0.0 0.0 0.0 0.0 0.0		DNAN Degrad	ation:	Mass R	tatio vs.	Time			
	60	93.2842	9.3371 On: Concentration v	rs. Time	•	1.1 1.0 0.9 0.8 0.7 Mass Ratio 0.6 (C_n / C_o) 0.5 0.4 0.3 0.3 0.2 0.3 0.2 0.3 0.3 0.2 0.3 0.3 0.3 0.3 0.3 0.3 0.3 0.3 0.3 0.3		DNAN Degrad	ation:	Mass R	tatio vs.	Time			
	60	93.2842	9.3371	•	•	1.1 1.0 0.9 0.8 0.0 0.8 0.0 0.9 0.8 0.0 0.9 0.8 0.0 0.9 0.8 0.0 0.9 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0		DNAN Degrad	ation:	Mass R	tatio vs.	Time			
	60	93.2842	9.3371	•	•	111 10 09 08 07 Mass Ratio 0.6 (C_n / C_o) 0.5 0.4 0.3 0.2 0.1 0.0 0.0		DNAN Degrad	ation:	Mass R	latio vs.	Time			
	60	93.2842	9.3371	1.150	45 50 55 60	→ 1.1 1.0 0.9 0.8 0.0 0.8 0.2 0.9 0.8 0.9 0.8 0.9 0.8 0.9 0.8 0.9 0.8 0.9 0.9 0.8 0.9 0.0 0.9 0.0 0.9 0.0 0.0 0.0 0.0 0.0	0	5 10 15 2	ation:	0 Mass R	tatio vs.	Time	45	50 5	5 60
	60	93.2842	9.3371	1.150 rs. Time	45 50 55 60	111 10 09 08 07 Mass Ratio 0.6 (C_n / C_o) 0.5 04 0.3 0.2 0.1 0.0	0	DNAN Degrad	ation:	Mass R	tatio vs. *	10000000000000000000000000000000000000	45	50 5	5 60
	60	93.2842	9.3371 9.3371 0.1 0.1 0.1 0.1 0.1 0.1 0.1 0	1.150 rs. Time	094.3	→ 1.1 1.0 0.9 0.8 0.7 Mass Ratio 0.6 (C_n / C_0) 0.5 0.4 0.2 0.1 0.0 0.0	0	DNAN Degrad	ation:	Mass R	tatio vs. *	10000000000000000000000000000000000000	45	50 5	5 60
	60	93.2842	9.3371	• • • • • • • • • • • • • • • • • • •	45 50 55 60	111 10 09 08 07 Mass Ratio 0.6 (C_n / C_o) 0.5 04 0.3 0.2 0.1 0.0	0	DNAN Degrad	ation:	Mass R	35 nin)	Time	45	50 5	5 60
	60	93.2842	9.3371	rs. Time	094.3	11 10 09 08 07 Mass Ratio 0.6 (C_n / C_0) 0.5 0.4 0.3 0.2 0.0 0.0	0	DNAN Degrad		0 Mass R	atio vs. *	Time	45	50 5	5 60
	60	93.2842	9.3371	1.150	45 50 55 60	111 10 0.9 0.8 0.7 Mass Ratio 0.6 (C_n / C_o) 0.5 0.4 0.3 0.2 0.1 0.0	0	DNAN Degrad		Mass R	tatio vs.	10000000000000000000000000000000000000	45	50 5	5 60
Quality	60 Concentration (ppm)	93.2842	9.3371	1.150	094.3	111 10 0.9 0.8 0.8 0.7 Mass Ratio 0.6 (C_n / C_P) 0.5 0.4 0.3 0.2 0.1 0.0	0	DNAN Degrad		Mass R	25880	10000000000000000000000000000000000000	45		5 60
Quality	60 Concentration (ppm) (Control Checks: QC 6 Area	93.2842	9.3371	1.150	45 50 55 60	111 10 0.9 0.8 0.7 Mass Ratio 0.6 (C_n / C_o) 0.5 0.4 0.3 0.2 0.1 0.0	0	DNAN Degrad		Mass R Mass R	attio vs.	Time	45		5 60
Quality Line 9	60 Concentration (ppm) (Control Checks: QC 6 Area 445.7	93.2842	9.3371	rs. Time	094.3	1.1 1.0 0.9 0.8 0.7 Mass Ratio 0.6 (C_n / C_0) 0.5 0.4 0.3 0.2 0.1 0.0	0	5 10 15		C Mass R S S S S S S S S	atio vs. *	Time	45	50 5	5 60
Quality Line 9 17	60 Concentration (ppm) Control Checks: QC 6 Area 445.7 45.15	93.2842	9.3371	s. Time	45 50 55 60	111 10 0.9 0.8 0.7 Mass Ratio 0.6 (C_n / C_o) 0.5 0.4 0.3 0.2 0.1 0.0	0	DNAN Degrad		0 Mass R	latio vs. *	40	45	50 5	5 60
Qualith Line 9 17 26	60 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	93.2842	9.3371	s. Time	094.5	1.1 1.0 0.9 0.8 0.7 Mass Ratio 0.6 (C_n / C_O) 0.5 0.4 0.3 0.2 0.1 0.0	0	DNAN Degrad		C Mass R L L L L L L S JO R	25 min)	Time	45	50 5	5 60



























			1			_		-										_		
Data File Name	20200716_DNAN_JH			Notes																
DNAN Prepared	7/13/2020		DNAN pippetted @ 67	'6 and 600	μl to get 1276 μl.															
DNAN Conc (mg/Lor ppm)	10.009200																			
Divide conc (mg/c or ppm)	10.005500		-			-		-												
pH	6.932																			
H2O2 Vol (µl)	1276																			
CAS weight (g)	0.2504																			
0101010	100					-		-												
CAS VOI (µI)	100							_				_								
Start Setup	6:45																			
Start Control	8:45																			
	0.45		-					-				-								
Stop Experiment	10:47																			
Ran in HPLC	11:00																			
					1															
		-	liberation Come				C	alibra	tion Cu	rve: C	ancent	ration	(%)	us Aros	. 253	nm				
			alibration Curve				C	anura	nion cu	ive. o	JIICEIII	lation	(70) V	/s. Alea	. 2551					
		Concentration (%)	Concentration (ppm)	RT (min)	Area (meas. @ 253 nm))	10	0.0000										•		
		0.0000	0.0000	0.000	0.0		9	90.0000								_	and a start of the			
		0.0000	0.0000	0.000	0.0			0000								and a series				
		10.0000	1.0009	1.104	81.7	_		20.0000							and the second					
		20.0000	2.0019	1.108	139.8			0.0000						a second						
		40,0000	4.0037	1.11	284.2	DNA	N Concentration	50.0000						100		y = 0.	.1398x-C	1.1256		
		60,0000	6.0056	1 114	437.1		(%)	50.0000					100			R	* = 0.999	16		
		00.0000	0.0050	1.114	427.1			\$0.0000												
		80.0000	8.0074	1.113	569.2		3	80.0000			and the second									
		100.0000	10.0093	1.114	722.4		2	20.0000												
							1	10.0000		1 ¹⁰										
								0.0000	and the second s											
		Slope	0.1398						0.0	100.0	200.0	300.0	40	0.0 5/	00.0	600.0	700	.0	800.0	
		y-intercept	-0.1256										Ares @	253 nm						
													ca @							
		-						_												1
		Co	ntrol Experiment									-								
HPLC Type	Sample Time (min)	Concentration (%)	Concentration (ppm)	RT (min)	Area (meas. @ 253 nm)) C_o = A	vg Ctrl Conc. (pp	om)												
C1	0	91 /002	9 1594	1 112	655.4		9 3010											-		
C1	0	21.4225	3.1304	1.115	033.4		3.3010					-						+		
C2	10	94.7986	9.4887	1.116	679.0															
C3	20	93.8759	9.3963	1.114	672.4															
C4	20	02 1250	9 2222	1 1 1 2	667.1															
04	50	55.1550	5.5222	1.115	007.1	_		-				-								
C5	40	92.1424	9.2228	1.112	660.0															
C6	50	91.7090	9.1794	1.114	656.9															
67	60	02 2027	0 2200	1 114	669.2			_												
0	60	93.3027	9.5590	1.114	000.5	_														
		Experi	ment: 1000:1 (1 of 3)																	
			DNAN				By	nrodu	rts											
				nm (1)				produ		~ ~				10 1						
HPLC Type	Sample Time (min)	Concentration (%)	Concentration (ppm)	RT (min)	Area (meas. @ 253 nm))	RT (min)	1	Area (me	as. @ 2	53 nm)	Mas	is Rati	io (C_n /	C_0)					
C o (starting Conc)	0		9.3010										1.	.0000						
R1	5	78.1065	7.8179	1.112	559.600								0.	.8405						
R2	10	73.9125	7.3981	1.115	529.600								0.	.7954						
								-				-								
P2	15	69 9024	6 9967	1 1 1 2	500 200								0	7512						
1.5	15	09.8024	0.5607	1.115	300.200								υ.	./312						
								_												
R4	20	68.2785	6.8342	1.114	489.300								0.	.7348						
		67 6 10 1	6 774 9																	
R5	25	67.6494	6.//12	1.114	484.800								0.	.7280						
							0.000	-				-								
B6	35	66 2095	6 6271	1 113	474 500		0.832			0.760			0	7125						
110	55	00.2000	0.0271	1.115	474.500								0.	711.5						
R7	45	67.0623	6.7125	1.113	480.600								0.	.7217						
						_		_										_		
80	60	66 2252	6 6207		475 400								~	7420						
R8	60	66.3353	6.6397	1.114	475.400								0.	./139						
						-		-				-								
		DNAN Dograde	ion: Concentration	C Time					DNA	N Do-	radat'	an. 64-	acc D -	atio	Time					
		DINAIN Degradat	ion. concentration v	/s. iimė					UNA	un neg	auatio	JII. IVIa	122 KS	JUU VS.	11116					
	1	0.0					1.0000	•												
		95					0.9000	-												
		··· .							+											
							0.8000			•										
		9.0					0 7000			L 1	•	+				•				
							u. /000							T					1	
		8.5					0.600													
							Adama Datela													
	Concentration (ppm)	8.0					IVIASS KATIO 0.5000	-												
		•					(C_n / C_o)													
		7.5					0.4000	-												
							0.3000													
		7.0					0.0000													
			T 📍 🗌	• I	• •		u.2000													
		6.5		1			0.1000													
							0.1000													
		6.0					0.0000													
		0 5 10 1	20 25 30	35 40	45 50 55 60		2.0000	0	5	10 1	5 20	25	30	35	40	45	50	55	60	, [
			Time (min)							-			Time /	min)		-				
			rime (min)										nme (I							
			i					_												
						_														
Qualit	v Control Checks: OC 6	0%						-										1		
Qualit	, (C 0	Delether D. C. and						-				-						+		
Line	Area	Relative Error (< 10%)				_						-						_		
9	428.1	0.2341																		
17	427.3	0.0468																		
27	422.5	0.0400				-		-				-						+		
27	423.5	0.8429																		



								-														
Data File Name	20200723_DNAN_A_JH			Notes																		
DNAN Prepared	7/20/2020		Conducting this experi	iment. and	1000-1 #	3 on the	same															
DNAN Conc (mg/Lor nom)	10.0052		day Used same CAS s	olution fo	r hoth evr	orimente																
Diverse conc (mg/ c or ppin)	10.0055		uay. Used same CAS s		i boui exp	Jennients				-										-		
pH	6.238		Total reset after comp	letion of t	his experi	ment prio	or to															
H2O2 Vol (µl)	1276		starting 1000-1 # 3.																			
CAS weight (g)	0.2504		1 -																			
CAC V(al (ul)	100							-														
CAS VOI (µI)	100									-				_						-		
Start Setup	5:15																					
Start Control	7:20																					
Step Experiment	0:20							-		-				-						-		
Stop Experiment	9.20									-				_						-		
Ran in HPLC	9:28																					
		0	libration Curve						Calib	oratio	on Cur	ve: Co	ncen	tratio	n (%)	vs. Area	a: 253	nm				
		4	andration curve						cum	Jiacia	, cui		,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,	ci a cio	(/0)							
		Concentration (%)	Concentration (ppm)	RT (min)	Area (m	eas. @ 25	3 nm)		100.0	000										•		
		0.0000	0.0000	0.000		0.0			90.0	000									and the second			
		10.0000	1.0005	1.000		60.4			80.0	000								• • • • • •				
		10.0000	1.0005	1.088		69.4			70.0	000							and the second					
		20.0000	2.0011	1.09		143.6			50.00	200												
		40.0000	4.0021	1.09		289.8			DNAN Concentration	000						100		y = 0.	1386x + 0	.1324		
		60.0000	6 0022	1 002		421.6			(%) 50.01	00					and the second			F	R ² = 0.999	9		
		80.0000	0.0032	1.095		451.0			40.0	000 -												
		80.0000	8.0042	1.093		573.1			30.0	000			and a second									
		100.0000	10.0053	1.094		722.6			20.0	000												
									10.0	000												
									0.0	100 📥	and the											
		Slope	0.1386							0.0	10	0.0	200.0	300	0 40	0.00	500.0	600.0	700	0	800.0	
		v-intercept	0.1324							0.0	-	10.0	200.0				200.0	000.0	700.	-	000.0	
		,													wieg @	203 nm						
										_				_						_		
		Co	ntrol Experiment																			
HPLC Type	Sample Time (min)	Concentration (%)	Concentration (pnm)	RT (min)	Area (m	eas. @ 25	3 nm)	C	o = Avg Ctrl Conc. (nnm)													
		01 2010	0.4240	4.004						-				-						-		
U	U	91.2619	9.1310	1.094		057.5		-	9.5583	-				-						-		
C2	10	96.5703	9.6621	1.094		695.8																
C2	20	96 9445	9 6996	1 002		609 5																
	20	50.5445	9.0990	1.095		090.5		-		-				_						-		
C4	30	95.6417	9.5692	1.094		689.1																
C5	40	96.4317	9.6483	1.095		694.8																
C6	50	OF 7803	0 5921	1.004		600.1		-												-		
6	50	95.7803	9.5831	1.094		690.1		_		-				_						_		
C7	60	96.0990	9.6150	1.093		692.4																
		Evneri	mont: 1000:1 (2 of 2)					-		-										-		
		Expen	nent: 1000.1 (2 01 3)											_						-		
			DNAN						Bypro	ducts												
HPLC Type	Sample Time (min)	Concentration (%)	Concentration (ppm)	RT (min)	Area (m	eas. @ 25	3 nm)		RT (min)	Are	a (mea	s.@2	53 nm) M	ass Rat	io (C. n.	(C 0)					
C a (stasting Cana)	Sumple time (timi)	concentration (70)	o scoo		/ucu (iiii	cus. @ 25	5 mm	-		744	u (mee	J. @ 1	55 1111	,	435 1444	0000	c_0)			-		
C_o (starting Conc)	0		9.5583					_		_					1	.0000				_		
	-	70 2422	7 0204	1.005		574 500										0205						
R1	5	/9.3423	7.9384	1.095		571.500									0	.8305						
								-		-										-		
P2	10	75 9012	7 5021	1 005		546 600									0	7044						
112	10	75.0512	7.5551	1.055		540.000									0	./ 544						
R3	15	73.4518	7.3491	1.095		529.000									0	7689				-		
R4	20	72.2598	7.2298	1.094		520.400									0	.7564				-		
										_												
05	25	74 4202	7.4466	1.005												7477						
KS	25	/1.4282	7.1400	1.095		514.400									U	./4//						
								-		-										-		
R6	35	68 8780	6 8915	1 094		496 000									0	7210						
NO	35	00.0700	0.0515	1.054		450.000									0	.7210						
R7	45	67.7553	6.7791	1.094		487.900									0	.7092				-		
P.0		C7 4007	6 7	4.000		405 500									-	705.0						
R8	60	67.4227	6.7458	1.096		485.500									0	.7058						
								-		-										-		
				_																		
		DNAN Degradat	ion: Concentration v	/s. Time							DNA	v Deg	radati	on: N	nass R	atio vs.	fime					
	10	0							1 0000													
	10							-														
									0.9000													
	9	3									.											
									0.8000		•		_									
	. 9	0						-				1						1				
									0.7000							1		1			•	
	8	5							0.0007													
									0.6000													
	Concentration (nom)	0							Mass Ratio													
	concentration (ppm) 8	~							(C_n / C_o)													
									0.4000													
	7	5 T																				
			• 🛓 🗌						0.3000													
	7	0	Ī																			
				T	•		•		0.2000													
	6	5																				
								-	0.1000													
	6	0 5 10 17	20 25 20	35 /0	45	50 57	60		0.0000					0 0	e ~		40	45	50			
		v 5 10 15	zu 25 30	ab 40	45	ou 55	60		0	-	10	, 19	21	v 2	ə 30	35	40	45	50	55	60	
			Time (min)					-							Time (min)						
								-		-										1		
								-		-				-						-		
Quality	y Control Checks: QC 60	%																				
Line	Area	Relative Error (< 10%)																				
٥	428.4	0.7/1/						-		-										1		
9	426.4	0.7414						-		-				-						-		
17	432.4	0.1854																				
27	430.9	0.1622																				















			[
Data File Name	20200806_DNAN_2_J	н		Notes														
DNAN Prepared	8/3/2020		Conducted same day a	is 250:1 #1	L													
DNAN Conc (mg/L or ppm)	10.0040																	
-11	5 400																	
рн	5.188					_						_						
H2O2 Vol (µl)	319																	
CAS weight (g)	0.2501																	
CAS Vol (ul)	100					_						-			-			
CA5 V0I (µI)	100					_						_						
Start Setup	8:50																	
Start Control	9:00																	
Stop Exportment	11:00																	
Stop Experiment	11.00					-												
Ran in HPLC	11:10																	
		0	libration Curve					Calib	pration C	urve: O	oncentr	ation (%) vs. Are	a: 253 r	m			
		e																
		Concentration (%)	Concentration (ppm)	RI (min)	Area (meas. @ 253	nm)		100.000	, <u> </u>									
		0.0000	0.0000	0.000	0.0			90.000								and the second		
		10,0000	1 0004	1 098	72.2			80.000							•			
		10.0000	1.0004	1.050	72.2			70.000						and the second				
		20.0000	2.0008	1.097	141.2			60.000						er.				
		40.0000	4.0016	1.098	301.8		DNAN Concentration	50.000							y = 0.	.1376x - 0.	.0774	
		60.0000	6.0024	1.096	435.8		(%)	40.000				and a state of the				x- = 0.999		
		80,0000	8 0022	1 100	570.0			40.000			Sec. 1							
		80.0000	8.0032	1.100	579.9			30.000	,		and the second							
		100.0000	10.0040	1.100	726.4			20.000	,									
								10.000	D									
		flana	0 1276					0.000) •····									
		Siupe	0.1570						0.0 1	00.0	200.0	300.0	400.0	500.0	600.0	700.0	800	.0
		y-intercept	-0.0774									Area	@ 253 nm					
		Co	ntrol Experiment															
UDICT	Concelle Three (c. 1. 1	Concentration (n)	Concentration (DT (ml.)	A (a Aur Chiller 1					-			+			
HPLC Type	sample Lime (min)	concentration (%)	concentration (ppm)	кı (min)	Area (meas. @ 253	nm) C	_o = Avg ctrl Conc. (opm)										
C1	0	96.8480	9.6887	1.099	704.4		9.7363											
0	10	96.8205	9.6859	1.098	704.2													
<u> </u>	20	07 (122	0.7454	1 100	707.2	-						-						
	20	97.4122	9.7451	1.100	/08.5													
C4	30	96.3527	9.6391	1.099	700.8													
(5	40	98.7469	9.8786	1.098	718.2													
	-10	00.0014	0.0074	1.000	710.2							-						
Lb	50	98.0314	9.8071	1.100	/13.0							_						
C7	60	97.0544	9.7093	1.099	705.9													
		Experi	ment: 250:1 (2 of 3)															
		Experi							d			-						
			DNAN					Bypro	ducts									
HPLC Type	Sample Time (min)	Concentration (%)	Concentration (ppm)	RT (min)	Area (meas. @ 253	nm)	RT (min)		Area (m	eas. @ 2	253 nm)	Mass	Ratio (C	n/Co)				
C o (starting Conc)	0		9 7363	. ,			. ,						1 0000	1 1				
c_o (starting conc)	0		5.7505										1.0000					
R1	5	81.0103	8.1043	1.098	589.300								0.8324					
	-																	
R2	10	76.4832	7.6514	1.099	556.400								0.7859					
02	15	71.0619	7 1000	1.009	E17.000								0 7202					
1.5	15	/1.0018	7.1090	1.090	517.000								0.7502					
R4	20	69.9748	7.0003	1.101	509.100								0.7190					
RS	25	69.0391	6.9067	1.100	502.300								0.7094					
R6	35	67.6218	6.7649	1.100	492.000							_	0.6948					
R7	45	67.2916	6.7318	1.098	489.600								0.6914					
												-						
RR	60	67,2640	6.7291	1.102	489 400								0.6911					
		07.2040	0.7231	4.402	-03.400								0.0011					
		DNAN Degradat	on: Concentration v	s. Time		-			DN.	AN Dee	radatio	n: Mass	Ratio vs.	Time				
										-6								
	1	0.0					1.00	00 🔶										
		•					0.00											
		9.5					0.90	~										
							0.80	00	•									
		9.0								ΤĹ	1							
							0.70	00		- T		•	•		-+-			•
		8.5																
							0.60	00										
	Concontration (n===)						Mass Ratio											
	concentration (ppm)	5.0					(C_n / C_o) 0.50											
							0.40	00										
		7.5					0.40	· · ·										
							0.30	00										
		7.0	+															
			T	•	•	•	0.20	00 - 00										
		6.5																
							0.10	00										
		50					0.00	no 🗀										
		0 5 10 19	20 25 30	35 40	45 50 55	60	0.00	0	5	10 10	20	25	30 25	40	45	50	55	60
			Time (c1-)	0		~				- 15	10	ті	55 a (min)	40		50		50
			time (min)									i im	e (mm)					
								-										
Quality	Control Checks: OC 6	0%																
Quality	Ar	Bolothuo Error / - 4000										-						
Line	Area	Relative Error (< 10%)						_										
9	438.2	0.5507																
17	445.4	2.2028																
	422.5	0 5379										1			+			
21	405.0	0.5278																







Image: control in the second of the	Data File New -	20200012 041441 2	u		N				٦													
Disk Program Disk Program Disk Program Disk Program 1123 Veld 5.22 1023 Veld 6.00 0.00 <td< th=""><th>Data File Name</th><th>20200813_DNAN_2_</th><th>п</th><th></th><th>Notes</th><th></th><th></th><th></th><th>4</th><th></th><th></th><th></th><th></th><th></th><th></th><th></th><th></th><th></th><th></th><th></th><th></th><th></th></td<>	Data File Name	20200813_DNAN_2_	п		Notes				4													
$ \frac{1}{10} (1) (1) (1) (1) (1) (1) (1) (1) (1) (1)$	DNAN Prepared	8/10/2020		Conducted same day	as 250:1 #3	3.									_							
pit 0	DNAN Conc (mg/L or ppm)	10.0147																				
Hit2 Wolf in G See Sing 500 See Sing 500	pH	5.232																				
Oble wately Bar Coale Bar Coale Main Min Object Same Coale Same Coale Same Coale Main Min Object Same Coale Same Coale	H2O2 Vol (µl)	64																				
	CAS weight (g)	0.25																				
Bit Bode Bit Convert 100 Bit Solution 100 Convert 100 Conv	CAS Vol (µl)	100																				
Ban Canadiant Ban Canadiant Concentration (N) C	Start Setup	9:00							-													
Dime beam 1100 Concentration (i) Concentration	Start Control	9:05																				
Basis Brid. 13.00 Image: Brid. Discretion for concentration (b) or concentration (Stop Exportment	11:05													-							
Dame Decide and and a set of a set	Den is UDLC	12:00		-											-							
Image: constraint (n)	Ran In HPLC	12:00																				
Cale Cale <th< th=""><th></th><th></th><th></th><th></th><th></th><th></th><th></th><th></th><th>4</th><th></th><th>Calib</th><th>otion C</th><th></th><th></th><th>rotion</th><th>(0/)</th><th></th><th></th><th></th><th></th><th></th><th></th></th<>									4		Calib	otion C			rotion	(0/)						
			Ca	alibration Curve							Calib	ation C	urve. c	oncent	ration	(70)	vs. Area	1. 200				
$ \begin{array}{ c c c } \hline \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ $			Concentration (%)	Concentration (ppm)	RT (min)	Area (m	eas. @ 2	53 nm)			100.000	0								1.0	•	
$ \begin{array}{ c c c c c } \hline 1 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 &$			0.0000	0.0000	0.000		0.0				90.000	10								and the second		
			10.0000	1.0015	1.096		65.3				80.000	10										
$ \begin{array}{ c c c c c c c c c c c c c c c c c c c$			20.0000	2.0029	1.096		141.6				70.000	10						and the second				
$ \begin{array}{ c c c c c } \hline \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ $			40.0000	4.0059	1.096		288.4		D	NAN Concentratio	60.000	10					1997 C		y = 0.1	359x + 0.	3414	
$ \begin{array}{ c c c c c c c c c c c c c c c c c c c$			60,0000	6.0088	1 094		462.1			(%)	50.000	0				and the second			R	= 0.9985		
$ \begin{array}{ c c c c c c c c c c c c c c c c c c c$			80.0000	0.0000	1.004		F80.0				40.000	0			1997 B							
No. No. <th></th> <th></th> <th>80.0000</th> <th>0.0110</th> <th>1.094</th> <th></th> <th>300.9</th> <th></th> <th></th> <th></th> <th>20.000</th> <th>0</th> <th></th> <th>100</th> <th></th> <th></th> <th></th> <th></th> <th></th> <th></th> <th></th> <th></th>			80.0000	0.0110	1.094		300.9				20.000	0		100								
$ \begin{array}{ c c c c c c c c c c c c c c c c c c c$			100.0000	10.0147	1.095		/25.5				10.000		and the second second									
Image 0.199 <t< th=""><th></th><th></th><th></th><th></th><th></th><th></th><th></th><th></th><th></th><th></th><th>0.000</th><th>in a 1111</th><th></th><th></th><th></th><th></th><th></th><th></th><th></th><th></th><th></th><th></th></t<>											0.000	in a 1111										
Image: contraction (b) Co			Slope	0.1359							0.000	0.0	100.0	200.0	300.0	40	00.0 5	500.0	600.0	700.0	800.	.0
Image: concentration by concentra			y-intercept	0.3414												Area @	253 nm					
INC. Type of the series of the series in																						
Network Sequence (more) Concentration (som Provide (som) Concentration (som) Provide (som) <			Co	ntrol Experiment																		
n 0 0 000000000000000000000000000000000000	HPLC Type	Sample Time (min)	Concentration (%)	Concentration (ppm)	RT (min)	Area (m	eas. @ 2	53 nm)	C o =	= Avg Ctrl Conc.	(ppm)											
C2 10 95.067 95203 1.03 070.6 0 G3 00 95.688 95300 1.03 701.6 0	C1	0	93,0796	9,3216	1.092		682.4	,	1	9,5464												
G D S	(7	10	95,0637	9,5203	1.093		697.0			2.5404												
G SS SS A	(2	20	05 6000	0.5200	1.000		701.6		-													
Col So So So So All S All S C5 60 95/29 95/29 1093 70.5 100<	L3 C4	20	95.0888	9.5830	1.093		701.0		-													
CS 40 96.334 96.73 10.93 705.6 10000	C4	30	95.6481	9.5789	1.093		/01.3		_						_							
C6 50 55.873 9.620 1.092 701.5 901	C5	40	96.2324	9.6374	1.093		705.6															
C7 60 95.07.3 9.38.6 1.94 701.5 Part of the sequence	C6	50	95.8791	9.6020	1.092		703.0															
Image: contraction (b)	C7	60	95.6753	9.5816	1.094		701.5															
Image: Transmitter in the set of the s																						
Image: martine contraction Image: martin Image: martine contraction I			Exper	riment: 50:1 (1 of 3)																		
HPC Type Sample Time (mm) Concentration (m) Generation (m) Generation (m) Masc (mass. @ 23 m) Mass (mass. @ 23 m) Mass (mass. @				DNAN							Byproc	ucts										
C 0 (stating Con) 0	HPLC Type	Sample Time (min)	Concentration (%)	Concentration (ppm)	RT (min)	Area (m	eas @ 2	53 nm)		BT (min)		Area (m	eas.@2	53 nm)	Mas	ss Rati	io (C. n./	(C o)				
C Unitaria (only) C C (only) C (only) <td>C a (starting Cons)</td> <td>o o</td> <td>concentration (70)</td> <td>0 5464</td> <td></td> <td>/ucu (m</td> <td>cus. e 1.</td> <td>55 mm</td> <td></td> <td>,</td> <td></td> <td>74 64 (11</td> <td>cus. e .</td> <td></td> <td></td> <td>1</td> <td>0000</td> <td>0_07</td> <td></td> <td></td> <td></td> <td></td>	C a (starting Cons)	o o	concentration (70)	0 5464		/ucu (m	cus. e 1.	55 mm		,		74 64 (11	cus. e .			1	0000	0_07				
R1 5 8.57817 8.598 1.09 628.700 628.700 6.68.700 6.68.700 6.68.700 6.68.700 6.68.700 6.77.705 6.79.705 7.7950 7.7970 1.092 5.66.700 9.7000 9.7000 9.80470	C_0 (starting conc)	0		9.3404												1	.0000					
R2 10 84.9256 8.500 1.09 622.400 0.800 0.8000 0.8000 R3 15 79.7478 7.985 1.09 59.300 0.99 0.8000 0.8000 R4 20 79.924 7.985 1.09 59.300 0.99 0.8000 0.8306 R5 25 77.785 7.781 1.09 569.500 0.8100 0.8155 0.8157 R6 35 76.703 7.781 1.09 569.500 0.8100 0.8101 0.8100 R7 45 77.827 7.7742 1.09 568.700 0.8144 0.8144 0.8144 0 0.8144 0.91 <	R1	5	85.7817	8.5908	1.093		628.700									0	.8999					
R2 10 84.9256 8.900 1.03 622.400 0.809 0.8090 0.8090 0.8090 R3 15 7.7478 7.385 1.02 584.300 0.8100 0.8366 0.8356 0.8366									_						_							
No.	R2	10	84.9256	8.5050	1.093		622.400									0	8909					
R3 15 79.478 7.965 1.02 58.430 $(1 - 1)^{-1}$ $(1 - 2)^{-1}$ $(1$		10	04.5250	0.5050	1.055		022.400										.0505					
R3 1.5 7.9.878 7.9665 1.02 384.30 0 0.8.800 0 0.8.800 0 R4 20 7.8.9324 7.9048 1.092 578.300 0 0.8.820 0.8.820 0 0.8.820 0 0.8.820 0 0.8.820 0 0.8.820 0 0.8.820 0 0.8.815 0 0.8.815 0 0.8.815 0 0.8.815 0 0.8.815 0 0.8.815 0 0.8.815 0 0.8.815 0 0.8.815 0 0.8.815 0 0.8.815 0 0.8.815 0 0.8.815 0 0.8.814 0 0.8.814 0 0.8.814 0 0.8.814 0 0.8.814 0 0.8.814 0 0.8.814 0 0.8.814 0 0.8.814 0 0.8.814 0 0.8.814 0 0.8.814 0 0.8.814 0 0.8.814 0 0.8.814 0 0.8.914 0 0.8.914 0 0.8.914 0 0.8.914 0 0.8.914 0 0.8.914 0 0.9.916<		45	70 7470	7.0005	1 000		504 200										0200					
R4 20 78.9324 7.908 1.02 578.300 Image: Constraint of the sector of the sec	К3	15	/9./4/8	7.9865	1.092		584.300									U	.8300					
R4 20 78.3324 7.308 1.092 578.300 0 0.6280 R5 25 77.785 7.7851 1.092 569.500 0 0.8155 0.8017 R6 35 76.7036 7.7851 1.092 566.700 0 0.8017 0.8017 R7 45 77.3559 7.7470 1.092 566.700 0 0.8144 R8 60 77.5277 7.7742 1.093 568.700 0 0.8144 0 0.8144 0.8144 0.8144 0.8144 0.8144 0 0.8144 0.914 0.914 0.914 0.914 0 0.914 0.914 0.914 0.914 0.914 0 0.914 0.914 0.914 0.914 0.914 0 0.914 0.914 0.914 0.914 0.914 0 0.914 0.914 0.914 0.914 0.914 0 0.914 0.914 0.914 0.914 0.914 0 0.914 0.914 0.914 0.914 0.914 0 0.914 0.914 0.914 0.914 0.914 0 0.914 0.914																						
R5 25 77.7851 1.02 569.500 Image: Concentration of the concentratin of the concentratin of the concentratin of th	R4	20	78.9324	7.9048	1.092		578.300									0	.8280					
R5 25 77.785 7.785 1.02 569.500 0 0 0.8155 0 R6 35 76.7036 7.6816 1.02 561.500 0 0 0.8047 0 R7 45 77.3559 7.7470 1.02 566.700 1 0 0.8115 0 R8 60 77.6277 7.7742 1.03 568.700 1 0 0.8114 0 NAN Degradulor: Concentration (pen) 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0																						
R6 35 76.7036 7.6816 1.092 561.900 0.8047 0.8047 R7 45 77.3559 7.7470 1.092 566.700 0.8144 0.8144 R8 60 77.6277 7.7470 1.093 566.700 0.8144 0.8144 DNAN Degradation: Concentration vs. Time 0.8144 0.8144 0.8144 0.8144 0.0007 0.914 0.914 0.914 0.914 0.914 0.914 0.0007 0.914 0.914 0.914 0.914 0.914 0.914 0.914 0.0007 0.914 <td>R5</td> <td>25</td> <td>77.7365</td> <td>7.7851</td> <td>1.092</td> <td></td> <td>569.500</td> <td></td> <td></td> <td></td> <td></td> <td></td> <td></td> <td></td> <td></td> <td>0</td> <td>.8155</td> <td></td> <td></td> <td></td> <td></td> <td></td>	R5	25	77.7365	7.7851	1.092		569.500									0	.8155					
R6 35 76.703 7.6816 1.092 561.900 $$ 0.8047 $$ R7 45 77.3559 7.7470 1.093 566.700 $$ 0.8115 $$ R8 60 77.6277 7.7742 1.093 566.700 $$ 0.8144 $$ 0.8144 $$ R8 60 77.6277 7.7742 1.093 566.700 $$																						
R7 45 77.3559 7.7470 1092 566.700 Image: Concentration of the	R6	35	76.7036	7.6816	1.092		561.900									0	.8047					
R7 45 77.3559 7.7470 1.09 566.700 Image: Consent and on general sectors of the consent an																						
In <	R7	45	77 3559	7 7470	1.092		566 700									0	8115					
R8 60 77.6277 7.7742 1.09 568.700 <	10	45	77.5555	7.7470	1.052		500.700										.0115					
NS 60 77.0271 77.742 1093 308.700 700 700 700 DNAN Degradation: Concentration vs. Time Image: Concentration ppm Image: Conc	50	c0	77 (277	7 7740	1 000		F CO 700															
Image: concentration (p) Point (p)	KS	60	//.02//	1.1142	1.093		568.700									U	.8144					
DNAN Degradation: Concentration vs. Time DNAN Degradation: Concentration vs. Time DNAN Degradation: Mass Ratio vs. Time 0																						
DNAN Degradation: Concentration vs. Time DNAN Degradation: Mass Ratio vs. Time 0000 <th></th> <th></th> <th></th> <th></th> <th></th> <th></th> <th></th> <th></th> <th>-</th> <th></th>									-													
100 1			DNAN Degradat	ion: Concentration	/s. Time							DN.	AN Deg	radatio	on: Ma	ass Ra	atio vs.	Time				
Generation (p) 0		1	0.0							1												
0 0										-		1										
Quality Control Checks: QC 500- Relative Error (< 10%) Image: Control Checks: QC 10%			9.5 •							- 0.	9000	•	•									
Answer									-	- 0.	8000		-	•	•		+					•
Another interview Anoother interview Another interview A			9.0																			
concentration (ppm) a										- 0.	/000											
Concentration (pm) 0			8.5							. 0.	6000 -											
concentration (gpm) 23 73 1										Mass Ratio												
A A <td></td> <td>Concentration (ppm)</td> <td>8.U •</td> <td>• 1 </td> <td></td> <td></td> <td></td> <td></td> <td></td> <td>(C_n / C_o) 0.</td> <td>5000</td> <td></td>		Concentration (ppm)	8.U •	• 1						(C_n / C_o) 0.	5000											
1 1			7.6	T I	•			1		0.	4000 -											
1 1 <td></td> <td></td> <td>1.5</td> <td></td>			1.5																			
6.5 0 5 10 15 20 25 30 35 40 45 50 55 10 15 20 25 30 35 40 45 50 55 10 15 20 25 30 35 40 45 50 55 10 15 20 25 30 35 40 45 50 55 10 15 20 25 30 35 40 45 50 55 10 15 20 25 30 35 40 45 50 55 10 15 20 25 30 35 40 45 50 55 10 15 20 25 30 35 40 45 50 55 10 15 20 25 30 35 40 45 50 55 10 15 20 25 30 35 40 45 50 55 10 15 20 25 30 35 40 45 50			7.0							0.	3000											
a a <td></td> <td></td> <td>1.0</td> <td></td> <td></td> <td></td> <td></td> <td></td> <td></td> <td>0.</td> <td>2000</td> <td></td>			1.0							0.	2000											
0 0 <td></td> <td></td> <td>6.5</td> <td></td> <td></td> <td></td> <td></td> <td></td> <td></td> <td>1</td> <td></td>			6.5							1												
Action Action<										. 0.	1000											
0 5 10 15 20 25 30 35 40 45 50 55 00 15 20 25 30 35 40 45 50 55 00 15 20 25 30 35 40 45 50 55 00 16 15 20 25 30 35 40 45 50 55 00 16 <td< td=""><td></td><td></td><td>6.0</td><td></td><td></td><td></td><td></td><td></td><td></td><td>0.</td><td>0000 -</td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td></td<>			6.0							0.	0000 -											
Image: Description of the descriptic description of the description of the descriptio			0 5 10 15	20 25 30	35 40	45	50 55	60			0	5	10 1	5 20	25	30	35	40	45	50	55	60
Quality Control Checks: QC 60% Image: Control Checks: QC 60% I				Time (min)												Time (min)					
Quality Control Checks: QC 60//- Area Relative Error (< 10%) Area Relative Error (< 10%) Area Relative Error (< 10%) Area Area Relative Error (< 10%) Area			1	1																		
Quality Control Checks: QC 60% Part of the																						
Quality Control Checks: QC 60% 6 7 7 7 7 7 0.2164 0.2164 0																						
Line Area Relative Fron (< 10%) 9 457.2 1.0604 17 463.1 0.2164	Qualit	y Control Checks: QC 6	0%																			
9 457.2 1.0604 17 463.1 0.2164	Line	Area	Relative Error (< 10%)																			
17 463.1 0.2164	9	457.2	1.0604																			
	17	463.1	0.2164																			
27 465.9 0.9007	27	465.9	0.2104						-													



Data fills Mar	20200020 20000							1													
Data File Name	20200820_DNAN_1_J	н		Notes										_							
DNAN Prepared	8/17/2020		Conducted same day a	as 50:1 #3.																	
DNAN Conc (mg/L or ppm)	10.0027																				
pH	5,197																				
H2O2 Vel (ul)	64													_							
Η202 V0I (μΙ)	64													_							
CAS weight (g)	0.2502													_							
CAS Vol (µI)	100																				
Start Setup	5:15																				
Start Control	7:05		1																		
	0.05													-					-		
Stop Experiment	9:05													_							
Ran in HPLC	9:10																				
		Ci	alibration Curve							Calib	ration C	urve: C	oncen	tratio	י (%) חי	vs. Area	ı: 253 r	nm			
		Concentration (%)	Concentration (nnm)	RT (min)	Area (m	eas @ 21	53 nm)			100.00	0										
		0.0000	0.0000	0.000	/ucu (iii	0.0	<i>55</i> mm	+		00.00	0										
		0.0000	0.0000	0.000		0.0				90.00	0							a constant			
		10.0000	1.0003	1.099		72.8				20.00	0										
		20.0000	2.0005	1.099		139.2				70.00						and the	- T				
		40.0000	4.0011	1.097		288.3		D	NAN Concentratio	in 50.00	0					1		y = 0.1	37x + 0.2	536	
		60.0000	6.0016	1.101		437.9			(%)	40.00	0				and the second second			R	= 0.9998		
		00.0000	0.0010	4.000		500.0		+		40.00	0										
		80.0000	8.0022	1.099		588.0		-		30.00	0		and the second								
		100.0000	10.0027	1.100		723.9				20.00	00										
										10.00		•									
		Slope	0.1370							0.00	00	400.0	200.0	200				coo o	700.0		
		wintercent	0.2536					ti -			0.0	100.0	200.0	300	.0 40	00.0 5	00.0	0.000	/00.0	ະບບ.0	
		, mercept	0.2000					H							Area @	9 253 nm					
														_							
		Co	ntrol Experiment											_							
HPLC Type	Sample Time (min)	Concentration (%)	Concentration (ppm)	RT (min)	Area (me	eas. @ 25	53 nm)	C_0 =	= Avg Ctrl Conc	. (ppm)											
C1	0	92.5779	9.2603	1.101		673.9		_	9.5551												
	10	95 5097	9 5535	1 099		695.3			*					-							
C2	10	55.3057	0.0000	1.099		333.3		-						-					-		
63	20	96.4002	9.6426	1.100		/01.8								_							
C4	30	96.7701	9.6796	1.100		704.5															
C5	40	96.2221	9.6248	1.099		700.5															
C6	50	95,2905	9.5316	1.098		693.7															
67	50	05.0070	0.5020	4.404		000.0		-						-					-		
۲,	60	95.9070	9.5933	1.101		698.2								_							
														_							
		Exper	iment: 50:1 (2 of 3)																		
			DNAN							Byproc	lucts										
HPLC Type	Sample Time (min)	Concentration (%)	Concentration (ppm)	RT (min)	Area (me	eas. @ 25	53 nm)		RT (min)		Area (m	eas. @	253 nm) M	ass Rat	io (Cn/	C 0)				
C. o (starting Cons)	0		0 5551				,		,					,	1	0000	/				
C_0 (starting conc)	U		9.5551											_		.0000					
R1	5	86.7965	8.6820	1.098	6	631.700									0	.9086					
	40	02 4442	0.2124	1 000												0700					
RZ	10	83.1112	8.3134	1.099		604.800									0	1.8700					
R3	15	81.1247	8.1147	1.099	5	590.300									0	.8492					
														_							
P4	20	70 6962	7 9709	1 100		570 900									0	9242					
144	20	75.0002	7.5700	1.100		575.000									0	.0342					
R5	25	78.8642	7.8885	1.098	-	573.800									0	.8256					
														-							
R6	35	78.4258	7.8447	1.098	5	570.600									0	.8210					
														_							
87	45	70 41 21	7 0422	1 000		570 500										0000					
K7	45	70.4121	/.0455	1.099	-	570.500									0	1.6209					
R8	60	77.4805	7.7501	1.102	5	563.700									0	0.8111					
								-						_							
		DNAN Dogradati	ion: Concontration	r Timo							DN		radat	ion: N	Abec P	atio vr	Timo				
		Dishis Degradat	Sin concentration v								DI	, an Def	, audt	N	.a	000 45.	and				
	1	0.0							1	.0000 🔶											
										9000											
		9.5							1			•									
									0.	.8000 -			-	- 1	•	•		•			۰.
		9.0																			
		•							0.	7000											
		8.5								.6000											
									Marc Pati-												
	Concentration (ppm)	8.0	+						(C n / C n)	.5000 -											
			T I	T	- T		•		(C_11/C_0)	1000											
		7.5																			
									0.	3000											
		7.0																			
									0.	2000											
		6.5								1000											
									1												
		6.0							0.	.0000 -											
		0 5 10 15	20 25 30	35 40	45 5	50 55	60			0	5	10	15 2	0 2	15 30	0 35	40	45	50	55 f	60
			Time (min)												Time ((min)					
Quality	Control Checks: OC 6	0%												-							
quality	, control criecks. QU b	Deletion Fr. 1 - FC17						-						-					-		
Line	Area	Relative Error (< 10%)												_							
9	429.9	1.8269						_													
17	425.0	2.9459																			
27	439.3	0.3197																			



Data Filo Namo	20200920 08448 2 1	ш		Notos			٦													
Data File Name	20200820_DINAIN_2_J	in .		Notes	-		-						-							
DNAN Prepared	8/1//2020		Conducted same day a	as 50:1 #2.	. в															
DNAN Conc (mg/L or ppm)	10.0013												_							
рН	5.232												_							
H2O2 Vol (µl)	64																			
CAS weight (g)	0.2502																			
CAS Vol (µl)	100																			
Start Setup	9:10																			
Start Control	9:15																			
Stop Experiment	11:15																			
Ran in HPI C	11:20						-		_								-			
Kaninini Eo	11.20						_		_											
			liberation Come				4		alihra	tion Cu	rve. C	oncent	ration	(%)	vs Area	a. 253	nm			
		G	alibration Curve						Janbie	nion cu	iive. e	oncem	ation	(70) (v3. AIC	1. 200				
		Concentration (%)	Concentration (ppm)	RT (min)	Area (meas.	. @ 253 nm	<u> </u>		100.0000											
		0.0000	0.0000	0.000	0.	.0			90.0000	-							and the			
		10.0000	1.0001	1.1	72	2.1			80.0000											
		20.0000	2.0003	1.099	14	2.9			70.0000						-	1997				
		40.0000	4.0005	1.101	28	3.8	DN	AN Concentration	50.0000						1		y = 0.1	375x + 0.2	2763	
		60.0000	6.0008	1.1	43	1.5		(%)	40.0000					1997 - C			R	= 0.9998		
		80.0000	8.0010	1.099	58	7.0			30.0000											
		100.0000	10.0013	1.098	72	2.9			20.0000			and the second second								
		100.0000	10.0015	1.050	12.	2.5			10.0000		an and a second									
									0.0000	and the second						_				
		Siope	0.1375				+			0.0	100.0	200.0	300.0	40	0.0	\$00.0	600.0	700.0	800.0)
		y-intercept	0.2763				-11							Area @	253 nm					
		Co	ntrol Experiment																	
HPLC Type	Sample Time (min)	Concentration (%)	Concentration (ppm)	RT (min)	Area (meas.	@ 253 nm	C_0 = 4	Avg Ctrl Conc. (p	pm)											
C1	0	94.7663	9.4779	1.098	68	7.2		9.6456												
C2	10	96.3751	9.6388	1.098	69	8.9														
63	20	96 6638	9.6676	1.098	70	1.0			-								-			
C4	20	07.0499	9 7061	1.053	70	2.9	-		-				-				-			
64	50	97.0400	9.7001	1.097	70.	5.0 0.0							-							
6	40	96.5263	9.6539	1.097	70	0.0														
C6	50	96.8701	9.6883	1.097	70.	2.5							_							
C7	60	96.8563	9.6869	1.098	70	2.4														
		Exper	riment: 50:1 (3 of 3)																	
			DNAN					В	yprodu	cts										
HPLC Type	Sample Time (min)	Concentration (%)	Concentration (ppm)	RT (min)	Area (meas.	@ 253 nm		RT (min)		Area (me	as. @	253 nm)	Ma	ss Rati	io (Cn/	/C o)				
C o (starting Conc)	0		9.6456	. ,				. ,						1	0000					
e_o (starting conc)			5.0450						-											
R1	5	86.9426	8.6954	1.100	630	.300								0	.9015					
													-							
R2	10	83.4776	8.3488	1.101	605	.100								0	.8656					
							_						_							
83	15	81 81 38	8 1824	1 100	593	000								0	8483					
10	15	01.0150	0.1024	1.100	555	.000									.0105					
P.4	20	70 6651	7 9675	1 009	570	100								0	0157					
N4	20	78.0051	7.0075	1.096	570.	.100								0.	.0137					
R5	25	/8.8301	7.8840	1.103	5/1	.300								0.	.81/4					
R6	35	77.8263	7.7836	1.100	564	.000								0	.8070					
R7	45	77.9088	7.7919	1.098	564	.600								0	.8078					
													-							
R8	60	77.4413	7.7451	1.099	561	.200								0	.8030					
							_		_											
		DNAN Dogradat	ion: Concentration	is Time						DNA		radati	- h.A.	acc D	atio vr	Time				
		DIAMA DEGLAGAT	ion. concentration \	.s. iiiie						UNA	"A D68	audtli	JII. IVI	100 100	uciu VS.	unite				
	1	10.0						1.00	0											
								0.90	0											
		9.5							.		• •									1
		90						0.80	10			1	1		•		-			•
		5.0						0 701	0											
		85																		
		•						0.60	10 - 01											
	Concentration (ppm)	8.0						Mass Ratio 0.50	0											
			• •	•	•	•		(C_n / C_o)												
		7.5						0.401	10											
								0.30	10											
		7.0																		
								0.201	10											
		6.5						0.10	0											
		0 5 10 15	20 25 20	25 40	45 50	55 60		0.001	0	c -	10 1	5 20	25	ar	1 25	40	45	50	55	60
		5 3 10 15	- 10 23 30 Time/!-!		40 OC	33 60			0	э.		., 20	25	JU Time '	, 35 min)	чU	43	30	33	
			time (min)											mie (
							1		I.											
							-		-				-							
Q Pr	Control Charles CCC	£0%					-						-							
Quality	Control Checks: QC 6	Delethus Ferrar (+ 1000)							-				-				-			
Line	Area	nelative Error (< 10%)											-							
9	431.6	0.0232											-							
17	421.2	2.3870																		





Appendix C: AOP ANOVA, t-Test, and Regression Analysis

This treatment was for five levels, 1-5. Non-linear scaling.

- 1: 50
- 2: 100
- 3: 250
- 4: 500
- 5: 1000







Trial	Ratio	k_s (Y)	Treatment			
1	100	0.023	2			
2	100	0.02	2			
3	100	0.02	2			
4	500	0.029	4			
5	500	0.029	4			
6	500	0.028	4			
7	1000	0.026	5			
8	1000	0.026	5			
9	1000	0.038	5			
10	250	0.027	3			
11	250	0.029	3			
12	250	0.025	3			
13	50	0.015	1			
14	50	0.015	1			
15	50	0.016	1			
Ratio	Treatment	Mean	Stdev	tvalue	family alpha	0.05
100	1	0.0210	0.0017	5.597568367	comparison alpha	0.005
500	2	0.0287	0.0006			
1000	3	0.0300	0.0069			
250	4	0.0270	0.0020			
50	5	0.0153	0.0006			
Comparison	Margin of error	LB	UB	Significant		
50 - 100	0.0051	-0.0108	-0.0006	Y		
50 - 250	0.0058	-0.0175	-0.0058	Y		
50 - 500	0.0023	-0.0156	-0.0110	Y		
50 - 1000	0.0195	-0.0341	0.0048	Ν		
100 - 250	0.0074	-0.0134	0.0014	Ν		
100 - 500	0.0051	-0.0128	-0.0026	Y		
100 - 1000	0.0200	-0.0290	0.0110	Ν		
250 - 500	0.0058	-0.0075	0.0042	Ν		
250 - 1000	0.0202	-0.0232	0.0172	N		
F00 4000	0.0405	0 0000	0.04.04	NI		



H2O2:DNAN	(H2O2:DNAN) ²	k _s (min ⁻¹)						
0	0	0						
50	2500	0.015						
50	2500	0.015						
50	2500	0.016						
100	10000	0.023						
100	10000	0.02						
100	10000	0.02						
250	62500	0.027						
250	62500	0.029						
250	62500	0.025						
500	250000	0.029						
500	250000	0.029						
500	250000	0.028						
1000	1000000	0.026						
1000	1000000	0.026						
1000	1000000	0.038						
SUMMARY OU	JTPUT: LINEAR							
Regre	ssion Statistics							
Multiple R	0.833230718							
R Square	0.69427343							
Adjusted R Sq	0.62/606/63							
Standard Erro	0.013909126							
Observations	16							
ANOVA	df	CC	MC	5	Cignificanco F			
Pogrossion	uj	33	0.006500042	F	4 22000E 0E			
Regression	10	0.000390043	0.000390043	34.00344900	4.32009L-03			
Total	15	0.002901937	0.000193404					
Total	10	0.003452						
	Coefficients	Standard Error	t Stat	P-value	Lower 95%	Upper 95%	Lower 95.0%	Upper 95.0%
Intercept	0	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A
H2O2:DNAN	4.0717E-05	6.9764E-06	5.836390071	3.2751E-05	2.58471E-05	5.55868E-05	2.58471E-05	5.55868E-05
RESIDUAL OU	TPUT							
Observation	Predicted ks (min-1)	Residuals						
1	0	0						
2	0.002035849	0.012964151						
3	0.002035849	0.012964151						
4	0.002035849	0.013964151						
5	0.004071698	0.018928302						
6	0.004071698	0.015928302						
/	0.004071698	0.015928302						
8	0.010179245	0.010820755						
9	0.010179245	0.018820755						
10	0.0101/9245	0.014820755						
11	0.020336491	0.008641509						
12	0.020556491	0.006041509						
13	0.020336491	-0.014716081						
14	0.040716091	-0.014716021						
15	0.040710901	-0.014/10301						
16	0.040716981	-0 002716921						



SUMMARY OU	UTPUT: QUADRATIC FO	RCED THROUGH INTERC	EPT					
Regre	ession Statistics							
Multiple R	0.950181394							
R Square	0.902844681							
Adjusted R Sq	0.824476444							
Standard Erro	0.008116114							
Observations	16							
ANOVA								
	df	SS	MS	F	Significance F			
Regression	2	0.008569802	0.004284901	65.0495805	1.6943E-07			
Residual	14	0.000922198	6.58713E-05					
Total	16	0.009492						
	Coefficients	Standard Error	t Stat	P-value	Lower 95%	Upper 95%	Lower 95.0%	Upper 95.0%
Intercept	0	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A
H2O2:DNAN	0.000117706	1.46215E-05	8.050213817	1.27316E-06	8.63462E-05	0.000149066	8.63462E-05	0.000149066
(H2O2:DNAN)	-8.9346E-08	1.62974E-08	-5.482238799	8.07563E-05	-1.243E-07	-5.43916E-08	-1.243E-07	-5.43916E-08
RESIDUAL OU	TPUT							
<u> </u>								
Observation	Predicted ks (min-1)	Residuals						
1	0	0						
2	0.005661947	0.009338053						
3	0.005661947	0.009338053						
4	0.005661947	0.010338053						
5	0.010877164	0.012122836						
6	0.010877164	0.009122836						
7	0.010877164	0.009122836						
8	0.023842435	0.003157565						
9	0.023842435	0.005157565						
10	0.023842435	0.001157565						
11	0.036516625	-0.007516625						
12	0.036516625	-0.007516625						
13	0.036516625	-0.008516625						
14	0.028360265	-0.002360265						
15	0.028360265	-0.002360265						
16	0.028360265	0.009639735						
SUIVIIVIART								
Deare	anian Chatistics							
Regre								
R Square	0.057074088							
Adjusted P So	0.55805244							
Standard Erro	0.005068939							
Observations	16							
Observations	10							
ANOVA	df	22	MS	E	Significance E			
Pegression	uj 2	0.000785726	0.000303863	T 15 28008015	0 000284828			
Regidual	12	0.000783720	2 56941E-05	13.28558515	0.000384828			
Total	15	0.000334024	2.505411-05					
	15	0.001113/3						
	Coefficients	Standard Error	t Stat	P-value	Lower 95%	Unner 95%	Lower 95.0%	Unner 95.0%
Intercept	0.011710863	0.00244767	4,784494521	0.000356625	0.006422994	0.016998737	0.006422994	0.016998732
H2O2:DNAN	6.28003E-05	1.46658E-05	4.282096484	0.000892405	3.11168E-05	9.44839E-05	3.11168E-05	9.44839E-05
(H2O2:DNAN)	-4.51159E-08	1.375E-08	-3.281153575	0.005959972	-7.4821E-08	-1.54108E-08	-7.4821E-08	-1.54108E-08
RESIDUAL OU	TPUT							
Observation	Predicted ks (min-1)	Residuals						
1	0.011710863	-0.011710863						
2	0.01473809	0.00026191						
3	0.01473809	0.00026191						
4	0.01473809	0.00126191						
5	0.017539738	0.005460262						
6	0.017539738	0.002460262						
7	0.017539738	0.002460262						
8	0.024591203	0.002408797						
9	0.024591203	0.004408797						
10	0.024591203	0.000408797						
11								
	0.031832055	-0.002832055						
12	0.031832055 0.031832055	-0.002832055 -0.002832055						
12	0.031832055 0.031832055 0.031832055	-0.002832055 -0.002832055 -0.003832055						
11 12 13 14	0.031832055 0.031832055 0.031832055 0.029395293	-0.002832055 -0.002832055 -0.003832055 -0.003395293						
11 12 13 14 15	0.031832055 0.031832055 0.031832055 0.029395293 0.029395293	-0.002832055 -0.002832055 -0.003832055 -0.003395293 -0.003395293						



Appendix D: MATLAB Code

%DNAN Code
%June, 2020
%Author: W. Harper & J. Hart
%Project: UV LED Project (sponsored by AFCEC/DERA)
%This program is used to model DNAN removal in a UV LED reactor

%the clock is here to help determine the runtime. It does not affect the process simulation tstart = clock;

%global declarations - the purpose of these declarations is to make these parameter values %available to light3.

%global declarations

global rateconstant reactorvolume flow xo Cinit global realdata11 realdata12 realdata13 realdata14 realdata15 realdata16 realdata17 realdata18 realdata19 realdata110 realdata111 realdata112 realdata113 realdata114 realdata115 realdata21 realdata22 realdata23 realdata24 realdata25 realdata26 realdata27 realdata28 realdata29 realdata210 realdata211 realdata212 realdata213 realdata214 realdata215

%The parameters in the matrix are respectively: %effluent concentration of DNAN (1)

%the units of the rateconstant are inverse time (1/min)

%the units of volume are ml reactorvolume = 35;

%the units of flow are ml/minutes flow = 2.0;

tau = reactorvolume./flow;

%parameters needed for simulation alpha = 0.001; beta = 0.001; gamma = 0.05;

%additional matrices needed for data processing nnn = 100000; ZZZ1 = zeros(7,nnn); BEST = zeros(6,1); BEST1 = zeros(1,1); ZZZ2 = zeros(7,nnn); BEST2 = zeros(1,1); ZZZ3 = zeros(1,1); ZZZ4 = zeros(1,1); ZZZ4 = zeros(1,1); ZZZ5 = zeros(1,1); ZZZ5 = zeros(7,nnn);



BEST5 = zeros(1,1);
ZZZ6 = zeros(7,nnn);
BEST6 = zeros(1,1);
ZZZ7 = zeros(7,nnn);
BEST7 = zeros(1,1);
ZZZ8 = zeros(7,nnn);
BEST8 = zeros(1,1);
ZZZ9 = zeros(7,nnn);
BEST9 = zeros(1,1);
ZZZ10 = zeros(7,nnn);
BEST10 = zeros(1,1);
ZZZ11 = zeros(7,nnn);
BEST11 = zeros(1,1);
ZZZ12 = zeros(7,nnn);
BEST12 = zeros(1,1);
ZZZ13 = zeros(7,nnn);
BEST13 = zeros(1,1);
ZZZ14 = zeros(7,nnn);
BEST14 = zeros(1,1);
ZZZ15 = zeros(7,nnn);
BEST15 = zeros(1,1);

%the following are process parameters to = 0; %the units are minutes tf = 60;

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%aaa is needed to determine the best parameter combination aaa1 = 1000000000; aaa2 = aaa1;aaa3 = aaa1;aaa4 = aaa1;aaa5 = aaa1; aaa6 = aaa1;aaa7 = aaa1;aaa8 = aaa1; aaa9 = aaa1;aaa10 = aaa1;aaa11 = aaa1; aaa12 = aaa1;aaa13 = aaa1;aaa14 = aaa1; aaa15 = aaa1;

%this is a counter counttt = 1;

%the simulation logic begins here



%This is for the first experimental data set: 100:1 #1 for rateconstant = alpha:beta:gamma % %Initial Conditions Matrix xo = Cinit(1,1);%Solve the differential equations [t,x] = ode45('light3',realdata11,xo,[],tau); $MMM1 = abs((realdata21 - x(:,1)./Cinit(1,1))).^2;$ ttt1 = cumsum(MMM1); bbb1 = ttt1(end)./size(realdata21,1); $rrr1 = ((bbb1)^{(0.5)})./max(realdata21);$ ZZZ1(1,counttt) = rrr1; ZZZ1(2,counttt) = rateconstant; if ZZZ1(1,counttt) < aaa1 aaa1 = ZZZ1(1,counttt); BEST(1,1) = rateconstant; zipa = x(:,1)./Cinit(1,1); zipat = t; end counttt = counttt + 1; end

%

counttt = 1;

ttt2 = cumsum(MMM2); bbb2 = ttt2(end)./size(realdata22,1); rrr2 = ((bbb2)^(0.5))./max(realdata22);

ZZZ2(1,counttt) = rrr2; ZZZ2(2,counttt) = rateconstant;

```
if ZZZ2(1,counttt) < aaa2
aaa2 = ZZZ2(1,counttt);
BEST(2,1) = rateconstant;
zipb = x(:,1)./Cinit(2,1);
zipbt = t;
```



```
end
counttt = counttt + 1;
end
counttt = 1;
%This is for the third experimental data set: 100:1 #3
for rateconstant = alpha:beta:gamma
%
%Initial Conditions Matrix
xo = Cinit(3,1);
%Solve the differential equations
[t,x] = ode45('light3',realdata13,xo,[],tau);
MMM3 = abs((realdata23 - x(:,1)./Cinit(3,1))).^2;
ttt3 = cumsum(MMM3);
bbb3 = ttt3(end)./size(realdata23,1);
rrr3 = ((bbb3)^(0.5))./max(realdata23);
ZZZ3(1,counttt) = rrr3;
ZZZ3(2,counttt) = rateconstant;
if ZZZ3(1,counttt) < aaa3
  aaa3 = ZZZ3(1,counttt);
  BEST(3,1) = rateconstant;
  zipc = x(:,1)./Cinit(3,1);
  zipct = t;
end
counttt = counttt + 1;
end
counttt = 1;
%This is for the fourth experimental data set: 500:1 #1
for rateconstant = alpha:beta:gamma
%
%Initial Conditions Matrix
xo = Cinit(4,1);
%Solve the differential equations
[t,x] = ode45('light3',realdata14,xo,[],tau);
MMM4 = abs((realdata24 - x(:,1)./Cinit(4,1))).^2;
ttt4 = cumsum(MMM4);
bbb4 = ttt4(end)./size(realdata24,1);
rrr4 = ((bbb4)^(0.5))./max(realdata24);
ZZZ4(1,counttt) = rrr4;
ZZZ4(2,counttt) = rateconstant;
```

```
if ZZZ4(1,counttt) < aaa4
    aaa4 = ZZZ4(1,counttt);</pre>
```



```
BEST(4,1) = rateconstant;
  zipd = x(:,1)./Cinit(4,1);
  zipdt = t;
end
counttt = counttt + 1;
end
counttt = 1;
%This is for the fifth experimental data set: 500:1 #2
for rateconstant = alpha:beta:gamma
%
%Initial Conditions Matrix
xo = Cinit(5,1);
%Solve the differential equations
[t,x] = ode45('light3',realdata15,xo,[],tau);
MMM5 = abs((realdata25 - x(:,1)./Cinit(5,1))).^2;
ttt5 = cumsum(MMM5);
bbb5 = ttt5(end)./size(realdata25,1);
rrr5 = ((bbb5)^(0.5))./max(realdata25);
ZZZ5(1,counttt) = rrr5;
ZZZ5(2,counttt) = rateconstant;
if ZZZ5(1,counttt) < aaa5
  aaa5 = ZZZ5(1,counttt);
  BEST(5,1) = rateconstant;
  zipe = x(:,1)./Cinit(5,1);
  zipet = t;
end
counttt = counttt + 1;
end
counttt = 1;
%This is for the sixth experimental data set: 500:1 #3
for rateconstant = alpha:beta:gamma
%
%Initial Conditions Matrix
xo = Cinit(6,1);
%Solve the differential equations
[t,x] = ode45('light3',realdata16,xo,[],tau);
MMM6 = abs((realdata26 - x(:,1)./Cinit(6,1))).^2;
ttt6 = cumsum(MMM6);
bbb6 = ttt6(end)./size(realdata26,1);
rrr6 = ((bbb6)^(0.5))./max(realdata26);
```

ZZZ6(1,counttt) = rrr6;



```
ZZZ6(2,counttt) = rateconstant;
if ZZZ6(1,counttt) < aaa6
  aaa6 = ZZZ6(1,counttt);
  BEST(6,1) = rateconstant;
  zipf = x(:,1)./Cinit(6,1);
  zipft = t;
end
counttt = counttt + 1;
end
%This is for the seventh experimental data set: 1000:1 #1
for rateconstant = alpha:beta:gamma
%
%Initial Conditions Matrix
xo = Cinit(7,1);
%Solve the differential equations
[t,x] = ode45('light3',realdata17,xo,[],tau);
MMM7 = abs((realdata27 - x(:,1)./Cinit(7,1))).^2;
ttt7 = cumsum(MMM7);
bbb7 = ttt7(end)./size(realdata27,1);
rrr7 = ((bbb7)^(0.5))./max(realdata27);
ZZZ7(1,counttt) = rrr7;
ZZZ7(2,counttt) = rateconstant;
if ZZZ7(1,counttt) < aaa7
  aaa7 = ZZZ7(1,counttt);
  BEST(7,1) = rateconstant;
  zipg = x(:,1)./Cinit(7,1);
  zipgt = t;
end
counttt = counttt + 1;
end
%This is for the eigth experimental data set: 1000:1 #2
for rateconstant = alpha:beta:gamma
%
%Initial Conditions Matrix
xo = Cinit(8,1);
%Solve the differential equations
[t,x] = ode45('light3',realdata18,xo,[],tau);
MMM8 = abs((realdata28 - x(:,1)./Cinit(8,1))).^2;
ttt8 = cumsum(MMM8);
bbb8 = ttt8(end)./size(realdata28,1);
```

ZZZ8(1,counttt) = rrr8; ZZZ8(2,counttt) = rateconstant;

rrr8 = ((bbb8)^(0.5))./max(realdata28);



```
if ZZZ8(1,counttt) < aaa8
  aaa8 = ZZZ8(1,counttt);
  BEST(8,1) = rateconstant;
  ziph = x(:,1)./Cinit(8,1);
  zipht = t;
end
counttt = counttt + 1;
end
```

%This is for the ninth experimental data set: 1000:1 #3 for rateconstant = alpha:beta:gamma %________%Initial Conditions Matrix xo = Cinit(9,1);

%Solve the differential equations [t,x] = ode45('light3',realdata19,xo,[],tau);

```
MMM9 = abs((realdata29 - x(:,1)./Cinit(9,1))).^2;
ttt9 = cumsum(MMM9);
bbb9 = ttt9(end)./size(realdata29,1);
rrr9 = ((bbb9)^(0.5))./max(realdata29);
```

```
ZZZ9(1,counttt) = rrr9;
ZZZ9(2,counttt) = rateconstant;
```

```
if ZZZ9(1,counttt) < aaa9
  aaa9 = ZZZ9(1,counttt);
  BEST(9,1) = rateconstant;
  zipi = x(:,1)./Cinit(9,1);
  zipit = t;
end
counttt = counttt + 1;
end
```

%This is for the tenth experimental data set: 250:1 #1

```
for rateconstant = alpha:beta:gamma
%__________%Initial Conditions Matrix
```

xo = Cinit(10,1); %Solve the differential equations [t,x] = ode45('light3',realdata110,xo,[],tau);

```
MMM10 = abs((realdata210 - x(:,1)./Cinit(10,1))).^2;
ttt10 = cumsum(MMM10);
bbb10 = ttt10(end)./size(realdata210,1);
rrr10 = ((bbb10)^(0.5))./max(realdata210);
```

```
ZZZ10(1,counttt) = rrr10;
ZZZ10(2,counttt) = rateconstant;
```



```
if ZZZ10(1,counttt) < aaa10
  aaa10 = ZZZ10(1,counttt);
  BEST(10,1) = rateconstant;
  zipj = x(:,1)./Cinit(10,1);
  zipjt = t;
end
counttt = counttt + 1;
end
%This is for the eleventh experimental data set: 250:1 #2
for rateconstant = alpha:beta:gamma
%
%Initial Conditions Matrix
xo = Cinit(11,1);
%Solve the differential equations
[t,x] = ode45('light3',realdata111,xo,[],tau);
MMM11 = abs((realdata211 - x(:,1)./Cinit(11,1))).^2;
ttt11 = cumsum(MMM11);
bbb11 = ttt11(end)./size(realdata211,1);
rrr11 = ((bbb11)^(0.5))./max(realdata211);
ZZZ11(1,counttt) = rrr11;
ZZZ11(2,counttt) = rateconstant;
if ZZZ11(1,counttt) < aaa11
  aaa11 = ZZZ11(1,counttt);
  BEST(11,1) = rateconstant;
  zipk = x(:,1)./Cinit(11,1);
  zipkt = t;
end
counttt = counttt + 1;
end
%This is for the twelfth experimental data set: 250:1 #3
for rateconstant = alpha:beta:gamma
%_
%Initial Conditions Matrix
xo = Cinit(12,1);
%Solve the differential equations
[t,x] = ode45('light3',realdata112,xo,[],tau);
MMM12 = abs((realdata212 - x(:,1)./Cinit(12,1))).^2;
ttt12 = cumsum(MMM12);
bbb12 = ttt12(end)./size(realdata212,1);
rrr12 = ((bbb12)^{(0.5)})./max(realdata212);
```

```
ZZZ12(1,counttt) = rrr12;
ZZZ12(2,counttt) = rateconstant;
```

if ZZZ12(1,counttt) < aaa12


```
aaa12 = ZZZ12(1,counttt);
BEST(12,1) = rateconstant;
zipl = x(:,1)./Cinit(12,1);
ziplt = t;
end
counttt = counttt + 1;
end
```

```
%This is for the thirteenth experimental data set: 50:1 #1
for rateconstant = alpha:beta:gamma
%_____
```

```
%Initial Conditions Matrix
xo = Cinit(13,1);
%Solve the differential equations
[t,x] = ode45('light3',realdata113,xo,[],tau);
```

```
MMM13 = abs((realdata213 - x(:,1)./Cinit(13,1))).^2;
ttt13 = cumsum(MMM13);
bbb13 = ttt13(end)./size(realdata213,1);
rrr13 = ((bbb13)^(0.5))./max(realdata213);
```

```
ZZZ13(1,counttt) = rrr13;
ZZZ13(2,counttt) = rateconstant;
```

```
if ZZZ13(1,counttt) < aaa13
    aaa13 = ZZZ13(1,counttt);
    BEST(13,1) = rateconstant;
    zipm = x(:,1)./Cinit(13,1);
    zipmt = t;
end
counttt = counttt + 1;
end</pre>
```

```
%This is for the fourteenth experimental data set: 50:1 #2
for rateconstant = alpha:beta:gamma
%_____
```

```
%Initial Conditions Matrix
xo = Cinit(14,1);
%Solve the differential equations
[t,x] = ode45('light3',realdata114,xo,[],tau);
```

```
MMM14 = abs((realdata214 - x(:,1)./Cinit(14,1))).^2;
ttt14 = cumsum(MMM14);
bbb14 = ttt14(end)./size(realdata214,1);
rrr14 = ((bbb14)^(0.5))./max(realdata214);
```

```
ZZZ14(1,counttt) = rrr14;
ZZZ14(2,counttt) = rateconstant;
```

```
if ZZZ14(1,counttt) < aaa14
  aaa14 = ZZZ14(1,counttt);
```



```
BEST(14,1) = rateconstant;
zipn = x(:,1)./Cinit(14,1);
zipnt = t;
end
counttt = counttt + 1;
end
```

```
%This is for the fifteenth experimental data set: 50:1 #3
for rateconstant = alpha:beta:gamma
%_______%Initial Conditions Matrix
```

```
xo = Cinit(15,1);
%Solve the differential equations
[t,x] = ode45('light3',realdata115,xo,[],tau);
```

```
MMM15 = abs((realdata215 - x(:,1)./Cinit(15,1))).^2;
ttt15 = cumsum(MMM15);
bbb15 = ttt15(end)./size(realdata215,1);
rrr15 = ((bbb15)^(0.5))./max(realdata215);
```

```
ZZZ15(1,counttt) = rrr15;
ZZZ15(2,counttt) = rateconstant;
```

```
if ZZZ15(1,counttt) < aaa15
  aaa15 = ZZZ15(1,counttt);
  BEST(15,1) = rateconstant;
  zipo = x(:,1)./Cinit(15,1);
  zipot = t;
end
counttt = counttt + 1;
end
```

```
%End of calculations and use of ODE function %
```

%These are individual (each trial for each experiment) plots:

```
figure(1)
plot(realdata11,realdata21,'bd',zipat,zipa(:,1),'k-.')
title('DNAN Removal, Molar Ratio 100:1, 1 of 3')
xlabel('Time (minutes)')
ylabel('Relative concentration C/Co')
legend('data','model')
axis([0 60 0.50 1])
```

figure(2) plot(realdata12,realdata22,'bd',zipbt,zipb(:,1),'k-.') title('DNAN Removal, Molar Ratio 100:1, 2 of 3') xlabel('Time (minutes)') ylabel('Relative concentration C/Co')



```
legend('data','model')
axis([0 60 0.50 1])
```

figure(3) plot(realdata13,realdata23,'bd',zipct,zipc(:,1),'k-.') title('DNAN Removal, Molar Ratio 100:1, 3 of 3') xlabel('Time (minutes)') ylabel('Relative concentration C/Co') legend('data','model') axis([0 60 0.50 1])

figure(4) plot(realdata14,realdata24,'bd',zipdt,zipd(:,1),'k-.') title('DNAN Removal, Molar Ratio 500:1, 1 of 3') xlabel('Time (minutes)') ylabel('Relative concentration C/Co') legend('data','model') axis([0 60 0.50 1])

figure(5) plot(realdata15,realdata25,'bd',zipet,zipe(:,1),'k-.') title('DNAN Removal, Molar Ratio 500:1, 2 of 3') xlabel('Time (minutes)') ylabel('Relative concentration C/Co') legend('data','model') axis([0 60 0.50 1])

figure(6) plot(realdata16,realdata26,'bd',zipft,zipf(:,1),'k-.') title('DNAN Removal, Molar Ratio 500:1, 3 of 3') xlabel('Time (minutes)') ylabel('Relative concentration C/Co') legend('data','model') axis([0 60 0.50 1])

figure(7) plot(realdata17,realdata27,'bd',zipgt,zipg(:,1),'k-.') title('DNAN Removal, Molar Ratio 1000:1, 1 of 3') xlabel('Time (minutes)') ylabel('Relative concentration C/Co') legend('data','model') axis([0 60 0.50 1])

figure(8) plot(realdata18,realdata28,'bd',zipht,ziph(:,1),'k-.') title('DNAN Removal, Molar Ratio 1000:1, 2 of 3') xlabel('Time (minutes)') ylabel('Relative concentration C/Co') legend('data','model') axis([0 60 0.50 1])



figure(9) plot(realdata19,realdata29,'bd',zipit,zipi(:,1),'k-.') title('DNAN Removal, Molar Ratio 1000:1, 3 of 3') xlabel('Time (minutes)') ylabel('Relative concentration C/Co') legend('data','model') axis([0 60 0.50 1])

figure(10) plot(realdata110,realdata210,'bd',zipjt,zipj(:,1),'k-.') title('DNAN Removal, Molar Ratio 250:1, 1 of 3') xlabel('Time (minutes)') ylabel('Relative concentration C/Co') legend('data','model') axis([0 60 0.50 1])

figure(11) plot(realdata111,realdata211,'bd',zipkt,zipk(:,1),'k-.') title('DNAN Removal, Molar Ratio 250:1, 2 of 3') xlabel('Time (minutes)') ylabel('Relative concentration C/Co') legend('data','model') axis([0 60 0.50 1])

figure(12) plot(realdata112,realdata212,'bd',ziplt,zipl(:,1),'k-.') title('DNAN Removal, Molar Ratio 250:1, 3 of 3') xlabel('Time (minutes)') ylabel('Relative concentration C/Co') legend('data','model') axis([0 60 0.50 1])

figure(13) plot(realdata113,realdata213,'bd',zipmt,zipm(:,1),'k-.') title('DNAN Removal, Molar Ratio 50:1, 1 of 3') xlabel('Time (minutes)') ylabel('Relative concentration C/Co') legend('data','model') axis([0 60 0.50 1])

figure(14) plot(realdata114,realdata214,'bd',zipnt,zipn(:,1),'k-.') title('DNAN Removal, Molar Ratio 50:1, 2 of 3') xlabel('Time (minutes)') ylabel('Relative concentration C/Co') legend('data','model') axis([0 60 0.50 1])

figure(15) plot(realdata115,realdata215,'bd',zipot,zipo(:,1),'k-.') title('DNAN Removal, Molar Ratio 50:1, 3 of 3')



xlabel('Time (minutes)') ylabel('Relative concentration C/Co') legend('data','model') axis([0 60 0.50 1])

%

%These are plots categorized by molar ratio with x3 trials plotted:

figure(100) plot(realdata11,realdata21,'bd',zipat,zipa(:,1),'b-.') title('DNAN Removal, Molar Ratio 100:1, 3 Trials') xlabel('Time (minutes)') ylabel('Relative concentration C/Co') axis([0 60 0.50 1]) hold on plot(realdata12,realdata22,'rd',zipbt,zipb(:,1),'r-.') plot(realdata13,realdata23,'gd',zipct,zipc(:,1),'g-.') legend ('Trial 1','Model 1','Trial 2','Model 2','Trial 3','Model 3') hold off

figure(500) plot(realdata14,realdata24,'bd',zipdt,zipd(:,1),'b-.') title('DNAN Removal, Molar Ratio 500:1, 3 Trials') xlabel('Time (minutes)') ylabel('Relative concentration C/Co') axis([0 60 0.50 1]) hold on plot(realdata15,realdata25,'rd',zipet,zipe(:,1),'r-.') plot(realdata16,realdata26,'gd',zipft,zipf(:,1),'g-.') legend ('Trial 1','Model 1','Trial 2','Model 2','Trial 3','Model 3') hold off

```
figure(1000)

plot(realdata17,realdata27,'bd',zipgt,zipg(:,1),'b-.')

title('DNAN Removal, Molar Ratio 1000:1, Trials')

xlabel('Time (minutes)')

ylabel('Relative concentration C/Co')

axis([0 60 0.50 1])

hold on

plot(realdata18,realdata28,'rd',zipht,ziph(:,1),'r-.')

plot(realdata19,realdata29,'gd',zipit,zipi(:,1),'g-.')

legend ('Trial 1','Model 1','Trial 2','Model 2','Trial 3','Model 3')

hold off
```

figure(250) plot(realdata110,realdata210,'bd',zipjt,zipj(:,1),'b-.') title('DNAN Removal, Molar Ratio 250:1, 3 Trials') xlabel('Time (minutes)') ylabel('Relative concentration C/Co')



```
axis([0 60 0.50 1])
hold on
plot(realdata111,realdata211,'rd',zipkt,zipk(:,1),'r-.')
plot(realdata112,realdata212,'gd',ziplt,zipl(:,1),'g-.')
legend ('Trial 1','Model 1','Trial 2','Model 2','Trial 3','Model 3')
hold off
```

figure(50)

plot(realdata113,realdata213,'bd',zipmt,zipm(:,1),'b-.') title('DNAN Removal, Molar Ratio 50:1, 3 Trials') xlabel('Time (minutes)') ylabel('Relative concentration C/Co') axis([0 60 0.50 1]) hold on plot(realdata114,realdata214,'rd',zipnt,zipn(:,1),'r-.') plot(realdata115,realdata215,'gd',zipot,zipo(:,1),'g-.') legend ('Trial 1','Model 1','Trial 2','Model 2','Trial 3','Model 3') hold off

xlswrite('DNANregressions.xls',zipa,'100-1#1','B6'); xlswrite('DNANregressions.xls',zipat,'100-1#1','C6'); xlswrite('DNANregressions.xls',zipb,'100-1#2','B6'); xlswrite('DNANregressions.xls',zipbt,'100-1#2','C6'); xlswrite('DNANregressions.xls',zipc,'100-1#3','B6'); xlswrite('DNANregressions.xls',zipct,'100-1#3','C6'); xlswrite('DNANregressions.xls',zipd,'500-1#1','B6'); xlswrite('DNANregressions.xls',zipdt,'500-1#1','C6'); xlswrite('DNANregressions.xls',zipe,'500-1#2','B6'); xlswrite('DNANregressions.xls',zipet,'500-1#2','C6'); xlswrite('DNANregressions.xls',zipf,'500-1#3','B6'); xlswrite('DNANregressions.xls',zipft,'500-1#3','C6'); xlswrite('DNANregressions.xls',zipg,'1000-1#1','B6'); xlswrite('DNANregressions.xls',zipgt,'1000-1#1','C6'); xlswrite('DNANregressions.xls',ziph,'1000-1#2','B6'); xlswrite('DNANregressions.xls',zipht,'1000-1#2','C6'); xlswrite('DNANregressions.xls',zipi,'1000-1#3','B6'); xlswrite('DNANregressions.xls',zipit,'1000-1#3','C6'); xlswrite('DNANregressions.xls',zipj,'250-1#1','B6'); xlswrite('DNANregressions.xls',zipjt,'250-1#1','C6'); xlswrite('DNANregressions.xls',zipk,'250-1#2','B6'); xlswrite('DNANregressions.xls',zipkt,'250-1#2','C6'); xlswrite('DNANregressions.xls',zipl,'250-1#3','B6'); xlswrite('DNANregressions.xls',ziplt,'250-1#3','C6'); xlswrite('DNANregressions.xls',zipm,'50-1#1','B6'); xlswrite('DNANregressions.xls',zipmt,'50-1#1','C6'); xlswrite('DNANregressions.xls',zipn,'50-1#2','B6'); xlswrite('DNANregressions.xls',zipnt,'50-1#2','C6'); xlswrite('DNANregressions.xls',zipo,'50-1#3','B6'); xlswrite('DNANregressions.xls',zipot,'50-1#3','C6');

xlswrite('DNANregressions.xls',BEST(:,1),'BEST','C6');



%the following block is needed to calculate and display the runtime. tstop = clock; runtime = etime(tstop,tstart)./60; disp('length of run in minutes:') disp(runtime)

Matlab DNAN Data File

%June 2020 - AFIT %Authors: W. Harper and J. Hart %Project: 2019-20 UV LED project

global Cinit realdata11 realdata12 realdata13 realdata14 realdata15 realdata16 realdata17 realdata18 realdata19 realdata110 realdata111 realdata112 realdata113 realdata114 realdata115 realdata21 realdata22 realdata23 realdata24 realdata25 realdata26 realdata27 realdata28 realdata29 realdata210 realdata211 realdata211 realdata212 realdata213 realdata214 realdata215

%this is a data file
%realdata1* entries are time in minutes
%realdata2* entries are relative concentration
%Cinit is the matrix of initial concentrations
%
%
Cinit = [9.5831
9.3578
9.4945
9.6071
9.1886
9.3263
9.3010
9.5583
9.6419
9.5980
9.7363
9.4572
9.5464
9.5551
9.6456];
%

%_

%molar ratio = 100:1 %Experiment #1 of 3 %time data: realdata11 = [0 5



10

15

20 25

35

45

60];

%relative concentration C/Co

%NOTE: These relative concentrations use the concentration (C_t) calculated %by the calibration curve slope and measured concentration for that %particular experiment (which changes for each day). The initial %concentration which each C_t is divided by to normalize the data is an %average of the control experiment concentrations measured over 1 hour %prior to the actual experiment with the UV LED powered. Therefore, the %starting concentration for the DNAN solution entering the reactor changes %for each day and this is normalized so that the relative concentration is %1.0 for each experiment.

realdata21 = [1.0000

0.8936 0.8271 0.7860 0.7753 0.7525 0.7324 0.7320 0.7187]; %

%

%molar ratio = 100:1
%Experiment #2 of 3
%time data:
realdata12 = [0
5
10
15
20
25
35
45

60];

%relative concentration C/Co %Note: None realdata22 = [1.0000 0.9199 0.8536 0.8224 0.7913



0.7654 0.7548 0.7500 0.7444]; %Note: Check this graph and rate constant to ensure it isn't messing up due to the lack of a value for 60min. %

%_

%molar ratio = 100:1 %Experiment #3 of 3 %time data: realdata13 = [0 5 10 15 20 25 35 45 60];

%relative concentration C/Co

realdata23 = [1.0000 0.9194 0.8559 0.8254 0.8037 0.7816 0.7648 0.7588 0.7294]; %

%____

%molar ratio = 500:1
%Experiment #1 of 3
%time data:
realdata14 = [0
5
10
15
20
25
35
45
60];

%relative concentration C/Co



realdata24 = [1.0000 0.8606 0.8135 0.7557 0.7432 0.7212 0.6908 0.6848 0.6286]; %______

%

%molar ratio = 500:1 %Experiment #2 of 3 %time data: realdata15 = [0 5 10 15 20 25 35 45 60]; %relative concentration C/Co realdata25 = [1.0000 0.8661 0.7671 0.7567 0.7114 0.7062 0.6989 0.6900 0.6832]; %____

%____

```
%molar ratio = 500:1
%Experiment #3 of 3
%time data:
realdata16 = [0
5
10
15
20
25
35
45
```



60];

%relative concentration C/Co
realdata26 = [1.0000
0.8483
0.7752
0.7540
0.7295
0.7149
0.7142
0.6932
0.6879];
%

%

5

%molar ratio = 1000:1 %Experiment #1 of 3 %time data: realdata17 = [0 10 15 20 25 35 45 60]; %relative concentration C/Co realdata27 = [1.0000 0.8405 0.7954 0.7512 0.7348 0.7280 0.7125 0.7217 0.7139]; %_____ %molar ratio = 1000:1 %Experiment #2 of 3

%time data: realdata18 = [0 5 10 15 20

%



25 35 45

60];

%relative concentration C/Co realdata28 = [1.0000 0.8305 0.7944 0.7689 0.7564 0.7477

0.7210 0.7092

0.7058]; %_____

%_

%molar ratio = 1000:1 %Experiment #3 of 3 %time data: realdata19 = [0 5 10 15 20 25 35 45 60];

%relative concentration C/Co

realdata29 = [1.0000 0.7636 0.7057 0.6808 0.6676 0.6529 0.6446 0.6387 0.6259];

%_

%

%molar ratio = 250:1 %Experiment #1 of 3 %time data: realdata110 = [0



5 10

15

20

25

35 45

60];

%relative concentration C/Co realdata210 = [1.0000 0.8455 0.7949 0.7697 0.7306 0.7152 0.7098 0.7008 0.6859];

%_

%_

%molar ratio = 250:1 %Experiment #2 of 3 %time data: realdata111 = [0 5 10 15 20 25 35 45 60]; %relative concentration C/Co realdata211= [1.0000 0.8324 0.7859 0.7302 0.7190 0.7094 0.6948 0.6914 0.6911];

%_



%_

%molar ratio = 250:1
%Experiment #3 of 3
%time data:
realdata112 = [0
5
10
15
20
25
25
45 col.
00];
0/relative concentration C/Ca
%relative concentration C/Co
realdata $212 = [1.0000]$
0.8454
0.8055
0.7629
0.7365
0.7363
0.7278
0.7289
0.7149];
%
%
% %
% %
%% % molar ratio = 50:1
%%%%%%
% % %molar ratio = 50:1 %Experiment #1 of 3 %time data:
% % %molar ratio = 50:1 %Experiment #1 of 3 %time data: realdata113 = [0
% % %molar ratio = 50:1 %Experiment #1 of 3 %time data: realdata113 = [0 5
% % %molar ratio = 50:1 %Experiment #1 of 3 %time data: realdata113 = [0 5 10
%% %% %molar ratio = 50:1 %Experiment #1 of 3 %time data: realdata113 = [0 5 10 15
%% %% %molar ratio = 50:1 %Experiment #1 of 3 %time data: realdata113 = [0 5 10 15 20
%% %% %molar ratio = 50:1 %Experiment #1 of 3 %time data: realdata113 = [0 5 10 15 20 25
%% %% %molar ratio = 50:1 %Experiment #1 of 3 %time data: realdata113 = [0 5 10 15 20 25 35
% % %molar ratio = 50:1 %Experiment #1 of 3 %time data: realdata113 = [0 5 10 15 20 25 35 45
% % %molar ratio = 50:1 %Experiment #1 of 3 %time data: realdata113 = [0 5 10 15 20 25 35 45 60];
%% %% %molar ratio = 50:1 %Experiment #1 of 3 %time data: realdata113 = [0 5 10 15 20 25 35 45 60];
%% %% %molar ratio = 50:1 %Experiment #1 of 3 %time data: realdata113 = [0 5 10 15 20 25 35 45 60]; %relative concentration C/Co
%% % %molar ratio = 50:1 %Experiment #1 of 3 %time data: realdata113 = [0 5 10 15 20 25 35 45 60]; %relative concentration C/Co realdata213 = [1.0000
%% %% %molar ratio = 50:1 %Experiment #1 of 3 %time data: realdata113 = [0 5 10 15 20 25 35 45 60]; %relative concentration C/Co realdata213 = [1.0000 0.8999
% % %molar ratio = 50:1 %Experiment #1 of 3 %time data: realdata113 = [0 5 10 15 20 25 35 45 60]; %relative concentration C/Co realdata213 = [1.0000 0.8999 0.8909
%% %% %molar ratio = 50:1 %Experiment #1 of 3 %time data: realdata113 = [0 5 10 15 20 25 35 45 60]; %relative concentration C/Co realdata213 = [1.0000 0.8999 0.8909 0.8366
%% %% %molar ratio = 50:1 %Experiment #1 of 3 %time data: realdata113 = [0 5 10 15 20 25 35 45 60]; %relative concentration C/Co realdata213 = [1.0000 0.8999 0.8909 0.8366 0.8280
%% % %% %molar ratio = 50:1 %Experiment #1 of 3 %time data: realdata113 = [0 5 10 15 20 25 35 45 60]; %relative concentration C/Co realdata213 = [1.0000 0.8999 0.8909 0.8366 0.8280 0.8155
%% %% %molar ratio = 50:1 %Experiment #1 of 3 %time data: realdata113 = [0 5 10 15 20 25 35 45 60]; %relative concentration C/Co realdata213 = [1.0000 0.8999 0.8909 0.8366 0.8280 0.8155 0.8047



0.8115 0.8144];

%_

%

%molar ratio = 50:1 %Experiment #2 of 3 %time data: realdata114 = [0 5 10 15 20 25 35 45 60];

%relative concentration C/Co

realdata214 = [1.0000 0.9086 0.8700 0.8492 0.8342 0.8256 0.8210 0.8209 0.8111];

%____

%_

%molar ratio = 50:1 %Experiment #3 of 3 %time data: realdata115 = [0 5 10 15 20 25 35 45 60];

%relative concentration C/Co realdata215 = [1.0000 0.9015



0.8656
0.8483
0.8157
0.8174
0.8070
0.8078
0.8030];

%_

%



Appendix E: HPLC Method File Data

Data File : D:\data\20200529_DNAN_A 2020-05-29 10-57-18\1ED-1301.D Acq. Method: 20200220_BBP_D_DAD_MS_DLF.M

The Acq. Method's Instrument Parameters for the Run were :

------ FLD

FLD (G1321B)

=================

Detection Mode:		Fluorescence M	ode
Peakwidth:	> 0.2 min (4 s	s resp. time) (2.3	1 Hz)
PMT gain:		10	
Baseline Behaviou	ır Mode:	Appe	nd
Fit spectra range of	on:	Yes	
Analog Output So	urce Channel	1:	1
Analog Output So	urce Channel	2:	2
Signal polarity:		Positive (+)	
Posttime			
Posttime Mode:		Off	
Multiple Wavelen	gths		
Multi Wavelength	Mode:	Off	
Analog Output 1			
Analog 1 Attenuat	tion:	100 LU	
Analog 1 Zero Offs	set:	5 %	
Analas Output 2			
Analog Output 2		100.111	
Analog 2 Attenuat	lion:	100 LU	
Analog 2 Zero Ons	set:	5 %	
Lamn Settings			
Lamp on only duri	ng run.	Yes	
Lamp on required	for analysis:	No)
Lamp economy m	ode on:	No)
Lamp energy refe	rence mode o	n:	No
Fluorescence Scar	n Range		
	-		
Excitation Scan			
Scan Excitation W	L From:	220 nr	n
Scan Excitation W	L To:	380 nm	
Scan Excitation W	L Step:	5 nm	



Emission Scan Scan Emission WL From: Scan Emission WL To: Scan Emission WL Step:	300 nm 500 nm 5 nm
Signal A	
Excitation	
Use Signal:	Yes
Signal:	Signal A
Wavelength Mode:	Zero order
Emission	
Use Signal:	Yes
Signal:	Signal A
Wavelength Mode:	Zero order
Stoptime	
Stoptime Mode:	As pump/injector
Timetable	
DAD	
DAD (G1315C)	
=========	
Peakwidth: >0.10 min (2	2.0 s response time) (2.5 Hz)
Slit:	4 nm
UV Lamp Required:	Yes
Vis Lamp Required:	Yes
Analog Output 1	
Analog 1 Attenuation:	1000 mAU
Analog 1 Zero Offset:	5 %
Analog Output 2	
Analog 2 Attenuation:	1000 mAU
Analog 2 Zero Offset:	5 %
Signals	
Signal table	
Use Sig. Signal Waveleng nm nr	th Bandwidth Use Ref. I
Yes Signal A 253	10 No



Yes Signal B 300 200 No Yes Signal C 300 20 No Yes Signal D 270 10 No No Signal E No Signal F No Signal G No Signal H
Prepare Mode Margin for negative Absorbance: 100 mAU
AutobalanceAutobalance Prerun:YesAutobalance Postrun:No
Spectrum Spectrum Store: None
Stoptime Stoptime Mode: As pump/injector
Posttime Posttime Mode: Off
Timetable
Instrument Curves Store Board Temperature: No Store Optical Unit Temperature: No Store UV Lamp Anode Voltage: No
Column Comp.
Column Comp. (G1316A)
Valve Position: Port 1 -> 2
Left Temperature ControlTemperature Control Mode:Temperature SetTemperature:30.00 °C
Enable Analysis Left Temperature Enable Analysis Left Temperature On: Yes Enable Analysis Left Temperature Value: 0.80 °C



Right Temperature Control Right temperature Control Mo Right temperature:	ode: Temperature 30.00 °C	Set
Enable Analysis Right Temper Enable Analysis Right Temper Enable Analysis Right Temper	ature ature On: Yes ature Value: 0.80 °C	2
Stop Time Stoptime Mode:	As pump/injector	
Post Time Posttime Mode:	Off	
Timetable		
Instrument Curves Store Left Temperature: Store Right Temperature:	Yes No	
HiP Sampler		
HiP Sampler (G1367E) =======		
Auxiliary Draw Speed: Eject Speed: Draw Position Offset: Wait Time After Drawing: Sample Flush Out Factor: Vial/Well bottom sensing:	100.0 μl/min 100.0 μl/min 0.0 mm 2.0 s 5.0 No	
Injection Injection Mode: Injection Volume:	Standard injection 20.00 μL	
High throughput Automaitc Delay Volume Redu Overlapped Injection Enable Overlapped Injection:	uction: No No	
Valve Switching Valve Movements:	0	



Valve Switch Time 1 Switch Time 1 Enabled:	No
Valve Switch Time 2 Switch Time 2 Enabled:	Νο
Valve Switch Time 3 Switch Time 3 Enabled:	Νο
Valve Switch Time 4 Switch Time 4 Enabled:	Νο
Stop Time Stoptime Mode:	As pump/No limit
Post Time Posttime Mode:	Off
Timetable	
Instrument Curves Store Temperature:	No
Valve	
 Valve (G1170A) =======	
Position Switching Mode: Valve position: After Run Position Switching M	Use valve position 1 ode: Do not switch
Stop Time Stoptime Mode:	As pump/injector
Post Time Posttime Mode:	Off
Timetable	
Position Description Position Position Description	1
 1 dad 2	



3	flo
4	Channel 4
5	Channel 5
6	Channel 6
7	Channel 7
8	Channel 8
9	by pass
10	MS
11	Channel 11
12	Channel 12

______ Quat. Pump

0.00 bar 550.00 bar

Automatic

100.000 ml/min²

Yes

Quat. Pump (G1311B)

Flow:	0.600 ml/min
Low Pressure Limit:	0.00 k
High Pressure Limit:	550.00
Maximum Flow Gradient:	100.0
Primary Channel:	Autom

Stroke Automatic Stroke Calculation:

Compress	
Compressibility Mode:	Compressibility Value Set
Compressibility:	100 10e-6/bar

Stop Time	
Stoptime Mode:	Time set
Stoptime:	2.50 min

Post Time Posttime Mode: Off

Timetable

Solvent Composition Channel Name 1 Used Percent % А Yes 50.0 В No

С	Yes	10.0
D	Yes	40.0



Instrument Curves	
Store Pressure:	Yes
Store Flow:	Yes
Store Solvent Ratio A:	Yes
Store Solvent Ratio B:	Yes
Store Solvent Ratio C:	Yes
Store Solvent Ratio D:	Yes
Store Direction of Piston A:	No

Mass Spectrometer Detector

General Information

Use MSD	: Enabled
Tune File	: tunes20200218.tun
StopTime	: No Limit
Time Filter	: Enabled
Data Storage	: Condensed
Peakwidth	: 0.05 min
Fast Scan	: Disabled
Fast Scan Data	Reconstruction: Disabled
Polarity Switch	Delay : 50 ms
Ionization Swit	ch Delay : 50 ms

Signals

[Signal 1]

Ionization Mode: API-ESPolarity: PositiveFragmentor Ramp: DisabledPercent Cycle Time: 100.00 %

Scan Parameters

 Time |
 Mass Range
 |Frag- | Gain | Thres- | Step-(min) |
 Low |
 High | mentor |
 EMV |
 hold |
 size

 ----- ----- |----- |----- |----- |-----

 0.00
 175.00
 250.00
 35
 1.0
 150
 0.20

[Signal 2] Not Active



[Signal 3] Not Active [Signal 4] Not Active Spray Chamber ____ [MSZones] Gas Temp : 300 C maximum 350 C DryingGas : 10.0 l/min maximum 13.0 l/min Neb Pres : 45 psig maximum 60 psig Quad Temp : 0 C maximum 0 C VCap (Positive) : 4000 V : 3500 V VCap (Negative) [Time Table] Time Table is empty. END OF MS ACQUISITION PARAMETERS _____ **FIA Series** ______ FIA Series in this Method : Disabled **Time Setting** Time between Injections : 0.15 min Injection Loop Flush Time : 0.17 min _____ Column(s) Column Description : Eclipse XDB-C18 Serial# : autoID-11 Product# : 993967-902 Batch# : Diameter :4.6 mm Length : 150.0 mm Particle size : 5.0 µm Void volume : 60.0 % Maximum Pressure : 400.0 bar Maximum pH : 9.0 Minimum pH : 2.0 Maximum Temperature: 60.0 °C Comment :



Calibration Curve 250:1 Blank





Calibration Curve 250:1 10%





Calibration Curve 250:1 20%





Calibration Curve 250:1 40%



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Calibration Curve 250:1 60%





Calibration Curve 250:1 80%



Sampling Rate 0.0067 min (0.402 sec), 375 datapoints

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Calibration Curve 250:1 100%





Control 250:10 min



	File Information
LC-File	1EA-1001.D
File Path	D:\DATA\20200806_DNAN_1_JH 2020-08-06 08-52-21\
Date	06-Aug-20, 09:26:23
Sample	C1 Omin
Sample Info	
Barcode	
Operator	user
Method	20200220_BBP_D_DAD_MS_DLF.M
Analysis Time	2.493 min
Sampling Rate	0.0067 min (0.402 sec), 375 datapoints

#	Time	Area	Height	Width	Area%	Symmetry
1	0.105	70.2	4.2	0.2193	4.787	0.278
2	0.362	728.5	150.1	0.0786	49.649	1.259
3	1.099	668.6	108.1	0.0882	45.564	0.403
3	1.099	668.6	108.1	0.0882	45.564	0.403



Control 250:1 10 min





Control 250:1 20 min



	File Information
LC-File	1EC-1201.D
File Path	D:\DATA\20200806_DNAN_1_JH 2020-08-06 08-52-21\
Date	06-Aug-20, 09:33:41
Sample	C3 20min
Sample Info	
Barcode	
Operator	user
Method	20200220_BBP_D_DAD_MS_DLF.M
Analysis Time	2.5 min
Sampling Rate	0.0067 min (0.402 sec), 376 datapoints

#	Time	Area	Height	Width	Area%	Symmetry
1	0.159	70.4	5.8	0.1814	4.570	0.982
2	0.362	734.9	150.7	0.0789	47.713	1.248
3	1.098	694.5	112.5	0.0861	45.088	0.405
4	1.797	40.5	1.5	0.3473	2.629	0.721



Control 250:1 30 min



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Control 250:1 40 min





Analysis Time 2.493 min

Sampling Rate 0.0067 min (0.402 sec), 375 datapoints
Control 250:1 50 min



	File Information
LC-File	1EF-1501.D
File Path	D:\DATA\20200806_DNAN_1_JH 2020-08-06 08-52-21\
Date	06-Aug-20, 09:44:37
Sample	C6 50min
Sample Info	
Barcode	
Operator	user
Method	20200220_BBP_D_DAD_MS_DLF.M
Analysis Time	2.493 min
Sampling Rate	0.0067 min (0.402 sec), 375 datapoints

	#	Time	Area	Height	Width	Area%	Symmetry
	1	0.363	701.7	148.3	0.0772	49.415	1.188
- [2	1.098	718.4	113.9	0.0896	50.585	0.416



Control 250:1 60 min



	File Information
LC-File	1EG-1601.D
File Path	D:\DATA\20200806_DNAN_1_JH 2020-08-06 08-52-21\
Date	06-Aug-20, 09:48:16
Sample	C7 60min
Sample Info	
Barcode	
Operator	user
Method	20200220_BBP_D_DAD_MS_DLF.M
Analysis Time	2.493 min
Sampling Rate	0.0067 min (0.402 sec), 375 datapoints



Experiment 250:1 5 min



Experiment 250:1 10 min



Experiment 250:1 15 min



	File Information
LC-File	1DC-2001.D
File Path	D:\DATA\20200806_DNAN_1_JH 2020-08-06 08-52-21\
Date	06-Aug-20, 10:02:50
Sample	R3 15min
Sample Info	
Barcode	
Operator	user
Method	20200220_BBP_D_DAD_MS_DLF.M
Analysis Time	2.493 min
Sampling Rate	0.0067 min (0.402 sec), 375 datapoints

#	Time	Area	Height	Width	Area%	Symmetry
1	0.364	706.5	148.9	0.0774	55.297	1.178
2	0.632	33.2	2.1	0.232	2.595	10.03
3	0.823	1.3	5.2E-1	0.0439	0.104	1.522
4	1.1	536.6	85.7	0.0891	42.003	0.395



Experiment 250:1 20 min



	File Information
LC-File	1DD-2101.D
File Path	D:\DATA\20200806_DNAN_1_JH 2020-08-06 08-52-21\
Date	06-Aug-20, 10:06:29
Sample	R4 20min
Sample Info	
Barcode	
Operator	user
Method	20200220_BBP_D_DAD_MS_DLF.M
Analysis Time	2.5 min
Sampling Rate	0.0067 min (0.402 sec), 376 datapoints
Operator Method Analysis Time Sampling Rate	user 20200220_BBP_D_DAD_MS_DLF:M 2.5 min 0.0067 min (0.402 sec), 376 datapoints

#	Time	Area	Height	Width	Area%	Symmetry
1	0.141	57.4	4.3	0.1818	4.279	0.74
2	0.364	743.7	151.5	0.0793	55.392	1.227
3	0.64	30.6	1.8	0.2459	2.281	12.481
4	0.825	1.6	5.7E-1	0.0458	0.116	1.831
5	1.099	509.3	81.8	0.0866	37.933	0.399



Experiment 250:1 25 min

Sampling Rate 0.0067 min (0.402 sec), 376 datapoints





Experiment 250:1 35 min



	File Information
LC-File	1DF-2301.D
File Path	D:\DATA\20200806_DNAN_1_JH 2020-08-06 08-52-21\
Date	06-Aug-20, 10:13:48
Sample	R6 35min
Sample Info	
Barcode	
Operator	user
Method	20200220_BBP_D_DAD_MS_DLF.M
Analysis Time	2.493 min
Sampling Rate	0.0067 min (0.402 sec), 375 datapoints

#	Time	Area	neight	width	Area%	Symmetry
1	0.363	796	151.8	0.0832	60.198	1.44
2	0.638	30.1	1.7	0.2543	2.278	13.394
3	0.82	1.4	5.4E-1	0.0434	0.103	1.31
4	1.097	494.8	78.9	0.0892	37.421	0.393



Experiment 250:1 45 min



	File Information
LC-File	1DG-2401.D
File Path	D:\DATA\20200806_DNAN_1_JH 2020-08-06 08-52-21\
Date	06-Aug-20, 10:17:27
Sample	R7 45min
Sample Info	
Barcode	
Operator	user
Method	20200220_BBP_D_DAD_MS_DLF.M
Analysis Time	2.5 min
Sampling Rate	0.0067 min (0.402 sec), 376 datapoints

#	Time	Area	Height	Width	Area%	Symmetry
1	0.364	709.9	149	0.0776	57.513	1.178
2	0.638	34.4	2.1	0.2467	2.790	12.44
3	0.819	1.5	5.7E-1	0.0435	0.118	1.082
4	1.097	488.5	79.1	0.086	39.579	0.401



Experiment 250:1 60 min



	The Information
LC-File	1DH-2501.D
File Path	D:\DATA\20200806_DNAN_1_JH 2020-08-06 08-52-21\
Date	06-Aug-20, 10:21:05
Sample	R8 60min
Sample Info	
Barcode	
Operator	user
Method	20200220_BBP_D_DAD_MS_DLF.M
Analysis Time	2.5 min
Sampling Rate	0.0067 min (0.402 sec), 376 datapoints

#	Time	Area	Height	Width	Area%	Symmetry
1	0.363	801.8	151.3	0.0838	61.156	1.449
2	0.64	29.8	1.7	0.2544	2.274	13.561
3	0.828	1.4	5.1E-1	0.0454	0.106	2.32
4	1.097	478.1	77.3	0.0861	36.464	0.399



Appendix G: Potential Byproduct Mass Spectroscopy

100:1 Trial

Sequence Name	Line	Vial	Sample Name	Region	RT	AMU
20200622_DNAN_JH_MS	2	P1-D-04	R4-H	Н	1.175	240





10	0:1	Trial
IU	<i>i</i> 0.1	Inai

Sequence Name	Line	Vial	Sample Name	Region	RT	AMU
20200622_DNAN_JH_MS	2	P1-D-04	R4-H	Н	1.175	240





Sequence Name	Line	Vial	Sample Name	Region	RT	AMU
20200622_DNAN_JH_MS	3	P1-D-04	R4-M	Μ	0.371	146



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Sequence Name	Line	Vial	Sample Name	Region	RT	AMU
20200622_DNAN_JH_MS	3	P1-D-04	R4-M	Μ	0.371	146





Sequence Name	Line	Vial	Sample Name	Region	RT	AMU
20200622_DNAN_JH_MS	9	P1-D-08	R8-H	Н	1.164	240





Sequence Name	Line	Vial	Sample Name	Region	RT	AMU
20200622_DNAN_JH_MS	9	P1-D-08	R8-H	Н	1.164	240



Sequence Name	Line	Vial	Sample Name	Region	RT	AMU
20200622_DNAN_JH_MS	10	P1-D-08	R8-M	Μ	0.372	146





1	00):1	Trial

Sequence Name	Line	Vial	Sample Name	Region	RT	AMU
20200622_DNAN_JH_MS	10	P1-D-08	R8-M	Μ	0.372	146





Sequence Name	Line	Vial	Sample Name	Region	RT	AMU
20200813_MS_DNAN_250-1_JH	2	P1-E-03	С3-Н	Н	0.376	192





Sequence Name	Line	Vial	Sample Name	Region	RT	AMU
20200813_MS_DNAN_250-1_JH	2	P1-E-03	С3-Н	Н	0.376	192





Sequence Name	Line		Vial	Sample Name	Region	RT	AMU
20200723_MS_DNAN_B_JH		2	P1-E-03	С3-Н	Н	0.377	192





Sequence Name	Line		Vial	Sample Name	Region	RT	AMU
20200723_MS_DNAN_B_JH		2	P1-E-03	С3-Н	Н	0.377	192





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