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## The Exploration of Chirality for Improved Druggability within the Human Kinome

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### Abstract

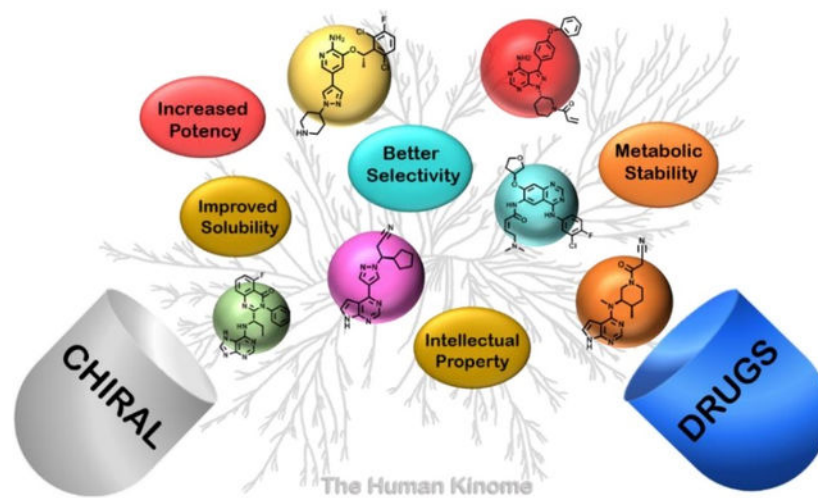
Chirality is important in drug discovery since stereoselective drugs can ameliorate therapeutic difficulties including adverse toxicity and poor pharmacokinetic profiles. The human kinome, a major druggable, enzyme class, has encountered a push for chiral drug development. As a consequence, kinase inhibitors have been exploited to treat a wide range of diseases. However, many kinase inhibitors are planar and overlap in chemical space, which leads to selectivity and toxicity issues. By exploring chirality within the kinome, a new iteration of kinase inhibitors are being developed to better exploit the three-dimensional nature of the kinase active site. Exploration into novel chemical space, in turn, will also improve drug solubility and pharmacokinetic profiles. This perspective explores the role of chirality to improve kinome druggability and will serve as a resource for pioneering kinase inhibitor development to address current therapeutic needs.

### Graphical Abstract

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## 1. Introduction

Stereochemistry has a vital role in pharmacology by dictating pharmacokinetic and pharmacodynamic properties of a drug molecule.<sup>1-2</sup> The enantiomers of a chiral drug may have identical physical and chemical properties but, in a chiral environment, enantiomeric effects can be significantly different.<sup>3</sup> Hypothetically, an active enantiomer will perfectly fit into the receptor binding site to produce a pharmacological effect whereas the inactive enantiomer (distomer) does not and will not generate any active response.<sup>4-5</sup> Moreover, the distomer may interact at a site elsewhere and cause an unwanted or adverse effect as a consequence of its pharmacodynamics *eg.* Thalidomide, a drug used for morning sickness in the late 1950's, caused teratogenic effects in offspring (phocomelia).<sup>6-9</sup> Later, it was discovered that only the *S*-isomer could cross the blood-placental barrier and was responsible for teratogenicity.<sup>10</sup> Considering the possible detrimental effects of the distomer, the FDA provided guidelines to assure stereoisomeric composition of a drug and pharmacokinetics of specific enantiomers.<sup>11-12</sup>

In certain drugs, such as atropisomers,<sup>13</sup> a chiral center does not exist but hindrance around a rotatable bond generates axial chirality. Compounds with axial chirality exhibit similar properties to that of traditional enantiomers, which can significantly impact drug properties. Recently, drug design and synthetic campaigns have been carried out to address the issue of atropisomers in pharmaceutical development. Since axial chirality can give rise to a single, stereochemically stable drug with improved efficacy and safety, atropisomers are being developed in a similar fashion to that of enantiomers to enhance drug properties.<sup>14-15</sup>

Chiral drug discovery has gained much attention in the human kinome as a method to improve drug properties of kinase inhibitors. As is known, the kinome represents promising drug targets because of their pivotal roles in cellular signalling.<sup>16</sup> Kinase inhibitors are divided between type I (ATP competitive), II (ATP non-competitive), and III (allosteric) and are typically planar, non-chiral structures.<sup>17, 18</sup> An emerging paradigm to improve kinome selectivity is to explore the three-dimensional nature of the kinase active site by generating chiral inhibitors. Researchers have investigated this strategy to successfully address potency

and selectivity issues.<sup>19</sup> For example, FDA approved drugs crizotinib and lorlatinib were developed by exploiting chirality to improve potency, selectivity, and pharmacokinetics.<sup>20–21</sup> Additionally, the FDA approved drug tofacitinib was selectively developed for JAK3 by evaluating selectivity of diastereomers.<sup>22</sup> In general, chirality can be engineered into kinase inhibitors to improve drug properties. Various approved enantio-specific kinase inhibitors are listed in Table 1.

In this perspective, we consider the role of chirality in the discovery of safer, more efficacious kinase inhibitors to treat chronic diseases with an emphasis on malignancies. A comprehensive overview is provided outlining the discovery of clinically approved chiral kinase inhibitors or inhibitors under clinical development. This perspective serves as a resource for pioneering kinase inhibitor discovery to address new therapeutic needs through enantio-specific approaches.

## 2. Chiral Kinase Inhibitors

### 2.1 ALK and c-MET Receptor Tyrosine Kinases

Receptor tyrosine kinases (RTKs) are transmembrane receptors activated by growth factors, cytokines, or hormones. They transfer the  $\gamma$ -phosphate of ATP to a tyrosine residue of a downstream signaling partner. RTKs play fundamental roles in cellular processes such as proliferation, migration, metabolism, differentiation, and survival.<sup>31</sup> Uncontrolled RTK activities are associated with various types of cancers and numerous small molecules targeting RKTs have been approved for the treatment of cancers.<sup>32</sup> In particular, hepatocyte growth factor receptor (HGFR) and anaplastic lymphoma kinase (ALK) have been targeted for their roles in non-small cell lung cancer.<sup>33–34</sup>

HGFR, also known as c-MET, has participating roles in normal cellular processes with subsequent signaling from RTKs. Consequently, aberrant c-MET signaling is correlated with poor prognosis and metastatic progression in a number of major cancers.<sup>35–37</sup> ALK, belonging to the insulin receptor superfamily, was first discovered as a NPM-ALK fusion protein in anaplastic lymphoma.<sup>38</sup> ALK chromosomal alterations have been observed in anaplastic large cell lymphoma (50%–60%), inflammatory myofibroblastic tumors (27%), and non-small cell lung cancer (NSCLC) (4%–7%). Hence, both c-MET and ALK underwent extensive targeting strategies for the treatment of cancer.<sup>39</sup>

#### 2.1.1 FDA-Approved RTK Drugs

**A. Crizotinib (Aug 2011, XALKORI<sup>®</sup>, Pfizer):** In 2011, **crizotinib** (7, PF-02341066) became the first FDA approved chiral ALK kinase inhibitor for the treatment of NSCLC.<sup>40</sup> Crizotinib demonstrates concentration-dependent inhibition of ALK and c-MET and has antitumor activity in mice bearing tumor xenografts with c-MET and EML4- or NPM-ALK fusion proteins.<sup>41</sup> Although originally approved for ALK fusion oncogenes, crizotinib is also a potent inhibitor of c-MET and ROS1. Crizotinib was discovered through lead-based optimization, which focused on improving selectivity and pharmacokinetic properties of lead candidates by exploiting chirality.

The discovery of crizotinib initiated with the identification of compound **1** (PHA-665752) (Scheme 1), which is a *c*-MET inhibitor with cellular potency ( $IC_{50} = 0.009 \mu M$  in GTL-16 cell line) and moderate selectivity (>50-fold for *c*-MET compared to other kinases).<sup>42</sup> However, poor pharmacokinetic properties of **1** led to an optimization campaign to improve drug properties as well as kinase selectivity. The co-crystal structure<sup>43</sup> of compound **1** with *c*-MET revealed inefficient interaction within the ATP pocket so the warhead was re-engineered to 4-(6-amino-5-((2,6-dichlorobenzyl)oxy)pyridin-3-yl)phenol (**2**), which led to an increase in receptor affinity ( $K_i = 3.83 \mu M$ ). Scaffold **2** was further optimized to improve solubility to afford **3** ( $K_i = 0.46 \mu M$ ).

Further modification of the linkage between the 2-aminopyridine core and the phenyl ring was investigated due to a small lipophilic pocket adjacent to the binding location of the 3-benzyloxy linker. Addition of a small  $\alpha$ -methyl group enhanced the binding efficiency of **4** ( $K_i = 0.068 \mu M$ ,  $IC_{50} = 0.14 \mu M$ ) along with lipophilicity (LipE  $K_i = 4.20$ ; LipE  $IC_{50} = 3.86$ ). Also, the  $\alpha$ -methyl group improved pharmacokinetics by impairing benzylic oxidation and created a chiral center. Finally, the combination of 2,6-dichloro, 3-fluoro, and  $\alpha$ -methyl into compound **5** provided the greatest inhibition against *c*-MET and the highest LipE values (enzymatic LipE = 4.82, cell LipE = 4.60;  $K_i = 0.012 \mu M$ , cell  $IC_{50} = 0.020 \mu M$ ).

Aforementioned, the addition of the  $\alpha$ -methyl introduced a chiral center (**5**), and the two enantiomers of compound **5** were synthesized and assessed. The *R*-enantiomer (**7**) exhibited better potency than the racemate (**5**) and *S*-isomer (**6**), which can be attributed to improved solubility, binding affinity, and assay variation. Hence, compound **7** efficiently binds *c*-MET resulting in improved cell-based ligand efficacy (LE) and LipE values with blocked benzylic oxidation.

The co-crystal structure of compound **7**<sup>20</sup> bound to nonphosphorylated *c*-MET was solved (Figure 1; left panel). 2-Aminopyridine is involved in two hydrogen bonds with the hinge region (Pro1158 and Met1160). The chiral methyl group interacts with the *c*-MET A-loop, which rigidifies the benzyl group and occupies a small lipophilic pocket between Val1092 and Leu1157 (Figure 1; right panel). Moreover, the chiral benzyl group orients in a  $\pi$ - $\pi$  interaction with Tyr1230. It can be concluded from structural analysis that the *R*-enantiomer preferentially interacts with Val1092, Leu1157, and Tyr1230; the *S*-enantiomer, however, would sterically clash with the *c*-MET back pocket and justifies the 100-fold loss in activity. Therefore, by exploiting chirality, *R*-enantiomer **7** was developed with enhanced enzymatic activity and improved pharmacokinetic profiles over the *S*-enantiomer **6**.

**B. Lorlatinib (Nov 2018; LORBRENA<sup>®</sup>, Pfizer):** Due to poor blood brain barrier permeability of crizotinib, modifications were made to the molecule to better target ALK-positive NSCLC brain metastasis (Scheme 2).<sup>44-45</sup> It was hypothesized that simultaneous improvement in cellular potency and multidrug resistance (MDR) BA/AB ratios (<2.5) could be achieved if crizotinib was redesigned with a restricted conformation and removal of the highly basic amine.<sup>21</sup> The co-crystal structure of compound **8** bound to ALK highlighted an acyclic U-shaped pose with the fluorophenyl and heteroaromatic tail in proximity to the binding site. This suggested that novel macrocyclic design templates, with restricted

conformations, could retain potency while achieving desirable central nervous system (CNS) ADME properties.

A series of 12 to 14-membered macrocycles (**8a-c**) were tested and **8a** exhibited an improvement in potency (ALK  $K_i = 0.0002 \mu\text{M}$ , ALK-L1196M  $K_i = 0.00029 \mu\text{M}$ ) against both wild-type and mutant ALK compared with the *S*-enantiomer (**8b**) (ALK  $K_i = 0.0017 \mu\text{M}$ , ALK-L1196M  $K_i = 0.0021 \mu\text{M}$ ). This stereochemical preference of the *R*-isomer accounts for a 210-fold improvement compared to the *S*-enantiomer. Additional modifications were performed to obtain the required combination of potency, ADME, and CNS availability, which provided compound **9** (lorlatinib). Interestingly, **9** was found to exhibit atropisomerism *via* a “ring-flip”. But, due to a high energy barrier, only a single diastereomer is physiologically relevant.<sup>46</sup>

Selectivity of the macrocycles for ALK over the highly conserved TrkB kinase was investigated because of the importance of TrkB in CNS homeostasis.<sup>47</sup> It was found that the cyano group of compound **9** (lorlatinib) was highly selective for the ALK mutation L1196M.<sup>48–49</sup> The chiral  $\alpha$ -methyl on compound **9** orients the fluorobenzene into a lipophilic pocket formed by Leu1256, Cys1255 and Gly1269 (Figure 2; right panel). Consequently, in TrkB, the cyano moiety of **9** is oriented to Tyr635. This interaction causes unfavorable desolvation energies between the nitrile and Tyr635 resulting in 40-fold selectivity for ALK over TrkB. The co-crystal structure of **8c** bound to ALK depicts key hydrogen bonding of the  $\text{NH}_2$  and ring nitrogen of the 2-aminopyrazine core with hinge residues Glu1197 and Met1199 (Figure 2; left panel).

The macrocycles were examined for CNS availability by analyzing MDR BA/AB efflux. Compound **9** exhibited low efflux potential, low clearance, and improved potency against wild-type and ALK mutants compared to crizotinib. On November 2, 2018, the FDA granted accelerated approval of compound **9** for ALK-positive NSCLC with metastatic disease.<sup>50</sup> By exploiting chirality and macrocyclic atropisomerism, compound **9** achieved enhanced CNS penetration and improved kinome selectivity.

**2.1.2 RTK Inhibitors Under Clinical Development**—Although crizotinib provides upfront efficacy, patients frequently develop resistance to treatment because of ALK mutations (L1196M, G1269A, S1206Y, C1156Y, F1174L, L1152R and 1151Tins). Therefore, crizotinib was reengineered and optimized for ALK mutations by using a combination of LipE analysis and structure-based drug design.<sup>51</sup> Comparing the crizotinib-ALK co-crystal structure to its apo form suggested a smaller C2 group would relax the Gly1269 carbonyl and enhance ALK mutant potency. Hence, strategies focused on optimizing the 2,6-dichloro-3-fluorophenyl group as well as limiting structural bulk at the pyrazolopiperidine tail (Scheme 3).

Optimization efforts uncovered that a triazole on C6 and a thiazole with a tertiary alcohol (**10b**) afforded the best potency and lipophilic values (L1196M cell  $\text{IC}_{50} = 0.027 \mu\text{M}$ ,  $\log D = 3.6$ ). The alcohol formed a hydrogen bond with the carbonyl group of Asp1203 and structural analysis suggested another alcohol in proximity to Asp1203 could improve binding site interactions. The resulting *R* and *S* enantiomers with a primary alcohol were

synthesized, amongst which the *S* enantiomer **12** (PF-06439015) exhibited an improved LipE value and an increase in cellular potency compared to crizotinib. Importantly, compound **12** also exhibited activity against ALK mutations L1196M and G1269A of which crizotinib is not active.

The co-crystal structure of compound **12** with wild-type ALK illustrates that the hydroxy group formed two hydrogen-bonds with Asp1203 (Figure 3). Moreover, introduction of the additional hydroxy group reduces lipophilicity but maintains membrane permeability because of intramolecular hydrogen bonding. Interestingly, the *R*-enantiomer of the chiral alcohol (**11**) demonstrated a reduced LipE value suggesting that an optimal chiral alignment is essential for improved drug properties.

Harmange *et al* discovered a series of triazolo-pyridines/pyridazines<sup>52</sup> exhibiting cellular and enzymatic potency against *c*-MET.<sup>53</sup> The U-shaped inhibitors adopt a unique *c*-MET binding mode and presented with exciting selectivity properties over other kinases. The first series was based on *O*-linked (**13**) and *N*-linked triazolopyridazine (**14**), but both suffered from poor solubility and rapid clearance in a patient-derived xenograft (PDX) model.<sup>54</sup> These limitations were addressed with the generation of compound **15**. The combination of a PEG-like ethoxy solubilizing group, a fluorine to block aromatic oxidation, and an *R*  $\alpha$ -methyl to block benzylic oxidation furnished the best combination of potency and pharmacokinetic properties. However, efficacy was not optimal in PDX models (Scheme 4).<sup>55</sup> Further improvements were investigated to improve drug properties, which resulted in compound **16** (AMG 337). Compound **16** was predicted to form intramolecular hydrogen bonds to reinforce the rigidity of the U-shaped binding mode.<sup>56</sup> Compound **16** exhibited an improved half-life, high oral bioavailability (~65%), and strong inhibition of *c*-MET over a 12 h period. Compound **16** was also evaluated in a *c*-MET dependent xenograft model and exhibited an ED<sub>50</sub> of 0.3 mg/kg.

Boezio *et al.* produced a co-crystal structure of compound **16** with unphosphorylated *c*-MET<sup>56</sup> and confirmed that the inhibitor adopts the predicted U-shaped binding mode. The chiral benzylic methyl forces the compound in a stable U-shaped binding mode around Met1211 (Figure 4, left panel), which would cause a steric clash with the *S*-enantiomer. The naphthyridinone nitrogen hydrogen bonds with the hinge at Met1160, whereas the nitrogen of the fluorotriazolopyridine engages the amide backbone of Asp1222. Furthermore, Tyr1230 and the fluorotriazolopyridine ring system exhibit face-to-face  $\pi$ - $\pi$  stacking. The bulky fluorotriazolopyridine orients towards the solvent front, which is unlikely for the *S*-analogue because of geometric constraints in the *c*-MET back pocket. Interestingly, the *R*-configuration is encapsulated in a small, lipophilic pocket generated by Val1092, Leu1157, and Lys1110 (Figure 4, right panel), but the *S*-enantiomer is unable to interact in the same pocket. Also, the fluorine atom on fluorotriazolopyridine is confined to a small cleft perpendicular to the amide backbone of Asn1209. Compound **16** was selected as a clinical candidate and is currently in phase II clinical trials for *c*-MET amplified gastric/esophageal adenocarcinoma and other solid tumors (NCT02016534).

Katz *et al.*<sup>57</sup> uncovered inhibitor **17** while screening a Merck library. Follow on studies identified **17** as a potent ATP competitive inhibitor of *c*-MET (IC<sub>50</sub> = 0.031  $\mu$ M). The

tricyclic heptanone core is a unique kinase warhead; therefore, optimization efforts focused on the phenyl and sulfonamide regions while keeping the warhead fixed. Aryl and heteroaryl derivatives were tested at the 3-position, amongst which the *N*-methyl pyrazolyl analogue **18** displayed a 27-fold increase in potency ( $IC_{50} = 0.004 \mu M$ ). To improve solubility, alterations were examined on the 7-position sulfonamide with analogues such as vinyl, phenyl, imidazolyl, trifluoromethyl, and *tert*-butyl. Further modifying the pyrazole substituent and diversifying the sulfonamide moiety led to free amine **18a** (*c*-MET  $IC_{50} = 0.003 \mu M$ ) and monomethyl amine **18b** (*c*-MET  $IC_{50} = 0.002 \mu M$ ), which were subjected to metabolic profiling. Metabolic studies revealed that rapid dealkylation of the sulfonamide was the main metabolic path. To block dealkylation, cyclic analogues were generated, which exhibited optimal cell-based activities and pharmacokinetics. The *R*-dioxanyl cyclic analogue **20** (**MK-2461**), displayed the best cell potency (GTL-16  $IC_{50} = 0.056 \mu M$ ), and excellent rat pharmacokinetics ( $Cl_p = 10 \text{ mL/min/kg}$ ,  $t_{1/2} = 1.3 \text{ h}$ ).

A piperidine analogue of compound **20**, **18c** (*c*-MET  $IC_{50} = 0.0026 \mu M$ ), was co-crystallized with *c*-MET and adopts a similar pose as compound **20**. The analogue forms a hydrogen bond with Met1160 at the hinge region, and the substituent on the pyrazole moiety extends into the solvent (Figure 5). Other key interactions include a hydrogen bond with Asp1222 and a hydrogen bond between the (*R*)-1,4-dioxane moiety and Arg1086. The sulfonamide moiety is buried near the catalytic lysine and the glycine rich loop. The stereospecific alignment of (*R*)-1,4-dioxane allows a water mediated hydrogen bond between the most proximal dioxanyl oxygen and the carbonyl oxygen of the central core. As a result, the tricyclic core adopts a conformation slightly out of plane. Hence, inclusion of the chiral (*R*)-analogue generates a unique binding mode for compound **20** in *c*-Met and effectively interacts with the solvent improving pharmacokinetic properties. Compound **20** has progressed into clinical studies and is the first candidate to enter phase II clinical trials from the tricyclic series ([NCT00518739](#)).

Insulin-like growth factor (IGF) receptor is another RTK that has been targeted with chiral molecules.<sup>58</sup> The IGF system is comprised of three receptors (IR, IGF-1R, IGF-2R), three ligands (insulin, IGF-1, IGF-2), and six 3-indole-D-glycerol-3'-phosphate (IGP) binding proteins (IGFBP1–6). The IGF-1R downstream signaling pathway is activated by insulin receptor (IR) substrates-1–4 and Src-homology collagen proteins as adapter molecules. Activation of the receptor triggers both PI3K/Akt and Ras/Raf pathways, thereby controlling apoptosis. Several studies have highlighted the key roles IGF-1R plays in cancer cell proliferation and metastasis. Over-expression of IGF-1R has been associated with colorectal and breast cancer.<sup>59</sup> In addition, increased levels of IGF-1 have been associated with prostate cancer and pre-menopausal breast cancer.<sup>60–61</sup> The two main approaches to control IGF-1R signaling include monoclonal antibody therapy and small molecule inhibition.<sup>62</sup>

**BMS-754807 (23)** is a pyrrolo-triazine based IGF-1R inhibitor exhibiting good clinical results.<sup>66</sup> For development, structural modifications were performed on compound **21** (Scheme 7). The core of the inhibitor was developed into pyrrolo-triazine with cyclopropyl substitution on pyrazole **22** providing further scope of structure-activity relationship (SAR) studies on the C2 amine.

The primary amide (**22a**) was found to be potent against IGF-1R but also exhibited CDK2E inhibition. The *S*-amide (**22**) was found to be five-fold more potent than the *R*-amide (**22b**). Other substituents, such as phenyl, thiazole, and pyridine, showed improved potency, but the (*S*)-2-methyl analogues, with heterocyclic amides (**22c**), maintained potency with better selectivity. By optimizing the pyridyl substitution, analogue **23** was discovered and had an optimal combination of both potency ( $IC_{50} = 0.002 \mu M$ ). It exhibited lower toxicity and good pharmacokinetic properties.

The co-crystal structure of compound **23** with IGF-1R demonstrates a donor/acceptor/donor hydrogen bonding motif with Met1052, Leu1051, and Glu1050 at the hinge. Moreover, the pyridyl ring nitrogen is involved in a hydrogen bond with the backbone of Asp1123. In the *S*-enantiomer, the cyclopropyl substituent on pyrazole could accommodate the gatekeeper (Met1049) and the fluoropyridyl amide engages the back pocket. The less active *R*-enantiomer would have a steric clash between the fluoropyridyl ring and the Gly-rich loop of the kinase. Because of the favorable interactions, the *S*-isomer (**23**) exhibits better potency compared to the *R*-isomer (Figure 6).<sup>66</sup>

Additional chiral RTK inhibitors (Scheme 8) are being evaluated in clinical studies including LY2874455, AZD4547, and BMS-582664. Compound **24** (**LY2874455**) is a novel pan-FGFR inhibitor and is in phase I clinical trials for solid tumors ([NCT01212107](#)).<sup>67</sup> Compound **25** (**BMS-582664**) is a prodrug for dual inhibition of VEGFR-2/FGFR-1 and is in phase II clinical trials for hepatocellular carcinoma.<sup>69</sup> Clearly, chirality is an important chemical addition to target RTKs, which can improve potency, selectivity, and pharmacokinetic profiles and can result in improved target inhibition.

## 2.2 Non-Receptor Tyrosine Kinase Inhibitors

Non-receptor tyrosine kinases (nRTKs) are a subgroup of tyrosine kinases with the same primary function as RTKs except that they are solubilized, cytoplasmic enzymes. NRTK phosphorylation is associated with activation of T-cell receptors (TCR), B-cell receptors (BCR), IL-2 receptors (IL-2R), Ig, and prolactin receptors, thereby contributing to the immune system and immune response.<sup>70</sup> Also, oncogenic nRTK mutations (*e.g.* BCR-ABL) are prevalent in a variety of hematological malignancies. Several small molecule nRTK inhibitors have been investigated for both cancer and immune disorders.<sup>71–73</sup>

### 2.2.1 FDA-Approved Non-RTK Drugs

**A. Ruxolitinib (Nov. 2011, JAKAFI<sup>®</sup>, Incyte) and tofacitinib (Nov. 2012, XELJANZ<sup>®</sup>, Pfizer):** Ruxolitinib and tofacitinib are the first-generation Janus kinase (JAK) inhibitors approved for primary myelofibrosis and immunological diseases (Scheme 9).<sup>74–75</sup> The JAK family is comprised of JAK1, JAK2, JAK3, and tyrosine kinase 2 (TYK2). The JAK pathway is activated upon binding of a cytokine to a cytokine receptor leading to the phosphorylation of JAK. In its active, phosphorylated form, JAK signals through STAT, which translocates to the nucleus and regulates gene transcription and cellular function.<sup>76–77</sup>

Ruxolitinib (**26**, INCB018424)<sup>78</sup> was the first FDA approved JAK inhibitor for the treatment of myelofibrosis, and is selective for JAK1/JAK2 over JAK3/TYK2 ([NCT01164163](#)). To



date, the preclinical drug discovery and development campaign of ruxolitinib has not been disclosed. There are reports of resistance to ruxolitinib, but the exact mechanism is still unknown and is likely patient dependent.<sup>79</sup> Resistance could be due to on-target, JAK2 mutations or from mutations in the heterodimerization domain between JAK2 and JAK1.<sup>78</sup>

Tofacitinib (**27**, CP-690550) received regulatory approval in 2012 for the treatment of severe rheumatoid arthritis. It has also been developed for other disorders such as psoriasis, psoriatic arthritis, ankylosing spondylitis, ulcerative colitis, and Crohn's disease.<sup>80</sup> Because tofacitinib is approved to treat chronic, non-lethal disease, the side effect profile should be minimal. In the discovery of tofacitinib, chirality was exploited for JAK3 selectivity, which resulted in low off-target liabilities and a well-tolerated side effect profile.

Tofacitinib was discovered through high-throughput screening, which uncovered a series of pyrrolo[2,3-*d*]pyrimidines (**28**) (Scheme 10).<sup>22</sup> The pyrrolopyrimidine warhead was hypothesized to bind the hinge of JAK3, and different heterocyclic substitutions were examined, but all reduced potency. To reduce bulk at the binding site, the tricyclic ring system was truncated to *N*-methylcycloalkyl, which increased potency (**29**). Substitutions were further explored on the cyclohexane ring and it was found that the introduction of 2',5'-dimethyl groups increased activity (**30**). Compound **30** is a complex mixture of 8 isomers so stereospecific isomers were synthesized and tested. It was found that a natural product-like terpenoid derivative (**31**) provided optimal activity but required further optimization because of the exposed alkene and stereochemical complexity. To improve drug-like properties, piperidine-based analogues were explored, which was hypothesized to provide access the JAK3 activation loop. Through the analysis of piperidine analogues, a cyanoacetamide substituent was found to provide the best combination of potency and selectivity resulting in tofacitinib (**27**).<sup>81–82</sup>

Compound **27** was docked into the JAK3 binding pocket and demonstrated that the 7-deazapurine warhead hydrogen bonds to the JAK3 hinge (Figure 7). In addition, the nitrile group hydrogen bonds with Arg953 at the opening of the JAK3 cleft. This docking pose in JAK3 illustrates that the 4*R*-methyl group is equatorial while the 3*R*-base moiety is axial, suggesting stereo-specific JAK3 binding.

To investigate the stereo-specificity of compound **27** for JAK3, its three stereoisomers were synthesized and subjected to cell-based assays, molecular modeling studies, and target profiling. JAK3 and JAK2/TYK2 serve as a shared receptor for selected cytokines and is downregulated by STAT5 and STAT4 phosphorylation, respectively. Hence, the degree of STAT5 and STAT4 phosphorylation was evaluated *via* immunoblotting with each stereoisomer and only compound **27** (Scheme 11) could affect STAT5 phosphorylation at the concentration of 0.5  $\mu$ M and no clear inhibition of STAT4 phosphorylation was observed.

Next, the selectivity profile over other kinases was determined and all four isomers were JAK selective, but compound **27** was more selective for JAK3 ( $K_d = 0.0075 \mu$ M for JAK3).<sup>83</sup> Further, the stereoisomers were docked into the JAK3 catalytic cleft.<sup>84</sup> The lowest energy conformations of the unbound compounds **27** and **27a-c** were super-imposed with their respective best docked poses (Figure 8). It was found that only compound **27** (3*R*, 4*R*) binds

to JAK3 in a conformation that best resembles its minimum energy conformation, whereas the other isomers, **27a** (3*R*, 4*S*) and **27b** (3*S*, 4*R*), resemble an unstable half chair and a twisted boat conformation. The (3*S*, 4*S*) isomer **27c** assumes a chair conformation in JAK3 but the axial and equatorial substitutions on the cyclohexane are high energy, respectively. Therefore, by exploiting chirality, tofacitinib was developed as a selective JAK3 inhibitor that is well tolerated for non-lethal indications of inflammation.

**2.2.2 Non-RTK Inhibitors in Clinical Development**—Proliferation and differentiation of T-cells or B-cells is induced by cytokines or chemokines *via* the JAK/STAT pathway.<sup>85</sup> Amongst the four members of the JAK family, JAK1 is activated by  $\gamma$ -common chain cytokines, IFN $\gamma$ , IL-6, and other gp130 cytokines.<sup>86</sup> Whereas TYK2 plays a significant role in cytokine signaling from IL-dependent type I interferons and IL-12 and IL-23. Thus, the idea of dual inhibition of JAK1 and TYK2 with selectivity over JAK2/JAK3 (minimizing erythropoietin signaling pathway) was envisioned.<sup>87</sup>

To identify JAK1/TYK2 dual inhibitors, a series of constrained 2,4-diamino pyrimidines were investigated (compounds **33a-d**) (Scheme 12).<sup>88</sup> A piperazine ring was found optimal at the 4-position of 2,4-diamino pyrimidine and the ring could tolerate a methylene bridge, which generated two enantiomers. The preferential *S,S*-enantiomer **33a** exhibited better activity (TYK2 IC<sub>50</sub> = 0.023  $\mu$ M) compared to *R,R*-enantiomer **33b** (TYK2 IC<sub>50</sub> = 2.690  $\mu$ M). The SAR was expanded to include more bridged diamines, which provided compound **34** with a 3,8-diazabicyclo[3.2.1]octane ring, *N*-methyl pyrazole, enhanced potency, and high LipE. Next, keeping the *N*-methyl pyrazole constant, a series of acylated derivatives, amides, and ureas were screened and uncovered that 1,1-difluoro-cyclopropane was very effective at this position (compounds **35a-c**). The eutomer *S*-1,1-difluoro cyclopropane **36a** (**PF-06700841**) provided a more balanced, potent JAK1/TYK2 profile (TYK2 and JAK1 IC<sub>50</sub> = 0.023 and 0.017  $\mu$ M) compared to the *R*-enantiomer **36b** (TYK2 and JAK1 IC<sub>50</sub> = 0.702  $\mu$ M and 0.842  $\mu$ M).

The co-crystal structure of compound **36a** with TYK2 shows the formation of two hydrogen bonds at the hinge region, whereas the ethylene bridge of the [3.2.1]-diazabicyclo protrudes into a hydrophobic pocket between Gly1040 and Leu1030. The difluoromethylene of the cyclopropyl amide orients towards the P-loop of the ATP binding site composed of Gly909 and Lys910 (Figure 9). With the (*R*)-distomer (**36b**), the difluoromethylene group orients into a negative electrostatic-potential region formed by side chain residues Asp1041 and Asn1028. This explains the remarkable 40-fold potency difference between the *S* and *R* isomers with respect to TYK2 binding. Compound **36a** also binds JAK1 in a similar manner, justifying the similar potencies against both enzymes.

Compound **36a** was progressed through a variety of pre-clinical testing and exhibited an excellent off-target polypharmacology profile and an ADME profile consistent with once-daily dosing. Compound **36a** is currently in phase II clinical trials for psoriasis (NCT02969018). Clearly, the application of chirality in the development of compound **36a** enabled enhanced target selectivity and improved drug properties.

Bruton's tyrosine kinase (BTK) is another nRTK and plays a key role in BCR-mediated activation and development. Phosphorylated BTK activates downstream NFAT and NF $\kappa$ B pathways, resulting in proliferation, cytokine production, and expression of stimulatory molecules. As a result, inhibiting BTK regulates BCR signaling and Fc $\gamma$  and Fc $\epsilon$  pathways, thereby ameliorating autoimmune diseases such as rheumatoid arthritis (RA), lupus, and multiple sclerosis *etc.*<sup>89-91</sup>

After much effort in identifying a reversible BTK inhibitor, compound **37** was discovered as a promising lead.<sup>92</sup> SAR exploration led to compound **38 (BMS-935177)** (Scheme 13) with reasonable potency against BTK (IC<sub>50</sub> = 0.003  $\mu$ M),<sup>93</sup> but the compound presented with a very narrow therapeutic window (< 20-fold). Researchers believed the toxicity was a result of four inter-converting atropisomers with different selectivity and toxicity profiles. Hence, it was envisioned that trapping a single atropisomer, with simultaneous improvement in potency and selectivity, could enhance drug safety. For this reason, another carbonyl was introduced into the quinazolinone ring generating derivative **39** that provided better pharmacokinetic properties. The two enantiomers were separated and the (*S*)-isomer was found to be more potent against human whole blood cells (BTK IC<sub>50</sub> = 0.0023  $\pm$  0.0012  $\mu$ M). Next, a second point of chirality was introduced by locking carbazole C4 through the addition of a C3 chloro substituent, which was found to be 1900-fold selective for BTK over JAK2 with improved potency. Anticipating improvement in kinase selectivity and the overall PK profile, SARs were expanded to an additional point of chirality on tetrahydrocarbazoles **40**.

Ultimately, adding (*S*)-dimethyl carbinol on tetrahydrocarbazoles and locking the carbazole C4 in the bioactive (*R*)-analogue by a fluoro substituent exhibited good potency (BTK IC<sub>50</sub> = 0.0005  $\mu$ M and hWB IC<sub>50</sub> = 0.090  $\mu$ M) and pharmacokinetic properties (AUC = 39  $\mu$ M\*h). The optimized analogue **41 (BMS-986142)** inhibited only five TEC family kinases with less than 100-fold selectivity for BTK, exhibited a good pharmacokinetic profile in mice (with <4% formation of the main des-methylquinazoline dione metabolite) and a clean liability profile.

Compound **41** was co-crystalized with BTK<sup>94</sup> and revealed that the tetrahydrocarbazole NH and the carboxamide carbonyl form two hydrogen bonds at the hinge region (Figure 10). The C2 dimethyl carbinol is directed towards the solvent front and does not exhibit any specific interaction. The (*R*)-configuration of the C5 phenyl linker projects the methyl group into a hydrophobic pocket adjacent to Cys481. The orthogonal nature of the phenyl linker orients the (*S*)-quinazolinone into the active site. In the (*S*)-configuration, the methyl group would be pushed out of the hydrophobic pocket causing an increase in entropy. Compound **41** demonstrated a desirable safety profile in multiple species and completed its phase II trials recently for moderate to severe rheumatoid arthritis (NCT02638948). The drug discovery campaign of compound **41** illustrates the use of axial chirality leading to a single, stable atropisomeric compound with enhanced potency and selectivity profiles.

With continued interest in discovering BTK inhibitors, compound **42 (CGI-1746)**<sup>95</sup> was developed as a highly selective and potent BTK inhibitor with excellent selectivity but suffered from poor ADME properties. Pharmacokinetic optimization of compound **42**

focused on two main regions (Scheme 14).<sup>96</sup> The first region was analogued with moieties to engage the solvent exposed pocket (Region 1, H2 Pocket). The second region was explored by varying substitution on the phenyl ring or replacing it with alternate arenes or heterocycles (Region 2, H3 Pocket). Adding polarity to the phenyl ring by substituting different heterocyclic arenes caused a decrease in binding affinity. Finally, a hydrobenzothiophene substituent at the H3 pocket and dimethyl-3-oxopiperazin-2-yl group on the H2 region optimized potency and pharmacokinetic properties. The (*R*)-isomer of substituent **44** ( $IC_{50} = 0.006 \mu\text{M}$ ;  $CL = 4.4 \text{ mL/min/Kg}$ ;  $F = 35\%$ ) provided a 3-fold improvement in potency and clearance from its enantiomeric (*S*)-isomer ( $IC_{50} = 0.02 \mu\text{M}$ ;  $CL = 11 \text{ mL/min/Kg}$ ;  $F = 41\%$ ). Additionally, compound **44** (**GDC-0834**) was found to have excellent selectivity against a panel of 331 kinases and minimal off-target receptor activity.

The co-crystal structure of compound **44** in complex with BTK revealed that the tetrahydrobenzothiophene moiety engages the hydrophobic pocket created by Leu542, Val546, Ser543, and Tyr551 of the activation loop (Figure 11). The amide linking the central aryl to the tetrahydro benzothiophene forms a hydrogen bond to Lys430. The pyrazinone binds Met477 at the hinge while the dimethyl-3-oxopiperazin-2-yl extends into the solvent front. In the discovery of compound **44**, chirality was used to improve pharmacokinetic properties and receptor potency.

### 2.3 Serine/Threonine Kinase Inhibitors

The human kinome consist of more than 500 human kinases of which 300 are serine/threonine kinases (STK).<sup>97</sup> As with any kinase, the prime function of an STK is to phosphorylate an amino acid hydroxy group (serine or threonine), thereby turning on or off a pathway. STKs are regulators of cell proliferation, apoptosis, cell differentiation, and embryonic development, and have relevance in numerous forms of disease. STKs can be receptors, which are categorized as type I (including activin like receptors [ALKs], TGF $\beta$ R1 [transforming growth factor beta receptor 1]), type II (ActR2, ActR2B, MISR2, BMPR1A, TGF $\beta$ R2), and type III (TGF $\beta$ R3), or solubilized, cytosolic proteins such as protein kinase A, B (Akt kinase), and C.<sup>98</sup> Other major classes of STKs include second messenger-dependent protein kinases (cAMP kinase, cGMP kinase, Ca<sup>2+</sup>/calmodulin kinase, Protein kinase C), MAP kinases (ERKs, JNKs or SAPKs), MAPKinase-regulating kinases (MEKs, SEKs, Raf, MEK kinases), CDKs, CDK-regulating kinases (CAK, CAK kinase), GRKs, RSKs and casein kinases.<sup>99</sup> STKs also include dual specificity kinases that act on both tyrosine as well as serine/threonine residues, such as MEKs. Additionally, STKs are activated in signal transduction pathways triggered by many RTKs and other receptors.<sup>100</sup> Another class of serine-threonine kinases include cyclin-dependent kinases (CDKs), known for cell cycle progression. Hence, CDK inhibitors exhibit therapeutic relevance for several diseases including cancer, diabetes, renal, neurodegenerative, and infectious diseases.

**2.3.1 FDA-Orphan Drug Designation**—CDK inhibitors have undergone clinical development with no disclosed explanation for incorporating chirality into the clinical candidate. **Alvocidib (45)**, a flavonoid CDK9 inhibitor, was granted with FDA orphan drug designation in 2014 for AML (acute myeloid leukemia).<sup>101</sup> Among other CDK inhibitors, **seliciclib (46, R-roscovitine, CYCLACEL<sup>®</sup>)** is a CDK-2,7,9 inhibitor under phase II

development<sup>102</sup> whereas **dinaciclib (47)**, a CDK-2,7,9 inhibitor, is in phase II clinical trials for advanced breast cancer and NSCLC (NCT00732810).<sup>103</sup>

**Cobimetinib (48)**, COTELLIC<sup>®</sup>, GDC-0973, XL518), a MEK1/2 inhibitor, obtained orphan drug status for malignant melanoma exhibiting BRAF<sup>V600</sup> mutations in 2014.<sup>104</sup> Compound **48** is a carboxamide-based, selective MEK inhibitor (100-fold selective over 100 other serine–threonine and tyrosine kinases)<sup>105</sup> and exhibits higher efficacy in BRAF mutated tumors because of its strong MEK inhibition.<sup>12</sup>

### 2.3.2 Additional STK Inhibitors under Clinical Development—Lee *et al.*

(2017)<sup>106</sup> initiated a drug discovery campaign against IRAK4 (Interleukin-1-receptor associated kinase 4) for the treatment of inflammation. IRAK4 is activated by the cytokine receptor interleukin-1-receptor in response to binding of interleukin-1 (IL-1). In addition, IRAK4 is involved in the innate and adaptive immune system and is expressed in T- and B-lymphocytes. Therefore, IRAK4 is an attractive target for treating inflammatory and autoimmune diseases. To initiate development, Lee *et al.* completed a fragment based screening using the Pfizer Global Fragment Initiative library. 10 best hits were co-crystallized with IRAK4. Co-crystal structure analysis suggests that exploration of the three-dimensional space within the ATP pocket could simultaneously improve potency, pharmacological and pharmaceutical properties. Binding of the carboxamide **49** to IRAK4 suggested switching the core to a more polar heterocyclic system, such as quinoline or isoquinoline, would improve potency. Compound **50** was generated and the resulting protein-ligand complex (Scheme 16) suggested interactions at the base of the binding pocket could be optimized. The piperidine was replaced with a five-membered lactam ring generating compound **51**. The (*S*)-isomer (**51a**) was found to be significantly more potent than the (*R*)-isomer (**51b**). The increase in potency of the (*S*)-isomer stems from its stereochemistry that enables the lactam ring to efficiently hydrogen bond to Ala315 and Asn316. In addition, the carbonyl accepts hydrogen bonds from Ser328 and an interaction between the isoquinoline nitrogen and Asp272 *via* a water molecule.

Compound **51a** achieved a good pharmacokinetic profile (CL = 23 L/hr/Kg, T<sub>1/2</sub> = 1.2 h, *F* = 57% in rat), which suggested oral administration was feasible for dosing. Unfortunately, allometric scaling to determine the human dose led to termination of the compound. To improve pharmacokinetics, compound **51** was further modified at the lactam position, thereby reducing the planarity of the molecule. A fluoro substituent with *syn* stereochemistry (**52a**) to the ether linker provided better potency than the *anti*-isomer (**52b**). However, *α-syn* fluorine substituent and a *β*-3-ethyl substituent led to compound **53 (PF-0665083)** with improved potency (IRAK4 IC<sub>50</sub> = 0.001 μM, PBMC IC<sub>50</sub> = 0.0024 μM) and optimized ADME properties (LE = 0.52, LipE = 7.4). The potency rise can be attributed to enhanced hydrogen bonding capability of the lactam ring conferred by appropriate positioning of the fluoro substituent.

The co-crystal structure of **53** bound to IRAK4 is shown in Figure 12, illustrating key interactions. The terminal, primary amide group forms two hydrogen bonds with Val263 and Met265. The cyclic lactam is involved in a hydrogen bond with the bottom pocket of IRAK4. The (*S*)-stereochemistry orients the lactam amide into a favorable position to

take part in hydrogen bonding with Ala315. Moreover, the ethyl group on the cyclic amide is encapsulated in a lipophilic pocket formed by Gly195, Lys213 and Val261. Hence, introduction of 3 points of chirality into **53** reduced planarity, which improved binding site interactions, solubility, and pharmacokinetics.

Another serine/threonine kinase closely related to the IRAK family is receptor interacting protein 1 (RIP1). RIP1 is involved in cell death/growth signaling circuits and is affected by exposure to several stress signals such as inflammatory cytokines, infections, and genotoxic stress.<sup>107</sup> Functions of RIP1 include T-cell homeostasis, activation of NF- $\kappa$ B, and activation of mitogen activated protein kinases (MAPKs), such as p38 MAPK, JNK, and ERK.<sup>108</sup> It was also found that RIP1 plays a significant role in various downstream pathways of the death receptors TNFR1, FasL, TRAIL, and Toll-like receptors. Thus, obstructing this pathway may be therapeutically relevant for various inflammatory diseases.<sup>109</sup>

Initial RIP1 inhibitors suffered from poor pharmacodynamics and pharmacokinetic properties. To identify a more viable RIP1 inhibitor, a GSK DNA-encoded library was screened *via* high-throughput screening, which uncovered compound **54a** (GSK-481), a more selective RIP1 benzoxazepinone pharmacophore. The binding interactions of the (*S*)-analogue **54a** with the protein is of significance as the (*R*)-analogue **54b** is not active. Therefore, chirality is integral for RIP1 activity.<sup>110</sup>

Replacing the heteroatom in the benzoxepinone with -N, -S, -CH<sub>2</sub>, -NMe provided high RIP1 *in vitro* potency (Scheme 17). Altering the size of the benzoxazepine or removal of the benzo function yielded inactive analogues as the benzoxazepinone moiety fits tightly into the RIP1 pocket. Heteroaryl substitutions on the aryl ring at 7,8-positions suffered from low solubility. For example, oxazole (**56a**) and imidazole (**56e**) were found to be more active than their isomers, whereas thiazole (**56b**) exhibited lower activity. Also, *N*-benzyl-1,2,3-triazole (**56g**) displayed better rat oral exposure than its 1,2,4-triazole (**56f**) analogue, but, the 3-benzyl-1,2,4-triazole isomer provided the best combination of *in vitro* potency, lipophilicity (logD 3.8), and rat oral exposure (AUC<sub>0-∞</sub> 2.3 μg/h/mL at a dosage of 2 mg/kg). All other tetrazole, phenyl, or pyridine analogues suffered from high lipophilicity and low solubility. Thus, compound **57** (GSK-2982772) was progressed for further development and has entered phase IIa clinical trials for ulcerative colitis. (NCT02903966)

The co-crystal structure of benzoxazepinone **57** bound to RIP1 demonstrates<sup>111</sup> the binding of the seven-membered ring to an allosteric site between the *N*-terminal and *C*-terminal domains without any interaction at the hinge region (Figure 13). The triazole and benzyl groups occupy an allosteric lipophilic pocket at the back of the ATP binding site. The benzoxazepinone ring resides in a pocket formed by two  $\beta$ -strands defined by Leu90-Val91-Met92 and Ile43-Met44-Lys45. The amide carbonyl linker makes a direct hydrogen-bond with the backbone of Asp156. The (*S*)-stereochemistry of the molecule allows the benzyl triazole amide access into a hydrophobic tunnel, while the (*R*)-analogue is not able to access this tunnel and is virtually inactive (> 10,000-fold potency). Hence, any change in chirality or conformation of the seven membered ring is not tolerated.

Polo-like kinases (PLKs), which are serine/threonine kinases, are well-validated cell cycle targets with vital roles in mitosis, spindle formation, chromosome segregation, and cytokinesis.<sup>112</sup> They include PLK1, PLK2 (SNK), PLK3 (PRK/FNK) and PLK4 (SAK), among which PLK1 is the most studied in oncology with an established correlation between PLK1 expression and cancer prognosis.<sup>113</sup> As such, there have been numerous campaigns targeting PLKs for antineoplastic drug development.

The PLK1 inhibitor **58** exhibited strong activity against PLK1, but was also active on PLK3 and lacked desirable drug properties warranting further clinical studies. Compound **58** was further optimized to improve potency and pharmacokinetic properties (Scheme 18). Incorporating a methyl group at the benzylic carbon displayed an improvement in cell potency (40-fold). The (*R*)-analogue (**59a**) exhibited approximately 40-fold improvement in growth inhibition of HCT116 (colorectal carcinoma) over the (*S*)-analogue (**59b**).<sup>114</sup> Further, improvement in solubility was considered by incorporating of more polar groups. By analyzing the binding of **59a** in the active site of PLK1, it was found that the 6-position of benzimidazole orients towards the solvent and could tolerate polar groups.

Methyl ether analogs at the 6-position of benzimidazole (**60a**) displayed high protein binding but poor solubility. Potency was further refined by eliminating the methylene spacer between the oxygen atom and the piperidine ring (**60b**). The basic amine analogs displayed an excellent combination of potency, solubility, and reduced protein binding with selectivity over PLK2/PLK3. Homology modeling of compound **60c** bound to the ATP-binding site of PLK1 displayed a hydrogen bond interaction between Glu140 and the piperidine nitrogen. Whereas in PLK3 and PLK2, Glu140 is replaced by a histidine, whose interaction with the charged amine is not favorable, resulting in reduced potency. Subsequently, more cyclic amines were screened to obtain suitable potency, selectivity, and solubility, which resulted in the discovery of compound **61** (**GSK461364**). Compound **61** is currently under evaluation in phase I clinical trials for non-Hodgkin's lymphoma ([NCT00536835](#)).

## 2.3 Lipid kinase Inhibitors

**2.3.1 FDA-Approved Lipid Kinase Drugs**—Lipid kinases are responsible for phosphorylation of lipids in the cell, which in turn change the reactivity and localization of lipids causing signal transduction.<sup>115</sup> For instance, Sphingosine kinase, a lipid kinase, catalyzes the conversion of sphingosine to sphingosine-1-phosphate (S1P) whereas phosphatidylinositol kinases generate phosphatidylinositol 3,4-bisphosphate (PI(3,4)P<sub>2</sub>), phosphatidylinositol 3,4,5-trisphosphate (PIP<sub>3</sub>), and phosphatidylinositol 3-phosphate (PI3P).<sup>116</sup> This family of kinases include phosphoinositide 3-kinases (PI3Ks), phosphatidylinositol-4-phosphate 3-kinase, and phosphatidylinositol-4,5-bisphosphate 3-kinase.<sup>117</sup> PI3Ks are lipid kinases that phosphorylate the 3' position of inositol in phosphatidylinositol, which functions as a secondary messenger that regulates proliferation, motility, and differentiation. PI3Ks are further classified into three classes, among which class I plays a critical role in regulating PIP<sub>3</sub> levels in the cell. PIP<sub>3</sub> is an essential cellular mediator involved in activation of downstream signaling cascades, which is generated through the phosphorylation of PIP<sub>2</sub>.<sup>118</sup> A lack of regulation in PIP<sub>3</sub> levels, such as impairment in PTEN function, is found in numerous, aggressive cancers.<sup>119</sup>

**A. Idelalisib (Jul. 2014, ZYDELIG<sup>®</sup>, Gilead):** In July 2014, **idelalisib** (**62**, GS-1101, CAL-101, IC489666) received FDA approval for treatment of relapsed chronic lymphocytic leukemia, follicular B-cell non-Hodgkin's lymphoma, and small lymphocytic lymphoma.<sup>120</sup> Idelalisib is the first-in-class small molecule PI3K inhibitor, selectively targeting PI3K $\delta$ . PI3K $\delta$  is a class I PI3K comprised of p110 $\delta$  as a catalytic subunit and p85 as a regulatory subunit. PI3K $\delta$  expression is restricted to leukocytes making it an excellent therapeutic target to selectively impair the PI3K-AKT pathway in hematopoietic cells.<sup>121–123</sup> Idelalisib is similar to **63** (IC87114), which was discovered by the ICOS corporation and has been studied comprehensively as a PI3K $\delta$  inhibitor.<sup>124</sup> Idelalisib has an IC<sub>50</sub> for PI3K $\delta$  of 0.019  $\mu$ M and exhibits better potency and metabolic stability than compound **63** (IC87114) (Scheme 19).<sup>125,126</sup> Further, idelalisib is selective for PI3K $\delta$  with relatively weak inhibition of PI3K $\alpha$ , PI3K $\beta$ , and PI3K $\gamma$  isoforms (IC<sub>50</sub> = 8.6, 4.0, and 2.10  $\mu$ M, respectively).<sup>127,128</sup>

Idelalisib interacts with PI3K $\delta$  hinge residues Val828 and Glu826 *via* the N3 and N9 nitrogens of the purine group, respectively (Figure 14). The (*S*)-chiral carbon directs the ethyl group of idelalisib into the hydrophobic pocket of PI3K $\delta$  formed by Ile910, Met900, and Met752. The ATP-binding pocket of PI3K $\delta$  undergoes a conformational change (from the apo-enzyme PDB: 2WXR) to accommodate the fluoro quinazolinone ring in a hydrophobic pocket (the specificity pocket) made up of Met752, Trp760, and Lys708 on the top of the active site.<sup>129,130</sup> It is hypothesized the energy required to open the specificity pocket defines the selectivity of idelalisib for PI3K $\delta$  over other isoforms. Further, because of geometric constraints in the selectivity pocket, the *R*-enantiomer of idelalisib does not fit properly in the PI3K $\delta$  active site. The chiral attributes of idelalisib, as well as low energy binding for PI3K $\delta$ , enable selectivity in the PI3K family. The selectivity, in turn, improves toxicity profiles and drug properties of idelalisib.

In 2012, Amgen disclosed compound **64**, an inhibitor of Class I PI3Ks with activity in biochemical ( $K_i$  values of 0.012, 0.005, 0.002 and 0.004  $\mu$ M for PI3K $\alpha$ , PI3K $\beta$ , PI3K $\delta$ , and PI3K $\gamma$ , respectively) and cellular (U87 MG IC<sub>50</sub> = 0.016  $\mu$ M) assays (Scheme 20). The compound exhibited promising *in vivo* activity, but exhibited rapid clearance (CL = 2.5 L/h/kg) with a very short mean residence time (MRT = 1.6 h for both); hence, it did not have appropriate drug-like properties.<sup>131</sup> Upon further investigation, it was found that the metabolites were the product of oxidative metabolism, including *O*-demethylation (**65a**) and benzylic oxidation (**65b**). To reduce metabolism of **64**, further optimization was completed, which resulted in compound **67a** (AMG 511).<sup>131</sup>

To improve drug properties of **64**, Norman *et al.* explored altering electron density of the terminal pyridine ring.<sup>131</sup> Introducing a fluorine atom at the C3 position of the pyridine ring furnished compound **66c** ( $K_i$  for PI3K $\delta$  = 0.006  $\mu$ M and  $K_i$  for PI3K $\alpha$ , PI3K $\beta$ , PI3K $\gamma$  are 0.018, 0.008, 0.021  $\mu$ M respectively) and reduced *O*-demethylation but did not improve clearance. Introduction of a benzylic methyl decreased PI3K $\delta$  selectivity either with or without substitution at the piperazine position. There was no significant stereo-chemical preference for PI3K inhibition, but pharmacokinetic properties improved with one isomer. When exploring rat microsomal stability, the (*R*)-Methyl benzylic isomer (**67a**; IC<sub>50</sub> = 0.004  $\mu$ M for U87 MG) was more stable than the (*S*)-Methylpiperazine isomer (**67b**; IC<sub>50</sub> = 0.007  $\mu$ M for U87 MG). Therefore, compound **67a** was selected for clinical investigation.



The co-crystal structure of **67a** bound to PI3K $\gamma$  showed the aminotriazine of compound **67a** forms two hydrogen bonds with Val882 at the hinge region (Figure 15). The methyl substituent on the triazine occupies a small hydrophobic pocket found only in PI3Ks (near Tyr867), which is responsible for kinase selectivity. Both the methoxy oxygen and the 3-fluoro substituent exhibit a favorable interaction with Lys833 within the affinity pocket. The nitrogen in the pyridine central core forms a network of water-mediated hydrogen bonds with Asp964. The benzylic (*R*)-methyl group efficiently occupies a hydrophobic pocket at the floor of the enzyme formed by Thr887, Ile963, and Asp950. This directs the methylsulfonamide piperidine moiety to engage in hydrogen bonds with Lys802 and Ala805.

Compound **67a** was subjected to a kinase panel against phosphatidylinositol 3-kinase-related kinases and exhibited good selectivity against mTOR ( $K_d > 10.0 \mu\text{M}$ ), hVPS34 ( $K_d > 9.0 \mu\text{M}$ ) and DNA-PK ( $K_d > 10.0 \mu\text{M}$ ). From the series, compound **67a** exhibited the highest stability in rat microsomes ( $CL_{\text{int}} = 20 \mu\text{L}/\text{min}/\text{mg}$ ) and also the lowest *in-vivo* clearance ( $CL = 0.4 \text{ L}/\text{kg}/\text{h}$ ) with a high mean residence time of ~2–5h. Compound **67a** also possessed high oral bioavailability ( $F = 60\%$ ) commensurate with a large oral exposure ( $AUC = 5.0 \mu\text{Mh}$ ). Furthermore, compound **67a** was also shown to potently block the PI3K pathway in an *in vivo* model and exhibited a dose-dependent decrease in AKT phosphorylation with an  $EC_{50}$  of 228 ng/mL. In a U87 MG xenograft model, compound **67a** effectively inhibited tumor growth with an  $ED_{50}$  of 0.6 mg/Kg. Hence, by introducing a chiral methyl at the benzylic position, compound **67a** achieved enhanced metabolic stability, which improved clearance and mean residence time.

Scientists at Amgen discovered another PI3K drug candidate, compound **71** (AMG 319), which completed phase I/II studies against relapsed or refractory lymphoid malignancies. Compound **71** was also examined for the treatment of human papillomavirus (HPV) and head and neck squamous cell carcinoma (HNSCC). However, clinical investigation of compound **71** was terminated due to safety concerns (NCT02540928).<sup>132</sup>

Compound **71** was discovered through modeling known PI3K inhibitors from the literature, which uncovered lead compound **68** (Scheme 21). Compound **68** served as a validated starting point since the compound achieved an  $IC_{50}$  of  $0.24 \mu\text{M}$  against PI3K $\delta$ . However, the thioether of **68** was sensitive to *in vivo* oxidation.<sup>133</sup> SAR exploration revealed that an ether (**69b**) or amino (**69c**) linker improved potency against PI3K and also improved selectivity for PI3K $\delta$  over PI3K $\gamma$ . However, the ether and amino analogs were still poorly soluble and exhibited microsomal instability. In order to minimize benzylic oxidation, a methyl was introduced at the  $\alpha$ -position to both ether and amine linkers (**70a-b**). Microsomal stability did not improve yet enzymatic potency against PI3K $\delta$  did improve (**70a**) ( $PI3K\delta IC_{50} = 0.071 \mu\text{M}$ ). The introduction of a methyl at this position limits free rotation and rigidified the structure in a low energy state, which may mimic the binding state. Upon further analysis, it was observed that the (*S*)-methyl isomer (**70a**) ( $IC_{50} = 0.071 \mu\text{M}$ ) was significantly preferred over the (*R*)-methyl isomer (**70b**) ( $IC_{50} = 2.6 \mu\text{M}$ ) due to steric interference. Further SAR exploration resulted in identification of compound **71**, which involved removal of the metabolically labile methyl, deactivating the quinoline with a fluorine, and substituting 2-aryl for 2-pyridyl. Compound **71** exhibited decent pharmacokinetic properties and solubility

(PI3K $\delta$  IC<sub>50</sub> = 0.018  $\mu$ M; PI3K $\beta$  IC<sub>50</sub> = 2.7  $\mu$ M; PI3K $\alpha$  IC<sub>50</sub> = 33  $\mu$ M; PI3K $\gamma$  IC<sub>50</sub> = 0.85  $\mu$ M, sol. (PBS) 146 mg/ $\mu$ L, rat PK CL = 0.34 L/h/kg; *F* = 54%).

Compound **71** has been co-crystallized in the PI3K $\gamma$  active site. The 7-fluoroquinoline lies in the inducible specificity pocket between Trp812 and Met804, and the pyridine orients towards a hydrophobic pocket comprised of Val882 and Lys890. The chiral (*S*)-methyl group on the benzylic position efficiently occupies a hydrophobic pocket adjacent to the hinge region formed by Thr887, Ile963, and Asp905 (Figure 16). The purine core binds to the hinge region at Val882 and Glu880. The (*R*)-enantiomer is unable to form similar interactions in PI3K $\gamma$  and therefore has substantially less activity. Therefore, by exploiting chirality, (*S*)-AMG 319 exhibited improved selectivity, solubility, and pharmacokinetic properties.

A series of 4*H*-pyrido[1,2-*a*]pyrimidin-4-ones, illustrated by compound **72** (**TGX-221**) (PI3K $\beta$  IC<sub>50</sub> = 0.022  $\mu$ M), were reported as PI3K $\beta$  inhibitors. Compound **72** has a benzylic, chiral center but previous investigations were completed with the racemic mixture. Chirality of compound **72** was later resolved, and it was observed that the *R*-enantiomer (**73a**) (PI3K $\beta$  IC<sub>50</sub> = 0.006  $\mu$ M) was 100-fold more potent than the *S*-enantiomer (**73b**) (PI3K $\beta$  IC<sub>50</sub> = 0.80  $\mu$ M). This suggests that chirality plays a crucial role in receptor binding and was further investigated to obtain insight about the receptor/ligand complex. Compound **72** was modeled in a homology model of PI3K $\beta$  and identified that morpholine interacts with Val854 at the hinge and the pyrido-pyrimidinone core interacts in the central pocket formed by Met926 and Ile residues 803, 851, and 936. The carbonyl group engages the back-pocket Tyr839 *via* a hydrogen bond network. Also, the aniline ring of compound **73a** (**TGX-221-R**) is believed to induce a conformational switch in the P-loop at the top of the ATP binding site, forming a specificity pocket as observed with other PI3K inhibitors. Because of the energetics of PI3K $\beta$ , induction of the specificity pocket by **73a** is selective for the  $\beta$ -isoform over others.<sup>134,-135</sup>

Further efforts by AstraZeneca resulted in the discovery of another PI3K $\beta$  inhibitor, **AZD6482** (**74a**) (Scheme 22).<sup>135</sup> Similar to **73a**, compound **74a** (PI3K $\beta$  IC<sub>50</sub> = 0.04  $\mu$ M) exhibited 200 times more activity than the (*S*)-enantiomer (**74b**) (PI3K $\beta$  IC<sub>50</sub> = 2.3  $\mu$ M). **74a** was evaluated for anti-platelet effects *via* ADP-induced impedance aggregometry and exhibited efficacy in humans.<sup>137</sup>

Barlaam *et al.* sought to identify an orally available PI3K $\beta$  inhibitor and utilized compounds **73a** and **74a**. For this investigation, the researchers considered removing the carboxylic acid on **74a**, believing the acid was responsible for poor oral exposure. With the objective of balancing lipophilicity and permeability, the researchers identified the *R*-isomer (**75**), with a difluoro substituted aniline and a tertiary amide on the core. Compound (*R*)-**75** had average metabolic stability and exhibited good cell potency (IC<sub>50</sub> = 0.003  $\mu$ M), 31% oral bioavailability, and a clearance of 82 mL/min/kg. However, due to solubility issues (*R*)-**75** was terminated.<sup>136</sup>

The same research group sought to further optimize (*R*)-**75** with the intention of generating a more hydrophilic molecule with improved solubility and metabolic stability. By modifying

(*R*)-**75**, **AZD8186 (76)** was discovered that has a similar difluoro substituted aniline and a tertiary amide on a different core. Compound **76** exhibited a significant increase in both potency and selectivity (PI3K $\beta$  IC<sub>50</sub> = 0.0004  $\mu$ M; PI3K $\alpha$  IC<sub>50</sub> = 0.035  $\mu$ M; PI3K $\delta$  IC<sub>50</sub> = 0.012  $\mu$ M; PI3K $\gamma$  IC<sub>50</sub> = 0.675  $\mu$ M, in cell, MDA-MB-468 pAKT IC<sub>50</sub> = 0.003  $\mu$ M) than compound **75**. Further, through oral administration, **76** blocked Akt phosphorylation in PTEN-deficient PC3 xenografts. With moderate permeability (Caco-2 P<sub>app</sub> 8.0 $\times$ 10<sup>-6</sup> cm/s), high metabolic stability, and potency, **76** was progressed into clinical studies for patients with advanced castration-resistant prostate cancer (CRPC), squamous NSCLC, triple negative breast cancer (TNBC), and PTEN-deficient/mutated or PIK3CB mutated/amplified advanced, solid malignancies (NCT03218826).<sup>138</sup>

In an attempt to develop a PI3K $\delta$  inhibitor that could be administered *via* inhalation to treat NSCLC, Erra *et al.* developed **LAS195319 (78)**, which displayed less side effects than idelalisib (Scheme 23).<sup>139</sup> Modifications to **63** were performed to reduce systemic side effects by deliberately increasing clearance. These efforts resulted in compound **78**, which exhibited improved lung retention and potency against PI3K $\delta$  (PI3K $\delta$  IC<sub>50</sub> = 0.0005  $\mu$ M, PI3K $\alpha$  IC<sub>50</sub> = 1.9  $\mu$ M, PI3K $\beta$  IC<sub>50</sub> = 0.01  $\mu$ M, PI3K $\gamma$  IC<sub>50</sub> = 0.036  $\mu$ M, M-CSF-induced AKT in THP-1 cells IC<sub>50</sub> = 0.027  $\mu$ M, rat PK AUC = 171 ng/h/mL, *F* = 1%).<sup>140</sup> Erra *et al.* developed another pyrrolotriazine based inhibitor by adding a methyl group on the benzylic carbon to minimize benzylic oxidation on IC87114 (Scheme 23). Additional modifications uncovered compound **80 (LAS191954)**, which entered clinical development for the treatment of pemphigus (PI3K $\delta$  IC<sub>50</sub> = 0.026  $\mu$ M, PI3K $\alpha$  IC<sub>50</sub> = 8.2  $\mu$ M, PI3K $\beta$  IC<sub>50</sub> = 94.0  $\mu$ M, PI3K $\gamma$  IC<sub>50</sub> = 72.0  $\mu$ M, M-CSF-induced AKT in THP-1 cells IC<sub>50</sub> = 0.078  $\mu$ M, rat PK CL = 1.4mL/min/Kg, *F* = 98%).<sup>141</sup>

The co-crystal structure of compound **81** (an analogue of **78**) bound to PI3K $\delta$  revealed that the molecule adopts a chirality-induced conformation. The pyrrolopyrimidine forms hydrogen bonds to Glu826 and Val828 at the hinge. As a result, the pyrrolotriazinone moiety is sandwiched orthogonally into the specificity pocket between Trp760 and Met752 (Figure 17). Also, the sulfone forms a hydrogen bond with the side chain of Lys779, and the phenol group hydrogen bonds to Asp787.

Compound **82** (an analogue of **80**) occupies the prototypical binding pose in PI3K $\delta$  where the pyrrolotriazinone moiety enters the hydrophobic specificity pocket between Trp760 and Met752; the cyanopyrimidine binds to Val828 and Glu826 at the hinge (Figure 17). The *R*-enantiomer of analogue **82** cannot enter the specificity pocket with the correct geometry and would therefore form undesirable steric clashes in the binding pocket.

Additional inhibitors of the PI3K family are under clinical development. This includes **umbralisib (83)**, a selective PI3K $\delta$  inhibitor in phase II clinical trials for chronic lymphocytic leukemia with resistance to BTK inhibitors or prior PI3K $\delta$  inhibitor therapy (NCT03801525) (Scheme 24).<sup>141-142</sup> This also includes **duvelisib (84)**, a dual PI3K $\delta$  and PI3K $\gamma$  inhibitor in clinical trials for advanced hematologic malignancies and relapsed or refractory peripheral T-cell lymphoma (NCT01476657, NCT03372057), and **tenalisib (85)**, another dual PI3K $\delta$  and PI3K $\gamma$  inhibitor in phase II clinical trials for relapsed/refractory indolent non-Hodgkin's lymphoma and T-cell lymphoma (NCT03711578). The additional

PI3K inhibitors are chiral and the *S*-enantiomers are active. The *S*-chiral configuration permits appropriate geometric alignment in the selectivity pocket.

## 2.5 Irreversible Chiral Kinase Inhibitors

Irreversible kinase inhibitors form covalent bonds with the target kinase.<sup>143</sup> This occurs *via* nucleophilic attack by a cysteine residue on an electrophilic center of the irreversible inhibitor. The typical electrophilic centers used for this purpose include acrylamides, vinyl sulphonates, quinones, alkynyl amides, propargylic acid derivatives,  $\alpha$ -halo ketones, thiocyanates, epoxides, *etc.* Covalent inhibition serves as a platform to fine tune selectivity and affinity for the target kinase.<sup>144</sup> Kinase classes explored with covalent inhibitors include EGFR, Her-2, Her-4, the Tec family (BMX, BTK, ITK, TEC and TXK), and one member of the Src family (BLK).<sup>145</sup> Among clinically approved covalent candidates, two chiral molecules have been approved by the FDA, afatinib and ibrutinib.

### 2.5.1 FDA-Approved Irreversible Kinase Inhibitors

**A. Afatinib (Jul 2013, GILOTRIF<sup>®</sup>, Boehringer Ingelheim Corp):** In 2009, afatinib (**88**, BIBW-2992) was the first quinazoline-based, irreversible kinase inhibitor approved by the FDA for treatment of NSCLC. Compound **88** covalently binds to Cys797 (EGFR) and Cys805 (HER2) and exhibits potent phosphorylation inhibition on both EGFR (IC<sub>50</sub> = 0.005  $\mu$ M) and HER2 (IC<sub>50</sub> = 0.014  $\mu$ M) compared to other irreversible kinase inhibitors (EKB-569 and HKI-272) (Scheme 25).<sup>146,147</sup>

The drug discovery campaign for compound **88** has not been disclosed, but its co-crystal structure with EGFR illustrates a key covalent bond formation between Cys797 and the electrophilic center of afatinib along with a hydrogen bond with Met793 at the hinge region (Figure 19). The specific role of the chiral tetrahydrofuran ring has not been described but, since that region is in the solvent, it can be inferred the chirality does not influence the substrate-ligand complex.<sup>148</sup> Instead, the chiral tetrahydrofuran ring likely influences pharmacokinetic properties of compound **88**. Metabolic studies reveal minimal cytochrome P450 (CYP) metabolism, while the majority of **88** is excreted as a covalent adduct with plasma proteins.<sup>149</sup> Also, compound **88** exhibits a low renal elimination rate (5%).<sup>149</sup>

**B. Ibrutinib (Nov 2013, IMBRUVICA<sup>®</sup>, Pharmacyclics):** Ibrutinib (**90b**, PCI-32765) is another irreversible inhibitor approved for B-cell non-Hodgkin's lymphoma. To identify compound **90b**, a library was screened against the BTK kinase and compound **89** (PCI-29732) was identified as a hit compound (BTK IC<sub>50</sub> = 0.082  $\mu$ M) (Scheme 26).<sup>150</sup>

A series of molecules were synthesized bearing different electrophilic centers to engage the conserved cysteine residue in BTK (Cys481). On the electrophilic center, adding a *trans* methyl group to the vinyl group reduced potency whereas addition of a tertiary amine improved potency. Investigation into piperidine and pyrrolidine based Michael acceptors was completed, and it was found that a piperidine based Michael acceptor with absolute (*R*)-configuration provided optimal potency (IC<sub>50</sub> = 0.0005  $\mu$ M).<sup>151</sup>

Drug-receptor interaction studies were completed by modeling compound **90b** in BTK. The 4-amino group hydrogen bonds to Thr474 (gatekeeper) and Glu475, whereas the N-H of the

pyrazolo[3,4-*d*]pyrimidine core forms a hydrogen bond with Met477 at the hinge (Figure 20). The thiol group of Cys481 covalently binds to the electrophilic center of compound **90b**. Chirality of the piperidine ring places compound **90b** in an orientation appropriate for covalent interaction with Cys481 and optimizes hydrogen bonding and hydrophobic interactions within the protein.

Although ibrutinib is effective against B-cell malignancies, the inhibitor has numerous off-target activities due to irreversible binding to other kinases [*e.g.*, EGFR, tyrosine kinase expressed in hepatocellular carcinoma (TEC), interleukin-2-inducible T-cell kinase (ITK), and T-cell X chromosome kinase (TXK)]. This led to the development of more selective, second-generation, irreversible BTK inhibitors **tirabrutinib**<sup>152</sup> (**91**, ONO/GS-4059) and **acalabrutinib** (**92**, ACP-196, CALQUENCE®, AstraZeneca Pharmaceuticals Inc.) (Scheme 27).<sup>153</sup> Compound **92** was developed for selectivity while maintaining an efficacious, irreversible profile against BTK. It received FDA approval in 2017 for treatment of adult patients with relapsed mantle cell lymphoma (MCL).<sup>25</sup>

It should be noted that the JAK inhibitors **26** and **27** as described above are also irreversible kinase inhibitors.

### 3. Conclusion and Future Perspectives

Chirality is a prominent attribute in the biological world. Many organic molecules, including sugars and most natural amino acids, are chiral. Furthermore, all biomolecules within the central dogma of biology are chiral. Incorporating chirality into drug discovery is an important technique to better engage biological targets with enhanced drug properties. During drug discovery, the majority of failures are due to a lack of either efficacy or safety, which can be attributed to poor ADME properties of the drug.<sup>154</sup> Consequently, a balance of optimized pharmacokinetic and pharmacodynamic parameters maximizes the safety and efficacy of a drug candidate. Chirality has the potential to remedy both challenges of drug optimization by exploiting the three dimensional nature of biology. As such, chiral small molecules are emerging as an attractive clinical advantage in drug discovery.

In kinase drug discovery, most approved inhibitors are planar and have no stereocenters. Although planar structures are efficacious, some drug discovery efforts within the kinome are currently focused on the generation of kinase inhibitors with stereocenters. These efforts emphasize chirality as a property to improve pharmacokinetics and selectivity within the kinome. Solubility is also a major liability in drug development, especially with planar drug structures. Since most kinase inhibitors mimic adenine, the structures are planar and aromatic and exhibit intramolecular  $\pi$ - $\pi$  stacking interaction that limits their aqueous solubility. Hence, incorporation of a chiral center can reduce  $\pi$ - $\pi$  stacking interaction, thus improving drug solubility and absorption. Axial chirality is also being explored within the kinome by generating atropisomeric structures. Dynamics of such axial systems permits fine-tuning of receptor/ligand interactions. Further, chirality provides a new dimension to access new chemical space increasing novelty in structure and thereby accelerating drug discovery.

Understanding the importance of chirality in interdisciplinary areas of drug development may contribute to major progress in kinase inhibitor development. Crizotinib, the first FDA approved chiral kinase inhibitor for NSCLC, supports the importance of chirality in kinase drug discovery. On similar lines, the recent approval of lorlatinib for the treatment of NSCLC has further galvanized the importance of chirality in kinase research. The recent major advancements in new asymmetric synthetic methodologies and enantiomeric separation techniques encourage the effort of chiral drug development. Other evolving medicinal chemistry practices, such as kinome profiling and X-ray crystallography, are providing better insight into the role of chirality in kinase receptor engagement and receptor selectivity. Hence, developing chiral kinase inhibitors can help enhance druggability within the kinome. It is expected that chirality-driven, drug discovery campaigns will promote the development of kinase inhibitors with improved selectivity, potency, and drug properties. A surge of chiral kinase inhibitors are under clinical investigation and many have been approved in recent years. Enhancing druggability by implementing chirality-focused drug discovery will expand structural diversity when targeting the kinome. This, in turn, will uncover new chemotypes with augmented pharmacokinetic and pharmacodynamic profiles for improved druggability within the human kinome.

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### List of Non-standard Abbreviations

<b>BTK</b>	Bruton's tyrosine kinase
<b>BCR</b>	B-cell receptors
<b>BLK</b>	B Lymphocyte Kinase
<b>CDKs</b>	Cyclin-dependent kinases
<b>CL</b>	Blood Clearance
<b>CRPC</b>	Castration-resistant prostate cancer
<b>ERKs</b>	Extracellular signal-regulated kinases
<b>FLT3</b>	FMS like tyrosine kinase 3
<b>GSK</b>	Glaxo smith Kline
<b>HER2</b>	Human epidermal growth factor receptor 2
<b>ITK</b>	Interleukin-2-inducible T-cell kinase

<b>IFN<math>\gamma</math></b>	Interferon gamma
<b>IGF</b>	Insulin-like growth factor-1 receptor
<b>IL-2R</b>	IL-2 receptors
<b>IRAK4</b>	Interleukin-1-receptor associated kinase
<b>ITK</b>	Interleukin-2-inducible T-cell kinase
<b>JAK</b>	Janus Kinase
<b>JNKs</b>	c-Jun N-terminal kinases
<b>MAPKs</b>	Mitogen activated protein kinases
<b>MDA-MB</b>	M.D. Anderson Metastasis Breast cancer
<b>MDR</b>	Multi drug resistance
<b>NFAT</b>	Nuclear factor of activated T-cell
<b>PBMC</b>	Peripheral blood monomorphonuclear cells
<b>PDX</b>	Patient-derived xenograft
<b>PI(3,4)P2</b>	Phosphatidylinositol 3,4-bisphosphate
<b>PI3K</b>	Phosphoinositide 3-kinase
<b>PI3P</b>	Phosphatidylinositol 3-phosphate
<b>PIP3</b>	Phosphatidylinositol 3,4,5-trisphosphate
<b>PLKs</b>	Polo-like kinases
<b>PTEN</b>	Phosphatase and tensin homolog
<b>RIP1</b>	Receptor interacting protein 1
<b>S1P</b>	Sphingosine-1-phosphate
<b>STAT</b>	Signal transducer and activator of transcription
<b>STK</b>	Serine threonine Kinase
<b>TCR</b>	T-cell receptors
<b>TGF<math>\beta</math>R1</b>	Transforming growth factor beta receptor 1
<b>TNBC</b>	Triple negative breast cancer

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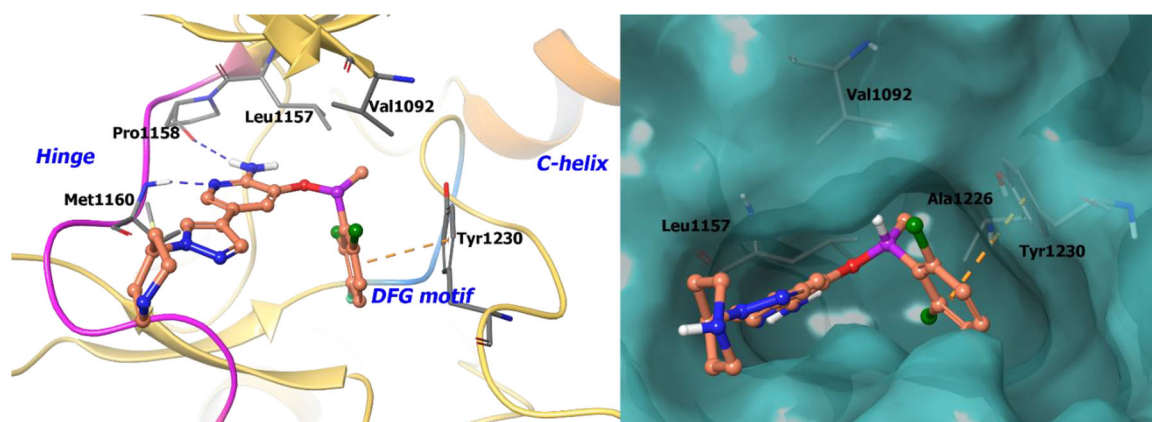
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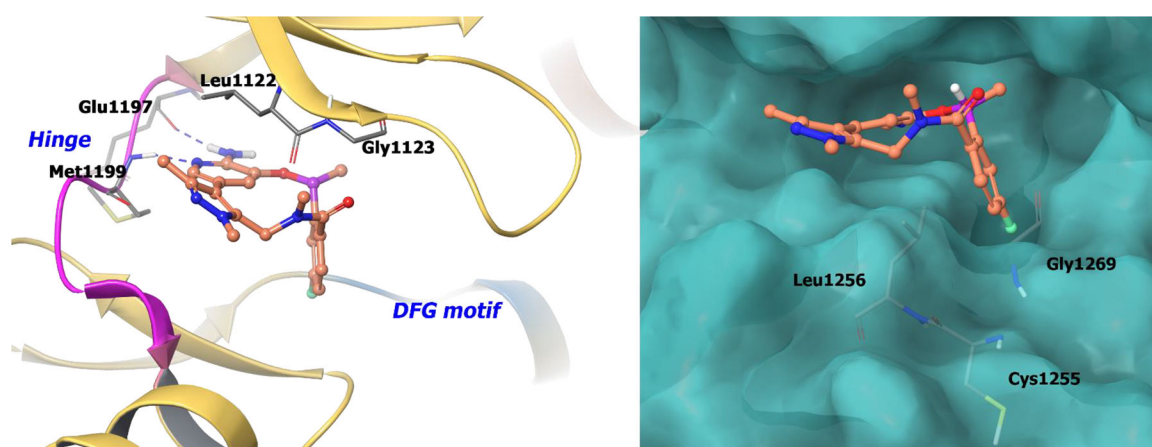
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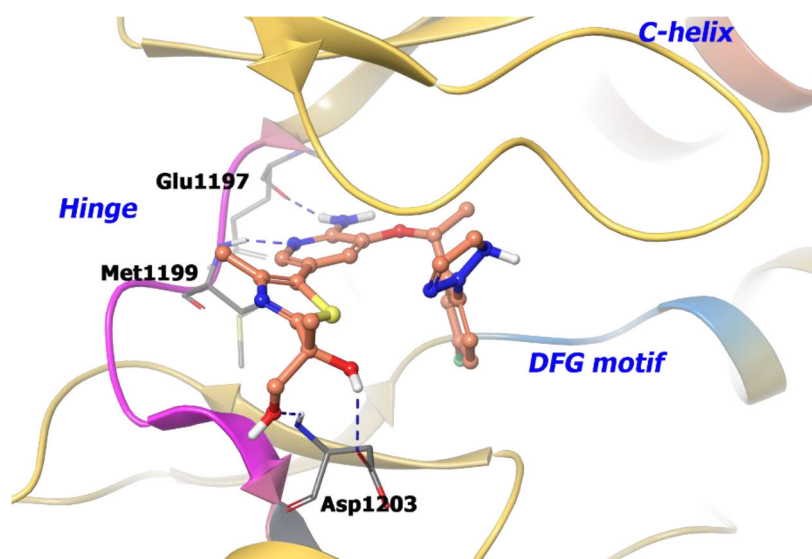


**Figure 1.**

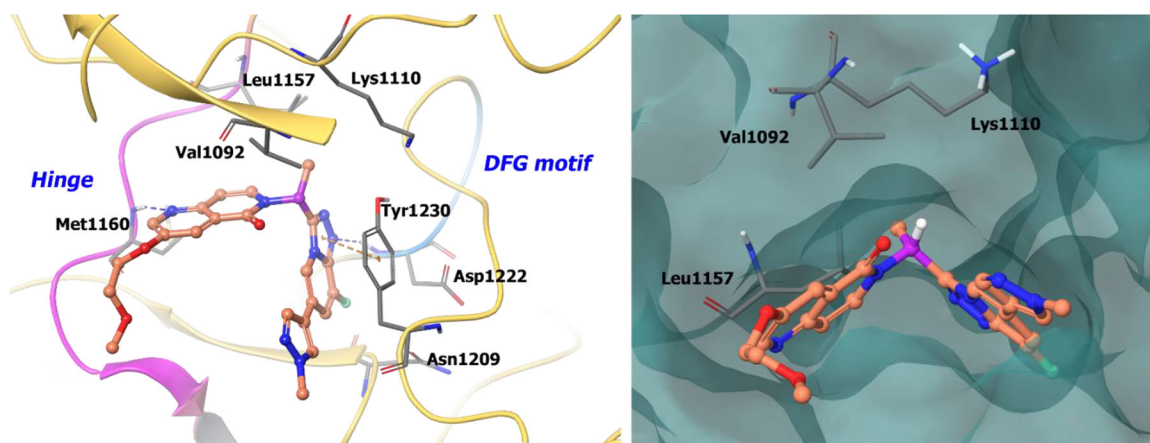
The co-crystal structure of compound 7 bound to c-MET (PDB 2WGJ, 2.0 Å). Left Panel: Interaction of compound 7 with the protein. The protein is depicted as yellow ribbons, and hydrogen bonds are illustrated with blue dashed lines; Right panel: The compound 7 binding site in c-MET. The surface of the protein is depicted in blue. compound 7 atoms are colored as follows: carbon, red-orange; nitrogen, blue; oxygen, red; chlorine, green; fluorine, jade; hydrogen, white; the chiral carbon is highlighted in violet.



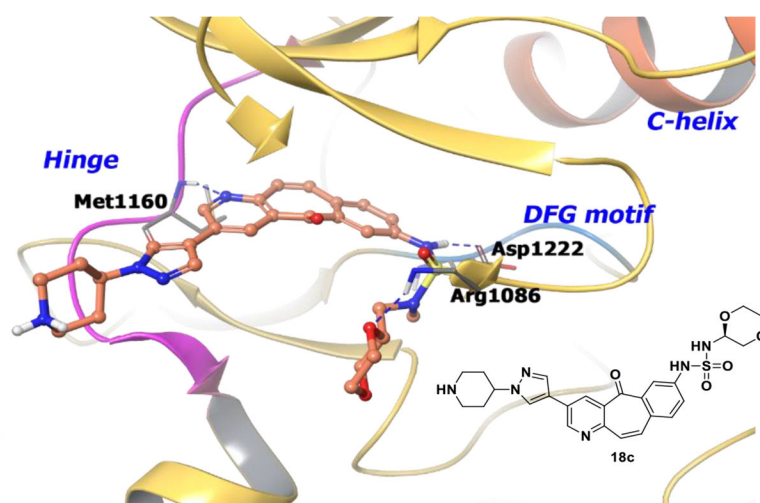
**Figure 2.** The co-crystal structure of compound **9** bound to ALK (PDB 4CMU, 1.8 Å). Left panel: Interaction of compound **9** with the protein. The protein is depicted as yellow ribbons, and the hydrogen bonds are illustrated with blue dashed lines; Right panel: The compound **9** binding site in ALK, protein is shown as surface. Compound **9** atoms are colored as follows: carbon, red-orange; nitrogen, blue; oxygen, red; chlorine, green; fluorine, jade; hydrogen, white; the chiral carbon is highlighted in violet.



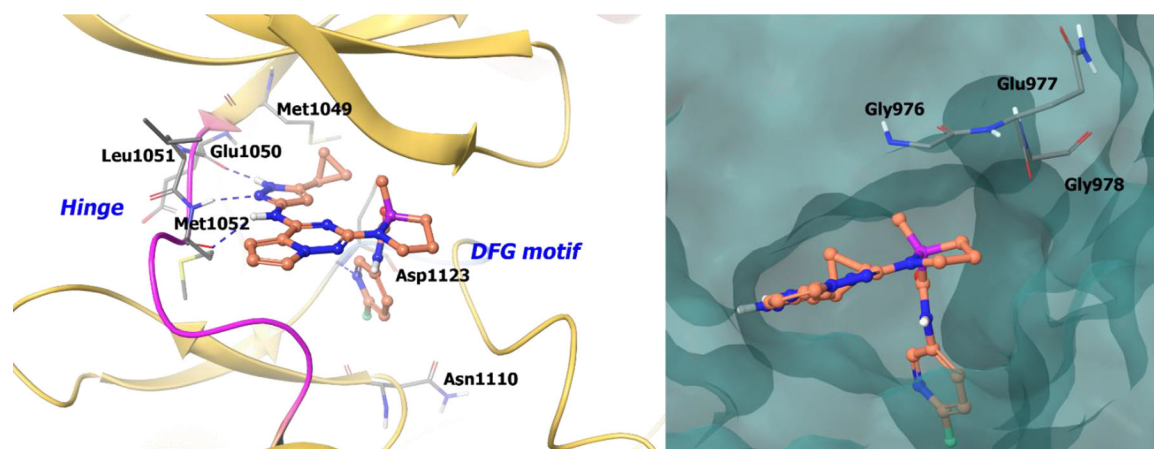
**Figure 3.** The co-crystal structure of compound **12** bound to ALK L1196M protein (PDB 4CD0, 2.23 Å). Interaction of compound **12** into the binding site of the protein. The protein is depicted as yellow ribbons, and the hydrogen bonds are illustrated with blue dashed lines. Compound **12** atoms are colored as follows: carbon, red-orange; nitrogen, blue; oxygen, red; chlorine, green; fluorine, jade; hydrogen, white; the chiral carbon is highlighted in violet.



**Figure 4.** The co-crystal structure of compound **16** bound to *c*-MET (PDB 5EYD, 1.85 Å). Left panel: Interaction of compound **16** with the protein. The protein is depicted as yellow ribbons, and the hydrogen bonds are illustrated with blue dashed lines; Right panel: Compound **16** binding site in *c*-MET, protein is shown as surface. Compound **16** atoms are colored as follows: carbon, red-orange; nitrogen, blue; oxygen, red; chlorine, green; fluorine, jade; hydrogen, white; the chiral carbon is highlighted in violet.



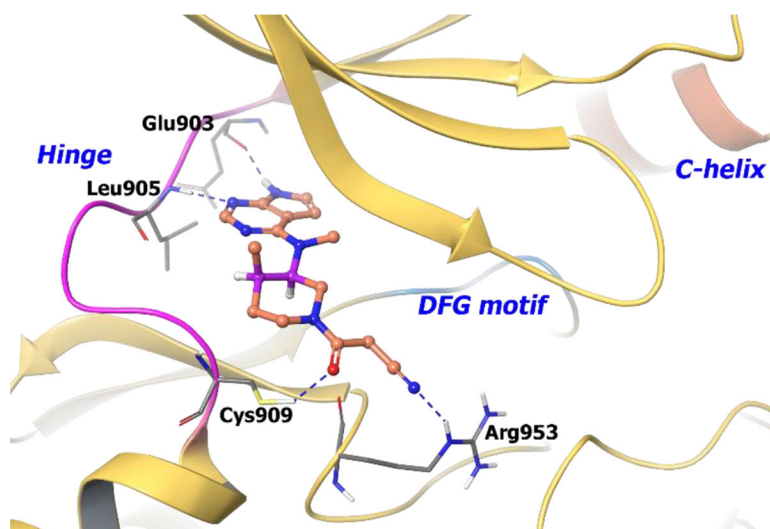
**Figure 5.** The co-crystal structure of analogue **18c** bound to *c*-MET (PDB 3R7O, 2.3 Å). Interaction of analogue **18c** at the binding site of the protein. The protein is depicted as yellow ribbons, and the hydrogen bonds are illustrated with blue dashed lines. Compound **18c** atoms are colored as follows: carbon, red-orange; nitrogen, blue; oxygen, red; chlorine, green; fluorine, jade; hydrogen, white; the chiral carbon is highlighted in violet.



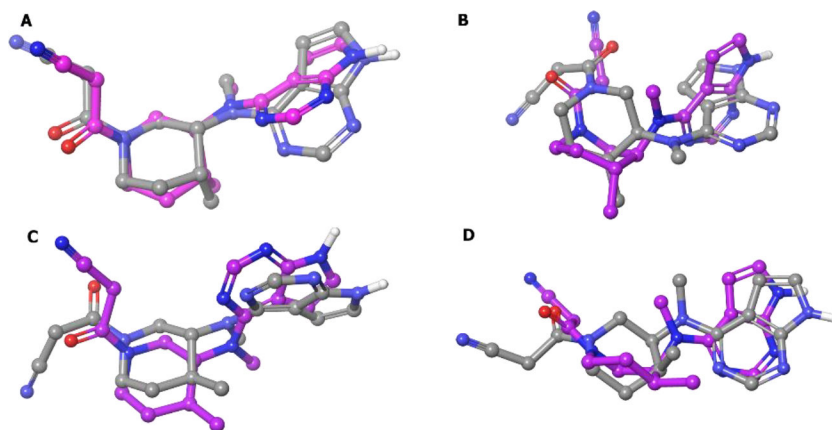
**Figure 6.**

The co-crystal structure of compound **23** bound to IGF-1R (PDB 3I81, 2.08 Å). Left Panel: Interaction of compound **23** with the protein. The protein is depicted as yellow ribbons, and the hydrogen bonds are illustrated with blue dashed lines; Right panel: The binding site of compound **23** in IGFR-1R. The surface of the protein is depicted in blue. Compound **23** atoms are colored as follows: carbon, red-orange; nitrogen, blue; oxygen, red; chlorine, green; fluorine, jade; hydrogen, white; the chiral carbon is highlighted in violet.

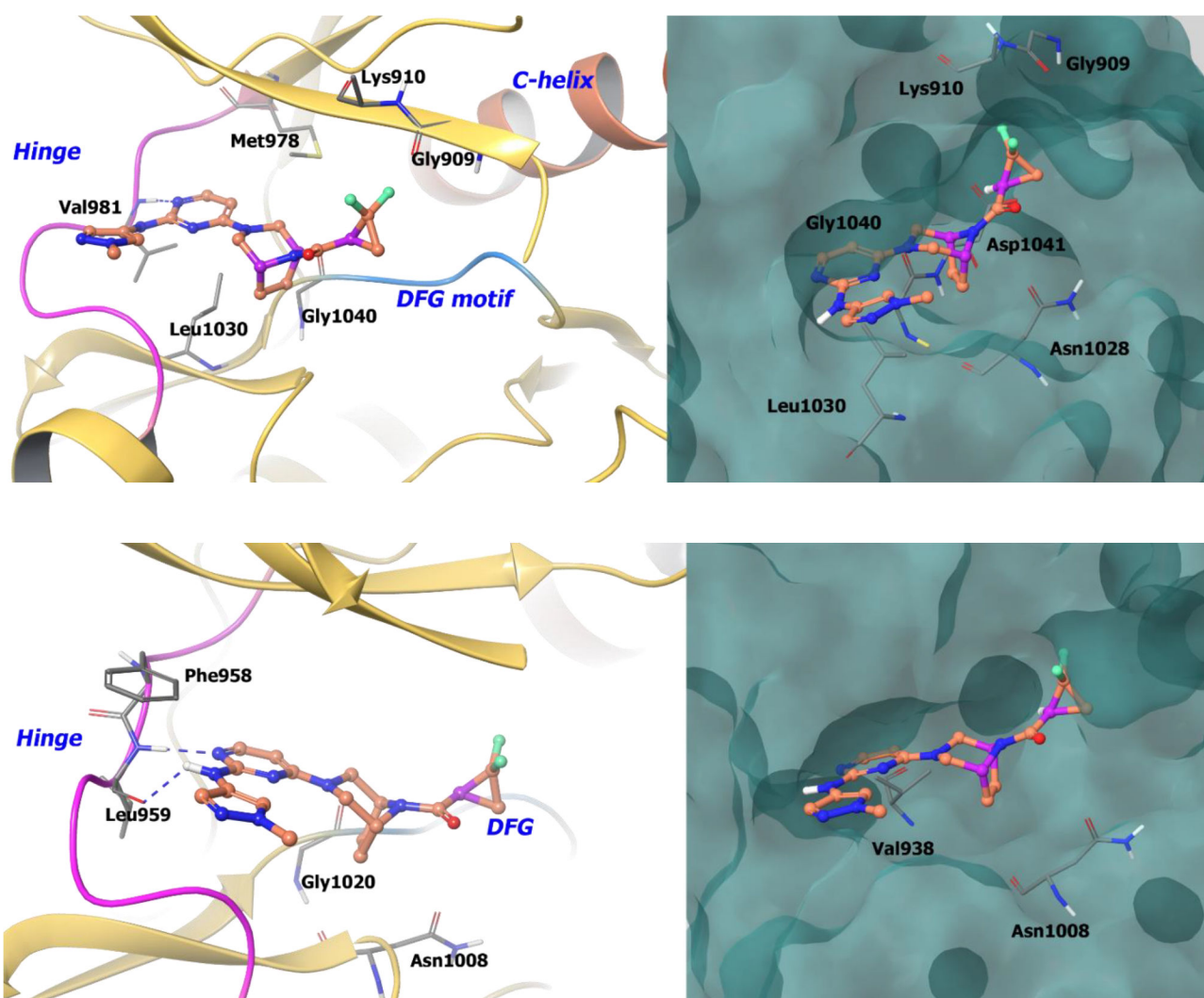




**Figure 7.** The binding of compound **27** into JAK3 active site (PDB 1YVJ, 2.55 Å). Interaction of compound **27** at the binding site of protein. The protein is depicted as yellow ribbons, and the hydrogen bonds are illustrated with blue dashed lines; Compound **27** atoms are colored as follows: carbon, red-orange; nitrogen, blue; oxygen, red; chlorine, green; fluorine, jade; hydrogen, white; the chiral carbon is highlighted in violet.

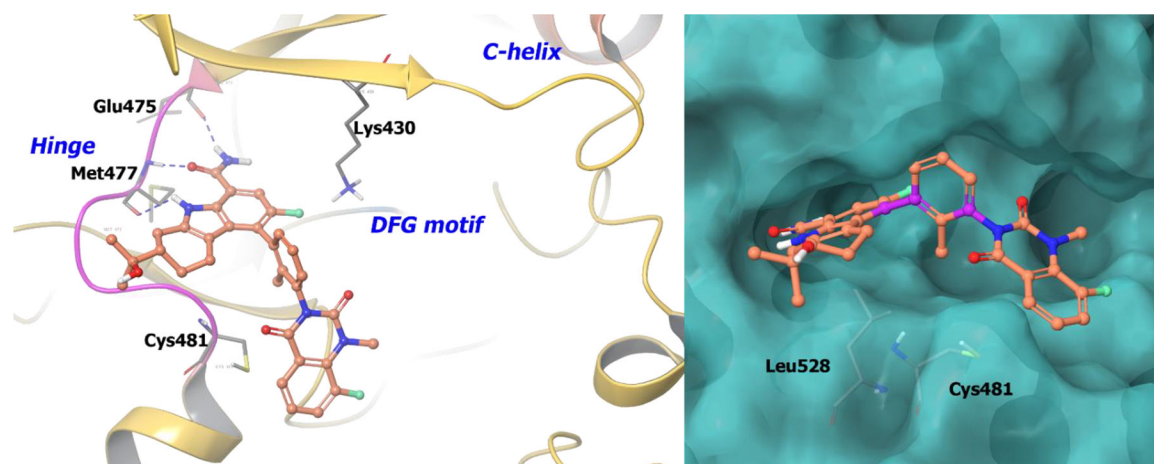


**Figure 8.** Superimposition of the six-membered ring of the lowest energy conformation (MM2 energy minimization) of compounds **A**:[27 (*R,R*)]; **B**:[27a (*R,S*)]; **C**:[27b (*S,R*)]; **D**: [27c (*S,S*)] (colored by atom type) and their respective best docked poses (colored in pink).



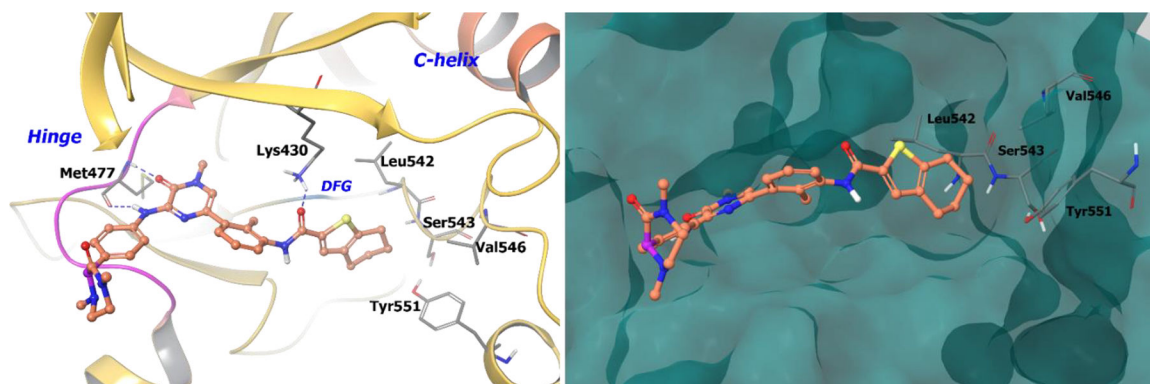
**Figure 9:**

**A.** The co-crystal structure of compound **36a** bound to TYK2 (PDB 6DBM, 2.36 Å). Left Panel: Interaction of compound **36a** with TYK2, the protein is depicted as yellow ribbons, and the hydrogen bonds are illustrated with blue dashed lines; Right panel: The binding site of compound **36a** in TYK2. The surface of the protein is depicted in blue. **B.** The co-crystal structure of compound **36a** bound to JAK1 (PDB 6DBN, 2.48 Å). Left Panel: Interaction of compound **36a** with JAK1. The protein is depicted as yellow ribbons, and the hydrogen bonds are illustrated with blue dashed lines; Right panel: The compound **36a** binding site in JAK1. The surface of the protein is depicted in blue. Compound **36a** atoms are colored as follows: carbon, red-orange; nitrogen, blue; oxygen, red; chlorine, green; fluorine, jade; hydrogen, white; the chiral carbon is highlighted in violet.



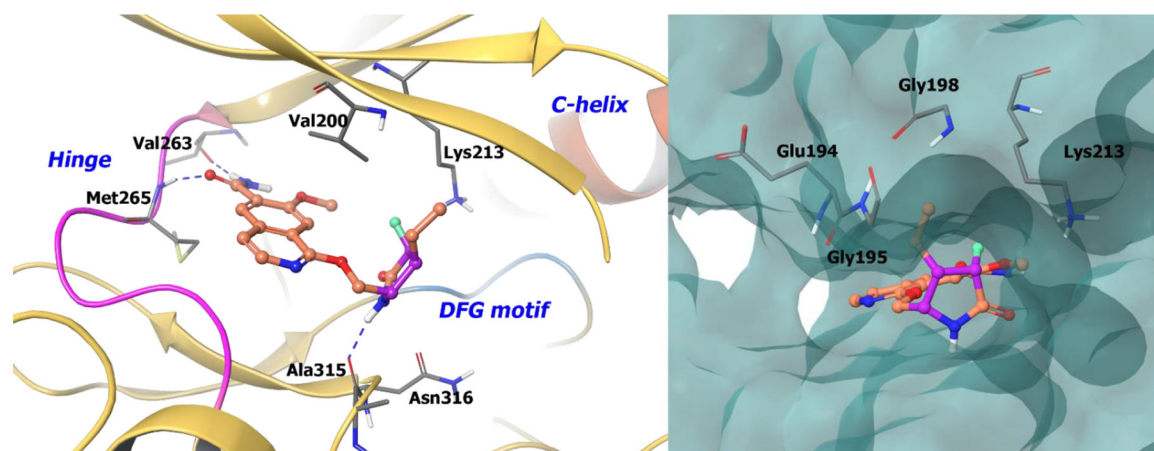
**Figure 10.**

The co-crystal structure of compound **41** bound to BTK (PDB 5T18, 1.5 Å). Left Panel: Interaction of compound **41** with the protein. The protein is depicted as yellow ribbons, and the hydrogen bonds are illustrated with blue dashed lines; Right panel: The binding site of compound **41**, The surface of the protein is depicted in blue. compound **41** atoms are colored as follows: carbon, red-orange; nitrogen, blue; oxygen, red; chlorine, green; fluorine, jade; hydrogen, white; the chiral carbon is highlighted in violet.



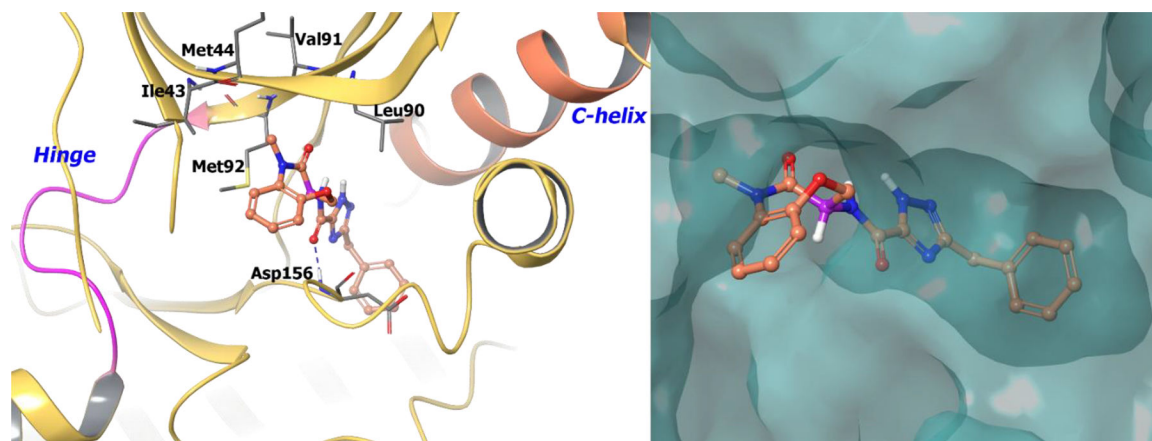
**Figure 11.**

The co-crystal structure of compound **44** bound to BTK (PDB 4OTF, 1.95 Å). Left Panel: Interaction of compound **44** with the protein. The protein is depicted as yellow ribbons, and the hydrogen bonds are illustrated with blue dashed lines; Right panel: The binding site of compound **44** in BTK. The surface of the protein is depicted in blue. compound **44** atoms are colored as follows: carbon, red-orange; nitrogen, blue; oxygen, red; chlorine, green; fluorine, jade; hydrogen, white; the chiral carbon is highlighted in violet.



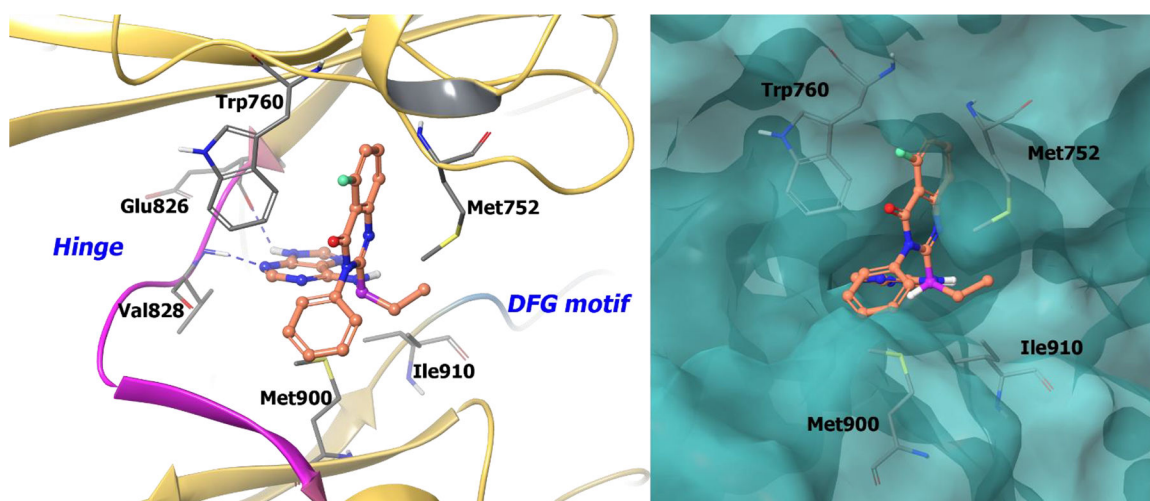
**Figure 12.**

The co-crystal structure of compound **53** bound to IRAK4 (PDB 5UIU, 2.02 Å). Left Panel: Interaction of compound **53** with the protein. The protein is depicted as yellow ribbons, and the hydrogen bonds are illustrated with blue dashed lines; Right panel: The binding site of compound **53** in IRAK4. The surface of the protein is depicted in blue. compound **53** atoms are colored as follows: carbon, red-orange; nitrogen, blue; oxygen, red; chlorine, green; fluorine, jade; hydrogen, white; the chiral carbon is highlighted in violet.



**Figure 13.**

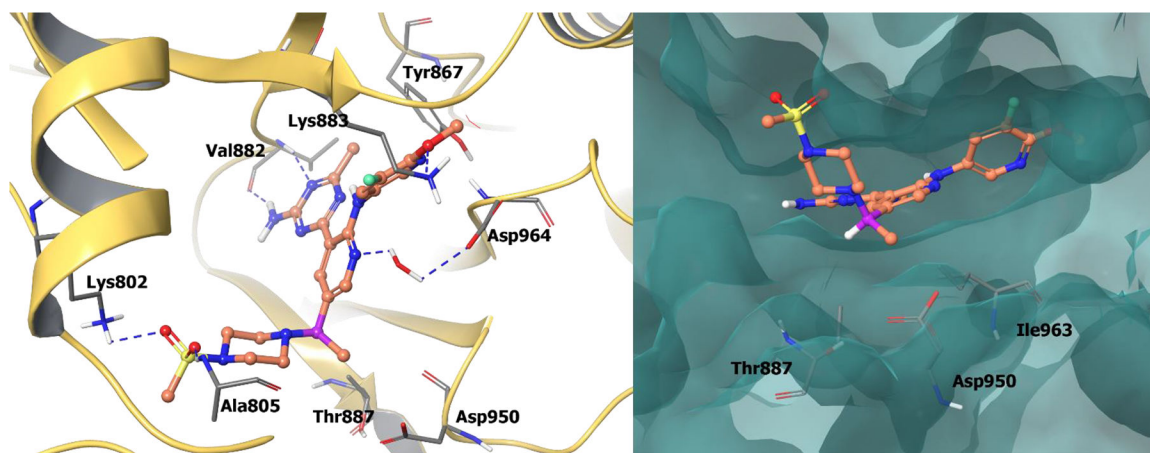
The co-crystal structure of compound **57** bound to RIP1 (PDB 5TX5, 2.56 Å). Left Panel: Interaction of compound **61** with the protein. The protein is depicted as yellow ribbons, and the hydrogen bonds are illustrated with blue dashed lines; Right panel: The binding site of compound **57** in RIP1, The protein surface is depicted in blue. Compound **57** atoms are colored as follows: carbon, red-orange; nitrogen, blue; oxygen, red; chlorine, green; fluorine, jade; hydrogen, white; the chiral carbon is highlighted in violet.



**Figure 14.**

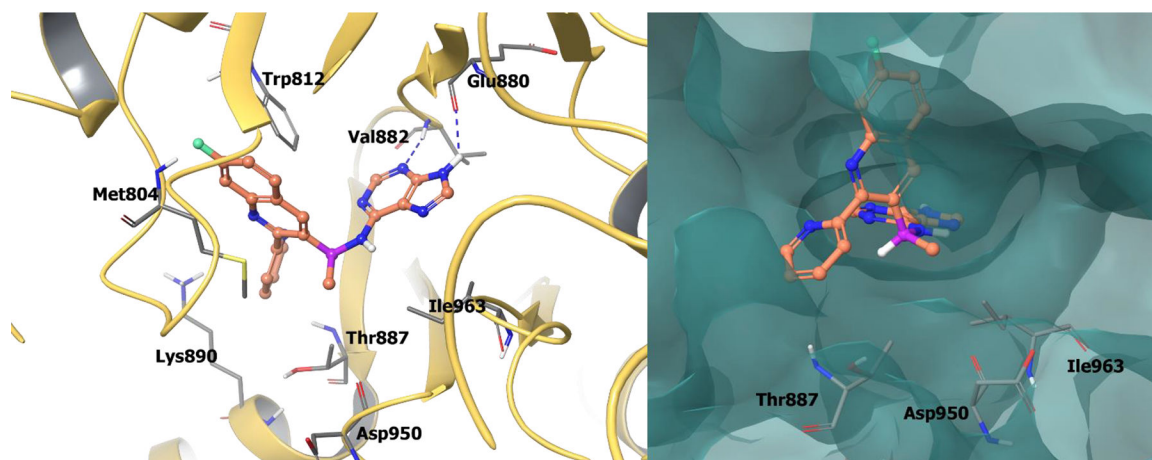
The co-crystal structure of compound **62** bound to PI3K $\delta$  (PDB 4XE0, 2.35 Å). Left Panel: Interaction of compound **62** with the protein. The protein is depicted as yellow ribbons, and the hydrogen bonds are illustrated with blue dashed lines; Right panel: The binding site of compound **62** in PI3K $\delta$ . The protein surface is depicted in blue. Compound **62** atoms are colored as follows: carbon, red-orange; nitrogen, blue; oxygen, red; chlorine, green; fluorine, jade; hydrogen, white; the chiral carbon is highlighted in violet.





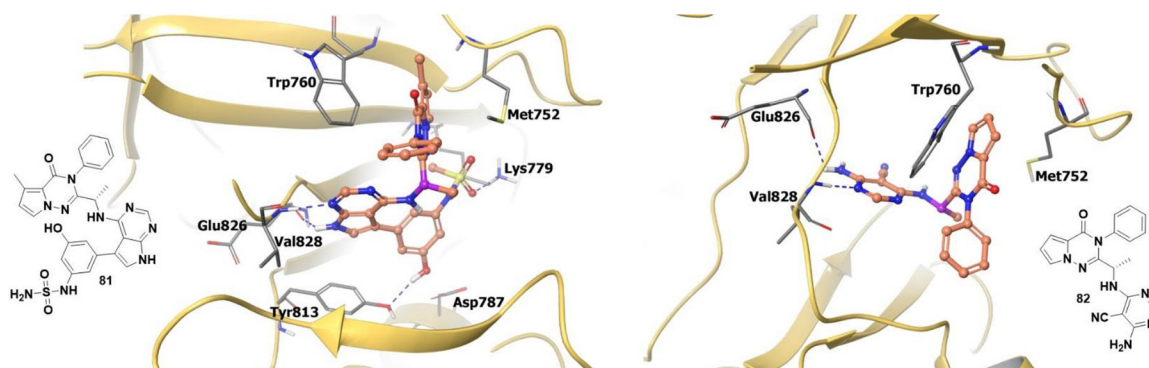
**Figure 15.**

The co-crystal structure of compound **67a** bound to PI3K  $\gamma$  (PDB 4FLH, 2.6 Å). Left Panel: Interaction of compound **67a** with the protein. The protein is depicted as yellow ribbons, and the hydrogen bonds are illustrated with blue dashed lines; Right panel: The binding site of compound **67a** in PI3K  $\gamma$ . The protein surface is depicted in blue. Compound **67a** atoms are colored as follows: carbon, red-orange; nitrogen, blue; oxygen, red; chlorine, green; fluorine, jade; hydrogen, white; the chiral carbon is highlighted in violet.



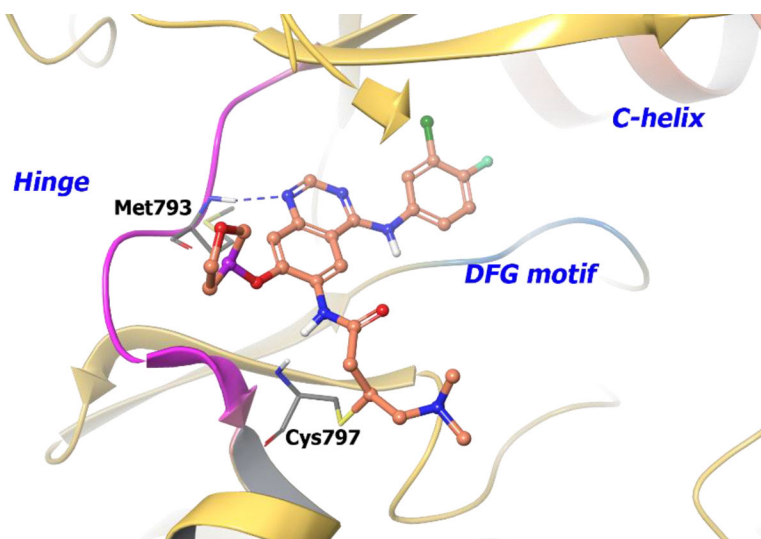
**Figure 16.**

The co-crystal structure of compound **71** bound to PI3K  $\gamma$  (PDB 4WWN, 2.7 Å). Left Panel: Interaction of compound **71** with the protein. The protein is depicted as yellow ribbons, and hydrogen bonds are illustrated with blue dashed lines; Right panel: The compound **71** binding site in PI3K  $\gamma$ . The surface of the protein is depicted in blue. Compound **71** atoms are colored as follows: carbon, red-orange; nitrogen, blue; oxygen, red; chlorine, green; fluorine, jade; hydrogen, white; the chiral carbon is highlighted in violet.

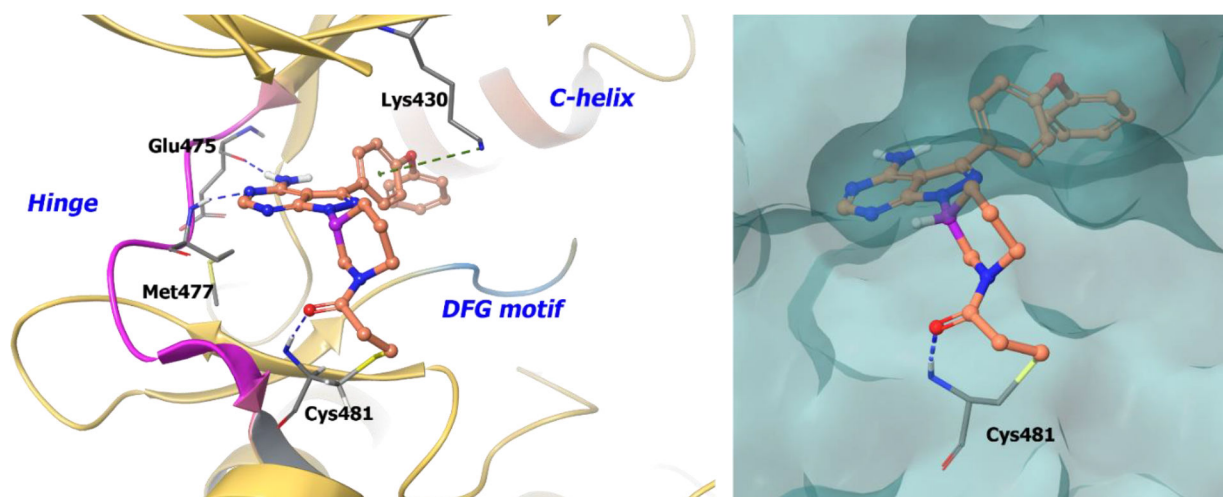


**Figure 17.**

Left Panel: The co-crystal structure of analogue **81** bound to catalytic site of PI3K $\delta$  (PDB 6G6W, 2.72 Å). Right Panel: The co-crystal structure of analogue **82** bound to catalytic site of PI3K $\delta$  (PDB 5M6U, 2.85 Å). The protein is depicted as yellow ribbons, and the hydrogen bonds are illustrated with blue dashed lines; Analogue **81** and **82** atoms are colored as follows: carbon, red-orange; nitrogen, blue; oxygen, red; chlorine, green; fluorine, jade; hydrogen, white; the chiral carbon is highlighted in violet.

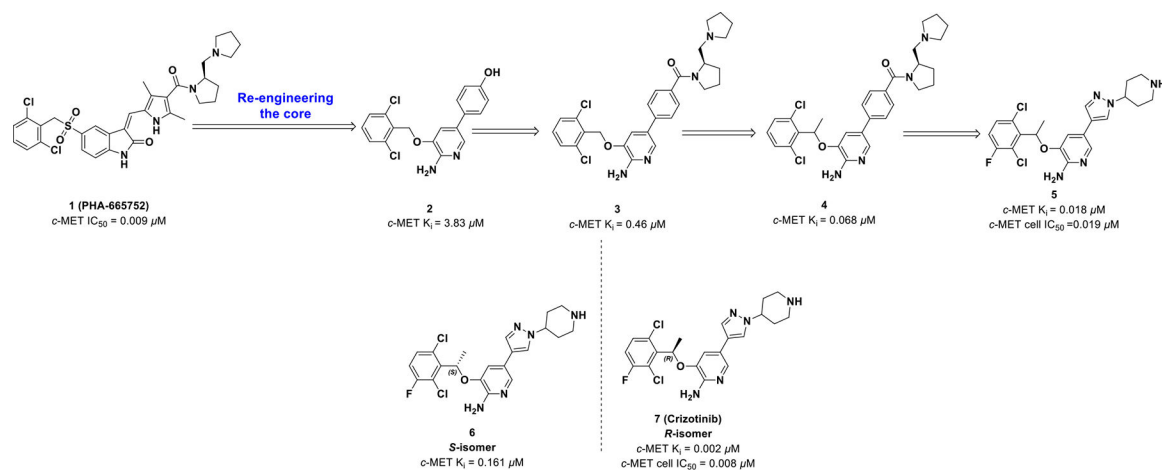


**Figure 19.** The co-crystal structure of compound **88** bound to EGFR<sup>T790M</sup> mutant (PDB 4G5P, 3.17 Å). The protein is depicted as yellow ribbons, and the hydrogen bonds are illustrated with blue dashed lines. Compound **88** atoms are colored as follows: carbon, red-orange; nitrogen, blue; oxygen, red; chlorine, green; fluorine, jade; hydrogen, white; the chiral carbon is highlighted in violet..

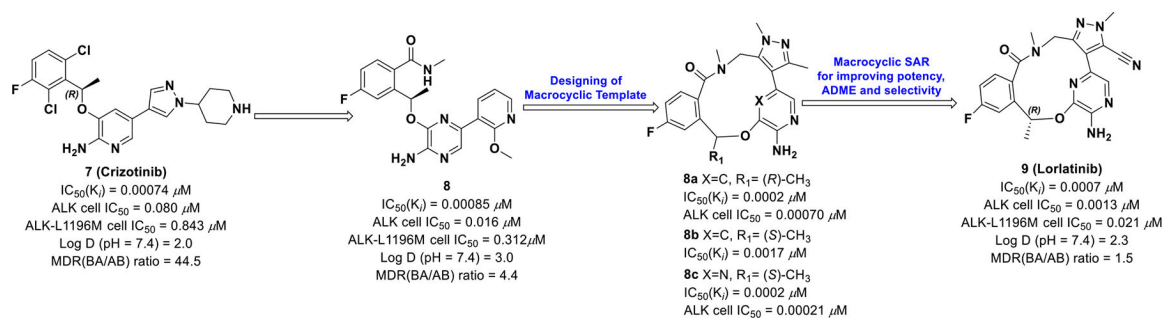


**Figure 20.**

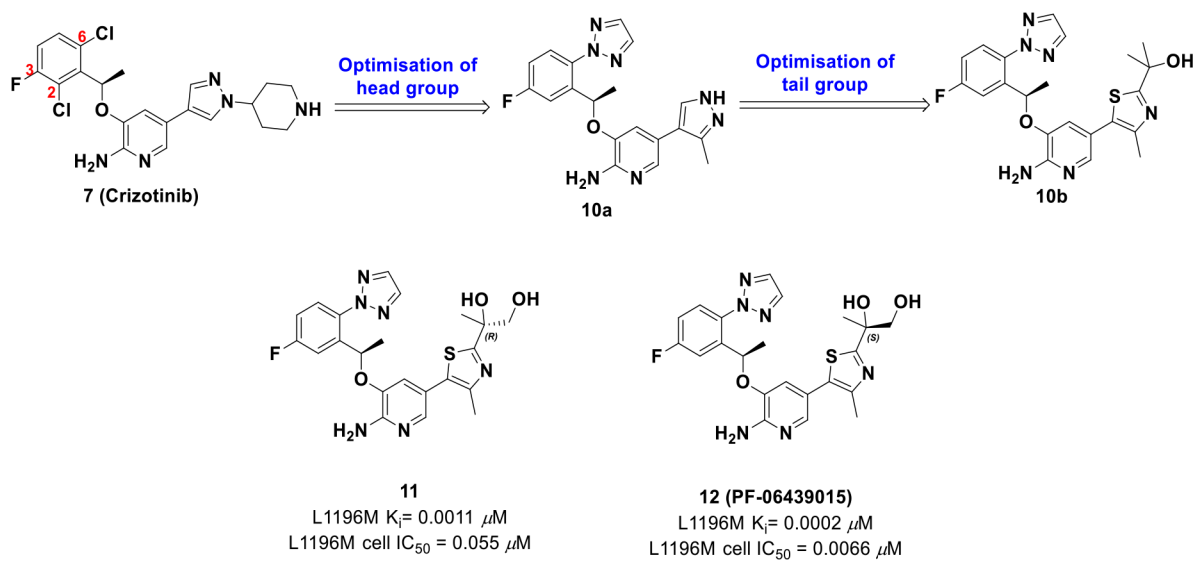
Compound **90b** docked into the ATP binding pocket of EGFR (PDB 5FBN, 3.17 Å). Left Panel: Interaction of compound **90b** with the protein. The protein is depicted as yellow ribbons, and the hydrogen bonds are illustrated with blue dashed lines; Right panel: The binding site of compound **90b** in EGFR. The protein surface is depicted in blue. Compound **90b** atoms are colored as follows: carbon, red-orange; nitrogen, blue; oxygen, red; chlorine, green; fluorine, jade; hydrogen, white; the chiral carbon is highlighted in violet..



**Scheme 1.**  
Drug design of compound 7.

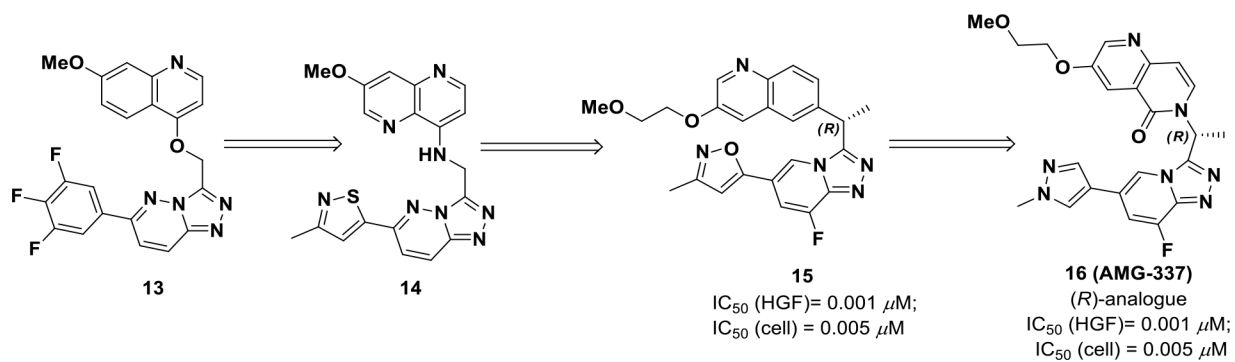


**Scheme 2.**  
 Drug design of compound **9**.

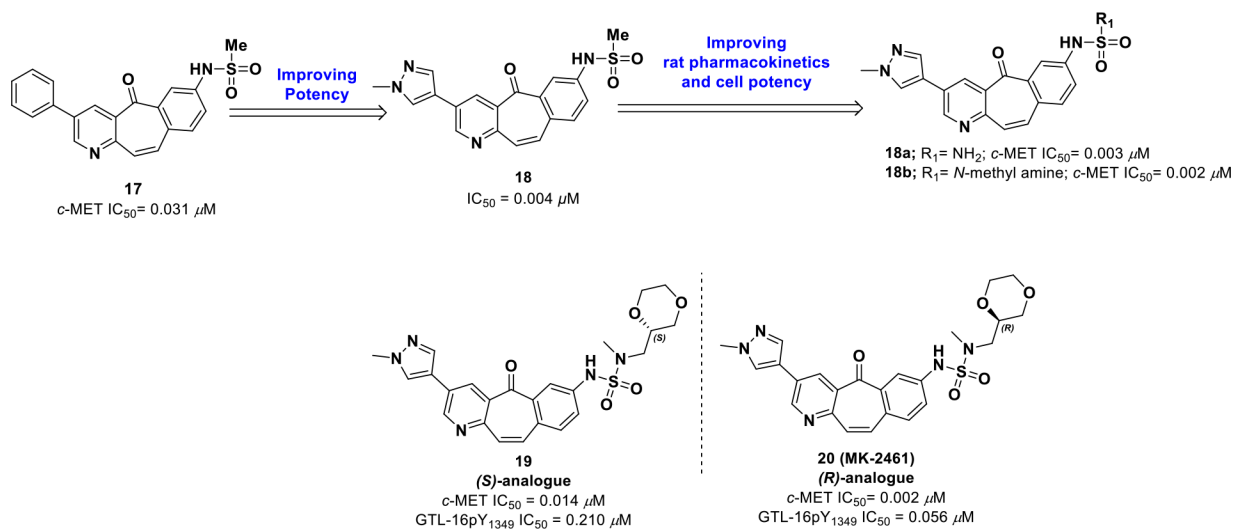


**Scheme 3.**  
Drug design of compound **12**

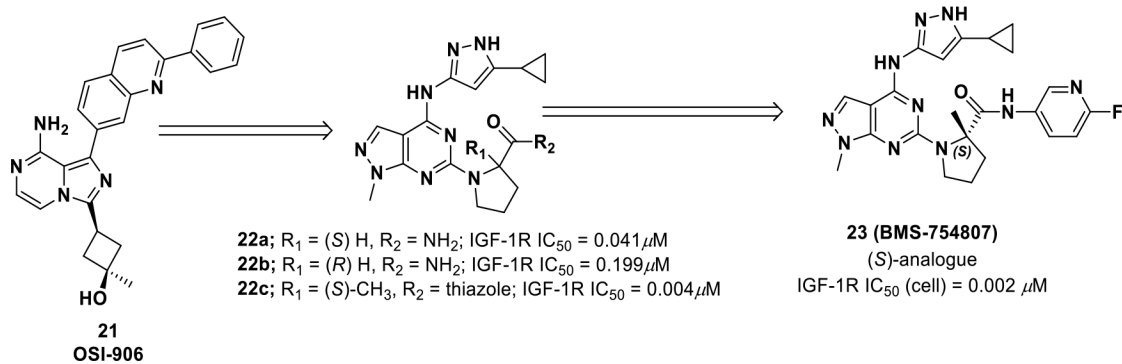




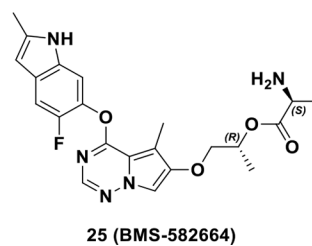
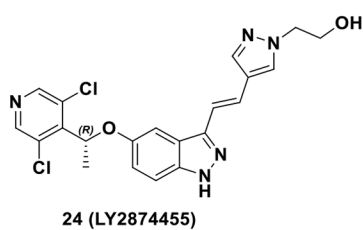
**Scheme 4.**  
Drug design of compound **16**



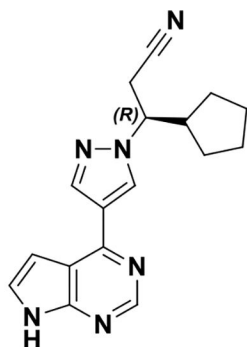
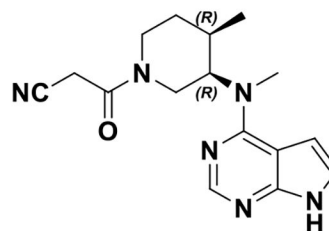
**Scheme 5.**  
 Drug design of compound **18**



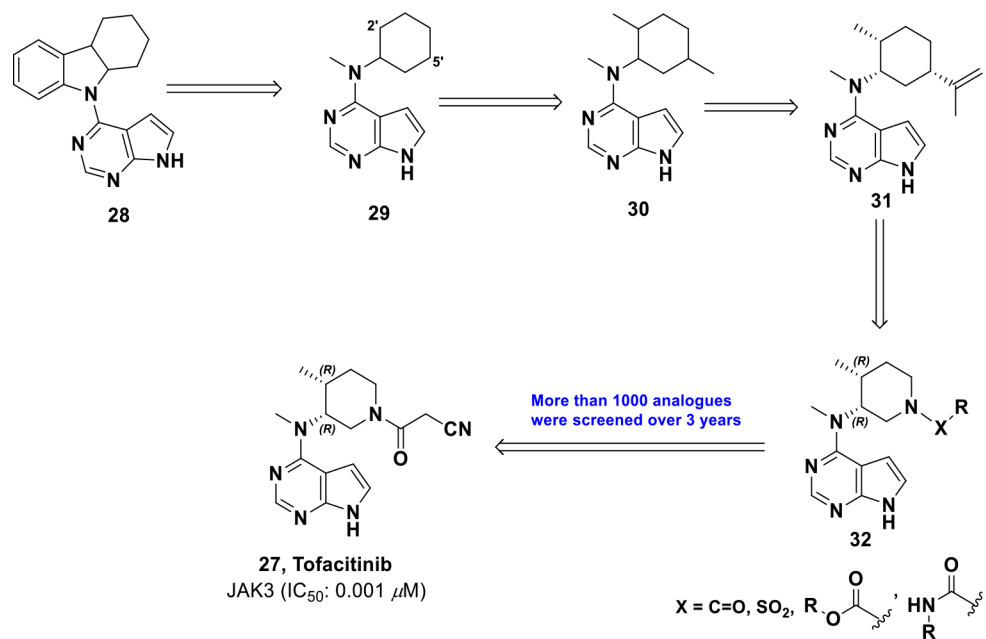
**Scheme 7.**  
Drug design of compound **23**

**Scheme 8.**

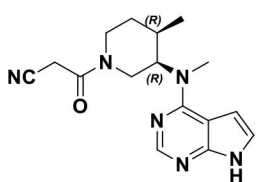
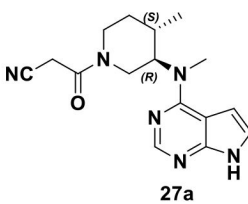
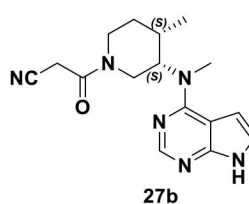
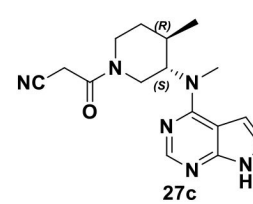
Chemical structures of chiral RTK inhibitors **24** and **25**.

**26 (Ruxolitinib)**JAK1 (IC<sub>50</sub>: 0.0033 μM)JAK2 (IC<sub>50</sub>: 0.0028 μM)JAK3 (IC<sub>50</sub>: 0.428 μM)**27 (Tofacitinib)**JAK3 (IC<sub>50</sub>: 0.001 μM)**Scheme 9.**

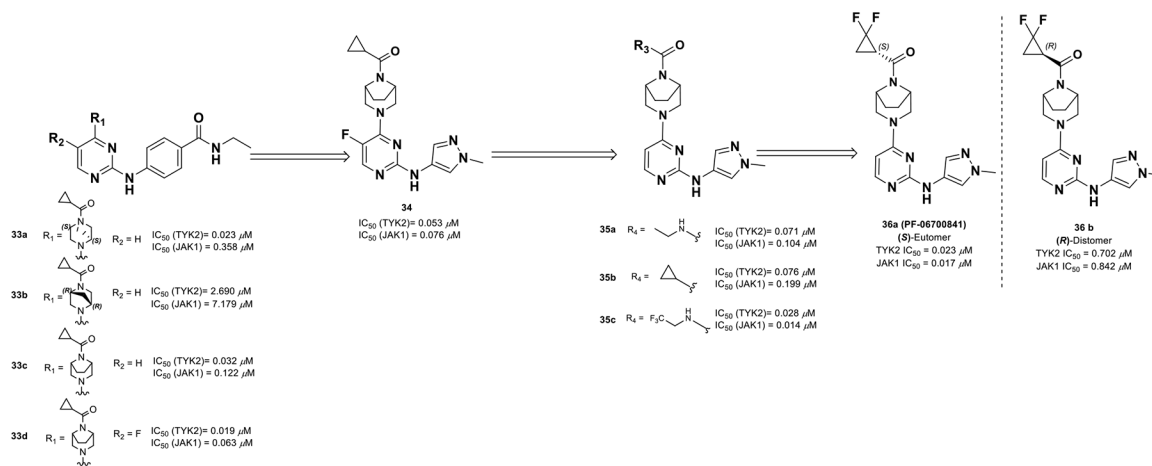
FDA approved chiral JAK inhibitors



**Scheme 10.**  
Drug development of compound 27

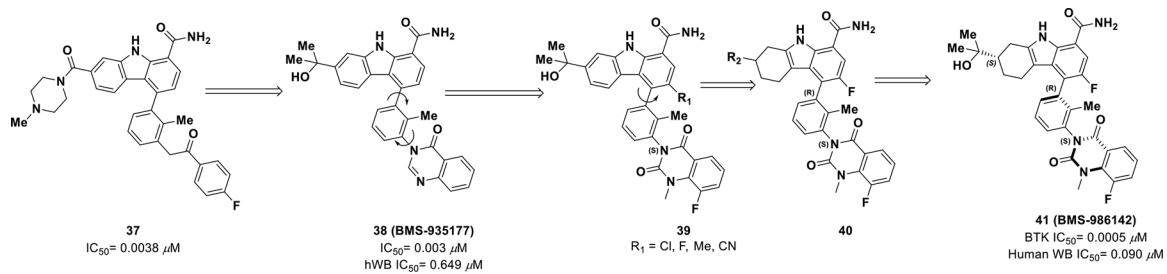
**27 (Tofacitinib)** $IC_{50}$  (JAK3) = 0.001  $\mu$ M $IC_{50}$  (JAK2) = 0.020  $\mu$ M**27a****27b****27c****Scheme 11.**

Four stereoisomers of tofacitinib

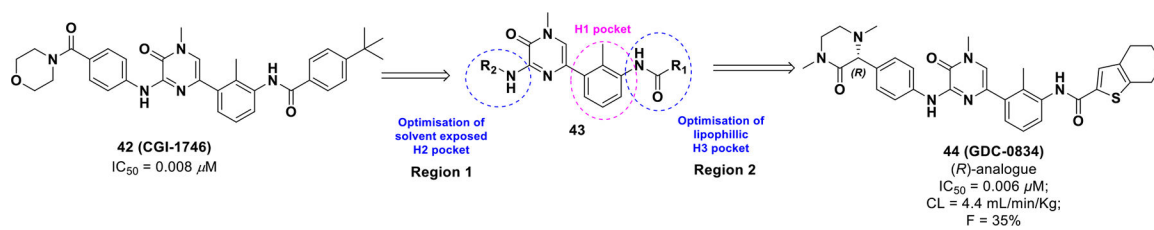


**Scheme 12.**  
Discovery of compound **36a** profile.

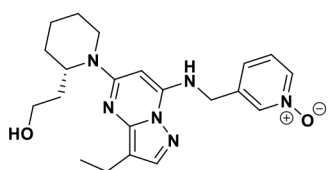




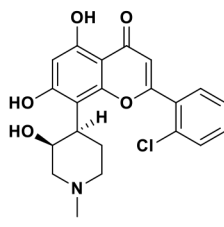
**Scheme 13.**  
Drug discovery of compound **41**



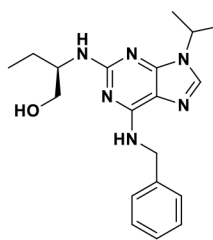
**Scheme 14.**  
Drug discovery of compound 44



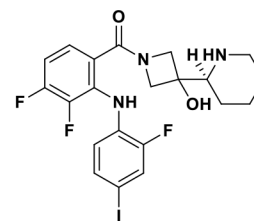
**45 (Dinaciclib)**  
CDK inhibitor  
Merc & Co.



**46 (Alvocidib)**  
CDK9 kinase inhibitor  
Tolero Pharmaceuticals, Inc.

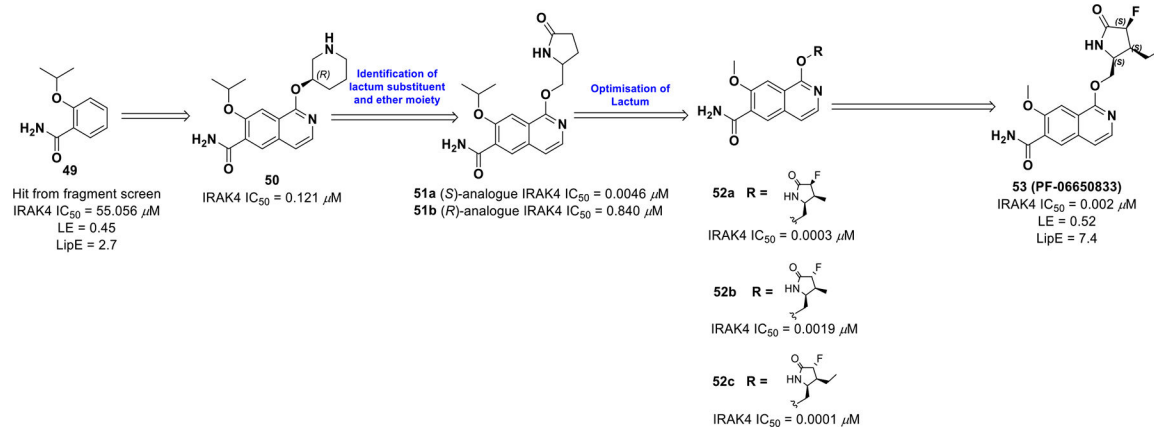


**47 (Seliciclib)**  
CDK2/CDK7/CDK9 Inhibitor

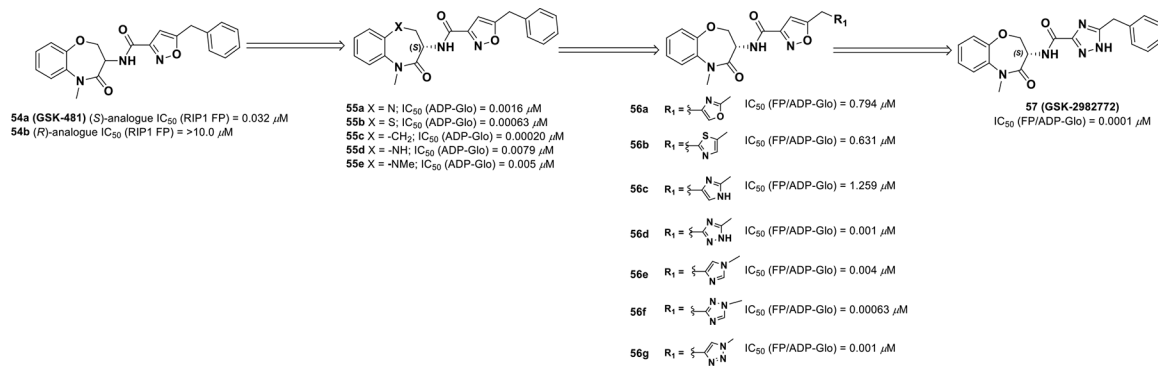


**48 (Cobimetinib)**  
MEK inhibitor  
Exelixis and Genentech (Roche)

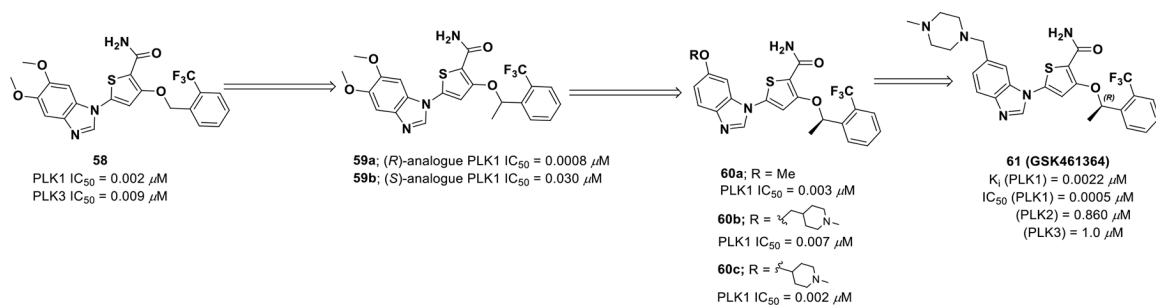
**Scheme 15:**  
Chemical structures of approved CDK and MEK inhibitors



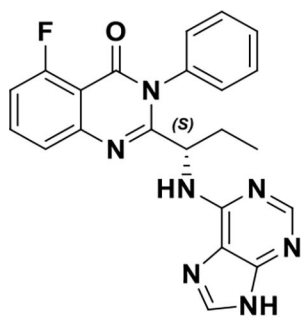
**Scheme 16.**  
 Drug discovery of compound **53**



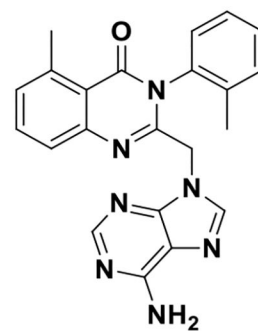
**Scheme 17.**  
Drug discovery of compound **57**



**Scheme 18.**  
Drug discovery of compound **61**

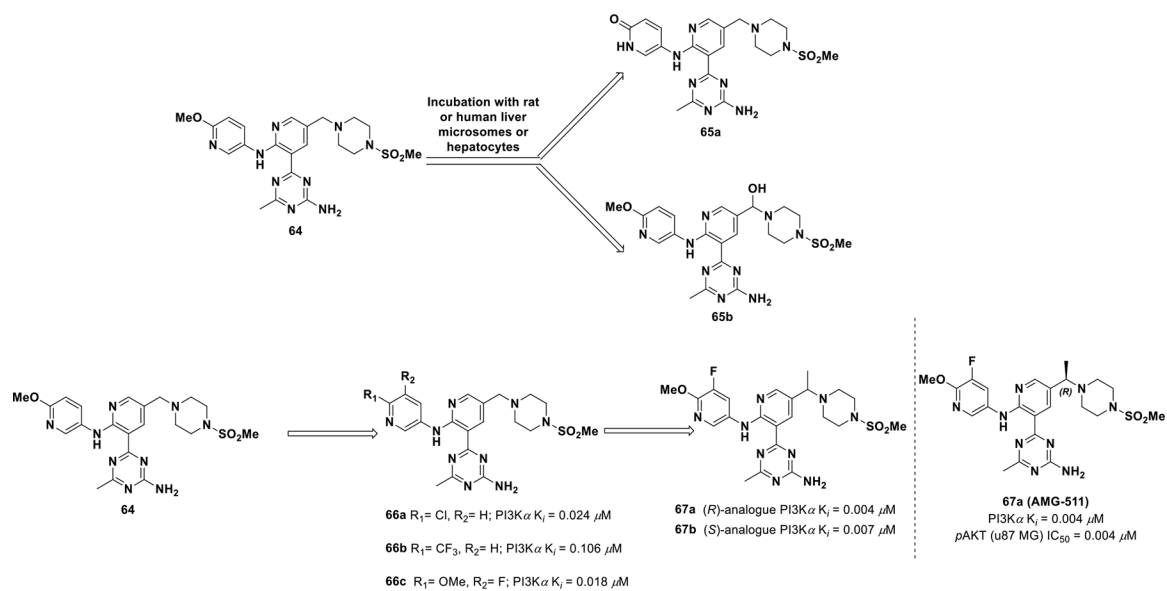


**62 (Idelalisib)**  
PI3K $\delta$  IC<sub>50</sub> = 0.019  $\mu$ M



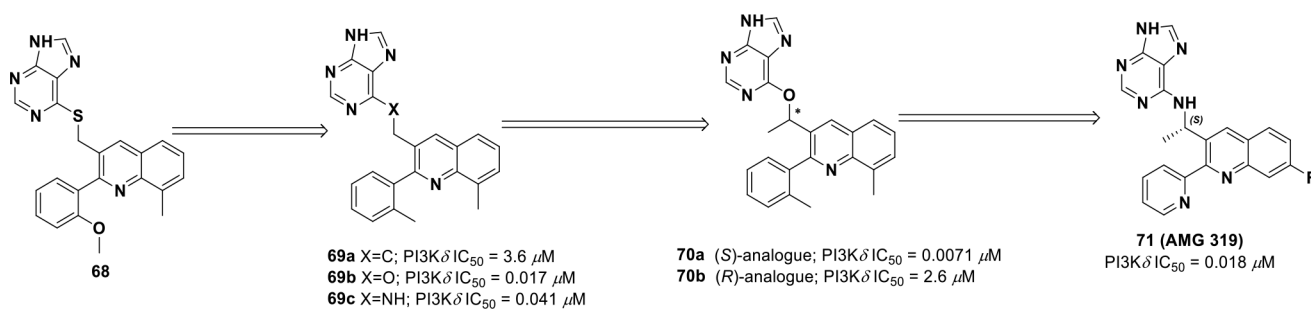
**63 (IC87114)**

**Scheme 19.**  
FDA approved drug **62** and its chemotype **63**

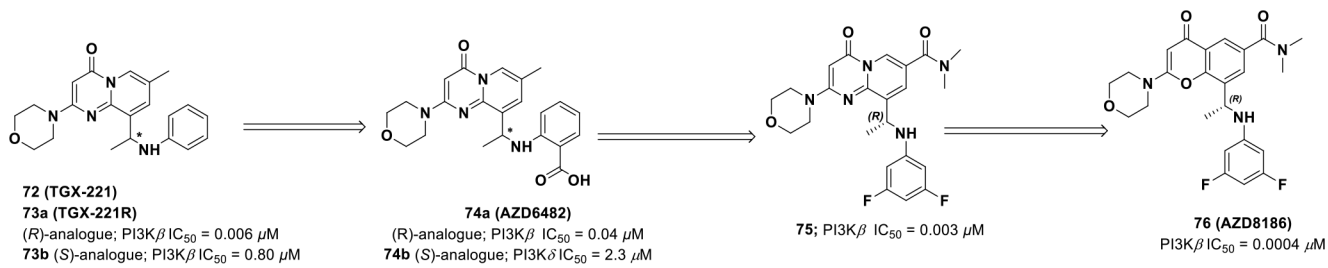


**Scheme 20.**  
Drug discovery of compound **67a**

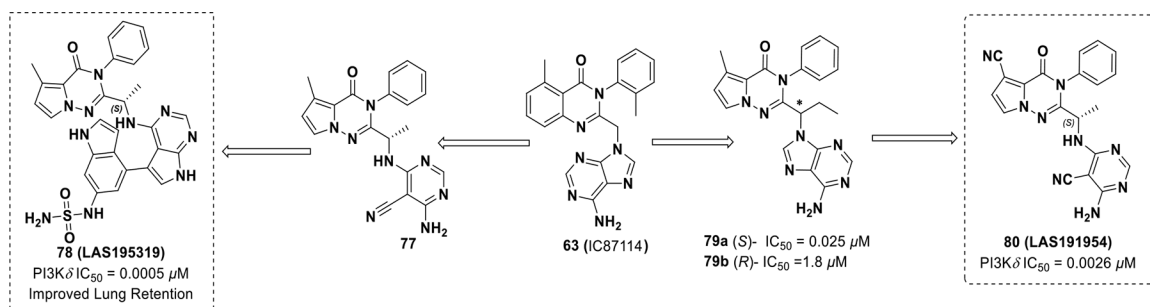




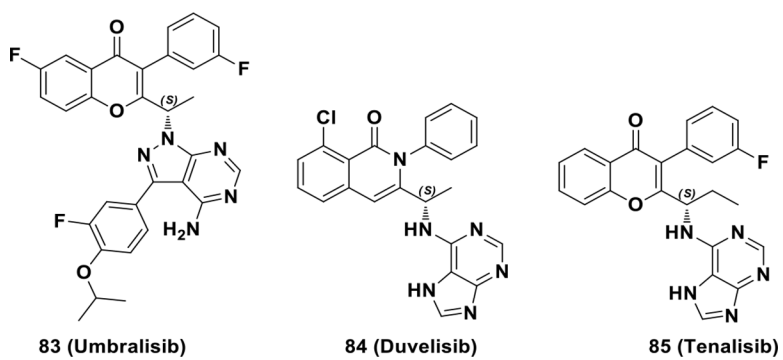
**Scheme 21.**  
Drug discovery of compound **71**



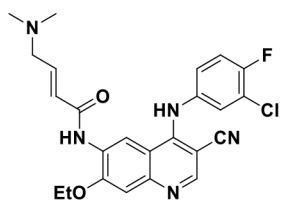
**Scheme 22.**  
Drug discovery of compound **74a** and **76**.



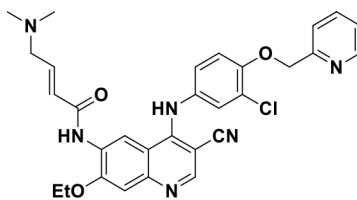
**Scheme 23.**  
Drug discovery of compound **78** and **80**

**Scheme 24.**

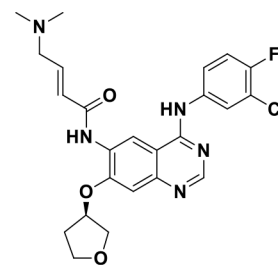
Chemical structures of PI3K clinical candidates **83**, **84** and **85**



**86 (Pelitinib, EKB-569)**  
EGFR:  $IC_{50} = 0.08 \mu M$   
Her2:  $IC_{50} = 1.23 \mu M$



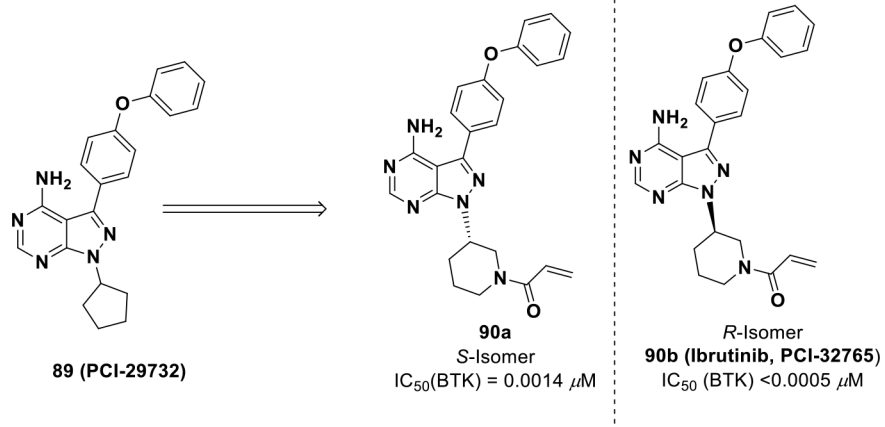
**87 (Napatanib, HKI-272)**  
EGFR:  $IC_{50} = 0.092 \mu M$   
Her2:  $IC_{50} = 0.059 \mu M$



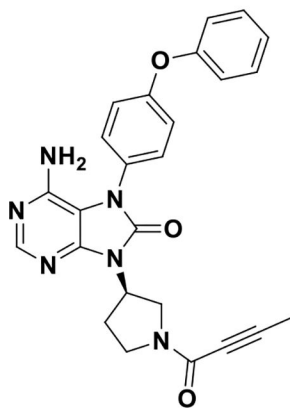
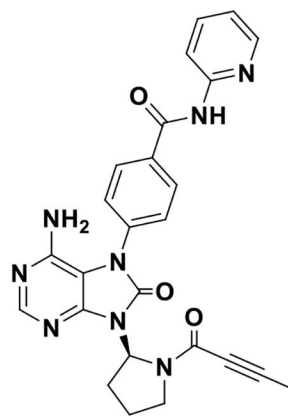
**88 (Afatinib, BIBW-2992)**  
EGFR:  $IC_{50} = 0.0005 \mu M$   
Her2:  $IC_{50} = 0.014 \mu M$

### Scheme 25.

Chemical structures of irreversible EGFR and Her2 inhibitors **86**, **87** and **88**



**Scheme 26.**  
Drug development of compound **90b**

**91 (Tirabrutinib)****92 (Acalabrutinib)**

**Scheme 27:**  
Second generation irreversible BTK inhibitors **91** and **92**.

**Table 1:**

Various approved chiral kinase inhibitors

Drug Name	Tradename	Approval	Developer	Target	Indication
Sirolimus <sup>*</sup>	RAPAMUNE <sup>®</sup>	1999 <sup>23</sup>	Wyeth-Ayerst Research	FKBP12/mTOR	Immunosuppressant
Temsirolimus <sup>*</sup>	TORISEL <sup>®</sup>	2007 <sup>24</sup>	Wyeth Pharmaceuticals	FKBP12/mTOR	Advanced RCC <sup>a</sup>
Everolimus <sup>*</sup>	AFINITOR <sup>®</sup>	2009	Novartis	FKBP12/mTOR	Immunosuppressant
Crizotinib	XALKORI <sup>®</sup>	2011	Pfizer	ALK, c-MET, HGFR	NSCLC
Ruxolitinib	JAKAFI <sup>®</sup>	2011	Incyte	JAK1, JAK2	Myelofibrosis
Tofacitinib	XELJANZ <sup>®</sup>	2012	Pfizer	JAK2, JAK3	RA <sup>b</sup>
Afatinib	GILOTRIF <sup>®</sup>	2013	Boehringer Ingelheim	EGFR, HER2	NSCLC <sup>c</sup>
Inbrutinib	IMBRUVICA <sup>®</sup>	2013	Pharmacyclics	BTK	CLL <sup>d</sup> , MCL <sup>e</sup>
Idelalisib	ZYDELIG <sup>®</sup>	2014	Gilead	PI3K $\delta$	Haematological cancers
Cobimetinib	COTELLIC <sup>®</sup>	2015 <sup>25</sup>	Exelixis and Genentech	MEK1/2	Melanoma
Midostaurin <sup>*</sup>	RYDAPT <sup>®</sup>	2017 <sup>26</sup>	Novartis	FLT3	AML <sup>f</sup>
Netarsudil	RHOPRESSA <sup>®</sup>	2018 <sup>27</sup>	Aerie Pharm.	Rho Kinase	Glaucoma
Acalabrutinib	CALQUENCE <sup>®</sup>	2017 <sup>28</sup>	Acerta Pharm	BTK	MCL <sup>e</sup>
Encorafenib	BRAFTOVI <sup>®</sup>	2018 <sup>29</sup>	Array BioPharma	B-Raf <sup>V600E/K</sup>	Melanoma
Larotrectinib	VITRAKVI <sup>®</sup>	2018 <sup>30</sup>	Bayer	NTRK	NTRK positive solid tumors

<sup>\*</sup> Natural-product derived.

<sup>a</sup> RCC, renal cell carcinoma.

<sup>b</sup> RA, rheumatoid arthritis.

<sup>c</sup> NSCLC, non-small cell lung cancer.

<sup>d</sup> CLL, chronic lymphocytic leukemia.

<sup>e</sup> MCL, mantle cell lymphoma.

<sup>f</sup> AML, acute myeloid leukemia.