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Amide Bond Bioisosteres: Strategies, Synthesis, and Successes

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Abstract

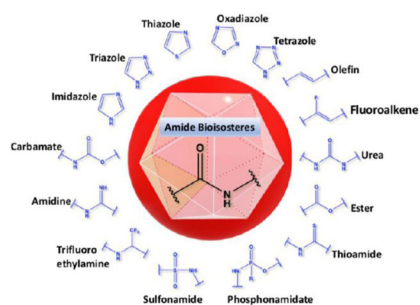
The amide functional group plays a key role in the composition of biomolecules, including many clinically approved drugs. Bioisosterism is widely employed in the rational modification of lead compounds, being used to increase potency, enhance selectivity, improve pharmacokinetic properties, eliminate toxicity, and acquire novel chemical space to secure intellectual property. The introduction of a bioisostere leads to structural changes in molecular size, shape, electronic distribution, polarity, pK_a , dipole or polarizability, which can be either favorable or detrimental to biological activity. This approach has opened up new avenues in drug design and development resulting in more efficient drug candidates introduced onto the market as well as in the clinical pipeline. Herein, we review the strategic decisions in selecting an amide bioisostere (the why), synthetic routes to each (the how), and success stories of each bioisostere (the implementation) to provide a comprehensive overview of this important toolbox for medicinal chemists.

Graphical Abstract

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INTRODUCTION

The amide functional group plays a critical role in the composition of many biologically active molecules. This includes peptides and proteins, a wide variety of chemical probes and clinically approved and experimental synthetic and naturally derived drug molecules. Consequently, the amide functionality is of extreme interest to both medicinal chemists and chemical biologists.^{1,2} The amide group enjoys significant attention due to its unique ability to form relevant hydrogen bonding interactions. An amide typically (the keto tautomer predominating) consists of two types of hydrogen bonding sites, the carbonyl group and the amine group, which may act as a hydrogen bond acceptor (HBA) and hydrogen bond donor (HBD), respectively.³ The lone pair of the amine nitrogen is not available to accept a hydrogen bond due to its role in the resonance system of the functional group which installs significant conformational rigidity that further enhances or weakens the strength of the hydrogen bonds.

A peptide bond, a term erroneously used interchangeably with an amide bond, consists of an amide composed from the linkage of an α -amino nitrogen from one amino acid with the carbonyl carbon of a second amino acid. In peptide chemistry, the partial double-bond character of the amide group (due to delocalization of the lone pair of the nitrogen) results in planar geometry and thus allows adaptation of either the *cis* or *trans* conformation. In *cis* conformation, the two α -carbon atoms ($C\alpha-C$ and $N-C\alpha$) lie on the same side of the peptide bond, whereas in the *trans* conformation these two carbon atoms are transposed. Nearly all proteins in their folded state adopt the *trans* configuration over *cis* to reduce steric hindrance between groups attached to the α -carbon atoms.⁴

The most common synthetic access to amides is provided by the reaction between a suitably functionalized carboxylic acid with a suitably functionalized amine, the same reaction that forms peptide bonds between amino acids to build proteins in biological systems.⁵ At the bench, to increase yields, shorten reaction times, and react sterically hindered or other low reactivity substrates, the most frequently employed method for the preparation of amides involves the reaction of an activated carboxylic acid derivative, such as acid chlorides, anhydrides, or esters, with amines or alternatively, the union of carboxylic acids with amines aided by stoichiometric amounts of dedicated coupling reagents, such as carbodiimides or 1*H*-benzotriazole derivatives, which achieve activation of the carboxylic acid in situ.⁶⁻⁹

The role of the amide bond has gained increasing prominence in drug design and development as more detailed knowledge about its properties has been revealed in the past century. Several top-selling drugs (Figure 1) such as lidocaine (**1**), paracetamol (**2**), the penicillins (embodied by the core structure **3**), atorvastatin (**4**), chloramphenicol (**5**), moclobemide (**6**), captopril (**7**), acetazolamide (**8**), ponatinib (**9**), methotrexate (**10**), trimethobenzamide (**11**), among others contain an amide functional group as part of their pharmacophore or auxophore.

One of the initial hurdles to overcome in the drug discovery process is the identification of a lead compound that engages a validated target in a disease of interest. In most cases, the hit compound that forms the basic structural blueprint for hit-to-lead discovery and indeed the initial lead is deficient in one or several properties required for clinical success, the required level of potency, selectivity, suitable pharmacokinetic (PK), or pharmacodynamic (PD) parameters, that impart obstacles along the path to the identification of a clinical candidate.¹⁰ To counteract many of these issues, one of the most frequently employed strategies in hit-to-lead and lead optimization involves the replacement of a selected fragment within a compound of interest with another fragment that is known to closely mimic the properties of the original fragment or functional group. This process of replacement or modification of functional groups, having similar properties, is known as isosteric or bioisosteric replacement and has become a mainstay of the medicinal chemist's toolbox.^{11–13}

Bioisosterism is considered a qualitative technique to achieve the rational modification and optimization of a bioactive compound that can provide several beneficial effects including increased potency, enhanced selectivity, improvements in PK and PD properties, elimination or attenuation of toxicity and facilitate access to novel chemical space to attain patent protection.¹⁴ Bioisosteres can be categorized into classical and nonclassical subtypes. Classical bioisosteres are functional groups that satisfy Grimm's hydride displacement law as well as Erlenmeyer's concepts of isosteres and can be subdivided into five categories: (a) monovalent atoms or groups, (b) divalent atoms or groups, (c) trivalent atoms or groups, (d) tetravalent atoms or groups, and (e) ring equivalents (Table 1). On the other hand, nonclassical bioisosteres possess more advanced mimicry of their emulated counterparts and do not fulfill the criteria of steric and electronic factors required for classical isosteres (Table 1).^{15–17,11}

The installation of a bioisostere leads to structural changes that can be either beneficial or deleterious to biological activity depending upon the effect on overall molecular size, shape, electronic distribution, lipophilicity, dipole moment, and polarizability.¹⁶ For example, the tetrazole heterocycle is a well-known bioisostere of a carboxylic acid.¹⁸ Several studies have demonstrated that the 1,2,3-triazole moiety is an amide surrogate.¹⁹ The utilization of this approach has opened new avenues in drug design and development, resulting in more efficient drug candidates that have reached the clinic as well as countless numbers in the pipeline.

The amide functional group is enzymatically very labile *in vivo*; therefore, amide bond bioisosteres that improve metabolic stability are of great interest, particularly for applications in peptide chemistry and the development of peptidomimetics.²⁰ Peptide drugs

represent a major class of pharmacologically active compounds, composed of small molecules and proteins that have been deployed to treat cancer, diabetes, infectious diseases, and cardiovascular diseases among other indications.^{21–23} The U.S. Food and Drug Administration (FDA) has approved over 60 peptide drugs, and approximately 140 new peptide therapeutics are currently being evaluated in clinical trials at the time of writing.²⁴ Although peptides are endowed with high specificity and low toxicity and are generally well-tolerated in humans, many therapeutic peptides suffer from poor metabolic stability due to the rapid degradation of the amide bond by proteases.^{25,26} Thus, the introduction of structural motifs that mimic the physicochemical properties of the amide bond provides greater metabolic stability. The replacement of the amide bond by a bioisostere can afford new peptidomimetics with improved biological properties and retention of the desired therapeutic effect. To date, several amide bioisostere classes are known, including 1,2,3-triazole, oxadiazole, imidazole, tetrazole, pyrazole, indole, pyridine, pyrazine, retroinverted and reverse amide, urea, olefin, fluoroalkene, trifluoroethylamine, amidine, ester, sulfonamide, phosphoramidate, thioamide, and carbamate. The past decade has seen enormous success in the application of these amide bioisosteres in the construction of more sophisticated and often more active compounds. Choosing the most appropriate bioisostere is a complex task. Consideration of feasible synthetic routes, modification strategies, and bioactivity effects of prior successes in the field of amide bioisosteric replacement can provide valuable insights into drug discovery projects.

There are a number of prior articles available in the literature that discuss the application of several types of classical and nonclassical bioisosteres in drug design^{27–31} along with a more recent review focused on amide bioisosteres.³² This Perspective aims to be a reference guide for medicinal chemists to peruse a selection of the most common amide bond bioisosteres and make an informed choice on a potentially appropriate moiety to employ in their project, with the caveat that any hit or lead compound of interest will possess distinct properties that may preclude some or all of the highlighted bioisosteres from either a synthetic or biological perspective. We review a broad range of amide bioisosteres covering their successful design, application of modification strategies, bioisosteric relationships, and pharmacological advancements along with a summary of synthetic methodologies adopted to access more potent therapeutic agents. In this context, we have categorized amide bioisosteres into 13 categories: heterocycles, retroinverted and reverse amide, urea, carbamate, amidine, thioamide, trifluoroethylamine, sulfonamide, phosphoramidate, ester, olefin, fluoroalkene, and finally miscellaneous bioisosteres.

FIVE-MEMBERED RING HETEROCYCLES AS AMIDE BIOISOSTERES

A. Triazole.

The triazole moiety has repeatedly shown potential application in refining the therapeutic ability of amide bond-containing molecules and therefore is considered an excellent nonclassical bioisostere. Most importantly, the triazole motif is proficient in mimicking the configuration of the *trans* amide bond; either a *trans* or a *cis* conformation can be achieved around the heterocycle depending on the substitution pattern of the triazole.³³ The 1,4-disubstituted 1,2,3-triazole scaffold is isosteric to the *trans* amide bond and has gained

widespread use (Figure 2). The 1,5-disubstituted 1,2,3-triazole moiety mimics the *cis* amide bond, and its use is much less common.³⁴ The distance between the substituents at the 1- and 4-position of the triazole ring is 5.0–5.1 Å, which is approximate to the 3.8–3.9 Å distance between *trans* amide substituents.³⁵ Several fundamental properties, such as planarity, dipole moment and hydrogen bonding properties of the 1,2,3-triazole, are comparable to those of an amide.

Similarly, the dipole moment of the amide (~4 D) and 1,2,3-triazole (~5 D) is not significantly different.³⁶ The two indicated nitrogen atoms (Figure 2) in the triazole moiety possess lone pairs of electrons that act as hydrogen bond acceptors, playing a similar role as the oxygen atom in the amide. The CH bond within the triazole exhibits a strong dipole moment and therefore can function as a hydrogen bond donor, analogous to the amide NH.³⁷ The 1,2,3-triazole unit is particularly resistant to cleavage mediated by proteases, oxidation, and hydrolysis.³⁸ In summary, the 1,2,3-triazole moiety possesses characteristics that could afford protease-resistant peptidomimetics with retained or even improved biological activity. Much literature has been published in recent years that have shown the advantages of the 1,2,3-triazole moiety.¹⁹ Successful replacement of the amide bond within bioactive scaffolds with a 1,2,3-triazole has led to the discovery of many potent bioactive molecules, including approved marketed drugs to combat human immunodeficiency virus (HIV) infection and acquired immune deficiency syndrome (AIDS), bacterial infections, cancer, and neurological disorders.

The Rana research group has investigated the RN-18 class of small molecules to target HIV-1 accessory protein viral infectivity factor (Vif) to identify novel antagonists.^{39–41} The 23 kDa Vif protein is critical for *in vivo* viral replication and has emerged as a validated target for HIV-1/AIDS drug development.^{42,43} Initially, the group had identified a lead compound RN-18 (**12**, Figure 3) that specifically antagonizes HIV-1 Vif protein function [in H9 (nonpermissive cells), IC₅₀ = 6 μM] and obstructs viral replication. Compound **12** does not inhibit viral infectivity in permissive cells, MT4 (human T-lymphoid cells), even at 100 μM which highlights its Vif specificity.

However, two significant concerns related to the potency and metabolic stability of RN-18-based Vif antagonists became an obstacle to further clinical development. In a follow-up study, the authors used the concept of bioisosterism and replaced the amide bond in **12** with 2,5-disubstituted-1,3,4-oxadiazole, 3,5-disubstituted-1,2,4-oxadiazole, 1,4-disubstituted-1*H*-1,2,3-triazole, or 1,5-disubstituted-1*H*-1,2,3-triazole moieties, aiming to improve the pharmacological profile. In the original paper, the authors did not comment on any structural role for the amide in **12**. However, they synthesized new analogs that were tested *in vitro* using wild-type HIV-1 in both H9 and MT-4 cells. Results of this experiment have shown that the installation of only the 1,4-disubstituted-1,2,3-triazole moiety (compound **13**; IC₅₀ = 1.2 μM; H9 cells, Figure 3) as an amide bond bioisostere resulted in increased potency over the parent compound (IC₅₀ = 6 μM; H9 cells). The general synthetic method (i) to access compound **13** through the application of copper catalyzed azide-alkyne cycloaddition (CuAAC) click chemistry is delineated in Scheme 1, i. Overall, compound **13** was determined to be a potent Vif antagonist. Inspired by the obtained results, a subseries of

new triazole containing analogs (based on **13**) was also synthesized that resulted in the discovery of more potent HIV-1 inhibitors than compound **13** itself.⁴⁴

Vismodegib (GDC-0449, compound **17**) is a highly specific small molecule synthetic smoothened (SMO) antagonist that inhibits the Hedgehog (Hh) signaling pathway, upregulated in basal-cell carcinoma (BCC).⁴⁵ Compound **17** was approved by the FDA in 2012 to treat locally advanced and metastatic unresectable BCC. Several clinical studies indicated that many BCC patients experienced substantial benefits from **17**; however, they developed side effects including muscle spasms, alopecia, dysgeusia, fatigue, and weight loss.^{46,47} Additionally, patients acquired resistance upon treatment with compound **17**, which was associated with Hh pathway reactivation.⁴⁸ Considering these problems, Passarella and colleagues modified the structural framework of compound **17**, aiming to improve potency as well as other pharmacological features.⁴⁹ Initially, a virtual library of 140 triazole-containing derivatives were screened. On the basis of the obtained docking results, several analogs were synthesized wherein a 1,2,3-triazole bioisostere was introduced in place of the amide of compound **17**, along with additional alterations of the substituents on the phenyl rings (Figure 4).

The *in vitro* antiproliferative activity of all synthesized compounds was determined in three cancer lines (L1210, murine leukemia cells; CEM, human T-lymphocyte cells; HeLa, human cervix carcinoma), and two endothelial cell lines (HMEC-1, human microvascular endothelial cells; BAEC, bovine aortic endothelial cells). Compound **18** possessing the 1,2,3-triazole ring in place of the amide bond (**17**) displayed an appreciable activity benefit in HMEC-1 cells ($IC_{50} = 9.6 \pm 0.7 \mu M$) as compared to parent **17** ($IC_{50} = 41 \pm 3 \mu M$). Thus, it can be considered that the triazole ring is solely responsible for lowering IC_{50} in this context. The most potent compound of the series **19**, containing further structural changes beyond the bioisostere, possessed greater influence on all tested cell lines compared with compound **17** (Figure 4). The general synthetic method (i) to obtain compounds **18** and **19** is depicted in Scheme 1, i. Overall, results suggested the 1,2,3-triazole scaffold provided favorable bioactivity outcomes on this pharmacophore.

In another study, the Passarella group synthesized triflorcas and a close analog containing a 1,2,3-triazole as an amide bond surrogate. *In silico* docking studies showed that the -NH-CO-function is involved in hydrogen bonding with Glu₁₁₂₇ and Lys₁₁₁₀ in the same way that the triazole ring is stabilized by polar interactions with Lys₁₁₁₀. Overall, docking results confirmed the binding of the 1,2,3-triazole bioisostere into the adenosine triphosphate (ATP) binding site of *N*-methyl-*N'*-nitrosoguanidine human osteosarcoma transforming gene (MET) in a similar fashion as triflorcas. Results of hepatocyte growth factor (HGF)-induced scattering of Madin-Darby canine kidney (MDCK) epithelial cells and *in vitro* tumorigenesis of H1437 cells (non-small-cell lung cancer) and GTL-16 cells (human gastric carcinoma) showed that the 1,2,3-triazole bioisostere was nearly equipotent with triflorcas. The overall results of this study suggest that the replacement of the amide bond with 1,2,3-triazole ring maintained the tumorigenesis inhibitory potential of the lead compound triflorcas.⁵⁰⁻⁵²

Imatinib is a tyrosine-kinase inhibitor that is approved for the treatment of chronic myelogenous leukemia (CML), certain types of gastrointestinal stromal tumors (GIST), and

a number of other malignancies.^{53–57} The development of resistance to imatinib called for the need to develop small molecule inhibitors that could overcome imatinib resistant in CML patients.⁵⁸ Passarella and colleagues reported the first example of amide bioisosterism in imatinib via a 1,2,3-triazole. Among all tested analogs, the most potent compound (FA030; structure not shown) possessing the 1,2,3-triazole motif in place of the amide bond of imatinib showed similar binding patterns in molecular modeling studies. FA030 displayed potent antienzymatic activity against recombinant Abl kinase but decreased activity in the imatinib-resistant mutant Abl T3151. In addition to this, FA030 decreased the phosphorylation of break point cluster region Abelson kinase (Bcr-Abl), c-Abl, signal transducer and activator of transcription 5 (STAT-5), and Src, a protooncogene encoding a non-receptor tyrosine kinase in a dose-dependent manner similar to imatinib.⁵²

Modulation of the dopamine-3 subtype receptor (D3-R) influences neuronal activity in some parts of the brain; therefore, the D3-R has gained special attention in the development of therapeutics to treat neurological diseases such as schizophrenia, Parkinson's disease (PD), and associated dyskinesias, as well as neuropsychiatric (particularly drug addiction) disorders.^{59,60} The development of selective D3-R ligands is an extremely challenging task due to their very close homology with dopamine-2 subtype receptor (D2-R).⁶¹ The Hauck Newman group discovered PG648 (**20**), OMO5–057 (**21**), and NGB2904 (**22**) as highly potent and selective D3-R ligands (Figure 5).^{62,63}

Prior structure-activity relationship (SAR) studies disclosed a molecular sketch design that consists of an amalgamation of two pharmacophores, a phenylpiperazine moiety and an extended aryl ring unit, linked via a butyl chain essential to produce D3-R partial agonism/or antagonism.⁶⁴ Moreover, the amide function provided a necessary element to impart maximum D3-R over D2-R selectivity.⁶⁵ Although **20**, **21**, and **22** have shown potent D3-R binding affinity, their poor metabolic stability, mainly due to the presence of the amide, has impeded translation of these candidates to clinical use. To resolve this issue and in an effort to find more potent and D3-R selective ligands, a library of structurally modified analogs of **20**, **21**, and **22** were synthesized, in which the amide bond was replaced with a 1,2,3-triazole scaffold to generate a library of compounds.⁶⁶

In this context, a 1,2,3-triazole was tested as a bioisosteric surrogate for the amide group in a series of compounds consisting of a substituted phenylpiperazine connected via an appropriate carbon linker to an aryl unit, with synthetic access provide by CuAAC click chemistry (Scheme 1, ii). This modification led to the discovery of compound **23**, which showed promising D3-R binding affinity and 165-fold selectivity over the D2-R, evaluated by radioligand competition binding experiments using human embryonic kidney 293 (HEK293) cells, expressing human dopamine receptor subtypes. Compound **23** displayed better metabolic stability (35%) toward mouse liver microsomes (MLM) in phase 1 metabolic stability assay experiments than **20** (11%), remaining after 1 h incubation. Thus, it indicated that 1,2,3-triazole containing molecules could provide specific resistance to CYP450-mediated phase 1 metabolism over amide bioisosteres.

In a study aiming to replace an amide linker that would be capable of sustaining and modulating amide-related bioactivity, structural modifications to capsaicin (**24**) were

explored in the context of a 1,2,3-triazole group as a bioisosteric element (Figure 6).⁶⁷ The vanilloid and cannabinoid (CB) profiles of synthesized analogs were compared with compound **24** and other capsaicinoids. Success was achieved with compound **25**, which presented antagonistic activity for vanilloid receptor 1, transient receptor potential cation channel subfamily V member 1 (TRPV1) with an IC_{50} of $0.69 \pm 0.16 \mu\text{M}$ (found inactive as TRPV1 agonist with $EC_{50} > 10000 \text{ nM}$ and therefore tested as a TRPV1 antagonist). Compound **25** was synthesized by using copper iodide (CuI) catalyzed click chemistry as shown in the Scheme 1, iii. This compound also showed a significant submicromolar affinity for human cannabinoid 1 (hCB₁) ($K_i = 0.44 \mu\text{M}$), the psychotropic cannabinoid receptor. In conclusion, the installation of a 1,2,3-triazole ring within the pharmacophore of compound **25** resulted in potent TRPV1 and CB₁ selective antagonist activity. The authors in the original paper commented on the usefulness of compound **25** as a dual and unique TRPV1/CB₁ antagonist; however, there was no mention that this was due solely to the 1,2,3-triazole bioisostere.

An example of developing potent and selective cannabinoid-2 (CB₂) receptor ligands using a bioisosteric approach was reported by Corelli and co-workers.⁶⁸ Ligands selective to the CB₂ receptor are desirable for treating pain associated with inflammation, cancer, and neuropathic conditions, which avoids the unwanted psychoactive effects typically induced by activation of the cannabinoid-1 (CB₁) receptor.^{69–71} Aiming to optimize the physicochemical properties of a previously developed lead (**26**), the authors experimented with different heteroaromatic rings as amide surrogates in a series of 4-quinolone,3-carboxylic acid derivatives. The 1,2,3-triazole ring in **27** was prepared by microwave-assisted, CuI-catalyzed azide-alkyne 1,3-dipolar cycloaddition (Scheme 1, iv). The installation of a 1,2,3-triazole motif in place of the amide bond led to the development of the most potent compound among the series, **27** (Figure 7). This compound resolved solubility issues present in the lead compound (**26**) and also showed attractive results in *in vitro* CB₁ and CB₂ binding assays.

A series of novel α -lipoic acid (LA) derivatives tethered to a chroman ring were designed, where the amide bond in previously synthesized analogs⁷² was replaced with several five-membered heterocyclic amide isosteres to study effects on the neuroprotective activity (Figure 8).⁷³ Compound **29** possessing a 1,2,3-triazole was obtained by CuAAC click chemistry, as illustrated in Scheme 1, i.

α -Lipoic acid or 1,2-dithiolane-3-pentanoic acid, reported as a therapeutic agent against oxidative stress models of death, and its structural analogs were found to be effective against reperfusion arrhythmias,⁷⁴ acetylcholinesterase inhibition,⁷⁵ butyrylcholinesterase inhibition,⁷⁶ and nitric oxide synthase inhibition.⁷⁷ Several studies also showed LA analogs as potent antiproliferative^{78–80} and anti-inflammatory agents.⁸¹ Results of neuroprotective activity experiments showed that bioisosteric replacement of the amide group in compound **28**, by a 1,2,3-triazole (**29**), improved glutamate induced oxidative stress in mouse hippocampal neurons (HT22), $EC_{50} = 2.10 \pm 0.40 \mu\text{M}$ and $EC_{50} = 0.90 \pm 0.04 \mu\text{M}$, respectively. In Figure 8, the relative potency was calculated by EC_{50} of standard/ EC_{50} of tested compound, whereas the % efficacy was calculated at a fixed concentration of $10 \mu\text{M}$ (compounds were considered to be fully, partially, or weakly neuroprotective if % efficacy is

>66–100%, >33–66%, and 33%, respectively). The SAR analysis revealed that the presence of a nitrogen heterocycle was mostly well tolerated and strongly influenced the neuroprotective activity of 5-substituted chroman derivatives, depending on the nature of the heterocycle.

An example wherein the 1,2,4-triazole was successfully installed as an amide bioisostere within a rigid ring system is found in the short-acting benzodiazepine alprazolam (**31**) (Figure 9). Benzodiazepines are a class of drugs used as anxiolytics, sedative-hypnotics, anticonvulsants, and muscle relaxants and have achieved significant economic success.^{82,83} This interesting journey started in 1963 when diazepam (**30**) was discovered and later approved for clinical use to treat anxiety, epilepsy, muscle spasms, and alcohol withdrawal symptoms.^{84–86} Compound **30** is a potent orally bioavailable central nervous system (CNS) penetrant small molecule, acting predominantly via positive allosteric modulation of γ -aminobutyric acid A (GABA_A) chloride channels in the brain.⁸⁷

In humans, **30** is metabolized by the liver cytochrome (CYP) P450 enzyme system into three pharmacologically active metabolites (Figure 10). Demethylation of **30** by CYP 2C9, 2C19, 2B6, 3A4, and 3A5 yields *N*-desmethyldiazepam/nordazepam (**32**), which is then oxidized to oxazepam (**33**). This metabolite **32** is a major circulating active metabolite (half-life of 50–120 h) equipotent to **30**. As seen in Figure 10, the oxidation at C₃ of **30** by CYP 3A4 and CYP 3A5 led to temazepam (**34**). The end product of **30** metabolism is **33** which is excreted in the urine. Each of these metabolites has a half-life of more than 24 h which in turn causes diazepam-induced toxicity. Subsequently, **33**, **32**, and **34** were developed and marketed as individual drugs.⁸⁸

In 1971, Hester and co-workers reported several close analogs of **30**, including **31**, wherein the amide functionality was replaced with a triazole moiety. Compound **31** was synthesized by refluxing 7-chloro-5-phenyl-1,3-dihydro-2*H*-benzo[*e*][1,4]diazepine-2-thione (**35**) with acethydrazide in *n*-butanol (Scheme 2) for 4 h.⁸⁹ This compound was evaluated *in vivo* using CF-1 male albino mice and was found to be more potent than the parent, compound **30**, in a variety of pharmacological assays. A few years later, **31** was approved by the FDA for the treatment of anxiety disorders. Human PD studies indicated that **31** did not produce active metabolites, resulting in significant suppression of diazepam-induced toxicity.⁹⁰

B. Oxadiazoles.

Oxadiazoles are members of the azole class of heterocycles composed of two carbons, two nitrogens, and one oxygen atom. The oxadiazole ring exists in several different regioisomeric forms: 1,2,4-isomers (two forms), 1,3,4-isomer (one form), and 1,2,5-isomer (one form) (Figure 11).⁹¹

The oxadiazole moiety is a weak base because of the inductive effect of the extra heteroatom. Electrophilic substitutions at the carbon atom of the oxadiazole ring are difficult to accomplish due to the low electron density on the carbon atom, attributed to the electron withdrawing effect of the pyridine-type nitrogen. Electrophilic attack occurs at the nitrogen if the oxadiazole ring is substituted with an electron donating group (EDG). Oxadiazoles are largely resistant to nucleophilic attack but can undergo nucleophilic substitution in the same

manner as an aliphatic sp^2 carbon. These highlighted physicochemical properties of the oxadiazole motif impart versatility for its use in medicinal chemistry, and it has been utilized in the discovery of potent anti-HIV, anticancer, antimicrobial, anti-inflammatory, antidiabetic, and antiobesity agents.⁹² Moreover, several oxadiazole-containing molecules are known as D3-R ligands,⁹³ benzodiazepine receptor agonists,⁹⁴ muscarinic receptor agonists,⁹⁵ mono-aminoxidase B inhibitors,⁹⁶ selective adenosine A_{2B} receptor antagonists,⁹⁷ and 5-hydroxytryptamine (5-HT) receptor antagonists.⁹⁸

Improved metabolic stability, membrane permeability, and bioavailability may be achieved with oxadiazoles, and they are often used as amide bioisosteres.^{92,99} Among the different regioisomeric forms, the 1,2,4-isomer and 1,3,4-isomer are most commonly employed in the bioisosteric replacement of an amide bond.¹⁰⁰ Both of these isomers can mimic the molecular planarity and dipole moment of an amide, but being a nonclassical amide bioisostere, the heterocycle shows variation in aromatic, electrostatic, and hydrogen bonding character.¹⁰¹

Researchers at Bristol-Myers Squibb evaluated the 1,2,4-oxadiazole ring as a bioisostere for the amide functionality within compound **36**, which provided BMS-708163 (**37**), a compound that proved to have potent as well as selective inhibition for γ -secretase and possessed excellent PK properties in animal models as compared to the parent (Figure 12).

The abnormal aggregation of the amyloid- β ($A\beta$) peptide is a known hallmark of Alzheimer disease (AD). Inhibition of γ -secretase is being explored to lower $A\beta$ production in the AD patient's brain.¹⁰² The γ -secretase enzyme also plays an essential role in the Notch signaling pathway, and the normal functioning of this pathway is important for proper development in all multicellular organisms.^{103,104} Therefore, the identification of a γ -secretase inhibitor with no effects at the Notch receptor is desirable.¹⁰⁵

The oxadiazole moiety of compound **37** was introduced as depicted in Scheme 3, i. *In vitro* evaluation showed that compound **37** potently inhibited both $A\beta_{40}$ ($IC_{50} = 0.30 \pm 0.15$ nM (mean \pm SD) and $A\beta_{42}$ ($IC_{50} = 0.27 \pm 0.12$ nM) cleavage in H4-8Sw cells. As designed, this compound demonstrated poor potency for Notch inhibition. Even though the parent amide-containing compound **36** showed potent γ -secretase inhibition, it possessed poor metabolic stability, indicating the potential for rapid *in vivo* clearance. In contrast, the replacement of the enzymatically labile amide bond with the oxadiazole ring significantly improved the metabolic stability of **37** [% remaining after 10 min of incubation is 32% (rat), 75% (dog), and 97% (human)]. Moreover, upon oral administration compound **37** notably reduced $A\beta_{40}$ levels in the brain, plasma, and cerebrospinal fluid in both rats and dogs.

In search of new structural lipoic acid (LA) analogs as potent neuroprotective agents, a set of 1,2-dithiolane/chroman hybrids was designed and synthesized by Koufaki et al.⁷³ Compound **28** is an amide-containing LA structural analog which was previously reported (Figure 13).⁷² Initially, this compound was found to be effective against reperfusion arrhythmias and was included in this study to check its neuroprotective ability. To explore the SAR, the amide bond in **28** was replaced by different amide bioisosteres (triazole isostere **29** is discussed previously in the 1,2,3-triazole section). The general synthetic

method to obtain a 1,2,4-oxadiazole bioisostere (**40**, Scheme 3, ii) was achieved by intermolecular cyclization of respective acyl amidoxime in the presence of tetrabutylammonium fluoride (TBAF). The neuroprotective potential of both compounds (**28** and **40**) was assessed in HT22 cells, challenged with glutamate to mediate excitotoxicity, which in turn could mimic cytotoxic conditions arising due to oxidative stress in AD and other neurodegenerative disorders. Compound **40** demonstrated substantial improvement in activity against glutamate-induced oxidative stress in HT22 cells (Figure 13) as compared to parent **28**.

In another study reported by Koufaki et al., an amide bond replacement on chroman linked with two methylene carbons to a 3,4-dimethoxyphenyl ring (**41**) was used in the identification of a potent neuroprotective agent (Figure 14).¹⁰⁶ Compound **42** bearing a 1,2,4-oxadiazole moiety was synthesized by following the general procedure as shown in Scheme 3, ii. Results of the *in vitro* evaluation of newly synthesized analogs, using glutamate-challenged HT22 cells, showed that several compounds displayed good neuroprotective ability, but among all, compound **42** demonstrated notable neuroprotection ($EC_{50} = 254 \pm 65$ nM). Hence, the amide replacement with 1,2,4-oxadiazole proved to be successful in protecting neuronal cells from oxidative stress-induced cell death.

Another example describing the potential of the oxadiazole ring as an amide surrogate was published by the Lindsley group, aiming to discover potent metabotropic glutamate receptor subtype-7 negative allosteric modulators (mGlu₇-NAMs).¹⁰⁷ Initially, two compounds **43** and **44** were identified as potent mGlu₇-NAMs.^{108,109} Both **43** and **44** displayed strong efficiency for the mGlu₇-receptor, but their poor metabolic stability attributed to the amide linker hindered their further development (Figure 15). The authors decided to replace the amide linker with several amide bioisosteres. Success was achieved with the identification of a 1,3,4-oxadiazole in compound **45**¹⁰⁷ (Figure 15) that not only demonstrated potent mGlu₇-NAM activity but also showed favorable plasma protein binding (rat $f_u = 0.10$), low predicted hepatic clearance in microsomal incubations (rat $CL_{hep} = 27.7$ mL min⁻¹ kg⁻¹), and high CNS penetration (rat $K_p = 4.9$, $K_{p,uu} = 0.65$); however, the authors did not mention the CNS penetration properties (rat f_u and rat K_p) for the parent amides **43** and **44**. Compound **45** exhibited a favorable selectivity index over another seven mGlu receptors (>10 μ M vs mGlu_{1-6,8}). As shown in Scheme 4, 2-(1*H*-imidazol-1-yl)-5-(trifluoromethoxy)benzoic acid (**46**) undergoes a propylphosphonic anhydride mediated microwave-assisted condensation of 3,4-dimethoxybenzohydrazide acid to furnish **45**.

The replacement of an amide with different isomeric forms of oxadiazole has been employed to improve metabolic stability of the parent compound in numerous bioactive compounds. One efficient example of this is found in β -homophenylalanine-based dipeptidyl peptidase enzyme inhibitors.¹¹⁰ The inhibition of dipeptidyl peptidase-4 (DPP-4) is linked to augmentation of the biological activity of the “incretin” hormones (glucagon-like peptide 1; GLP-1) and glucose-dependent insulinotropic polypeptide (GIP), which in turn is responsible for diminishing the pathophysiological symptoms of diabetes.¹¹¹ Hence, DPP-4 inhibitors, or gliptins, emerged as a promising therapeutic target for novel oral antihyperglycemic agents. Initially, the Santhera group discovered β -homophenylalanine pyrrolidine-2-ylmethylamide derivative (**47**), a potent as well as selective DPP-4 inhibitor

(Figure 16). Unfortunately, **47** suffered from high efflux ratio and low Caco-2 permeability, accounting for its poor PK properties. The bioisosteric replacement of the problematic amide employed a 1,2,4-oxadiazole and related heterocycle. Some success was achieved with the identification of two different isomeric oxadiazole containing compounds (**48** and **49**). Both compounds were found to be nearly equipotent with the parent (**47**) in DPP-4 inhibition assays, with slight improvement *in vitro* metabolic stability. Therefore, on the basis of these obtained biological results, new analogs containing an isomeric oxadiazole moiety with different substituents, which could provide long plasma half-lives to the molecule, were designed and synthesized. The adopted drug modification approach proved efficacious and led to the development of **50** and **51**, which showed excellent DPP-4 inhibitory potential *in vitro* and improved oral glucose tolerance in *ob/ob* mice and also exhibited attractive PK profiles (Figure 16). The synthetic methods for the preparation of both **50** and **51** are depicted in Scheme 5.

The final reaction in mammalian triglyceride synthesis is catalyzed by two acyl CoA:diacylglycerol acyltransferase (DGAT) enzymes (DGAT-1 and DGAT-2); out of these, inhibition of DGAT-1 is known as a feasible strategy for the treatment of diabetes and obesity.¹¹² Recently, researchers at the Novartis Institutes of Biomedical Research have explored the 1,3,4-oxadiazole moiety as an amide bioisostere (**56**, Figure 17) in search of new potent DGAT-1 inhibitors.¹¹³

Initially compound **56**, a benzimidazole derivative containing an amide linker joining the western phenyl ring, was determined to be a potent inhibitor of DGAT1.¹¹⁴ Besides its potent DGAT-1 inhibitory activity ($IC_{50} = 39$ nM; C2C12 mouse myoblast cellular assay), this compound has shown a low A–B value (0.7×10^{-6} cm/s) in the Caco-2 permeability assay and a low oral bioavailability profile *in vivo*. To improve membrane permeability and reduce efflux of the parent **56**, the initial structural changes comprised bioisosteric replacement of the amide in **57** with oxazole (**58**) and oxadiazole (**59**), along with modifications on the carboxylic acid-containing fragment. The SAR studies revealed that replacement of the amide with oxazole and oxadiazole moieties, combined with removal of the propionic acid moiety, provided potent DGAT1 inhibition (Figure 17). On the basis of this SAR, the oxadiazole moiety was chosen as the amide surrogate to incorporate into this particular chemotype. The general synthetic method to furnish 1,3,4-oxadiazole bioisostere (as in **60**) using Burgess reagent is shown in Scheme 6, i. Overall, these efforts lead to the development of a benzimidazole derivative containing a 1,3,4-oxadiazole moiety, **60**, which displayed excellent DGAT-1 inhibition (Figure 17). Moreover, this compound desirably showed poor inhibition for DGAT-2 ($IC_{50} > 10$ μ M) and a low risk of mutagenicity in the Ames assay. Compound **60** suppressed postprandial plasma triglycerides in a dose-dependent manner in healthy human subjects.

In the optimization of a series of previously identified 6-substituted 4-quinolone-3-carboxamides as highly selective and potent CB₂ receptor ligands by Corelli and colleagues,¹¹⁵ the poor solubility profile of these compounds which hampered biological assays led to the use of a bioisosteric approach to give high-affinity CB₂ receptor ligands with good selectivity, along with acceptable physicochemical properties. In a follow-up study, the amide bond present in the central core of the parent compounds^{116,117} **63** and **64** was

replaced by three different amide surrogates: a 1,2,3-triazole, a 1,3,4-oxadiazole, and a 1,2,4-oxadiazole. Second, the quinolone ring was also substituted with 2-furyl, 4-bromo, and 4-isopropoxyphenyl moieties to derive the SAR (Figure 18).⁶⁸

Results of this experiment showed that the 1,2,3-triazole-containing derivative **27** (discussed in the 1,2,3-triazole section above) emerged as the most potent CB₂ receptor ligand with promising PD and physicochemical properties. Apart from this, the 1,3,4-oxadiazole (**65**) and 1,2,4-oxadiazole (**66**) derivatives showed notable CB₂ receptor binding affinity of 6.5 ± 2.2 nM and 0.4 ± 0.1 nM, respectively (Figure 18). Unfortunately, the latter (**66**) exhibited poor selectivity over the CB₁ receptor (80-fold), while compound **65** was nearly 1500-fold more selective to the CB₁ receptor over CB₂. Overall results were compared with lead compound **26**, which showed potent CB₂ receptor binding affinity with 14,000-fold selectivity over CB₁ receptor. The general synthetic routes to access compounds **65** and **66** are shown in Scheme 6, ii, and Scheme 3, iii, respectively.

C. Imidazole.

Arguably the most successful example of amide versus imidazole bioisosterism is presented in the discovery of midazolam (**67**) at Hoffmann-LaRoche, Inc., U.S.¹¹⁸ Compound **67** or 8-chloro-6-(2-fluorophenyl)-1-methyl-4*H*-imidazo[1,5-*a*][1,4]benzodiazepine is a structural analog of **30**, in which the amide bond has been successfully replaced by an imidazole moiety (Figure 19). This structural modification increased the basicity of the molecule due to the imidazole ring nitrogen, which allowed the formation of water-soluble salts for pure aqueous injectables.¹¹⁹ Moreover, it undergoes rapid metabolic inactivation as compared to **30** and the other classical benzodiazepines which is attributed mainly to the presence of the methyl group appended to the imidazole ring. This results in a short window of action allowing greater clinical management options.

Very recently, Taghizadeh et al. reported a one-pot condensation of benzodiazepines with the monoanion of tosylmethyl isocyanide or ethyl isocynoacetate under mild conditions, which provides rapid synthetic access to **67** (Scheme 7).¹²⁰ At present, midazolam is used for the treatment of seizures,¹²¹ irregular sleeping patterns,¹²² severe agitation, procedural sedation, and anesthesia.¹²³

Several preclinical and clinical studies have shown that blocking the calcitonin gene related peptide (CGRP) receptor could be beneficial to discover therapeutic agents for preventive treatment of migraine.^{124–126} Merck Research Laboratories previously reported a potent, orally bioavailable CGRP antagonist, telcagepant (MK-0974, compound **72**), for the treatment of migraines.^{127,128} Further improvements in potency and PK properties of this lead compound **72** were sought via the isosteric replacement of the caprolactam core of **72** with several heterocyclic rings.¹²⁹ It was assumed that the inclusion of the heterocyclic ring in place of the caprolactam core of **72** would improve solubility and reduce plasma protein binding, resulting in lower serum shifts. Initially, one fused triazole derivative (compound **73**) showed comparable CGRP antagonistic potencies in CGRP binding assay and in related cell-based functional assays to **72** (Figure 20).

Unfortunately, **73** displayed poor PK properties in rats ($F=2\%$), and low permeability ($P_{app}=4 \times 10^{-6}$ cm/s) compared to **72** (rat $F=20\%$; $P_{app}=21 \times 10^{-6}$ cm/s). Upon further optimization, a fused imidazole containing molecule **74** showed the highest augmentation in permeability ($P_{app}=24 \times 10^{-6}$ cm/s) and also improved rat oral bioavailability ($F=35\%$). On the basis of these encouraging results, several structural analogs of **74**, having different substituents at both C5 and C4 on the imidazole ring, were synthesized and tested for their *in vitro* CGRP antagonistic activities. Several structural analogs of **74** have shown potent CGRP antagonistic activity in the nanomolar range (structures not shown); out of them, compound **75** (Figure 20) showed improved potency compared to **74**. Despite excellent CGRP antagonistic binding affinity ($K_i=0.04$ nM), **75** presented poor rat oral bioavailability ($F=2\%$). Persistent efforts in finding potent CGRP antagonist with desirable PK properties were continued, and consequently, azaoxindole and azabenzoxazinone-containing analogs were synthesized. Among this series of analogs, compound **76** maintained good potency and showed improved bioavailability in three species, with rat ($F=33\%$), dog ($F=28\%$), and rhesus ($F=17\%$). But in another *in vivo* model, rhesus capsaicin induced dermal vasodilation (CIDV) assay; **76** unexpectedly showed lower efficacy. Moreover, unfavorable human ether-a-go-go-related gene (hERG) activity ($IC_{50}=3.3$ μ M) of **76** impeded its development. The next challenge was to overcome hERG related undesirable activity, and therefore, structural analogs of **76** were prepared by varying different oxygenated substituents on the fused imidazole ring. The synthetic approach to provide **77** containing imidazoazepane scaffold is shown in Scheme 8. Among these tested analogs, compound **77** consists of a tertiary methyl ether which displayed excellent CGRP antagonistic activity, acceptable oral bioavailability, and diminished hERG activity. Overall, this fascinating lead optimization journey of **72** has discovered the most promising compound **77** as a preclinical candidate for the treatment of acute migraine.

Very recently, a series of heterocyclic pyrimidinedione-based HIV-1 integrase inhibitors were prepared and tested by Peese and co-workers at Bristol-Myers Squibb, USA.¹³⁰ The purpose of this study was to search for a potent HIV-1 integrase inhibitor that can resolve the issues for the development of resistance mutations associated with the first generation integrase inhibitors raltegravir and elvitegravir. Recently, two new integrase strand transfer inhibitors (INSTI's), dolutegravir and bicitegravir, gained FDA approval, and because of their reduced resistance mutation profile, they have been considered second generation integrase inhibitors.¹³¹ Raltegravir, **80**, was discovered by Merck Research Laboratories¹³² in 2008, and BMS-707035, **81**, was reported in 2018 by Bristol-Meyers Squibb as a potent HIV-1 strand transfer inhibitor.¹³³ By considering the binding patterns of **80** and **81** into the integrase enzyme, Bristol-Meyers Squibb researchers decided to replace the amide within the pyrimidinedione chemotype (as present in **80** and **81**) with different bioisosteres to improve activity against first-generation-resistant mutants while maintaining activity against wild-type integrase. New synthesizedazole heterocyclic derivatives were initially screened for antiviral activity against the NL₄₋₃ virus in a cellular assay. The SAR analysis revealed that oxazole, thiazole, and imidazole containing heterocycles showed potent activity against wild-type virus either equipotent or better than the parent amide, **81**. However, with pyrazole, oxadiazole, and triazole, the antiviral activity was lost. These compounds were also tested for their activity toward the first-generation resistance mutations Q148R, G140S/

Q148H, and N155H. The imidazole containing derivative **82** presented desirably increased potency compared with parent **81** (Figure 21). Modeling studies within the active site of the PFV (3S3N) wild-type integrase binding pocket revealed that the benzyl group of **81** is tightly positioned between Q148 and E152 (Figure 22). However, compound **82** showed a structural difference between the binding site of the wild-type integrase and the G140S/Q148H mutant. In order to provide better insights toward the altered potential of compound **82** to chelate Mg^{2+} , bite angle (θ) and *N*-partial charge of the Mg^{2+} -coordinating nitrogen were calculated and compared with **81**. Overall, modeling results suggested that the wider geometry of imidazole **82** provided optimum Mg^{2+} binding which resulted in better steric occupancy of the mutant active site (Figure 22), and this can be correlated with the improved resistance toward G140S/Q148H.

The synthetic procedure to access **82** is delineated in Scheme 9. The authors assumed that an inhibitor with a wider geometry than parent **81** would provide better binding into the active site of first-generation resistant integrase. Results of fold resistance versus wild-type ($EC_{50\text{mutant}}/EC_{50\text{wt}}$) ratio, bite angle (θ), and *N*-partial charge, calculated using Schrodinger Maestro Elements, revealed that **82** improved resistance coverage due to its wide geometry and optimum Mg^{2+} binding into the mutant active site. In rat PK studies **82** displayed low clearance (CL ($L\ min^{-1}\ kg^{-1}$) = 10) and very low volume of distribution (V_{ss} (L/kg) = 0.3), resulting in moderate plasma exposure. Overall, the imidazole motif was identified to be a promising amide bioisostere, and the viability of this class could be used for further structural modification to the parent pyrimidinedione series.

Stearoyl-CoA desaturase (SCD) has two isoforms, SCD1 and SCD5, in humans. Stearoyl-CoA desaturase 1 (SCD1) plays a critical role in regulating skeletal muscle fat metabolism.¹³⁴ High SCD activity has been connected with several diseases, including diabetes, obesity, atherosclerosis, cancer, and viral infection. Therefore, inhibition of SCD1 emerged as a novel approach for the treatment of metabolic diseases, cancer, and viral infections. Shaoyi and colleagues reported thiazolylimidazolidinone-based SCD1 inhibitors and evaluated their potential for treating metabolic diseases.¹³⁵ Initially, the Xenon group identified 2-aminothiazole-based SCD1 inhibitor **85** with moderate activity (mouse SCD1; IC_{50} = 3400 nM), and structural modification of **85** identified the more potent SCD1 inhibitor **86** with an IC_{50} (mouse) of 512 nM. Unfortunately, compound **86** showed poor human SCD1 activity determined by human liver cancer (HepG2) cell assay (IC_{50} = 2677 nM), and it was assumed that amide moieties at the C2- and C4-position of the thiazole core are the potential contributors for its poor permeability or stability in HepG2 cells. In order to improve selectivity and metabolic stability, as well as PK properties, the replacement of the amide bond at the C2-position in compound **86** (Figure 23) was undertaken by introduction of different five- or six-membered heterocycles.

From this series of analogs, compound **87**, an imidazolidinone-containing bioisostere, was identified as the most potent inhibitor in both the mouse SCD1 assay (IC_{50} = 28 nM) and the HepG2 SCD1 (IC_{50} = 53 nM) assay, but its metabolic stability was poor (10% remaining after 30 min incubation with 0.5 mg/mL rat liver microsomes). To overcome this, SAR studies continued with the thiazolylimidazolidinone (**87**) as the center core structure and variation of substituents on both the left (R1) and right (R2) side in the new analogs.

A new SAR was derived from these analogs that showed homologation at R1 by just one carbon led to drastically decreased SCD1 activity. In contrast, on the right side, a longer chain length up to propyl was able to maintain the SCD1 inhibitory activity. As illustrated in Scheme 10, imidazolidinone bioisostere was prepared by reacting ethyl 2-amino-4-methylthiazole-5-carboxylate (**89**) with 2-chloroethyl isocyanate followed by in situ cyclization in the presence of potassium carbonate. Next, further alkylation of **90** with 4-fluorobenzyl bromide afforded the substituted imidazolidinone moiety (**88**). Compound **88** (R1= pyridine-3-ylmethyl; R2 = 4-fluorobenzyl) resulted in the most potent SCD1 (mouse SCD1 IC₅₀ = 6 nM; HepG2 SCD1 IC₅₀ = 10 nM) activity along with acceptable rat liver microsomal stability (67% remaining after 30 min incubation with 0.5 mg/mL rat liver microsomes). However, in the resultant clinical studies of **88**, adverse effects related to SCD1 inhibition were observed that impeded further development.

D. Tetrazole.

The tetrazole ring is frequently used as a metabolism-resistance bioisosteric replacement for carboxylic acids.^{18,136} However, several authors have also examined the capability of a tetrazole ring as an amide bioisostere, and subsequently, tetrazole gained attention due to its viability for amide bond replacement. In a first example from the protein arginine deiminases (PADs) inhibitor field, tetrazole Cl-amidine analogs were identified as potent PAD inhibitors that show better antiproliferative activities in U2OS (PAD-4 expressing osteosarcoma bone marrow) cells as compared to the parent **92**, Cl-amidine (Figure 24).¹³⁷

Human proteins undergo a range of post-translational modifications (PTMs) such as citrullination which is catalyzed by PADs, involving the hydrolysis of arginine residues to form citrulline. Abnormal PAD activity is linked with onset and progression of ulcerative colitis, inflammatory bowel disease, rheumatoid arthritis, lupus, and certain cancers.¹³⁸ Compound **92** belongs to the haloacetamidine class that showed efficacy in a variety of preclinical models of autoimmune diseases and cancer. As **92** is a peptide-based compound; it primarily suffers from metabolic degradation by proteolysis. In this context, structural modifications of the parent compound (**92**) by replacing the C-terminal amide bond with a tetrazole ring to improve potency, selectivity, and bioavailability were performed. Tetrazole analogs of compound **92** were initially screened for their potency and selectivity by determining $k_{\text{inact}}/K_{\text{I}}$ values (a measure of potency for an irreversible inhibitor) for PAD1, -2, -3, and -4. Compound **93**, a biphenyl tetrazole *tert*-butyl Cl-amidine (the synthetic route of **93** is given in Scheme 11), showed the best potency among all tested analogs and therefore was evaluated in an antiproliferative activity assay using U2OS cells at the fixed concentration of 20 μM . Results displayed that **93** (EC₅₀ = 10 \pm 2.5 μM) has 16-fold better activity than the parent **92** (EC₅₀ = 160 \pm 20 μM), which could be attributed to its increased hydrophobicity that enhanced cell penetration.

Previously it was shown that PAD-4 isozyme-mediated histone hypercitrullination induces heterochromatin decondensation and chromatin unfolding to form neutrophil extracellular trap (NET) which causes direct organ damage and can trigger endothelial as well as epithelial cell death.¹³⁹ Therefore, in this case, inhibiting PAD-4 would be helpful to reduce NET formation. Compound **92** has been shown to block NET formation and modulate the

lupus phenotype in animal models.¹⁴⁰ Although compound **93** had very poor *in vitro* inhibitory values against the PAD-4 isozyme compared to parent **92**, it was checked for its potential to block NET formation by using a DNA/neutrophil elastase overlap assay. Strikingly, **93** was significantly more potent than **92** in the NET assay, possibly due to its hydrophobic nature, which enhanced cellular uptake.

A similarly successful tactic has been described for the identification of potent neuroprotective agents in a series of 1,2-dithiolane-based analogs. Many studies reported that LA is a potent antioxidant and it can regenerate intracellular glutathione (GSH), vitamin C, and vitamin E levels.^{141,142} Also, it has beneficial effects in a number of pathological conditions such as inflammation, neurodegeneration, ischemia-reperfusion injury, diabetes, etc. related to oxidative stress.¹⁴³ Koufaki and co-workers designed a small library of LA (or 1,2-dithiolane) based analogs where the amide bond present in LA amide-dopamine conjugate (**96**) was bioisosterically replaced by several heterocyclic five-membered rings including triazole, oxadiazole, tetrazole, and thiazole to improve neuroprotective activity with that of parent **96**.¹⁴⁴ The authors did not comment on why they decided to make conformational changes from the natural *trans*-amide (**96**) to the *cis*-amide-like tetrazole (**97**). Results of *in vitro* neuroprotection assay using glutamate challenged HT22 cells revealed that the tetrazole containing analog (**97**) displayed the strongest neuroprotective activity compared to the parent **96** and also among all tested compounds (Figure 25).

The synthetic route to access **97** is delineated in Scheme 12, i, in which trimethylsilyl azide (TMSA) in the presence of triphenylphosphine and diisopropyl azodicarboxylate (DIAD) was used to obtain the desired tetrazole intermediate. The primary SAR analysis on this series of compounds showed that potent neuroprotective activity could be achieved by insertion of the heteroaromatic head in the alkyl-1,2-dithiolane chemotype in conjunction with other antioxidant moieties such as the catechol.

In 2009, Koufaki and co-workers again conducted a similar type of study in which novel 1,2-dithiolane/chroman hybrids were designed and evaluated for their neuroprotective potential in glutamate-challenged HT22 cells.⁷³ Several nonclassical bioisosteres such as triazole (discussed in the triazole section, **29**), oxadiazole (discussed in the oxadiazole section, **40**), and tetrazole were employed to replace the amide bond in the parent compound **28**. Here, we highlight the *in vitro* neuroprotection assay results obtained upon tetrazole installation in compound **100** (Figure 26). This compound was synthesized according to the general synthetic procedure depicted in Scheme 12, i. In this study, the authors did not discuss effects on activity related to the restricted conformation obtained with the *cis*-amide-like tetrazole (**100**) compared with the *trans*-amide (**28**). Being less flexible in comparison with other dithiolane/chroman hybrids of the same series, **100** exhibited a slight reduction in activity ($EC_{50} = 3.04 \pm 1.15 \mu M$) compared to the parent amide **28** ($EC_{50} = 2.10 \pm 0.40 \mu M$). However, the percentage efficacy of both **100** (100%) and **28** (95%) was almost equal, which signifies its potent neuroprotective ability.

Neuronal nicotinic acetylcholine receptors (nAChRs) belong to the “Cys-loop” superfamily of ligand-gated ion channels, widely expressed throughout the brain, and are suggested to be a potential therapeutic target for the treatment of cognitive disorders.^{145,146} Several studies

also indicate that $\alpha 7$ -AChRs share a target for therapeutic intervention in AD and schizophrenia.^{147,148} In an effort to identify more potent $\alpha 7$ -AChRs agonist with desirable drug-like properties, Beinat and colleagues¹⁴⁹ explored the SAR of SEN12333 (**101**), a potent $\alpha 7$ -AChR agonist ($K_i = 670 \pm 119$ nM) developed by another group at Siena Biotech and Wyeth (Figure 27).¹⁵⁰ Due to limited SAR studies for this chemotype (**101**), these authors have previously identified that the four-carbon chain linker is essential for optimal binding and functional activity at $\alpha 7$ -AChRs.¹⁵¹ In the present work, the authors investigated the role of the amide bond in **101**, particularly its connectivity and bioisosteric replacement (Figure 27).

Several compounds were synthesized and tested for their agonistic activity for $\alpha 7$ -AChRs. The transposition of amide **101** to the reverse amide (structure not shown here) resulted in a marked decrease of affinity at $\alpha 7$ -AChRs over that of **101**. The bioisosteric replacement of the amide in **101** with a tetrazole ring (a *cis* amide isostere) was undertaken to provide further mechanistic details into the binding mode of **101** at $\alpha 7$ -AChR and potentially reduce the number of rotatable bonds within the molecule. X-ray crystallographic studies were performed to identify the solid-state conformations for both **101** and a tetrazole containing bioisostere (**102**). Compound **102** was readily synthesized from a corresponding amide using phosphorus pentachloride to initially afford the respective imidoyl chloride derivative followed by the addition of trimethylsilylazide to furnish the tetrazole moiety (Scheme 12, ii). The obtained Oak Ridge thermal ellipsoid plots (ORTEPs) of **101** and **102** are shown in Figure 28. These plots revealed that amide (**101**) adopts a *trans*-conformation at the lowest energy. However, the tetrazole ring (**102**) locks the amide bond into *cis*-conformation and resides in a bent form. If the binding conformation of **101** is similar to the low energy (i.e., *trans*-conformation), these studies suggest the binding mode of **101** and **102** would be vastly different. Contrary to expectations of the tetrazole bioisostere (**102**), affinity to $\alpha 7$ -AChR was completely abolished (Figure 27), which may be due to increased steric hindrance or electronics of the tetrazole ring at the receptor-binding site. Thus, the obtained SAR results provided valuable insights about the essential molecular requirements of this particular chemotype and concluded that the original amide bond connectivity, as in **101**, is favorable for binding affinity as well as agonistic activity at $\alpha 7$ -AChRs.

E. Pyrazole.

Prolylcarboxypeptidase (PrCP) or prolinecarboxypeptidase represents a potential therapeutic target for the treatment of cardiovascular, inflammatory, and metabolic diseases, wherein substantial efforts have been made to generate potent PrCP inhibitors.^{152–154} A medicinal chemistry campaign to discover novel inhibitors of PrCP at Merck Research Laboratories investigated the use of a pyrazole scaffold as an amide bioisostere in a class of previously reported PrCP inhibitors **103** and **104** to modify their PK properties while maintaining potency for both human (h) and mouse (m) PrCPs.¹⁵⁵ Compounds **103** and **104** showed potent PrCP *in vitro* inhibitory activity of IC_{50} (h, m) = 3.5 and 5 nM and IC_{50} (h, m) = 2.5 and 1.4 nM, respectively (Figure 29). In mouse PK studies, **104** showed a long half-life, which results in improved oral bioavailability as compared to **103**, which suggested that the morpholine substituent replacement could be afforded without disturbing potency. Next, when the pyrazole ring was installed (compound **105**) in place of the amide function

on this chemotype, it brought a significant loss in PrCP inhibitory activity. Further optimization was made to regain the potency. In due course, compound **106** was identified as the most potent PrCP inhibitor containing a pyrazole bioisostere (Figure 29).

Moreover, this compound also showed a modest half-life and oral bioavailability in the mouse comparable to the original amides, i.e., **103** and **104**. In summary, the preliminary installation of the pyrazole (**105**) as an amide surrogate attenuated the *in vitro* PrCP potency; however, an exhaustive SAR analysis showed that the exchange of an amino-cyclohexane core with a piperidine motif was beneficial in restoring the *in vitro* PrCP activity. Moreover, simplified analogs with no stereogenic centers including **106** were also potent PrCP inhibitors.¹⁵⁶

F. Miscellaneous Heterocyclic Amide Bioisosteres.

Several studies have shown that the CB₁ receptor, a member of the G-protein-coupled receptor (GPCRs) family, is a promising therapeutic target against a wide range of pathological conditions including mood and anxiety disorders, neuropathic pain, Huntington's disease (HD), PD, multiple sclerosis, traumatic brain and spinal cord injury, glaucoma, obesity, myocardial infarction, stroke, and hypertension.^{157,158} Previously, the indole-3-carboxamide derivatives **107** and **108** were reported as CB₁ agonists which showed potent antinociceptive activity in the mouse tail-flick test after intravenous (iv) administration, and both demonstrated a fast onset and short duration of action.^{159,160} Efforts were made at improving metabolic stability through a bioisosteric approach, and thus, introduction of conformationally constrained and steric blocking groups in place of the piperazine amide (**107** and **108**) was evaluated (Figure 30).¹⁶¹

New compounds consisting of different bioisosteric heterocycles (oxazole, 1,2,4-oxadiazole, 1,3,4-oxadiazole, thiazole, and thiadiazole) with a simple tertiary amine were synthesized and evaluated for *in vitro* CB₁ agonist activity by using Chinese hamster ovary (CHO) cells doubly transfected with human CB₁ and luciferase. The SAR analysis of this series revealed that all new compounds retained CB₁ agonistic activity. However, the replacement of the piperazine amide by a 1,2,4-thiadiazole motif (**109**) provided the best combination to retain CB₁ agonist potency (pEC₅₀ = 7.7) and metabolic stability [MLM = 71; human liver microsome (HLM) = 89] within the series (Figure 30).

Next, SAR was explored around the amine moiety and several compounds were prepared and evaluated for CB₁ receptor agonistic activity and metabolic stability. These compounds showed CB₁ agonistic activities comparable with **109**. Success was achieved upon constraining the diethyl fragment into a pyrrolidine ring (compound **110**) and with compound **111** containing a similar sized ethyl group in place of the 7-methoxy group (Figure 30). This compound displayed comparable potency and stability to **110** and was therefore selected for advanced *in vitro* experiments. Results demonstrated that **111** showed high binding affinities for both human CB₁ (pK_i = 8.2) and CB₂ (pK_i = 8.5), tested by radioligand competition binding assay using [³H] CP 55940 binding to either human CB₁ or CB₂ receptors expressed in insect Sf9 membranes. Figure 31 shows the superimposed images of **111** and **107** suggesting appropriate biomimicry by the thiadiazole moiety.

Moreover, in the mouse tail-flick test, a preclinical model of nociception, **111** showed improved duration of action after iv administration compared to the parent **107**.¹⁶¹

The matrix metalloproteinases (MMPs), also called matrixins, belong to the metzincin group of proteases, which possess a conserved zinc-binding motif in their catalytic site. These MMPs play a crucial role in many physiological processes, and their expression is increased in various pathological conditions such as inflammation, angiogenesis, metabolic bone disease, and cancer. Therefore, inhibitors of MMPs are valuable compounds for therapeutic development in these diseases.^{162–164} A series of succinyl hydroxamate matrix metalloproteinase inhibitors were prepared by incorporating both aromatic and aliphatic substituents in place of an amide moiety present in general structure **112** (Figure 32).¹⁶⁵

Previously, the 3-acyl indole ring had been employed as an isosteric replacement for an aryl amide moiety in developing platelet-activating factor (PAF) antagonists. This modification enhanced the binding energy of the series and stabilized a hydrolysis-prone amide function which resulted in the identification of several PAF antagonists with good oral bioavailability.¹⁶⁶ In this study, the authors replicated this strategy and replaced the C-terminal amide (**113**) with 3-acyl indole (**114**) to ascertain its effects on MMP inhibitory potency and oral bioavailability. Results were encouraging, and as expected, **114** was found to be a potent broad-spectrum MMP inhibitor (Figure 32). The synthetic route for **114** is delineated in Scheme 13. This compound showed modest oral bioavailability in rats similar to **113**. Furthermore, in monkeys, **114** at an oral dose of 10 mg/kg exhibited a half-life of 20 h, which was comparable to marimastat (**115**) (oral dose, 10 mg/kg; 27 h), a broad-spectrum MMP inhibitor taken as reference (Figure 32).

An example where an acetamide functional group was replaced with a trifluoroethyl, pyridine, pyrimidine, pyrazine, or thiazole ring was reported in the optimization of antagonists of the adenosine A_{2A} (A_{2A}) receptor, a GPCR mediating the physiological actions of adenosine, involved in coordinating motor functions.^{167–169} Previously, the authors have reported a series of 2,4,6-trisubstituted pyrimidines that showed potent antagonism at the A_{2A} receptor and confirmed their efficacy in haloperidol-induced catalepsy. The molecular structures of all these compounds possess an acetamide group, due to which they showed varied stability under acidic conditions; therefore, this acetamido fragment was bioisosterically replaced from compound **119** (a preclinical candidate), chosen as the starting point (Figure 33).

Preladenant was selected as the standard reference compound *in vitro* human A_{2A} receptor binding assays.¹⁷⁰ Merck introduced preladenant (SCH 420814) as a potent A_{2A} receptor antagonist for the treatment of PD. Results from clinical trials suggested the discontinuation of preladenant due to adverse events.^{169,171} The preliminary SAR analysis showed that the installation of pyrazine with 1,2,3,4-tetrahydroisoquinoline (compound **120**) improved potency more than 10-fold compared to the parent **119**. It exhibits superior antagonistic potency of 1.1 nM at human A_{2A} receptor comparable to that of preladenant (1 nM). The synthetic route to obtain the pyrazine bioisostere **120** is given in Scheme 14. On the other hand, two more compounds consisting of a thiazole with (*R*)-2-(methoxymethyl)pyrrolidine (**121**) and a pyridine with pyrazole (**122**) also displayed superior potency compared to parent

119 (Figure 33). Thus, the observed SAR trend on this series was unclear, warranting further detailed investigations.

Tyrosine kinase 2 (TYK2) belongs to the Janus kinase (JAK) family and plays a critical role in driving interleukin 12 (IL-12) and interleukin 23 (IL-23) pathways, and these pathways are correlated with the pathogenesis of autoimmune diseases such as psoriasis, lupus, multiple sclerosis, and inflammatory bowel disease.¹⁷² Therefore, TYK2 appeared as a therapeutic target for various human autoimmune diseases. The challenging task is to develop a selective TYK2 inhibitor over other JAK family members (i.e., JAK1, -2, -3) because of their high sequence homology to TYK2.¹⁷³ Lead **125** was identified as a TYK2 inhibitor, and its subsequent optimization to a fluorocyclopropane analog **126** was reported. To improve TYK2 potency, the authors prepared several structurally constrained analogs derived from lead **126**, where the amide bond was cyclized onto the pyridine ring to form fused heterocycles (Figure 34).¹⁷⁴ The prepared analogs were evaluated for their TYK2 and JAK2 inhibition and resulted in some active scaffolds including imidazopyridine, oxazolopyridine, thiazolopyridine, and pyrazolopyridine. Among them, the imidazopyridine containing analog, **127**, showed an IC₅₀ value of 1.7 nM for TYK2 along with increased selectivity over JAK-2 compared to parent **125**.

These results show that the constrained core (**127**) is a better choice over the unconstrained amide core (**125**) in terms of improving the selectivity for JAK2. Further optimization of **127** by replacement of the cyclopropylamide portion with an aminopyrimidine moiety and appending a cyano group was performed. Earlier, it was observed, as in the case of unconstrained amide series (**126**), that the introduction of a cyano group at the fourth position of the dichlorophenyl ring led to significant improvement in *in vivo* clearance in rodents. Of these new analogs, compound **128** bearing a 6-methylpyrimidine showed potent inhibition of TYK2 ($K_i = 0.7$ nM) and the IL-23 pathways in cells (EC₅₀ = 66 nM) along with high selectivity over JAK2. As described in Scheme 15, compound **128** was synthesized by reacting 2,6-dichloro-4-iodobenzoic acid (**129**), 2-chloropyridine-3,4-diamine, and polyphosphoric acid. The resulting isolated product was treated with POBr₃ solution to give the desired compound **130** (4-bromo-2-(2,6-dichloro-4-iodophenyl)-3*H*-imidazo[4,5-*c*]pyridine). Next, the mixture of compound **130**, Zn(CN)₂, and Pd(PPh₃)₄ was heated to obtain compound **131**. Finally, microwave-assisted Pd-catalyzed coupling reaction of compound **131** and 6-methylpyrimidine-4-amine was done to obtain **128**. This compound demonstrated high permeability and exhibited moderate stability in liver microsomes. Moreover, in mice, **128** displayed a dose-dependent reduction of interleukin 17 (IL-17) production in a PK/PD model and in an imiquimod-induced psoriasis model.¹⁷⁴

During research to identify new dopamine D₂ receptor modulating agents, Baures and co-workers demonstrated the bioisosteric relationship existing between the amide bond (L-prolyl-L-leucylglycinamide **132**) and diketopiperazine (DKP) functionalities (**133**, **134**, and **135**) (Figure 35).¹⁷⁵ Earlier, these authors have reported that **132** modulates the dopamine D₂ receptor by increasing the affinity of the receptor for agonists.^{176,177} Compound **133** was designed previously¹⁷⁸ to mimic an N-terminal "C5" conformation involving an intermolecular hydrogen bond between the prolyl nitrogen and the lactam NH in an analog of parent **132** (structure not shown), which possessed better activity in a number of

pharmacological assays.^{179,180} In order to further explore SAR, the DKP containing compounds **134** and **135** were designed in which a “C5” conformational mimic was incorporated into the parent structure (**132**) and a bicyclic lactam moiety was assimilated (present in a potent **132** analog, structure not shown), respectively.¹⁸¹ The dopamine receptor modulation ability of **134** and **135** was assessed by measuring activity in a [³H]spiro-peridol/*N*-propylnorapomorphine (NPA) D₂ receptor competitive binding assay in the presence as well as absence of 5'-guanylyl imidodiphosphate (Gpp(NH)p); K_H and K_L represent the inhibitor constant (K_i) of agonist calculated for the high- and low-affinity components of the [³H]spiroperidol binding, respectively (Figure 35).

The obtained results suggested that both **134** and **135** increased the affinity of the dopamine receptor for agonists and the percentage of dopamine D₂ receptors which existed in the high-affinity state. However, the potency seen with **134** and **135** was greater than the parent **132**, whereas it was not as great as observed for **133**. Furthermore, compound **134** was found to be 10 times more potent than **135** which in turn was 10 times more potent than the parent **132** in an *in vivo* assay measuring apomorphine-induced rotational behavior in a 6-hydroxydopamine-lesioned rat model of PD. The synthesis of a diketopiperazine scaffold was accomplished by reacting *N*-chloroacetyl derivative (**136**) with L-leucine benzyl ester to obtain **137**, which further gave compound **134** over several steps (Scheme 16). Many authors have also shown the bioisosteric relationship between amide and DKP which has resulted in the identification of a number of peptidomimetics and β -turn mimetics.¹⁸²

RETROINVERTED AND REVERSE AMIDES AS AMIDE BIOISOSTERES

The retroinverted or retroinverso alteration (NH–C(O)) is a popular approach for improving the resistance of an amide-containing molecule toward enzymatic cleavage, wherein the amide bond geometry and topology are maintained. This modification can be achieved by retroinversion from N → C to C → N, which does not alter the conformational flexibility of the molecule but improves the *in vivo* stability and prevents amide bond hydrolysis by proteases. On the other hand, a reverse amide, also known as a retro-amide (–C(O)NH–), retains the hydrogen bonding properties of an amide but is diametrically opposed.¹¹ Several lines of experimental evidence suggest that the change in the location of the hydrogen bond donor and acceptor influences bioactivity.^{149,183,184} Here, examples where the use of a retroinverted or reverse amide produced beneficial as well as detrimental effects are discussed.

An interesting example where the installation of the retroinverted amide as an amide isostere significantly affected target specificity is a novel aldo-keto reductase 1C3 (AKR1C3) inhibitor for the potential treatment of acute myeloid leukemia (AML) and T-cell acute lymphoblastic leukemia (T-ALL).^{183,185–187} Several structural chemical classes, such as steroids, flavones, jasmonates, and nonsteroidal anti-inflammatory drugs (NSAIDs), have been tested to identify and develop potent AKR1C3 inhibitors.¹⁸³ Unfortunately, the lack of inhibitory potency and isoform selectivity had no observable clinical efficacy in castration-resistant prostate cancer (CRPC) patients,^{188–190} preventing further clinical development. It has been reported that baccharin, a natural product isolated from honeybee propolis, is a highly selective inhibitor (500-fold selectivity over AKR1C2) of AKR1C3, with an IC₅₀

value of 0.11 μM .¹⁹¹ This discovery has made baccharin a promising hit compound for the development of more potent and selective AKR1C3 inhibitors. Similarly, we previously reported the preliminary SAR of several baccharin analogs as AKR1C3 inhibitors.¹⁹² In another study, we reported the design, synthesis, and evaluation of potent AKR1C3 inhibitors containing a more stable amide bioisostere. However, their selectivity over AKR1C1 and AKR1C2 isoforms was relatively low.¹⁹³

A recent report describes a library of compounds that were designed utilizing the concept of bioisosterism to obtain an extensive SAR map for AKR1C3 inhibition based on a baccharin pharmacophore.¹⁸³ The results of *in vitro* enzyme inhibition assays indicated that several compounds produced a marked inhibition of AKR1C3 and had moderate to significant isoform selectivity for AKR1C3 over the other isoforms. Compound **138**, a *meta*-amide baccharin analog, had potent AKR1C3 inhibition (AKR1C3 IC_{50} = 0.066 μM), with a 109-fold selectivity for AKR1C3 (Figure 36). Alteration of the central ring substitution pattern to an all *meta* arrangement and installation of a retroamide bioisostere yielded compound **139**, which was equipotent with **138** (AKR1C3 IC_{50} = 0.07 μM). Most importantly, this compound had >2800-fold selectivity for C3 over C1 and C2, thus making it the most selective AKR1C3 inhibitor across all known classes of inhibitors reported thus far (Figure 36). Modeling experiments confirmed that **139** showed better binding affinity through the formation of strong hydrogen bonds to the carbonyl of the retroinverted amide, due to the reduced distance between the amino acid hydrogen bond donors and the amide carbonyl acceptor (Figure 37).

Compound **139** was synthesized in several synthetic steps, starting from 3-bromo-5-iodobenzoyl chloride (Scheme 17). The combination of compound **139** and the antileukemic drugs daunorubicin and cytarabine produced synergism against AML and patient derived T-ALL cells. Furthermore, **139** had a >100-fold dose reduction index in a daunorubicin-resistant AML cell line and >100-fold dose reduction of cytarabine in both AML cell lines and primary T-ALL cells.

In the search for a potent melatonergic receptor agonist, a series of melatonin-based compounds has been described by de la Fuente Revenga and co-workers, where the acetamido group of melatonin (**143**) was replaced with several amide bioisosteres such as a reversed amide, oxazole, 1,2,4-oxadiazole, 1,3,4-oxadiazole, 1,3,4-oxadiazol(thio)ones, 1,3,4-triazol(thio)-ones, and 1,3,4-thiadiazole.¹⁸⁴ Compound **143**, *N*-acetyl-5-methoxytryptamine, is a neurohormone secreted primarily by the pineal gland during the night.¹⁹⁴ The physiological and pharmacological effects of **143** are primarily mediated by the activation of the high-affinity GPCRs, melatonin receptor 1 (MT_1R) and melatonin receptor 2 (MT_2R).¹⁹⁵ Numerous studies have shown that **143** and its ligands have the potential to treat pathological conditions such as sleep disturbances, type 2 diabetes, obesity, major depression, mood disorders, neurodegeneration, severe pain, inflammation, and certain forms of cancer.^{196–198} Earlier attempts involving detailed SAR exploration indicated that modifications on the acetamido group of **143** were detrimental as they caused either a substantial decrease or complete loss of binding affinity and potency for melatonin receptors (MTRs).^{199–203} Furthermore, *in silico* studies indicated that the acetamido group of **143** can form captodative hydrogen bonds at the binding site of MTRs.²⁰⁴ Therefore, the authors

installed different amide bioisosteres to replace the *N*-acetyl fragment in **143** in order to ascertain the structural binding pocket of this fragment in terms of its size, shape, electronic distribution, and lipophilicity. The binding and functional activity studies of the prepared compounds were determined using human MT₁R or MT₂R stably transfected in the Chinese hamster ovary cells. The results indicated that the replacement of the acetamido group of the parent **143** by retroamides (**144** and **145**) produced the highest binding affinities, with K_i values in the low nanomolar and subnanomolar range (Figure 38).

The SAR analysis of retroamides with unsaturated side chains indicated that alkenyl or alkynyl substitution was well tolerated but the length of the spacer affected the potency of the compounds. For example, retroamides with one methylene unit (structures not shown here) did not produce favorable results. In contrast, both **144** and **145**, which had an ethylene spacer, retained potency at MTRs. The synthetic route to access **144** and **145** is delineated in Scheme 18 where commercially available 2-(5-methoxy-1*H*-indol-3-yl)alkanoic acid was activated with carbonyldiimidazole (CDI) and then reacted with propargylamine or allylamine to obtain **144** and **145**, respectively. Furthermore, compound **144** was analyzed for brain repairing efficacy, i.e., neurogenic potential, by using rat neural stem cells as an *in vitro* system. The results of this experiment indicated that **144** induces moderate cell differentiation but failed to stimulate neural maturation. Overall, the bioisosteric replacement of an amide with a retroamide yielded compounds that retained MTRs binding affinity, suggesting that the acetamido group could be transformed without a significant loss of binding affinity.¹⁸⁴

The above examples illustrate that despite their relatively simple structural differences, reverse amide bioisosteres can overcome issues related to the potency and selectivity of amide-containing counterparts. There are of course many examples where reverse amide surrogation does not produce beneficial pharmacological effects, and one such case is discussed in the tetrazole section of this review above, where Beinat and colleagues installed reverse amide and tetrazole isosteres to develop potent α 7-AChRs agonists.¹⁴⁹

UREA BIOISOSTERES

Urea has the ability to form multiple stable hydrogen bonds with a variety of protein and receptor targets, a very important element for its molecular recognition and bioactivity. The central carbonyl functions as a nucleophile and hydrogen bond acceptor with the ability to accept two hydrogen bonds. The protons on the two nitrogens serve as hydrogen bond donors, capable of providing two to four hydrogen bonds dependent on substitution.²⁰⁵ These interactions allow for specificity in drug action, biological activity, and manipulation of physicochemical properties, which is why urea derivatives are widely used in medicinal chemistry. Ghosh and co-workers proposed that substitution on the urea nitrogen atoms significantly affects the conformational preferences of urea derivatives due to the delocalization of nonbonded electrons α to the carbonyl atom.²⁰⁶ Urea is hydrotropic, meaning it can be used to promote the solubility of poorly soluble drugs and improve the permeability of molecules it is introduced into.²⁰⁵ In some cases, urea compounds can have poor solubility or permeability. However, various techniques can be used to address this issue, for instance, modulating the hydrogen bonding ability of ureas by introducing electron

donating or electron withdrawing groups (EWGs) on the substituents, disruption of molecular planarity to enhance solubility by introducing substituents on one urea nitrogen to make it nonsymmetrical and break planarity, or introducing a substituent at the *ortho* position of *N*-aryl groups of arylureas.²⁰⁶ Overall, solubility and permeability depend on other substitutions within the molecule. There are several FDA approved drugs containing the urea moiety for use in a variety of human diseases such as antidiabetics, antibacterials, anticancer, and other therapeutic agents. Urea derivatives play a vital role in the regulation of various pharmacological activities such as the ability to improve potency and target selectivity, modulation of physiochemical properties, and contribution to metabolic liability.

In order to identify the necessary structural motifs for potent acyl-coenzyme A:cholesterol acyltransferase (ACAT) inhibition *in vitro* and hypocholesterolemic agents *in vivo*, Roark and colleagues employed a peptidomimetic approach. Initially, a series of oleic and fatty acid analogs were synthesized wherein the peptide amide bonds in *N*-(2,4,6-trimethoxyphenyl)- and *N*-(2,6-dimethylphenyl)oleamides, and stearamides underwent various bioisosteric replacements to examine effect on biological activity. Results showed that only two urea bioisosteres **148** and **149** (Figure 39) retained considerable inhibitory activity *in vitro* ($IC_{50} = 0.32 \mu M$ and $0.16 \mu M$, respectively). Although **149** showed a 4-fold decrease in potency *in vitro* ($IC_{50} = 0.16 \mu M$) compared to its amide counterpart **147** ($IC_{50} = 0.043 \mu M$) (Figure 39), it was more potent *in vivo*. When **149** was dosed at 0.05% in the diet of cholesterol-fed rats, it lowered total cholesterol by 55% versus a 38% decrease in total cholesterol with the amide-based compound at the same dose. As a result, only bioisosteres having both hydrogen bond donor and acceptor functionalities yielded compounds that retained ACAT inhibitory potency activity *in vitro* as shown by sulfonamide, thioamide, retroamides, urea, carbamate, and thiocarbamate bioisosteres. Additionally, the location of the hydrogen bond donor and acceptor was crucial as retroinverted amides were less potent than the amides. Bioisosteric analogs with no, or one, hydrogen bond donor or acceptor functionality, as shown by ester, oxymethylene, thiomethylene, methyleneamino, sulfoxide, ketomethylene, and hydroxyethylene, led to uniformly inactive compounds. Therefore, the urea moiety was an acceptable bioisosteric replacement for the amide.²⁰⁷ Later the same group extended this original fatty acid amide series to encompass β -ketoamides.²⁰⁸ A simple series of *N,N'*-diphenylurea derivatives were also found to be potent ACAT inhibitors.²⁰⁹ Further evaluation led to the identification of a novel series of potent urea derivatives and a new ACAT inhibitors. Structure-activity relationship studies in this series revealed that a certain spatial arrangement, five atom spacer, between two phenyl rings is critical, lipophilic bulk is well tolerated, the 2,6-positions of the 2,6-diisopropylphenyl are essential to orient the required carbonyl group out of plane of the phenyl ring in order to obtain optimal enzyme interactions. Isosteric replacement of the urea moiety resulted in significantly less active compounds (10- to 1000-fold). From this series of analogs, a potent inhibitor of ACAT ($IC_{50} = 0.017 \mu M$) (**150**) (Figure 39) was discovered; it dose-dependently lowered plasma cholesterol in cholesterol-fed rats, but further investigations showed the compound was poorly absorbed. To overcome this, SAR studies continued with *N*-phenyl-*N'*-(1-phenylcyclopentyl)methyl]ureas and compound **151** (Figure 39) was discovered (Scheme 19, i) which did not produce adrenal toxicity in guinea pigs and had substantial lipid-modulating

activity in a chronic model of preestablished dyslipidemia in rats. The general synthetic route to obtain compound **151** is depicted in Scheme 19, i, where the urea moiety was furnished by reacting the corresponding isocyanate and amine. Overall, subsequent evaluation in animal models of hypercholesterolemia suggested that their physical properties were important determinants of their pharmacokinetics and efficiency.

Bioisosteric replacement of an amide bond in (\pm)-15-deoxyspergualin (DSG, **155**) (Figure 40), a synthetic derivative of spergualin, a product isolated from *Bacillus laterosporus*, was explored by Lebreton and co-workers.²¹⁰ Previously, **155** has been used as an anticancer agent and in animal transplantation either in allografts, xenografts, or graft-versus-host disease (GVHD) animal models. In 1994, **155** was commercialized in Japan as an immunosuppressive agent. However, **155** has three drawbacks limiting its use: low chemical stability in aqueous solution leading to hydroxylation, presence of the inactive (+)-**155** isomer in a racemic mixture which is not reported to be immunosuppressive and can contribute to acute toxicity, and low oral bioavailability (<5%) preventing oral administration. New analogs of **155** were synthesized and tested in a GVHD model in mice. By use of a bioisosteric replacement approach, variations were implemented at the hydroxyglycine central carbon atom to prevent issues associated with chirality and hydrolytic sensitivity. Initially, a malonic derivative was identified as the first analog of a new series of potent immunosuppressive agents where the retro-inverted amide bond was linked to a hexylguanidino moiety, **156** (Figure 40). Structure-activity relationship studies where the “western-amide” was reversed compared to **155** led to active analogs at 3 and 1 mg/kg. However, other “western-amide” replacements such as a two-methylene unit, carbamate, or urea led to inactive compounds. The “easternamide” of the malonic derivative was varied and led to more analogs wherein a urea derivative, **157** was active at 3 mg/kg. Replacing the NH atoms of the urea by oxygen led to compound **158** which was prepared via acid-amine coupling using HOBt and DCC in dichloromethane (Scheme 20). Compound **158** was found to be very active at 3 mg/kg in a GVHD model (Figure 40). However, when compound **158** was tested in a more demanding model for acute organ rejection after heart allotransplantation, the urea derivative (**157**) was only slightly active, whereas compound **158** was found to be the most potent and slightly more active than compound **155** in the heart allotransplantation model in rats. This was due to the absence of chirality leading to improved chemical stability when compared to compound **158** (Figure 40); therefore, compound **158** was selected as a drug candidate.

Successful bioisosteric replacement of an amide with a urea moiety was achieved based on 1,6-naphthyridine moieties in which the lead compound **161** had similar activity as ganciclovir, an antiviral drug for human cytomegalovirus (HCMV). Previous SAR studies revealed that the optimal positions for nitrogen atoms on the naphthyridine ring are at the 1- and 6-positions.²¹¹ Additionally, substitution at C-8 and a bulky alkoxy group at the 2' - position are beneficial for activity (Figure 41).²¹² It was also discovered that the internal hydrogen bond between the NH of the amide and heteroatoms labeled N1 and O2' (Figure 41) are key to maintaining the active conformation of the molecule. Chan and co-workers evaluated new naphthyridines, wherein bioisosteric replacement of the amide group with other groups can maintain hydrogen bonds, thioamides, and urea as new anti-HCMV

compounds. First, thioamide derivatives were studied due to their structural similarity to the amide motif and potential ability for *in vivo* stability. Results showed that methoxybenzylamine substitution was 3 times less active than the parent amide. There was only slight improvement with an increase in the bulk of alkoxy substituent to 2'-ethoxybenzylamine or 2'-isopropoxybenzylamine. Replacing the amide with a longer thioamide resulted in the loss of some desirable interaction at this position; therefore, thioamide derivatives were not further studied. Next, urea derivatives were evaluated since they have the potential to form two internal hydrogen bonds. More specifically, benzyl and phenylureas were studied due to previous SAR studies revealing that substitution on naphthyridine can enhance potency leading to substitutions at carbons 3 and 8 also being evaluated. The benzylureas revealed that unsubstituted analogs resulted in nonselective activity; the 2' methoxy analog was active, and increasing the bulk of the substituent to isopropoxy resulted in enhanced activity. Similar results were seen in the phenylurea derivatives where an unsubstituted analog gave an inactive derivative, an alkoxy group substituent led to active compounds, and an increase in the bulk of the alkoxy group resulted in enhanced activity. The 2' isopropoxy derivative **162** was the most active compound (Figure 41) with $IC_{50} = 30$ ng/mL in this series. Substitution on 1,6-naphthyridine indicated that a cyano or methyl group at C-3 eliminated activity, whereas introducing a bromine atom at C-8 did not improve potency in urea derivatives. These novel anti-HCMV compounds revealed that ureas and amides are maintained in similar active conformation through internal hydrogen bonding. The lack of 2'-alkoxy substituents led to toxicity or no activity due to the presence of only one internal hydrogen bond and more degrees of freedom being present around the amide bond. Overall, internal hydrogen bonding is an important feature in 1,6-naphthyridine urea derivatives for potent activity as HCMV inhibitors.²¹³

Bioisosteric replacement of an amide with a urea moiety was compared in ceramide analogs; B13, compound **163**, a ceramide analog consisting of a phenyl group instead of an alkenyl chain and (1*R*, 2*R*) configuration versus the (2*S*, 3*R*) configuration of natural ceramides, was synthesized.²¹⁴ Previously, **163** was shown to have potent cytotoxic activity in human colon cancer cells that underwent apoptosis.²¹⁵ It also displayed selective toxicity toward malignant cells over nonmalignant cells. Moreover, it prevented metastasis in liver colon cancer cells of a nude mouse model. This led to the synthesis and evaluation of 3-alkyl-1-(1-methyl-2-phenylethyl)-ureas, novel analogs of **163**.²¹⁶ The amide group of **163** underwent a bioisosteric replacement with urea in the presence or absence of a *p*-nitro group on the phenyl ring, two hydroxyl groups on the backbone, varying stereochemistry on the backbone along with varying chain length of the alkyl chain with octyl and dodecyl groups. These derivatives were evaluated for their cytotoxic activity in five human tumor cell lines (Caki-2, human renal cancer; HT-29, human colon cancer; A549, human lung cancer; PC-3, human prostate cancer; HL-60, human leukemia). Thus, compound **163**, displayed modest activity in the HL-60 cell line ($IC_{50} = 28$ μ M) and weak activity in each of the other four cell lines (Figure 42). A urea analog, **164**, was synthesized by following the general synthetic procedure as shown in Scheme 19, ii. Compound **164** had comparable cytotoxicity in Caki-2, A549, and HL-60 but showed significantly potent cytotoxicity in HT-29 and PC-3 when compared to **163** (Figure 42). Therefore, urea serves as a suitable amide bioisostere. When the *p*-nitro group was excised, it resulted in more than a 3-fold decrease in

cytotoxicity. When octyl and dodecyl groups were added to the urea moiety, the dodecyl analogs were more active compared to octyl. This is consistent with other studies of ceramide where biological activity was enhanced with increasing acyl chain length.^{217,218} This is a known phenomenon in medicinal chemistry wherein enhanced lipophilicity increases activity to a certain limit.²¹⁹ Results showed that retention of stereochemistry on the backbone may not be essential for potent cytotoxic activity. However, this may not be certain because the **163** urea analogs containing (1*R*, 2*R*) and (1*S*, 2*S*) enantiomers displayed similar activity, while enantiomers of unsubstituted phenyl rings and 1-hydroxymethyls were inactive, making a conclusive comparison challenging. Overall, the urea motif appeared to serve as a suitable bioisosteric replacement of an amide for novel ceramide analogs.²¹⁶

The antitrypanosomal activities of novel derivatives against *Trypanosoma brucei*, the causative agent of human African trypanosomiasis (HAT), were explored.²²⁰ Human African trypanosomiasis occurs in 36 nations of sub-Saharan Africa and is an insect vectored disease caused by *Trypanosoma brucei gambiense* which progresses slowly from early stage to late stage or can progress rapidly when caused by *Trypanosoma brucei rhodesiense*. In late-stage HAT, the central nervous system is infected and the disease becomes fatal if patients are left untreated regardless of the contributing parasite.²²¹ The compound 2-(2-benzamido)ethyl-4-phenylthiazole **165** (Figure 43) was one of 1035 compounds from a phenotypic high-throughput screen of 700,000 compounds that inhibited the growth of *T. brucei in vitro* at concentrations below 3.6 μM and was nontoxic to mammalian cells (Huh7). A total of 82 novel analogs were synthesized by Patrick and colleagues and tested against *T. brucei rhodesiense* STIB900 and L6 rat myoblast cells for cytotoxicity *in vitro*. It was found that 44 derivatives were more potent than **165** with antiparasitic IC₅₀ values ranging from 9 nM to >300 μM in which eight of them displayed IC₅₀ values below 100 nM. Overall, ureas were significantly more potent than amides in addition to being more selective for the parasite. From these, the most potent and selective for *T. brucei rhodesiense* was a piperidyl urea analog **166** with an IC₅₀ = 0.0090 μM . Thirty-three compounds with IC₅₀ values below 0.2 $\mu\text{g/mL}$ were tested in mice infected with *T.b. rhodesiense* STIB900. Despite these compounds displaying *in vitro* potencies, none of them cured any infected mice, although seven compounds did cause a reduction in parasitemia by at least 97% compared to the untreated control group. Relapses occurred in all cases. Further analysis was taken in which the stability of 15 compounds in MLM and HLM, with and without the nicotinamide adenine dinucleotide phosphate (NADPH) cofactor, was evaluated to determine if metabolic instability was the contributing factor for the lack of *in vivo* efficacy. The SAR studies revealed that the incorporation of a piperidyl urea moiety (**166**) significantly improved the potency against *T.b. brucei* when compared to **165**. However, compound **166** suffered from low metabolic stability in MLM ($t_{1/2}$ = 1.6 min) and also was the least stable to HLM ($t_{1/2}$ = 4.9 min) in comparison to **165** (Figure 43). These microsomal studies revealed that compound **166** collectively had poor metabolic stability and therefore was not further evaluated *in vivo*.²²⁰

In order to improve metabolic stability while maintaining potency, further optimization was attempted. This led to more promising compounds based around urea derivatives of 2-

arylbenzothiazol-5-amines, more specifically (*S*)-2-(3,4-difluorophenyl)-5-(3-fluoro-*N*-pyrrolidylamido)benzothiazole **167** (Figure 43). Herein modifications in other sites of **165** were performed, and in almost all cases except three analogs, the three-carbon bridge between the amide and thiazole nitrogen atoms of **165** was retained. Modifications were performed via replacement of the carbonyl oxygen of the amide with sulfur, various substituents on the piperidine ring of **166**, and alkylation or unsaturation of the ethylene linker. Results showed that none of these provided any advantage regarding the antitrypanosomal activity or metabolic stability. Enhanced metabolic stability was observed only in the presence of benzoxazole- or benzothiazole-5-amino moiety in fused ring analogs. However, antitrypanosomal activity was only retained in benzothiazole derivatives. Thus, the ethylene linker played a role in the poor metabolic stability of initial thiazole analogs. From this series, **167** was discovered which exhibited good activity *in vitro* (*T.b. brucei*; EC₅₀ = 0.0348 μM), had no detectable toxicity when tested in two human cell lines [human lymphoblast cells (CRL-8155) and HepG2], and possessed a half-life of >60 min in both MLM and HLM (Figure 43). The target compound **167** was prepared by reacting a primary amine (**168**) with triethylamine in dichloromethane. Triphosgene was added followed by the addition of (*S*)-3-fluoropyrrolidine hydrogen chloride (Scheme 21). Compound **167** was also tested in mice; oral administration of 5 mg/kg intraperitoneal (ip) dose resulted in C_{max} = 23.34 μM and AUC = 13,254 min·μM with excellent brain penetration (brain concentration of 9.07 μM and brain/plasma ratio of 4.00). The compound was advanced to *in vivo* efficacy studies in which oral dosing cured 5/5 acute and chronic models of HAT, making it a representative lead for the future development of drugs combating this disease.²²¹

In order to target the ThDP binding site of *Escherichia coli* pyruvate dehydrogenase complex E1 component (PDHc-E1), two novel “open-chain” linkers, comprising amide and urea functionality, were studied for their effect on *E. coli* PDHc-E1 inhibition. The pyruvate dehydrogenase complex (PDHc) catalyzes the conversion of pyruvate into acetyl-CoA, while PDHc-E1 catalyzes the first irreversible step of this multistep process. The PDHc-E1 protein has been reported to be a promising target for the development of fungicide and herbicide agents.²²² Several studies on small molecule inhibitors of PDHc-E1 have been reported, but they suffer from structural complexity and contain a highly charged pyrophosphate. Therefore, there is a need for the development of small molecules as inhibitors of PDHc-E1 that overcome these limitations. First, SAR studies revealed that placing iodine in the 5-position of the 1,2,3-triazole moiety of compounds under investigation had the potential to increase inhibitory and antifungal activity against *E. coli* PDHc-E1. Additionally, the linker was essential for biological activity, thus leading to the optimization of 1,2,3-triazole derivatives with amide and urea moieties as “open-chain” linker analogs of **169** (Figure 44). Amide and urea derivatives were evaluated for their *in vitro* inhibition of *E. coli* PDHc-E1. Most compounds had a good inhibitory activity with IC₅₀ < 20 μM. These studies revealed that compounds with an amide linkage possessed inhibitory activity highly correlated to substituents on the benzene ring; electron-withdrawing groups led to more potent inhibitory activity, as seen in **170** (Figure 44). This compound possessing a 4-NO₂ substituent resulted in the most potent inhibitory activity, IC₅₀ = 3.58 ± 0.52 μM (Figure 44). Overall, the amide linkage has higher inhibitory activity than parent triazole **169**. As for the urea linkage, inhibitory activity was improved compared to the corresponding amide derivatives with the

same substituents, thus resulting in compound **171**, which had the same potency as **170**. The synthetic method utilized for the preparation of compound **171** is outlined in Scheme 22. He and co-workers tried to synthesize a urea derivative with a 4-NO₂ in the benzene ring; however, they were unsuccessful. Next, they performed molecular docking studies that showed that the binding mode of **171** is similar to **170** in the active site of *E. coli* PDHc-E1 (Figure 45). However, the two NH groups of the urea form strong hydrogen bonds with Glu₅₂₂; the oxygen of the phenoxy also hydrogen bonds with Leu₂₆₄ which could be due to the increase in chain length afforded by the urea moiety. Overall, the amide and urea linkages have a beneficial effect on *E. coli* PDHc-E1 inhibition versus the 1,2,3-triazole derivatives.²²²

CARBAMATE BIOISOSTERES

Ghosh and co-workers have described that a carbamate motif can be considered as structurally related to an amide-ester hybrid. Carbamates can modulate inter- and intramolecular interactions with target enzymes or receptors. Additionally, they induce a degree of conformational restriction as a result of the delocalization of nonbonded electrons on the nitrogen atom. Hydrogen bonding also occurs via the carboxyl group and NH backbone. Carbamates possess a pseudo double bond; thus, two isomers, *syn* and *anti*, can coexist. They display close similarity to amides; however, they prefer the *anti*-isomer. Ultimately solvent, concentration, salts, and pH influence the adaptation of *syn* and *anti* isomers in carbamates. Overall, carbamates possess very good chemical and proteolytic stabilities. They serve as amide bioisosteres in peptidomimetics due to their chemical stability and ability to permeate cell membranes. Carbamate-based prodrugs must undergo extensive hydrolysis in order to release the active drug at a suitable rate to achieve the desired activity profile.²²³

The global pandemic of HIV/AIDS was first identified in 1983–1984. The protease enzyme of HIV cleaves the *kh* and *gag-pol* polyprotein into its essential structural parts. Protease inhibitors block this enzyme, thereby preventing the development of the HIV virus. Saquinavir **173** (Figure 46) was approved in 1995 as the first HIV protease inhibitor.^{224,225} Although **173** is a potent protease inhibitor, which is effective against both HIV-1 and HIV-2 proteases, this can also lead to reduced susceptibility to clinical resistance due to these enzymes being the most genetically divergent strains. Ghosh and co-workers investigated the replacement of the P₂-asparagine of **173** with (2*S*,3'*R*)-tetrahydrofuranylglycine **174** which led to increased enzyme affinities for HIV-1 and HIV-2 proteases and significant enhancement of antiviral potency.²²⁶ These compounds prevented HIV-1 in MT4 infected with 111b isolate; **174** was 3-fold more potent (CIC₉₅ = 8 ± 4 nM) than **173** (CIC₉₅ = 22 ± 7 nM). In HIV-2, **174** was 2-fold more potent (IC₅₀ = 0.24 nM) than **173** (IC₅₀ = 0.5 nM) (Figure 46).²²⁷ An X-ray crystal structure of **173** bound to the HIV-1 protease showed that the carbonyl oxygen of the asparagine is within hydrogen bonding distance to the NH group within both Asp₂₉ and Asp₃₀, present in the S₂ binding domain of the HIV-1 protease. On the basis of this, the authors hypothesized that the ether oxygen would conformationally constrain and lend its lone pairs for hydrogen bonding to the residues in the S₂ region of the active site. A model for **174** was superimposed on the structure of **173**, which revealed that

the tetrahydrofuran oxygen of **174** is indeed in close proximity to the carbonyl oxygen of asparagine. Overall, replacing the P₂-asparagine of **173** with (2*S*,3'*R*)-tetrahydrofuranylglycine **174** led to an over 4-fold increase in enzyme inhibition for HIV-1 (IC₅₀ = 0.23 ± 0.1 nM) and HIV-2 (IC₅₀ = 0.054 ± 0.027 nM), respectively.²²⁸

To continue their studies of designing novel, cyclic ligands for the HIV-1 protease substrate binding site, Ghosh and co-workers introduced urethanes instead of N-terminus acyclic *tert*-butylurethane.²²⁶ Incorporation of various 3-tetrahydrofuranyl- or 3-tetrahydropyranylurethanes as P₂ ligands in hydroxyethylamine and hydroxyethylene series was developed. Compound **175** (IC₅₀ = 160 nM) (Figure 46) bearing a tetrahydrofuranylurethane moiety exhibited more than an 18-fold potency increase relative to its BOC derivative (structure not shown) (IC₅₀ = 3000 nM). Replacing a BOC urethane with 3(*S*)-tetrahydrofuranylurethane (**176**) resulted in over a 10-fold increase in inhibitory potency (IC₅₀ = 0.03 nM) and prevented the spread of HIV-1 (CIC₉₅ = 3 nM) (structure not shown). The synthetic route leading to compound **176** is delineated in Scheme 23, where 3-(*S*)-tetrahydrofuranyl succinimidyl carbonate was reacted with amine **177** in the presence of triethylamine to afford **176**. It was concluded from this study that 3-tetrahydrofurans and pyrans are high-affinity ligands for the S₂ binding domain of HIV-1 protease resulting in potent inhibitors.

Inhibiting β -secretase may provide a promising target for AD.²²⁹ On the basis of a β -secretase inhibitor **178** (A β 40 (cell) IC₅₀ = 0.082 nM) (Figure 47),²³⁰ Peters and colleagues designed a series of carbamate derivatives of dibenzazepinone as potent and metabolically stable γ -secretase inhibitors.²³¹ First, they evaluated the potential of **178** as a lead structure by preparing close analogs, one of which was the carbamate analog **179** (Figure 47). However, **179** displayed poor activity (IC₅₀ = 1500 nM). Despite this, it was found that a carbamate in place of an amide was tolerated in further synthesized compounds. Moreover, although **179** was a weak γ -secretase inhibitor, it gave rise to the possibility of deriving a stereogenic center from the chiral pool such as lactic acid. Thus, it could possibly prevent the separation of diastereomers in the process of inhibitor synthesis. Changing a malanamide analog to a carbamate **180** (IC₅₀ = 1.7 nM) (Figure 47) gave an improvement in solubility and microsomal stability and led to reduced clearance *in vivo*. The synthetic procedure to obtain compound **180** is shown in Scheme 24. Arguably, a carbamate motif is biodegradable; however, in this case it was stable with plasma and buffer at various pH values (1.7, 4.7, and 7.8). At pH 12.8, slow degradation occurred (*t*_{1/2} = 57 h). In an *in vivo* AD model, both the malanomides and **180** dose-dependently increased the ratio of C-terminal fragment (A β PP) after oral administration with a minimal effective dose of three doses (3 mg/kg) over 2 days. Both the malanamide and carbamate analogs were potent γ -secretase inhibitors with single digit nanomolar inhibitory activity *in vivo* and were also efficacious in a mouse model of AD after oral administration.

Substance P (SP) is an 11 amino acid molecule that preferentially binds to the neurokinin-1 (NK-1) receptor, where it acts as a neurotransmitter and neuromodulator in the central and peripheral nervous system. Substance P is broken down into several bioactive fragments; substance P 1–7 (SP_{1–7}), a heptapeptide, is a major N-terminal metabolite that has been comprehensively evaluated. It has been shown to have high affinity to specific binding sites

in the spinal cord and brain. Numerous reports propose that it may have its own putative receptor. Fransson and colleagues were able to demonstrate that it could induce antihyperalgesia in diabetic mice.²³² It is thereby suggested that SP₁₋₇ peptidomimetics could have the potential to serve as therapeutic agents for neuropathic pain. Initially, alanine and subsequent N- and C-terminal modifications of SP₁₋₇ and endomorphin-2, and subsequent truncation gave rise to the lead compound **182** (Figure 48). This compound had a more pronounced effect in diabetic mice than SP₁₋₇ when administered intrathecally. Structure-activity relationship studies of dipeptide analogs and rigid analogs of H-Phe-Phe-NH₂ revealed that two benzyl moieties in the (*S,S*) configuration and a primary amine at the N-terminal with a crucial primary amide function in the C-terminal were the structural motifs optimal in order to achieve high binding affinity. However, this pharmacophore led to high efflux of the compound. Therefore, it was investigated what pharmacophore was essential through the exploration of compounds with fewer hydrogen bond donors. The N-terminal of the basic phenylalanine in **182** ($K_i = 1.5$ nM) was exchanged for a more lipophilic benzyloxycarbonyl moiety giving rise to **183** (Figure 48). The synthesis of compound **183** was accomplished through the reaction of C-terminal activated benzyloxycarbonyl protected phenylalanine (**184**) with ammonia (Scheme 25). Compound **183** was then evaluated in an SP₁₋₇ binding assay, which gave rise to a good binding affinity ($K_i = 5.2$ nM) while still maintaining interactions with the target. The *in vitro* profile of **182** displayed poor “drug-like” properties as a result of low membrane permeability, high *in vitro* clearance ($Cl_{int} = 97.3 \mu\text{L min}^{-1} \text{mg}^{-1}$) (Figure 48) and no measurable plasma protein binding. This could be due to rapid degradation in plasma; therefore, this compound was not further investigated *in vivo*. Compound **183**, in which the N-terminal amine was replaced with a carbamate motif, resulted in improved membrane permeability ($P_{app} = 31 \times 10^{-6}$ cm/s), low efflux, and moderate *in vitro* clearance ($Cl_{int} = 22.6 \mu\text{L min}^{-1} \text{mg}^{-1}$) (Figure 48). Despite these promising results, compound **183** experienced hydrolytic cleavage in rat blood/plasma, inducing extrahepatic clearance, thus preventing good exposure after a single dose in rats. When tested in human plasma, this was not an issue. Compound **183** was further evaluated with different C-terminal groups (hydroxamic acid, acyl cyanamide, acyl sulfonamide, acyl hydrazine, and 1,3,4-oxadiazole) using a bioisosteric approach. Overall, these analogs showed moderate to good binding affinities for the SP₁₋₇ binding site ($IC_{50} = 4\text{--}60$ nM). These C-terminally modified compounds were also evaluated for their uptake, metabolic stability, and permeability to determine the effect of bioisosterism on pharmacokinetic properties. When compared to **183**, the rat plasma stabilities were improved for all analogs except two. Additionally, three out of the five showed a low risk of oxidative metabolism and comparable Cl_{int} to **183**. Overall, isosteres provided compounds with increased permeability, low efflux, and good metabolic stability.²³²

AMIDINE BIOISOSTERES

Very late activating antigen-4 (VLA-4), a key cell surface integrin, is expressed in circulating leukocytes. It plays a critical role in inflammation via the promotion of leukocyte attachment and extravasation from the vasculature into peripheral tissues. Thus, VLA-4 antagonists could be useful for the treatment of multiple sclerosis, rheumatoid arthritis, and asthma.²³³ Kamenecka and co-workers previously reported potent and specific amide

VLA-4 antagonists **185** and **186** (Figure 49).²³⁴ These *N*-phenylsulfonylproline biphenylalanine derivatives suffered from poor pharmacokinetic properties such as low oral bioavailability ($F < 10\%$) and high plasma clearance in rat ($Cl_p > 90 \text{ mL min}^{-1} \text{ kg}^{-1}$) (Figure 49). This raised speculation of whether these deficiencies were a result of the amide bond, and so this group was either removed or modified. Bioisosteric replacement of the amide bond with an ester caused a 200-fold decrease in potency while *N*-methylation gave rise to a 4000-fold drop. Therefore, it was concluded that the NH was essential for potency. Removal of the amide carbonyl motif resulted in a 2000-fold reduction in potency. This could be the result of the secondary amine being too basic to engage in essential hydrogen bonding or as a result of a conformational change in the molecule leading to a reduction in potency. It was still unclear if the oxygen atom was needed, so Kamenecka and co-workers sought amidines as amide bond bioisosteres to help attenuate the basicity on the nitrogen group, thus giving rise to improved potency and pharmacokinetics. Results showed that changing the oxygen atom in **185** to an NH (**187**) resulted in almost equipotent VLA-4 inhibitory activity (Figure 49), thus confirming that the amide bond oxygen is not necessary for potency, but the amide oxygen or amide nitrogen can still act as a hydrogen bond acceptor. Next, the NH bond of **187** was modified by amalgamation with an EWG on the nitrogen linked with one methylene group (**188**). This modification did not produce significant improvement in antagonizing VLA-4; however, both compounds (**187** and **188**) displayed slightly better pharmacokinetic profiles than **185** and **186** (Figure 49). The synthetic procedure of amidine bioisosteres **187** and **188** is outlined in Scheme 26.²³³

THIOAMIDE BIOISOSTERES

The thioamide and amide functional groups share the same number of atoms and valence electrons, which are arranged similarly. The thiocarbonyl bond is longer than a carbonyl bond. Additionally, the C–N bond in the thioamide is shorter in comparison to the amide due to the larger contribution of resonance. Two structural deviations of the thioamide from the amide do exist: there is a more rigid out-of-plane bending vibration mode due to the nitrogen in the thioamide, and there is an increase in rotational barrier across the C–N bond in thioamides over amides by 2–3 kcal mol⁻¹. Thioamides, like amides and esters, can exist as *cis* and *trans* isomers. The proton affinity of sulfur in a thioamide (203 kcal mol⁻¹) is greater than that of oxygen (199 kcal mol⁻¹) in an amide. Despite this, thioamides are weak hydrogen bond acceptors compared to amides since this is negated by the unfavorable entropies that go with hydrogen bond formation in thioamides.²³⁵

Bacterial resistance is an emerging issue when combating bacterial infections and has led to the continuous search for novel antibiotics. Previously, Thorarensen and colleagues reported the optimization of anthranilic acid hit compound **190**, which led to the discovery of lead compound **191** displaying potent broad-spectrum antibacterial activity (Figure 50).²³⁶ This group sought to explore the role of the linker connecting the A- and B-rings in **191**. They decided to take the amide bioisostere approach based on the following two hypotheses: the amide linker was involved in an essential interaction with the target and disruption of this would be detrimental to activity, and the purpose of the amide linker was to act as a conformational control element thereby linking essential pharmacophores. They proceeded to select functional groups that were successful amide bioisosteres through their ability to

maintain essential recognition elements of an amide via incorporation of hydrogen bond acceptor or hydrogen bond donor properties. Some of their previous work revealed that electron-withdrawing groups (-Cl, -Br, -NO₂, and -CN) at the 5-position on the A ring were interchangeable and resulted in similar antibacterial activity. Additionally, 3- versus 4-substituted B-rings resulted in analogs with similar activity; however, 3-substitution had a slight improvement in potency. The selection of a B-ring substituent was influenced by the fact that the corresponding amide illustrated reasonable antibacterial activity. Next, substitution patterns were picked on the sole basis of the ease of synthesis. The thioamide moiety as in **192** was readily available via reflux in toluene with compound **193** and Lawesson's reagent. The hydrolysis of the ester fragment with treatment of lithium hydroxide gave rise to compound **192** (Scheme 27). The ability of the new linker to serve as an amide bioisosteric replacement was monitored based on its activity against *Staphylococcus aureus*. Results showed that the thioamide **192** (Scheme 27) was equipotent with its corresponding amide. The minimal inhibitory concentrations (MIC) were tested across five different bacterial strains, but improvements were seen in only three strains (*Staphylococcus aureus* UC 9218 (SAUR), *Staphylococcus epidermidis* UC 12084 (SEPI), and *Haemophilus influenzae* 30063 (HINF)) for the thioamide **192** in comparison to the amide **191** (Figure 50). However, the improvement in activity for the thioamide was not clear. Conversion from an amide to a thioamide is only a small change in linker construction. Nevertheless, results did show that removing this linker resulted in analogs devoid of activity. Replacing the linker with a five-membered ring heterocycle results in the abolishment of activity. Using an alkane caused faint antibacterial activity, but an alkene, more specifically an *E*-alkene, provided equipotent activity to its corresponding amide, suggesting a critical role in retaining bioactive conformation. It can be concluded that an amide is not necessary for activity but plays a role as a recognition element and adequately positions the aryl rings. Therefore, an amide can be replaced without significantly affecting MIC antibacterial activity of novel linkers.

TRIFLUOROETHYLAMINE BIOISOSTERES

The introduction of a trifluoroethylamine group [CH(CF₃)-NH] is an emerging mimic of the natural parent amide bond in a number of peptidomimetic compounds. In 2000, Zanda and co-workers published the first example of peptide mimics that incorporated a trifluoroethylamine group as a replacement for the amide moiety.²³⁷ The trifluoroethylamine motif has the ability to reduce the basicity of the NH while preserving hydrogen bond donating properties, retains the backbone geometry of the amide bond (bond angle close to 120°), and has structural similarity with a tetrahedral proteolytic transition state (TS), and the C-CF₃ bond is isopolar with the carbonyl bond.²³⁸ An additional benefit is the sp³ hybridization of the trifluoroethylamine functional group that can influence the conformation of substituent groups into a target receptors' active site, enhancing hydrogen bond strength. Zanda and co-workers replaced both a glycine amide bond and a malonamide to a partially modified retro-Ψ[NHCH(CF₃)] peptide (Figure 51).²³⁹ They also synthesized a Ψ[NHCH(CF₃)] retrothiorphan analog **197** (Figure 51) over the course of several steps starting with the reaction of *N*-trifluorocrotonoyloxazolidin-2-one (**198**) and *L*-phenyl alaninol (Scheme 28). Compound **197** was determined to be a potent and selective inhibitor

of metalloproteinase neutral endopeptidase (NEP) which does not inhibit the related zinc proteinase, angiotensin-converting enzyme (ACE), and plays a key role in controlling blood pressure.²³⁸ Compound **197** was evaluated for its inhibitory capacity toward NEP 24.11 achieving IC₅₀ values greater than the thiophan parent scaffold, with K_i values over 4 M. Results proved that there was loss of NEP inhibition capacity when comparing compound **197** and its stereoisomers with (*R*)- and (*S*)-retrothiorphan ($K_i = 2.3$ nM and 210 nM, respectively). Despite these results, it was found that the trifluoroethylamine unit possesses high metabolic stability and restricts the molecule into accessible conformational states, thereby resulting in well-defined conformational motifs. As a result, it is only an effective replacement if the carbonyl group of the parent peptide is not involved in key hydrogen bonding with the receptor.²³⁸

Successful replacement of an amide with a trifluoroethylamine isostere has progressed beyond peptidomimetics; it has also been used in the lead optimization of odanacatib, **202** (Figure 52), a highly potent and selective drug candidate for the inhibition of cathepsin K (Cat K).²⁴⁰ Cathepsin K, a lysosomal cysteine protease, is abundantly expressed in osteoclasts where it is responsible for degradation of the bone protein matrix. Blocking secreted cathepsin K can help prevent bone loss without affecting the ability of osteoblasts to build bone and thereby enhancing bone strength and quality.²⁴¹ Thus, Cat K inhibitors can be used as a therapeutic treatment for osteoporosis. Initially, X-ray crystallography showed that in an irreversible dipeptide inhibitor of Cat K, the P₁-P₂ amide hydrogen bonds with the enzyme backbone involving the NH and carbonyl groups. However, the P₂-P₃ amide bond only forms one hydrogen bond to Gly₆₆ with the NH while the oxygen points toward the solvent. Thus, the P₂-P₃ amide bond can be replaced with an isostere without having detrimental effects on potency. In order to identify a potent and selective inhibitor of Cat K, the initial lead **200** was synthesized (Figure 52). It proved highly selective over cathepsins B, L, and S in enzyme assays and displayed good PK properties.²⁴² However, further studies revealed that its lysosomotropic properties caused the loss of selectivity in cell-based assays, more specifically in a Cat S-dependent B cell line assay where it blocked antigen presentations. Overall, this initial lead compound resulted in reduced effective selectivity in whole-cell assays which could cause an increase in potential adverse effects in the clinic.²⁴³ Black and co-workers found that not only an analog of compound **200** containing a trifluoroethylamine moiety at the P₂-P₃ amide enhanced potency and selectivity over other cathepsins but the resulting compounds were also stable to P₁-P₂ amide bond cleavage similar to dipeptide inhibitors. Introduction of a trifluoroethylamine bioisostere was found to be a viable substitution at the P₂-P₃ amide for inhibitors of Cat K. Optimization studies led to the replacement of the P₂ amide bond with a trifluoroethylamine isostere; compound **201** showed nearly comparative Cat K inhibition as **200**. Additionally, **201** was nearly 26,000-fold more selective for Cat K over Cat B (Figure 52).²⁴⁴ *In vivo* studies of this compound showed it was orally bioavailable to rat, dog, and rhesus monkey; however, it had metabolic liabilities such as a short half-life (2 h) and clearance (7.5 mL min⁻¹ kg⁻¹) in monkey (Figure 52).²⁴³ In order to minimize leucine hydroxylation, amide hydrolysis, and lactonization, the P₁ and P₂ residues were modified and led to the final drug candidate **202**. The general synthetic route to obtain the trifluoroethylamine bioisostere **202** is outlined in Scheme 29, i. Compound **202** is a potent, selective, and neutral cathepsin K inhibitor that

maintains excellent selectivity and activity in both enzymatic and cell-based assays. It has minimal effects on intracellular collagen accumulation compared to other cathepsin K inhibitors, balicatib and relacatib, with long half-lives in preclinical species.²⁴⁰ The compound continued into clinical development for the treatment of postmenopausal osteoporosis and bone metastasis. It progressively increased bone mineral density over 5 years and reduced the risk of fractures in patients. However, development was discontinued before the filing of a new drug application (NDA) due to an increased risk of cardiovascular events and risk of stroke.²⁴⁵

An example of where an amide replacement with the trifluoroethylamine moiety affects selectivity of a drug toward different targets can be appreciated with telaprevir, **205**. It is a first-generation peptidomimetic and potent hepatitis C virus (HCV) NS3 protease inhibitor with $IC_{50} = 70$ nM (Figure 53). Moreover, **205** has the ability of inhibiting other cysteine proteases such as cathepsin B with an IC_{50} of approximately 210 nM and is also an antiviral agent, $EC_{50} = 210$ nM in the replicon. Replacing the P_4 amide moiety with a trifluoroethylamine surrogate identified two active inhibitors of cathepsin S with $IC_{50} = 2$ nM and 0.6 nM for compounds **206** and **207**, respectively (Figure 53). However, in contrast to the unfluorinated parent compound **205**, compounds **206** and **207** only exhibited a weak inhibition of HCV NS3 with 34% and 29% inhibition at 25 μ M in the HCV replicon, respectively, despite the structural changes being remote from the active site.¹⁶

Bioisosteric replacement of an amide with a trifluoroethylamine moiety was examined in the design of β -site amyloid precursor protein cleaving enzyme 1 (BACE-1) inhibitors. Inhibitors containing a P_1 or P_2 amide motif exhibit high efflux transporter liability along with metabolic lability.²⁴⁶ This was attributed to the release of aniline upon amide cleavage *in vivo*, thereby potentiating toxicity after metabolic activation. Butler and co-workers sought to identify an amide replacement that provided excellent potency but avoided the aniline structural motif and its toxicity. The X-ray cocrystal structure of a related BACE-1 inhibitor analog, compound **208** (Figure 54), showed that the amide NH is positioned in such a way that it engages with the backbone carbonyl of the Gly₂₃₀ residue in order to partake in a critical hydrogen bonding interaction. Therefore, preservation of the NH of the aniline is necessary. It was found that the planar aniline moiety has sp^3 nature on the benzylic carbon resulting in an orthogonal arrangement of the C–N bond relative to the fluorophenyl P_1 ring, facilitating an optimal geometry for hydrogen bonding to Gly₂₃₀. Due to uncertainty of what structural motifs were necessary, a parallel synthesis was performed in order to evaluate the SAR for BACE-1 which identified an ethylamine analog. This analog showed modest improvement in BACE-1 cell-free assay potency with $IC_{50} = 13.9$ μ M. However, it has a more potent increase in whole-cell assay potency of about 1000-fold. This was attributed to the basicity of the analog which increases the tendency for accumulation into the endosome, an acidic intracellular compartment where BACE-1 resides. Further optimization focused on utilization of electron-withdrawing groups and incorporation of branched amines to further enhance potency. In due course, a CF_3 -cyclopropane derivative, compound **209** (Figure 54), was synthesized via reductive amination with 1-(trifluoromethyl)cyclopropan-1-amine, followed by the removal of the amidine protecting group (Scheme 30). Compound **209** maintained good potency in both BACE-1 cell-free assay ($IC_{50} = 0.0069$ μ M) and whole-cell

assay ($IC_{50} = 0.018 \mu M$) and overall an optimal balance of properties. A cocrystal structure of compound **209** in BACE-1 was obtained, and results showed that the thioamidine and difluorophenyl ring are orientated similarly to previously described BACE-1 inhibitor structures. The difluorophenyl occupies the S_1 pocket as predicted, and the benzylic amine substituent adopts an orthogonal orientation toward the plane of the difluorophenyl P_1 group in order to involve the carbonyl of Gly₂₃₀. Results showed that improvements in BACE-1 cell-free assay potency using the CF_3 -containing lead was due to the CF_3 group pointing toward and filling the S_3 pocket while the cyclopropyl moiety fills a lipophilic pocket at the interface of the S_1 and S_3 pockets. In the end, compound **209** possessed significant inhibition activity toward cytochrome P₄₅₀ subtype 2D6 (CYP 2D6) and development was discontinued.²⁴⁶

An amide bond replacement on a malonyl moiety by an amide surrogate trifluoroethylamine was employed in the identification of novel receptor tyrosine kinases (RTKs) inhibitors, more specifically malonamide-type dual inhibitors of the vascular endothelial growth factor receptor-2 (VEGFR2) and c-Met receptors. Gaudette and colleagues initially investigated what changes were suitable for VEGFR2 and c-Met enzyme inhibition via initial SAR studies of compound **212**, the parent malonamide (Figure 55).²⁴⁷ First, the left-hand side of compound **212** was left unchanged and one amide moiety of the malonamide head group was replaced by a trifluoroethylamine moiety on the eastern side. Results showed that replacement of the eastern amide bond of the parent malonamide by the trifluoroethylamine moiety led to 23-fold and 11-fold decrease in activity for c-Met ($IC_{50} = 0.70 \mu M$) and VEGFR2 ($IC_{50} = 0.21 \mu M$), respectively, compared to compound **212** ($IC_{50} = 0.03 \mu M$ and $IC_{50} = 0.02 \mu M$ for c-Met and VEGFR2, respectively). The decrease in activity in VEGFR2 and c-Met could be due to the steric clash between the CF_3 group and hydrophobic back pocket of the kinase active site and/or the loss of the carbonyl group, a strong hydrogen bond acceptor in compound **212**. Replacement of the western amide bond by a trifluoroethylamine group caused a 4-fold decrease in activity against c-Met ($IC_{50} = 0.12 \mu M$). However, the compound showed similar VEGFR2 inhibitory activity ($IC_{50} = 0.01 \mu M$) as compound **212**. The same observations were seen in a pyrimidine-based series, compound **213** which was found to be of highly selective and potent for VEGFR2 ($IC_{50} = 0.04 \mu M$). It was also profiled against a set of eight kinases where it was also highly selective for VEGFR3. Lastly, there was a significant effect on VEGF-dependent angiogenic activity where there was inhibition of VEGF-dependent proliferation of human umbilical vein endothelial cells (HUVEC). Replacing an amide moiety of a malonamide head group by a trifluoroethylamine led to the identification of novel, potent, and selective inhibitors of VEGFR2 enzyme. Compound **213** was synthesized over the course of several steps starting with the coupling of a corresponding amine with trifluoroacetaldehyde ethyl hemiacetal (Scheme 29, ii).²⁴⁷

SULFONAMIDE BIOISOSTERES

Sulfonamide functional groups are structurally related to amides in which the carbonyl moiety is replaced with an isosteric SO_2 group. As in amide bioisosteres, sulfonamides are known to increase water solubility and could provide additional HBAs. Lim et al. reported a urea analog of B13, an aromatic ceramide analog with a phenyl ring in lieu of an alkenyl

chain, that exhibited slightly more potent cytotoxicity compared to **163** (Figure 56). As previously mentioned in the urea bioisostere section of this paper, results indicated that the urea appears to serve as a bioisostere of the amide.²¹⁶ A series of novel D-erythro ceramide analogs with alkylsulfonamido chains were synthesized and evaluated for their cellular toxicity against human tumor cell lines HeLa, Caki-2, PC-3, and HL-60. Modest cytotoxicity ($IC_{50} = 48 \mu M$) was displayed by **163** against HL-60 leukemic cells. An aromatic sulfonamide ceramide analog, **214**, was synthesized via the coupling of the acid (**216**) and amine (**215**) with HOBt and EDCI (Scheme 31). *In vitro* evaluation showed that compound **214** had comparable cytotoxicity in Caki-2 ($IC_{50} = 103 \mu M$) and HeLa cancer cells ($IC_{50} = 65 \mu M$) but the greatest potent cytotoxicity in HL-60 leukemic cells ($IC_{50} = 28 \mu M$) (Figure 56). Further comprehensive analysis of the sulfonamide ceramides is needed; however, their cytotoxic properties appear to be cancer cell specific due to their structural similarities to **163**. The introduction of a *para*-halogen onto the phenyl ring of D-erythro ceramide analogs resulted in compounds with comparable or somewhat lower activity than unsubstituted phenyl ceramide analogs. Variations in the alkyl sulfonyl chain length had a more significant influence on the activity of aromatic ceramide analogs, more specifically, an aromatic sulfonamido ceramide analog.²⁴⁸

The human isoprenylcysteine carboxyl methyltransferase (hIcmt) is a promising anticancer target. Proteins contain a C-terminal sequence motif called Caax box (where C is cysteine, aa is an aliphatic residue, and X is one of several amino acid residues). These motifs are post-translationally modified for cellular targeting, most common being membrane association. The protein K-Ras is one of the >120 proteins containing a Caax box; it undergoes farnesylation, endoproteolytic cleavage of the -aaX residues, and methyl esterification of the free carboxylate of the prenylated cysteine by isoprenylcysteine carboxyl methyltransferase (Icmt). When mutant K-Ras is in the constitutively active form in the GTP-bound conformation, it results in tumorigenesis. Inhibition of human Icmt has been thought of as blocking the activity of oncogenic Ras. *N*-Acetyl-*S*-farnesyl-*L*-cysteine (AFC) is a substrate for hIcmt, and previous work by Majmudar and co-workers has shown that amide modified farnesyl cysteine analogs (AMFCs) are low-micromolar inhibitors of hIcmt. No structural information on hIcmt exists, thereby possessing a challenge in designing Icmt inhibitors. It was hypothesized by Majmudar and co-workers that a bioisosteric replacement of an amide bond in AMFC would give rise to molecules with retained interaction with hIcmt and provide more insight on inhibition requirements. Compound **217** (Figure 57) represents one of the most potent AMFCs ($IC_{50} = 4.3 \mu M$) synthesized by Donelson et al.²⁴⁹ The goal was to determine the structural requirements for hIcmt inhibitors by prenylated cysteine derivatives with a sulfonamide bioisostere. Sulfonyl chlorides with varying electronic character, steric bulk, and alkyl aromatic scaffolds were incorporated. These new analogs were evaluated as substrates and inhibitors of human Icmt using a vapor diffusion assay (VDA). Results showed that no sulfonamide modified farnesyl cysteine analogs (SMFCs) are effective substrates but rather serve as moderate inhibitors of hIcmt. Compound **218** was obtained via reaction of a corresponding primary amine and sulfonyl chloride in the presence of sodium carbonate using dioxane as a solvent (Scheme 32, i). Compound **218** displayed 64% hIcmt inhibition at $10 \mu M$ using $25 \mu M$ AFC as the substrate with an $IC_{50} = 8.8 \pm 0.5 \mu M$ (Figure 57). It was hypothesized that the reason why

SMFCs are not substrates for hICmt is due to the reason that the amide bond or the carbonyl carbon is necessary for substrate activity. Additionally, SMFCs do inhibit Icmt but have varying strength of inhibition. Poor hICmt inhibitors were analogs containing highly bulky or rigid motifs. Compounds with electron-withdrawing groups were more potent than electron-donating groups; however, some exceptions do exist. A planar bulk next to the sulfonamide bond enhances inhibitory activity. The effect of the prenyl group was also evaluated, but none of these compounds exhibited substrate activity at 25 μM and were poor inhibitors of hICmt compared to their farnesyl analogs. As a result, the farnesyl group is highly important for hICmt inhibition by SMFCs. Overall, the determining factor for hICmt inhibition by SMFCs is related to the presence of the farnesyl chain, resulting in a specific binding interaction rather than just acting as hydrophobic bulk. Stereochemistry at the α carbon did not play a significant role in hICmt inhibition by SMFCs. When deviating from the carboxylate group, there is a reduction in hICmt inhibitory activity; however, this needs to be evaluated further with more analogs. Overall, the sulfonamide bond is a viable bioisosteric replacement for the amide bond in AFC derived hICmt inhibitors.²⁵⁰

Natural products have a successful history of being a source of new therapeutics as a result of their high chemical diversity and biochemical specificity.²⁵¹ Capsaicin **24**, the main pungent and irritating component of chili peppers, was reported to selectively inhibit the growth of various tumor cell lines. Early work gave rise to controversy regarding its mutagenic and carcinogenic abilities; however, recent studies have proven that it induces apoptosis in a large number of tumor cell types and that capsaicinoids possess *in vitro* and *in vivo* antitumor activity. Thus, **24** has the potential of serving as a lead against malignant tumors. However, some limitations such as its poor stability, attributed to the liable amide motif, and strong pungency limit its use and application in drug discovery.²⁵² The pungency of **24** is related to its ability to directly promote stimuli on transient receptor potential vanilloid subtype 1, thus causing Ca^{2+} influx and subsequently nociceptive hyperpolarization. The molecular mechanisms of capsaicin-induced cell death are still uncertain. Despite this, the capsaicinoid scaffold gave rise to molecules exhibiting improved physiochemical and pharmacological profiles. Ferreira and colleagues have investigated the optimization of capsaicin-like analogs as potential anticancer agents. The development of these compounds began with structural changes to the **24** structure (Figure 58), which was divided into three parts: the methylcatechol group (region A), the amide bond (region B), and an alkyl side chain (region C). In region A, cyclization was investigated which converted the methylcatechol group to the 1,3-benzodioxole bicyclic motif. This modification could give rise to important advantages since the benzodioxole system is a privileged structure for substances containing antitumor activity.²⁵³ In the first analog series, the amide bond linker (region B) was maintained or underwent a bioisosteric replacement by an ester, and the alkyl side chain (region C) was replaced by several alkyl/aryl groups to preserve the hydrophobic nature of this region. In the first series, amide (**222**) or ester analogs (**223**) (Figure 58) revealed that some of these analogs had equipotent cytotoxicity to **24** against *Mus musculus* skin melanoma cells (B16F10) and M. D. Anderson metastasis breast adenocarcinoma (MDA-MB-231). Despite this, these analogs suffered from poor chemical stability, as did **24**. The sulfonamide group, known to be very stable against chemical hydrolysis and other

physicochemical degradation processes, was used as a bioisosteric replacement of the amide and ester linkers to afford **224–226** (Figure 58).

Additionally, the use of the sulfonamide group was supported by the results of exploratory data analysis wherein the designed sulfonamide analogs clustered with the same set of compounds that had previously shown activity. Thus, aryl and alkyl sulfonamide bioisosteres were synthesized, giving rise to **224** and **225** (Figure 58). These analogs were a success because they resulted in slightly superior cytotoxic activity compared to **24**, displayed improved stability, but had poor solubility. In order to overcome this pitfall, a less hydrophobic sulfonamide analog was designed in which the eight-methylene unit of **225** was truncated to contain a four-carbon alkyl chain **226** leading to increased aqueous solubility. Compound **226** was synthesized by reacting a corresponding primary amine and sulfonyl chloride in the presence of sodium carbonate and water (Scheme 32, ii). A theoretical approach was taken in order to find more energetically favorable conformations for **24** and **226**, calculate molecular properties, and gain insight on SAR.²⁵² Next, the cytotoxic effects of **226** on MDA-MB-231 and human mammary epithelial cells (MCF10A) were evaluated. Results illustrated that both **24** and **226** both decreased the viability of MDA-MB-231 cells with IC₅₀ values of 120 and 87 μM , respectively; however, **226** is potentially more cytotoxic. Additionally, MCF10A cells were more resistant to treatment with **226** (IC₅₀ = 198 μM) and also induced a change in cell morphology. Results indicated that **226** is an antitumor candidate with a cytotoxic mechanism. This new capsaicin analog was capable of interrupting cell-cycle progression via S-phase arrest and inducing cell death in MDA-MB-231 cells and apoptosis via the downregulation of the antiapoptotic Bcl-2 protein. Results also showed that **226** leads to apoptosis through caspase-3 cleavage in the death-inducing signaling complexes, TRAIL-R1/DR4 and TRAIL-R2/DR-5. *In vivo* results also indicated that **226** has antitumor properties as it was more effective ($133.4 \pm 24.5 \text{ mm}^3$) than **24** ($281.3 \pm 78.5 \text{ mm}^3$) in reducing mean tumor volume and impairing tumor progression in the MDA-MB-231 model of breast cancer (Figure 58). Overall, the activity of **226** against MDA-MB-231, a well-established breast cancer model, and its lower pungency suggest its promising role as an anticancer agent for breast cancer.²⁵²

Novel irreversible HIV-1 protease inhibitors containing sulfonamide and sulfone groups as amide bond bioisosteres were discovered.²⁵⁴ Biotech Research Institute, Korea, reported an irreversible inhibitor **227** (Figure 59) with IC₅₀ = 20 nM containing an epoxide moiety as an active site isostere. The authors designed inhibitors with improved potency and fewer peptide bonds.²⁵⁴ First, the replacement of the amide carbonyl group in the C-terminus in compound **227** with sulfonamide occurred since the hydrogen bonding between inhibitor and water in the enzyme was reported. The sulfonamide group would be able to maintain this hydrogen bonding as well as improve stability against amide hydrolysis by proteolytic enzymes. Next, the P₂ site was taken into account for the design of new inhibitors since the pocket size of P₂ is large in order to fit asparagine and valine. Therefore, replacing asparagine with suitable amphiphilic groups could increase the potency of inhibitors. Thus, the following modifications were made: inserting a sulfonamide for the P₁–P₂ amide bond and a sulfone group for the P₂ asparagine, as seen in **228**. The sulfonamide bioisostere (**228**) installation was achieved through the use of 3-chloropropane-1-sulfonyl chloride which is

commercially available. Two sulfonamide bioisosteres of **227** were designed (**229** and **230**) (Figure 59). However, both of these bioisosteres were not the most potent of the series (IC_{50} = 30 nM and 20.2 nM, respectively). Results revealed that **228** was an inhibitor with high affinity, irreversibility, and high potency (IC_{50} = 6.6 nM) which could serve as a potential chemotherapeutic agent for the treatment of HIV.

PHOSPHONAMIDATE BIOISOSTERES

The RNA-dependent RNA polymerase (RdRp) of the hepatitis C virus, also known as nonstructural protein 5B (NS5B), is essential for the synthesis of viral RNA.²⁵⁵ The protein has no functional equivalent in the mammalian system, and thus it is a target for inhibition by both nucleoside and non-nucleoside inhibitors. The 3D structure of RdRp suggests that NS5B has a cupped right-hand-like structure with a finger, palm, and thumb domain.²⁵⁶ Several drugs such as filibuvir and lomibuvir bind to the thumb domain, whereas dasabuvir, GSK5852, HCV-796 bind to the palm domain.^{257,258} Phosphonamidate bioisosterism has been reported to represent a new class of non-nucleoside inhibitors of HCV NS5B. The sulfonamide and amide groups were modified in the small molecules, **231** and **232** (Figure 60), respectively, which are non-nucleoside NS5B inhibitors that bind to the allosteric site 2 of the thumb domain of the HCV viral polymerase (Figure 61).²⁵⁹

Compound **232** had potent activity in genotypes 1a and 1b infections in preclinical trials. In order to test the hypothesis of phosphonamidate bioisosterism, two compounds, **233** and **234**, were synthesized and evaluated for inhibition of HCV replication in the HCV replicon luciferase assay and inhibition of the 1b-J4 HCV NS5B polymerase.²⁵⁹ Only compound **234** produced a modest inhibition of the NS5B polymerase (IC_{50} = 3.74 μ M). Subsequently, detailed SAR investigations either on R¹-R²-R³-R⁴-substitutions or on the thiophene moiety were conducted to determine the effect on the potency of this new phosphonamidate class of compounds. Many analogs, with varying substituents, were synthesized and evaluated, and ultimately, compound **235** was identified as the most active analog, with efficacy greater than that of the parent compound, **232**. Scheme 33 describes the key synthetic route to generate the phosphonamidate bioisostere as in compound **235**. Compound **235** had broad genotype profile: IC_{50} = 0.0099 μ M, 0.2538 μ M, 0.1809 μ M, and 0.0257 μ M for genotypes 1b, 2a, 3a, and 4a, respectively. Furthermore, **235** had high selectivity index with subnanomolar potency in the replicon assay (EC_{50} = 0.0004 μ M) without producing cytotoxicity. Cocrystallization studies of **235** complexed with the viral NS5B indicated that the inhibitor is hydrogen bonded through the carboxylate functional group to the main chain of Ser476 and Tyr477 and to the side chain of Arg 501 with the oxo function of the phosphonamidate, confirming its interactions with the viral protein in the thumb 2 domain of NS5B (Figure 62). Compound **235**, designated IDX17119, was selected for further preclinical and PK studies. Overall, the phosphonamidate proved to be a viable bioisosteric replacement for the amide function in developing potent non-nucleoside NS5B inhibitors.

ESTER BIOISOSTERES

Geometrically an ester and amide are comparable. As with the resonance of an amide, in an ester, the lone pair of electrons on the oxygen delocalizes into the antibonding orbital of the

ester carbonyl group. Similar to what happens with amides, the electron delocalization results in *cis* and *trans* isomers. The *trans* conformation of an ester is more stable than the *cis* conformation, as seen with amides. Additionally, esters and amides differ based on hydrogen bond formation, thus affecting protein folding and stability. Esters are weak hydrogen bond acceptors and cannot hydrogen bond-donate. In addition to this, esters are vulnerable to hydrolysis *in vivo*.²³⁵ Amide isosteres can modulate polarity and bioavailability, while esters are used to address metabolism issues due to their vulnerability to cleavage *in vivo*, most often forming the cleavable component of prodrugs.¹⁶

Opioids are a common drug for the treatment of moderate to severe pain. The three major subtypes of opioid peptide receptors are μ (MOPr), δ (DOPr), and κ (KOPr). Leu-enkephalin (**238**) (Figure 63) is an agonist for the DOPr. However, **238** suffers from short half-life and high hydro-philicity, thereby hampering its ability to serve as a druggable compound. Additionally, enkephalins are rapidly metabolized by peptidases in the body as a result of their amide bonds and therefore cannot cross the blood-brain barrier (BBB) and reach opioid receptors in the central nervous system.²⁶⁰ Previously Rochon and co-workers have reported the effects of replacing the amide bonds in **238** with *E*-alkenes. When doing so, the replacement of the first amide bond by *E*-alkene did not affect the biological activity of **238**. Therefore, it was concluded that this bond is not involved in intramolecular or intermolecular interactions with the DOPr.²⁶⁰

Next, they sought to employ other amide bioisosteres including esters and *N*-methyl amides. The reason for the choice of these motifs, in particular, is their potential to act as hydrogen bond acceptors and not as hydrogen bond donors. The *N*-methyl group introduces a steric bulk, thereby distorting the planarity of the amide and restricting the conformation around the modified amide. An ester functional group is a better mimic of a peptide bond since it does not undergo many geometric alterations; however, the partial double bond nature of the ester bond is not as pronounced as the amide bond. Thus, esters are more structurally flexible. Rochon and co-workers replaced all of the amide bonds of **238** with an ester or an *N*-methyl amide. To evaluate the ability of each compound to bind the DOPr, competitive binding assays using GH3/DOPr cell membrane penetration were used. Results showed that replacing the fourth amide bond with an ester (**239**) or *N*-methyl amide (**240**) gave compounds with similar affinities to that of **238** (Figure 63). Compound **240** was synthesized by a multistep peptide approach where *N*-methylated leucine amino acid starting material was commercially available. When the third amide bond of **238** was replaced by an ester, most of the affinity for the DOPr was retained ($K_i = 34 \pm 17$). The phosphorylation of extracellular signal-regulated kinases 1 and 2 (ERK1/2) is used as an indicator of a compound's ability to act as an agonist. The activation of the DOPr by an agonist stimulates the rapid and transient phosphorylation of ERK1/2. However, the maximal effect of **238** is 5 min after stimulation; therefore, compounds were evaluated after 5 min of stimulation with varying concentrations (10^{-9} to 10^{-5} M). Compounds **239** and **240** at concentrations of 10^{-7} M produced significant phosphorylation of ERK1/2 similar to that of **238**.

Previously, this group reported the internalization of fluorescent chimeric DOPr (DOPr-GFp) in transfected DRGF11 cells in order to screen for active compounds. Compounds **239** and **240** were measured for their ability to induce internalization of DOPr-GFR. At 1 μ M,

238 produced an internalization that was visually seen within 5 min and complete by 30 min. The level of internalization by **239** and **240** was similar to that of **238**. These compounds were also tested for their ability to inhibit the electric-field induced contractions of the mouse vas deferens. Compound **240** has the greatest activity ($EC_{50} = 35 \pm 14$ nM) compared to **240** and **238** ($EC_{50} = 140 \pm 5$ nM and $EC_{50} = 74 \pm 1$ nM), respectively. A goal of these **238** analogs was their ability to cross the blood-brain barrier; therefore, their lipophilicity was assessed. On the basis of all the modifications, the *N*-methyl amide resulted in compounds with the highest lipophilicity. Compounds **239** and **240** had high total polar surface area (tPSA) values in comparison to CNS acting drugs. Results also indicated that compound **240** had an increase in half-life ($t_{1/2} = 10.7$ min) compared to **238** ($t_{1/2} = 4.6$ min), which is due to the replacement of the fourth amide bond with an *N*-methyl amide function, thereby increasing the stability of the third amide bond. On the other hand, when an ester is introduced to **239**, there was surprisingly little effect on the half-life ($t_{1/2} = 3.3$ min). These results showed that the systematic replacement of amides with bioisosteres such as an ester and *N*-methyl amide was an efficient way for designing novel peptide analogs of **238**.²⁶⁰

OLEFIN BIOISOSTERES

The bioisosteric replacement of a peptide bond with a nonhydrolyzable alkene functional group has been used to improve the “drug-like” properties of many parent compounds. The alkene bioisostere has been shown to mimic the planar geometrical features, but not the electronic and electrostatic properties, of an amide bond.^{261,262} The bond lengths and angles of an alkene are virtually identical to an amide. In contrast, an alkene does not have hydrogen bonding capacity due to the absence of heteroatoms.²³⁵ Furthermore, the value of the dipole moment is higher for an amide bond (3.6 D) than for an alkene (0.1 D).²⁶³ Several studies have reported that the replacement of an amide bond with an alkene bioisostere produces molecules that are efficacious. For example, dihydrouracil analog **241** is a potent inhibitor of the RNA-dependent RNA polymerase, NS5B protein of the hepatitis C virus genotypes GT1a ($EC_{50} = 51$ nM) and GT1b ($EC_{50} = 19$ nM).²⁶⁴ However, this compound had inherent pharmacokinetic issues; for example, **241** was rapidly cleared from plasma and thus had poor oral bioavailability ($F = 1.4\%$) in rats. These results could be explained by the low aqueous solubility ($<1.5 \mu\text{M}$ at pH 7.2) and poor membrane permeability of **241**. Modification of the amide linker in **241** with one that lacked one or both hydrogen bonding groups enhanced the overall membrane permeability potential.²⁶⁵ In order to identify a more potent HCV NS5B polymerase inhibitor with improved PK properties, the amide linkage was successfully replaced with a *trans* olefin, yielding compound ABT-072 (**242**) (Figure 64). The olefination of aldehyde group in **243** with diethyl (4-nitrobenzyl)phosphonate followed by the nitro reduction and methanesulfonylation gave **242** (Scheme 34). In the HCV genotype 1 (GT1) replicon assay, **242** had a greater potency for both the GT1a ($EC_{50} = 1$ nM) and GT1b ($EC_{50} = 0.3$ nM) polymerase compared to the parent compound **241**.

Moreover, in PK studies, the plasma clearance of **242** was significantly decreased, thereby producing greater oral bioavailability in both rat (5 mg/kg, per oral (po), $t_{1/2} = 3.1$ h, and $F = 44\%$) and dog (2.5 mg/kg, po, $t_{1/2} = 5.4$ h, and $F = 86\%$). On the basis of these results,

compound **242** was nominated for clinical studies. Pharmacokinetic studies in healthy human subjects indicated that **242** achieved maximum concentration within 5–9 h in plasma, with a mean terminal phase half-life of 7–9 h. Subsequently, phase II trials indicated that **242** was efficacious for treating genotype 1 infected HCV patients in combination with the other HCV protease inhibitor such as ritonavir, as well as ribavirin.

The calcitonin gene-related peptide is a 37 amino acid neuropeptide that has been shown to mediate various biological functions such as vasodilation and nociception.²⁶⁶ The CGRP is released from sensory nerves and plays an integral role in the pathophysiology of migraine.²⁶⁷ (*E*)-Alkene bioisosterism was used to develop acyclic CGRP antagonists, where the metabolically unstable central amide bond in a previously developed compound, **244** was replaced with an *E*-alkene linked to a substituted pyridyl moiety (**245**) (Figure 65).^{268,269} Compound **245** was synthesized via palladium-catalyzed Heck coupling reaction with an unsaturated halide (**246**) and an alkene (**247**). The general synthetic procedure is delineated in Scheme 35. These molecular structural changes substantially improved the bioavailability and pharmacokinetic profile of compound **245** in rats compared to **244** while maintaining antagonist activity at the CGRP receptor.

In 2007, Thorarensen et al. explored the SAR of the previously discovered lead compound, **249**, and newly synthesized anthranilic acid derivatives²⁷⁰ to elucidate the role of the linker connecting the two important pharmacophoric aryl A and B rings for antibacterial efficacy.²³⁶ The amide linker in **249** was successfully replaced by several amide bioisosteres, and the *E*-alkene-containing analog **250** was found to have significantly lower MIC values, particularly in *Staphylococcus aureus* UC9218 and *Staphylococcus epidermidis* UC 12084 (SEPI_d) (Figure 66), than the parent compound **249**. The general synthetic method showing Wittig olefination of an Wittig reagent (methyl 2-((bromotriphenyl- λ^5 -phosphaneyl)methyl)-5-cyanobenzoate) with an aldehyde (**251**) is described in Scheme 36, i. Overall, results suggest that the amide may not be essential for bioactivity, and it perhaps only keeps the pharmacophoric elements at the defined distances. Thus, an amide can be dispensable without causing a significant decrease in MIC values.

In another study exploring the modification of amide to alkene, utilizing amylin (20–29) as a parent structure, Brouwer and co-workers reported the synthesis of alkene dipeptide/alkene dipeptidosulfonamide isosteres using a solid phase cross metathesis method.²⁷¹ Amylin, or human islet amyloid polypeptide, is a peptide hormone composed of 37 amino acids, where amylin (20–29) refers to the highly amyloido-genic region that is involved in the pathogenesis of type 2 diabetes. The modification in amylin (20–29) to yield compound **254** was postulated to be beneficial in determining the peptide backbone interactions and peptide stabilization in enzymatic degradation. Given that the alkene moiety closely resembled the geometry of the amide bond and that the amalgamation of a sulfonamide bond may increase the flexibility of the backbone, the authors transformed the amide function (at positions 27 and 28) of **254** into the alkene derivative **255** and the alkenesulfonamide (**256**) dipeptide analogs (Figure 67). The adopted synthetic route for **255** and **256**, depicted in Scheme 37, used resin bound H-Ser(O^tBu) as a starting material.

Both compounds were characterized by electrospray mass spectrometry. Rapid gel formation, which was used to measure aggregation behavior, indicated that **255** and **256** decrease gel formation time by 30 and 60 min, respectively, compared to parent amylin (<10 min). Compared to **254**, both **255** and **256** displayed a significantly low number of amyloid fibrils in the transmission electron microscopy images. This retardation in fibril formation by both bioisosteres could be due to a lack of hydrogen bonding capabilities in the peptide backbone. Fourier transform infrared spectra (FTIR) and circular dichroism (CD) studies also validated that the modified dipeptide peptidomimetics exhibited superior activity in the retardation of fibril formation and altered β -sheet secondary structures when compared to the parent, **254**.

Another instance of application of amide bond replacement and amide bioisosterism is seen in Yamamoto et al. studies to find an efficient DNA minor groove binding agent where the group synthesized distamycin related structural analogs.²⁷² Distamycin (**262**) is a naturally occurring tripeptide antibiotic that binds to the nonintercalative minor groove of DNA, with high selectivity toward AT-rich sequences.²⁷³ The structural modification of the parent compound **262** at the distal C-terminal, by replacing the amidine group with a dimethylamino group, yielded compound **263**, and further alteration at the N-terminal in **263** yielded **264**, which had a nitro group. Compounds **263** and **264** were altered so as not to contain any amide bioisostere. One of the inter-pyrrole linkers (amide bond) of **264** was replaced by a *trans*-olefin to produce compound **265** to determine the effect of amide bond replacement or amide bioisosterism on its DNA binding properties (Figure 68).

The general synthetic route to access compound **265** is shown in Scheme 35, ii. The results of the ethidium displacement assay indicated that the modified compounds **263**, **264**, and **265** had a lower DNA binding affinity for poly(dA-dT) compared to **262**. However, the replacement of the amide bond with a *trans* olefin, as in compound **265**, produced the highest DNA binding for poly(dG-dC); $K_{app} = 7.4 \times 10^5 \text{ M}^{-1}$ compared with **262**, **263**, and **264**. Overall, the structural modification related to amide function could produce compounds that may have different DNA recognition patterns.

An interesting observation regarding the effect of replacing a peptide bond with an *E*-alkene is provided by the bombesin receptor antagonist **268**, derived from compound **266**, with speculation that the *E*-alkene bond could provide high lipophilicity and enhanced resistance to biodegradation.²⁷⁴ The biological results were compared to a short chain pseudopeptide **267**, which is also a bombesin analog. Both peptides **267** ([D-Phe⁶,Leu¹³Ψ(CH₂NH)Leu¹⁴]bombesin(6–14)) and **268** ([D-Phe⁶,Leu¹³Ψ[(*E*)-CH=CH]Leu¹⁴]-bombesin(6–14)) have similar structures except that **268** has a *E*-alkene bond inserted between the 13th and 14th position in bombesin (see cross-reference for synthetic procedure) (Figure 69).

The antagonistic activity of **268** for the bombesin receptor was 10 times greater than **267** in terms of its inhibition of bombesin-stimulated amylase release in rat pancreatic acini. Furthermore, additional pharmacological experiments revealed that **268** efficiently blocked bombesin-stimulated amylase release; however, **267**, even at the highest concentration used, failed to completely block amylase release, indicating that compound **268** is a very potent

and specific bombesin antagonist in rat pancreatic acini that could be a useful probe for studying the biological actions of bombesin and its related peptides.

Another example of an *E*-olefin bioisostere as an amide bond replacement are the mutants of A β (1–40) Phe19-Phe20 which inhibit amyloid A β peptide amyloidogenesis and have been implicated in the formation of many distinct quaternary structures involved in the pathogenesis of AD.^{275–277} The A β fibril structure is stabilized by various inter- and intramolecular hydrophobic interactions, salt bridges, and intermolecular hydrogen bonds. Therefore, interrupting intermolecular backbone-backbone hydrogen bonding in one of the hydrophobic subsequences, i.e., LVFFA (17–21) in A β (1–40), could prevent many peptides from forming cross- β -sheets-based amyloid fibrils. Subsequently, Kelly et al. in 2005 substituted a *trans* alkene moiety for an amide in the key Phe19-Phe20 subsequence, thereby eliminating a hydrogen bond donor and acceptor from the desired site (Figure 70).

Initially, the stereoselective *E*-olefin dipeptide isostere (**270**) was synthesized according to the general synthetic method shown in Scheme 36, ii, and then incorporated into the A β (1–40) peptide in place of phenylalanine 19 and 20 (abbreviated as Phe19-Phe20) by solid phase peptide synthesis using hexafluorophosphate azabenzotriazole tetramethyl uronium (HATU) activation. The final Phe19-Phe20 *E*-olefin analog of A β (1–40) was referred to as EOA β , and its efficacy to inhibit fibrillar aggregation into protofilaments and fibrils having a cross β -sheet structure was confirmed by circular dichroism and atomic force microscopy (AFM) methods.²⁷⁸

Researchers at the Neuroscience Research Pharmaceutical Product Division of Abbott Laboratories, prepared *E*-alkene bioisosteres of the amide bond in cholecystokinin (CCK) peptides, with the aim of developing potent and selective cholecystokinin brain (CCK-B) ligands.²⁷⁹ The systematic replacement of the amide linkage via an *E*-alkene was done to mimic the size, geometry, bond angle, and bond length of the amide. While the amide bond undergoes restricted rotation, it does still rotate, which is important for hydrogen bonding at the receptor binding site. In contrast, the *E*-alkene cannot form hydrogen bonds, and thus, the amide linkages at different positions of CCK peptides were replaced by an *E*-alkene and tested to determine if they were bioactive. This modification strategy was used as it was postulated that it would provide important information about the role of each amide bond in the CCK peptide. Among six pseudopeptides synthesized, the potency and functional activity of the **273** (Boc-Leu[*E*-CH=CH]Gly-Trp-Leu-Asp-PheNH₂) isostere was similar to that of the parent peptides, Boc-protected CCK-6 hexapeptide (Boc-Leu-Gly-Trp-Leu-Asp-PheNH₂; **272**) and Boc-protected (CCK-4) tetrapeptide (Boc-Trp-Met-Asp-PheNH₂; **271**) (Figure 71).

The target peptide, **273**, was synthesized by incorporating an *E*-alkene dipeptide isostere (i.e., Boc-Leu Ψ [*E*-CH=CH]Gly-OH) and a CCK residue using a standard peptide coupling procedure (Scheme 38). Overall, the results of this study indicated that the bioisosteric replacement of an amide bond at the Leu-Gly region of CCK-6 is acceptable for retaining the bioactive conformation required for receptor activation.²⁷⁹

FLUOROALKENE BIOISOSTERES

Fluoroalkene, also known as monofluoroalkene, has generated interest as a surrogate of the amide functional group. Geometrically, both the amide and fluoroalkene are similar; for example, the length of the C=O bond of the amide is 1.228 Å and the C–N bond is 1.368 Å, whereas the C–F bond is 1.376 Å and C=C bond is 1.333 Å. Furthermore, the fluorine atom mimics the oxygen atom of the carbonyl to a certain extent because both have similar van der Waals radii (1.47 Å for fluorine and 1.52 Å for oxygen).²⁸⁰ The double bond of the fluoroalkene imparts rigidity to the molecule. The high electronegative fluorine atom mimics the carbonyl oxygen of the amide and thus provides fluoroalkene with a dipole moment of 1.4 D (3.6 D in the case of an amide). Finally, the fluoroalkene isostere could serve as a weak hydrogen bond acceptor to make either intermolecular or intramolecular hydrogen bonds. Furthermore, the (*Z*)-fluoroalkene mimics the *s-trans* amide bond, whereas the (*E*)-fluoroalkene mimics the *s-cis* form, and it could be explained because no equilibrium exists between them. Also, the fluoroalkene moiety is more lipophilic than an amide and therefore could be potentially used as a metabolically stable amide bioisostere.²⁸⁰ In this context, several investigators have shown that the replacement of an amide bond with the fluoroalkene moiety produced superior metabolic stability, lipophilicity, and binding selectivity.

The search for a selective DOPr agonist is of interest for the development of novel medications to treat chronic pain, inflammation, and cancer pain. Compound **238** (Tyr¹-Gly²-Gly³-Phe⁴-Leu⁶) is a pentapeptide that is an endogenous ligand for the δ opioid receptor, but its therapeutic application is limited due to its extremely poor selectivity with respect to the μ opioid receptor and hydrophilic character.²⁸¹ Also, the *in vivo* administration of **238** is problematic due to poor PK properties, including the rapid cleavage of Tyr¹-Gly² by aminopeptidase N in human plasma ($t_{1/2}$ = 0.69 min) and Gly³-Phe⁴ by the angiotensin-converting enzyme present in the blood-brain barrier.^{282,283} To improve these pharmacological attributes of **238**, Altman and colleagues tactfully replaced the amide linkage of the Tyr¹-Gly² with a fluoroalkene (**275**) and trifluoroethylamine moiety to yield compounds (*S*)-**276** and (*R*)-**277**, respectively (Figure 72).^{284,285} The key synthetic steps to generate a fluoroalkene isostere in compound **275** are shown in Scheme 39.

The results indicated that compound **275** activated δ -receptors stably expressed in CHO cells (EC_{50} = 5 nM), whereas the progenitor **238** had a 60-fold higher activity (EC_{50} = 0.08 nM). However, **275** had a similar selectivity for μ versus δ as the parent peptide **238**. Most importantly, **275** had excellent stability in both Sprague-Dawley rat (76% remaining of **275** at 4 h versus $t_{1/2}$ < 5 min for **238**) and human plasma (68% remaining of **275** at 4 h versus $t_{1/2}$ < 12 min for **238**) compared to **238**. Furthermore, **275** had improved *in vivo* distribution in a BALB/c mouse model with 50 mg/kg intravenous dose and the plasma concentrations of **275** were detected for 2 h, whereas **238** was completely metabolized within 5 min. Also, **275** was orally bioavailable and plasma concentrations were detected up to 30 min after an oral dose of 400 mg/kg in the BALB/c mouse model.

These results suggested that **275** has significantly improved *in vivo* distribution (in both plasma and CNS), which was negligible for **238**. This improvement of **275** over **238** could

be explained by the σ -electron withdrawing effects of the fluorine atom, which decreased the basicity of the neighboring functional groups, making them less prone to hydrogen bond with H₂O, as well as the catalytic domains of the metabolizing enzymes. Neither (*S*)-**276** nor (*R*)-**277** were active at δ or μ receptors and therefore were not assessed for stability, metabolism, and distribution.

In another study by a different research group, the bioisosteric replacement of the Gly³-Phe⁴ amide bond was conducted by Nadon et al.²⁸⁶ Previously, these authors systematically replaced the Gly³-Phe⁴ amide linkage with a thioamide ($K_i = 47 \pm 17$ nM)²⁸⁷ and ester bioisostere ($K_i = 34 \pm 17$ nM) (Figure 73).²⁶⁰ These isosteres retained δ -opioid receptor activity, which suggested that a hydrogen bond donor at this site of **238** was not essential, and this led to the design of a fluoroalkene bioisostere (**283**). This compound was obtained by first synthesizing fmoc-protected benzyl fluoro-pentenoic acid intermediate (**286**) which was later used in solid-phase synthesis (SPPS) utilizing 2-chlorotrityl chloride resin (CTS). The synthetic route of **283** is shown in Scheme 40.

The δ -opioid receptor binding affinity of **238** and **283** was calculated by competitive binding assays using iodinated deltorphin I ([¹²⁵I]-deltorphin I) in membrane preparations obtained from HEK293 cells expressing a FLAG-tagged version of the mouse δ -opioid receptor. The results indicated that **283** had a high affinity for δ -opioid receptor ($K_i = 43 \pm 14$ nM), although its affinity was lower than the parent peptide **238** ($K_i = 6.9 \pm 2.3$ nM) (Figure 73). However, its affinity for the δ -opioid receptor was significantly greater than the *trans*-alkene isostere ($K_i = 587 \pm 19$ nM).²⁸⁸ This weak activity of the *trans*-alkene isostere highlighted the significant role of the fluorine atom as an effective functional mimicry of the hydrogen bond accepting feature of the amide.

Daclatasvir (formerly known as BMS-790052) (**290**) (Figure 74) is a small molecule inhibitor of HCV NS5A that has potent *in vitro* anti-HCV efficacy in the picomolar range in HCV replicons from various genotypes.²⁸⁹ In order to obtain an improved structural understanding of this chemotype template for designing novel NS5A inhibitors, Chang and co-workers synthesized fluoro-olefin-based structures, as they hypothesized they may provide a new peptidomimetic approach for developing potent and structurally unique inhibitors of HCV NS5A.²⁹⁰ The intermolecular hydrogen bonded amide group in **290** was successfully replaced with a fluoro-olefin motif to obtain compound **291**, and the synthetic route is depicted in Scheme 41.

The anti-HCV efficacy was measured in a clone A replicon whole cell assay, and the results indicated that **291** inhibited HCV genotype 1b replication in the picomolar range ($EC_{50} = 79$ pM), similar to the parent peptide **290** (Figure 74). Furthermore, the computational modeling studies indicated that this fluoro-olefin isostere favored a γ -turn substructure which is necessary for the interaction with the NS5A protein. Finally, **291** did not have any cytotoxicity up to the highest concentration tested ($CC_{50} > 10$ μ M).

MISCELLANEOUS AMIDE BIOISOSTERES

The signaling of RhoA/C is important for metastases and invasion of several cancers. Knockout and siRNA data have revealed an important *in vivo* role for RhoC in breast cancer metastasis as well as for megakaryoblastic leukemia transcriptional coactivator proteins (MKL1) and serum response factor (SRF) in breast and cancer metastases. These results reveal that Rho signaling and, more specifically, Rho-regulated gene transcription can be targets for cancer.²⁹¹ Evelyn and colleagues identified compound **301** (Figure 75), which blocks SRE-luciferase gene transcription when RhoA and RhoC signaling pathways are activated. Compound **301** potently inhibited LPA-induced DNA synthesis in PC-3 cells (<1 μM). Additionally, it inhibited the growth of RhoC-overexpressing melanoma cells at nanomolar concentrations but was less active in cell lines expressing lower levels of RhoC. Compound **301** inhibited spontaneous PC-3 prostate cancer cell Rho-dependent invasion through a Matrigel matrix but failed to do so *in vitro* in a $G\alpha_i$ -dependent lysophosphatidic acid (LPA-stimulated) SKOV-3 ovarian cancer cell invasion model. On the basis of these favorable results on cancer cell function, it was decided that **301** would be a promising lead. Compound **301** also showed acute cellular toxicity toward PC-3 cells at 24 h and consequently decrease in cell viability.

Therefore, the next goal was to make modifications in this initial lead to improve potency and or selectivity while diminishing its cytotoxicity. The three areas of concern from this initial lead were the nitrogen-oxygen bond between the two carboxamides being susceptible to cleavage by thiols, the two carboxamides limiting potency and interfering with cell penetration, and the two aromatic rings not being optimal motifs for potency and selectivity. The initial strategy to modify these areas included removing the nitrogen-oxygen bond and employing a bioisosteric replacement of the amides, and conformational restriction imposed between the two aromatic rings. Making changes on the tether between the two carboxamides of **301** was first evaluated. Results indicated that removing the methyl group led to little effect on activity or selectivity. Replacing the oxygen atom with a carbon atom eliminated acute toxicity even at higher doses. Next, modifications were made on the secondary amides. When the hydrogen bond donor was removed to improve cell permeability, this gave rise to a dramatic loss in activity. When the anilides were replaced, it had a detrimental effect, but reducing the amides to amines was more successful. A monoamine (**303**) (Figure 75) retained moderate selectivity with little cytotoxicity compared to another monoamine and diamine analogs. The bioisosteric replacement of the amide with triazoles, thiazole, and oxazole led to completely inactive compounds indicating “traditional” heterocyclic amide bioisosteres would be ineffective.

Several analogs were tested for their ability to inhibit PC-3 prostate cancer cell invasion in a Matrigel matrix (% inhibition invasion at 10 and 100 μM) as well as their ability to inhibit mitochondrial metabolism when using WST-1 (% inhibition WST-1 at 10 and 100 μM) in comparison to **301** (Figure 75). All conformationally restricted analogs had equivalent efficacies against SRE.L at 10 and 100 μM and had similar activity in a Matrigel assay. Compound **302** was slightly less toxic at 100 μM (23%) with an efficacy:toxicity profile at 100 μM higher than that of **301** (Figure 75). The monoamine bioisostere **305** was synthesized by alkylation of 4-chloroaniline with 3-bromopropylamine which led to

compound **303** over several steps (Scheme 42). Compound **303** had the best efficacy:cytotoxicity ratio in transfected cell SRE-luciferase studies. Additionally, it inhibits invasion at 10 μM (54%), similar to that of **301** (71%), with no apparent toxicity. At 100 μM concentration, there is almost complete inhibition of invasion (84%) with less toxicity (27%) compared to **301** at 10 μM (54%). Overall the nipecotic amide **302** and monamine **303** were able to inhibit $G\alpha_{12}\text{QL}$ -stimulated SRE.L-luciferase expression with efficacy equal to **301** but with reduced cytotoxicity. These studies revealed the correlation between inhibition of Rho-mediated gene expression to cell invasion in a Matrigel matrix model of metastasis.²⁹¹

A thiophenecarboxylic acid series is one of several chemical classes that has been reported to inhibit the function of NS5B in genotype 1a and 1b HCV at an allosteric thumb site near the active site.²⁹² Exploration of this series began with 3-arylsulfonamidothiophene-2-carboxylic acids and then proceeded to the application of aromatic and heteroaromatic amide isostere analogs. The problem with these amide bioisosteres was that they resulted in weaker enzyme inhibitors with reduced cellular potency. Therefore, Canales and colleagues turned to other structural motifs in order to identify novel NS5B inhibitors of the thiophenecarboxylic acid series.²⁹² They decided to use substituted *N*-acylhydrazines as tertiary amide replacements. Similar to amides, *N*-acylhydrazines are conformationally restricted due to resonance between the α -nitrogen and the carbonyl. As a result, trisubstituted *N*-acylhydrazines were synthesized, and a direct hydrazine analog (compound **307**) of the prototypical amide **306** ($\text{IC}_{50} = 0.086 \mu\text{M}$) (Figure 76) led to a compound with similar NS5B inhibitory potency ($\text{IC}_{50} = 0.088 \mu\text{M}$). A cocrystal structure of this direct hydrazine analog bound to NS5B proved the conformational similarity of the *N*-acylhydrazine to the amide. Additionally, the physicochemical properties were not significantly changed with the *N*-acylhydrazine replacement. It was then determined that the *N*-acylhydrazine was a reasonable tertiary amide bioisostere, thus resulting in the evaluation of a range of N^{β} substituents having increased steric bulk to further rigidify the orthogonal conformation along with adding polar substituents in order to engage the solvent-exposed region next to the binding pocket. Linear and cyclic alcohols resulted in similar binding affinities to that of **306**. Nonaromatic heterocycles gave rise to excellent binding affinities; however, inhibition of enzymatic activity was lower for these analogs in comparison to **306**. The synthetic method for a 4-Me-piperidinyl analog **308** is shown in Scheme 43. *In vitro* evaluation of compound **308** ($\text{IC}_{50} = 0.063 \mu\text{M}$) (Figure 76) showed significant improvement in cellular activity for both genotypes. This study showed that trisubstituted acylhydrazines could serve as tertiary amide bioisosteres.

CONCLUSION

The amide bond, beyond its critical function in protein structures, is most often encountered in hit, lead, and candidate compounds for therapeutic discovery across a wide range of disease indications. The resonance structure of the amide group gives way to restricted configuration engendering *trans* geometry of substituents, hydrogen bond accepting ability of the oxygen but not the nitrogen atom and hydrogen bond donating ability (if the nitrogen is not trisubstituted). These collective features provide for the often-critical role the amide plays in the pharmacophore or auxophore of bioactive compounds, providing either target binding interactions, positioning of bioactive configuration, or both. Successful bioisosteres

of the amide bond are required to closely mimic these features while overcoming the Achilles heel of the group: its metabolic lability. Thus, amide bioisosteres tend to see employment in lead compound optimization to improve absorption, distribution, metabolism, excretion, and toxicity (ADMET) properties.

Bioisosteres, by nature of their differing size, shape, and hydrogen bond donating and accepting profile, can convey additional target binding interactions to enhance (or degrade) activity depending on the interactions the amide bond makes with the target protein. However, this is often seen in combination with extensive SAR studies guided by *in silico* approaches that is often not directly attributed to the bioisostere itself but more a combination of differing substituents in differing configuration. While many potential bioisosteres of the amide group have been evaluated, there are a select few, summarized herein (Table 2), that provide a blend of similar hydrogen bonding pattern, restricted rotation, lipophilicity, and metabolic stability. For example, the ethane moiety has been employed as a bioisostere of the amide group that provides for significant metabolic stability but fails to mimic the hydrogen bonding, configurational, and hydrophilic character of the amide. Thus, ethane's use is limited to compounds wherein the amide is not present in the pharmacophore or auxophore. The ability of amide bioisosteres to confer additional properties beyond PK/PD modulation, such as engendering blood-brain barrier penetration, has been reported (see methylamide **240** as an example), although it is worth noting that this is not an inherent property of any bioisostere to date but more a design feature to remove penetration hindering molecular features of the amide bond, such as hydrogen bond donors and charged acids generated by metabolic cleavage, or simply to increase lipophilicity, three strategies widely employed in CNS drug discovery.²⁹³

Novel bioisosteres continue to be developed with new heterocyclic rings and inorganic elements being investigated for their suitability as amide bioisosteres. The amino oxetane moiety, wherein the amine is bound directly to the heterocycle, imparts increased metabolic and chemical stability to peptidomimetic derivatives; however, the impact of this novel bioisostere on biological activity remains to be fully elucidated.^{296,297} The loss of the rigidity of the amide bond and the increased separation of the oxygen from the backbone structure may have critical roles to play in retaining activity. Additionally, the oxetane ring has been utilized as a bioisostere for the methylene and gem-dimethyl groups¹⁶ and carboxylic acids,²⁹⁸ which may complicate its effects as a bioisostere for the amide group. The synthesis of oxetane-containing diketopiperazine bioisosteres, wherein the oxetane (or an azetidine) ring replaces the constrained amide carbonyl constituent, thus affording a spirocyclic system and combining the beneficial effects of two amide bioisosteres to maximize metabolic protection, has been reported.²⁹⁹ However, no biological activity associated with these structures has been published to the best of our knowledge, making the suitability of this spirocycle as a bioisostere of the amide bond unclear. In both cases the ability of the oxetane ring to introduce three-dimensionality over the two-dimensionality of a carbonyl benefits in moving away from planar "drug-like" structures and into more novel chemical space.³⁰⁰

Boron-containing structures continue to gain traction in medicinal chemistry.^{301,302} The boronamide structure B(OH)-NH is a theoretical bioisostere for the amide moiety. Initial

modeling studies of energy barriers to rotation performed on *N*-methyl methylboronamide illustrate the double bond character of the boron-nitrogen bond and single bond character of the B–O bond mimicking the natural amide bond.³⁰³ However, given synthetic challenges in accessing this particular functional group with the desired variety of substituents, the theory, to the best of our knowledge, has not been reduced to practice.

Silicon is gaining attention in medicinal chemistry for the role it can play in expanding chemical space.³⁰⁴ The reported use of silanols to mimic the transition state of protease inhibitors³⁰⁵ and to act as a bioisostere of terminal *N*-(hydroxy)amides in histone deacetylases (HDAC) inhibitors (albeit with reduced activity)³⁰⁶ is pointing the way for the direct investigation of silanols as amide bioisosteres. The pioneering work of Chris McGuigan in the development of phosphoramidate prodrug technology³⁰⁷ has led to a large amount of literature on the synthesis and biological stability of these moieties. These data can perhaps be mined to discover potential improvements on the traditional C–P bond-containing phosphoramidite bioisostere described above or to introduce the phosphoramidate moiety as an amide bioisostere itself, albeit with intracellular metabolic lability.

These few selected examples provide a glimpse of emerging novel amide bioisosteres that are under evaluation for adding to the medicinal chemist's toolbox. The examples illustrated in this Perspective were chosen to highlight the power of amide bond bioisosteres in hit-to-lead and lead optimization to preserve, or enhance, activity and selectivity and to enhance PK/PD properties. Included are many examples of clinical candidates and clinically approved drugs reflecting the importance of this approach to drug discovery.

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Angelica V. Carmona obtained her B.S. in Biochemistry from Mount Saint Mary's University Los Angeles, CA, U.S.. In 2018, she joined Dr. Paul C. Trippier's lab at Texas

Tech University Health Sciences Center and in 2019 moved to the University of Nebraska Medical Center as a Ph.D. scholar. Her current research work focuses on synthesizing novel neuroprotective compounds as potential therapeutics for the treatment of the rare pediatric disorder Batten disease.

Amit K. Tiwari obtained his B.Pharm. from the Ram-Eesh Institute of Technology, India. He received his M.S. and Ph.D. in Pharmaceutical Sciences from the St. John's University, Queens, NY (2008 and 2011, respectively). He then carried out postdoctoral research in Professor James Gallo's laboratory at Icahn School of Medicine (2011–2013) in the area of pharmacokinetics. He joined Tuskegee University as an Assistant Professor prior to joining the Department of Pharmacology and Experimental Therapeutics at the University of Toledo, Ohio, as an Assistant Professor in 2015. In 2019, he was promoted to Associate Professor with tenure. His research interests are in broad areas of cancer pharmacology, drug development, and medicinal chemistry.

Paul. C. Trippier gained his M.Chem. from the University of Hull (U.K.) and his D.Phil. in Synthetic Organic Chemistry from the University of Oxford under the mentorship of Professor Mark Moloney. After postdoctoral positions with Prof. Chris McGuigan (Cardiff University) and Prof. Richard Silverman (Northwestern University) he began his independent career at Texas Tech University Health Sciences Center where he was promoted to Associate Professor with tenure. In 2019, he moved to the College of Pharmacy at the University of Nebraska Medical Center where his research group investigates small molecule probe and drug discovery for cancer, ischemic stroke, and neurodegenerative diseases among other indications.

ABBREVIATIONS USED

Aβ	amyloid- β
A_{2A}	adenosine A _{2A}
A549	human lung cancer
ACAT	A:cholesterol acyltransferase
ACE	angiotensin-converting enzyme
ADMET	absorption, distribution, metabolism, excretion, and toxicity
AD	Alzheimer's disease
AFC	<i>N</i> -acetyl- <i>S</i> -farnesyl-L-cysteine
AFM	atomic force microscopy
AIDS	acquired immune deficiency syndrome
AKR1C3	aldo-keto reductase 1C3
AML	acute myeloid leukemia

AMFC	amide modified farnesyl cysteine analog
ATP	adenosine triphosphate
BBB	blood-brain barrier
B16F10	<i>Mus musculus</i> skin melanoma cells
BACE-1	β -site amyloid precursor protein cleaving enzyme 1
BAEC	bovine aortic endothelial cell
BCC	basal-cell carcinoma
Bcr-Abl	break point cluster region Abelson kinase
Caki-2	human renal cancer
CB	cannabinoid
CB₁	cannabinoid-1
CB₂	cannabinoid-2
CCK	cholecystokinin
CCK-B	cholecystokinin brain
CD	circular dichroism
Cat K	cathepsin K
CDI	carbonyldiimidazole
CEM	human T-lymphocyte cell
CGRP	calcitonin gene related peptide
CHO	Chinese hamster ovary
CIDV	capsaicin induced dermal vasodilation
CML	chronic myelogenous leukemia
CuAAC	copper(I)-catalyzed azide-alkyne cycloaddition
CuI	copper iodide
CNS	central nervous system
CRL-8155	human lymphoblast cell
CRPC	castration-resistant prostate cancer
CTC	2-chlorotriyl chloride resin
CyP	liver cytochrome

D2-R	dopamine-2 subtype receptor
D3-R	dopamine-3 subtype receptor
DGAT	acyl CoA:diacylglycerol acyltransferase
DKP	diketopiperazine
DOPr	δ opioid receptor
DPP-4	dipeptidyl peptidase-4
DIAD	diisopropyl azodicarboxylate
DSG	15-deoxyspergualin
EDG	electron donating group
ERK1/2	extracellular signal-regulated kinases 1 and 2
EWG	electron withdrawing group
FDA	Federal Drug Administration
FTIR	Fourier transform infrared
GABA_A	γ -aminobutyric acid A
GPCR	G-protein-coupled receptor
GIST	gastrointestinal stomatal tumor
GLP-1	glucagon-like peptide 1
GIP	glucose-dependent insulinotropic polypeptide
Gpp(NH)p	5'-guanylyl imidodiphosphate
GSH	glutathione
GT1	genotype 1
GTL-16	human gastric carcinoma
GVHD	graft-versus-host disease
h	human or hour
HATU	hexafluorophosphate azabenzotriazole tetramethyluranium
hCB₁	human cannabinoid 1

H1437	non-small-cell lung cancer
HAT	human African trypanosomiasis
HBA	hydrogen bond acceptor
HBD	hydrogen bond donor
HCV	hepatitis C virus
HCMV	human cytomegalovirus
HD	Huntington's disease
HDAC	histone deacetylase
HGF	hepatocyte growth factor
Hh	Hedgehog
hlcmt	human isoprenylcysteine carboxyl methyltransferase
HeLa	human cervix carcinoma
hERG	human ether-a-go-go-related gene
HEK293	human embryonic kidney 293
HepG2	human liver cancer
HINF	Haemophilus influenzae 30063
HIV	human immunodeficiency virus infection
HMEC-1	human microvascular endothelial cells
HL-60	human leukemia
HLM	human liver microsome
HT22	mouse hippocampal neuron
HT-29	human colon cancer
5-HT	5-hydroxytryptamine
HUVEC	human umbilical vein endothelial cell
Icmt	isoprenylcysteine carboxyl methyltransferase
ip	intraperitoneal
iv	intravenous
IL-12	interleukin 12
IL-17	interleukin 17

IL-23	interleukin 23
INSTI	integrase strand transfer inhibitor
JAK	Janus kinase
KOPr	κ opioid receptor
LA	α -lipoic acid
L1210	murine leukemia cell
m	mouse
MCF10A	human mammary epithelial cell
mGlu7-NAM	metabotropic glutamate receptor subtype-7 negative allosteric modulator
MDCK	Madin-Darby canine kidney
MDA-MB-231	M. D. Anderson metastasis breast adenocarcinoma
Met	<i>N</i> -methyl- <i>N'</i> -nitrosoguanidine human osteosarcoma transforming gene
MIC	minimal inhibitory concentration
MKL1	megakaryoblastic leukemia transcriptional coactivator protein
MLM	mouse liver microsome
MMP	matrix metalloproteinase
MOPr	μ opioid receptor
MT4	human T-lymphoid cell
MTR	melatonin receptor
MT₁R	melatonin receptor 1
MT₂R	melatonin receptor 2
MW	microwave
nAChR	neuronal nicotinic acetylcholine receptor
NADPH	nicotinamide adenine dinucleotide phosphate
NDA	new drug application
NEP	metalloproteinase neutral endopeptidase
NET	neutrophil extracellular trap

NK-1	neurokinin-1
NPA	[³ H]spiro-peridol/ <i>N</i> -propylnorapomorphine
NS5B	nonstructural protein 5B
NSAID	nonsteroidal anti-inflammatory drug
ORTEP	Oak Ridge thermal ellipsoid plot
PAD	protein arginine deiminase
PAF	platelet-activating factor
PC-3	human prostate cancer
PD	pharmacodynamic
PD	Parkinson's disease
PDHc	pyruvate dehydrogenase complex
PDHc-E1	pyruvate dehydrogenase complex-E1 component
PK	pharmacokinetic
PrCP	prolylcarboxypeptidase
po	per oral
PTM	post-translational modification
RdRp	RNA-dependent RNA polymerase
RTK	receptor tyrosine kinase
SAR	structure-activity relationship
SAUR	<i>Staphylococcus aureus</i> UC 9218
SCD	stearoyl-CoA desaturase
SCD1	stearoyl-CoA desaturase-1
SEP1d	<i>Staphylococcus epidermidis</i> UC 12084
SEPIId	<i>Staphylococcus epidermidis</i> (UC 12084)
SMO	smoothened
SMFC	sulfonamide modified farnesylcysteine analog
SP	substance P
SRF	serum response factor
SPPS	solid-phase synthesis

STAT-5	signal transducer and activator of transcription 5
T-ALL	T-cell acute lymphoblastic leukemia
TBAF	tetrabutylammonium fluoride
TMSA	trimethylsilyl azide
tPSA	total polar surface area
TRPV1	transient receptor potential cation channel subfamily V member 1
TS	transition state
TYK2	tyrosine kinase 2
U2OS	PAD-4 expressing osteosarcoma bone marrow
VEGFR2	vascular endothelial growth factor receptor-2
VDA	vapor diffusion assay
VLA-4	very late activating antigen-4
Vif	viral infectivity factor

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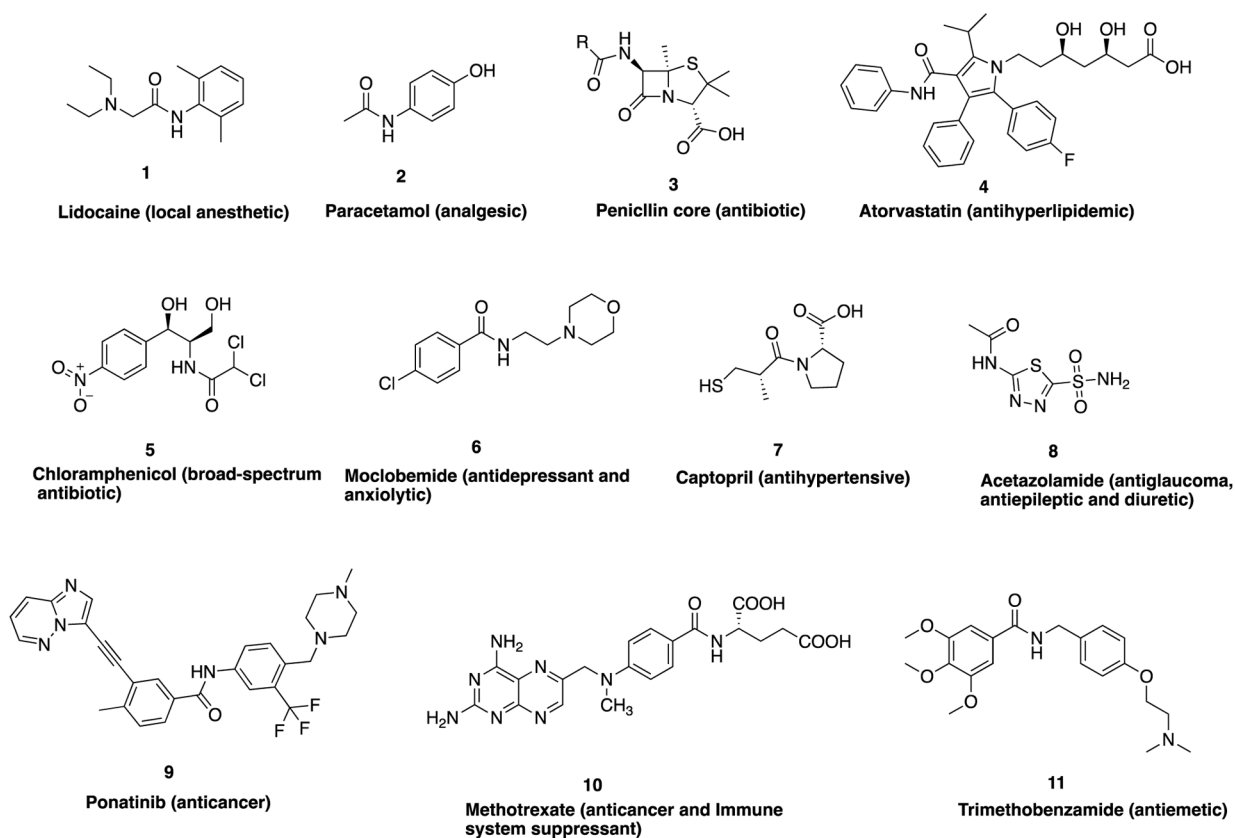


Figure 1. Structures of selected clinically approved drug molecules containing an amide bond and their biological function.

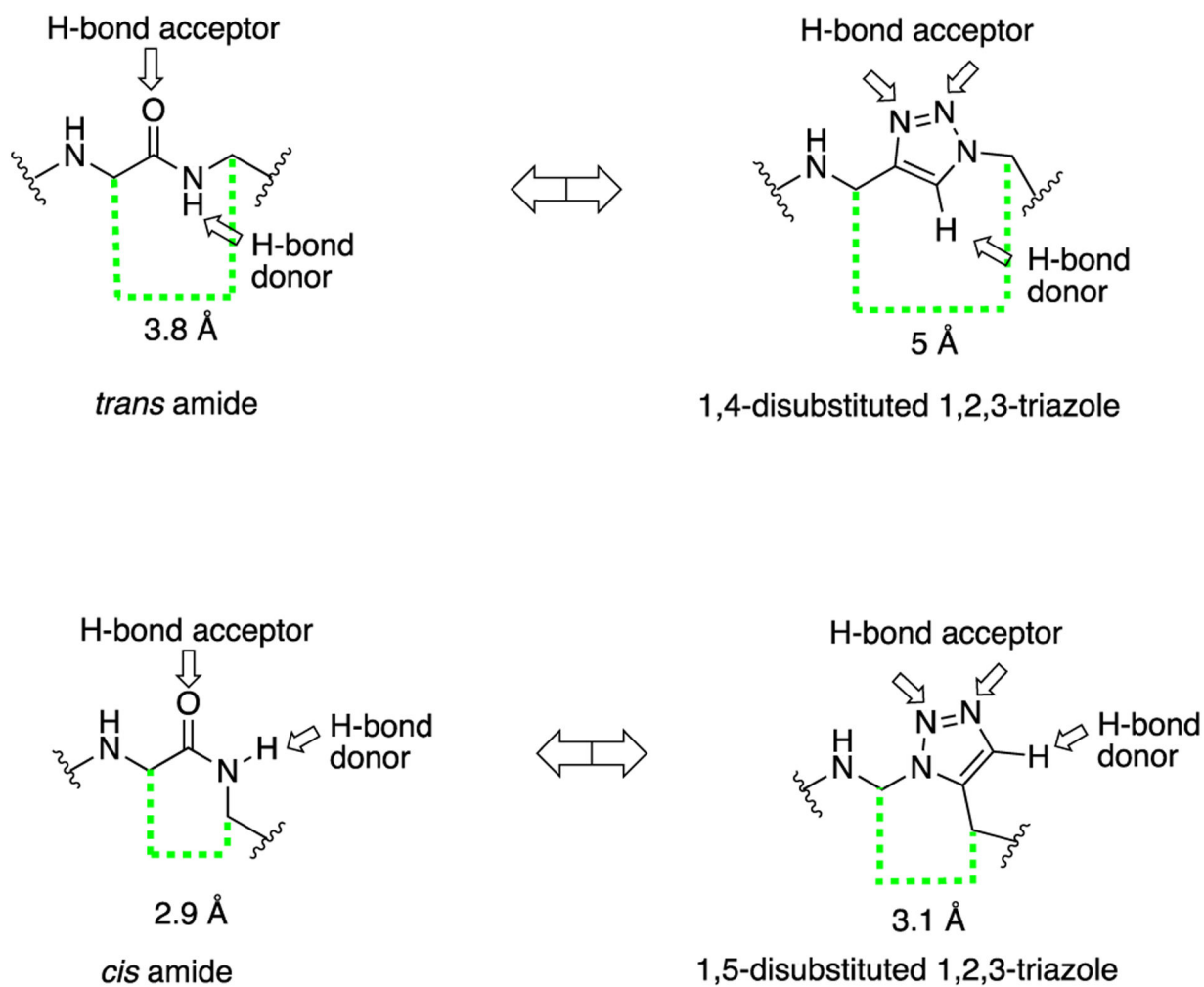


Figure 2. Representative structures of the *trans* and *cis* amide mimics 1,4-disubstituted 1,2,3-triazole and 1,5-disubstituted 1,2,3-triazole respectively, highlighting their distancing and hydrogen bonding capabilities.

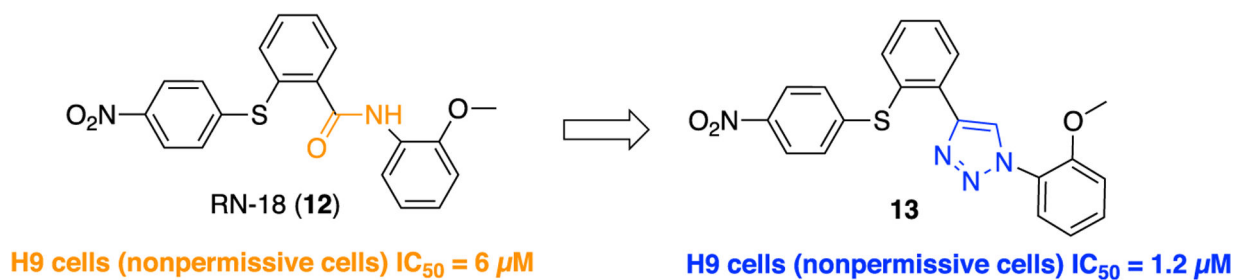
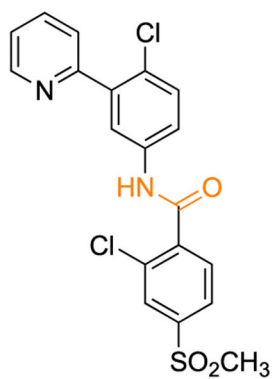


Figure 3. Replacement of the amide bond in RN-18 (**12**) with a 1,2,3-triazole moiety to afford compound **13** (1-(2-methoxyphenyl)-4-(2-((4-nitrophenyl)thio)phenyl)-1*H*-1,2,3-triazole).



Vismodegib (17)

Cell line = IC_{50} (μM) \pm SD

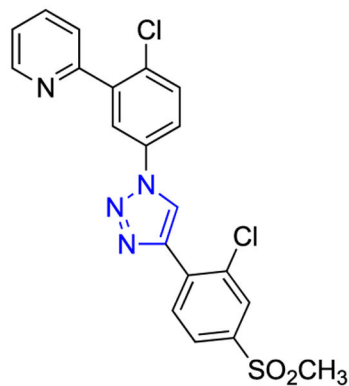
L1210 = 49 ± 9

CEM = 58 ± 6

HeLa = 64 ± 4

BAEC = 50 ± 4

HMEC-1 = 41 ± 3



18

Cell line = IC_{50} (μM) \pm SD

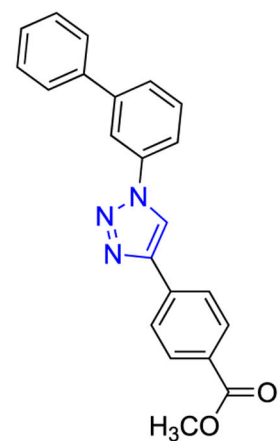
L1210 = 82 ± 72

CEM = 50 ± 12

HeLa = >100

BAEC = 40 ± 10

HMEC-1 = 9.6 ± 0.7



19

Cell line = IC_{50} (μM) \pm SD

L1210 = 1.1 ± 0.0

CEM = 0.92 ± 0.01

HeLa = 1.1 ± 0.3

BAEC = 0.42 ± 0.04

HMEC-1 = 0.62 ± 0.11

Figure 4.

Example of amide versus 1,2,3-triazole bioisosterism in vismodegib (17), a potent Hh signaling pathway inhibitor.

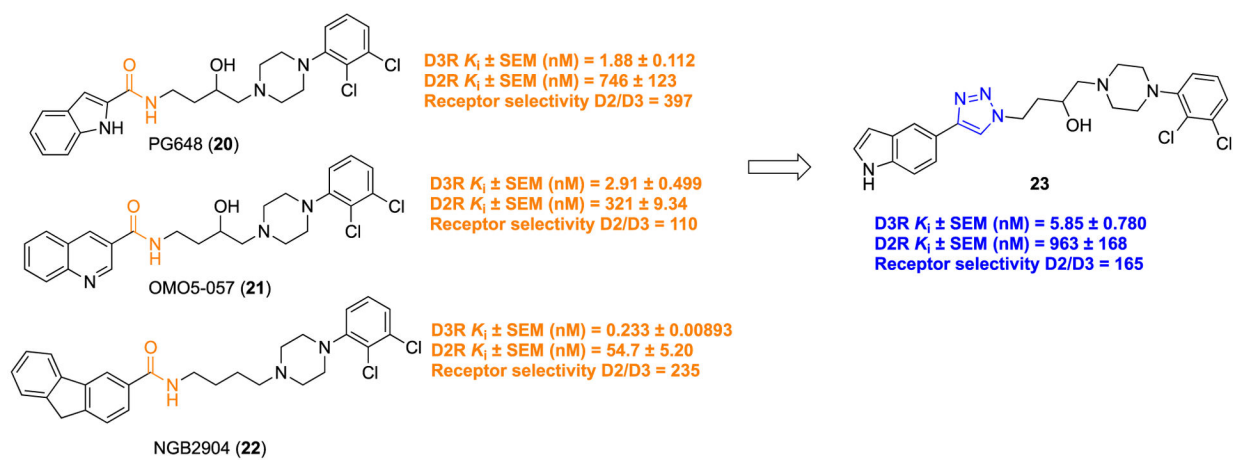


Figure 5. Molecular structures of highly potent D3-R ligands: **20**, **21**, **22** containing amide; **23**, a 1,2,3-triazole analog.

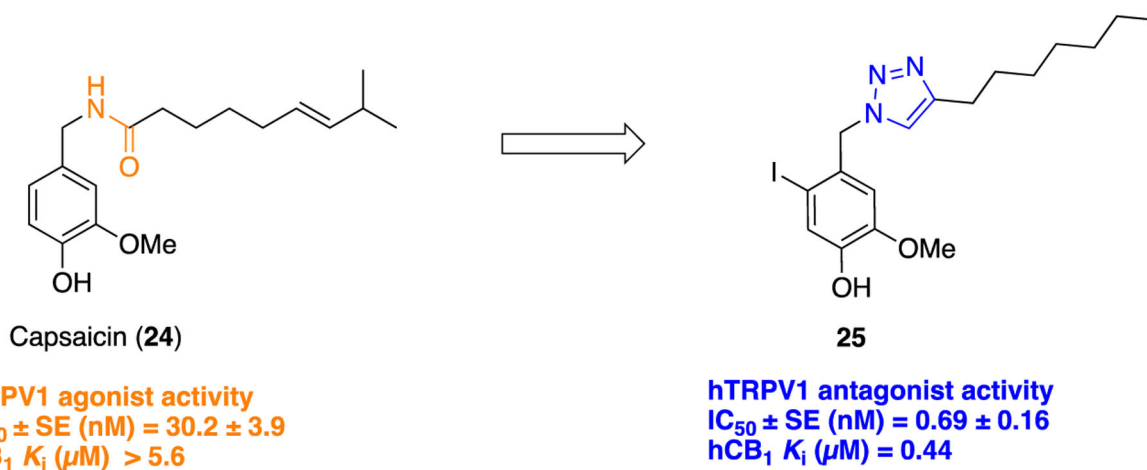


Figure 6.
1,2,3-Triazole as an amide bond bioisostere in a TRPV1/CB₁ antagonist.

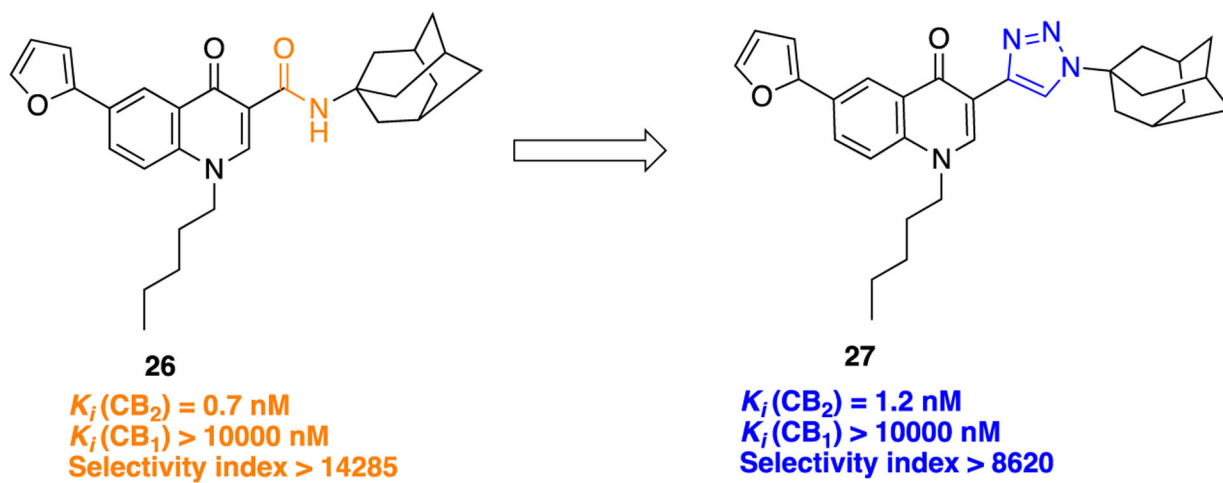


Figure 7.
Molecular structure of lead compound **26** and its bioisostere **27**.

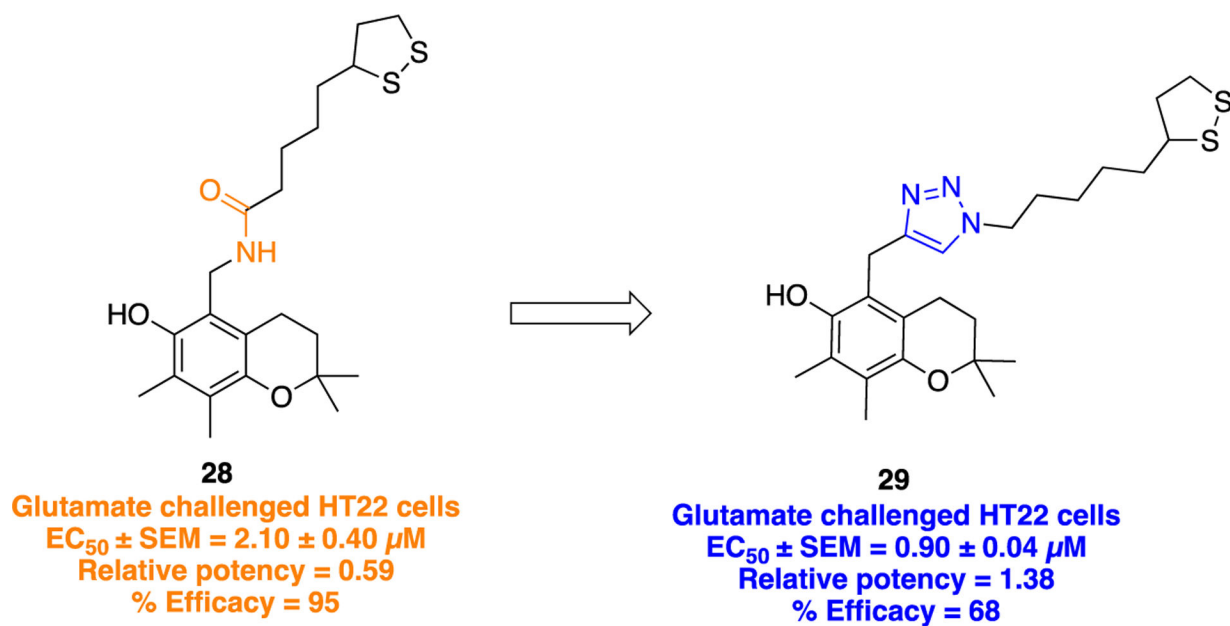
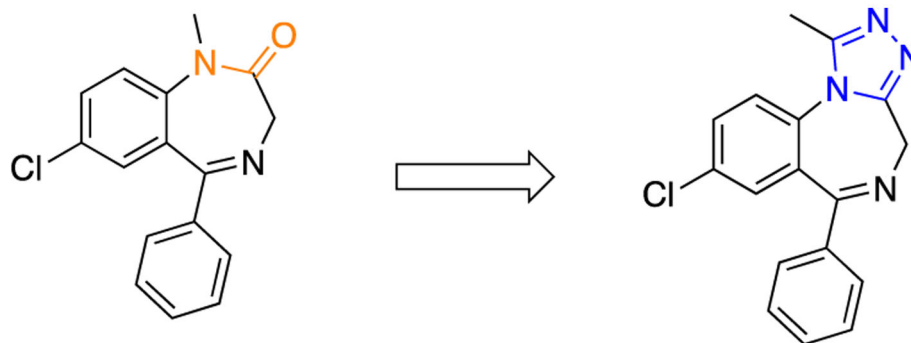


Figure 8.
Structural transformation of parent compound **28** into **29** illustrating amide/triazole bioisosterism.



Diazepam (**30**)

Human, $t_{1/2}$ = 40 - 120 h
Active metabolite (human) = Yes
Elimination (human) = Urine
(predominantly as glucuronide
conjugates)

Alprazolam (**31**)

Human, $t_{1/2}$ = 6.3 - 26.9 h
Active metabolite (human) = No
Elimination (human) = Urine (as
unchanged drug and metabolites)

Figure 9.
Replacement of an amide moiety with a 1,2,4-triazole: diazepam (**30**) to alprazolam (**31**).

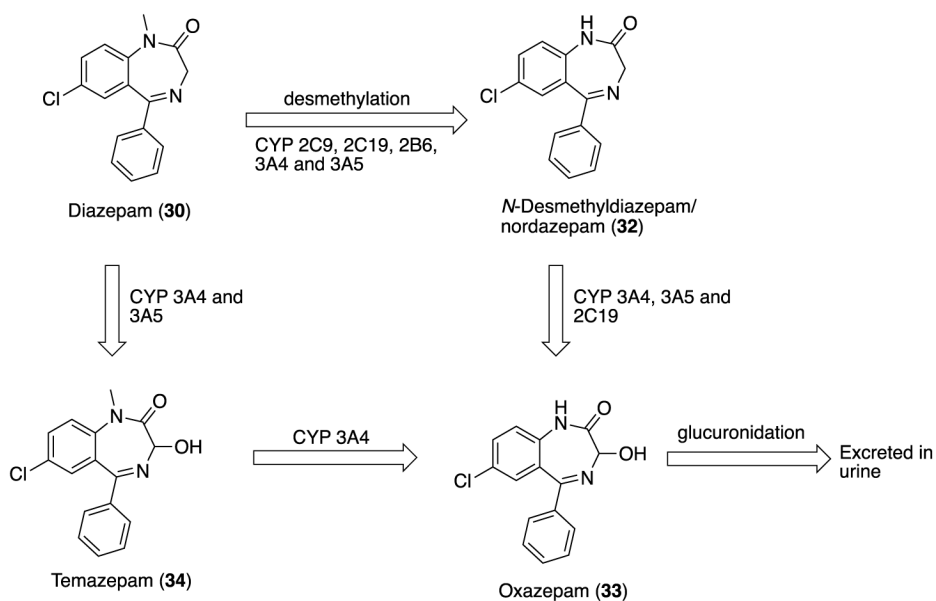
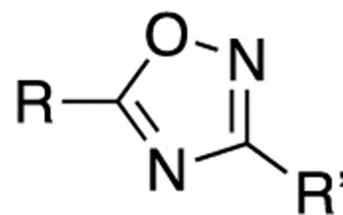
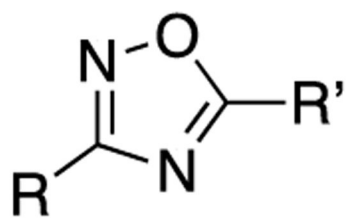
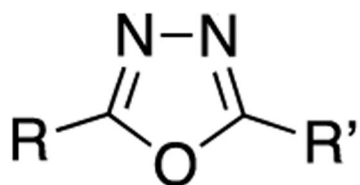


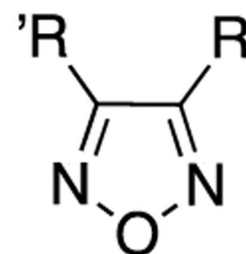
Figure 10. Metabolic transformation of diazepam (30) into three active metabolites: desmethyldiazepam/nordazepam (32), oxazepam (33), and temazepam (34).



1,2,4-isomers (if asymmetrically substituted)

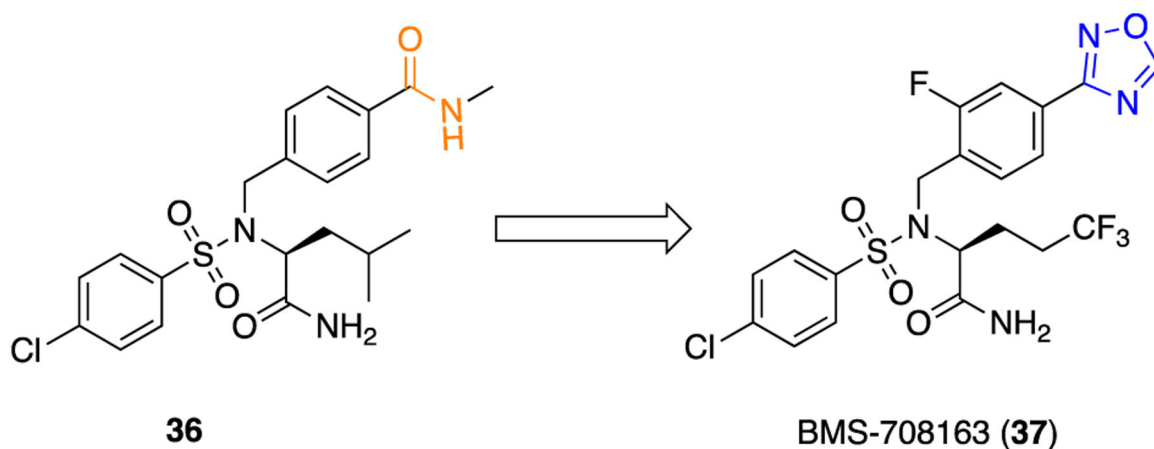


1,3,4-isomer



1,2,5-isomer

Figure 11.
Different regioisomeric forms of the oxadiazole ring.



$A\beta$ ($IC_{50} \pm SD$, nM) = 0.14 ± 0.05
Notch ($IC_{50} \pm SD$, nM) = 26 ± 9.1
Notch/APP ratio = 190

$A\beta$ ($IC_{50} \pm SD$, nM) = 0.30 ± 0.15
Notch ($IC_{50} \pm SD$, nM) = 58 ± 23
Notch/APP ratio = 193

Figure 12.
Amide bioisosteric replacement with an oxadiazole ring leading to a potent and selective γ -secretase inhibitor.

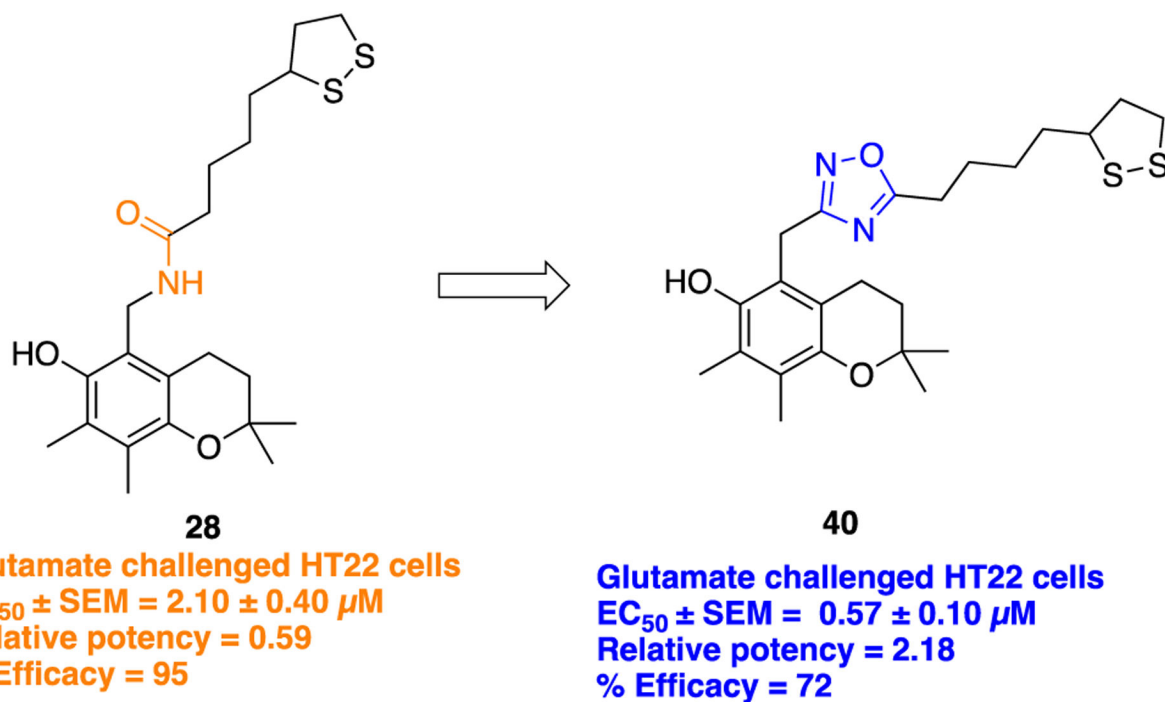


Figure 13.
Structures of parent amide-containing α -lipoic acid analog **28** and its 1,2,4-oxadiazole bioisostere **40**.

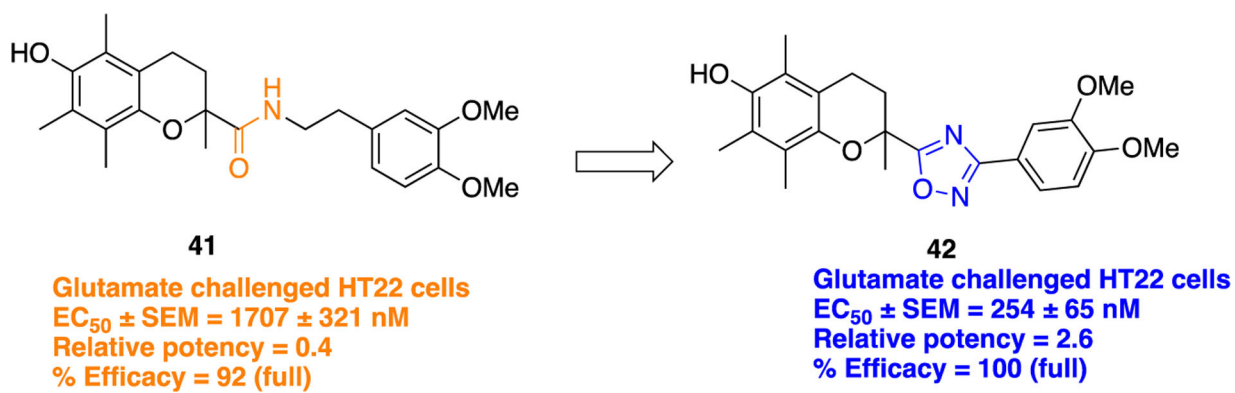


Figure 14.
Structures of parent chroman analog **41** and its 1,2,4-oxadiazole bioisostere **42**.

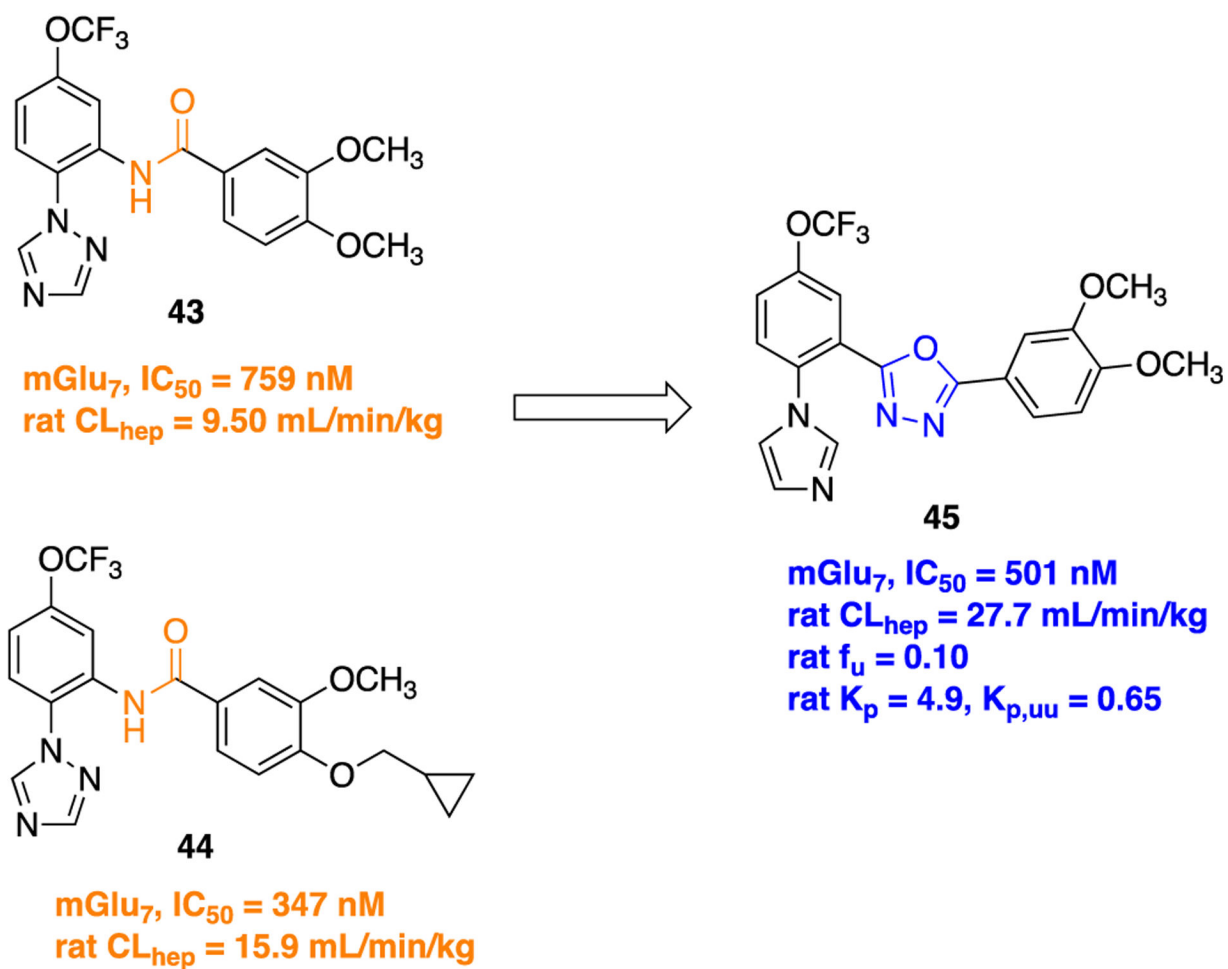
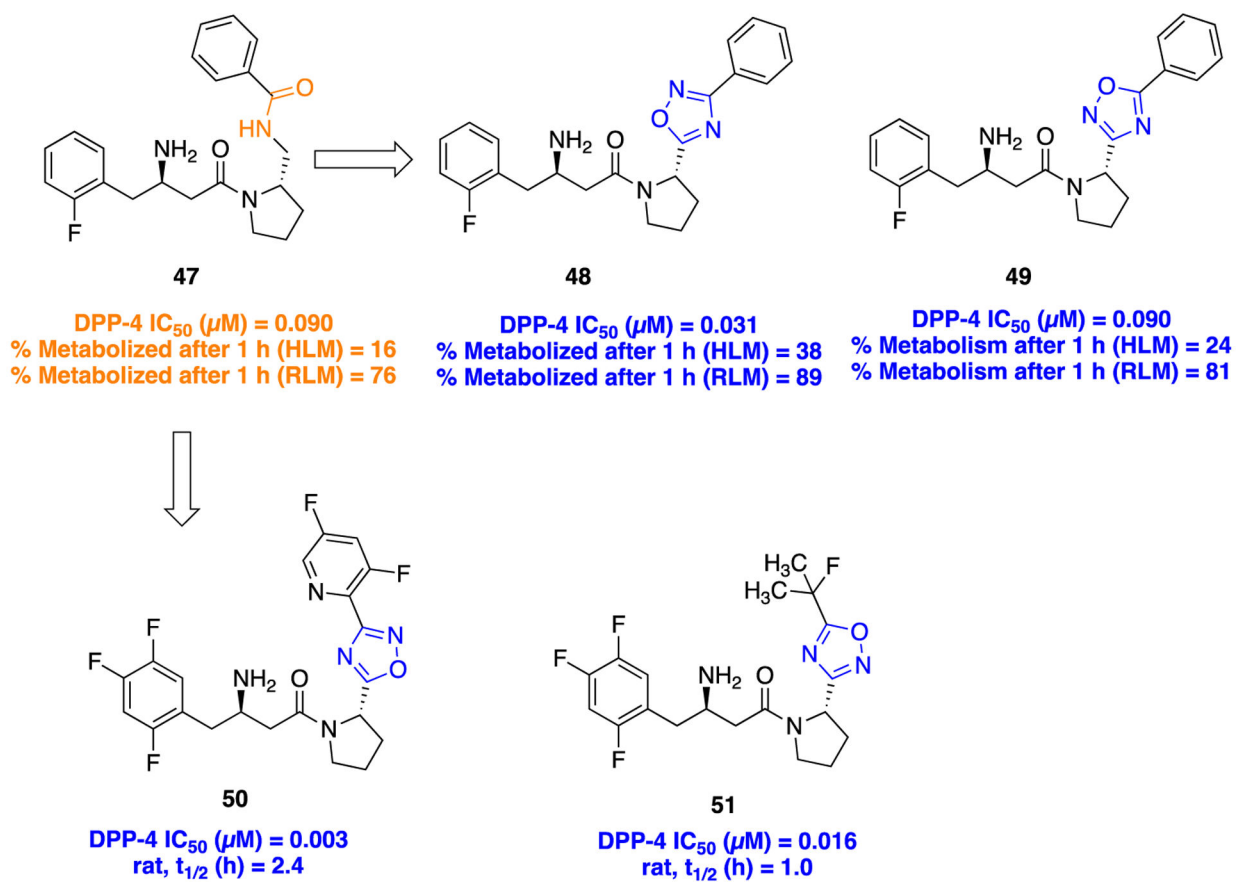


Figure 15.
Structures of parent amides **43** and **44**, potent mGlu₇-NAMs and the 1,3,4-oxadiazole bioisostere **45**.

**Figure 16.**

Structural optimization in the development of potent DPP-4 inhibitors to treat type 2 diabetes mellitus.

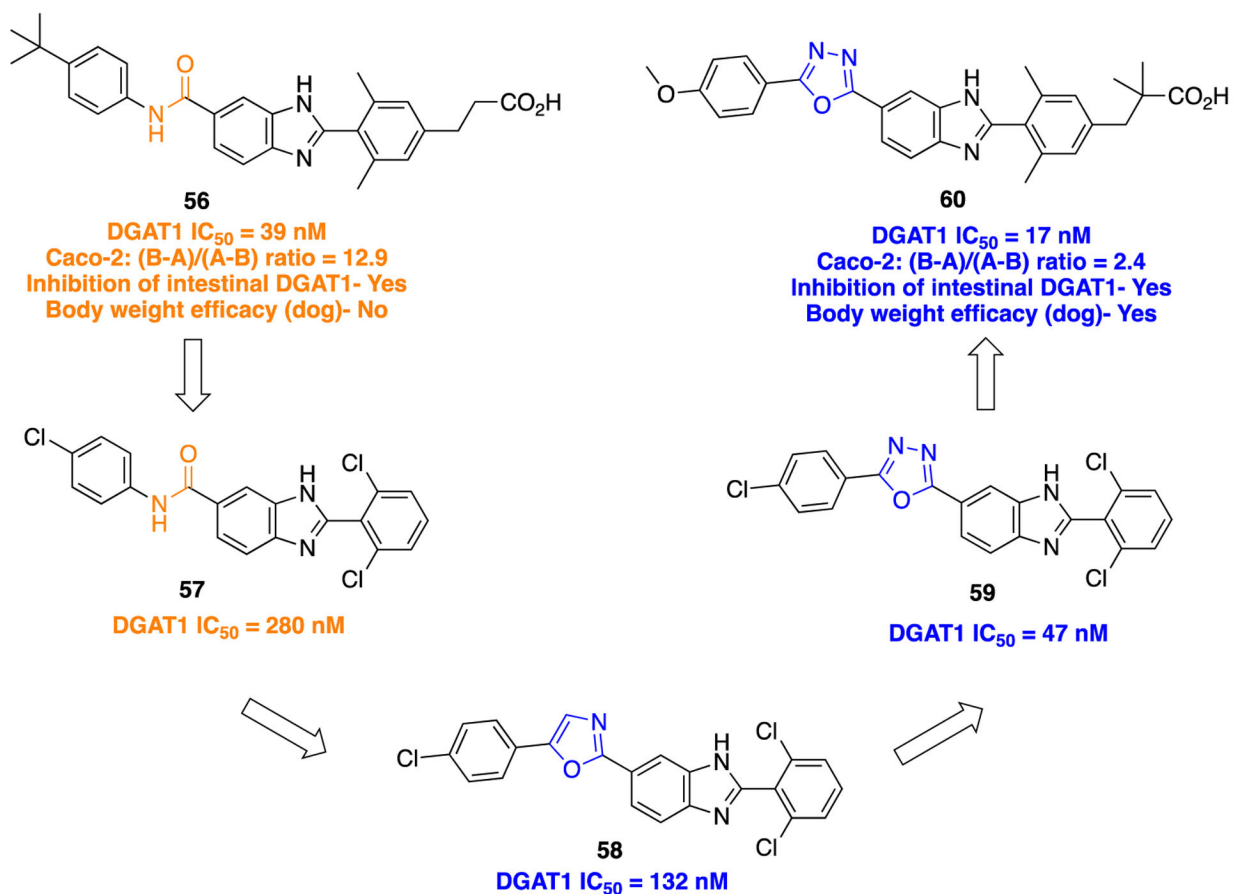


Figure 17.
Lead optimization journey to discover a potent and orally bioavailable DGAT-1 inhibitor.

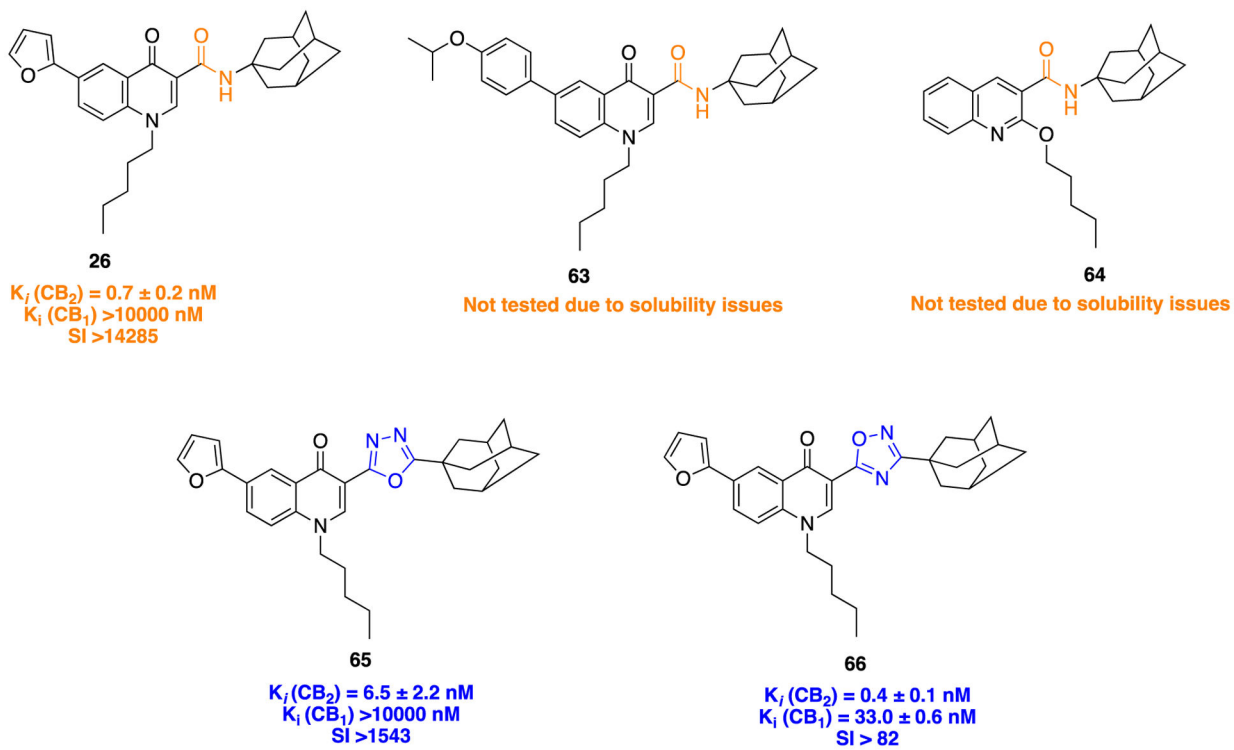


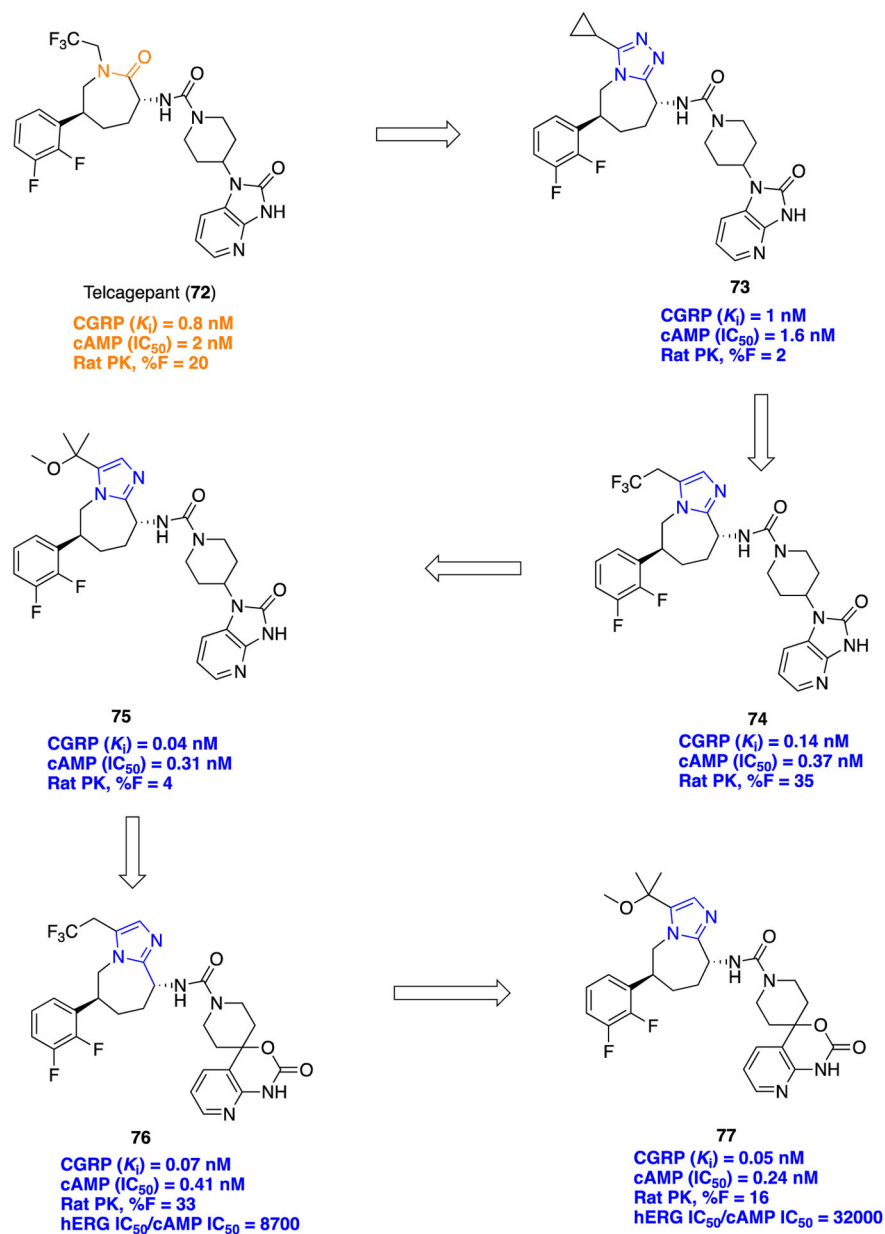
Figure 18.
Bioisosteric amide replacement via 1,3,4-oxadiazole (**65**) and 1,2,4-oxadiazole (**66**) in a series of CB₂ receptor ligands.



Long-acting benzodiazepine

Short-acting benzodiazepine

Figure 19.
Structures of diazepam and the imidazole-containing analog midazolam.

**Figure 20.**

Lead optimization journey of telcagepant (**72**) to discover **77**, a potent and orally bioavailable CGRP antagonist.

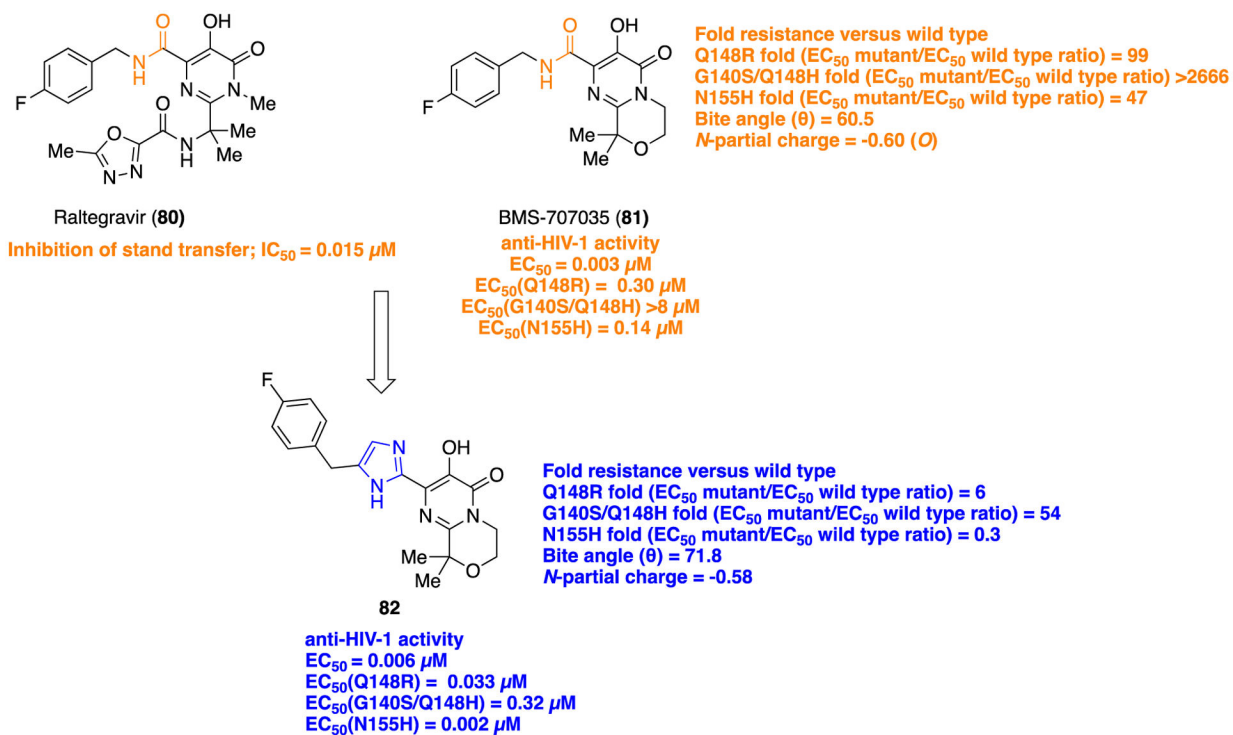


Figure 21.
Structures of **80**, **81**, and imidazole bioisostere **82**, potent HIV-1 integrase inhibitors.

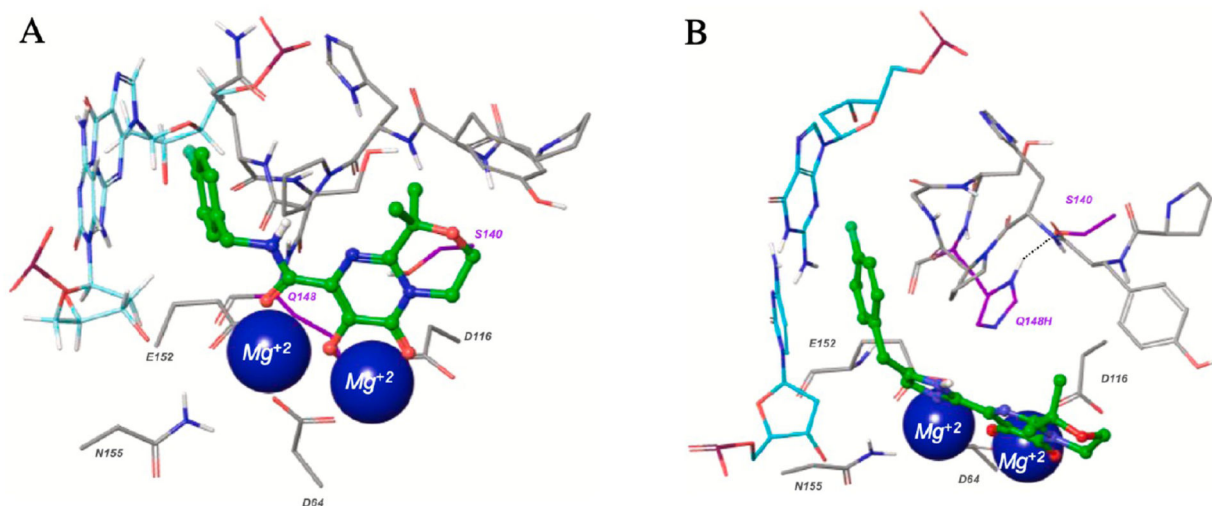


Figure 22.

Binding patterns of **81** and **82** into the active sites of PFV integrase (3S3N) wild-type (A) and Q148H/G140S mutant (B). Reproduced with permission from *Bioorganic & Medicinal Chemistry Letters* (<https://www.sciencedirect.com/journal/bioorganic-and-medicinal-chemistry-letters>), Volume 30, 126784, Peese, K. M.; Naidu, B. N.; Patel, M.; Li, C.; Langley, D. R.; Terry, B.; Protack, T.; Gali, V.; Lin, Z.; Samanta, H. K.; Zheng, M.; Jenkins, S.; Dicker, I. B.; Krystal, M. R.; Meanwell, N. A.; Walker, M. A., Heterocycle amide isosteres: an approach to overcoming resistance for HIV-1 integrase strand transfer inhibitors.¹³⁰ Copyright 2020 Elsevier.

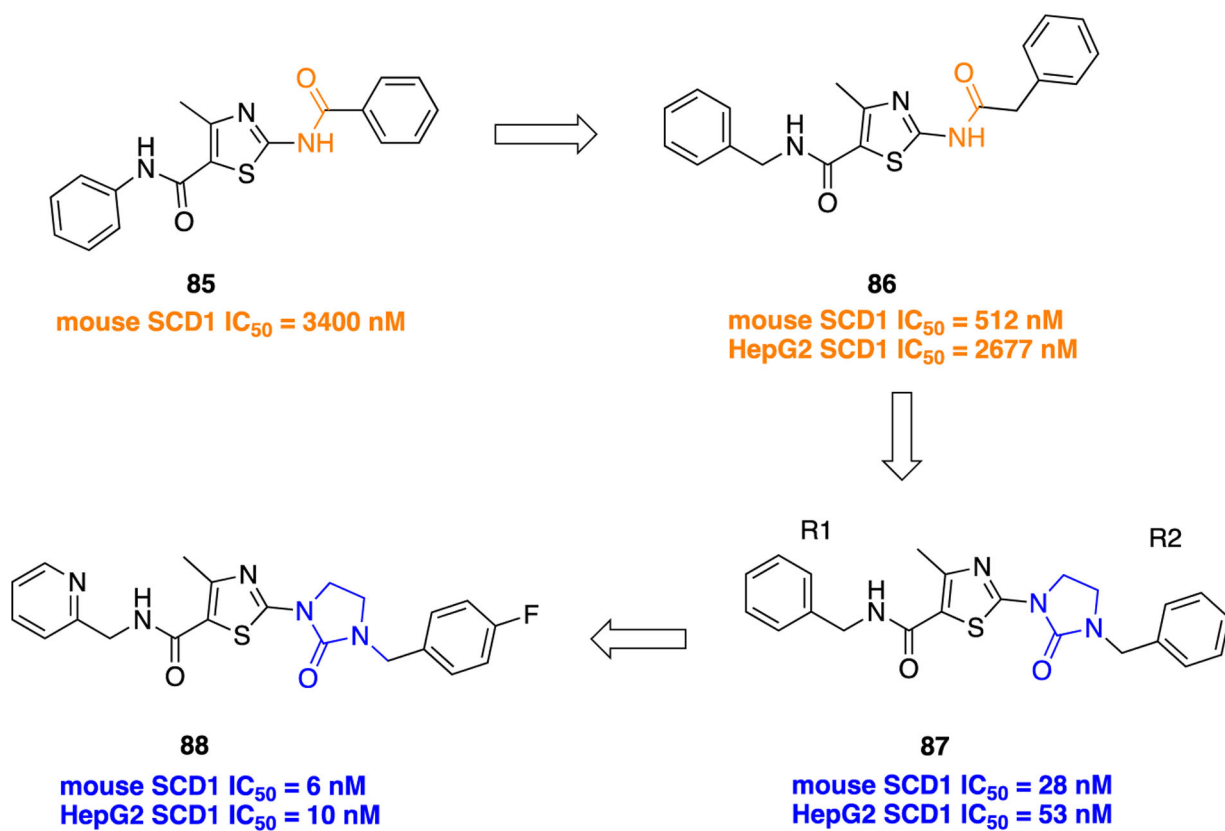


Figure 23.
Bioisosteric replacement of the amide functional group in the identification of potent SCD1 inhibitors.

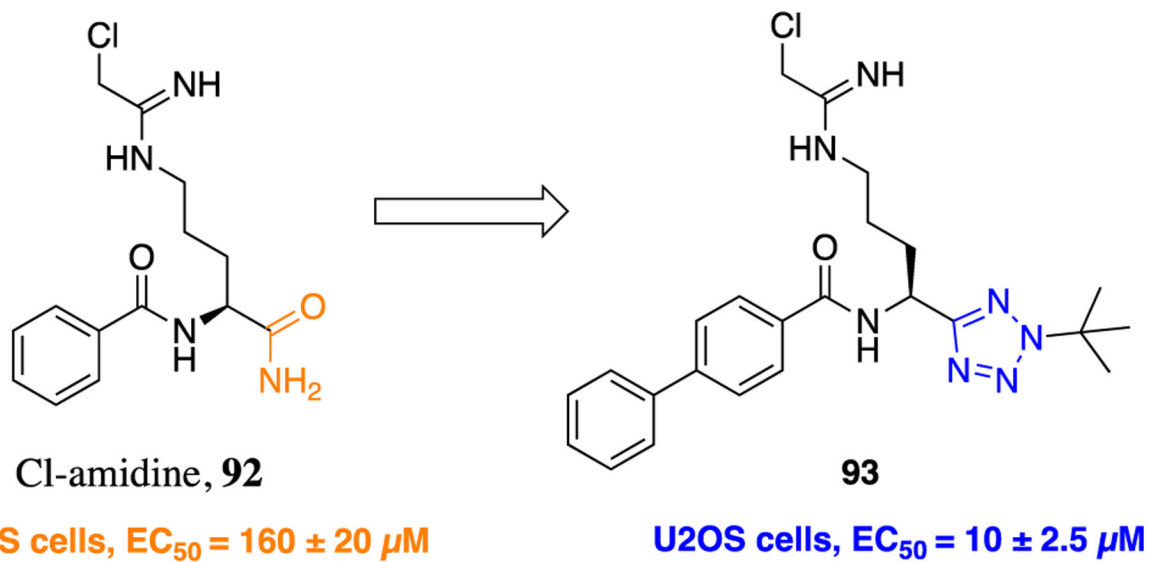


Figure 24.
Structure of **92** and its bioisostere **93**, potent PAD inhibitors.

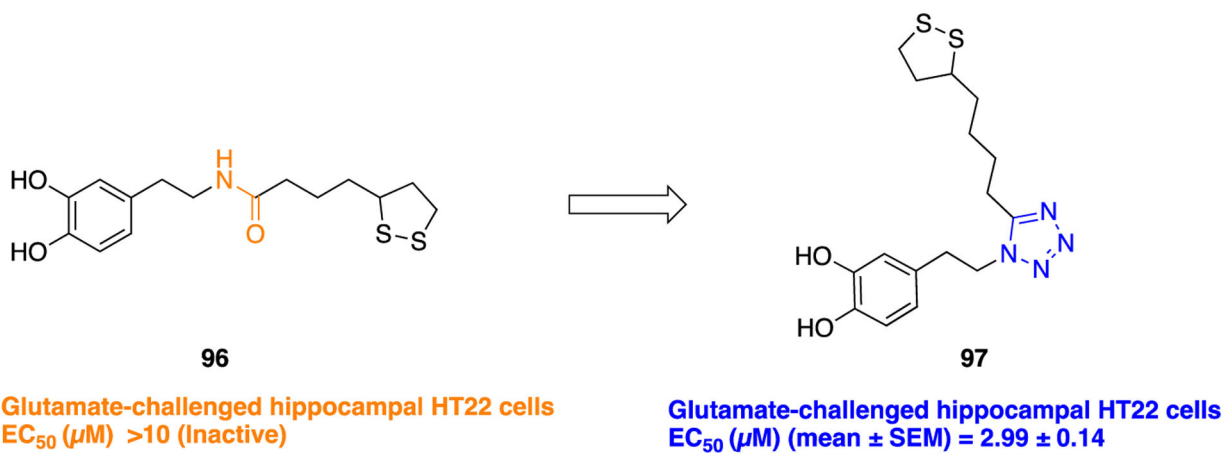


Figure 25.
Structures of LA amide-dopamine conjugate **96** and its tetrazole containing bioisostere **97**.

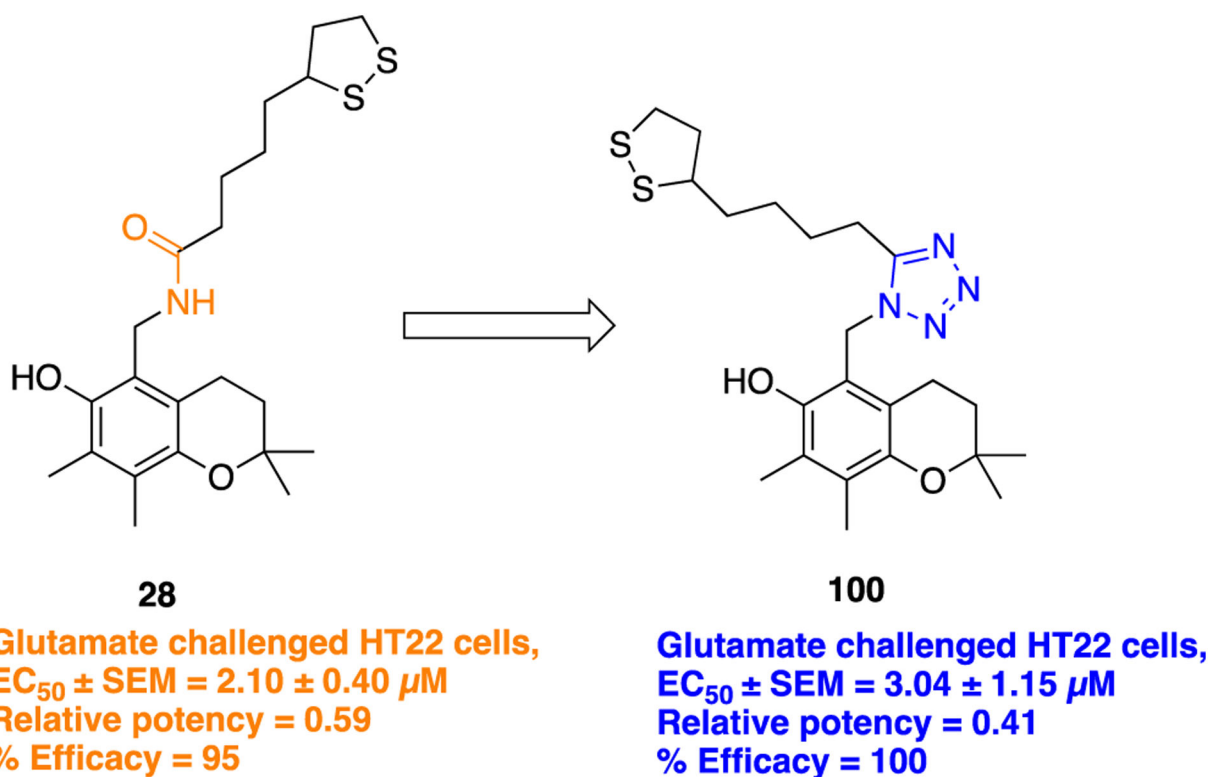


Figure 26.
Molecular structures of parent LA-amide analog **28** and its tetrazole bioisostere **100**.

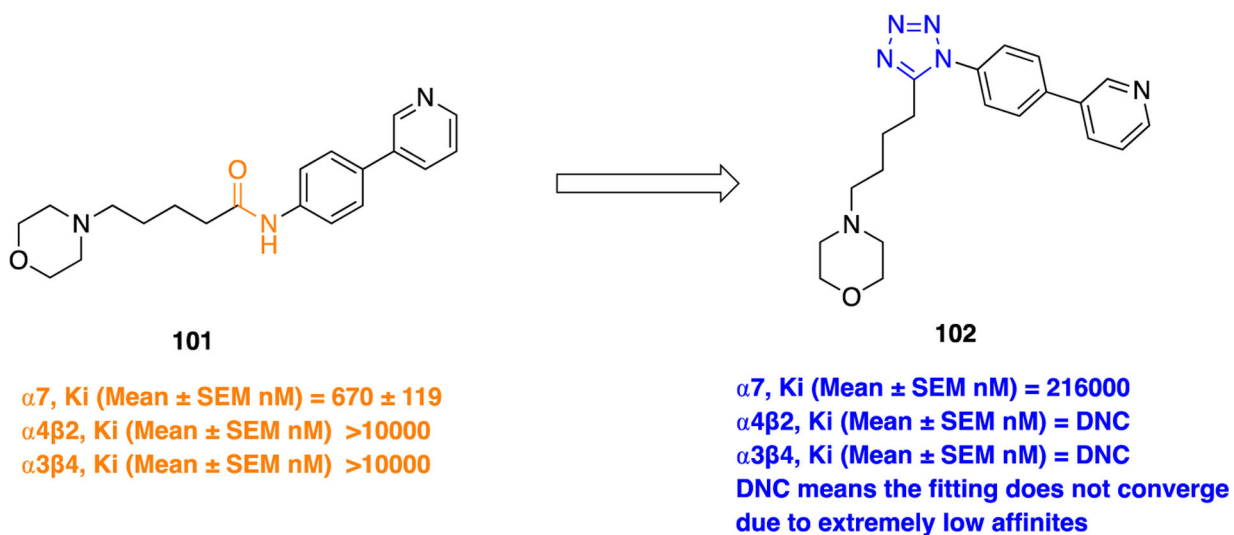


Figure 27.
Amide bond bioisosteric modification in **101** with a tetrazole functionality (**102**).

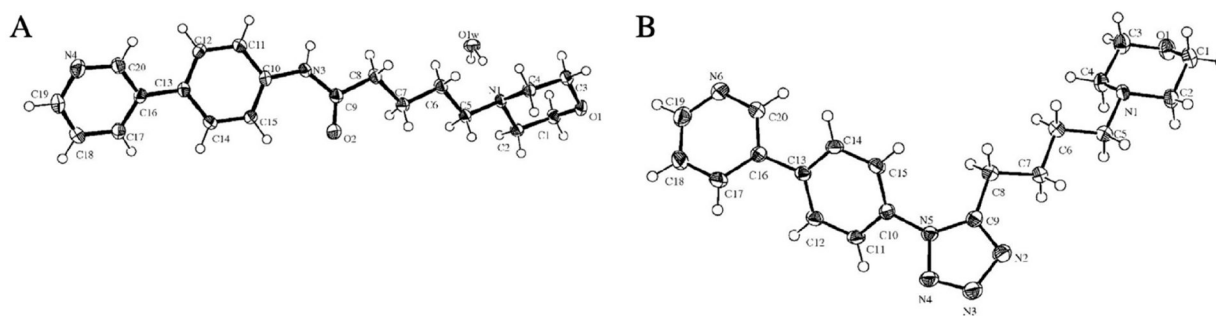
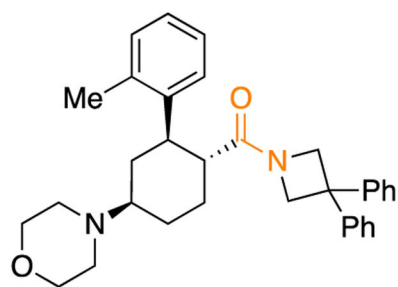
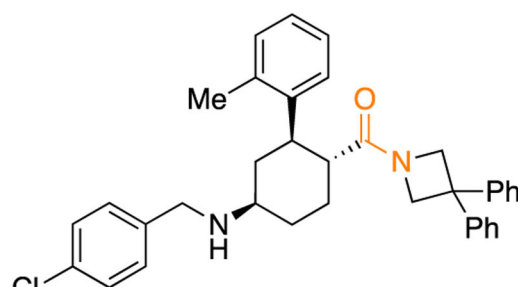


Figure 28.

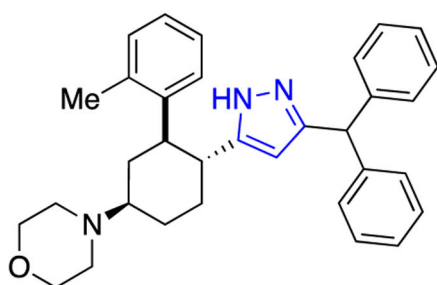
Oak Ridge thermal ellipsoid plots of **101** (A) and **102** (B). Reproduced with permission from *European Journal of Medicinal Chemistry* (<https://www.sciencedirect.com/journal/european-journal-of-medicinal-chemistry>), Volume 84, pp 200–205, Beinat, C.; Reekie, T.; Hibbs, D.; Xie, T.; Olson, T. T.; Xiao, Y.; Harvey, A.; O'Connor, S.; Coles, C.; Tsanaktsidis, J.; Kassiou, M., Investigations of amide bond variation and biaryl modification in analogues of $\alpha 7$ nAChR agonist SEN12333.¹⁴⁹ Copyright 2014 Elsevier.

**103**

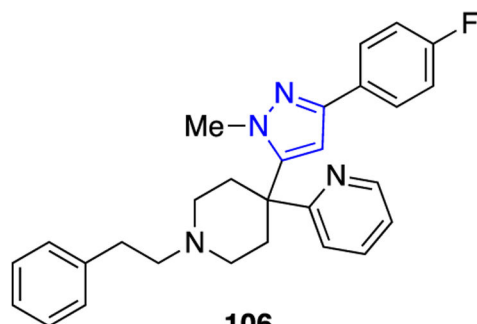
PrCP IC₅₀ (human) nM = 3.5
 PrCP IC₅₀ (mouse) nM = 5
 Plasma protein binding (human) = 2
 Plasma protein binding (mouse) = 4
 Cl (mL/min/kg) = 72.2 ± 5.5
 t_{1/2} (h) = 1.72 ± 0.2
 % F = 7.8

**104**

PrCP IC₅₀ (human) nM = 2.5
 PrCP IC₅₀ (mouse) nM = 1.4
 Plasma protein binding (human) < 1
 Plasma protein binding (mouse) < 1
 Cl (mL/min/kg) = 31.8 ± 8.0
 t_{1/2} (h) = 4.4 ± 2.0
 % F = 28

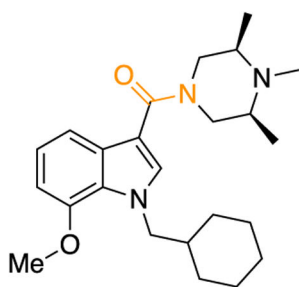
**105**

PrCP IC₅₀ (human) nM = 860
 PrCP IC₅₀ (mouse) nM = not tested

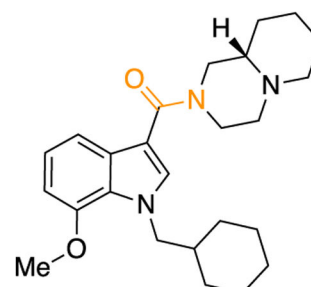
**106**

PrCP IC₅₀ (human) nM = 3.3
 PrCP IC₅₀ (mouse) nM = 0.7
 Plasma protein binding (human) = 1
 Plasma protein binding (mouse) = 4
 Cl (mL/min/kg) = 74.4 ± 16.3
 t_{1/2} (h) = 2.0 ± 0.3
 % F = 14

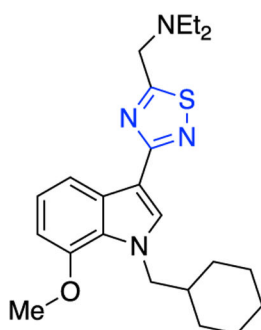
Figure 29.
 Bioisosteric replacement of amide (**103** and **104**) with pyrazole (**105** and **106**) to discover potent PrCP inhibitors.

**107**

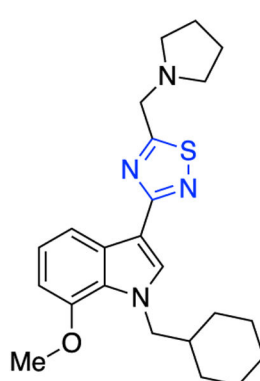
CB1, pEC₅₀ = 7.6
MLM stability > 270
HLM stability > 270

**108**

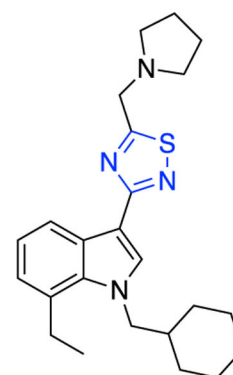
CB1, pEC₅₀ = 7.9
MLM stability > 270
HLM stability > 270

**109**

CB1, pEC₅₀ = 7.7
MLM stability = 71
HLM stability = 89

**110**

CB1, pEC₅₀ = 8.7
MLM stability = 41
HLM stability = 64

**111**

CB1, pEC₅₀ = 8.5
MLM stability = 34
HLM stability = 74

Figure 30.
Amide versus thiazazole bioisosterism in search of potent CB₁ agonist.

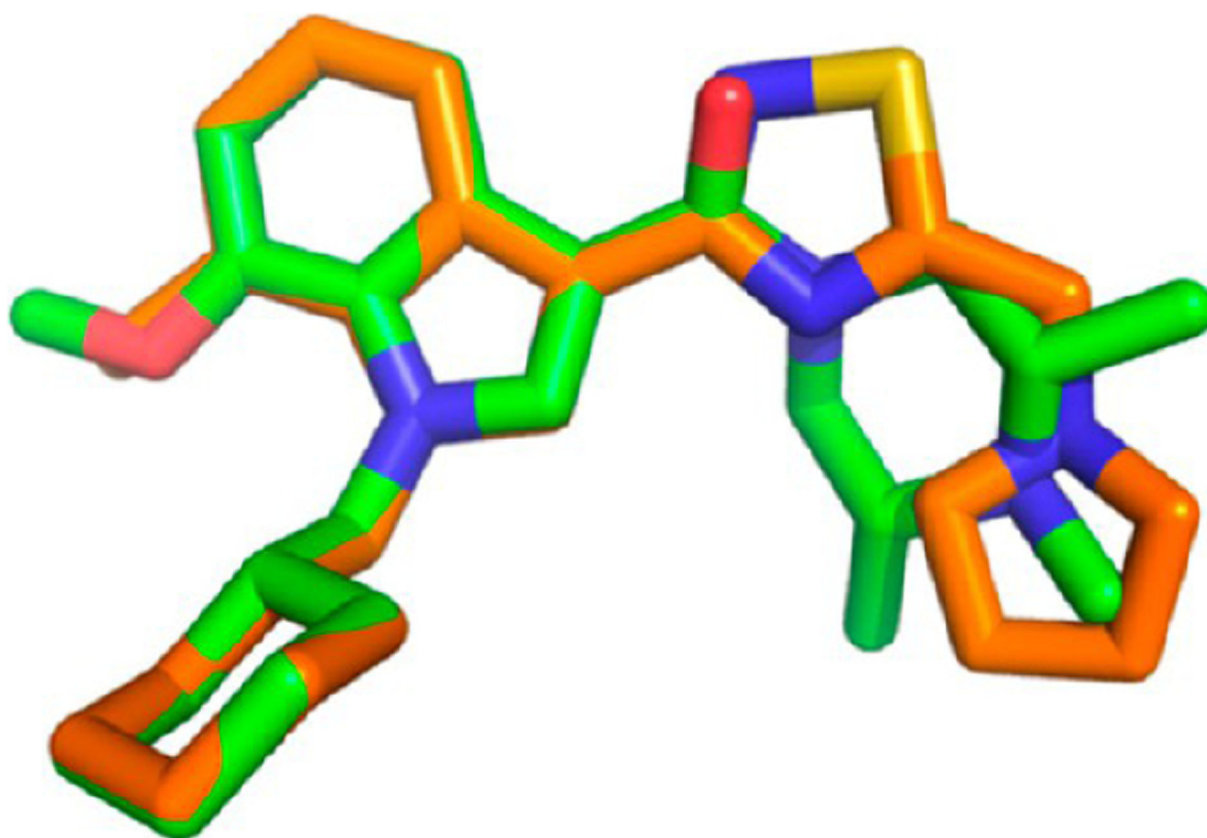
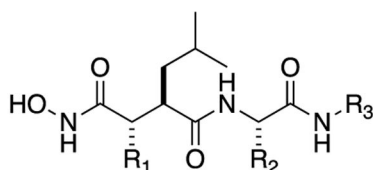
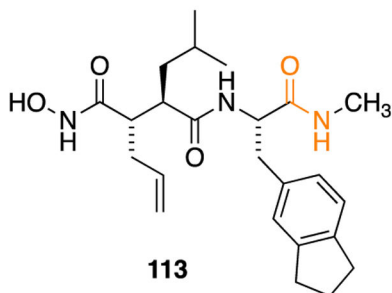


Figure 31.

Superimposition modeling image of **107** (green) and **111** (orange). Reproduced with permission from *Bioorganic & Medicinal Chemistry Letters* (<https://www.sciencedirect.com/journalbioorganic-and-medicinal-chemistry-letters/>), Volume 21, pp 506–509, Morrison, A. J.; Adam, J. M.; Baker, J. A.; Campbell, R. A.; Clark, J. K.; Cottney, J. E.; Deehan, M.; Easson, A. M.; Fields, R.; Francis, S.; Jeremiah, F.; Keddie, N.; Kiyoi, T.; McArthur, D. R.; Meyer, K.; Ratcliffe, P. D.; Schulz, J.; Wishart, G.; Yoshiizumi, K., Design, synthesis, and structure-activity relationships of indole-3-heterocycles as agonists of the CB1 receptor.¹⁶¹ Copyright 2011 Elsevier.

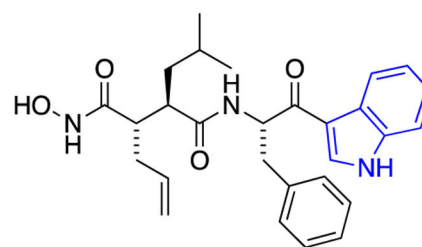


General structure (112)



113

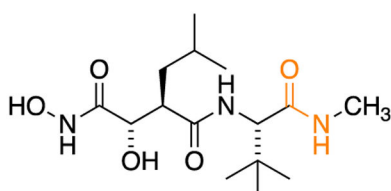
MMP-1, $IC_{50} = 2.2$ nM
 MMP-2, $IC_{50} = 1.8$ nM
 MMP-3, $IC_{50} = 12$ nM
 MMP-7, $IC_{50} = 11$ nM
 rat PK, 30 mg/kg/po
 $t_{1/2} = 0.35$ h
 $\%F = 0$



114

MMP-1, $IC_{50} = 1.1$ nM
 MMP-2, $IC_{50} = 1.1$ nM
 MMP-3, $IC_{50} = 2.3$ nM
 MMP-7, $IC_{50} = 2.2$ nM
 rat PK, 30 mg/kg/po
 $t_{1/2} = 1.45$ h
 $\%F = 7$

monkey PK, 10 mg/kg/po
 $t_{1/2} = 20$ h
 $\%F = 12$



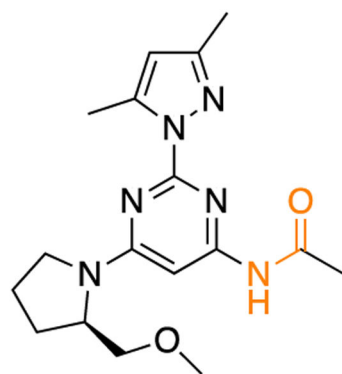
115

MMP-1, $IC_{50} = 1.1$ nM
 MMP-2, $IC_{50} = 0.85$ nM
 MMP-3, $IC_{50} = 10$ nM
 MMP-7, $IC_{50} = 11$ nM

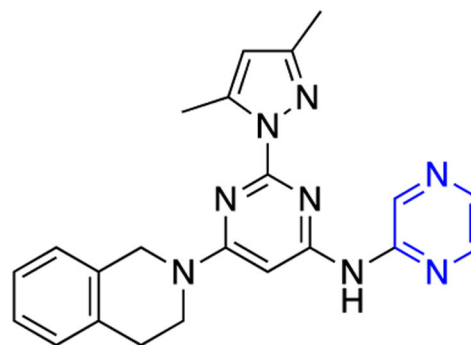
monkey PK, 10 mg/kg/po
 $t_{1/2} = 27$ h
 $\%F = 15$

Figure 32.

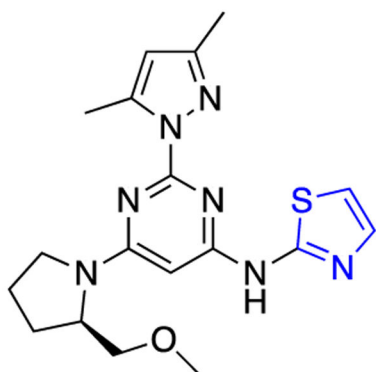
General structure (112) showing the molecular template for designing MMP inhibitors, isosteric replacement of the C-terminal amide bond in 113 with 3-acyl indole (114), and the structure of marimastat, (115), a broad-spectrum MMP inhibitor.

**119**

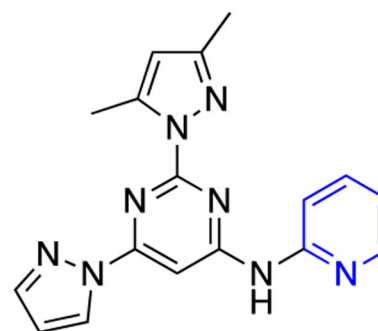
Inhibition % at 100 $\mu\text{mol/L}$ = 123
 $\text{hA}_{2\text{A}}$ K_i (nM) \pm SEM = 15 \pm 10

**120**

Inhibition % at 100 $\mu\text{mol/L}$ = 121
 $\text{hA}_{2\text{A}}$ K_i (nM) \pm SEM = 1.1 \pm 0.6

**121**

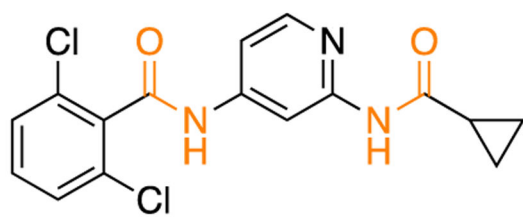
Inhibition % at 100 $\mu\text{mol/L}$ = 123
 $\text{hA}_{2\text{A}}$ K_i (nM) \pm SEM = 9.5 \pm 2.8

**122**

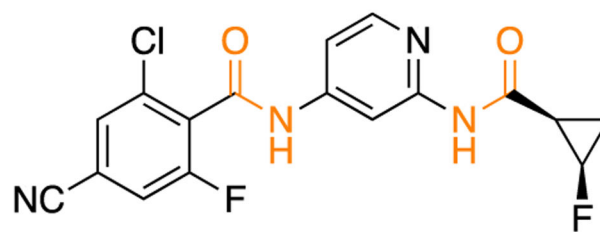
Inhibition % at 100 $\mu\text{mol/L}$ = 117
 $\text{hA}_{2\text{A}}$ K_i (nM) \pm SEM = 9.2 \pm 1.3

Figure 33.

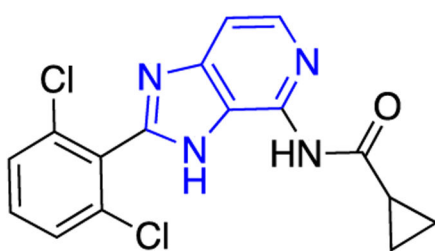
Molecular structures of the parent amide **119** and pyrazine (**120**), thiazole (**121**), and pyridine (**122**) bioisosteres.

**125**

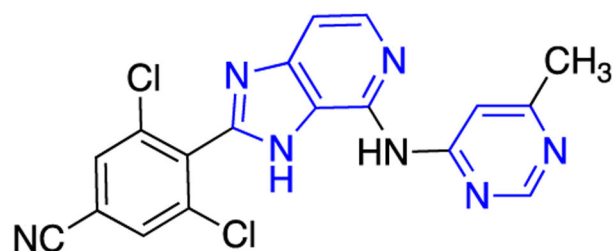
TYK2 K_i = 4.8 nM
JAK2 K_i = 28 nM

**126**

TYK2 K_i = 1.6 nM
JAK2 K_i = 62 nM

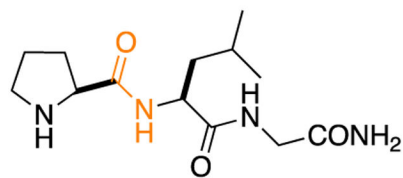
**127**

TYK2 K_i = 1.7 nM
JAK2 K_i = 150 nM

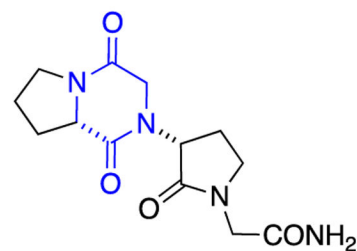
**128**

TYK2 K_i = 0.7 nM
JAK2 K_i = 22 nM

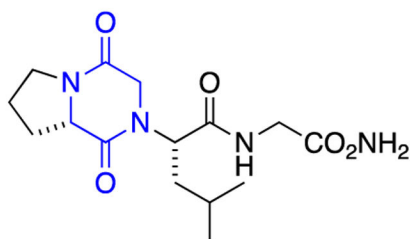
Figure 34.
Structures of lead TYR2 inhibitor **125** and its optimized analogs **126–128**.

**132**

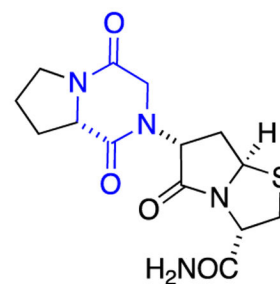
K_H (nM): K_L (nM)
 -Gpp(NH)p = 0.09 ± 0.005 : 73.2 ± 5.5
 +Gpp(NH)p = 0.13 ± 0.01 : 60.0 ± 8.6

**133**

K_H (nM): K_L (nM)
 -Gpp(NH)p = 0.08 ± 0.005 : 69 ± 3.5
 +Gpp(NH)p = 0.19 ± 0.02 : 50 ± 3

**134**

K_H (nM): K_L (nM)
 -Gpp(NH)p = 0.080 ± 0.001 : 120 ± 5
 +Gpp(NH)p = 0.120 ± 0.009 : 172 ± 7

**135**

K_H (nM): K_L (nM)
 -Gpp(NH)p = 0.098 ± 0.009 : 171 ± 18
 +Gpp(NH)p = 0.140 ± 0.064 : 183 ± 7

Figure 35.
 Bioisosteric replacement of the amide within **132**, with diketopiperazine (**133**, **134**, and **135**), to develop potent dopamine D_2 receptor modulators.

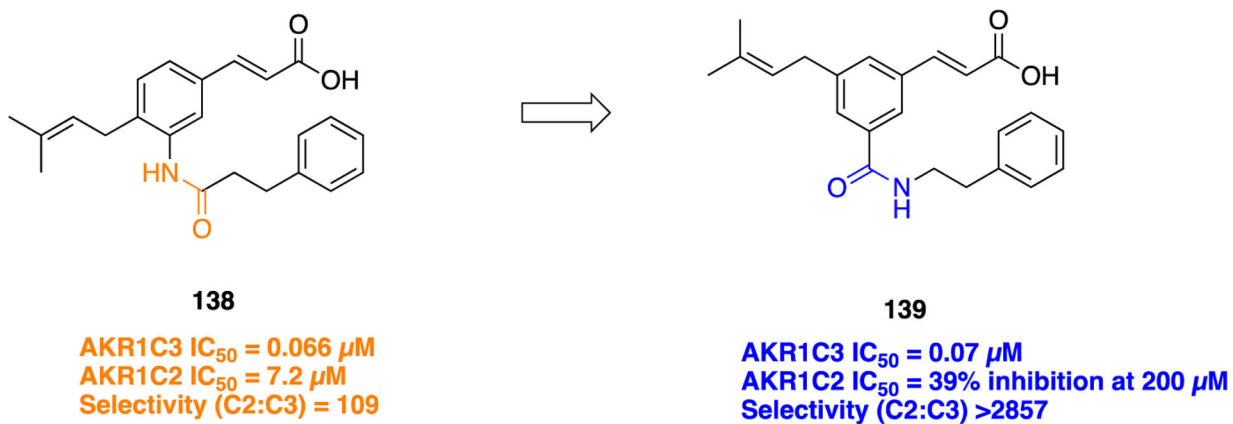


Figure 36. Structures of an amide-containing baccharin analog **138**, a potent but low selective AKR1C3 inhibitor, and **139**, a potent and highly selective retroinverted amide bioisostere.

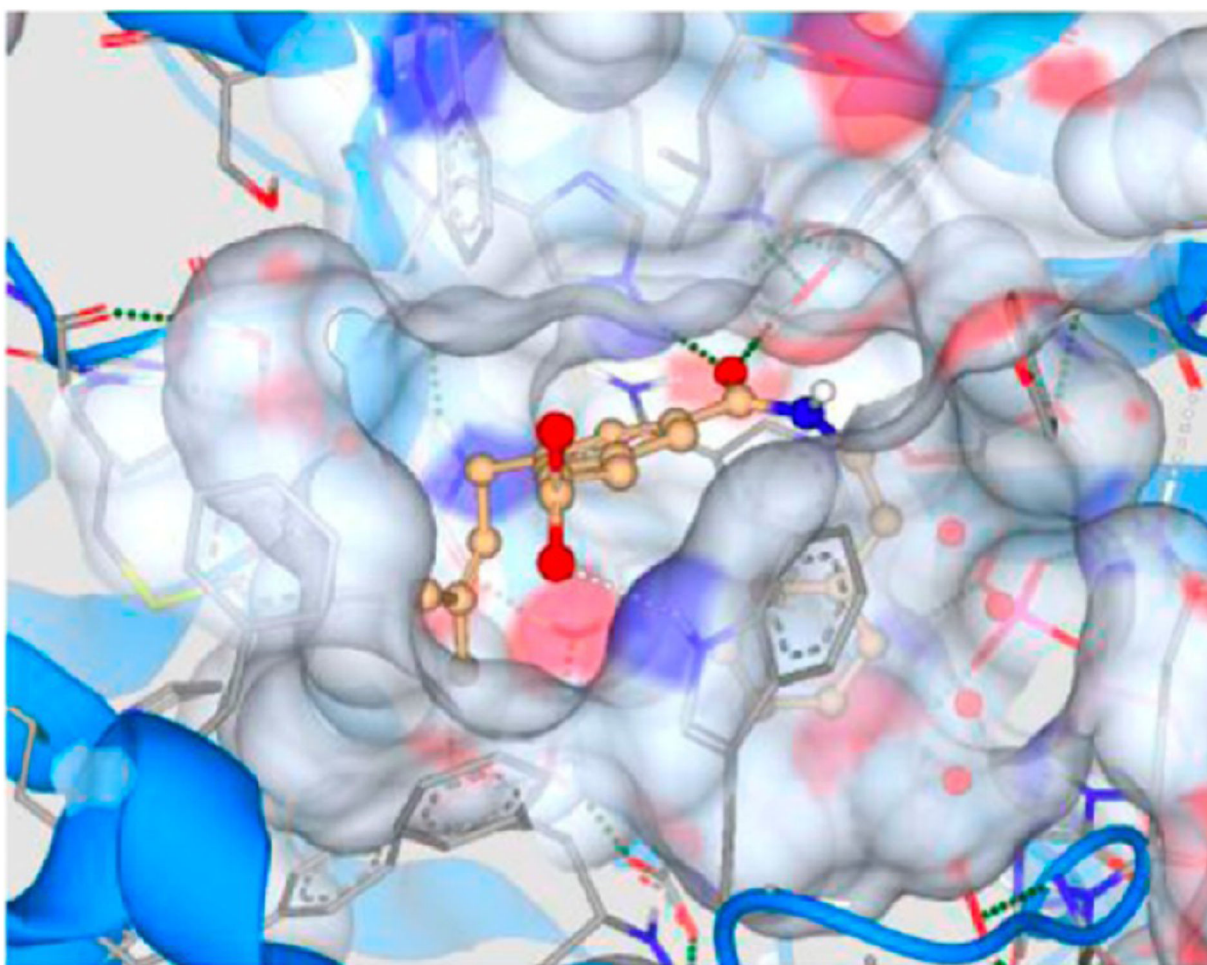
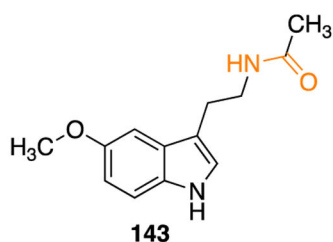


Figure 37. Compound **139** docked within the active site of AKR1C3 (gray, PDB code 3UG8): strong predicted hydrogen bond (green dotted line) and weak predicted hydrogen bond (white dotted line). Reproduced with permission from *Journal of Medicinal Chemistry*,¹⁸³ Copyright 2019 American Chemical Society.



Radioligand displacement binding studies at human MTRs

MT_1R ($K_i \pm SEM$, nM) = 0.091 ± 0.005

MT_2R ($K_i \pm SEM$, nM) = 0.15 ± 0.07

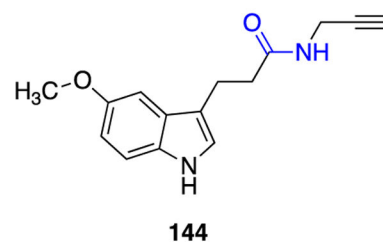
Functional studies (GTP γ S) at MTRs

MT_1R (EC_{50} , nM) = 0.098 ± 0.003

MT_1R (E_{max} , %) = 100

MT_2R (EC_{50} , nM) = 0.069 ± 0.003

MT_2R (E_{max} , %) = 100



Radioligand displacement binding studies at human MTRs

MT_1R ($K_i \pm SEM$, nM) = 5.0 ± 0.9

MT_2R ($K_i \pm SEM$, nM) = 1.0 ± 0.6

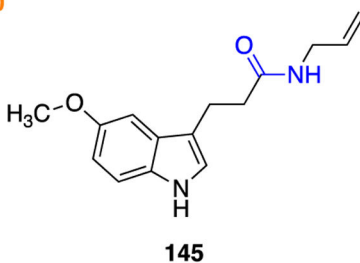
Functional studies (GTP γ S) at MTRs

MT_1R (EC_{50} , nM) = 38 ± 3

MT_1R (E_{max} , %) = 106 ± 9

MT_2R (EC_{50} , nM) = 3 ± 0.3

MT_2R (E_{max} , %) = 99 ± 9



Radioligand displacement binding studies at human MTRs

MT_1R ($K_i \pm SEM$, nM) = 2.5 ± 0.2

MT_2R ($K_i \pm SEM$, nM) = 0.45 ± 0.08

Functional studies (GTP γ S) at MTRs

MT_1R (EC_{50} , nM) = 204 ± 54

MT_1R (E_{max} , %) = 92 ± 2

MT_2R (EC_{50} , nM) = 11 ± 9

MT_2R (E_{max} , %) = 88 ± 4

Figure 38.

Structures of the parent amide **143** and the reverse amide bioisosteres **144** and **145**, MTR ligands.

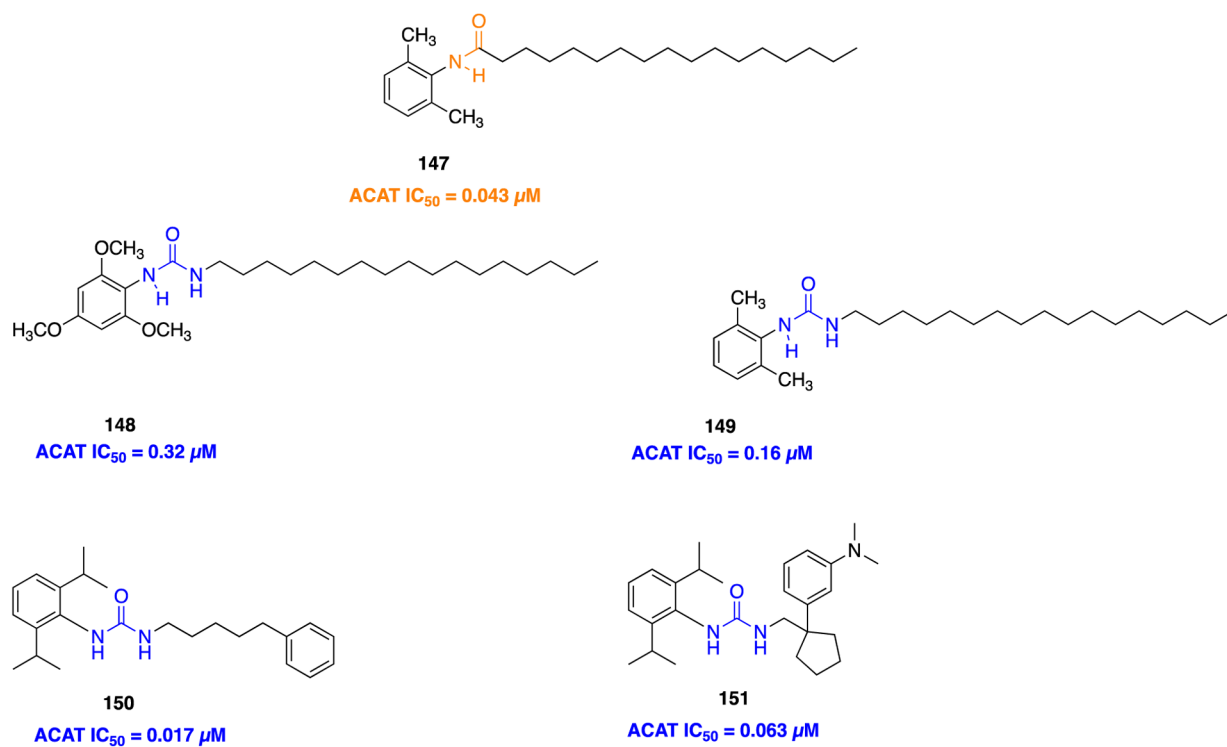
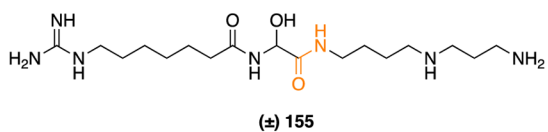
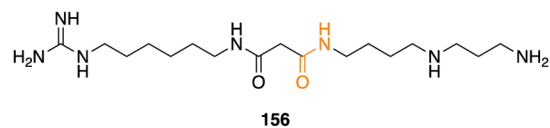


Figure 39.
Structures of parent amide **147**, urea bioisosteres **148**, **149**, and **150**, and **151**, a potent urea ACAT inhibitor.



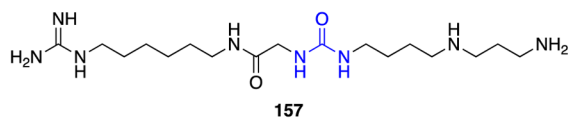
GVHD mean survival (days: M ± SD); 3 mg/kg = 57 ± 7
1 mg/kg = 38 ± 12

Heart Allotransplantation model (day: M ± SD); 6 mg/kg = 38 ± 30



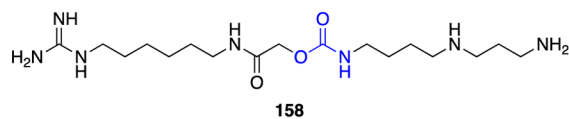
GVHD mean survival (days: M ± SD); 3 mg/kg = 52 ± 20
1 mg/kg = 53 ± 13

Heart Allotransplantation model (day: M ± SD); 6 mg/kg = 9 ± 3



GVHD mean survival (days: M ± SD); 3 mg/kg = 48 ± 12
1 mg/kg = 42 ± 21

Heart Allotransplantation model (day: M ± SD); 6 mg/kg = 12 ± 4



GVHD mean survival (days: M ± SD); 3 mg/kg = 58 ± 6
1 mg/kg = 46 ± 10

Heart Allotransplantation model (day: M ± SD); 6 mg/kg = 54 ± 34

Figure 40.
Structures of DSG (155) and bioisosteric analogs.

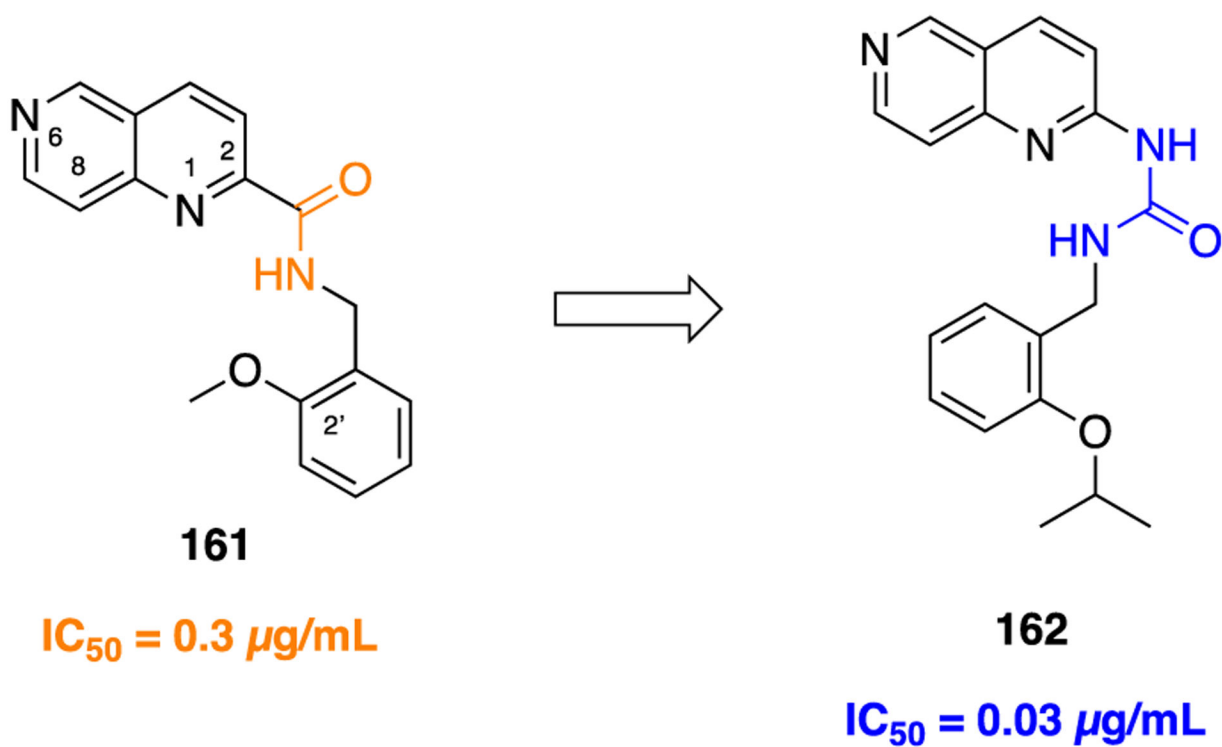


Figure 41. Structures of lead compound **161** for anti-human cytomegalovirus (HCMV) and 2'-isopropoxyurea bioisostere **162**.

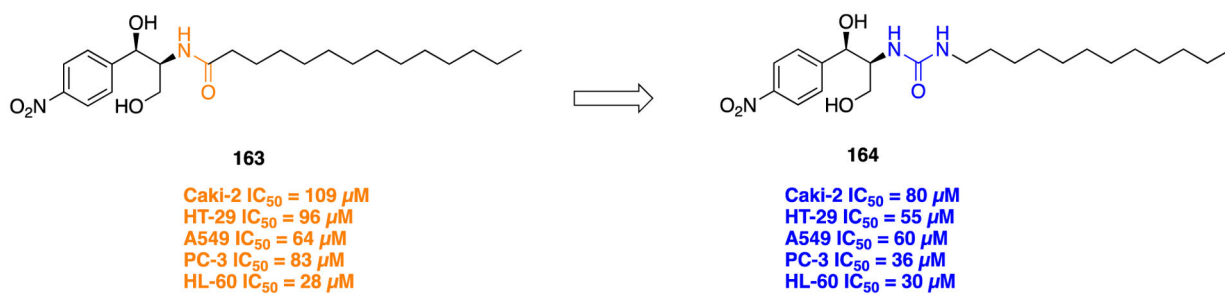


Figure 42.

Structures of **163**, B13, a ceramide analog tested for *in vitro* cytotoxicity against five human tumor cell lines, and **164**, a more potent urea bioisostere.

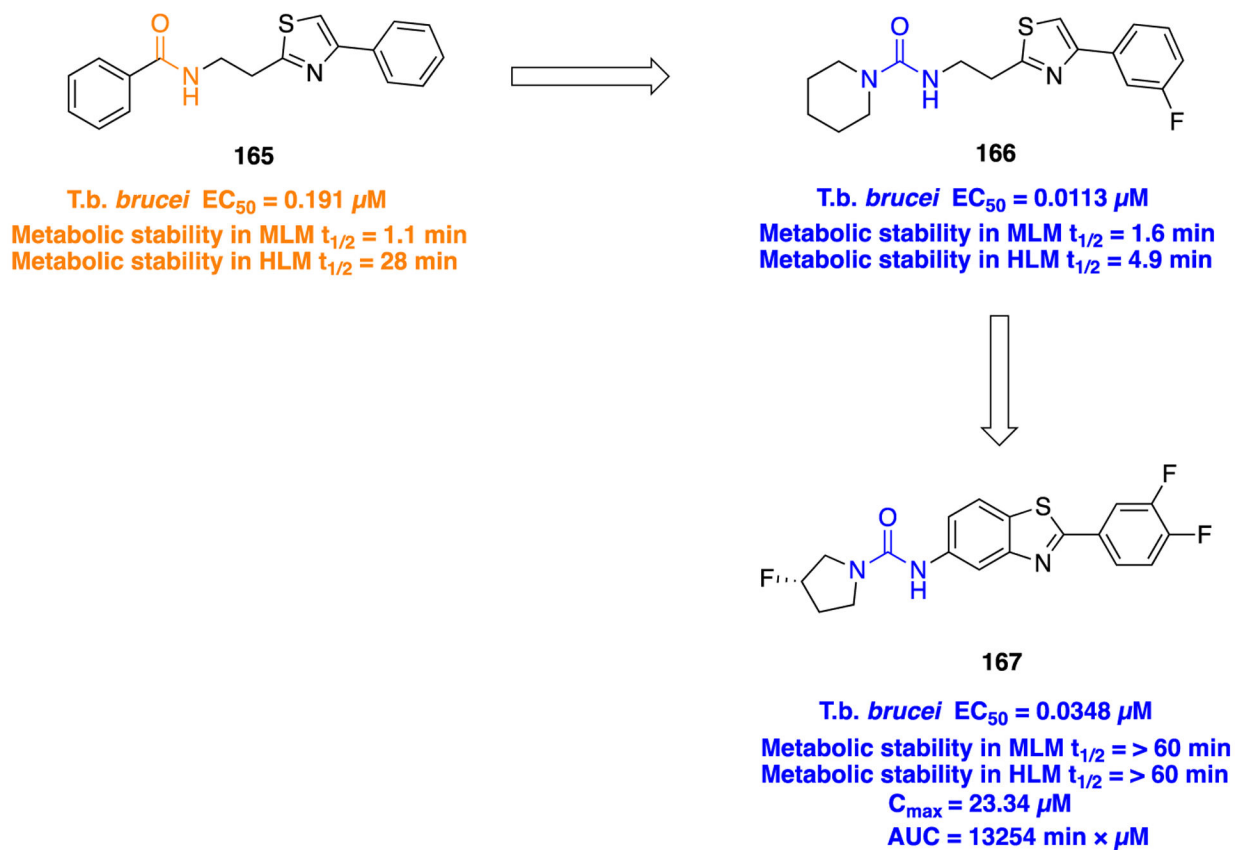


Figure 43.

Antitrypanosomal agent **165**, an amide derivative, was further optimized to urea derivatives **166** and **167**.

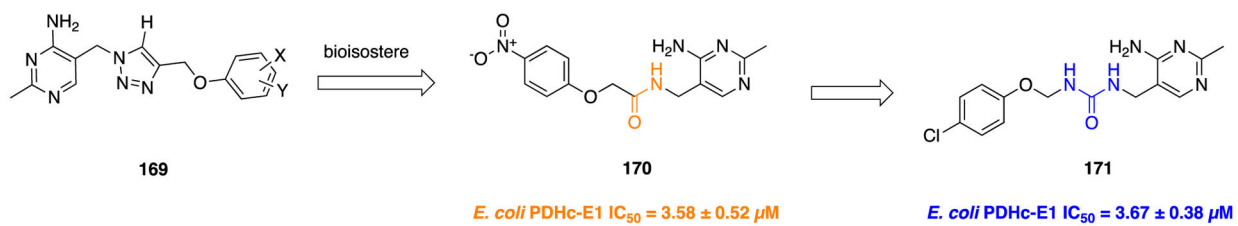


Figure 44.

Structures of the amide (**169**) and urea (**171**) bioisostere derivatives of the triazole-based *Escherichia coli* PDHc-E1 inhibitor **169**.

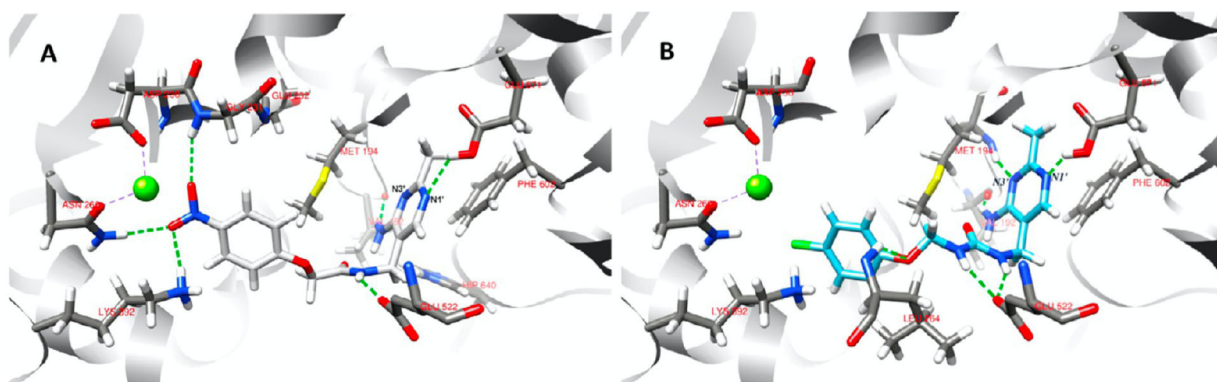


Figure 45.

Graphical representation of the binding modes of **170** (A) and **171** (B) into the active site of *E. coli* PDHc-E1 displayed in ribbon. Ligands and residues are depicted by stick, while the hydrogen and coordination bonds are shown with dashed lines (green). Reproduced with permission from *Bioorganic & Medicinal Chemistry* (<https://www.sciencedirect.com/journal/bioorganic-and-medicinal-chemistry>), Volume 22, pp 3180–3186, He, J. B.; Ren, Y. L.; Sun, Q. S.; You, G. Y.; Zhang, L.; Zou, P.; Feng, L. L.; Wan, J.; He, H. W., Design, synthesis and molecular docking of amide and urea derivatives as Escherichia coli PDHc-E1 inhibitors.²²² Copyright 2014 Elsevier.

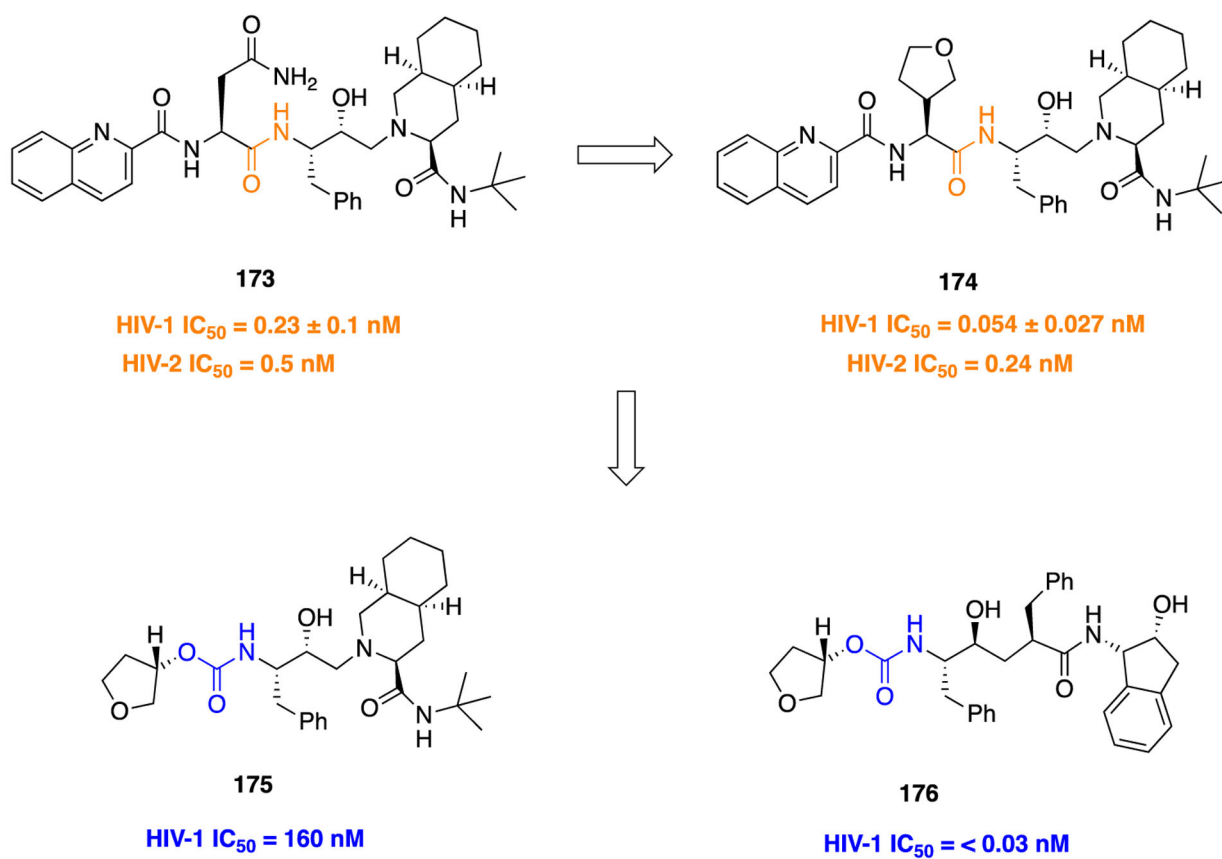


Figure 46.
Potent HIV protease inhibitors incorporating carbamate bioisosteres.

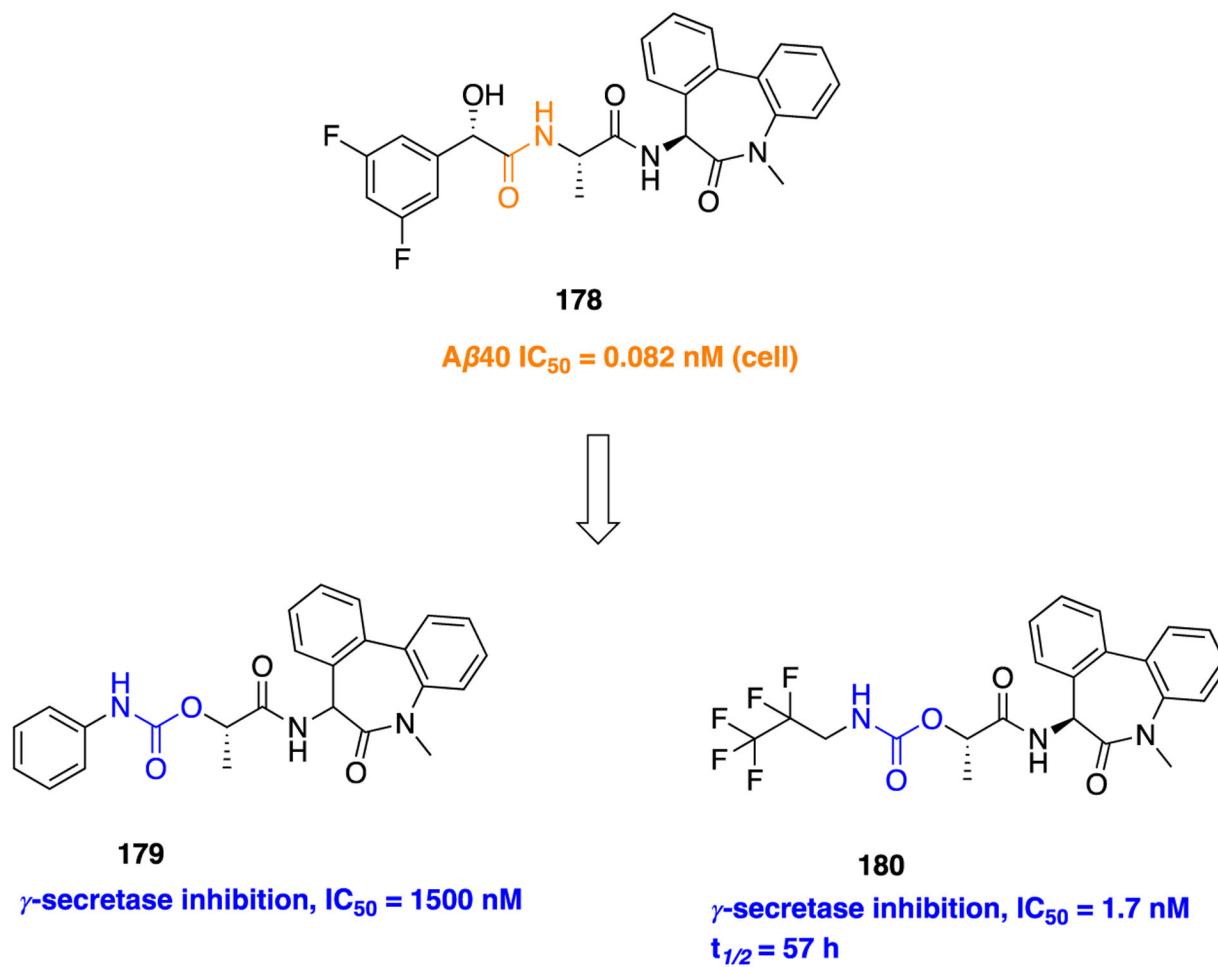


Figure 47. Structures of parent amide **178**, a γ -secretase inhibitor, and potent carbamate-based derivatives **179** and **180** for the treatment of AD.

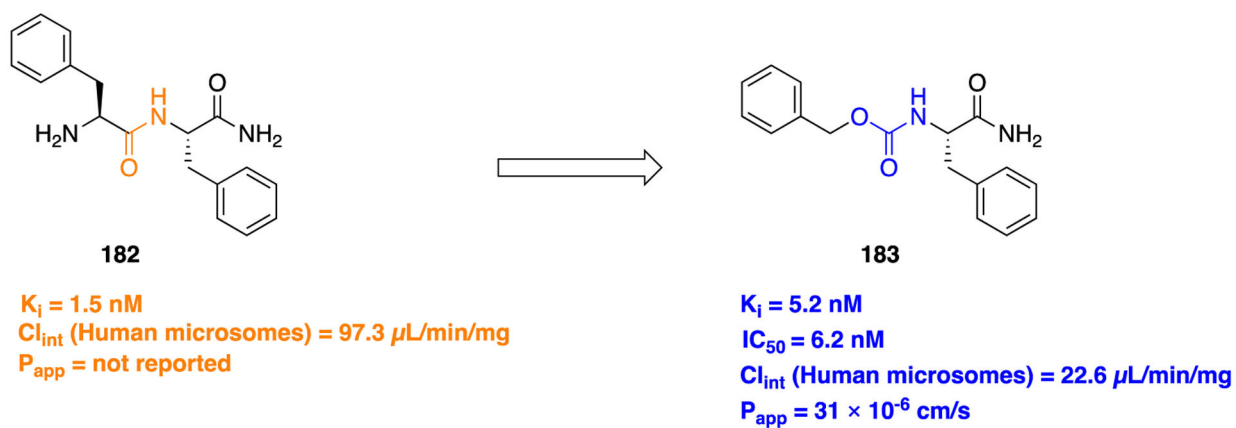


Figure 48.
Replacement of the amide bond in **182** with a carbamate moiety to afford compound **183**, novel SP₁₋₇ analogs as potential therapeutic agents for neuropathic pain.

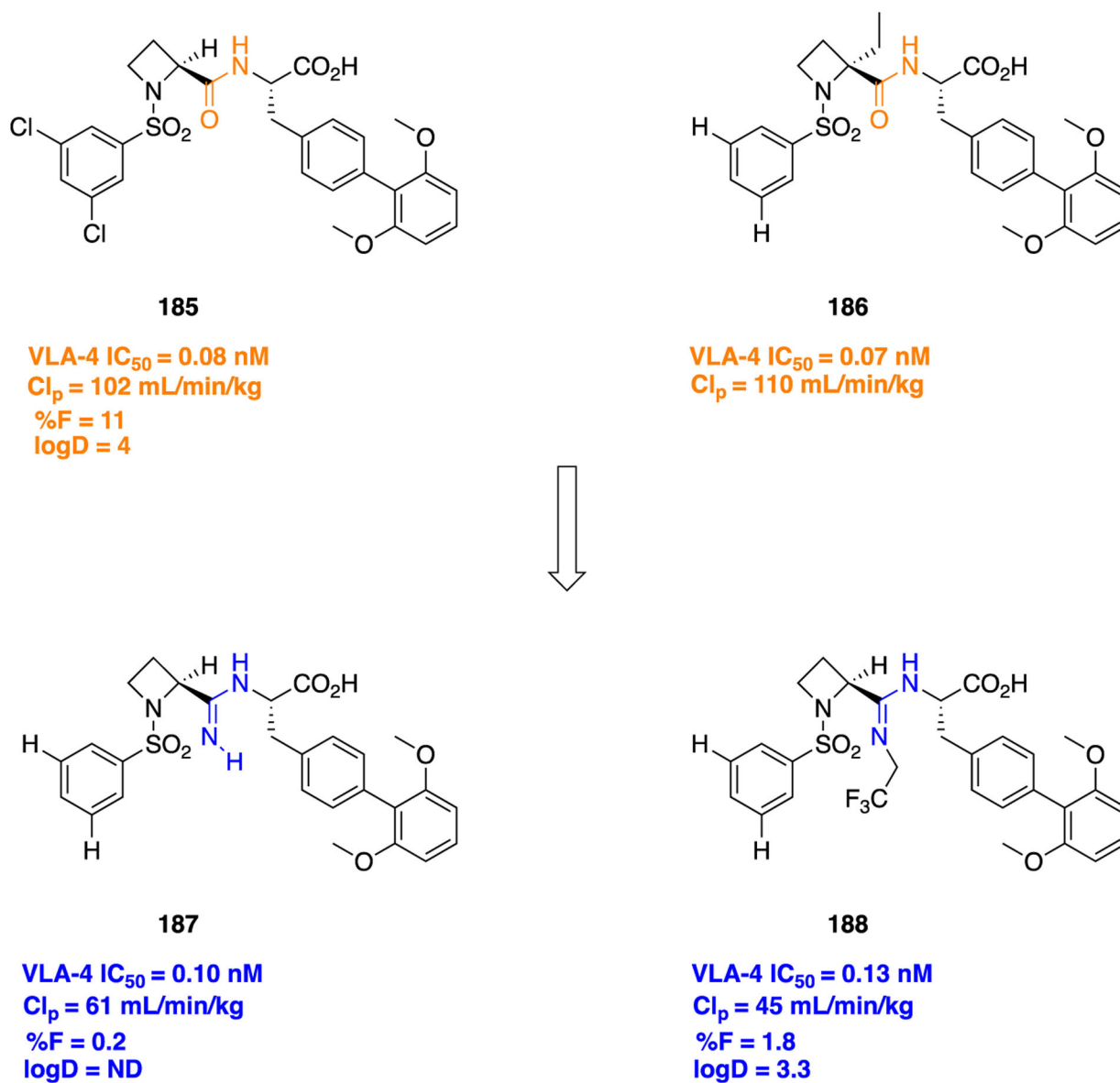


Figure 49.
Amidines as a bioisostere of the amide functionality in VLA-4 antagonists.

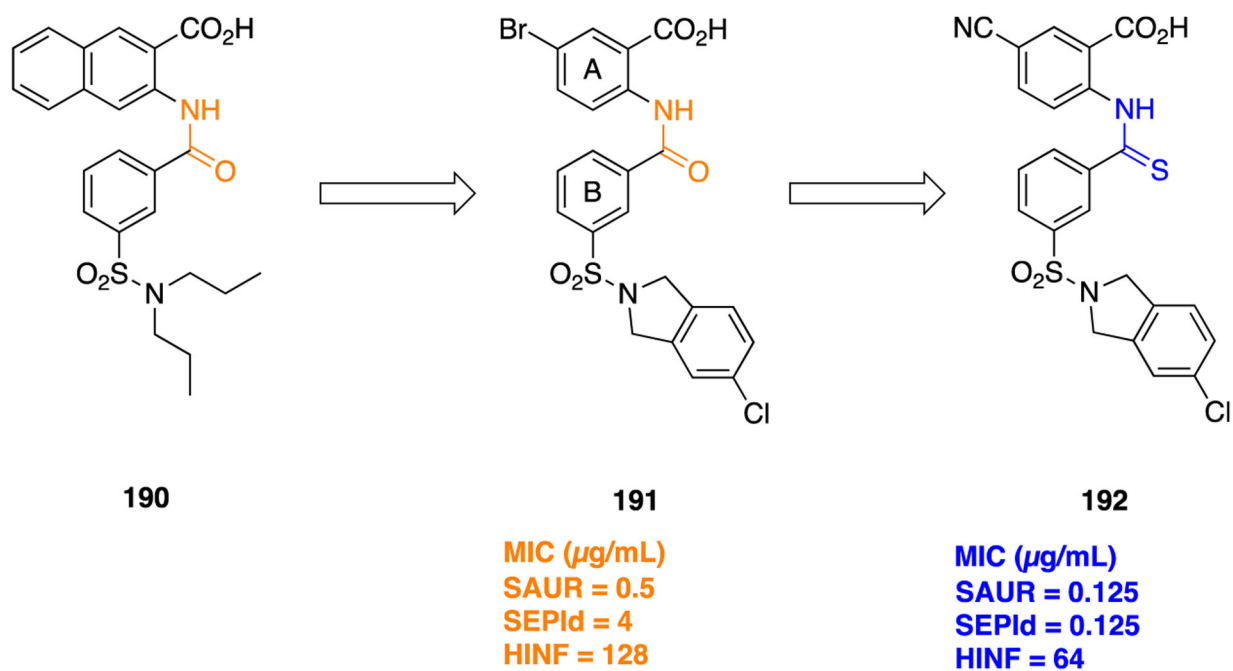


Figure 50. Anthranilic acid lead **190**, advanced lead **191**, and alternative thioamide bioisostere **192** as antibacterial agents.

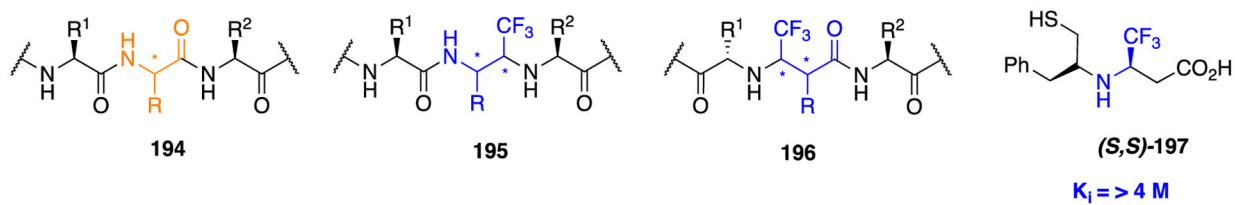
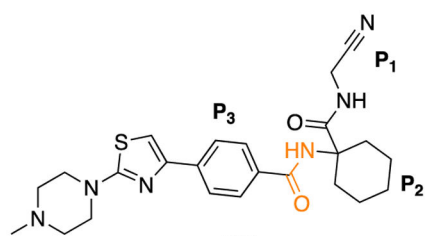
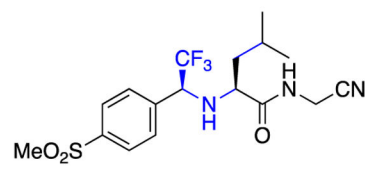


Figure 51. Molecular structures of natural **194** and bioisosteric $\Psi[\text{CH}(\text{CF}_3)\text{NH}]\text{Gly}$ **195** and **196** peptides and (*S,S*) [NHCH(CF₃)]-retrothiorphan diastereomer **197**.

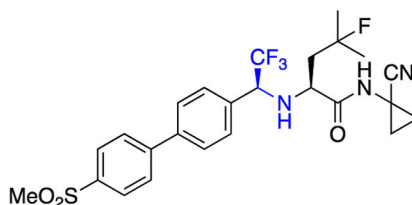
**200**

Cat K IC_{50} = 0.6 nM
 Cat B IC_{50} = 1050 nM
 Cat L IC_{50} = 3903 nM
 Cat S IC_{50} = > 10000 nM

**201**

Cat K IC_{50} = 0.2 nM
 Cat B IC_{50} = 5239 nM
 Cat L IC_{50} = 264 nM
 Cat S IC_{50} = 178 nM

Rat (10 mg/kg, po); %F = 40; $t_{1/2}$ (h) = 3
 Dog (10 mg/kg, po); %F = 65; $t_{1/2}$ (h) = 6
 Rhesus Monkey (5 mg/kg, po); %F = 24; $t_{1/2}$ (h) = 2

**202**

Cat K IC_{50} = 0.2 nM
 Cat B IC_{50} = 1034 nM
 Cat L IC_{50} = 2995 nM
 Cat S IC_{50} = 60 nM

Rat (10 mg/kg, po); %F = 8; $t_{1/2}$ (h) = 6
 Dog (5 mg/kg, po); %F = 6; $t_{1/2}$ (h) = 57
 Rhesus Monkey (5 mg/kg, po); %F = 7; $t_{1/2}$ (h) = 18

Figure 52.

Structures of **200** a reversible dipeptide inhibitor of cathepsin K, **201** a neutral cathepsin K inhibitor, and **202** a potent cathepsin K inhibitor containing the trifluoroethylamine bioisostere.

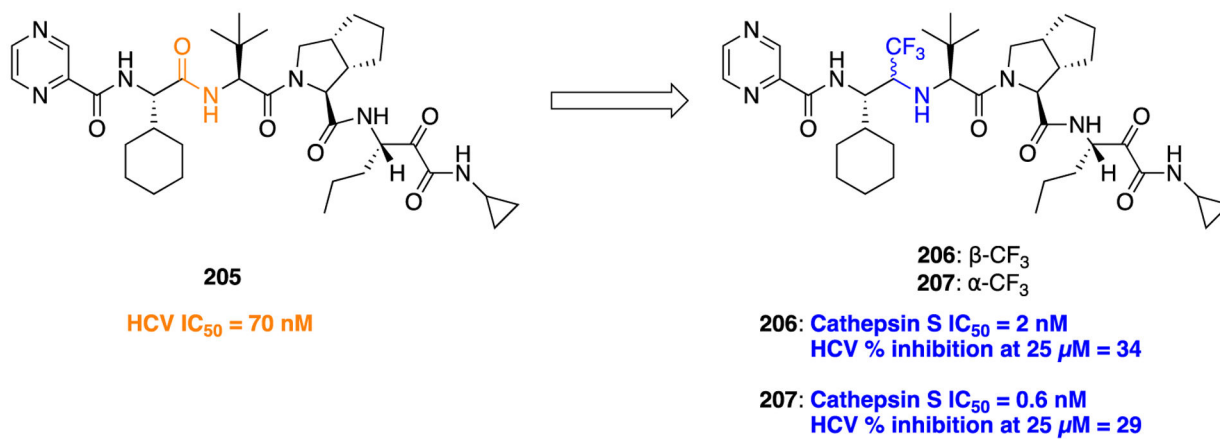


Figure 53. Structures of **205**, a potent hepatitis C virus (HCV) NS3 protease inhibitor, and trifluoromethylated-containing cathepsin S inhibitors **206** and **207**.

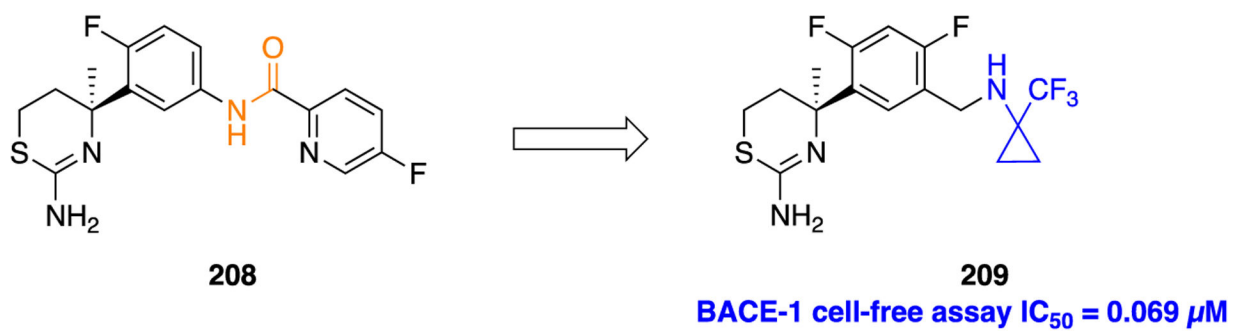


Figure 54.
Structures of **208**, an amide-based BACE-1 inhibitor, and CF_3 -cyclopropane bioisostere BACE-1 inhibitor **209**.

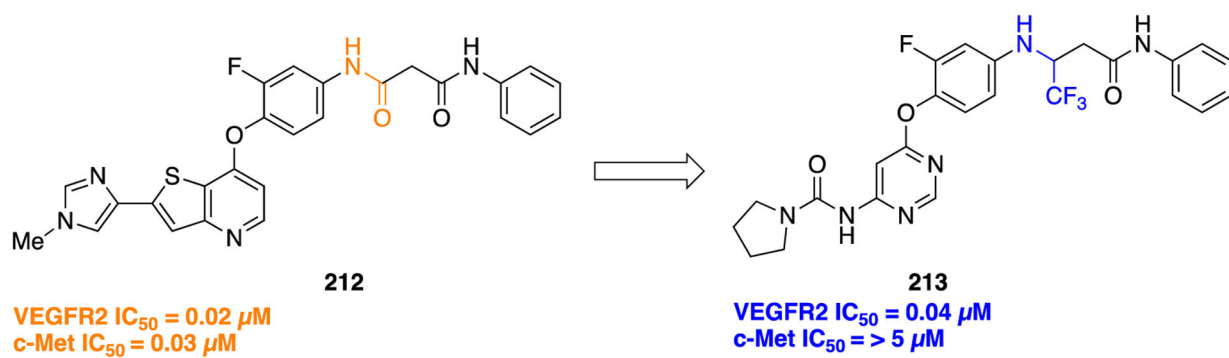


Figure 55.
Structures of parent malonamide **212** and selective and potent VEGFR2 inhibitor **213**.

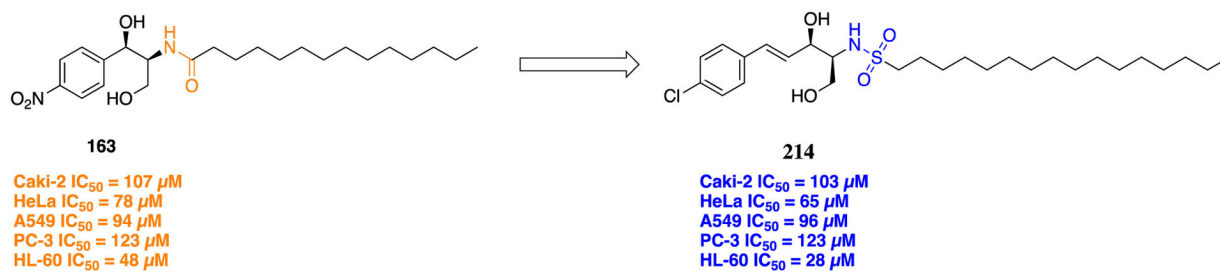


Figure 56. Structures of amide **163** and an aromatic sulfonamido ceramide bioisostere with more potent cytotoxic activity.

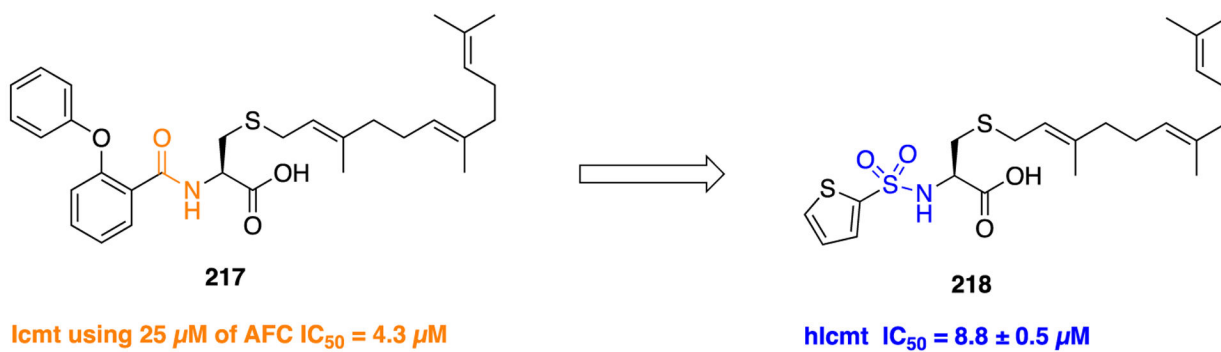
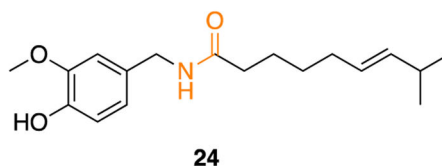
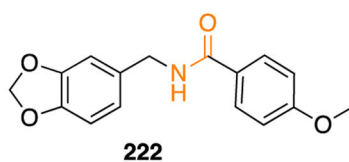


Figure 57.
Phenoxypheyl farnesylcysteine **217** and sulfonamide-modified farnesylcysteine (SMFC) analog **218**, as hIcmt inhibitors.



MDA-MB-231 cells, $IC_{50} = 120 \mu M$
In vivo MDA-MB-231 breast cancer model
(90 mg/kg; 15 days) = $281.3 \pm 78.5 \text{ mm}^3$

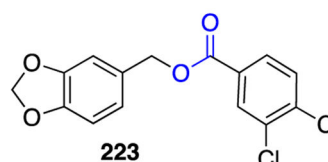
amide analog



222

MDA-MB-231 cells, $IC_{50} = > 200 \mu M$

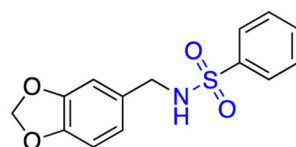
ester analog



223

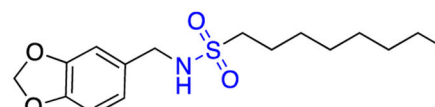
MDA-MB-231 cells, $IC_{50} = > 200 \mu M$

sulfonamide analogs



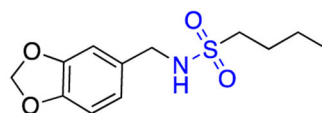
224

MDA-MB-231 cells, $IC_{50} = 14.2 \mu M$
Not further tested due to solubility issues



225

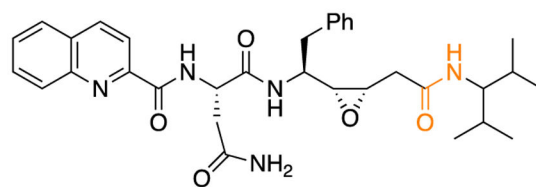
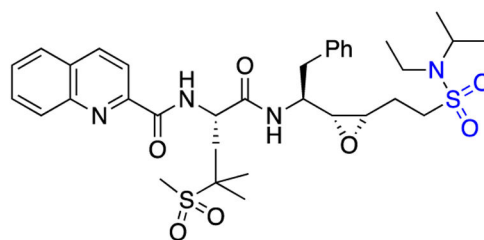
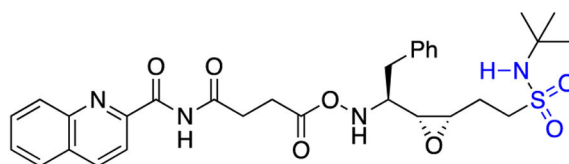
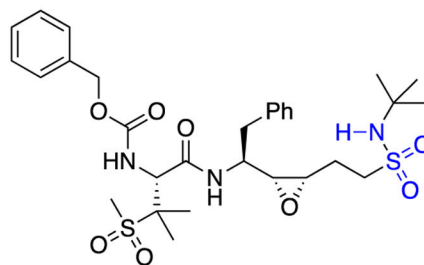
Not tested due to solubility issues



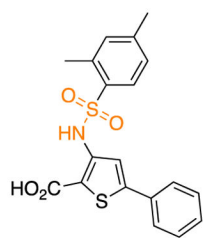
226

MDA-MB-231 cells, $IC_{50} = 87 \mu M$
In vivo MDA-MB-231 breast cancer model
(70 mg/kg; 15 days) = $133.4 \pm 24.5 \text{ mm}^3$

Figure 58.
 Capsaicin (**24**) and step by step development of novel capsaicin-like bioisosteric analogs **222–226**.

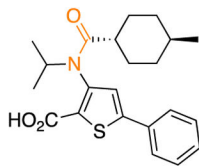
**227****IC₅₀ = 20 nM****228****IC₅₀ = 6.6 nM****229****IC₅₀ = 30 nM****230****IC₅₀ = 20.2 nM****Figure 59.**

Novel irreversible HIV-1 protease inhibitors encompassing sulfonamide and sulfone as amide bioisosteres.



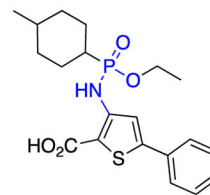
231

HCV NS5B polymerase inhibition
 $IC_{50} = 1.0 \mu M$
 Replicon cell-based assay
 $EC_{50} = 5.0 \mu M$



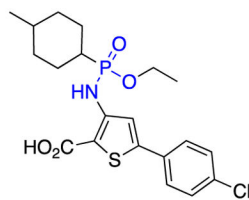
232

Inhibition of HCV replication cells
 $EC_{50} = 0.369 \mu M$
 Inhibition on the 1b-J4-HCV NS5B polymerase
 $IC_{50} = 0.035 \mu M$



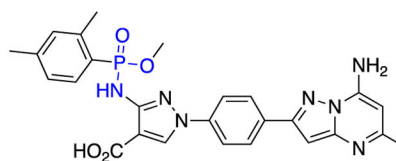
233

Inhibition of HCV replication cells
 $EC_{50} > 8.3 \mu M$
 Inhibition on the 1b-J4-HCV NS5B polymerase
 $IC_{50} > 10 \mu M$



234

Inhibition of HCV replication cells
 $EC_{50} > 8.3 \mu M$
 Inhibition on the 1b-J4-HCV NS5B polymerase
 $IC_{50} = 3.740 \mu M$



235

Inhibition of HCV replication cells
 $EC_{50} = 0.0004 \mu M$
 Inhibition on the 1b-Con1-HCV NS5B polymerase
 $IC_{50} = 0.0099 \mu M$
 Inhibition on the 2a-JFH-HCV NS5B polymerase
 $IC_{50} = 0.2538 \mu M$
 Inhibition on the 3a-NZL11-HCV NS5B polymerase
 $IC_{50} = 0.1809 \mu M$
 Inhibition on the 4a1-HCV NS5B polymerase
 $IC_{50} = 0.0257 \mu M$

Figure 60.

Non-nucleoside NS5B inhibitors (except **233**), containing the phosphonamidate group as an amide bioisostere (**233**, **234**, and **235**).

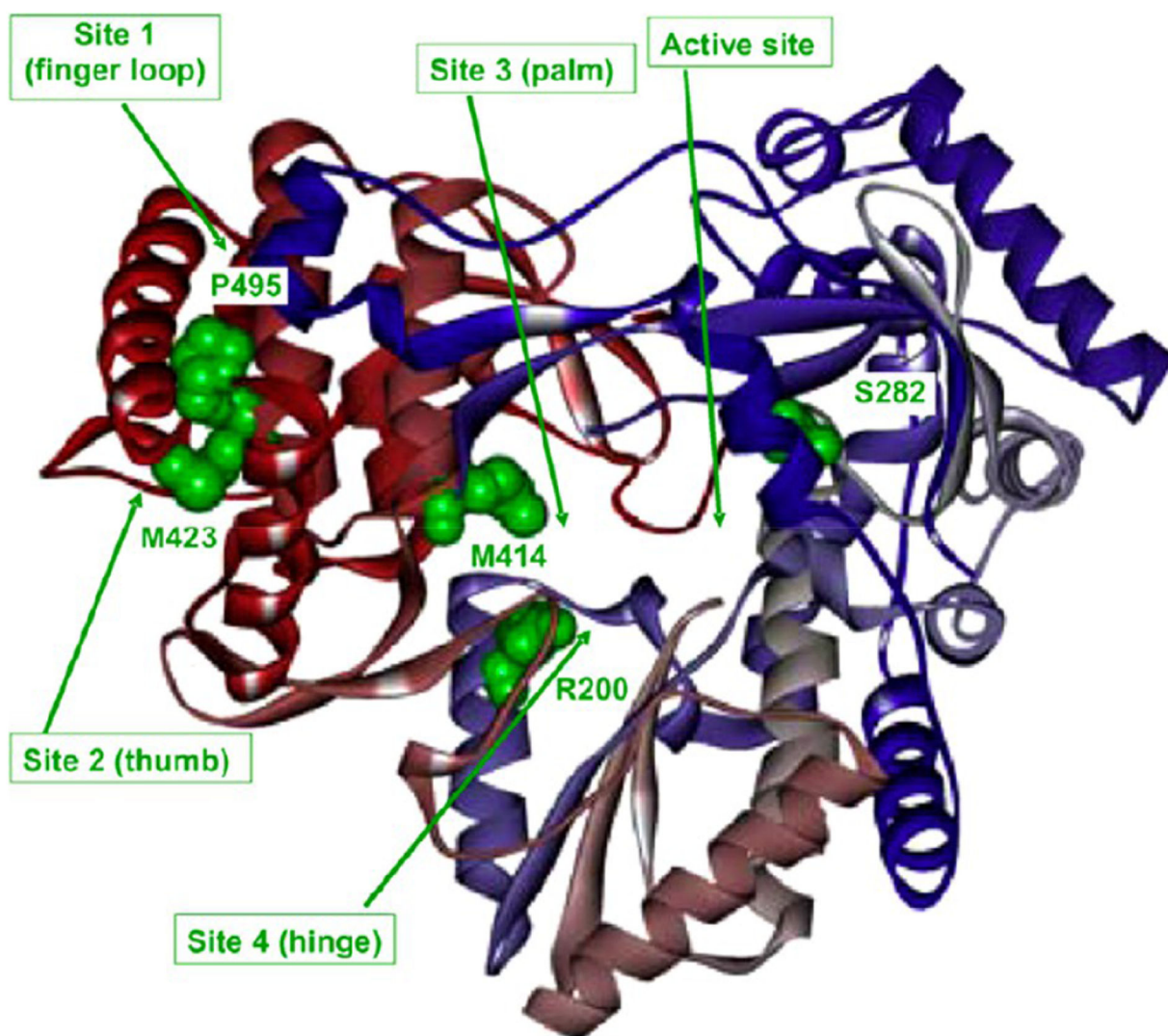


Figure 61.

Ribbon structure of NS5B HCV viral polymerase. Reproduced with permission from *Bioorganic & Medicinal Chemistry Letters* (<https://www.sciencedirect.com/journal/bioorganic-and-medicinal-chemistry-letters>), Volume 26, pp 4536–4541, Pierra Rouviere, C.; Amador, A.; Badaroux, E.; Convard, T.; Da Costa, D.; Dukhan, D.; Griffe, L.; Griffon, J. F.; LaColla, M.; Leroy, F.; Liuzzi, M.; Loi, A. G.; McCarville, J.; Mascia, V.; Milhau, J.; Onidi, L.; Paparin, J. L.; Rahali, R.; Sais, E.; Seifer, M.; Surleraux, D.; Standing, D.; Dousson, C., Synthesis of potent and broad genotypically active NS5B HCV non-nucleoside inhibitors binding to the thumb domain allosteric site 2 of the viral polymerase.²⁵⁹ Copyright 2016 Elsevier.

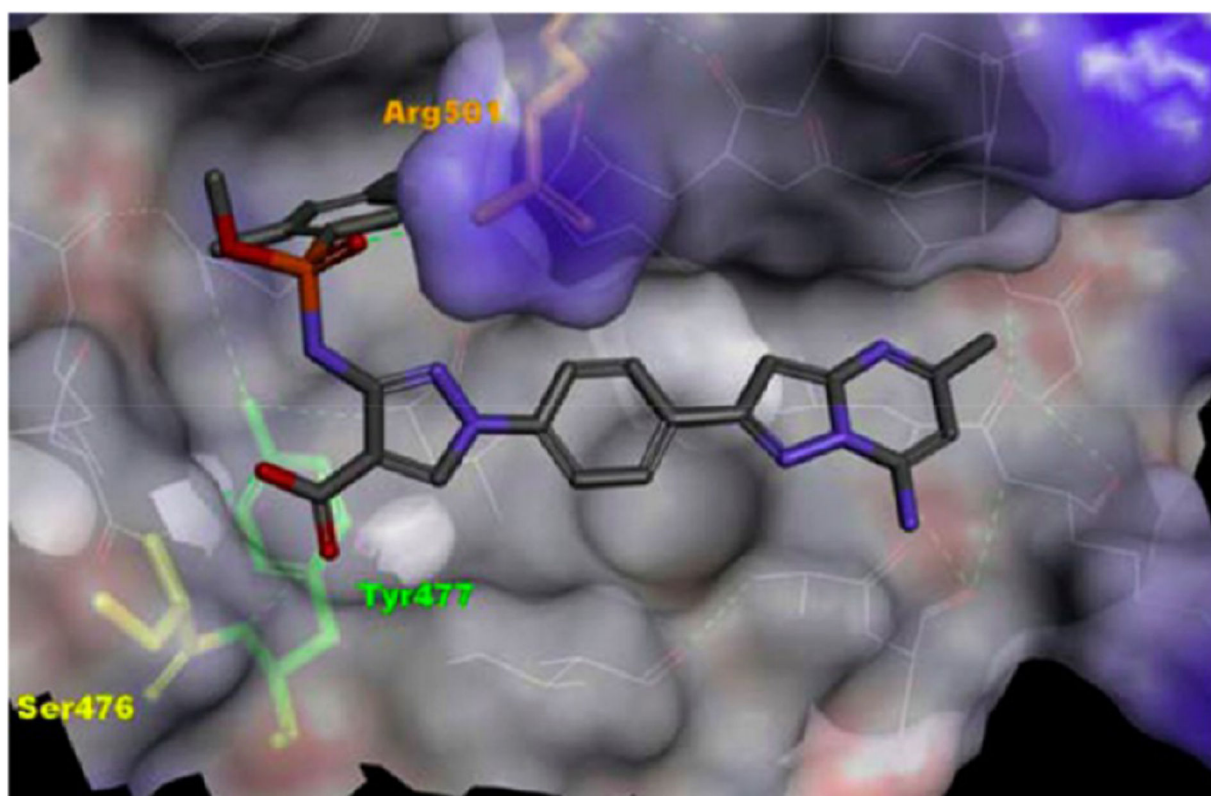


Figure 62.

Cocrystallization image of **235** complexed with the viral NS5B (PDB code 5CZB).

Reproduced with permission from *Bioorganic & Medicinal Chemistry Letters* (<https://www.sciencedirect.com/journal/bioorganic-and-medicinal-chemistry-letters>), Volume 26, pp 4536–4541, Pierra Rouviere, C.; Amador, A.; Badaroux, E.; Convard, T.; Da Costa, D.; Dukhan, D.; Griffe, L.; Griffon, J. F.; LaColla, M.; Leroy, F.; Liuzzi, M.; Loi, A. G.; McCarville, J.; Mascia, V.; Milhau, J.; Onidi, L.; Papparin, J. L.; Rahali, R.; Sais, E.; Seifer, M.; Surleraux, D.; Standing, D.; Dousson, C., Synthesis of potent and broad genotypically active NS5B HCV non-nucleoside inhibitors binding to the thumb domain allosteric site 2 of the viral polymerase.²⁵⁹ Copyright 2016 Elsevier.

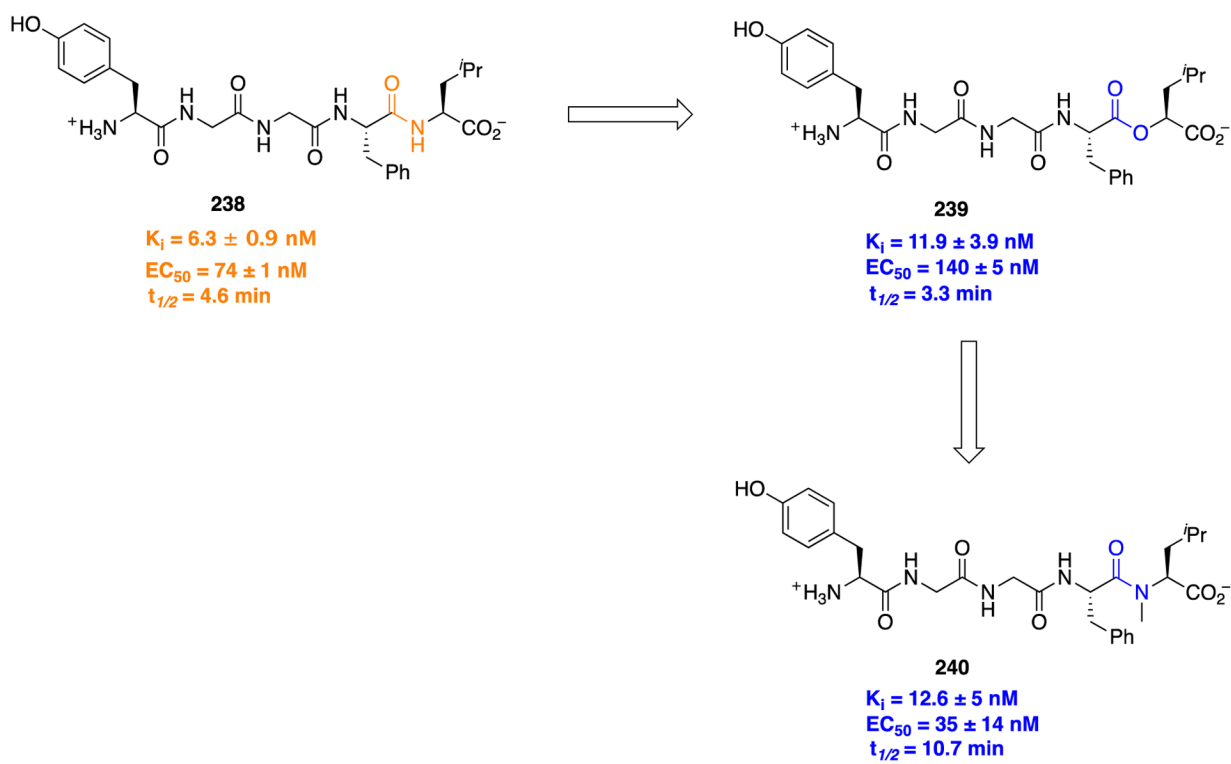


Figure 63. Structures of peptide **238** and analogs in which the amide bond was replaced by an ester **239** or *N*-methylamide bond **240**.

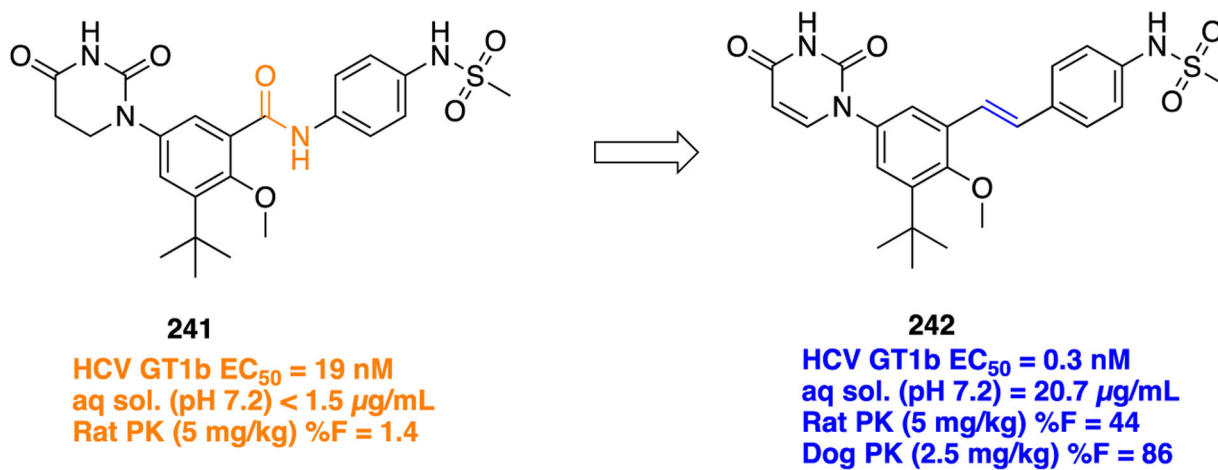


Figure 64.
Amide to *trans* olefin bioisosteric replacement leading to the clinical candidate **242**.

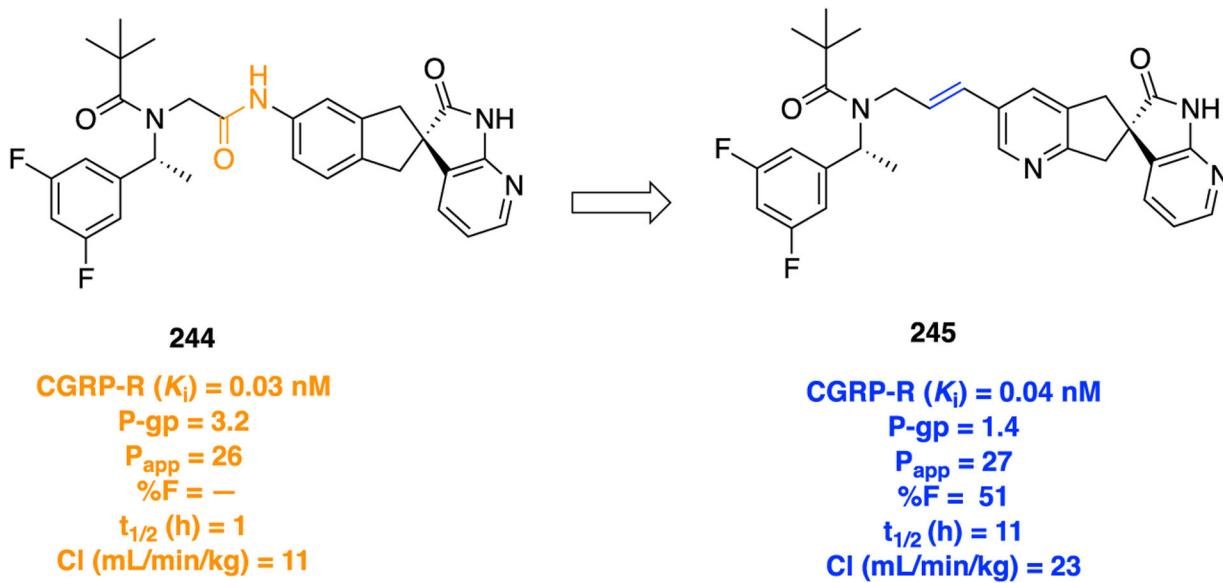


Figure 65.
Example of the replacement of a central amide of an azaoxindole derivative (**244**) with an *E*-alkene moiety **245**.

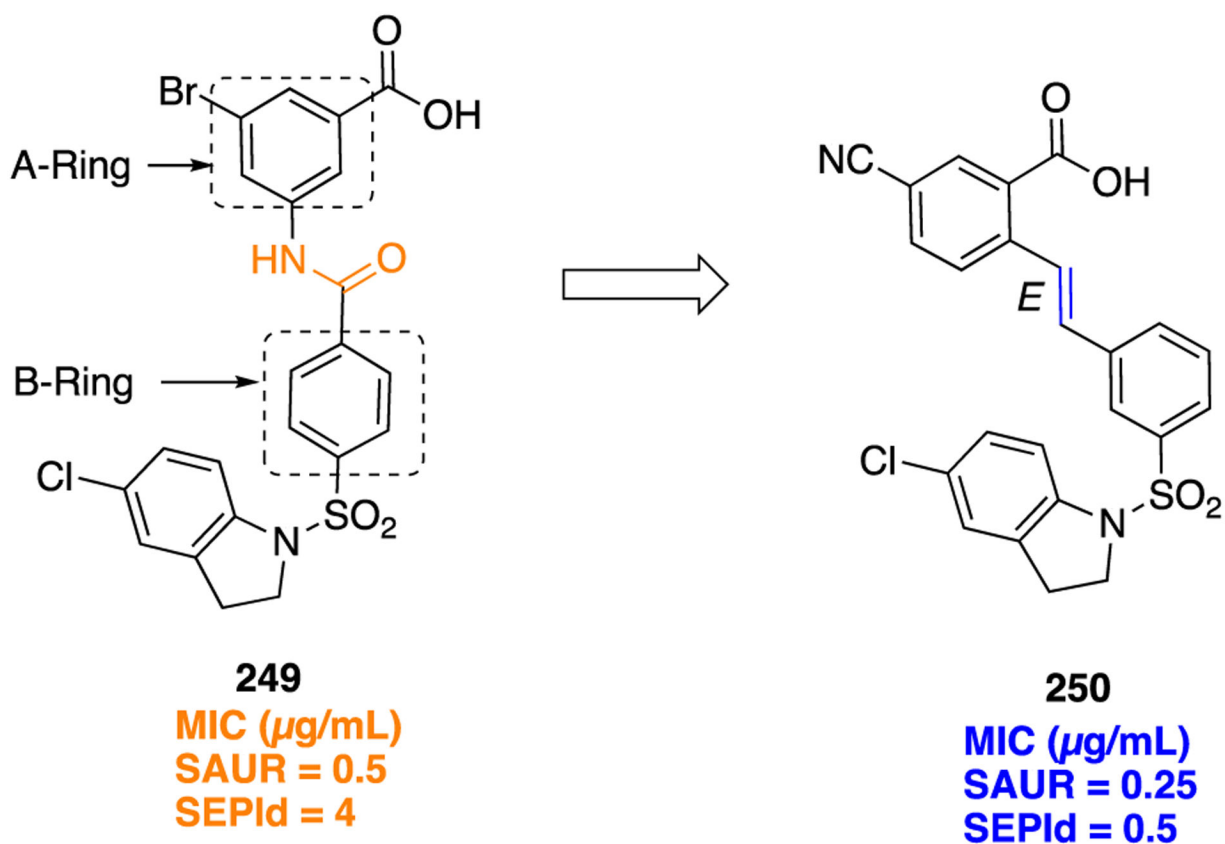


Figure 66.
Structural modification of an amide linker in **249** to an *E*-alkene in **250** that joins A and B rings.

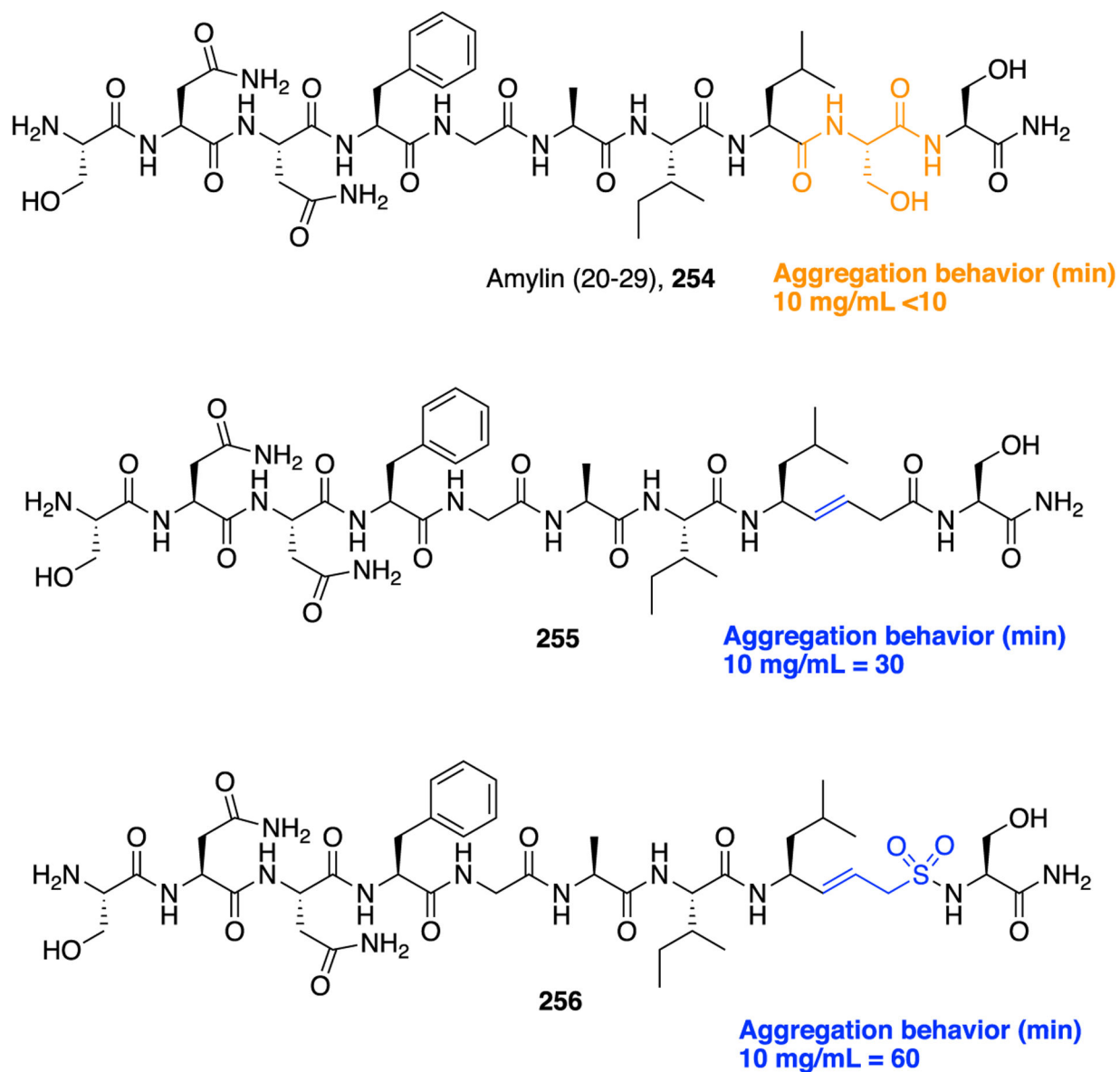
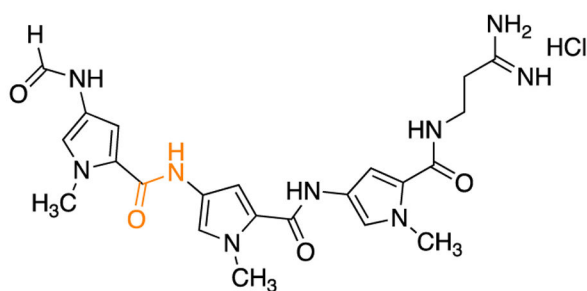
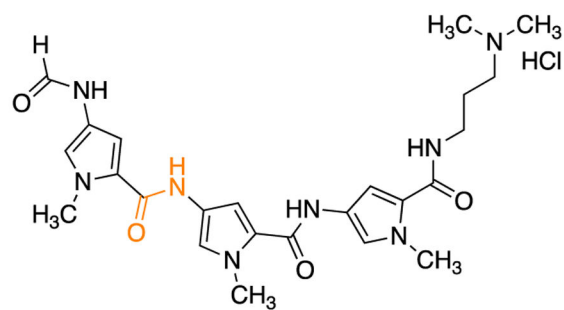


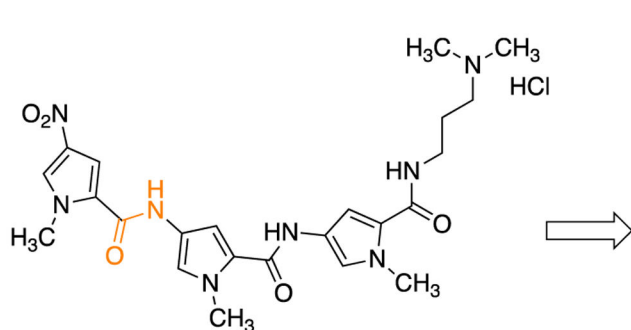
Figure 67.
Molecular structures of amylin (20–29) **254** and its modified bioisosteric analogs.

Distamycin (**262**)

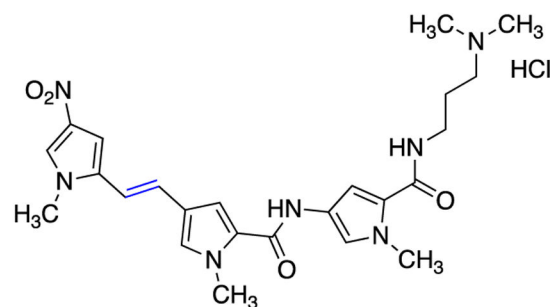
poly (dA-dT), $K_{app} = 345 \times 10^5 M^{-1}$
 poly (dG-dC), $K_{app} = 1.3 \times 10^5 M^{-1}$

**263**

poly (dA-dT), $K_{app} = 150 \times 10^5 M^{-1}$
 poly (dG-dC), $K_{app} = 0.9 \times 10^5 M^{-1}$

**264**

poly (dA-dT), $K_{app} = 8.7 \times 10^5 M^{-1}$
 poly (dG-dC), $K_{app} = 3.5 \times 10^5 M^{-1}$

**265**

poly (dA-dT), $K_{app} = 16.9 \times 10^5 M^{-1}$
 poly (dG-dC), $K_{app} = 7.4 \times 10^5 M^{-1}$

Figure 68.
 Distamycin (**262**) and its bioisosteric analogs.

1 2 3 4 5 6 7 8 9 10 11 12 13 14
pGlu-Gln-Arg-Leu-Gly-Asn-Gln-Trp-Ala-Val-Gly-His-Leu-Met-NH₂

Bombesin (**266**)

H-D-Phe-Gln-Trp-Ala-Val-Gly-His-Leu-ψ(CH₂-NH)-Leu-NH₂

267

**Amylase release inhibition;
IC₅₀ = 68.7 ± 16 nM**

H-D-Phe-Gln-Trp-Ala-Val-Gly-His-Leu-ψ[(E)-CH=CH]-Leu-NH₂

268

**Amylase release inhibition;
IC₅₀ = 6.7 ± 1.7 nM**

Figure 69.

Amino acid sequences of bombesin (**266**), pseudopeptide **267**, and *E*-alkene isostere **268**.

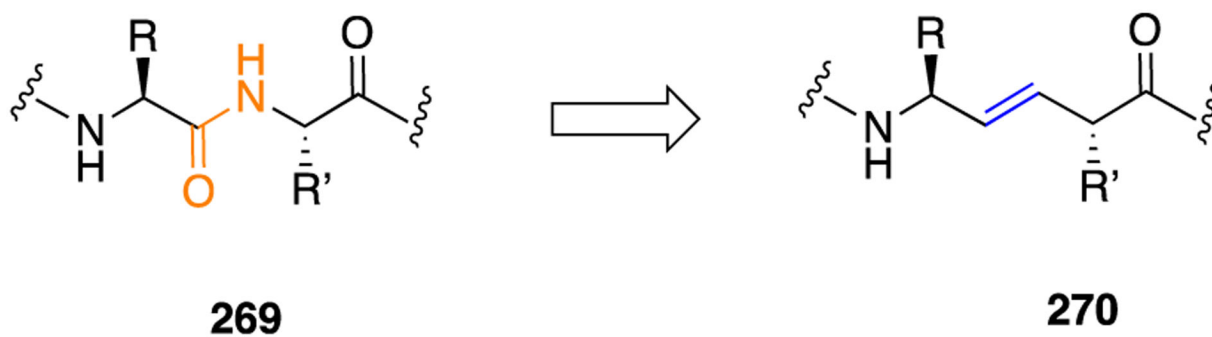
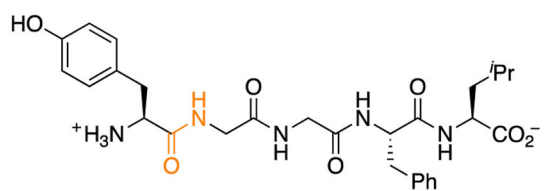


Figure 70.

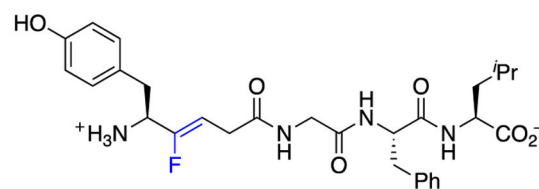
Graphical representation of the modification of peptide backbone from an amide to *E*-olefin, which is neither a hydrogen bond donor nor acceptor.

Boc-Trp-Met-Asp-PheNH₂**271****CCK-B (Cortex), binding of [¹²⁵I]BH-CCK-8, IC₅₀ = 25 ± 4.5 nM****CCK-A (Pancreas), binding of [¹²⁵I]BH-CCK-8 IC₅₀ = 1800 ± 630 nM****CCK-B calcium response in NCI-H345 cells,
Ca⁺² Release, EC₅₀ = 13 ± 0.6 nM, Max% = 99****Boc-Leu-Gly-Trp-Leu-Asp-PheNH₂****272****CCK-B (Cortex), binding of [¹²⁵I]BH-CCK-8, IC₅₀ = 54 ± 12 nM****CCK-A (Pancreas), binding of [¹²⁵I]BH-CCK-8 IC₅₀ = 1600 ± 820 nM****CCK-B calcium response in NCI-H345 cells,
Ca⁺² Release, EC₅₀ = 40 ± 9.9 nM, Max% = 99****Boc-Leu[*E*-CH=CH]Gly-Trp-Leu-Asp-PheNH₂****273****CCK-B (Cortex), binding of [¹²⁵I]BH-CCK-8, IC₅₀ = 37 ± 7.9 nM****CCK-A (Pancreas), binding of [¹²⁵I]BH-CCK-8 IC₅₀ = 2700 ± 720 nM****CCK-B calcium response in NCI-H345 cells,
Ca⁺² Release, EC₅₀ = 150 ± 18 nM, Max% = 103****Figure 71.**

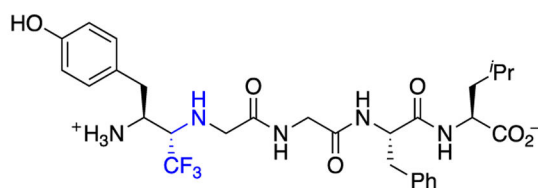
Bioisosteric replacement of amide linkages from parent CCK peptides **271** and **272** to develop *E*-alkene isostere **273**, a potent CCK-B receptor ligand.

**238**

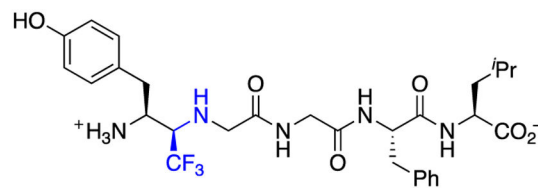
$EC_{50} \pm SEM$ (nM) $\delta = 0.08 \pm 0.01$
 $EC_{50} \pm SEM$ (nM) $\mu = 1.3 \pm 0.1$
 $EC_{50} \pm SEM$ (nM) $\kappa = 80 \pm 20$
 Selectivity μ/δ , $\kappa/\delta = 16, 1000$
 rat $t_{1/2} < 5$ min
 human plasma $t_{1/2} < 12$ min

**275**

$EC_{50} \pm SEM$ (nM) $\delta = 5.0 \pm 2$
 $EC_{50} \pm SEM$ (nM) $\mu = 60 \pm 15$
 $EC_{50} \pm SEM$ (nM) $\kappa > 10000$
 Selectivity μ/δ , $\kappa/\delta = 12, > 2000$
 rat $t_{1/2} = 4$ h
 human plasma $t_{1/2} = 4$ h

**(S)-276**

$EC_{50} \pm SEM$ (nM) $\delta, \mu, \kappa > 10000$

**(R)-277**

$EC_{50} \pm SEM$ (nM) $\delta, \mu, \kappa > 10000$

Figure 72.

Bioisosteric replacement of an amide bond at the Tyr¹-Gly² position in **238** with a fluoroalkene to produce **275** and a trifluoroethylamine moiety to produce (*S*)-**276** and (*R*)-**277**.

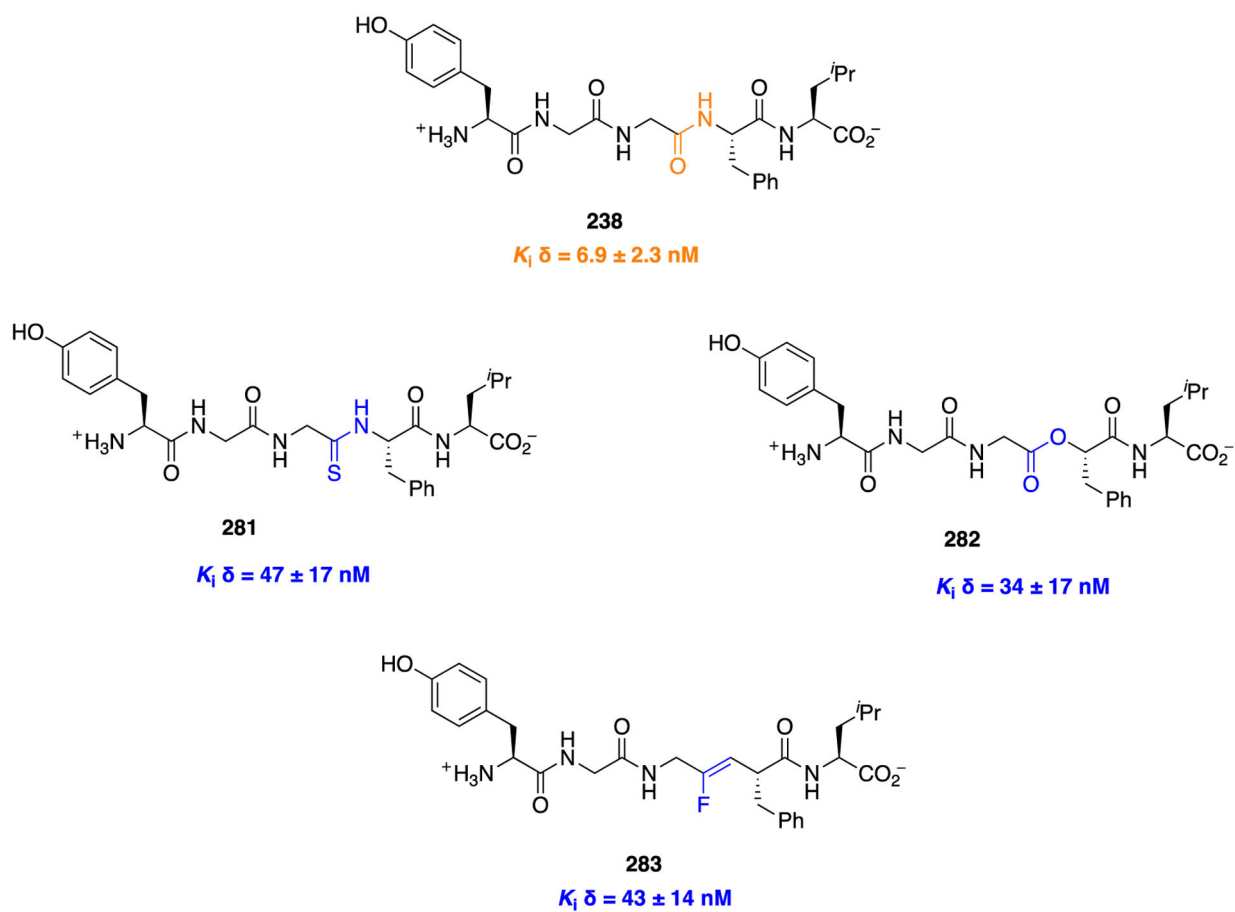


Figure 73.

Structures of the parent peptide **238** and its fluoroalkene isostere **283**.

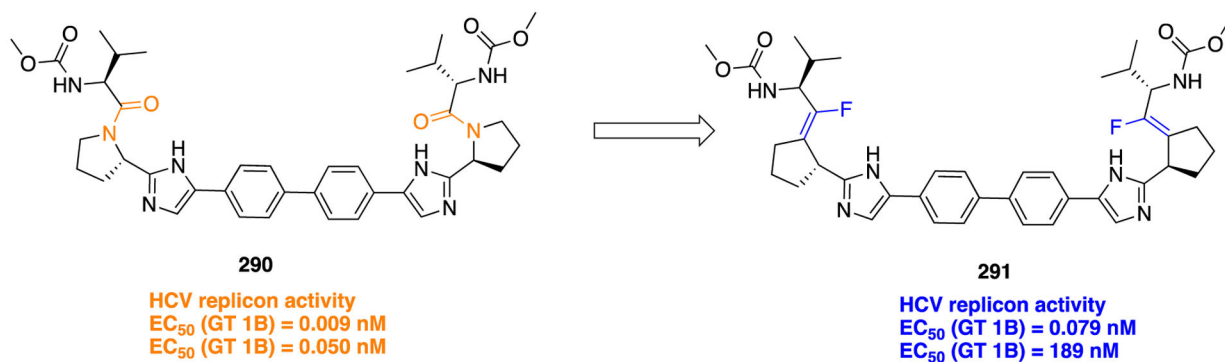


Figure 74.
Bioisosteric replacement of the amide function in daclatasvir, **290**, with a fluoro-olefin moiety to yield **291**.

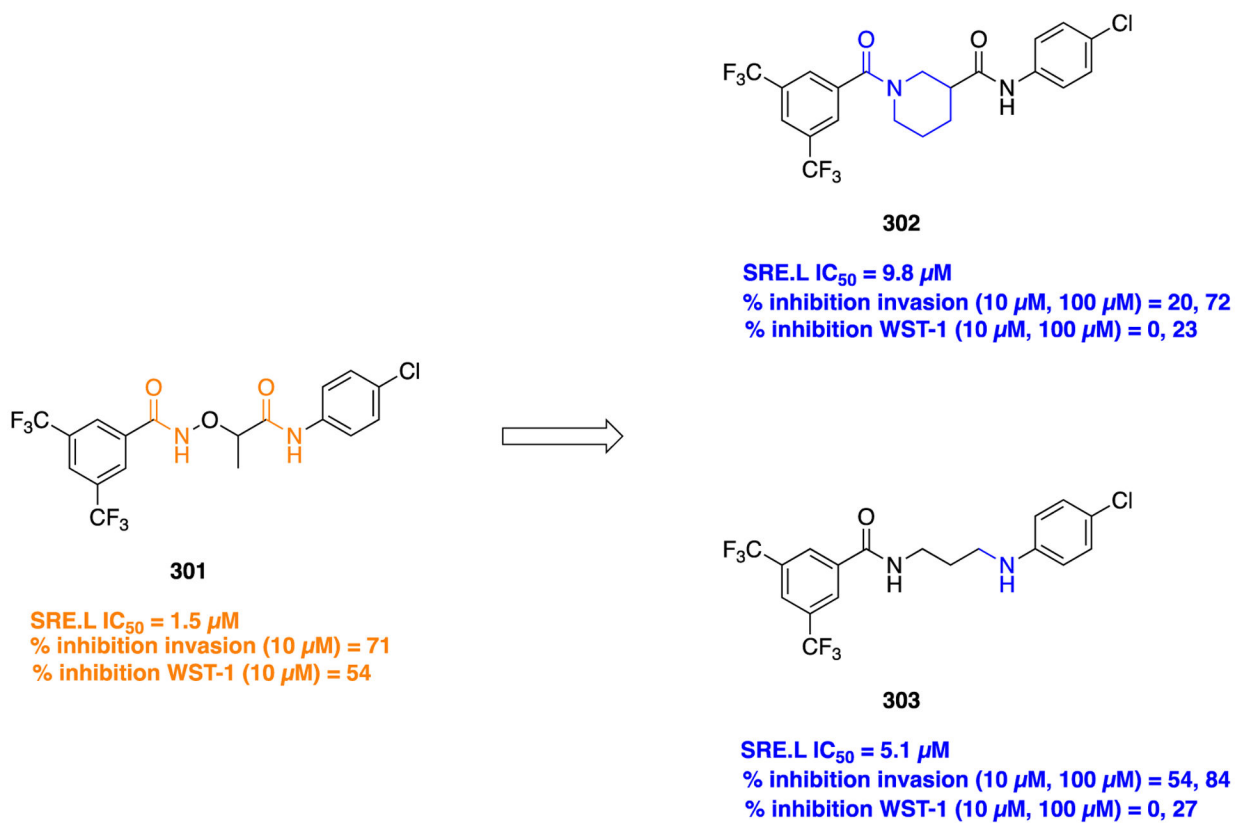


Figure 75.
 Inhibitor of Rho/MLK1 transcriptional pathway **301** and analogs with amide bioisosteric replacements **302** and **303**.

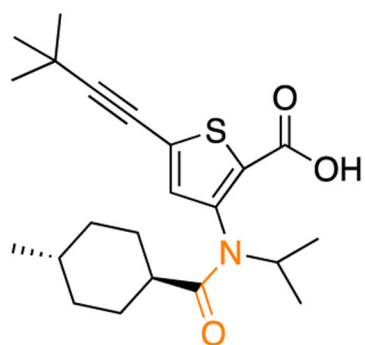
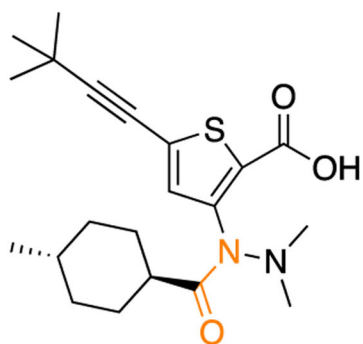
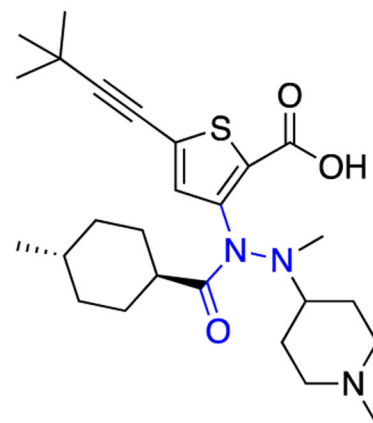
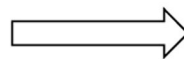
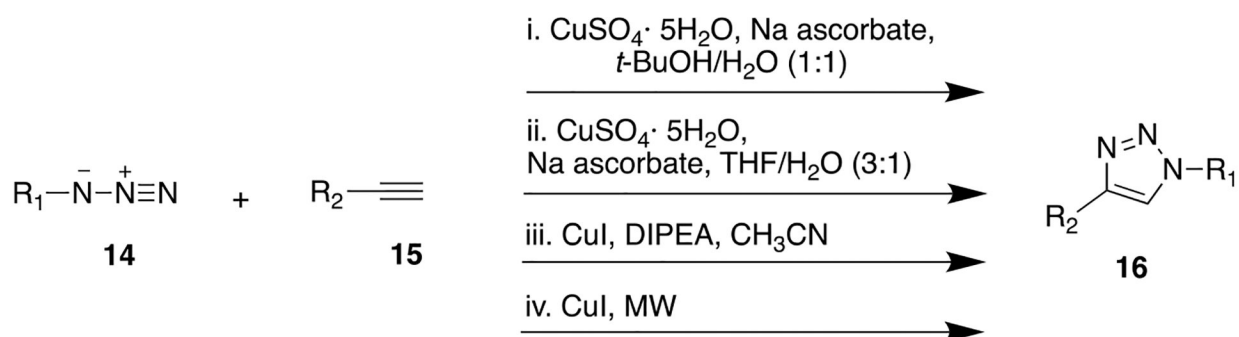
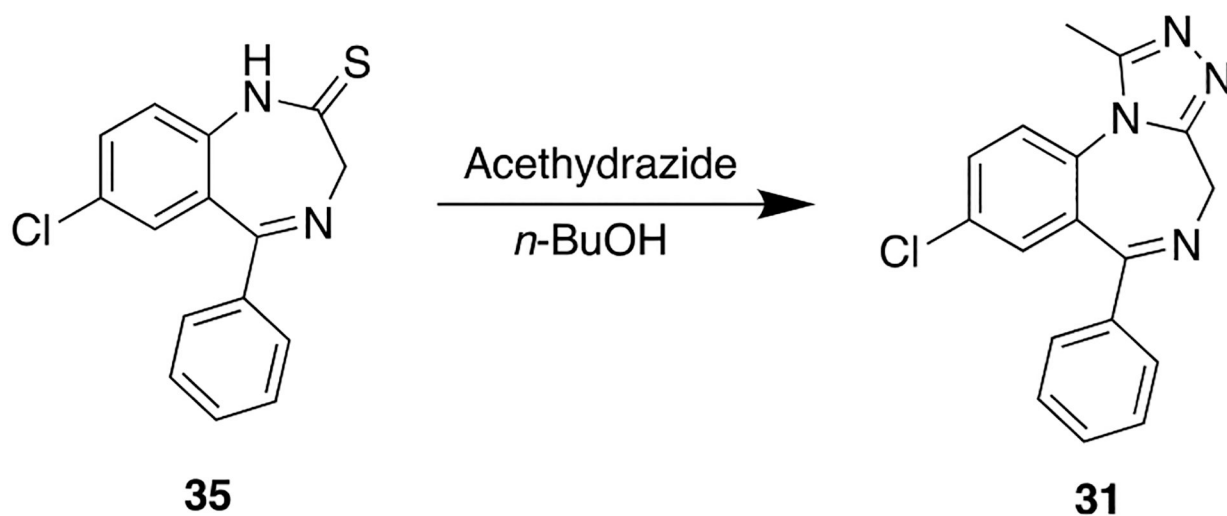
**306****NS5B IC₅₀ = 0.086 μM****307****NS5B IC₅₀ = 0.088 μM****308****NS5B IC₅₀ = 0.063 μM**

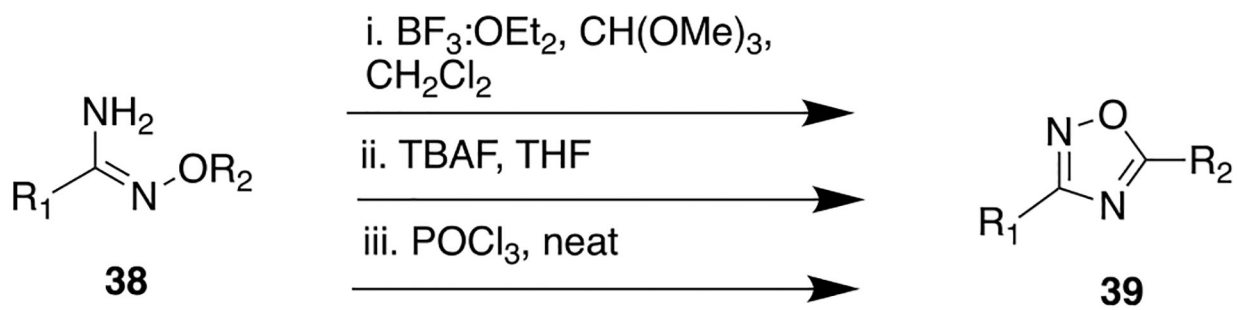
Figure 76.
Trisubstituted acylhydrazine as a tertiary amide bioisostere.

**Scheme 1.**

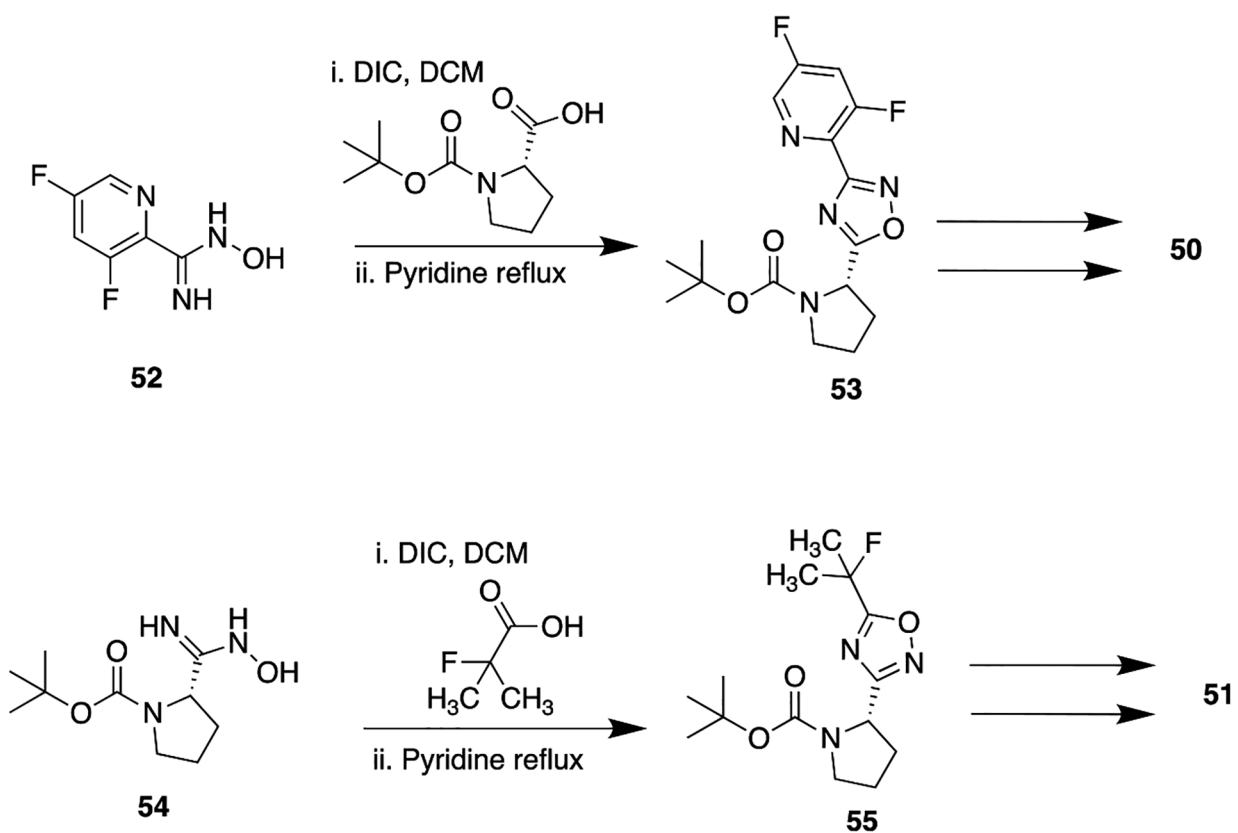
General Synthetic Pathway To Access Triazole Scaffold via Copper(I)-Catalyzed Azide-Alkyne Cycloaddition Click Chemistry

**Scheme 2.**

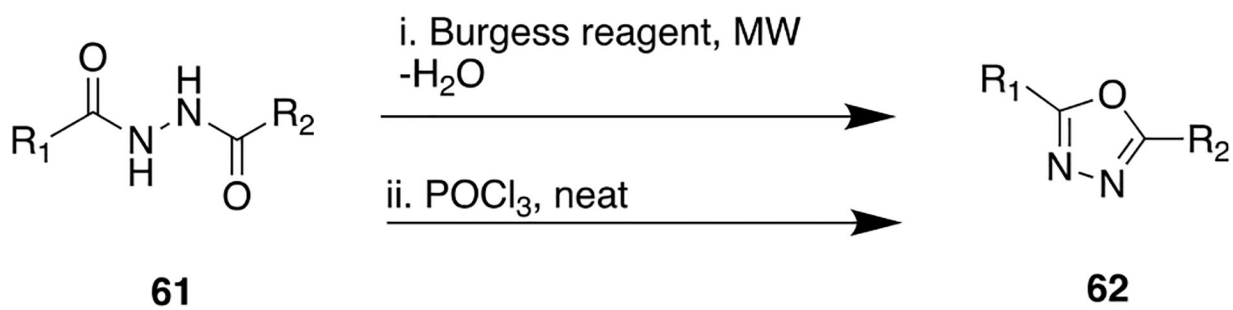
Synthesis of the Benzodiazepine Compound Alprazolam (31) from 7-Chloro-5-phenyl-1,3-dihydro-2*H*-benzo[*e*][1,4]diazepine-2-thione (35)

**Scheme 3.**

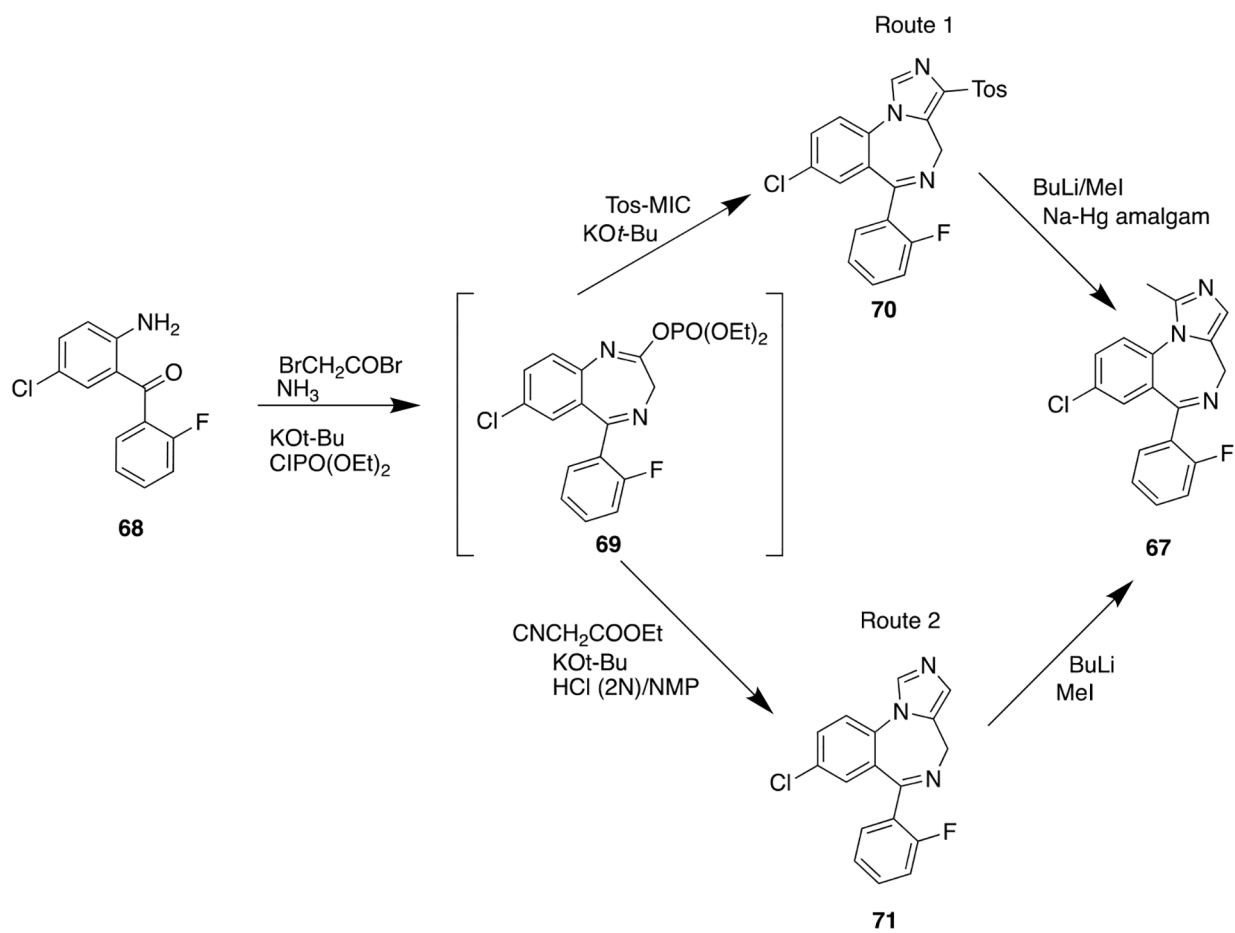
General Synthetic Route To Obtain the 1,2,4-Oxadiazole Moiety from an Amidoxime



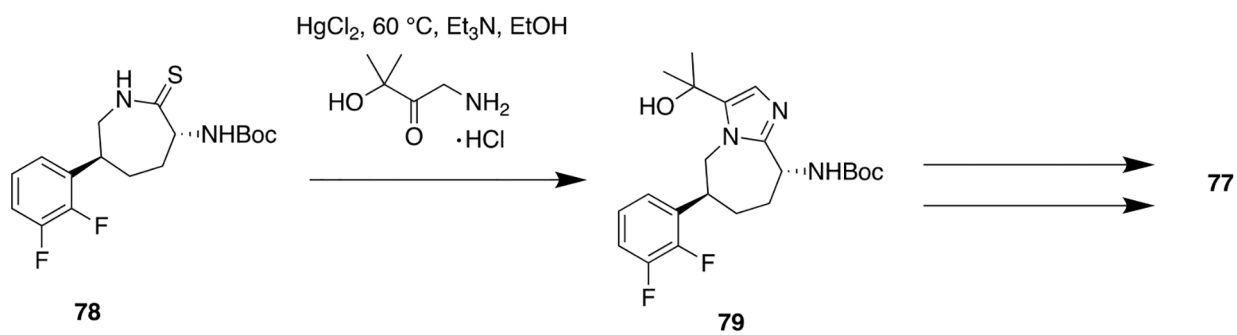
Scheme 5.
Synthetic Preparation of 50 and 51, Potent DPP Inhibitors



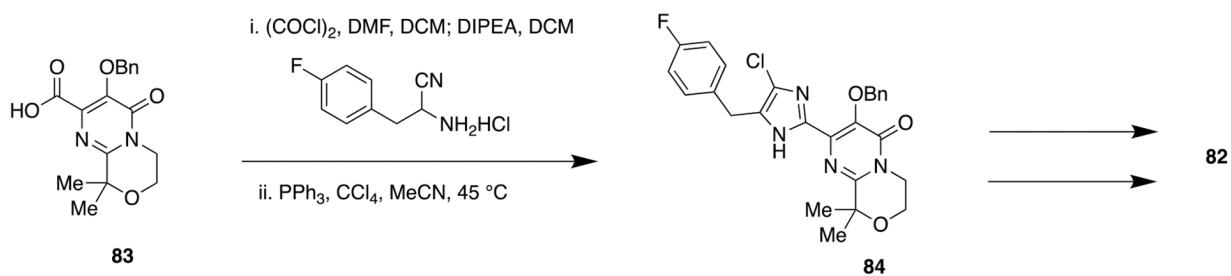
Scheme 6.
General Synthetic Route for Preparing 1,3,4-Oxadiazole from Diacylhydrazine



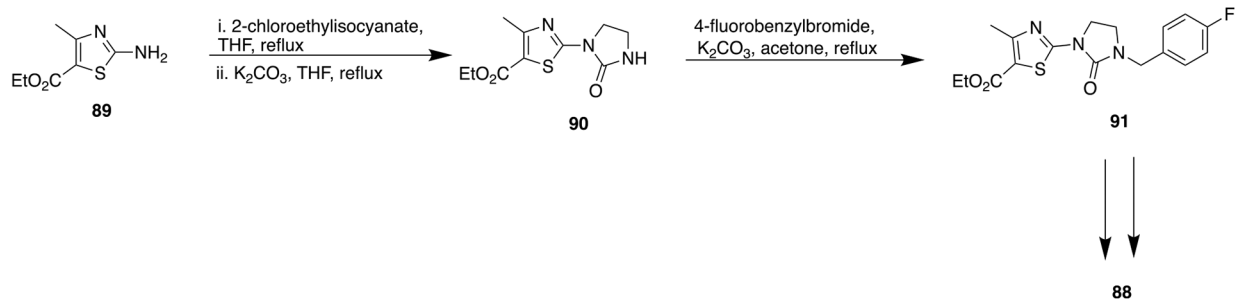
Scheme 7.
One-Pot Synthesis of Midazolam, 67, a Short Acting Benzodiazepine



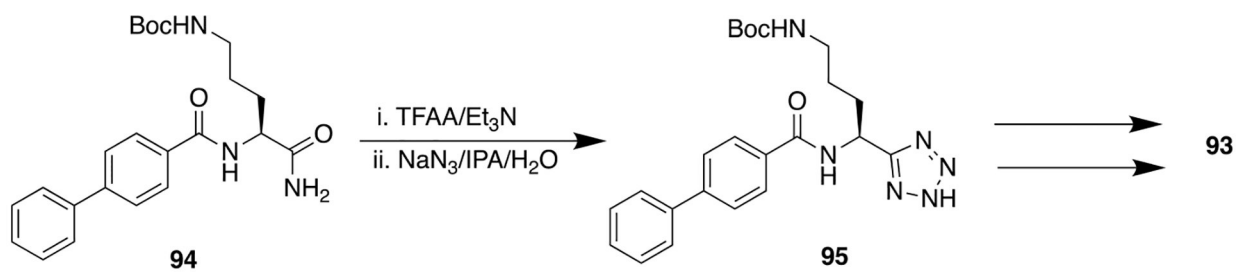
Scheme 8.
Synthetic Route for Compound 77

**Scheme 9.**

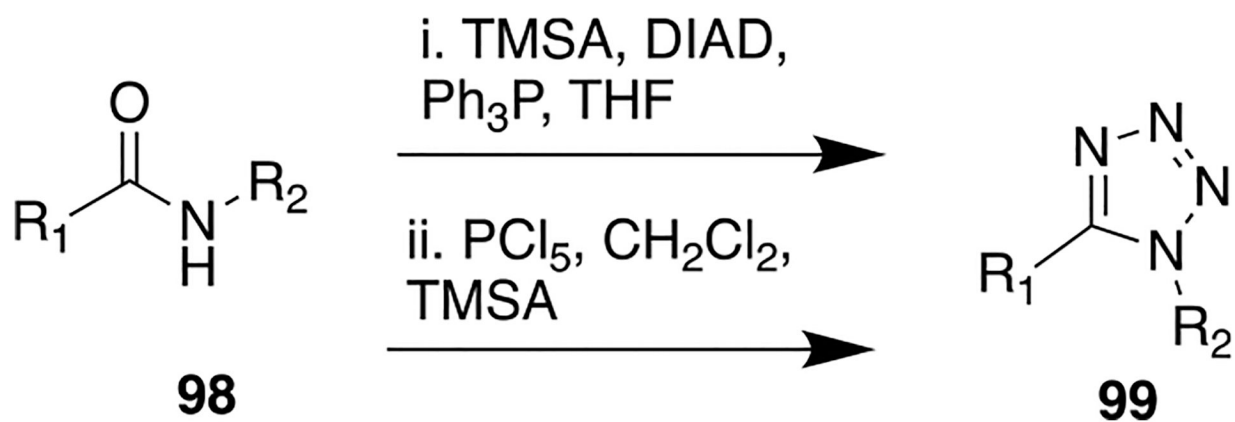
Synthetic Route To Access Imidazole Pyrimidinedione-Containing Derivative 82



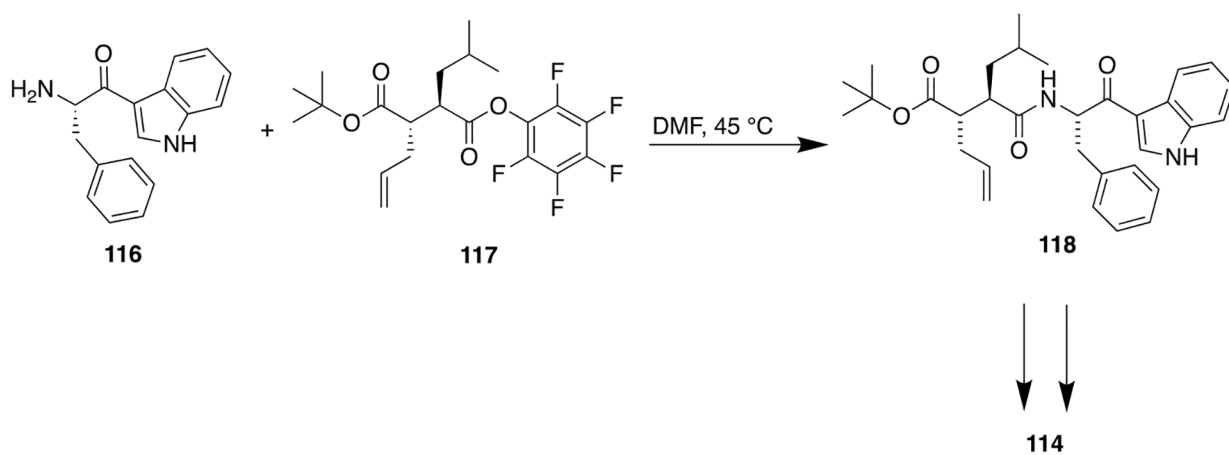
Scheme 10.
Synthetic Route for Compound 88



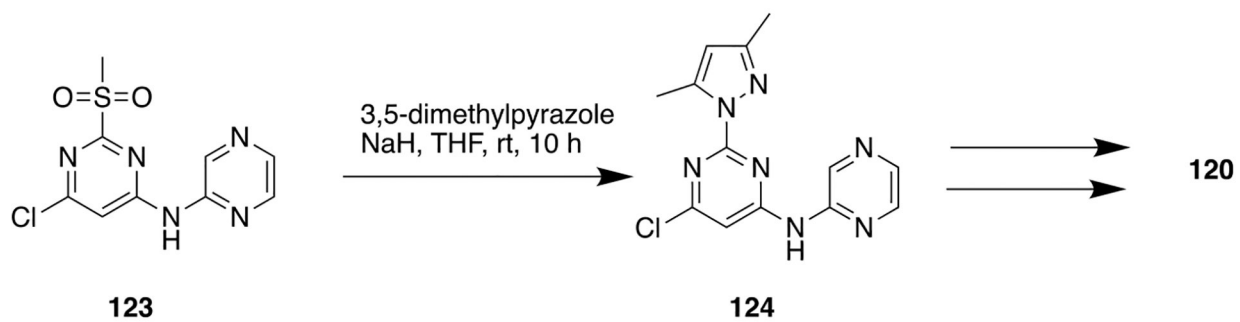
Scheme 11.
Synthetic Route To Access the Biphenyl Tetrazole *tert*-Butyl Cl-amidine-Containing PAD Inhibitor 93



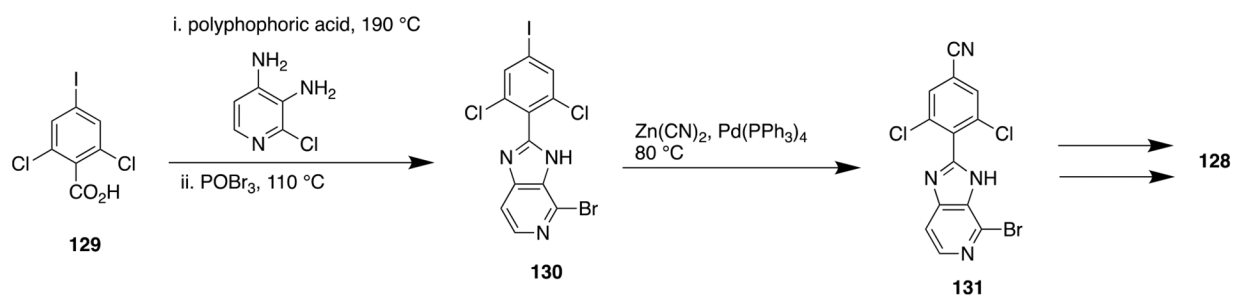
Scheme 12.
General Synthetic Route To Access Tetrazole, Nonclassical Amide Bioisostere



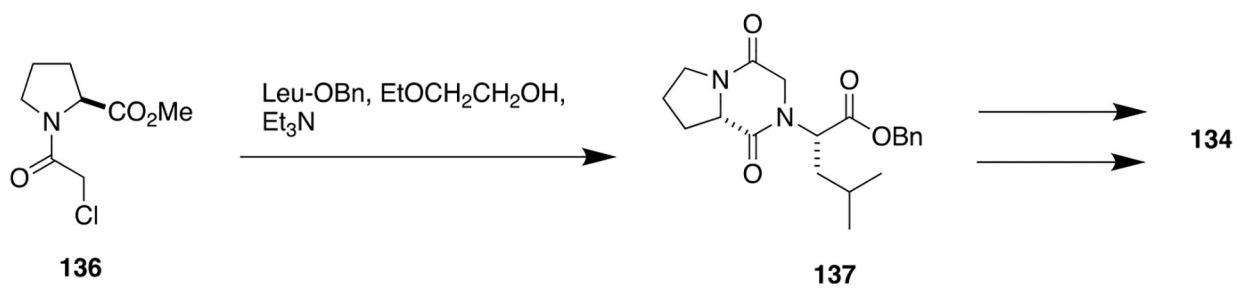
Scheme 13.
Synthesis of Indole Bioisostere 114, a Potent MMP Inhibitor



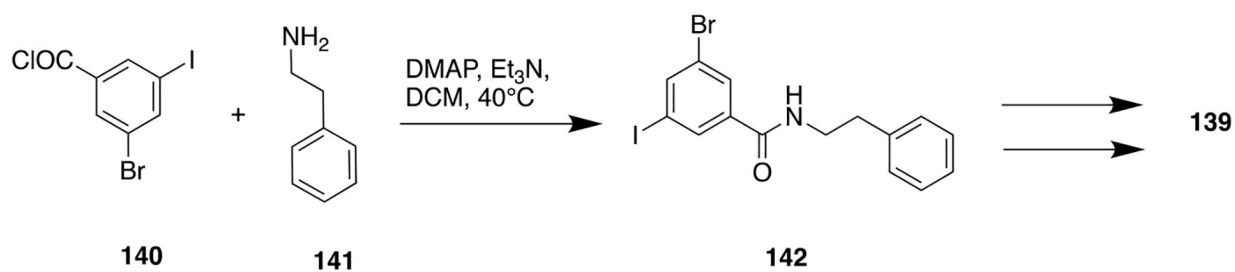
Scheme 14.
Synthetic Route for Obtaining the Pyrazine Bioisostere 120, a Potent A_{2A} Receptor Antagonist



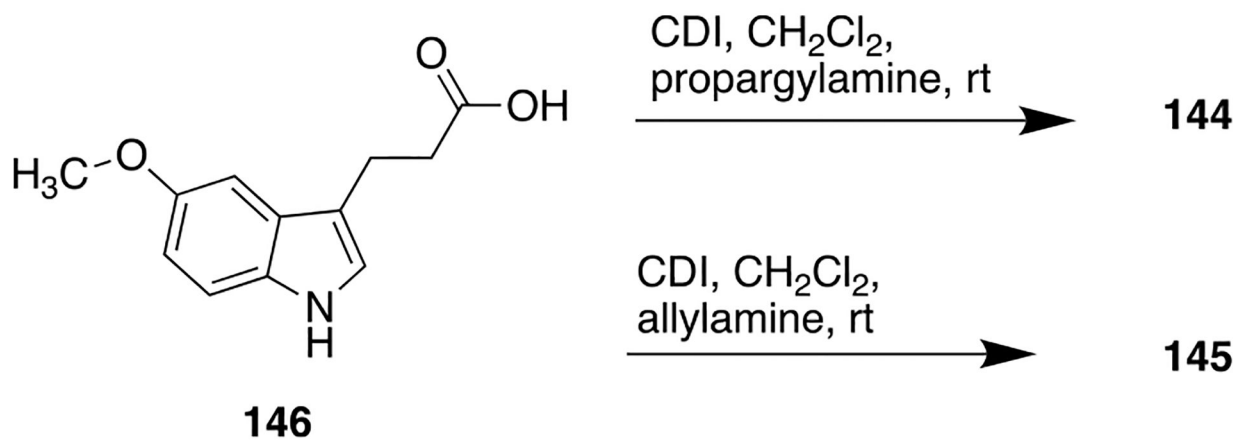
Scheme 15.
Synthetic Route To Obtain Compound 128, a Potent TYR2 Inhibitor

**Scheme 16.**

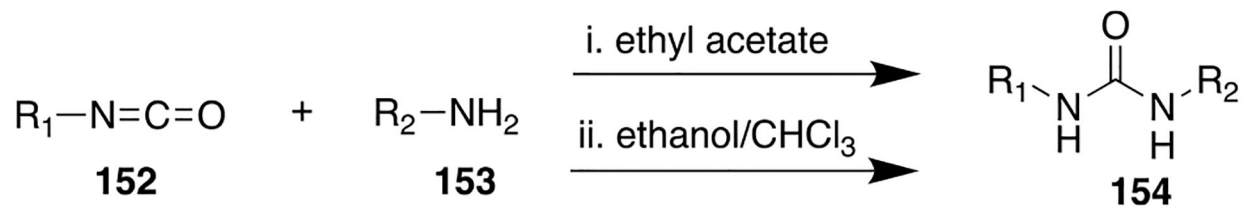
Diketopiperazine Bioisostere Synthesis from l-Proline To Obtain Compound 134

**Scheme 17.**

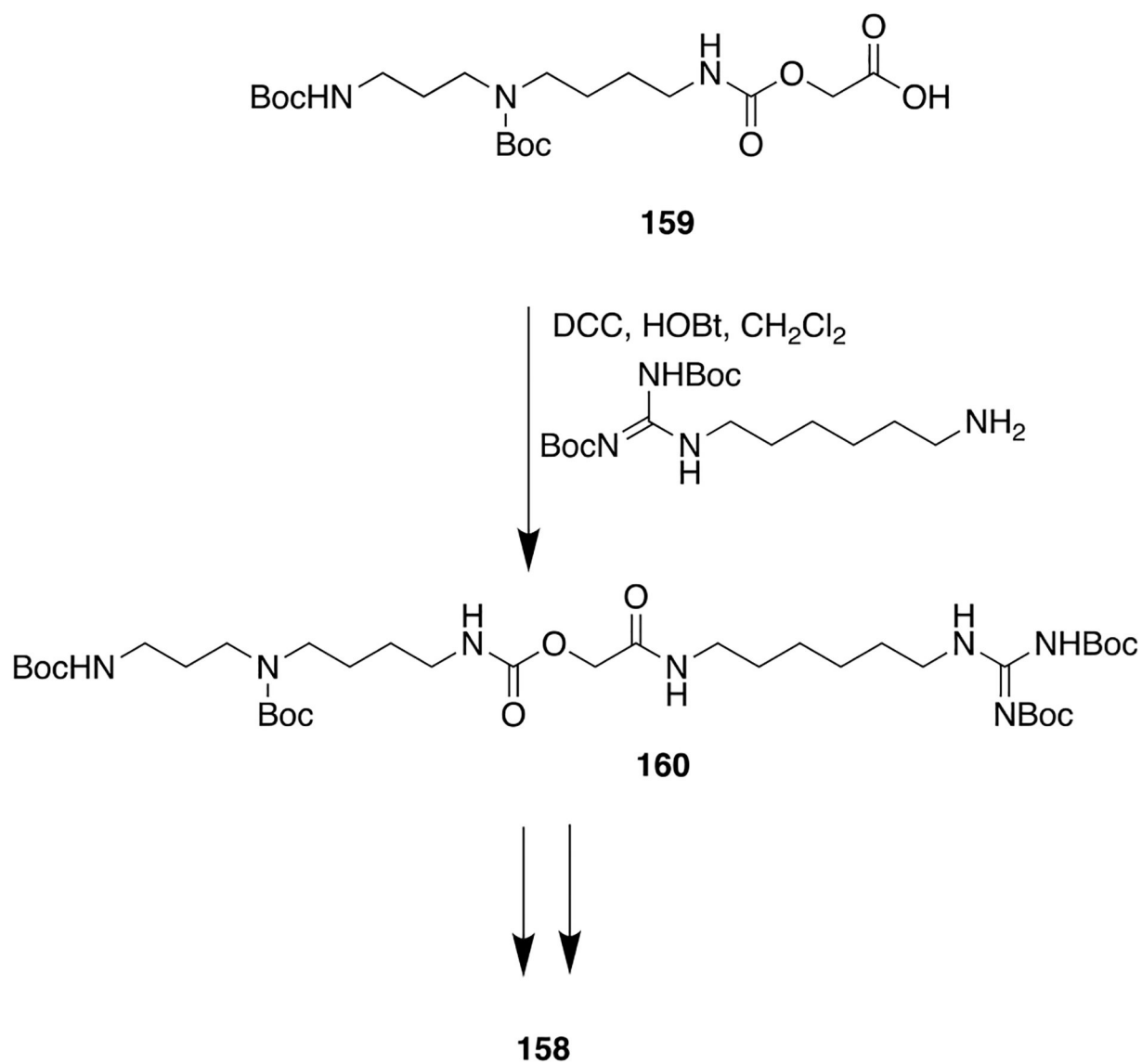
Synthetic Route To Access the Potent and Highly Selective AKR1C3 Inhibitor 139

**Scheme 18.**

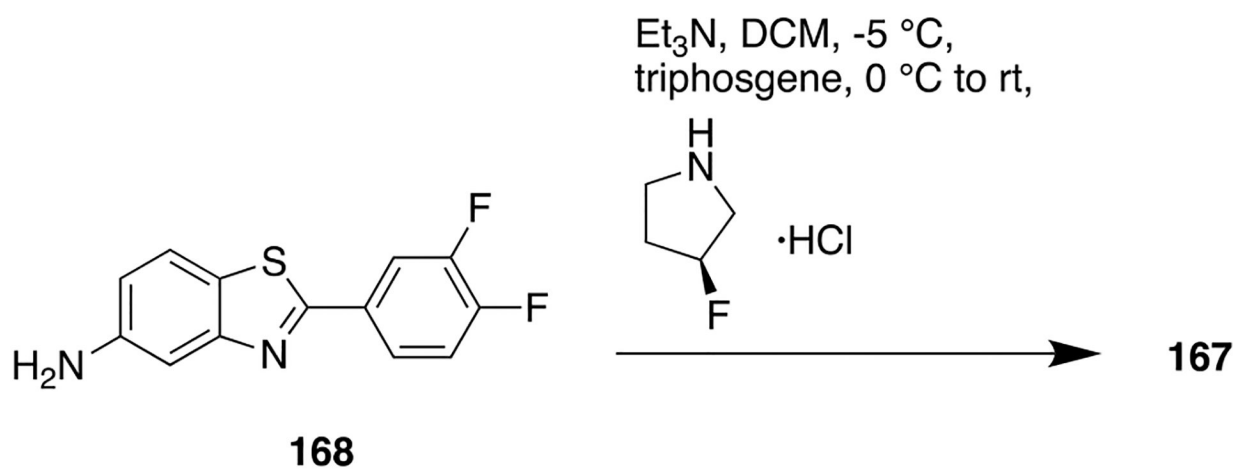
Synthetic Preparation of the Melatonin-Based Compounds 144 and 145



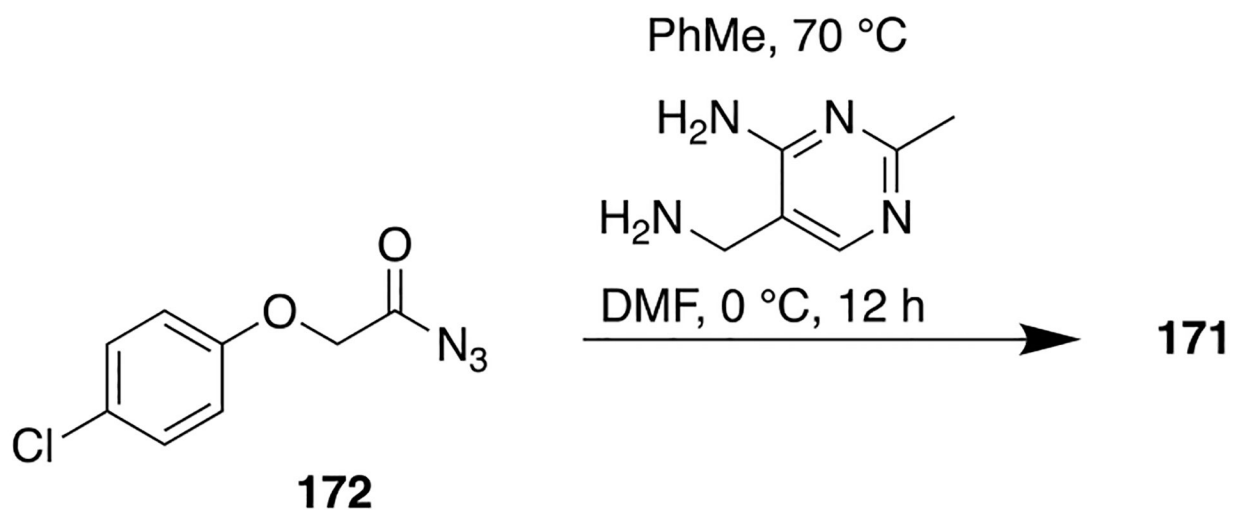
Scheme 19.
General Synthetic Route To Prepare Urea Bioisostere via Isocyanate

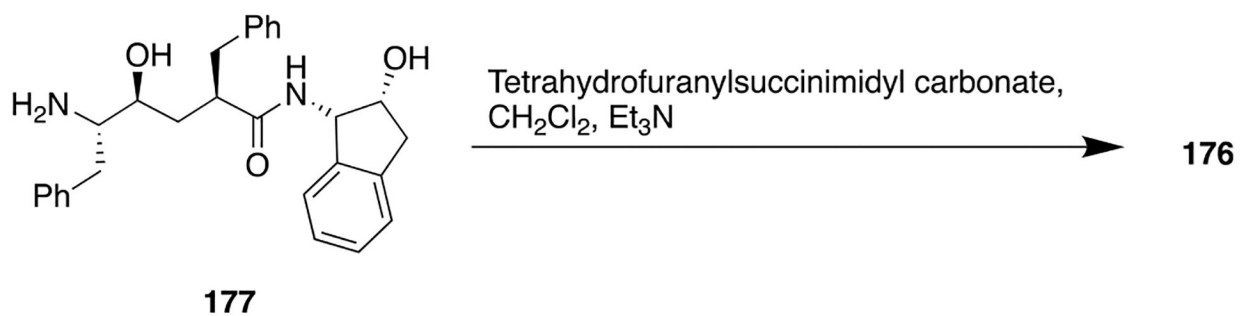


Scheme 20.
Synthetic Procedure To Access 158, a Potent Immunosuppressor

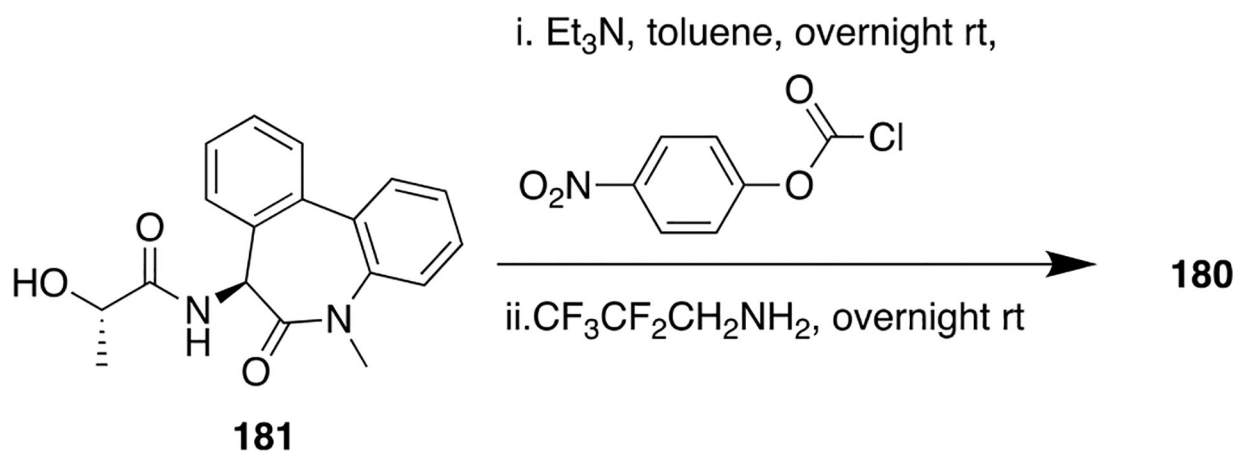
**Scheme 21.**

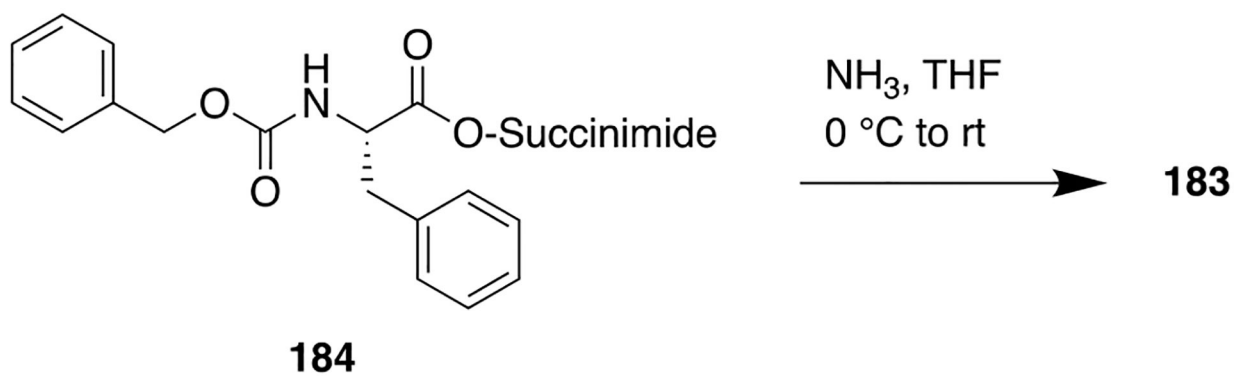
Synthesis of 167, a Novel and Potential Drug for Human African Trypanosomiasis

**Scheme 22.**Synthetic Route To Access the Potent Urea Derivative 171, an *E. coli* PDHc-E1 Inhibitor

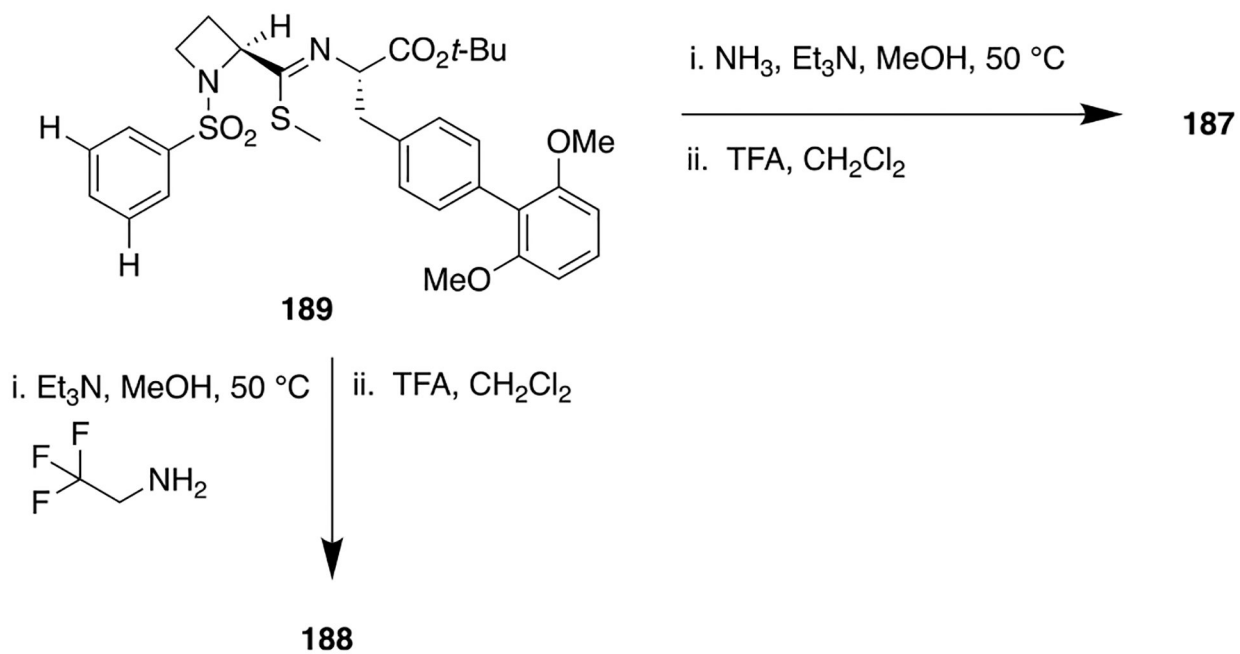
**Scheme 23.**

Synthetic Route To Access 3-(*S*)-Tetrahydrofuranylurethane-Containing Analog 176, a Potent HIV-1 Protease Inhibitor

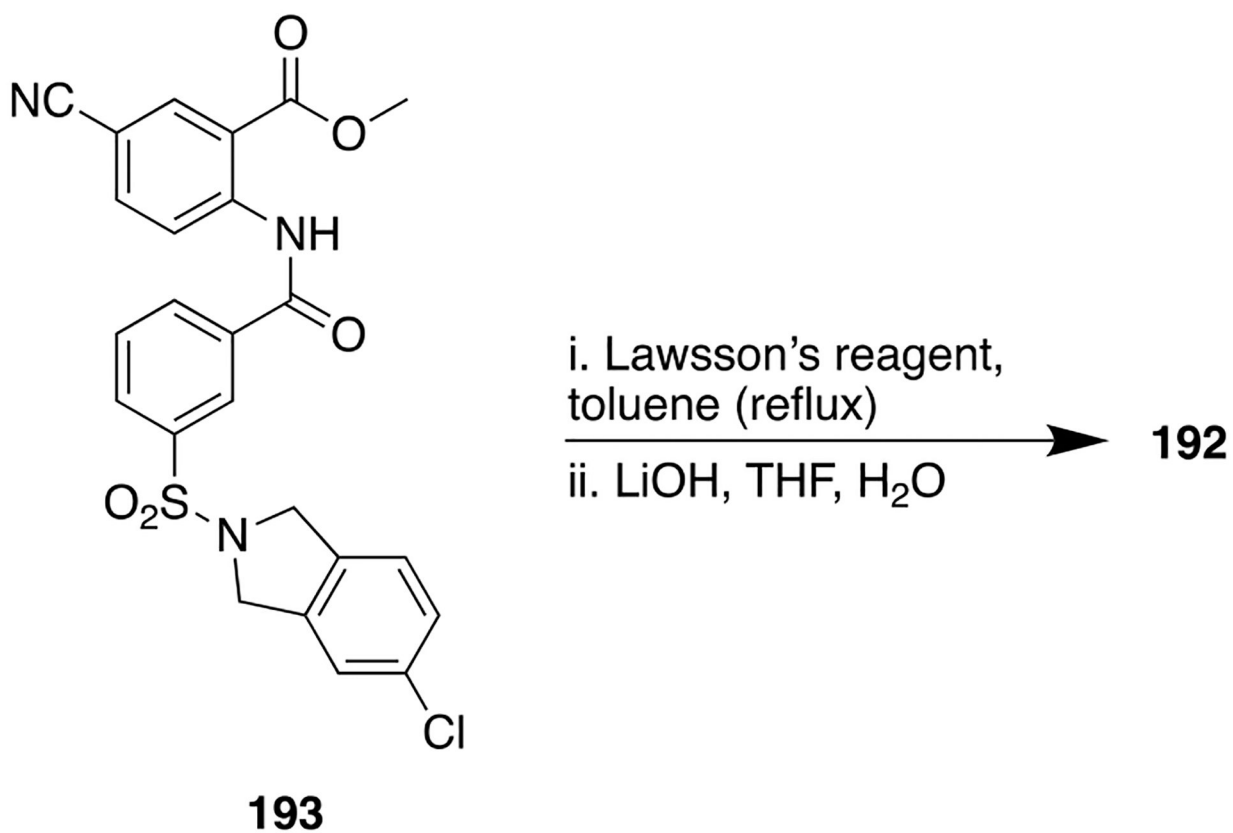
**Scheme 24.**Synthetic Route To Access the Dibenzazepinone-Based γ -Secretase Inhibitor 180



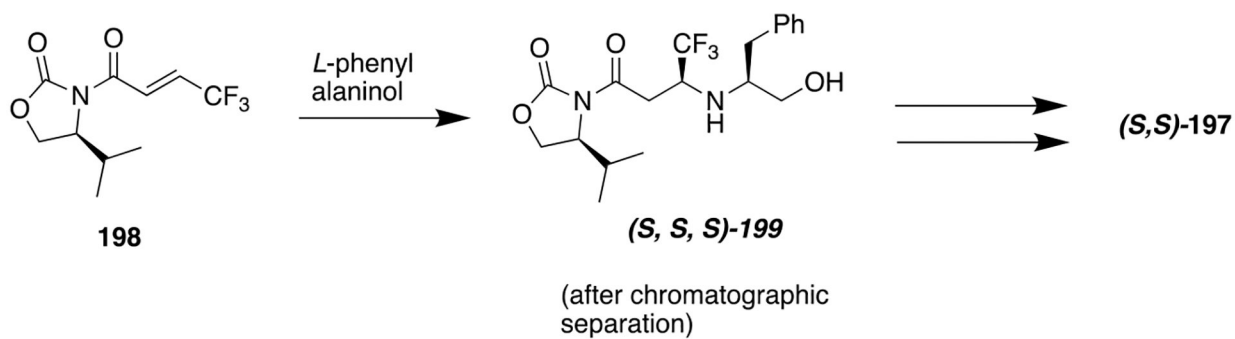
Scheme 25.
Synthetic Route To a Carbamate-Based Dipeptide SP_{1-7} Analog (183)

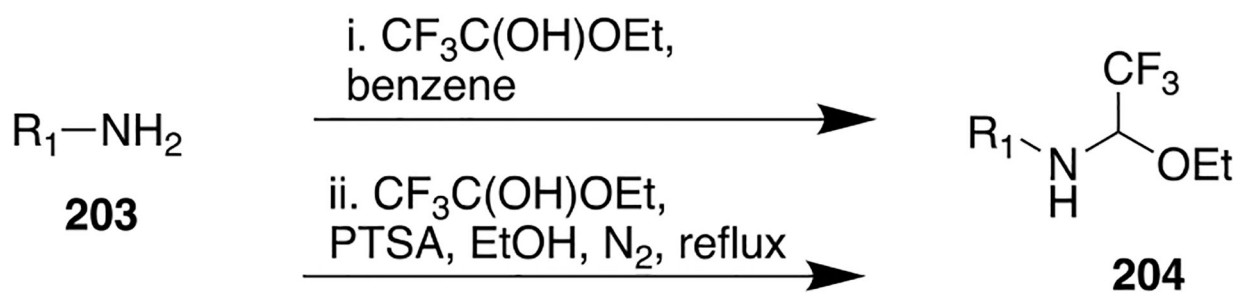


Scheme 26.
Synthetic Route To Access Amidine Derivatives as VLA-4 Antagonists

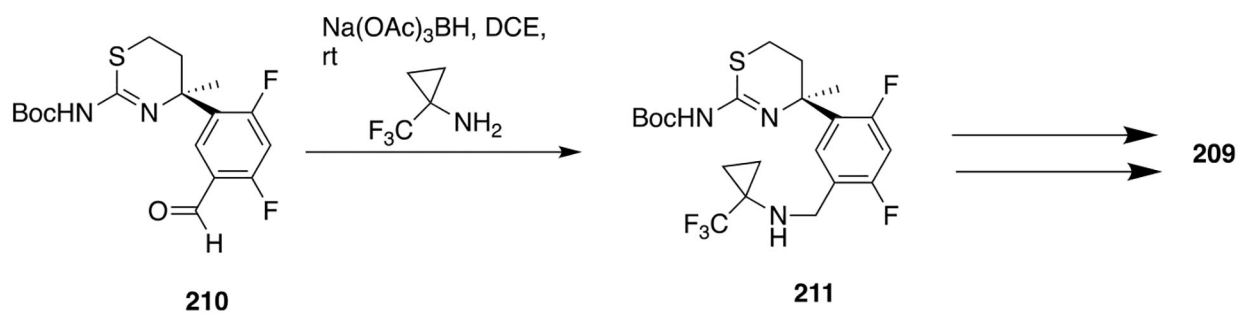


Scheme 27.
Synthetic Route To Access Thioamide 192

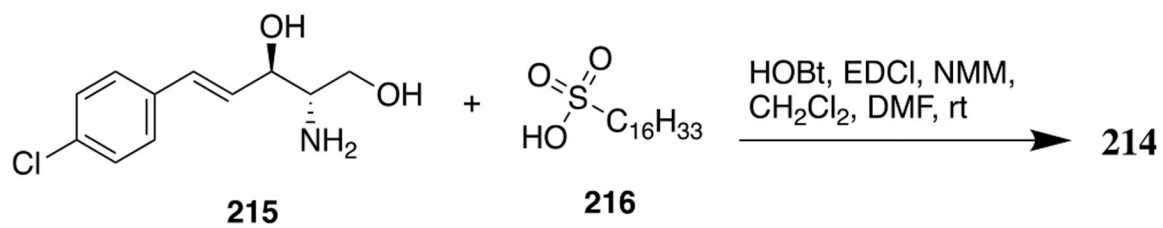
**Scheme 28.**Synthesis Route To Access Ψ [NHCH(CF₃)]-retro-thiorphan 197

**Scheme 29.**

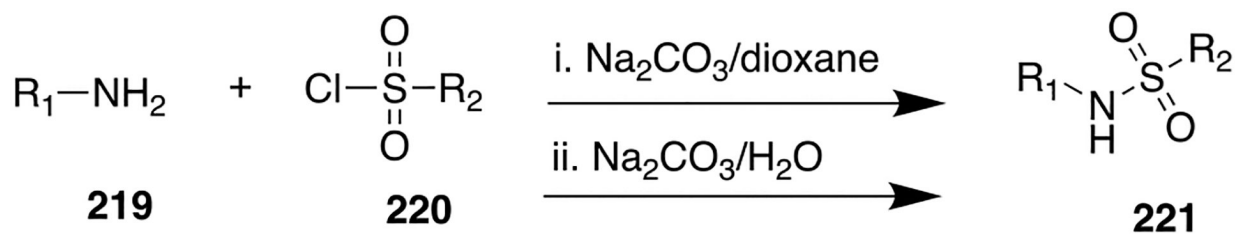
General Synthetic Route To Generate Trifluoroethylamine Bioisostere via a Trifluoroacetaldehyde Ethyl Hemiacetal



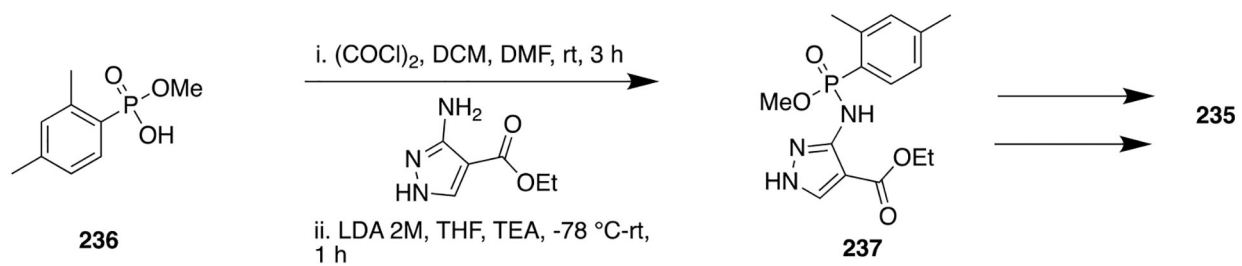
Scheme 30.
Synthetic Route To Access Compound 209, a BACE-1 Inhibitor

**Scheme 31.**

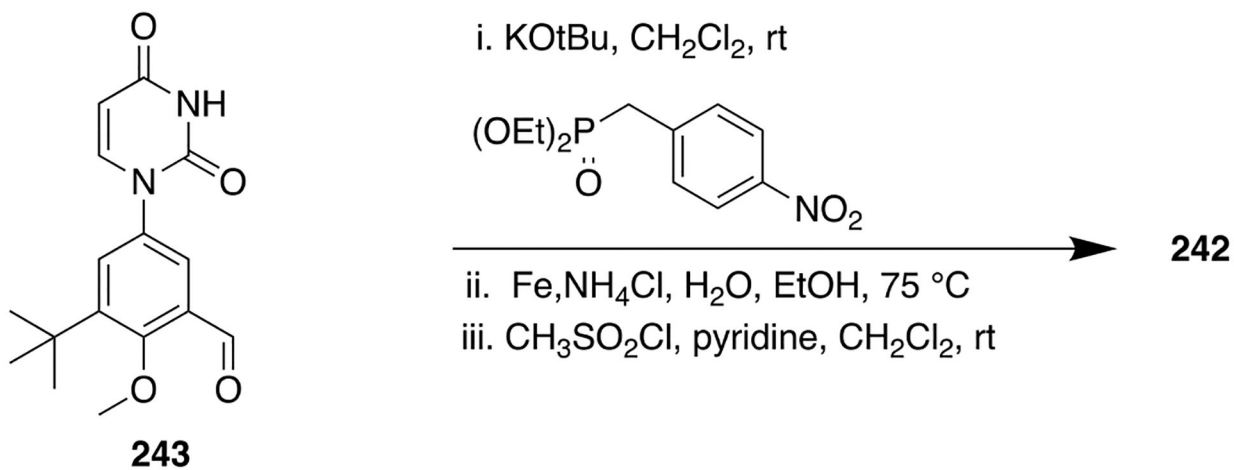
Synthetic Route To Access the Aromatic Alkyl Sulfonamido Ceramide Analog 214



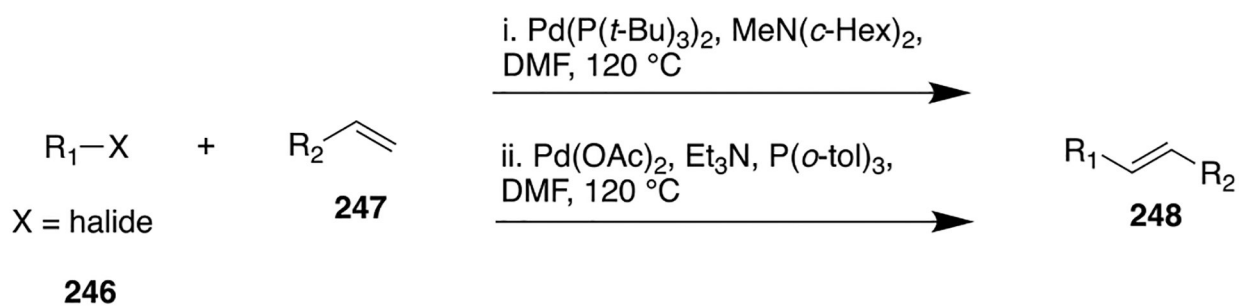
Scheme 32.
General Synthetic Procedure To Obtain Sulfonamide Bioisostere



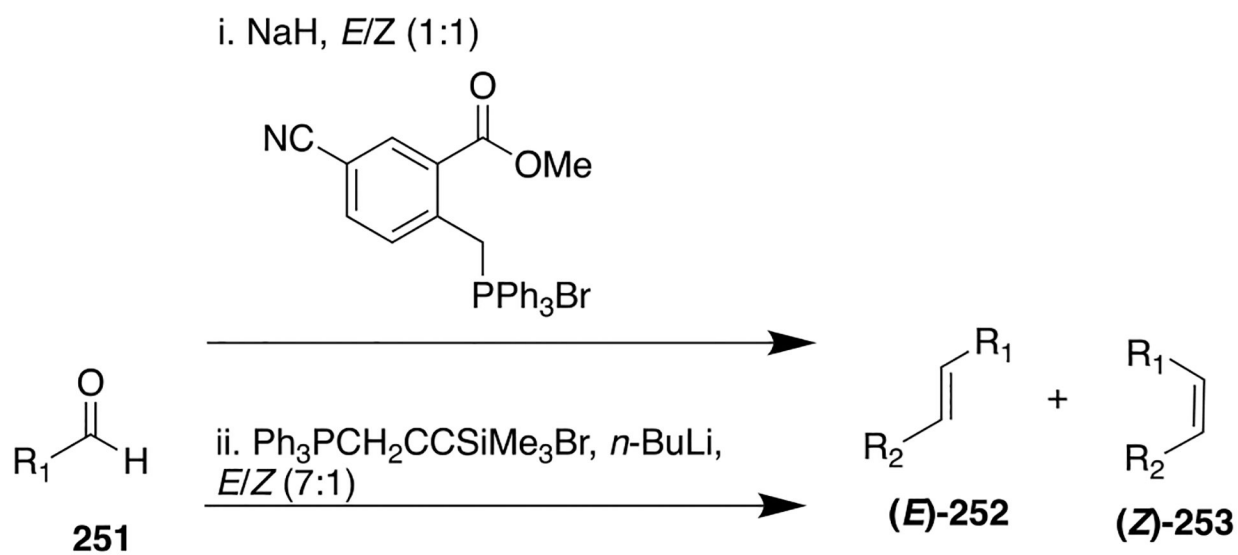
Scheme 33.
Synthetic Route To Access 235

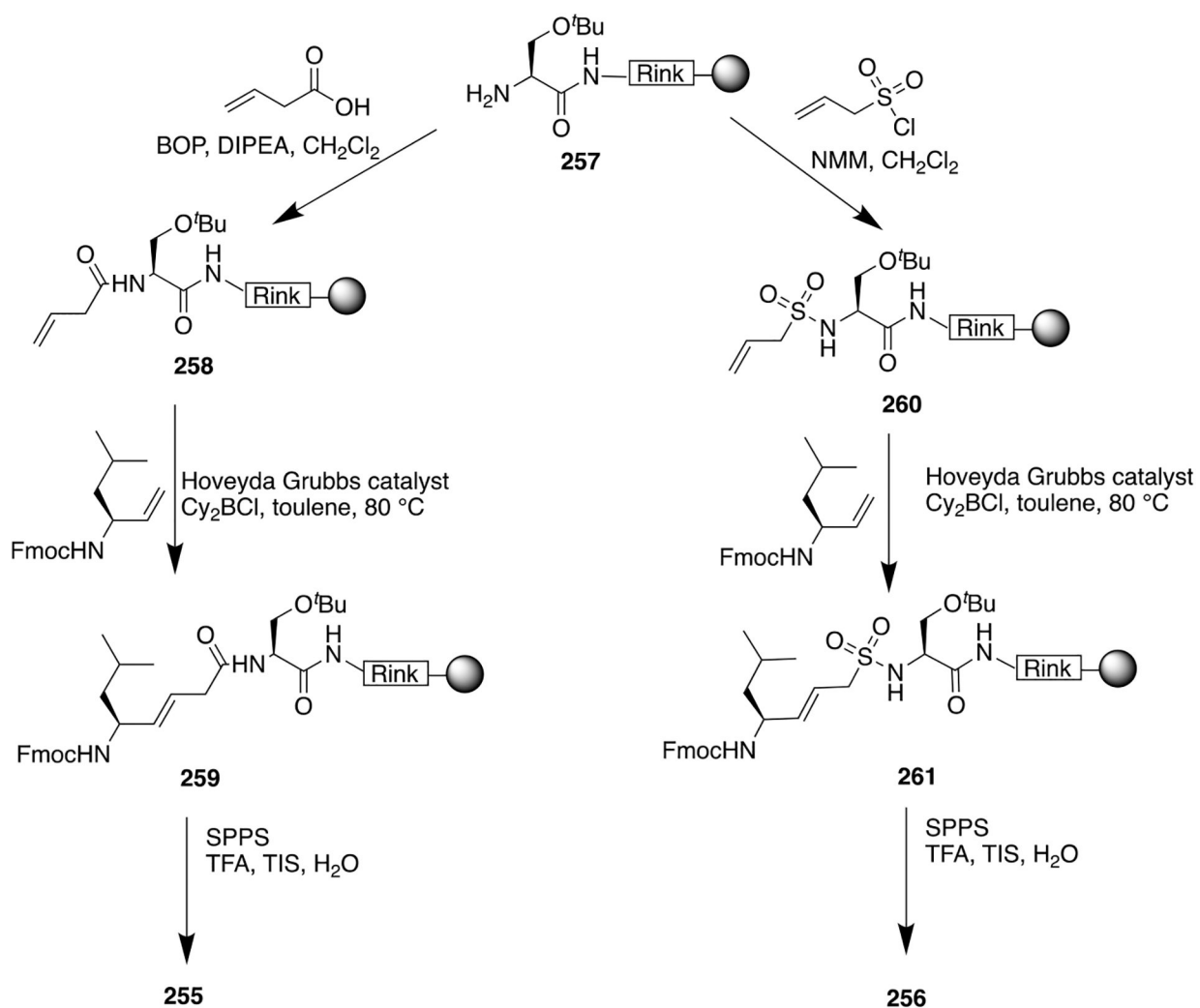
**Scheme 34.**

Synthetic Route To Access 242, a Non-Nucleoside HCV NS5B Polymerase Inhibitor

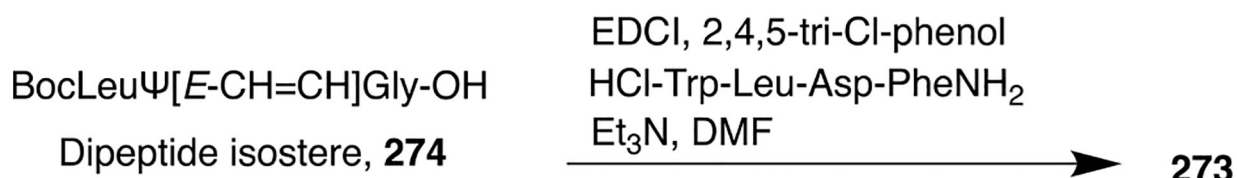


Scheme 35.
General Synthetic Route To Access Alkene Bioisosteres

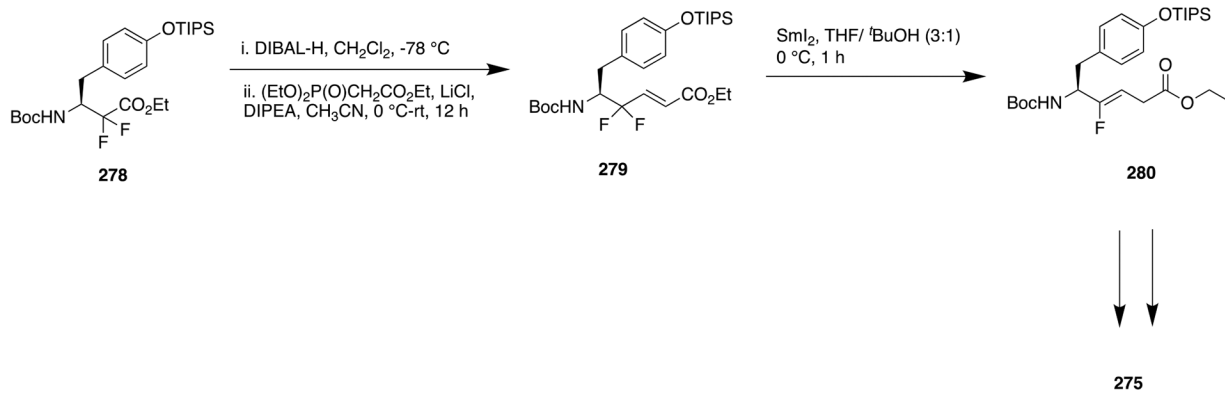
**Scheme 36.**General Synthesis of *E*-Alkene Bioisosteres from Respective Aldehyde



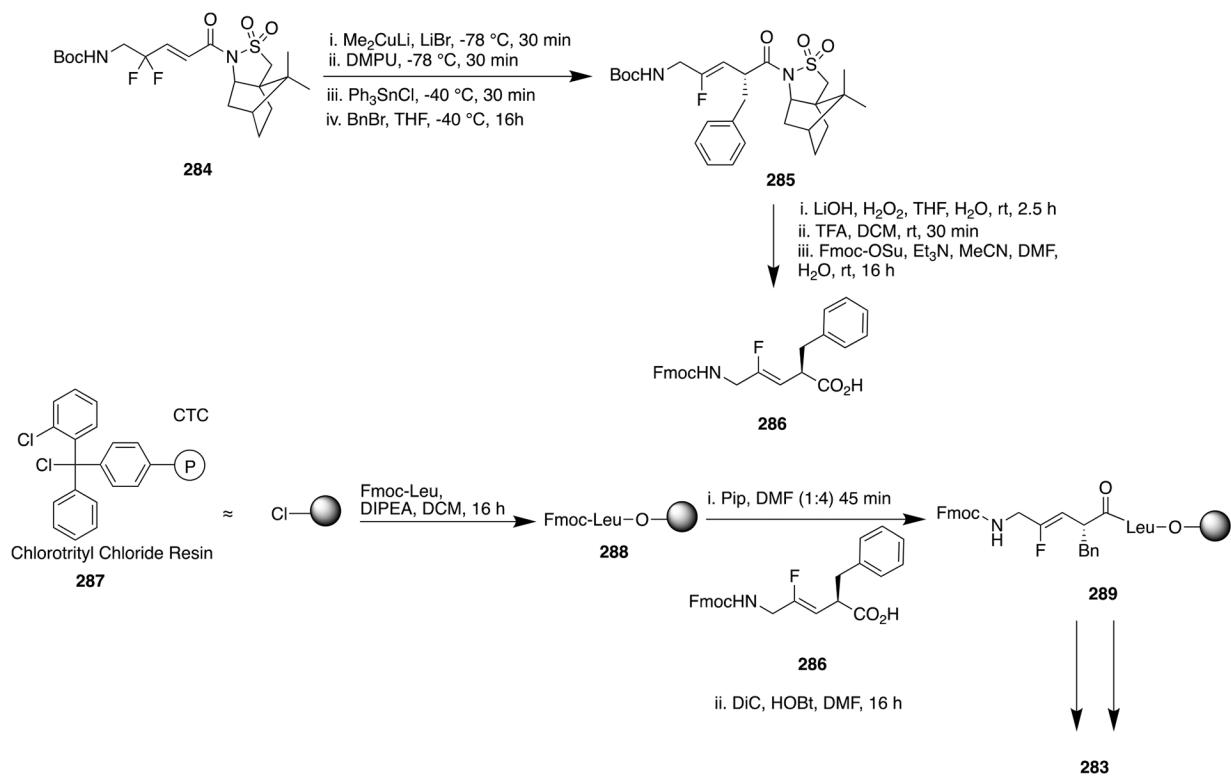
Scheme 37.
Solid Phase Synthesis of an Alkene Dipeptide (255) and Alkene Dipeptidosulfonamide
Isostere (256)

**Scheme 38.**

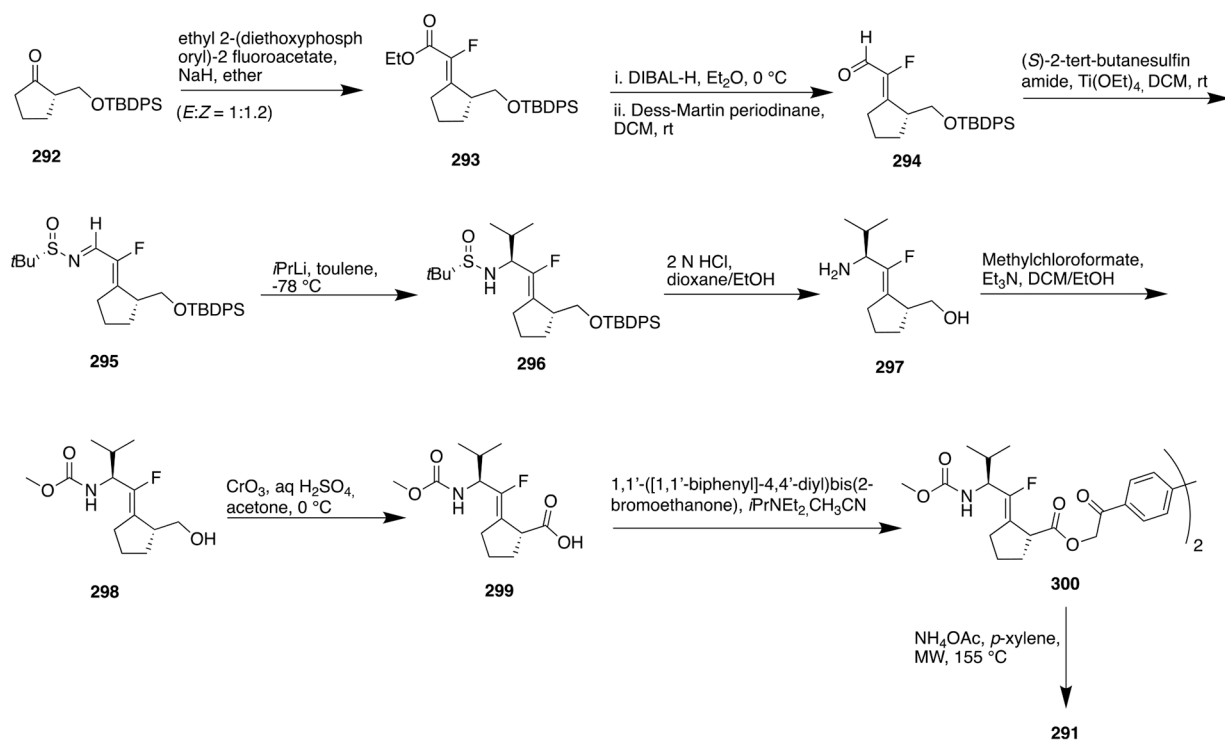
Synthetic Route Showing the Peptide Coupling of the Dipeptide Isostere with CCK
Fragment To Obtain Target Pseudopeptide 273



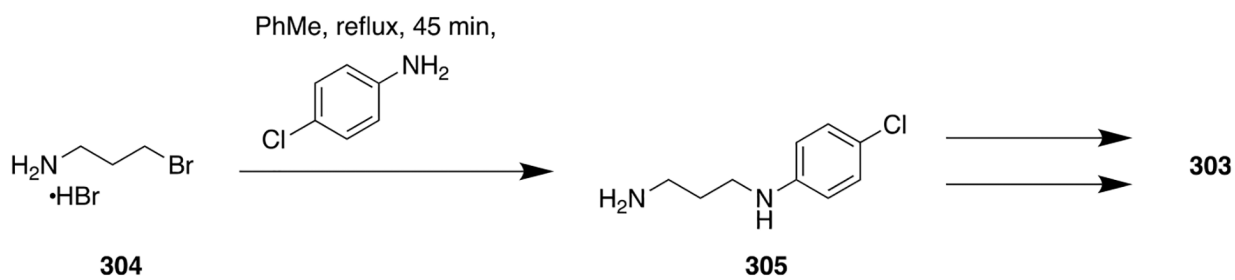
Scheme 39.
Synthetic Route To Access Leu-enkephalin Analog 275

**Scheme 40.**

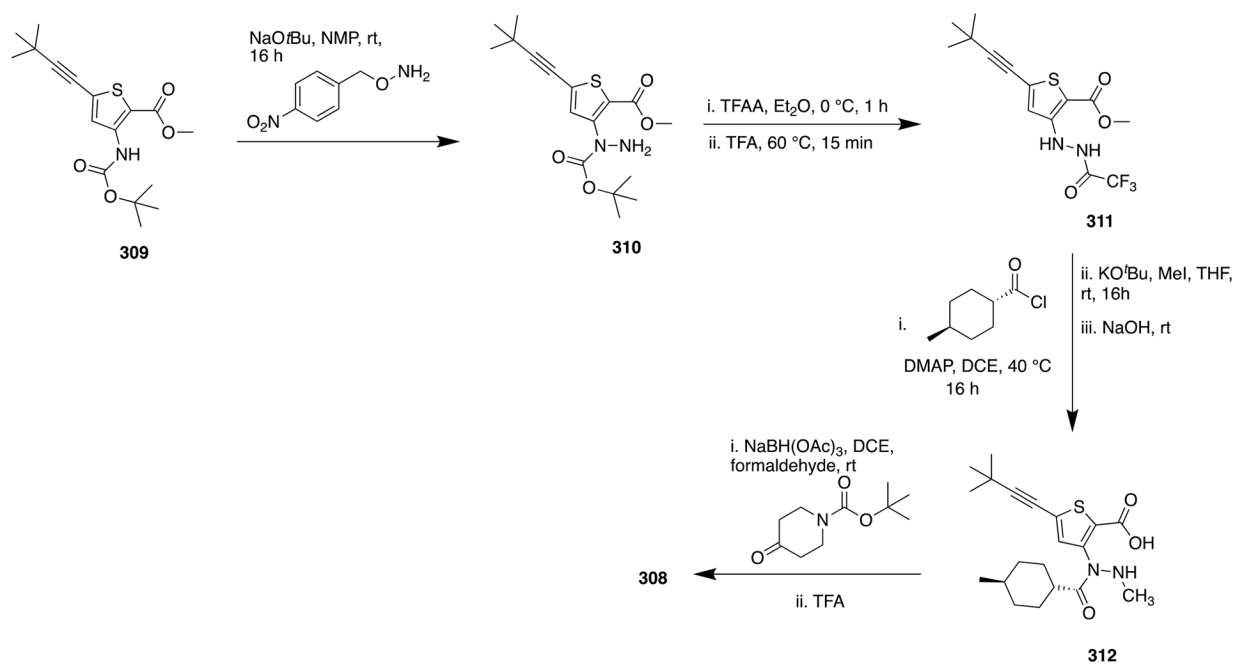
Synthetic Pathway To Obtain the Fluoroalkene Peptidomimetic Compound 283



Scheme 41.
Diastereoselective Synthesis of Fluoro-olefin Analog 291 by Chang and Co-workers

**Scheme 42.**

Synthetic Access To Amide Bioisostere Analog 303 of a Rho/MLK1 Transcriptional Pathway Inhibitor 301



Scheme 43.
Synthetic Route To Access 308, a HCV NS5B Thumb Site II Inhibitor








Table 1.



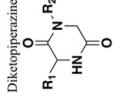






Classification of Classical and Nonclassical Bioisosteres

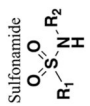
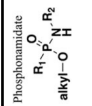
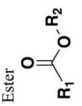
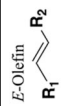
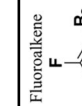
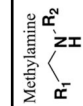
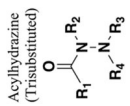
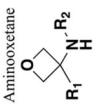
Classical bioisosteres	Nonclassical bioisosteres
<p>a. Monovalent atoms or groups F and H; D and H; NH and OH; C and Si; RSH and ROH; -F; -Cl; -Br; -I; -OH; -OR; -SH; -PH₂; -CH₃; -CF₃; -NH₂</p> <p>b. Divalent atoms or groups -O; -Se; -CH₂; -C≡N; -C≡S; -C≡C; -C≡O; -C≡NH; -COOR; -COSR; -CONHR; -COCH₂R</p> <p>c. Trivalent atoms or groups -As≡; -N≡; -P≡; -CH≡</p> <p>d. Tetravalent atoms or groups ≡C≡; ≡Si≡; ≡As⁺≡; ≡N⁺≡; ≡P⁺≡</p> <p>e. Ring equivalents benzene; tetrahydrofuran; thiophene; pyridine</p>	<p>a. Rings versus acyclic structures; Methyleneaminoxy methyl moiety (C=NOCH₂, MAOMM) as a bioisostere of aryl and other aromatic scaffold.</p> <p>b. Exchangeable groups, hydroxyl group bioisosteres, carbonyl group bioisosteres, amide group bioisosteres, thiourea group bioisosteres, halogen group bioisosteres, carboxylate group bioisosteres</p>

Table 2.

Summary of the Most Common Amide Bond Bioisosteres Discussed Herein, Their Physicochemical Properties, and Representative Examples of Pharmacokinetic Effects^a

Bioisostere	Physicochemical Properties Relative to Amide Bond	Representative Examples ^{1,2}	Design Considerations
 <p>Amide</p>	<p>Naturally occupies <i>trans</i> configuration. Substituent distance = 3.8–3.9 Å. Dipole moment = approx. 4 Debye. Functions as HBD and HBA. Susceptible to cleavage mediated by proteases, oxidation and hydrolysis (rate of cleavage depends on steric environment).</p>		
 <p>1,2,3-triazole</p>	<p>Mimics <i>trans</i> configuration upon 1,4-disubstitution (can mimic <i>cis</i> configuration upon 1,5-disubstitution). Substituent distance = 5.0–5.1 Å. Dipole moment = approx. 5 Debye. Functions as HBD and HBA. Resistant to cleavage mediated by proteases, oxidation and hydrolysis.</p>	<p>Removal of reactive metabolites but substantial decrease in human half-life (compare amide 30 to triazole bioisostere 31). Three-fold increase in metabolic stability (compare amide 20 with triazole bioisostere 23)</p>	<p>Increased sterics. If carbonyl of amide is a hydrogen bond acceptor the orientation of the nitrogens within the triazole alter distance and angle between donor and acceptor.</p>
 <p>Oxadiazole</p>	<p>Weak base. Functions as HBA only. Electrophilic substitution at carbon difficult. Electrophilic substitution at nitrogen possible with electron-donating group substituents. Resistant to nucleophilic attack but undergo nucleophilic substitution. Generally resistant to cleavage mediated by proteases, oxidation and hydrolysis.</p>	<p>Two-three-fold increase in clearance in a rat model (compare amide 43 to oxadiazole bioisostere 45). Reduced metabolic stability (compare amide 47 to oxadiazole bioisosteres 48 and 49).</p>	<p>Increased sterics. If amine of amide is a hydrogen bond donor this will be lost upon replacement.</p>
 <p>Imidazole</p>	<p>Mimics <i>trans</i> configuration. Functions as HBD (if nitrogen unsubstituted) and HBA. Mimics charge of amide nitrogen. Generally resistant to cleavage mediated by proteases, oxidation and hydrolysis.</p>	<p>Increased bioavailability (rat) (compare amide 72 to imidazole bioisostere 74). Retained bite angle and N-partial charge (compare amide 81 to imidazole bioisostere 82).</p>	<p>Increased sterics. If carbonyl of amide accepts two hydrogen bonds one will be lost upon replacement.</p>
 <p>Tetrazole</p>	<p>Functions as HBA only. Can mimic <i>trans</i> or <i>cis</i> configuration depending on substitution pattern. Generally resistant to cleavage mediated by proteases, oxidation and hydrolysis.</p>	102	<p>Increased sterics. If carbonyl of amide is a hydrogen bond acceptor or the amine a hydrogen bond donor these will be lost upon replacement.</p>
 <p>Pyrazole</p>	<p>Functions as a HBA and HBD (if nitrogen unsubstituted). Distance between substituents greater than in amide. Generally resistant to cleavage mediated by proteases, oxidation and hydrolysis.</p>	106	<p>Increased sterics. Increased lipophilicity. If carbonyl of amide is a hydrogen bond acceptor or the amine a hydrogen bond donor these will be lost upon replacement.</p>
 <p>1,2,4-thiadiazole</p>	<p>Functions as HBA only. Distance between substituents greater than in amide. Generally resistant to cleavage mediated by proteases, oxidation and hydrolysis.</p>	111	<p>Increased sterics. If carbonyl of amide is a hydrogen bond acceptor or the amine a hydrogen bond donor these will be lost upon replacement.</p>

Bioisostere	Physicochemical Properties Relative to Amide Bond	Representative Examples ^{1,2}	Design Considerations
3-acyl indole 	Bioisosteric with aryl amide. Much larger. HBD if nitrogen not substituted. Not a HBA as lone pair electrons involved in aromaticity.	40-fold increase in half-life and seven-fold increase in %F (compare amide 113 with 3-acyl indole bioisostere 114).	Increased sterics. Increased lipophilicity. If carbonyl of amide is a hydrogen bond acceptor this will be lost upon replacement.
Pyrazine  Constrained amide-containing cyclic systems.	Generally only bioisosteric with terminal amides. HBA only. Much larger size. Greater rigidity. Greater rigidity. Generally resistant to cleavage mediated by proteases, oxidation and hydrolysis. Provide locking of substituents into bioactive configuration.	120 Increase in target selectivity (compare amide 125 to constrained bioisostere 127).	Increased sterics. Increased charge. If carbonyl of amide accepts two hydrogen bonds one will be lost upon replacement. Increased sterics.
Diheteropyridazine 	Greater rigidity. Generally resistant to cleavage mediated by proteases, oxidation and hydrolysis. Provide locking of substituents into bioactive configuration. Ability to mimic β -turns.	134	Increased sterics. Chain length is increased by a methylene. If amine of amide is a hydrogen bond donor this will be lost upon replacement. Addition of hydrogen bond donor and acceptors maybe advantageous or deleterious to binding.
Reversed amide 	Very similar properties to amide but reversed orientation of HBD and HBA.	139	No improvement of PK properties.
Urea 	Additional HBA and HBDs. Increases solubility over equally substituted amide, especially when non-symmetrical. Extends chain length by one nitrogen group.	148	Increased length by one atom.
Carbamate 	Functions as HBD (if nitrogen unsubstituted) and HBA. Some degree of rigidity. Undergo rapid hydrolysis.	Exceptional long half-life example 180 . Reduced clearance (human microsomes) (compare amide 182 to carbamate bioisostere 183).	Little to no improvement in PK.
Amidime 	One additional HBD (if nitrogen not substituted). Greater charge. Similar distance and rotational constrictions.	Reduced plasma clearance but limited improvement of %F (amidine bioisostere 188).	Increased charged and likely reduction of BBB penetration.
Thioamide 	Thiocarbonyl bond is longer than carbonyl. C-N bond in thioamide is shorter. Increased rotational constrictions. Weak HBA, strong HBD.	192	Longer C-S bond may induce steric clash.
Trifluoromethylamine 	Reduced basicity of NH, but can HBD. Similar bond angle (120°). C-CF ₃ is isopolar with carbonyl group. Increased lipophilicity. Stereochemistry can be manipulated to enhance target binding interactions.	197	Steric effects of CF ₃ compared with O. If carbonyl of amide is a hydrogen bond acceptor this will be diminished or lost entirely upon replacement.

Bioisostere	Physicochemical Properties Relative to Amide Bond	Representative Examples ^{1,2}	Design Considerations
Sulfonamide 	Increased water solubility. Additional HBAs. No increase in chain length.	214	Increased steric bulk and chain length. Increased water solubility.
Phosphoramidate 	Increased water solubility and charge. Stereochemistry may increase (or decrease) interactions with target binding site. Additional HBAs. Metabolically labile.	233	Increased charge. Reduced cell permeability. Metabolically labile to different enzymes than amides.
Ester 	Decreased metabolic stability. Can mimic <i>cis</i> or <i>trans</i> conformation. Cannot HBD, weak HBA.	>Three-fold decrease of half-life (compare amide 239 with ester bioisostere 240).	Deteriorous to metabolic stability
<i>E</i> -Olefin 	Mimic geometry of <i>trans</i> amides. No HBAs or HBDs. Dipole moment much lower (0.1 Debye). Resistant to cleavage mediated by proteases, oxidation and hydrolysis.	Significantly increased bioavailability (compare amide 241 with <i>E</i> -olefin bioisostere 242). Significantly increased half-life (compare amide 244 with <i>E</i> -olefin bioisostere 245).	Geometric mimic only. If amide bond is engaged in binding interactions these will be lost upon replacement.
Fluoroalkene 	(<i>Z</i>)-fluoroalkene mimics the <i>s-trans</i> amide. (<i>B</i>)-fluoroalkene mimics the <i>s-cis</i> amide. Length of C-F bond (1.376 Å) is similar to carbonyl (1.228 Å). C-N and C=C bond length both approx. 1.3 Å. Fluorine has similar van der Waals radius to oxygen. Lower dipole moment (1.4 Debye). Resistant to cleavage mediated by proteases, oxidation and hydrolysis. Increased lipophilicity.	Significant increase in half-life (>20-fold) in human plasma (compare amide 238 to fluoroalkene bioisostere 275).	Geometric mimic. If carbonyl of amide is a hydrogen-bond acceptor or the amine a hydrogen bond donor these will be lost upon replacement.
Methylamine 	Functions as a HBD and acceptor. Free rotation around carbon and nitrogen. Same chain length.	303	Increased charge (depending on R ₂). If carbonyl of amide forms hydrogen bonds these are lost upon replacement.
Acylhydrazine (Trisubstituted) 	Trisubstituted acylhydrazine is bioisosteric to tertiary amide. Similar conformation. Functions as a HBA only. Increased chain length by one nitrogen. Less restricted rotation around N-N bond compared with amide.	308	Increased sterics. Increased chain length. If nitrogen of amide is a hydrogen bond donor this will be lost upon replacement.
Aminooxetane 	Influences basicity of proximal amine. Generally resistant to cleavage mediated by proteases, oxidation and hydrolysis. May increase steric bulk without increasing lipophilicity. ²⁹⁴ Decreases planarity.	Increases metabolic stability. Little details on effect on physicochemical, biological or PPOD properties. For an overview see reference. ²⁹⁵	Increased sterics. Loss of <i>trans</i> geometry.

²Footnotes:¹Improvements to potency and selectivity are generally excluded as they are most likely due to additional substituent modifications and/or increased target binding and cannot necessarily be attributed to the bioisostere alone.

² Comparisons are provided for compounds with the same or very similar substituents to the bioisostere where possible.

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