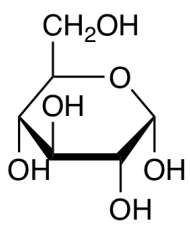
Corn starch → cheap polymer of α-D-Glucose

→ Converted to α-D-Glucose monomers using 2 enzymes:

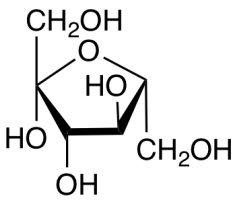
1) α-Amylase →

2) Glucoamylase →

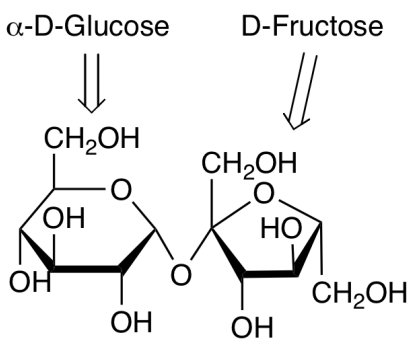
3) Some of the D-Glucose is converted to D-Fructose



α-D-Glucose



D-Fructose



Sucrose (Table Sugar)

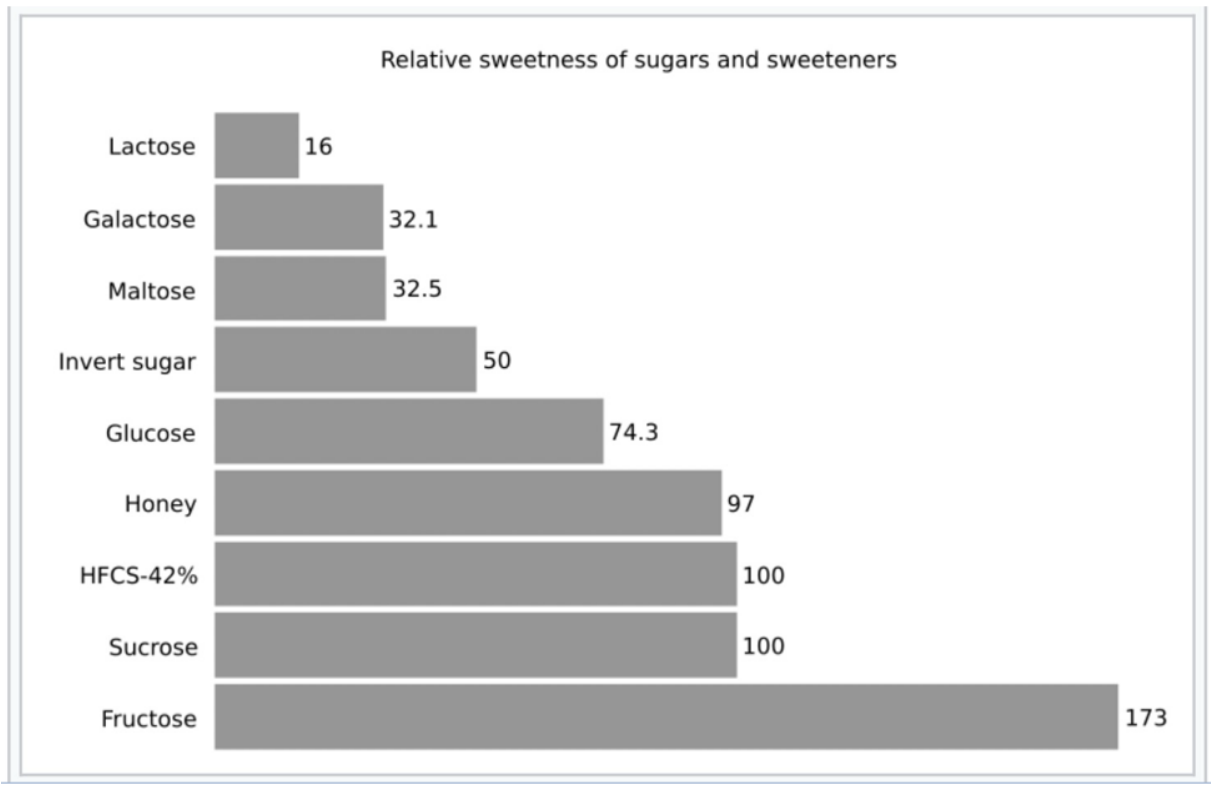
Final high fructose corn syrup:

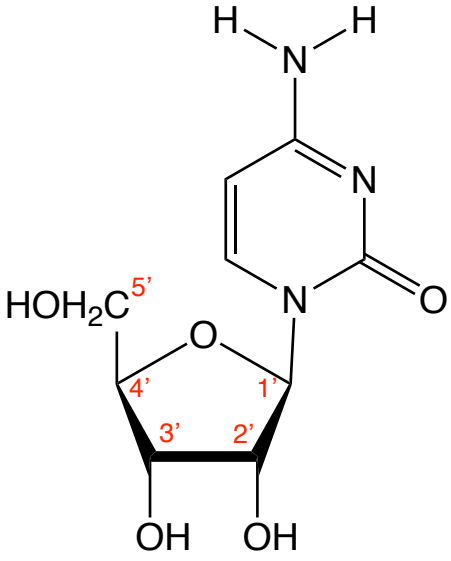
% D-Fructose % D-Glucose

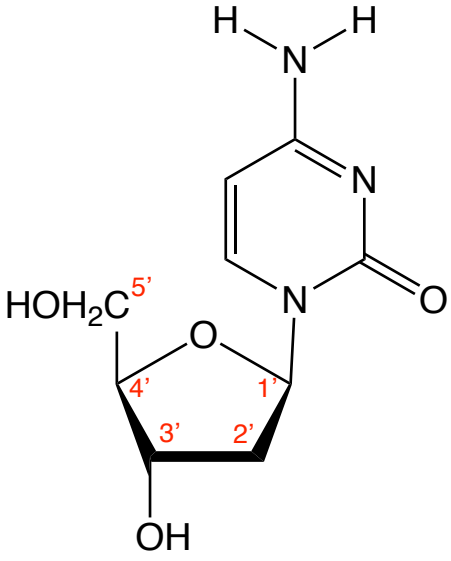
This is intended to mimic bee honey

% D-Fructose % D-Glucose

% Sucrose



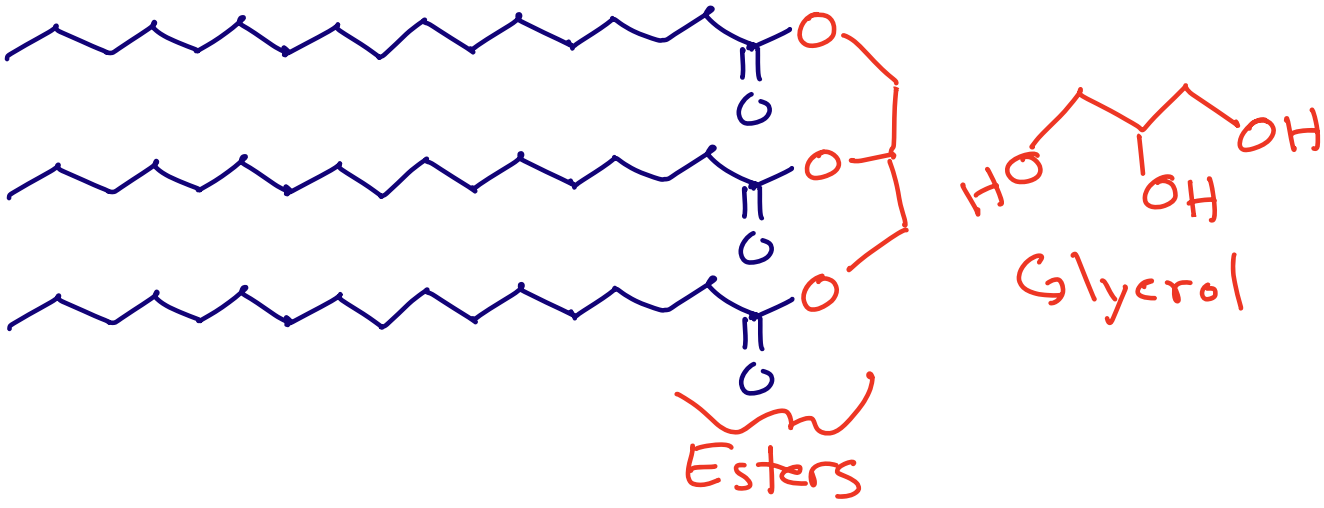


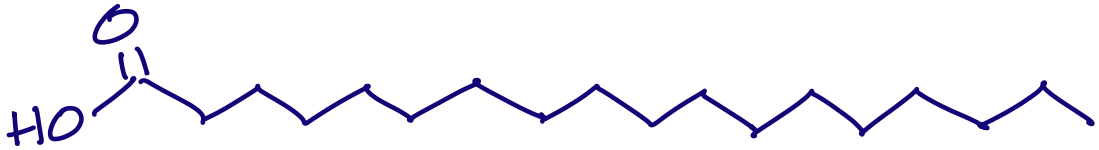


In RNA and DNA →

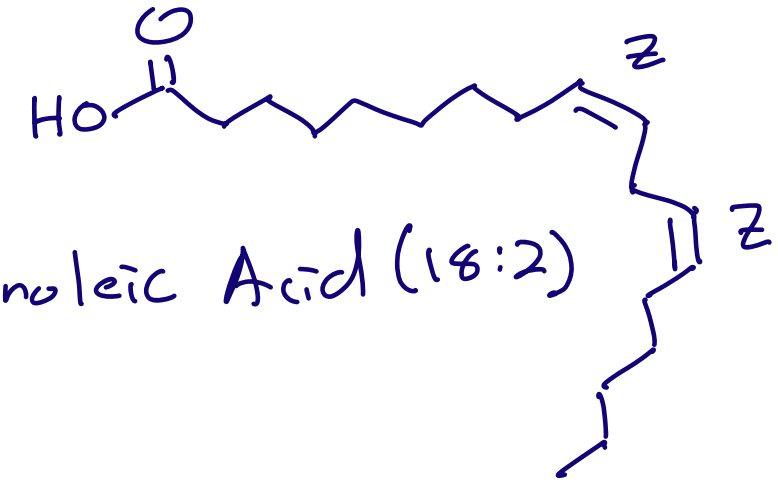
Lipids → Biological molecules that are not soluble in water

Triglycerides → Fats and oils





Stearic Acid (18:0)

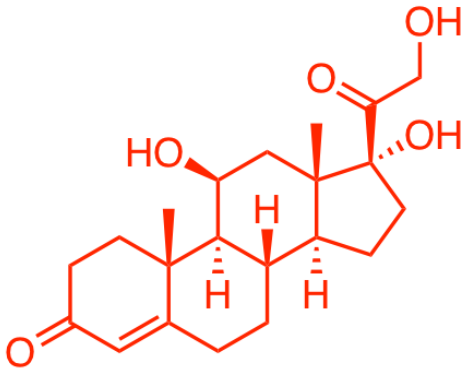


Linoleic Acid (18:2)

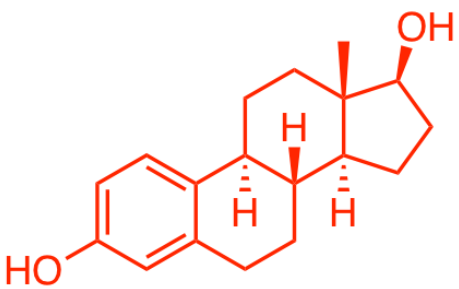
$Fa H_x$ Acids

Steroids → Rigid multiring structures that are important signals

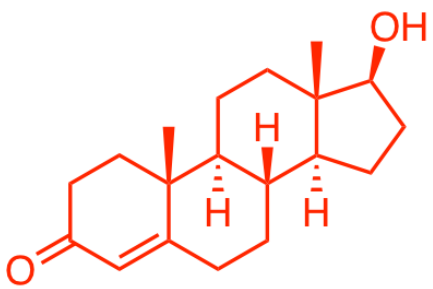
→ Rigid structure ensures high degree of for these critical functions



Cortisol

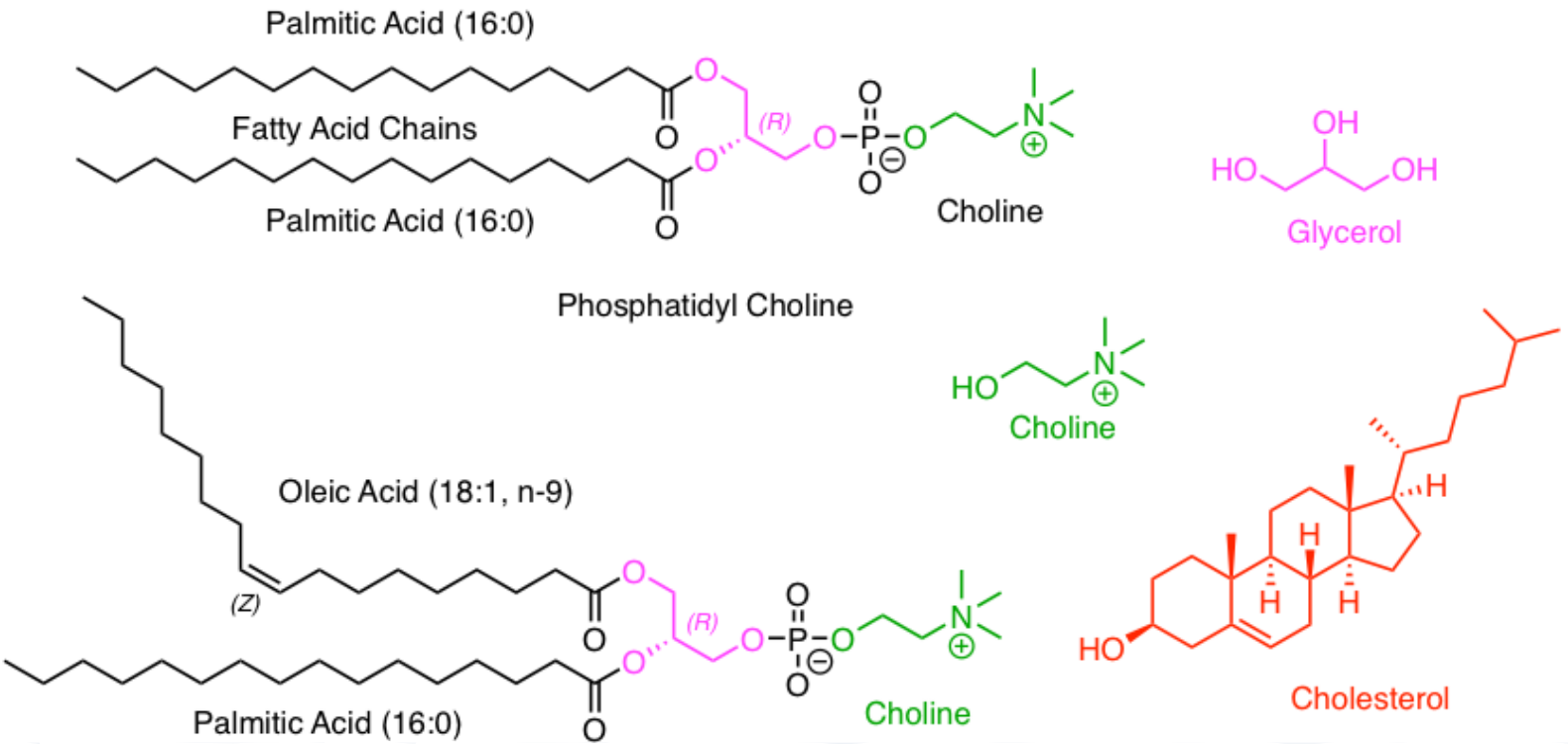


Estradiol

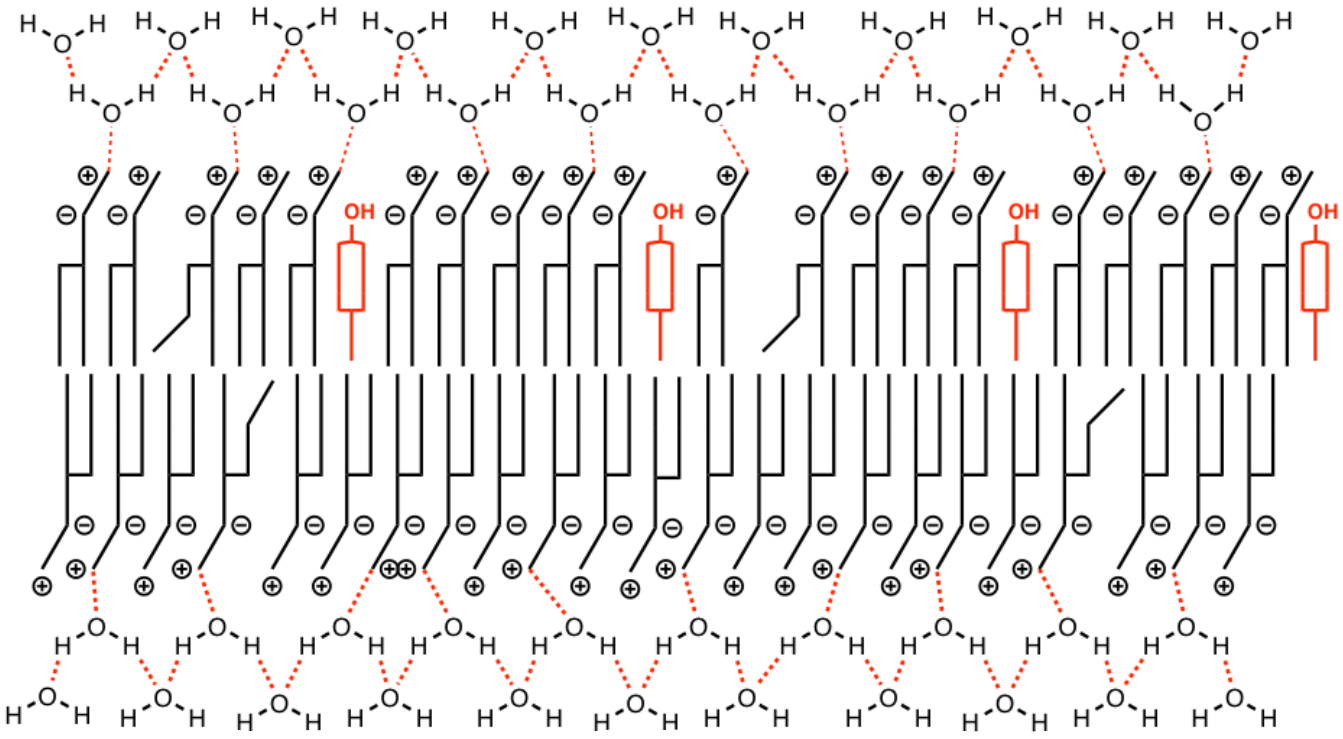


Testosterone

Phospholipids → Make up cellular membranes



Phospholipid membrane bilayers → The and combine to make the membranes enough to operate effectively



Lipid Bilayer Membrane

So what holds membranes together?

The fatty acid chains are not soluble in water → The in water prevent the from "dissolving" into the water → Only things that can interact with polar water molecules dissolve in water. → To break up hydrogen bonds a molecule must be charged and/or be capable of strong

"Like likes like" → Key rule of solvents

!!! ⟹ The cannot interact with water so they must therefore associate providing the to hold membranes together

How do energy drinks work?

Nutrition Facts
1 Serving Per Container
Serving Size 12 fl. oz (355mL)

Amount Per Serving	
Calories	**10**
	%Daily Value*
Total Fat 0mg	0%
Sodium 5mg	0%
Total Carbohydrate 0mg	0%
Protein 0mg	
Calcium 50mg	4%
Vitamin C 60mg	70%
Riboflavin 1.7mg	130%
Niacin 20mg	130%
Vitamin B6 2mg	120%
Vitamin B12 6mcg	250%
Biotin 300mcg	1000%
Pantothenic Acid 10mg	200%
Chromium 50mcg	140%

Not a significant source of sat fat, *trans* fat, cholesterol, dietary fiber, total sugar, added sugars, vitamin D, iron, and potassium.

The % Daily Value (DV) tells you how much a nutrient in a serving of food contributes to a daily diet. 2,000 calories a day is used for general nutrition advice.

Caffeine Content: 200mg

US BANG ENERGY BLUE RAZZ 16OZ. CAN

CONTAINS NO FRUIT JUICE

Nutrition Facts

Serving size	1 can
Amount per serving	
Calories	**0**
	% Daily Value*
Total Fat 0g	0%
Sodium 40mg	2%
Total Carbohydrate 2g	1%
Total Sugars 0g	
Includes 0g Added Sugars	0%
Protein 0g	
Potassium 90mg 2% •	Vitamin C 30%
Niacin 30% •	Vitamin B6 30%
Vitamin B12 60% •	Magnesium 2%

Not a significant source of saturated fat, trans fat, cholesterol, dietary fiber, vitamin D, calcium and iron.

*The % Daily Value (DV) tells you how much a nutrient in a serving of food contributes to a daily diet. 2,000 calories a day is used for general nutrition advice.

INGREDIENTS: CARBONATED WATER, CITRIC ACID, (pH CONTROL), NATURAL & ARTIFICIAL FLAVORS, CAFFEINE, SODIUM BENZOATE (PRESERVATIVE), POTASSIUM CITRATE, SUCRALOSE, ESSENTIAL AMINO ACIDS (L-LEUCINE, L-ISOLEUCINE, L-VALINE, L-LYSINE), POTASSIUM PHOSPHATE, ASCORBIC ACID (VIT.C), ACESULFAME POTASSIUM, POTASSIUM SORBATE (PRESERVATIVE), MAGNESIUM CHLORIDE, CALCIUM CHLORIDE, CALCIUM DISODIUM EDTA, NIACINAMIDE (VIT.B3), COENZYME Q-10, PYRIDOXINE HYDROCHLORIDE (VIT.B6), METHYLCOBALAMIN (VIT.B12).

MANUFACTURED FOR BANG ENERGY LLC. 2380 ANSELMO DRIVE, CORONA, CA 92879 U.S.A.
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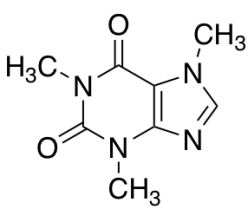
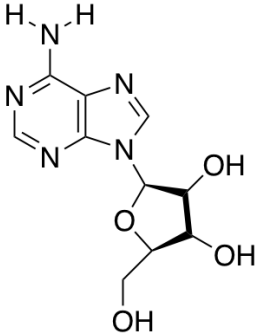


Caffeine



Adenosine

Coffee and tea drinks (coffee shops)	Serving size	Caffeine (mg)
Starbucks Coffee	20 oz. venti	390–490
Dutch Bros 9-1-1 Blended Freeze	large	440
Starbucks Coffee	16 oz. grande	315–390
Starbucks Iced Coffee	30 oz. trenta	320
Caribou Coffee	medium	305
Dunkin' Frozen Coffee	medium	295
Starbucks Coffee	12 oz. tall	235–290
Dunkin' Coffee	20 oz. large	270
Starbucks Caffè Americano	16 oz. grande	225
Dunkin' Coffee	14 oz. medium	210
Starbucks Cold Brew	16 oz. grande	205
Starbucks Flat White	16 oz. grande or 20 oz. venti	195

Caffeine → Turns off your

Antagonist

because it binds

binds where

to signal low and

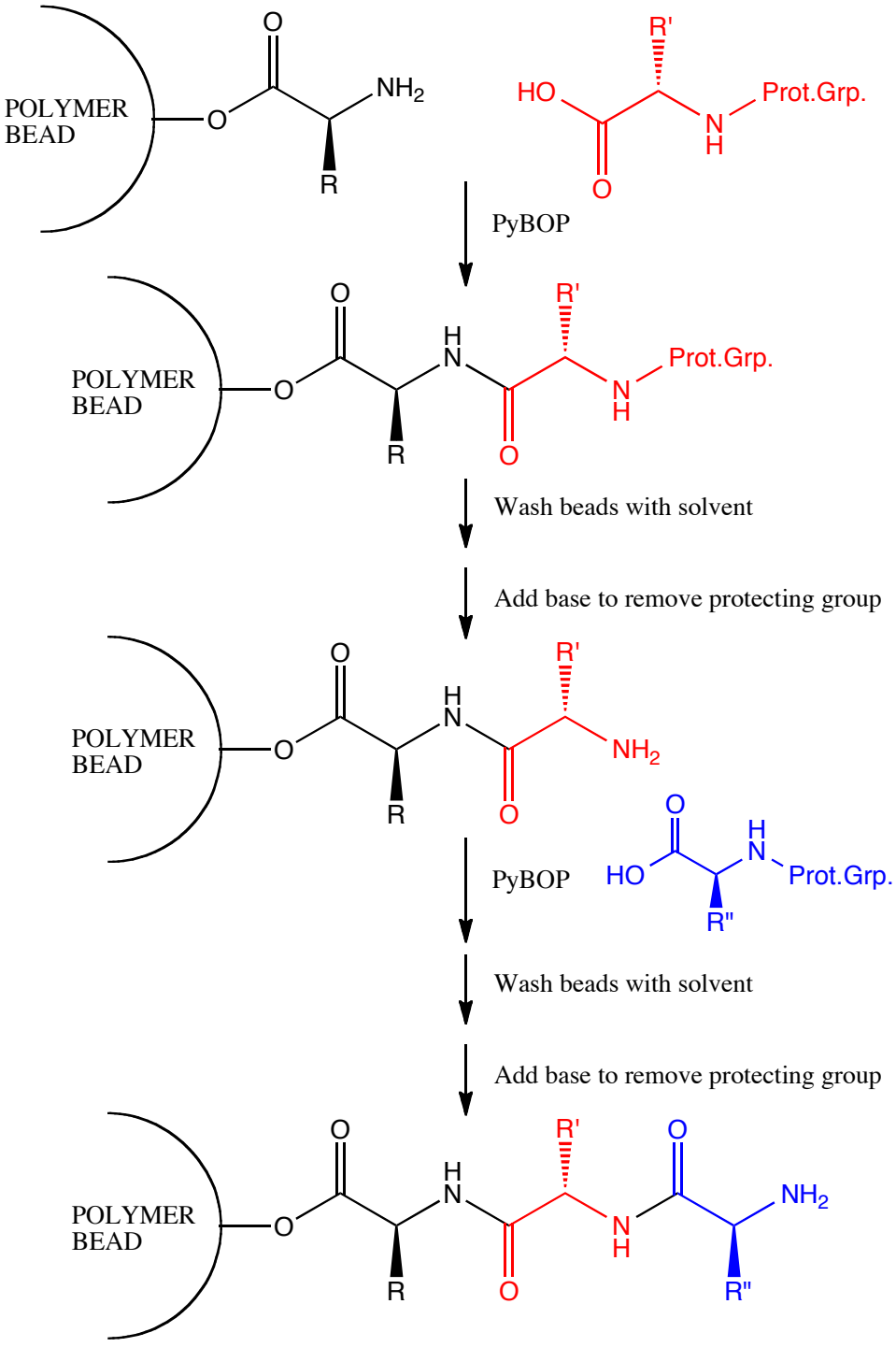
therefore .

Vitamins B_6 and B_{12} → stimulate

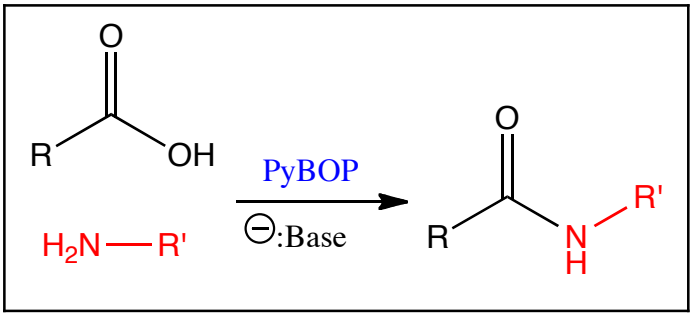
production of in your body

so you have available

Solid Phase Peptide Synthesis



Repeat as necessary then remove from resin. Can add up to 100 amino acids this way.



Good Leaving Group

PyBOP

overall an electrophile

REALLY Good Leaving Group

Good Nucleophile

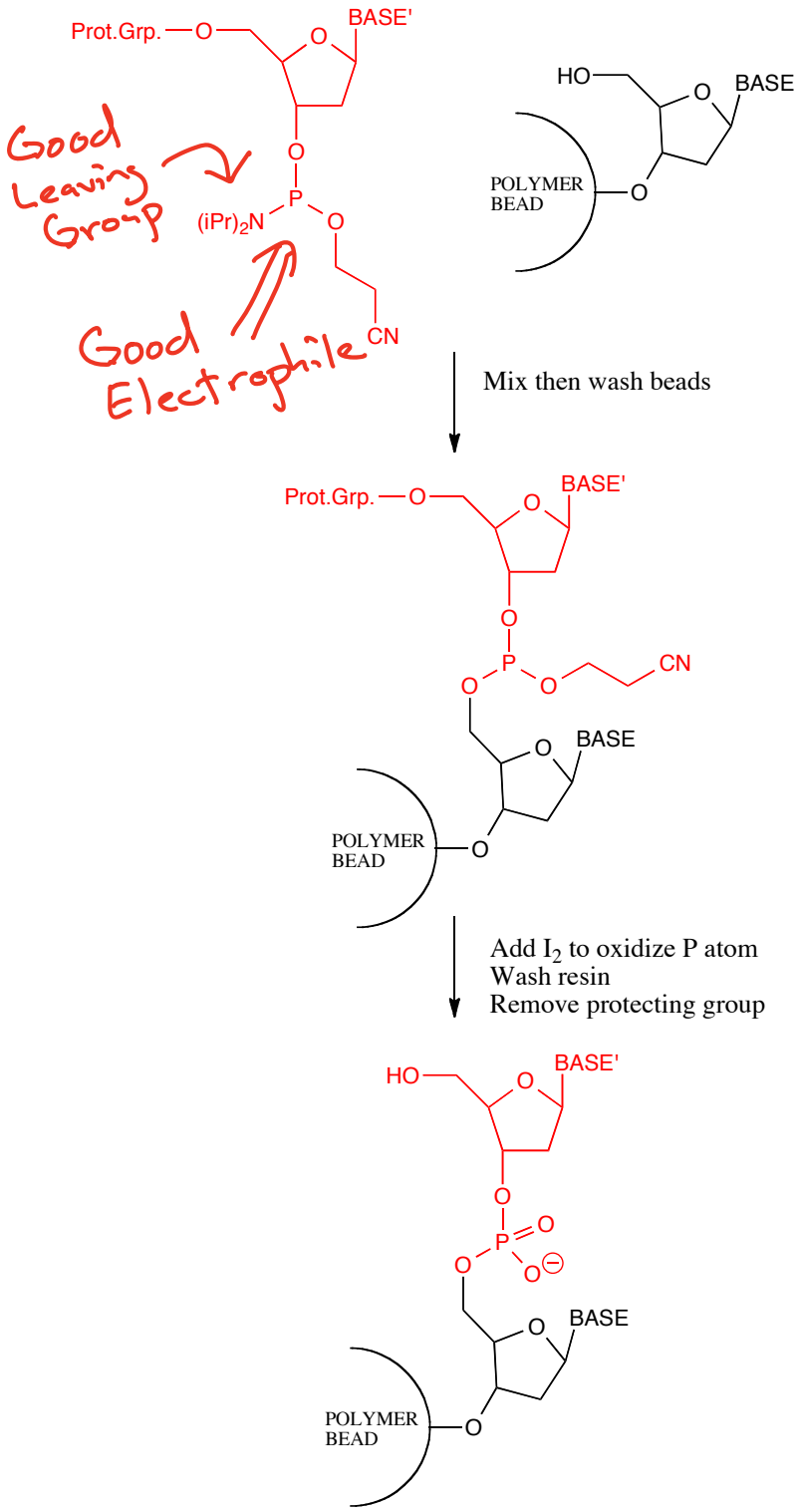
Good Leaving Group

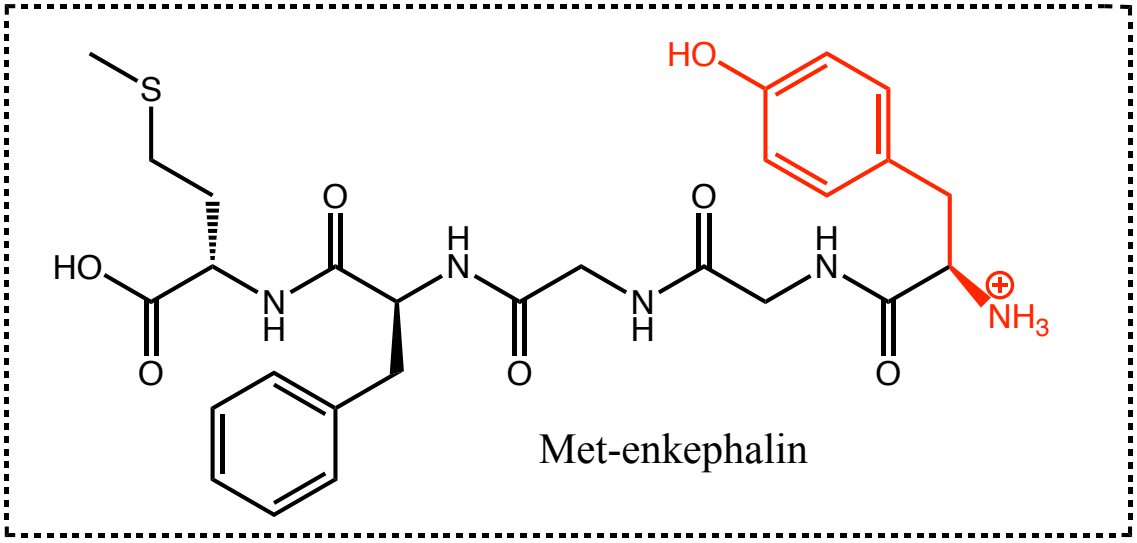
Formation of this strong bond drives reaction

Provides "Motive"

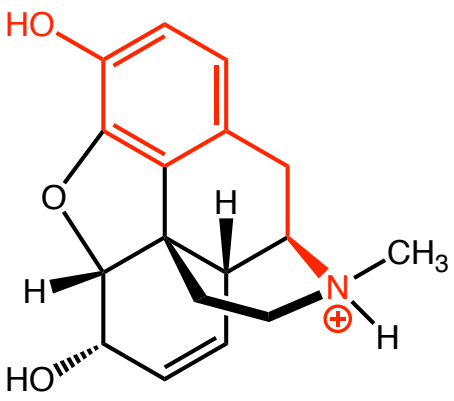
Just like the Wittig reaction!

Solid Phase Synthesis of DNA

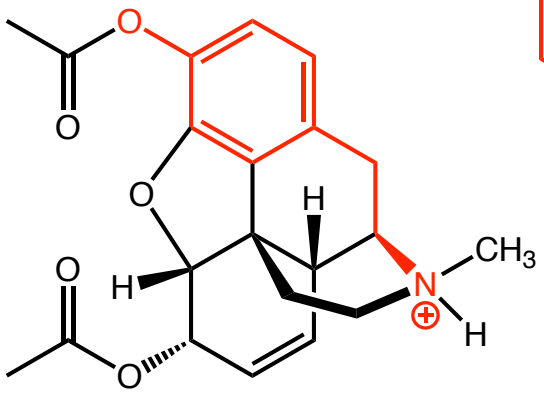




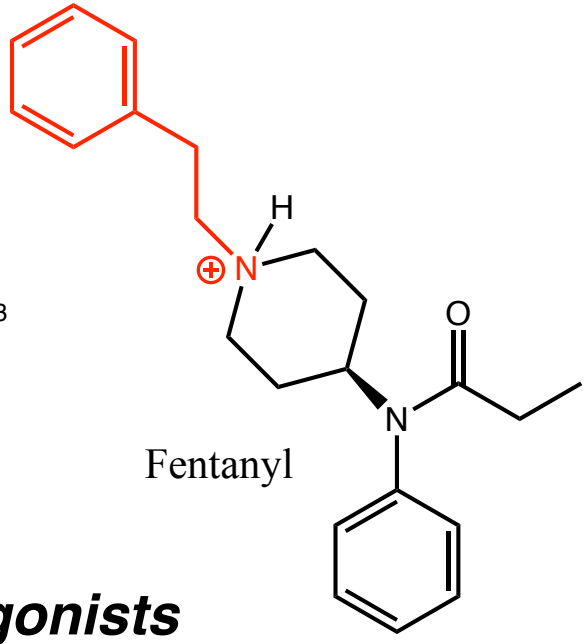
Met-enkephalin



Morphine

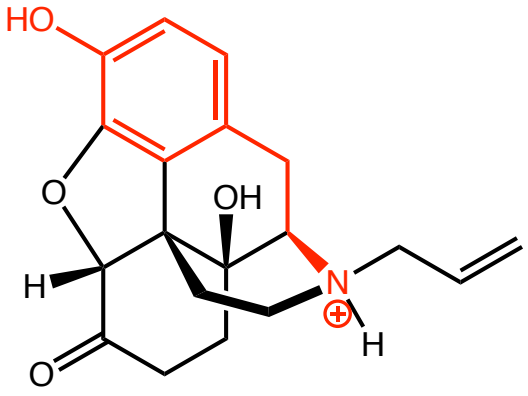


Heroin



Fentanyl

Mu-Receptor Agonists



Naloxone

Antagonist

HEALTH

Why fentanyl is deadlier than heroin, in a single photo

By Allison Bond Sept. 29, 2016 Reprints

DEA

Menu

ONE PILL CAN KILL

DEA Fentanyl Seizures in 2024

In 2023, DEA seized more than 79.5 million fentanyl-laced fake pills and nearly 12,000 pounds of fentanyl powder. The 2023 seizures are equivalent to more than 376.7 million lethal doses of fentanyl.

The 2024 fentanyl seizures represent over 93.7 million deadly doses. *

17,900,000+ Millions of Fentanyl Pills Seized

1,813+ lbs. Pounds of Fentanyl Powder Seized

* 2 mg of fentanyl equates to a potentially deadly dose

PRESS RELEASE

13 Arrested in Connection with an LSD, Fentanyl and Methamphetamine Trafficking and Money Laundering Scheme Occurring in the West Campus Area of the University of Texas at Austin

Friday, December 4, 2020

Share

For Immediate Release

U.S. Attorney's Office, Western District of Texas

Austin American-Statesman
SERVING OUR COMMUNITY SINCE 1871

Jake Ehlinger's family releases statement saying Texas player died of accidental overdose

Brian Davis
Hookem

Published 4:56 p.m. CT Oct. 21, 2021 | **Updated 3:54 p.m. CT Oct. 22, 2021**

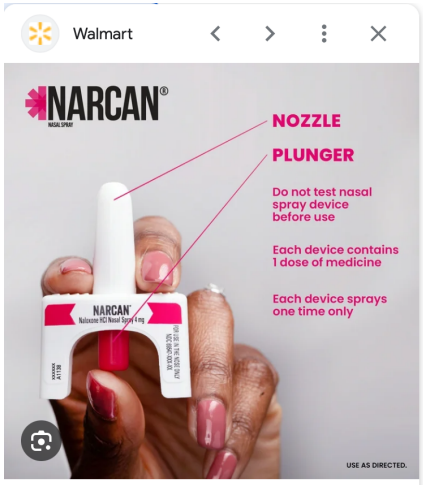
Remembering Texas linebacker Jake Ehlinger
Jake Ehlinger, younger brother of former Longhorns quarterback Sam Ehlinger, was found dead on May 6, Austin police said. *Austin American-Statesman*

SHIFT
THE CAMPUS CULTURE

SHIFT is ready for a different conversation.

For decades substance use and college campuses have been talked about as an inevitable rite of passage for college students, creating a norm that can far out shadow the dynamic pursuits of college students that revolve around academics and future opportunities.

SHIFT engages the community in dialogue that changes the culture of campus substance use from one of misuse to one of well-being.



Should I carry naloxone?

Sometimes it can be difficult to imagine how one person can have an impact on the culture of substance use – but you can! By carrying naloxone and learning the right way to administer it to someone having an opioid overdose, you have the potential to save a life. Even if you don't personally know anyone using opioids, you may find yourself in a situation where having naloxone on hand could make a huge difference. By showing that you care and taking the time to learn, you're helping to raise awareness about how important it is for each of us to play a part in shifting the culture of substance use.

How do I use naloxone?

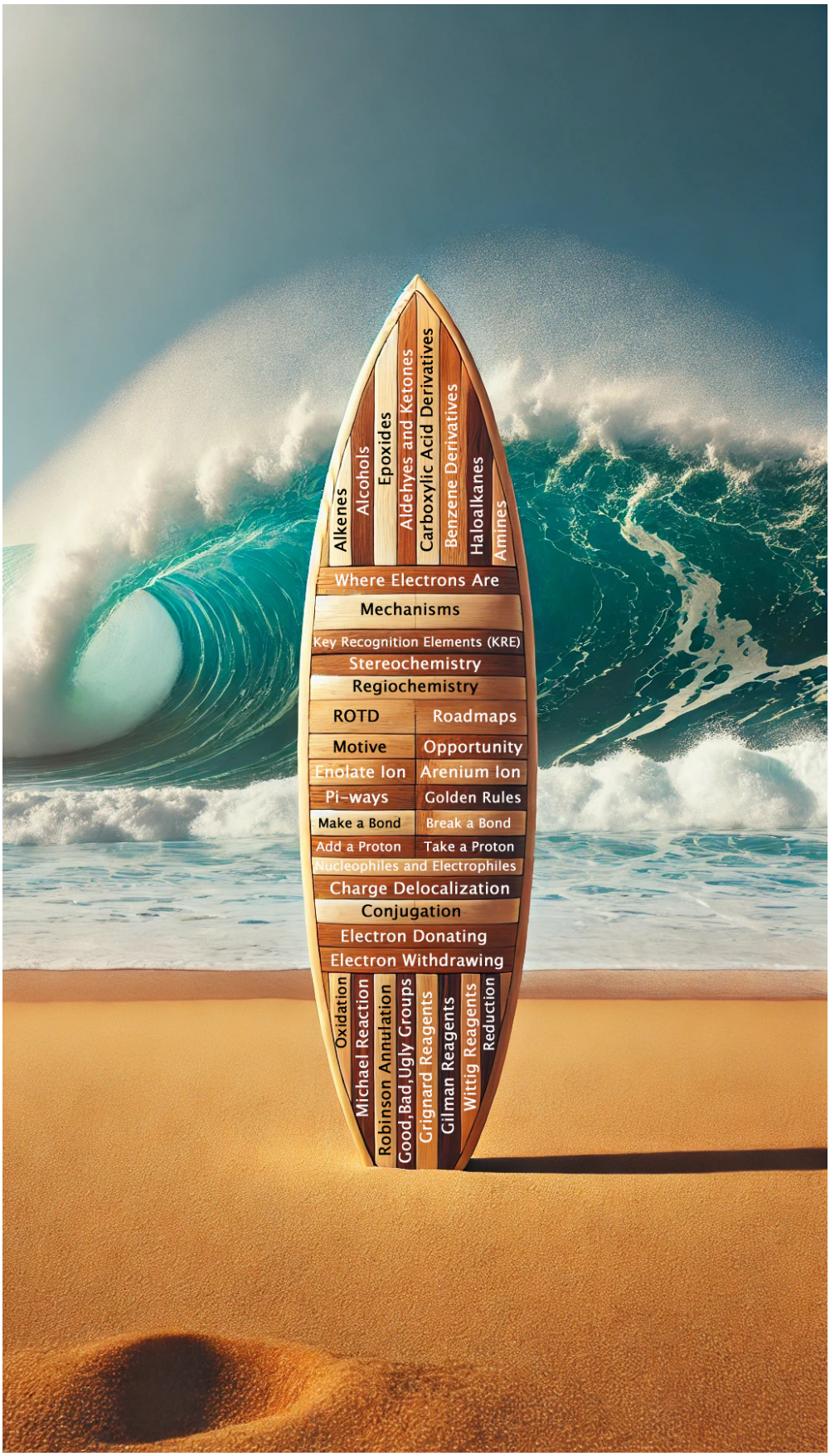
Okay, so now you know what naloxone is, and why it's so important – but how do you actually use it on someone experiencing an opioid overdose? Great question – luckily, Operation Naloxone at UT provides free trainings for students, staff, and faculty. Email shift@utexas.edu for more information. Request an Operation Naloxone training.

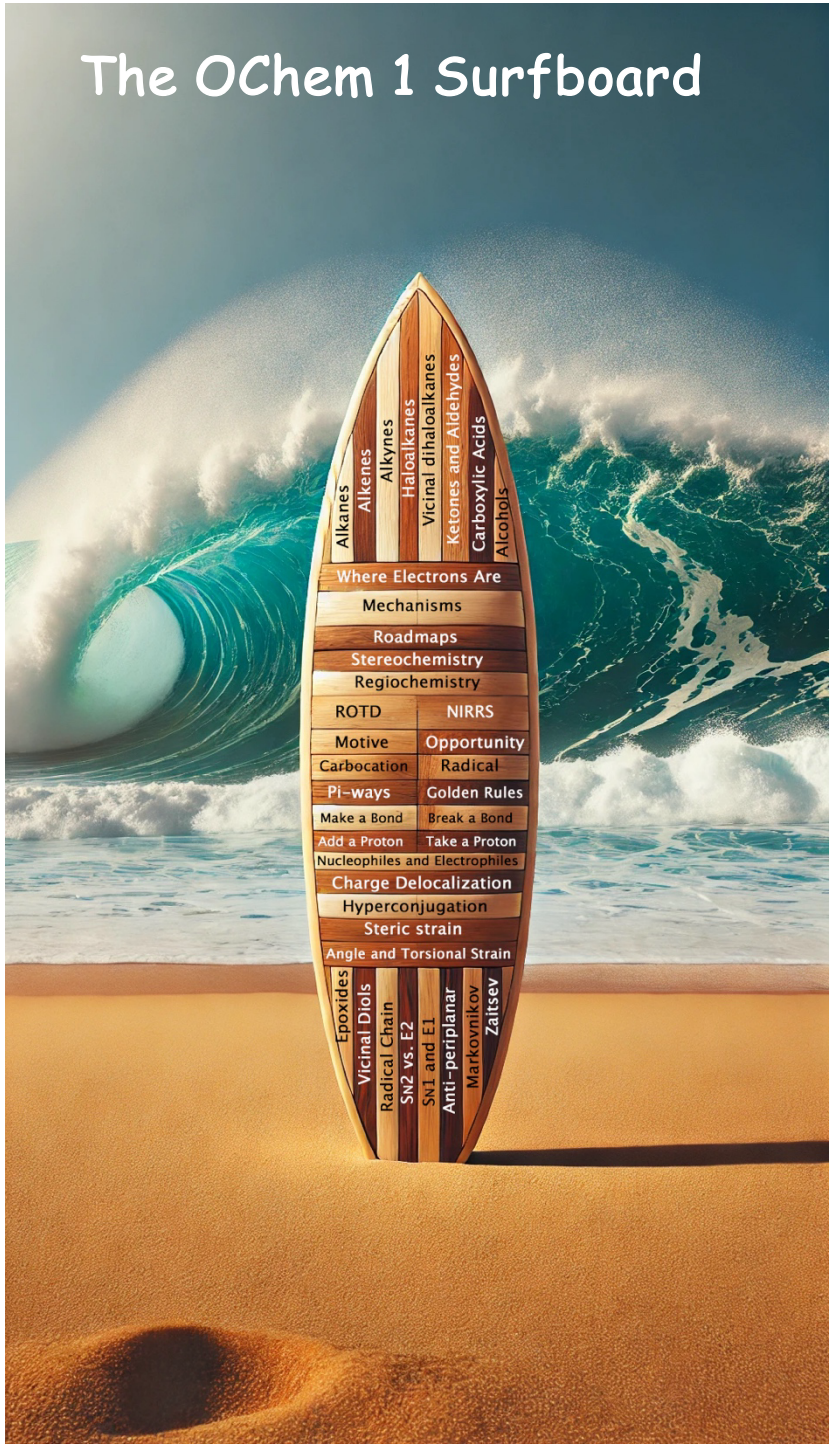
How do you administer the nasal spray version of naloxone (Narcan)?

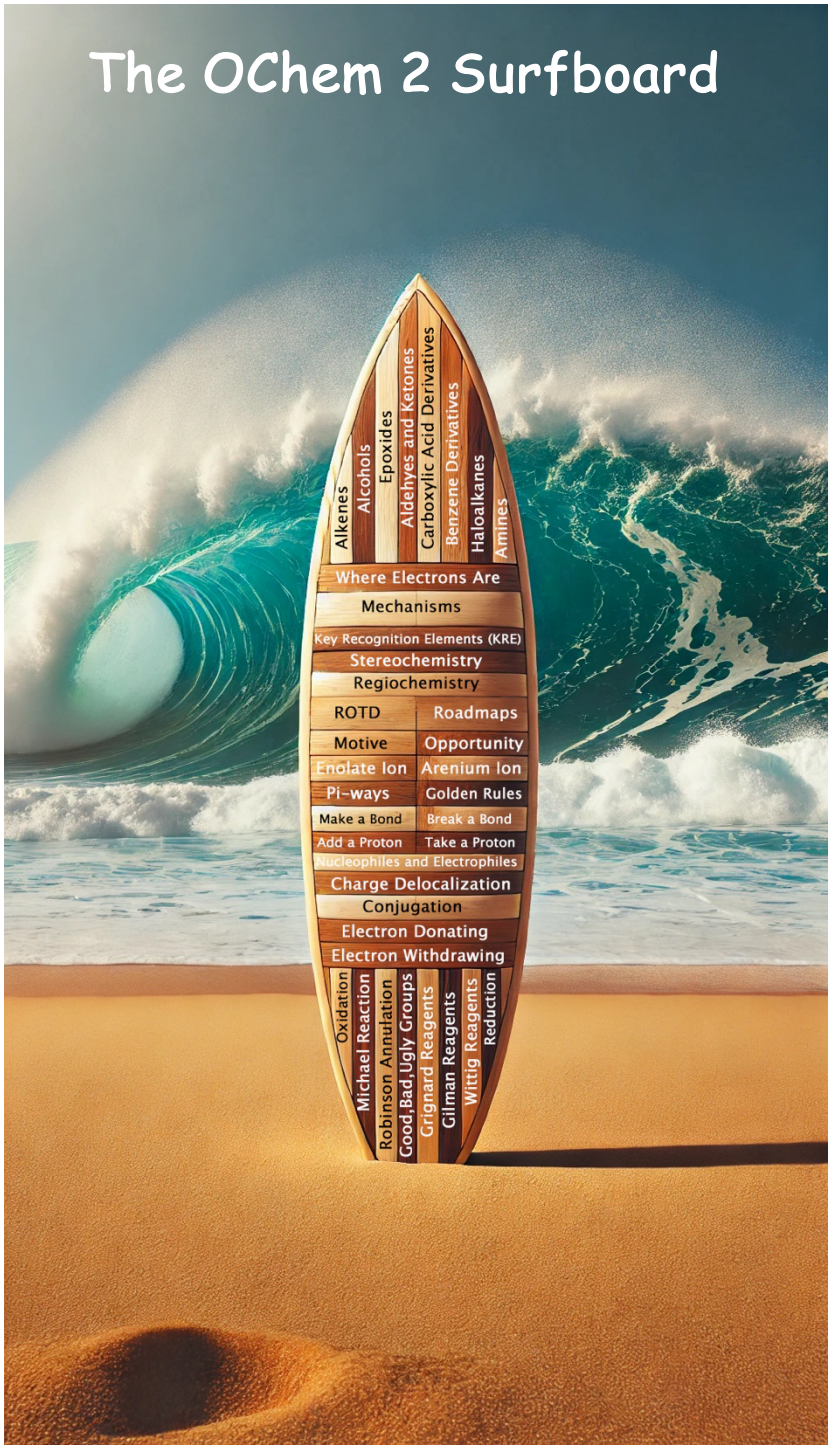
- Open the Narcan package, place the nozzle in the person's nostril and press the plunger.
- View the CDC video on how to administer Narcan.

Where can I find naloxone?

- Naloxone is available for distribution to all students, faculty, and staff at the Perry-Casteneda Library security front desk, the Longhorn Wellness Center (SSB 1.106), and the Center for Students in Recovery (Belmont 222).
- Naloxone is available for emergency access at all residence hall front desks, Sid Richardson Library, the Life Sciences Library, the Perry-Casteneda Library, and through UTPD.
- Many pharmacies dispense naloxone without a prescription, but there may be a copay depending on the insurer. You can call your insurance provider in advance to learn more about the potential copay cost.
- In Texas, you can request free naloxone via mail at MoreNarcanPlease.com.
- Map of free naloxone access sites in Austin.


Alkenes
Alcohols
Epoxides
Aldehyes and Ketones
Carboxylic Acid Derivatives
Benzene Derivatives
Haloalkanes
Amines
Where Electrons Are
Mechanisms
Key Recognition Elements (KRE)
Stereochemistry
Regiochemistry
ROTD
Roadmaps
Motive
Opportunity
Enolate Ion
Arenium Ion
Pi-ways
Golden Rules
Make a Bond
Break a Bond
Add a Proton
Take a Proton
Nucleophiles and Electrophiles
Charge Delocalization
Conjugation
Electron Donating
Electron Withdrawing
Oxidation
Michael Reaction
Robinson Annulation
Good,Bad,Ugly Groups
Grignard Reagents
Gilman Reagents
Wittig Reagents
Reduction


The OChem 1 Surfboard
Alkanes
Alkenes
Alkynes
Haloalkanes
Vicinal dihaloalkanes
Ketones and Aldehydes
Carboxylic Acids
Alcohols
Where Electrons Are
Mechanisms
Roadmaps
Stereochemistry
Regiochemistry
ROTD
NIRRS
Motive
Opportunity
Carbocation
Radical
Pi-ways
Golden Rules
Make a Bond
Break a Bond
Add a Proton
Take a Proton
Nucleophiles and Electrophiles
Charge Delocalization
Hyperconjugation
Steric strain
Angle and Torsional Strain
Epoxides
Vicinal Diols
Radical Chain
SN2 vs. E2
SN1 and E1
Anti-periplanar
Markovnikov
Zaitsev


The OChem 2 Surfboard
Alkenes
Alcohols
Epoxides
Aldehyes and Ketones
Carboxylic Acid Derivatives
Benzene Derivatives
Haloalkanes
Amines
Where Electrons Are
Mechanisms
Key Recognition Elements (KRE)
Stereochemistry
Regiochemistry
ROTD
Roadmaps
Motive
Opportunity
Enolate Ion
Arenium Ion
Pi-ways
Golden Rules
Make a Bond
Break a Bond
Add a Proton
Take a Proton
Nucleophiles and Electrophiles
Charge Delocalization
Conjugation
Electron Donating
Electron Withdrawing
Oxidation
Michael Reaction
Robinson Annulation
Good,Bad,Ugly Groups
Grignard Reagents
Gilman Reagents
Wittig Reagents
Reduction

Background on the HIV virus → AIDS

1) HIV is a retrovirus → single strand of RNA inside a protein coat → codes for 19 proteins

2) HIV infects cells of the immune system → HIV binds to specific receptors on these cells

3) Once inside the cell the RNA is reverse transcribed to DNA by a viral enzyme.
"Reverse transcriptase"

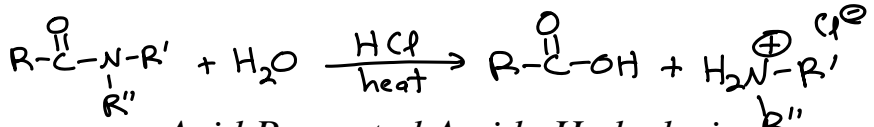
4) The DNA is integrated into the the host genome by another viral enzyme.
"Integrase"

→ The viral DNA remains inactive for some time within the DNA genome.

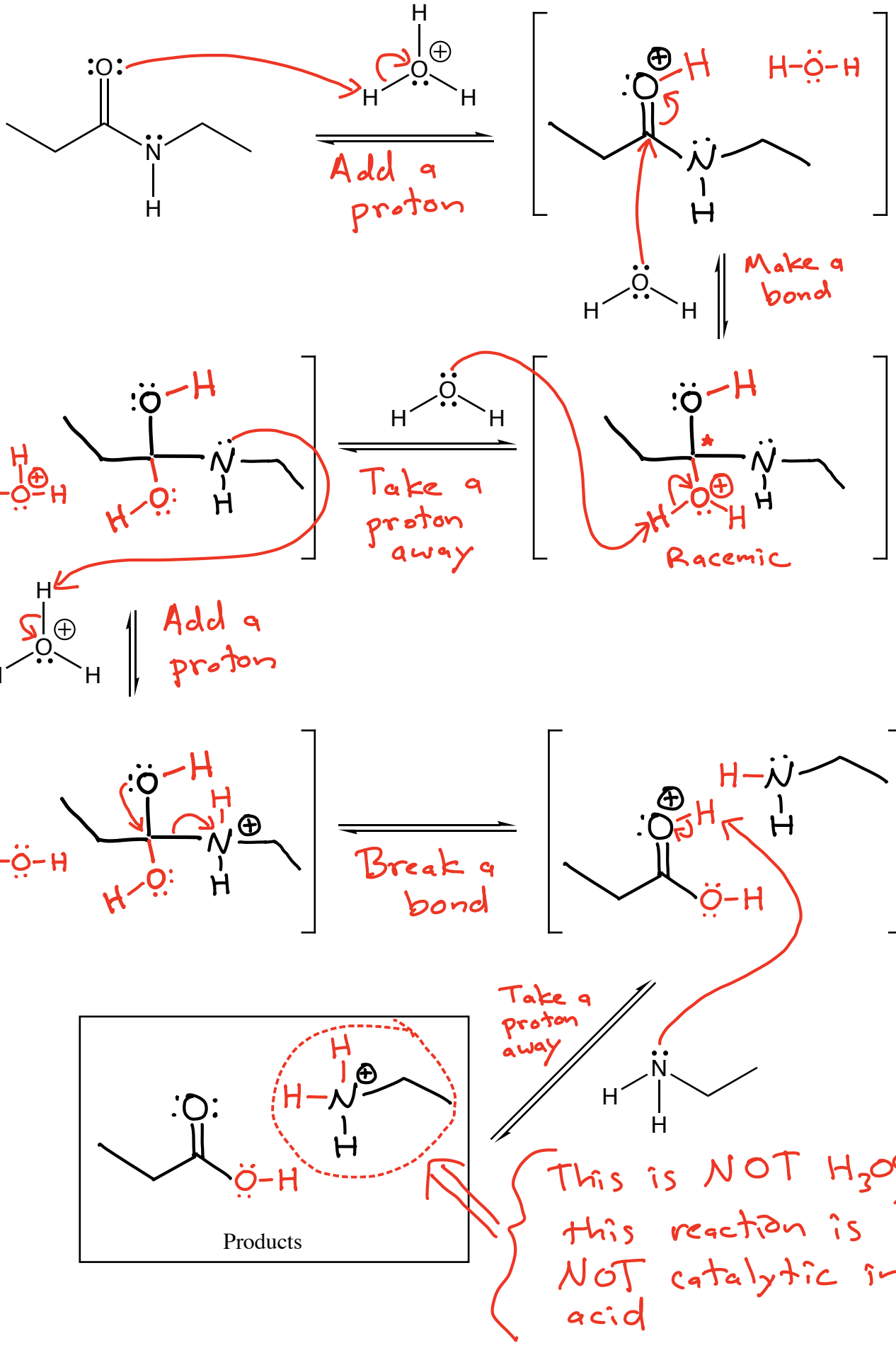
5) After an unknown signal, the viral DNA becomes active and produces a single long mRNA, that produces a very long HIV single protein. → called a polyprotein

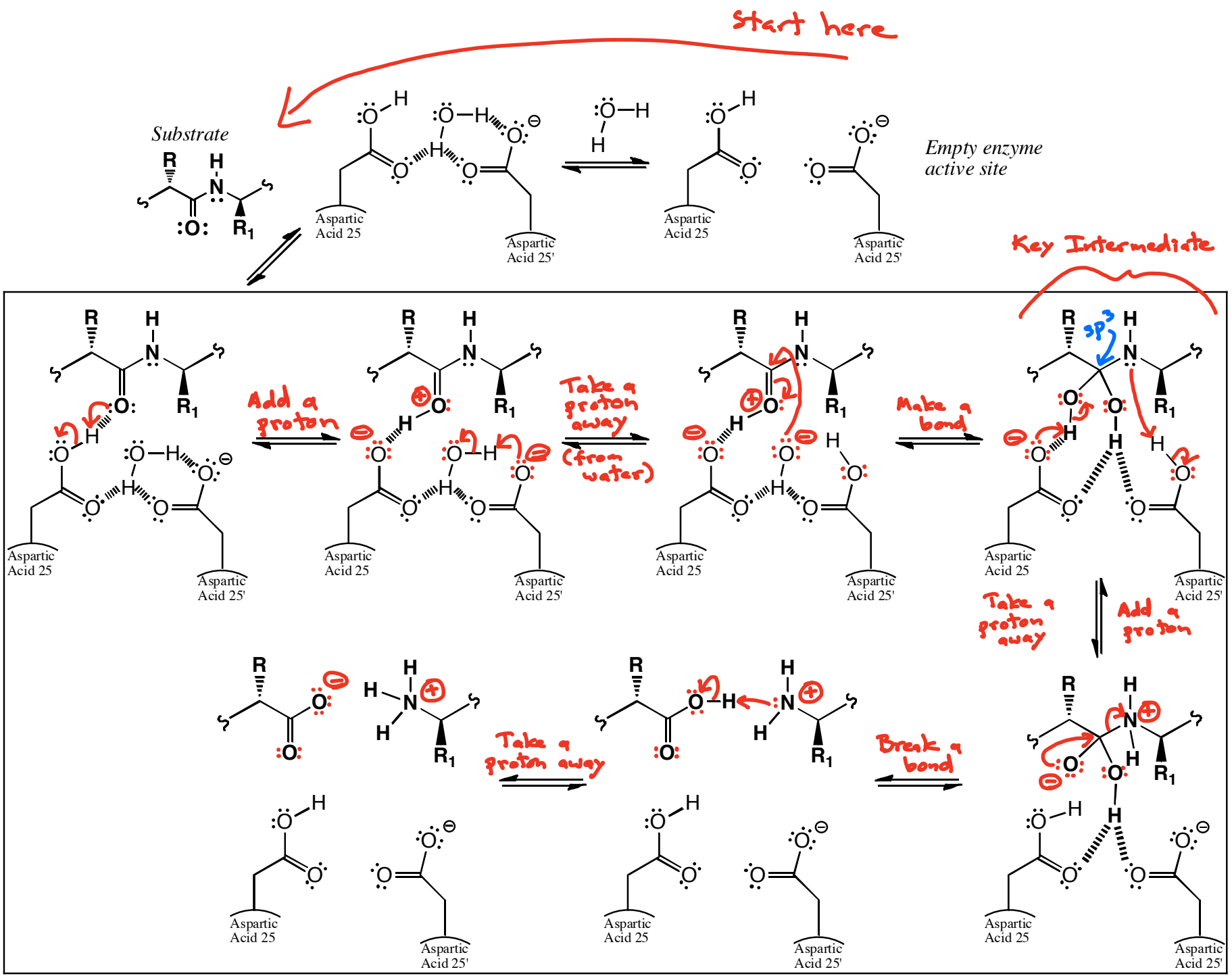
6) The HIV polyprotein is cleaved into individual proteins by another viral enzyme called the AIDS protease → cleaves amide bonds at the correct sequences. → has two carboxylic acids (Asp) at the correct location to cleave the amide bond. → called an aspartyl protease because of the two key carboxylic acid groups on aspartic acid amino acids (Asp).

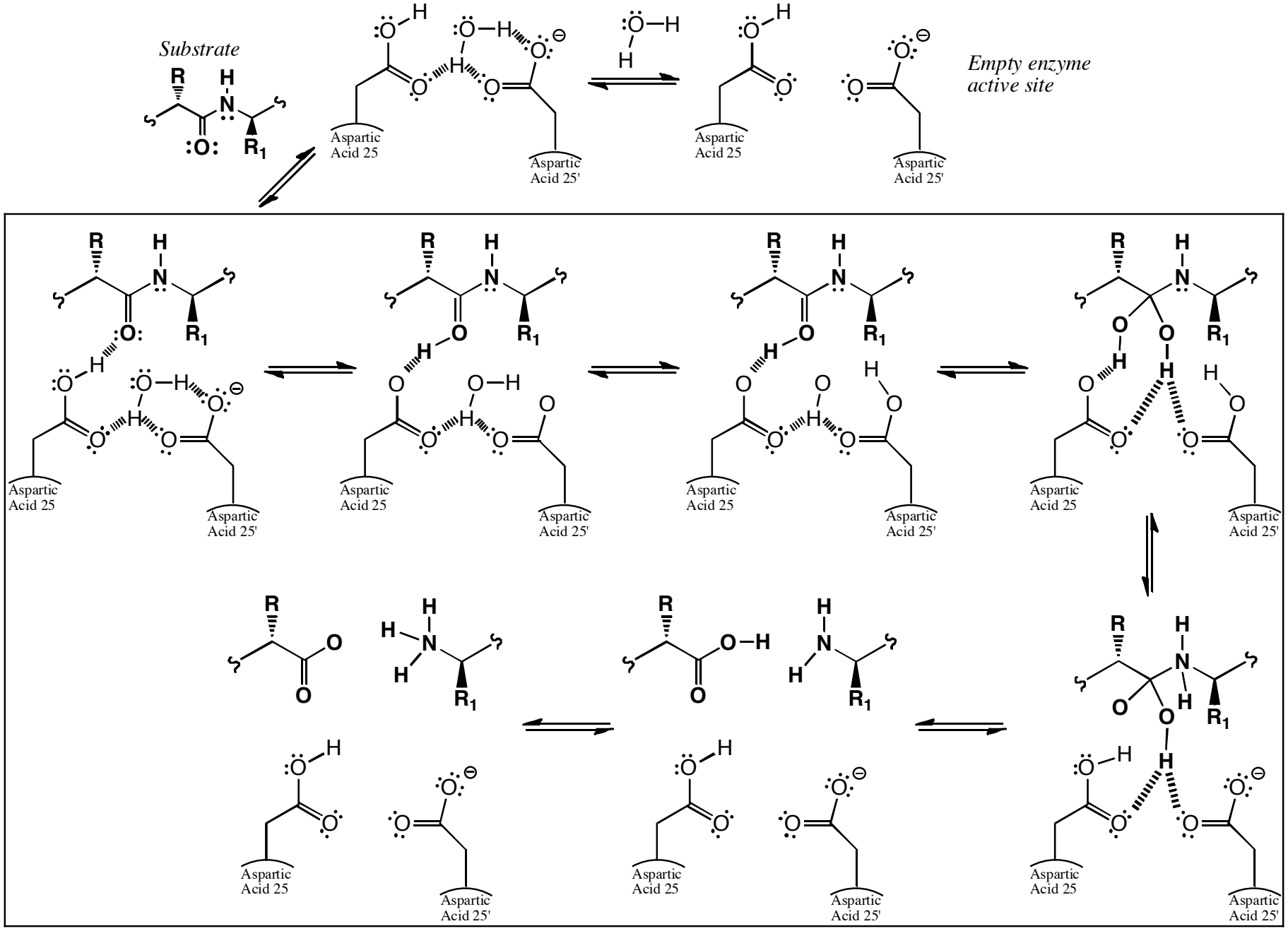
Enzymes → catalyze reactions by having an active site that places acids, bases nucleophiles and sometimes metal atoms in exactly the correct 3-d space to make the reaction happen → the active sites also lower the energy of reactions by stabilizing high energy intermediates



Acid Promoted Amide Hydrolysis




Start here
Substrate
Aspartic Acid 25
Aspartic Acid 25'
Empty enzyme active site
Key Intermediate
Add a proton
Take a proton away (from water)
Make a bond
Take a proton away
Add a proton
Take a proton away
Break a bond
sp3


Substrate
Aspartic Acid 25
Aspartic Acid 25'
Empty enzyme active site

PERSPECTIVE

OBC
www.rsc.org/obc

HIV-1 protease: mechanism and drug discovery

Ashraf Brik and Chi-Huey Wong *
Department of Chemistry and the Skaggs Institute for Chemical Biology, The Scripps Research Institute, 10550 North Torrey Pines Road, La Jolla, CA 92037, USA

Received 22nd August 2002
First published as an Advance Article on the web 26th November 2002

1 Introduction

It has now been two decades since acquired immunodeficiency syndrome (AIDS) was first reported by the US Center for Diseases Control (CDC). A few years later, it was found that a retrovirus called human immunodeficiency virus (HIV) is the causative agent in AIDS.[1] In a short time, AIDS increased to epidemic proportions throughout the world, affecting more than 40 million people today and killing so far more than 22 million (UNAIDS, 2001).

Since the outbreak of the AIDS epidemic, tremendous efforts have been directed towards development of antiretroviral therapies that target HIV type 1 in particular (HIV-1). The identification of the HIV retrovirus and the accumulated knowledge about the role of the different elements in its life cycle led researchers around the world to develop inhibitors that target different steps in the life cycle of the virus. One of these targets is HIV-1 protease (HIV PR), an essential enzyme needed in the proper assembly and maturation of infectious virions. Understanding the chemical mechanism of this enzyme has been a basic requirement in the development of efficient inhibitors. In this review, we summarize studies conducted in the last two decades on the mechanism of HIV PR and the impact of their conclusions on the drug discovery processes.

2 The life cycle of HIV

HIV belongs to the class of viruses called retroviruses, which carry genetic information in the form of RNA. HIV infects T cells that carry the CD4 antigen on their surface. The infection of the virus requires fusion of the viral and cellular membranes, a process that is mediated by the viral envelope glycoprotein (gp120, gp41) and receptors (CD4 and coreceptors, such as CCR5 or CXCR4) on the target cell. As the virus enters a cell, its RNA is reverse-transcribed to DNA by a virally encoded enzyme, the reverse transcriptase (RT). The viral DNA enters the cell nucleus, where it is integrated into the genetic material of the cell by a second virally encoded enzyme, the integrase. Activation of the host cell results in the transcription of the viral DNA into messenger RNA, which is then translated into viral proteins. HIV protease, the third virally encoded enzyme, is required in this step to cleave a viral polyprotein precursor into individual mature proteins. The viral RNA and viral proteins assemble at the cell surface into new virions, which then bud from the cell and are released to infect another cell. The extensive cell damage from the destruction of the host's genetic system to the budding and release of virions leads to the death of the infected cells.

3 HIV protease

3.1 HIV protease: a logical target for AIDS therapy

Unless the HIV life cycle is interrupted by specific treatment, the virus infection spreads rapidly throughout the body, which results in the weakness and destruction of the body's immune system. From the analysis of the HIV life cycle, one could conclude that there are several steps that might be interfered with, thus stopping the replication of the virus. For example, there are several commercially available drugs that inhibit the enzyme reverse transcriptase (RT). The first class of RT inhibitors is the nucleoside analogs such as AZT, ddI, ddC and d4T. These dideoxy compounds lack the 3′-hydroxy, causing DNA chain termination when they are incorporated into the growing DNA strand. The second class of inhibitors is the non-nucleoside inhibitors (NNIs); these inhibitors are known to bind in a pocket away from the polymerase active site, and are believed to cause a conformational change of the enzyme active site, and thus inhibit its action. Currently, there are three available non-nucleoside reverse transcriptase inhibitors (nevirapine, delavirdine, and efavirenz) for the treatment of AIDS.

Another critical step in the life cycle of HIV is the proteolytic cleavage of the polypeptide precursors into mature enzymes and structural proteins catalyzed by HIV PR. It has been shown that budded immature viral particles that contain catalytically inactive protease cannot undergo maturation to an infective form.[2] The necessity of this enzyme in the virus life cycle makes it a promising target for therapy of the HIV infection.[3]

3.2 Structure of HIV protease

Navia *et al.* from Merck laboratories were the first group to obtain a crystal structure of HIV PR;[4] a more accurate structure was reported subsequently by Kent and coworker.[5] HIV PR is a 99 amino acid aspartyl protease which functions as a homodimer with only one active site which is C_2-symmetric in the free form. More than 140 structures of the HIV-1 PR, its mutants and enzymes complexed with various inhibitors have been reported so far. A database dedicated to providing structural information about HIV PR has been created at the National Cancer Institute (http://www-fbsc.ncifcrf.gov/HIVdb/). The enzyme homodimer complexed with TL-3[6] is shown in Fig. 1 (PDB ID: 3TLH). Each monomer contains an extended β-sheet region (a glycine-rich loop) known as the flap, that constitutes in part the substrate-binding site and plays an important role in substrate binding, and one of the two essential aspartyl residues, Asp-25 and Asp-25′ which lie on the bottom of the cavity. The substrate binds in its extended conformation, in which its interactions with the different amino

Fig. 1 Structure of HIV PR complexed with TL-3 (PDB: 3TLH).

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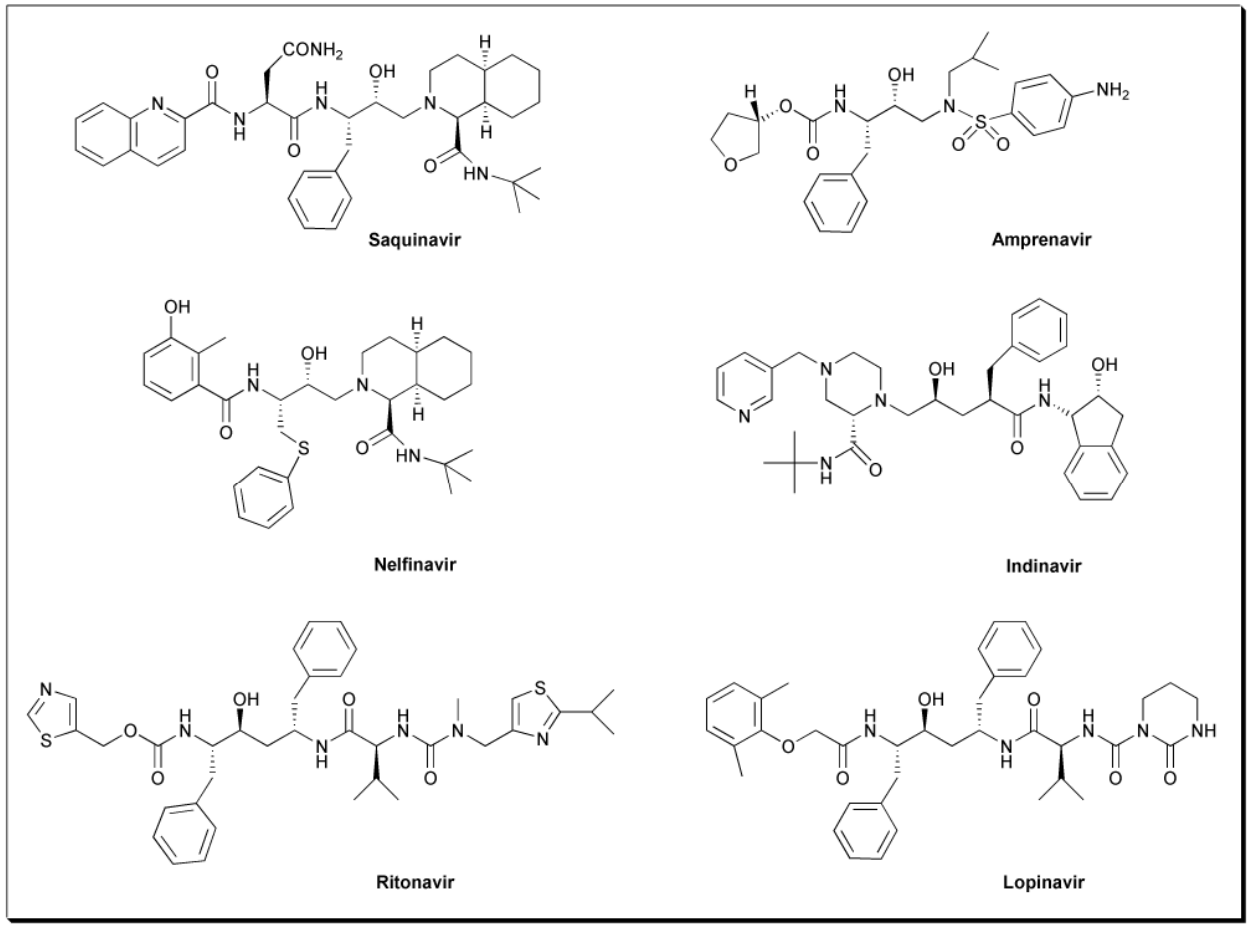
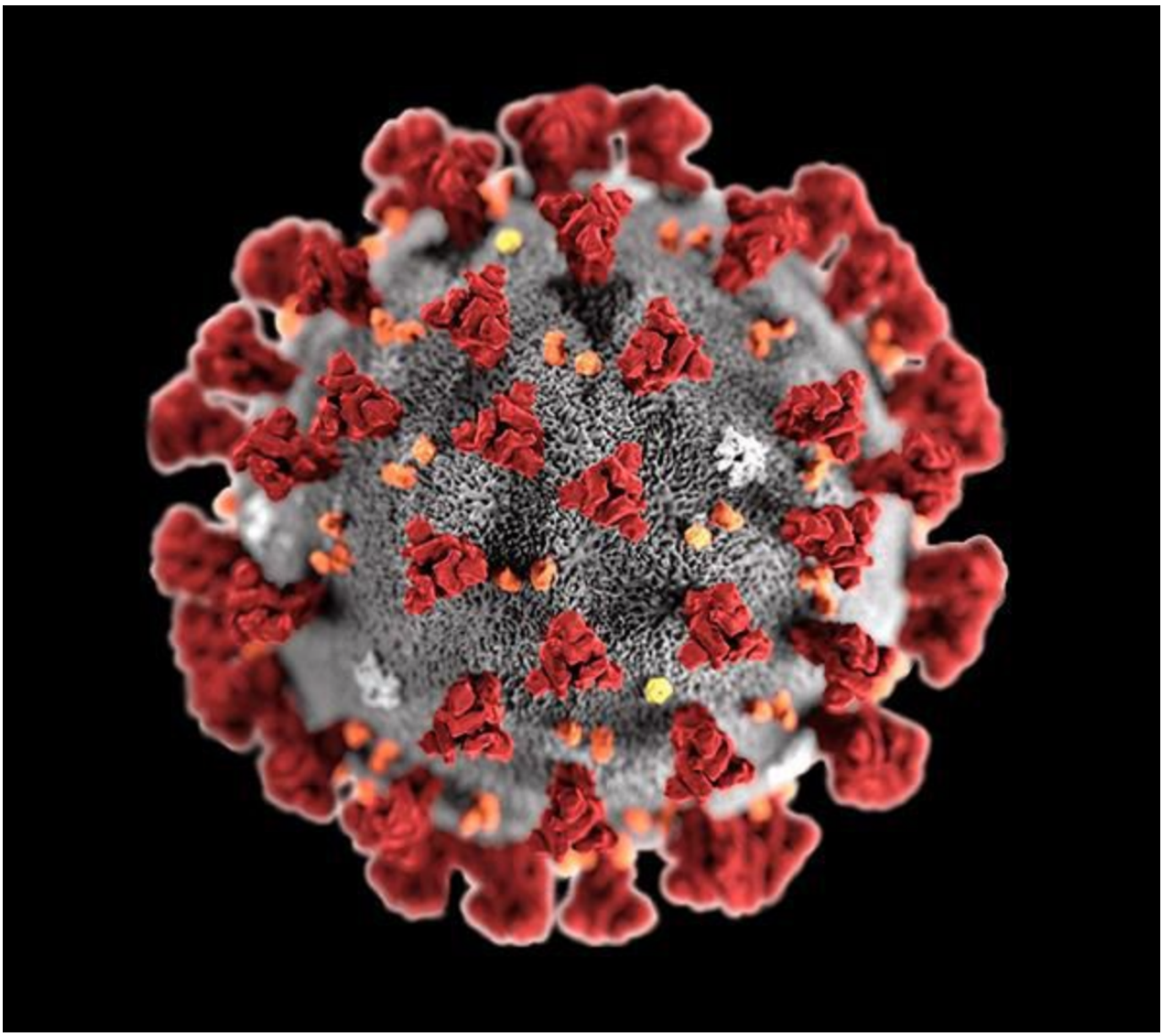


Fig. 10 FDA approved HIV-1 protease inhibitors.



Structure-based design of prefusion-stabilized SARS-CoV-2 spikes

Ching-Lin Hsieh[1], Jory A. Goldsmith[1], Jeffrey M. Schaub[1], Andrea M. DiVenere[2], Hung-Che Kuo[1], Kamyab Javanmardi[1], Kevin C. Le[2], Daniel Wrapp[1], Alison G. Lee[1], Yutong Liu[2], Chia-Wei Chou[1], Patrick O. Byrne[1], Christy K. Hjorth[1], Nicole V. Johnson[1], John Ludes-Meyers[1], Annalee W. Nguyen[2], Juyeon Park[1], Nianshuang Wang[1], Dzifa Amengor[1], Jason J. Lavinder[1,2], Gregory C. Ippolito[1,3], Jennifer A. Maynard[2]*, Ilya J. Finkelstein[1,4]*, Jason S. McLellan[1]*

[1]Department of Molecular Biosciences, University of Texas, Austin, TX 78712, USA. [2]Department of Chemical Engineering, University of Texas, Austin, TX 78712, USA. [3]Department of Oncology, Dell Medical School, University of Texas, Austin, TX 78712, USA. [4]Center for Systems and Synthetic Biology, University of Texas, Austin, TX 78712, USA.

*Corresponding author. Email: maynard@che.utexas.edu (J.A.M.); ilya@finkelsteinlab.org (I.J.F.); jmclellan@austin.utexas.edu (J.S.M.)

The COVID-19 pandemic has led to accelerated efforts to develop therapeutics and vaccines. A key target of these efforts is the spike (S) protein, which is metastable and difficult to produce recombinantly. Here, we characterized 100 structure-guided spike designs and identified 26 individual substitutions that increased protein yields and stability. Testing combinations of beneficial substitutions resulted in the identification of HexaPro, a variant with six beneficial proline substitutions exhibiting ~10-fold higher expression than its parental construct and the ability to withstand heat stress, storage at room temperature, and three freeze-thaw cycles. A 3.2 Å-resolution cryo-EM structure of HexaPro confirmed that it retains the prefusion spike conformation. High-yield production of a stabilized prefusion spike protein will accelerate the development of vaccines and serological diagnostics for SARS-CoV-2.

Mol Ther. 2008 November ; 16(11): 1833–1840. doi:10.1038/mt.2008.200.

Incorporation of Pseudouridine Into mRNA Yields Superior Nonimmunogenic Vector With Increased Translational Capacity and Biological Stability

Katalin Karikó[1], **Hiromi Muramatsu**[1], **Frank A Welsh**[1], **János Ludwig**[2], **Hiroki Kato**[3], **Shizuo Akira**[3], and **Drew Weissman**[4]

[1]Department of Neurosurgery, University of Pennsylvania, Philadelphia, Pennsylvania, USA

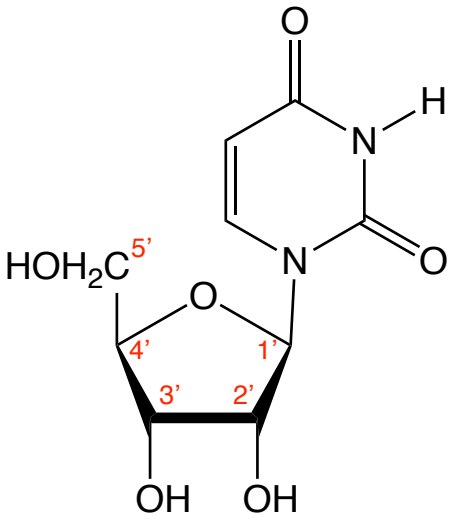
[2]Laboratory of RNA Molecular Biology, The Rockefeller University, New York, New York, USA

[3]Department of Host Defense, Research Institute for Microbial Diseases, Osaka University, Osaka, Japan

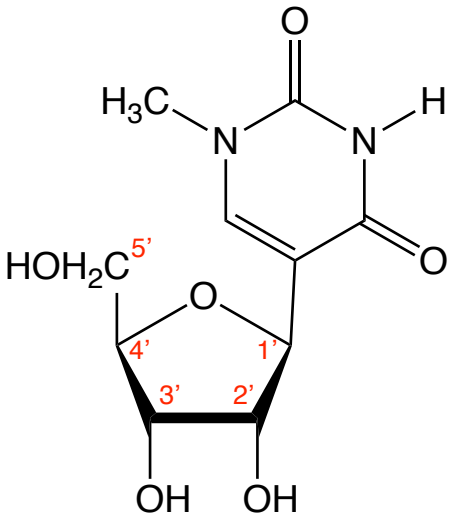
[4]Department of Medicine, University of Pennsylvania, Philadelphia, Pennsylvania, USA

Abstract

In vitro–transcribed mRNAs encoding physiologically important proteins have considerable potential for therapeutic applications. However, in its present form, mRNA is unfeasible for clinical use because of its labile and immunogenic nature. Here, we investigated whether incorporation of naturally modified nucleotides into transcripts would confer enhanced biological properties to mRNA. We found that mRNAs containing pseudouridines have a higher translational capacity than unmodified mRNAs when tested in mammalian cells and lysates or administered intravenously into mice at 0.015–0.15 mg/kg doses. The delivered mRNA and the encoded protein could be detected in the spleen at 1, 4, and 24 hours after the injection, where both products were at significantly higher levels when pseudouridine-containing mRNA was administered. Even at higher doses, only the unmodified mRNA was immunogenic, inducing high serum levels of interferon-α (IFN-α). These findings indicate that nucleoside modification is an effective approach to enhance stability and translational capacity of mRNA while diminishing its immunogenicity *in vivo*. Improved properties conferred by pseudouridine make such mRNA a promising tool for both gene replacement and vaccination.



Uridine



N1-methylpseudouridine
(m1Ψ)

Amy Rhoden Smith

Careers in Chemistry

Amy Rhoden Smith, PhD works at Precision BioSciences, a gene editing therapeutics company. As a program development leader, Dr. Rhoden Smith works with multiple teams to lead cell and gene editing therapy programs through preclinical and early clinical development. She loves working in biotechs and startups, where she can think about how to use cutting-edge science to bring meaningful therapies to patients. Dr. Rhoden Smith earned her BS in chemistry at the College of Charleston. She received her PhD in organic chemistry from the University of Texas at Austin.

Dr. Rhoden Smith has always been interested in applying her chemical knowledge to understand biological problems, so she started her career in biotechnology by joining Moderna Therapeutics. Her team used chemistry to create novel therapeutic mRNA conjugates for improved mRNA in vivo half-life and protein expression. She then moved to Intellia Therapeutics, where she led a team focused on generating Cas9 mRNA and synthetic guide RNAs for in vivo gene editing therapeutic applications. After working on projects that were discovery-based, she moved to Precision BioSciences, where she focuses on bringing products into the clinic.

Dr. Rhoden Smith says that organic chemistry gave her an understanding of how molecules interact with each other, which applies not only to small molecules, but also much larger ones like proteins, nucleic acids, and even cells. Just as importantly, it also taught her the value of problem-solving and gave her a passion for understanding complex problems, which she uses every day.

Molecular Therapy
Original Article

A Novel Amino Lipid Series for mRNA Delivery: Improved Endosomal Escape and Sustained Pharmacology and Safety in Non-human Primates

Staci Sabnis,[1] E. Sathyajith Kumarasinghe,[1] Timothy Salerno,[1] Cosmin Mihai,[1] Tatiana Ketova,[1] Joseph J. Senn,[1] Andy Lynn,[1] Alex Bulychev,[1] Iain McFadyen,[1] Joyce Chan,[1] Örn Almarsson,[1] Matthew G. Stanton,[1,2] and Kerry E. Benenato[1]

[1]Moderna Therapeutics, 200 Technology Square, Cambridge, MA 02139, USA

The success of mRNA-based therapies depends on the availability of a safe and efficient delivery vehicle. Lipid nanoparticles have been identified as a viable option. However, there are concerns whether an acceptable tolerability profile for chronic dosing can be achieved. The efficiency and tolerability of lipid nanoparticles has been attributed to the amino lipid. Therefore, we developed a new series of amino lipids that address this concern. Clear structure-activity relationships were developed that resulted in a new amino lipid that affords efficient mRNA delivery in rodent and primate models with optimal pharmacokinetics. A 1-month toxicology evaluation in rat and non-human primate demonstrated no adverse events with the new lipid nanoparticle system. Mechanistic studies demonstrate that the improved efficiency can be attributed to increased endosomal escape. This effort has resulted in the first example of the ability to safely repeat dose mRNA-containing lipid nanoparticles in non-human primate at therapeutically relevant levels.

INTRODUCTION

mRNA-based therapies have the potential to revolutionize the way we treat diseases. The surging interest in mRNA as a drug modality stems from the potential to deliver transmembrane and intracellular proteins, targets that standard biologics are unable to access due to their inability to cross the cell membrane.[1] One major challenge to making mRNA-based therapies a reality is the identification of an optimal delivery vehicle. Due to its large size, chemical instability, and potential immunogenicity, mRNA requires a delivery vehicle that can offer protection from endo- and exo-nucleases, as well as shield the cargo from immune sentinels. Lipid nanoparticles (LNPs) have been identified as a leading option in this regard.[2] Moderna Therapeutics has recently validated this approach by demonstrating safe and effective delivery of an mRNA-based vaccine formulated in LNPs.[3]

Key performance criteria for an LNP delivery system are to maximize cellular uptake and enable efficient release of mRNA from the endosome. At the same time, the LNP must provide a stable drug product and be able to be dosed safely at therapeutically relevant levels. LNPs are multi-component systems that typically consist of an amino lipid, phospholipid, cholesterol, and a PEG-lipid.[2] Each component is required for aspects of efficient delivery of the nucleic acid cargo and stability of the particle. The key component thought to drive cellular uptake, endosomal escape, and tolerability is the amino lipid. Cholesterol and the PEG-lipid contribute to the stability of the drug product both *in vivo* and on the shelf, while the phospholipid provides additional fusogenicity to the LNP, thus helping to drive endosomal escape and rendering the nucleic acid bioavailable in the cytosol of cells.

Several amino lipid series have been developed for oligonucleotide delivery over the past couple of decades.[4] The literature highlights direct links between the structure of the amino lipid and the resultant delivery efficiency and tolerability of the LNP. The amino lipid MC3 (DLin-MC3-DMA) is the most clinically advanced oligonucleotide delivery system, as siRNA formulated in MC3-based LNPs has progressed to phase III for the treatment of transthyretin-mediated amyloidosis.[5,6] More recently, literature reports have demonstrated the effectiveness of MC3-based LNPs to deliver mRNA.[7] LNPs of this class are quickly opsonized by apolipoprotein E (ApoE) when delivered intravenously (i.v.), which enables cellular uptake into hepatocytes by the low-density lipoprotein receptor (LDLr).[8] Concerns remain that MC3's long tissue half-life could contribute to unfavorable side effects hindering its use for chronic therapies.[9] In addition, LNPs can induce activation of the immune system resulting in complement activation-related pseudoallergy (CARPA), an acute immunological response that can lead to anaphylactic-like shock.[10]

To unleash the potential of mRNA therapies for humans, we required a class of LNPs with increased delivery efficiency along with a metabolic and toxicity profile that would enable chronic dosing in humans.

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[2]Present address: Generation Bio, 215 First Street, Suite 150, Cambridge, MA 02142, USA

Correspondence: Kerry E. Benenato, Moderna Therapeutics, 200 Technology Square, Cambridge, MA 02139, USA.
E-mail: kerry.benenato@modernatx.com

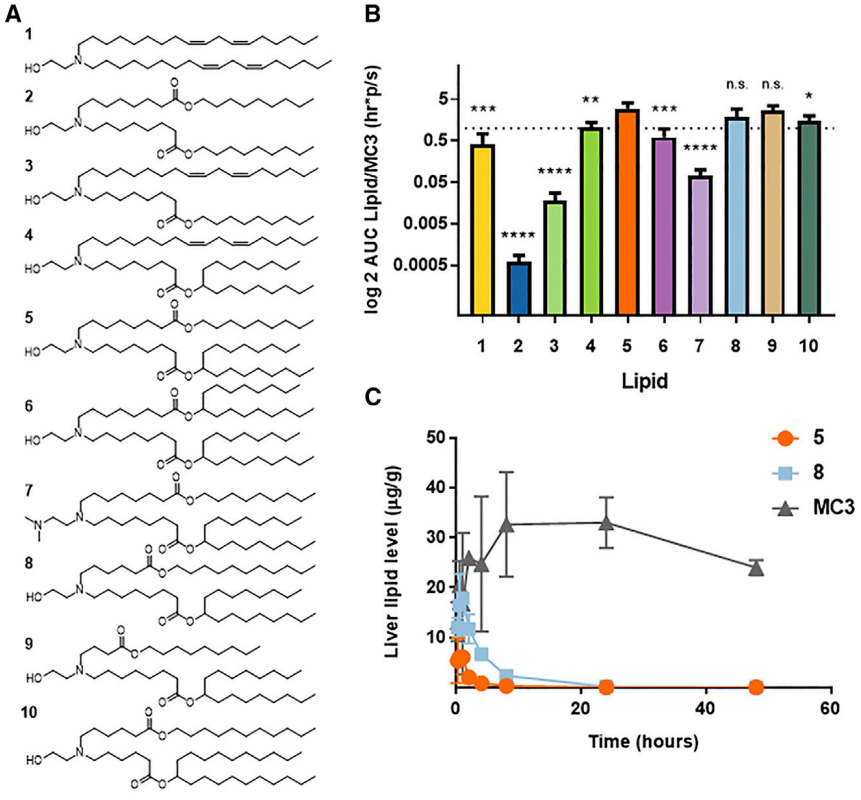


Figure 1. Optimization of Efficiency and Clearance of Amino Lipid

(A) Structures of amino lipids. (B) Whole-body luciferase bioluminescence AUC of novel LNPs versus MC3 LNPs, measured in CD-1 mice (n = 6 at 3 and 6 hr, n = 3 at 24 hr), 0.5 mg/kg dose firefly luciferase (ffLuc) mRNA, i.v. bolus, error bars indicate SD of the ratio of novel lipid AUC versus MC3 AUC. *p < 0.05, **p < 0.01, ***p < 0.001, ****p < 0.0001, n.s. = not statistically significant. (C) Parent amino lipid levels measured in liver tissue from Sprague-Dawley rats (n = 3 per time point), 0.2 mg/kg dose hEPO mRNA, mean ± SD, p < 0.05 for lipids 5 and 8 AUC relative to MC3.

We took a rational medicinal chemistry approach to amino lipid optimization aiming to identify structural motifs that provide chemical stability, optimal tissue clearance, and mRNA delivery efficiency. Our initial rodent screens led to the identification of a lead lipid with good delivery efficiency and pharmacokinetics. The lead LNP was profiled further in non-human primate for efficiency of delivery after single and repeat dosing. Finally, the optimized LNPs were evaluated in 1-month repeat dose toxicity studies in rat and non-human primate.

RESULTS

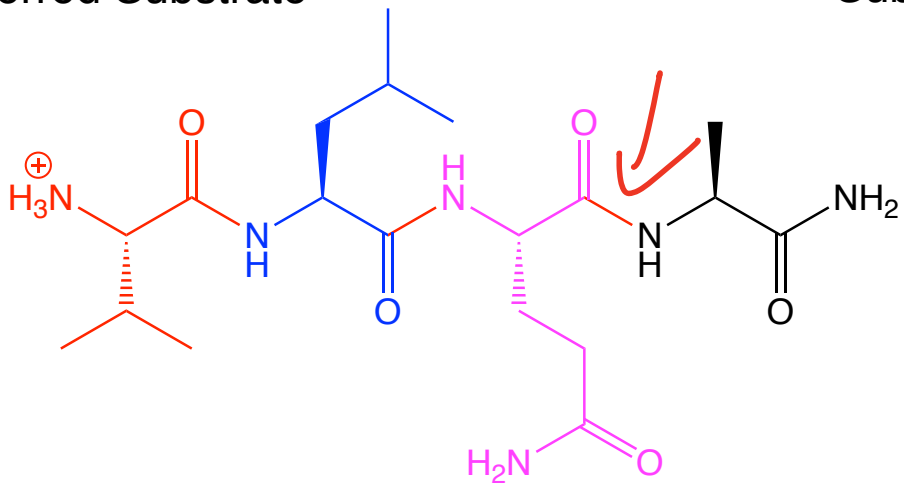
Initial screening of a broad chemical space identified ethanolamine as an amino lipid head group that could effectively drive mRNA encapsulation and provide LNPs with superior physiochemical properties. Combining the ethanolamine head group with di-linoleic lipid tails (lipid 1; Figure 1; Table 1) generated an LNP with high encapsulation of luciferase mRNA, small particle size, and low polydispersity index (PDI). The LNP with lipid 1 had a surface pK_a (apparent value for the particle) in the range that has been shown to be optimal for siRNA delivery.[11,12] To evaluate the efficiency of the new amino lipids, LNPs using the novel lipids were tested *in vivo* in mice using firefly luciferase mRNA as a reporter. An MC3 LNP was included as a control in each experiment, enabling us to compare LNPs from experiment to experiment. Measured luciferase activity also enabled us to determine protein bio-distribution. i.v. delivery of 0.5 mg/kg (mRNA dose level) of lipid 1-based LNPs to mice resulted in luciferase activity two-fold lower than an MC3 LNP control (Figure 1B). Whole-body imaging clearly demonstrated that the majority of protein expression was localized in the liver (Figure S1). We found that the lipid had similar clearance to MC3 from liver tissue with 66% of the original dose remaining in liver tissue of mice 24 hr post-dose (Table 1).

To improve tissue clearance, we introduced ester linkages in the lipid tails (lipids 2 and 3; Figure 1A), which are reported to trigger metabolism by esterases *in vivo*.[13] This has been shown to be a viable strategy to improve lipid clearance in a MC3-based lipid structure.[9] First, we established that the lipids were chemically stable by measuring ethanol stability at room temperature and 37°C (Table S1). We observed less than 1% change in purity for all lipids tested. LNPs formed with lipid 2 were significantly larger with a surface pK_a > 7 (Table 1). Removal of one ester (lipid 3) afforded LNPs with improved physiochemical characteristics and lower LNP surface pK_a. *In vivo*, neither lipid demonstrated efficient mRNA delivery (Figure 1B); however, we did observe rapid tissue clearance, with no lipid detected at 24 hr (Table 1).

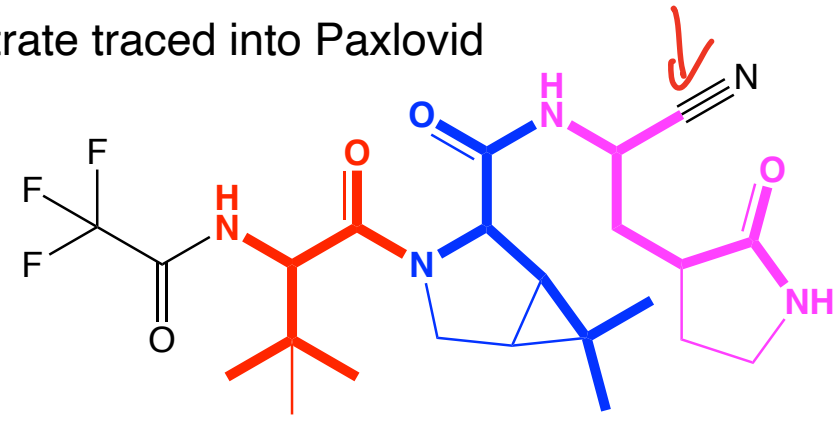
Improvement in protein expression was observed when a secondary ester was introduced (lipid 4; Figures 1A and 1B). We observed equivalent expression to MC3 LNPs, but the clearance rate was slower than lipids 2 and 3 (67% lipid remaining; Table 1). Replacement of the linoleic tail with a primary ester-containing lipid tail (lipid 5; Figure 1A) provided increased expression (3-fold higher than MC3; Figure 1B) and optimal tissue clearance (no lipid detected at 24 hr; Table 1). To further increase expression an additional secondary ester was introduced (6), but this resulted in a lowering of the surface pK_a to 6.00 and lower luciferase activity. In addition, the lipid had a significantly slower tissue clearance with 68% remaining at 24 hr.

With an optimal lipid tail structure identified we re-visited the ethanolamine head group. Lipid 7 is one representative example (Figure 1A) where the alcohol functionality is replaced with a dimethylamine. This generated an LNP with comparable physiochemical properties, but complete loss of delivery efficiency (Figure 1B).

Preferred Substrate



Substrate traced into Paxlovid



Paxlovid