

Synthetic and Medicinal Chemistry Approaches Toward WEE1 Kinase Inhibitors and Its Degraders

Vidya Jyothi Alli, Pawan Yadav, Vavilapalli Suresh, and Surender Singh Jadav*

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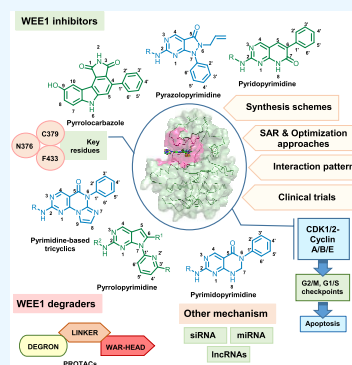
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ABSTRACT: WEE1 is a checkpoint kinase critical for mitotic events, especially in cell maturation and DNA repair. Most cancer cells' progression and survival are linked with elevated levels of WEE1 kinase. Thus, WEE1 kinase has become a new promising druggable target. A few classes of WEE1 inhibitors are designed by rationale or structure-based techniques and optimization approaches to identify selective acting anticancer agents. The discovery of the WEE1 inhibitor AZD1775 further emphasized WEE1 as a promising anticancer target. Therefore, the current review provides a comprehensive data on medicinal chemistry, synthetic approaches, optimization methods, and the interaction profile of WEE1 kinase inhibitors. In addition, WEE1 PROTAC degraders and their synthetic procedures, including a list of noncoding RNAs necessary for regulation of WEE1, are also highlighted. From the standpoint of medicinal chemistry, the contents of this compilation serve as an exemplar for the further design, synthesis, and optimization of promising WEE1-targeted anticancer agents.



1. INTRODUCTION

Genotoxic stress causes DNA damage, that triggers complex signaling pathways called DNA damage responses (DDR) to detect and repair DNA. The compromised pathways lead to tumor and cancer formation.¹ The breakage of DNA strands triggers the ATR-ATM (Ataxia-Telangiectasia mutated and Rad3-related-Ataxia-Telangiectasia mutated) cascade, which ultimately leads to apoptosis, senescence, or DNA patching (based on the degree of DNA damage). The ATR (single-strand DNA breakage) and the ATM (double-strand DNA breakage) activates distress signal messengers called the checkpoint kinases (CHK1 and CHK2, respectively).² Kinases are catalytic agents that transfer the γ -phosphate group from ATP to its substrate protein to either activate or deactivate the substrate, and the action is reversed by phosphatases (Figure 1).³ The kinase, CHK1 activates the guardian of the G2-M cell checkpoint, the WEE1 kinase (via phosphorylation), simultaneously deactivating the CDC25 (cell division cycle kinase 25, responsible for promoting the cell cycle).^{4–6} Conversely, CHK2 activates the tumor suppressor P53.^{7,8} The activated guardians disarm CDK1/2 (cell division kinases 1/2) and induce mitotic arrest, which ensures enough time to mend the DNA. The three members of the WEE protein kinase family, WEE1, WEE2, and MYT1 are negative regulators of cell cycle (by inhibiting CDKs). (1) WEE1 or WEE1A gene expression causes mitotic arrest and contributes to daughter cell maturation. Russell and Nurse et al. identified the WEE1 gene product of 112 kilobases (kb) as a protein kinase in fission yeast.⁹ Later, Igarashi et al. discovered the 2.8 kb long WEE1 gene and its gene product (432 amino acids long WEE1

protein) in humans.¹⁰ The WEE1 gene in humans is located on the 11th chromosome at the band 11p15, more precisely at 11p15.4, which contains 19,788 bases.^{11,12} It is a somatic nuclear serine/threonine (S/T) kinase responsible for cell cycle arrest by inhibiting CDKs via phosphorylating Y15 (in humans) and Y15 and T14 residues of CDC2/28 (homologue of CDK1 of fission and budding yeast).^{4,13–15} Though it phosphorylates Y and T residues, it is still classified as a S/T kinase and not a tyrosine kinase due to its structural and sequential similarities with S/T kinases.¹⁶ (2) WEE1B or WEE2 kinase is an oocyte-specific tyrosine kinase conserved from yeast to humans, responsible for premature oocyte arrest in the GV (germinal vesicle) state during prophase-1 and mature oocyte arrest during metaphase-2 before fertilization.^{17–19} Both meiotic arrests result from WEE2-catalyzed CDK1 inhibition (pY15).²⁰ (3) MYT1 (recently renamed as PKMYT1) is an odd membrane-associated kinase (endoplasmic reticulum and Golgi apparatus) that phosphorylates CDK1 at T14 and Y15 (preferentially T14 in humans) and causes cell cycle arrest at the G2-M checkpoint.^{21–24} Due to their role in cell cycle regulation, WEE1 and MYT1 have become potential anticancer targets.²⁵ In contrast, WEE2 has a role in fertilization but none in tumor induction.

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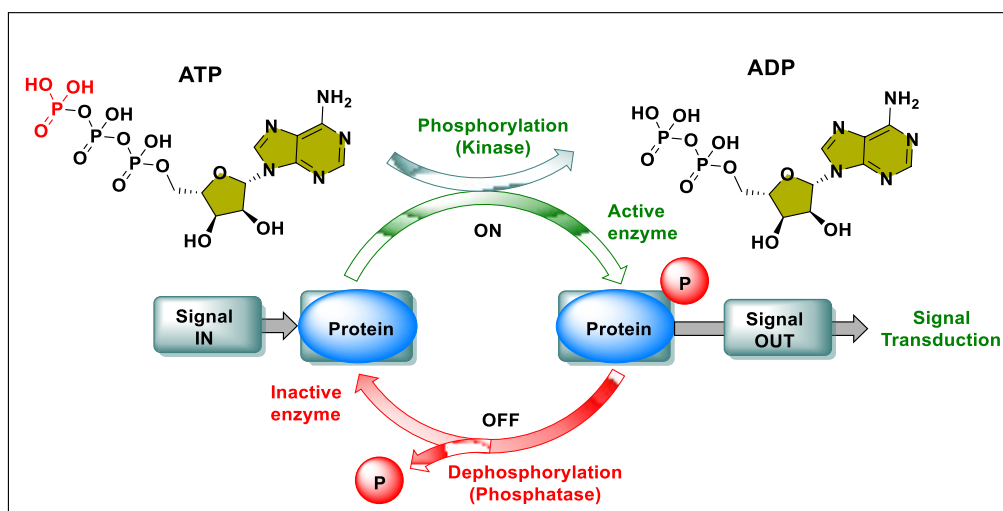


Figure 1. Mechanism of phosphorylation and dephosphorylation by kinase and phosphatases, respectively (adopted from Ha et al.³).

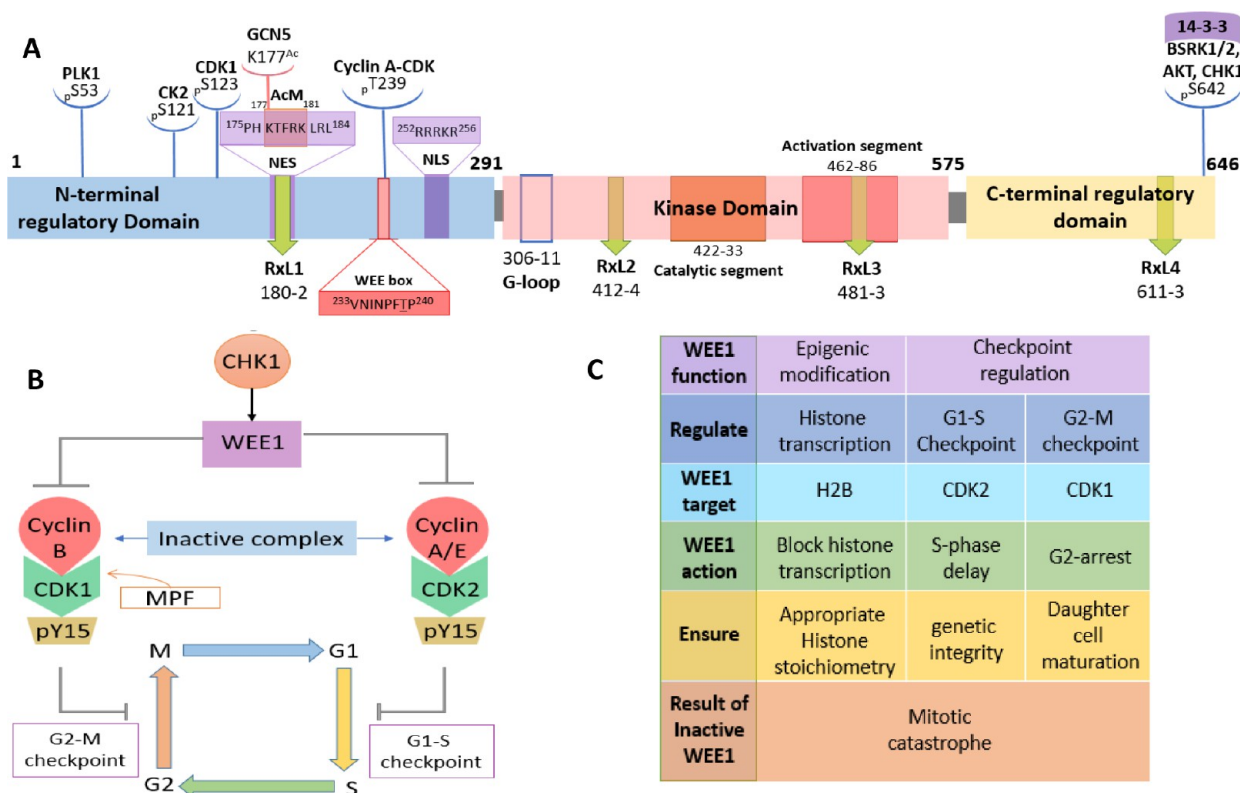


Figure 2. (A) Structure of WEE1 kinase (adopted from Watanabe et al.;²⁶ Matheson et al.;² Squire et al.;¹⁶ Li et al.;²⁸ Zhu et al.³¹). (B) Checkpoint arrest via WEE1 (adopted from Matheson et al.;² Elbaek et al.³⁸) and (C) functions of WEE1 kinase.

1.1. Structure of WEE1 Kinase. Squire et al. gave a detailed account of the structure of the WEE1 kinase using PDB ID: 1X8B (the cocystal structure of the WEE1 complexed with PD0407824).¹⁶ Initially, Watanabe et al. in 1995 constructed a full-length human WEE1 kinase containing 646 amino acids with an approximate molecular mass of 71,597 Da. They depicted the presence of the N-terminal regulatory domain (NRD), the central kinase domain (KD), and the C-terminal regulatory domain (CRD).²⁶ The NRD is equipped with many phosphorylation sites (P-sites), including P-sites for PLK1 (polo-like kinase 1) (S53) and CDK1 (S123), as well as a nuclear localization signal (NLS) (²⁵²RRRKR²⁵⁶)

and three PEST regions.²⁶ This domain furnishes a P-site at S121 for casein kinase 2 (CK2).²⁷ Squire et al. reported that the kinase domain of WEE1 contains a typical kinase structure, i.e., an N-terminal domain (NTD) and a C-terminal domain (CTD) linked by the active site cleft that contains a short catalytic segment (422–433) and a long activation segment (462–486). The catalytic segment retains an altered HRD motif at ⁴²⁴HMD⁴²⁶, while the activation segment conserves DFG and APE motifs with displaced residues, ⁴⁶³DLG⁴⁶⁵ and ⁴⁸⁴ANE⁴⁸⁶, respectively. These residue displacements are specific to WEE1.² The peptide connecting $\beta 5$ - α D is the hinge region (376–379). Additionally, the CRD has an

inhibitory P-site at S642 (via BRSK1/2, AKT, and CHK1) and the 14-3-3 chaperon-binding consensus (⁶³⁹RSVP⁶⁴⁴SLT⁶⁴⁴), which regulate WEE1 stability and subcellular localization.¹⁶ The WEE1 catalytic domain possesses a pair of Mg²⁺ ions, one is bound to N431 and the other to D463, along with three water molecules. ATP or a ligand is bound to the C379 hinge backbone and N376 gatekeeper residues. The adenine moiety or ligand scaffolds are encased in the hydrophobic pocket created by I305, V313, A326, and F433, forming π - π interactions with F433. The phosphate groups of ATP are bound to K328 and K428 residues.¹⁶ The active state conformations of WEE1 show striking similarities with CHK1 kinase.¹⁶ The full-length WEE1 contains a WEE box (²³³VNINPFT²³⁹P²⁴⁰) that encloses an inhibitory cyclin A-CDK complex P-site, T239. The role of the WEE box is to assist the catalytic activity of WEE1. Additionally, WEE1 conserves four RxL motifs, and the most conserved RxL1 binds to cyclin A-CDK to facilitate T239 phosphorylation.²⁸ Moreover, RxL1 is confined within the binding consensus of chromosomal maintenance 1 (CRM1) or exportin-1 or the nuclear export signal (NES) (¹⁷⁵PHKTERK¹⁸⁴LR¹⁸⁴).²⁸ The kinase domain also includes the binding motif of the SH2 domain of adaptor protein, CRK (⁴⁹²YTHL⁴⁹⁵). The NRD is highly rich in S, T, and Y residues ready to phosphorylate.^{29,30} An acetylation motif (AcM)¹⁷⁷KTFRK/R¹⁸¹ is incorporated within the NES, where acetylation and deacetylation of K177 activate and deactivate WEE1 kinase, respectively.³¹ Moreover, in humans, WEE1 is enriched with autophosphorylation sites like Y295 and Y362, whose roles are unknown. A summary of the full-length WEE1 structure is illustrated in Figure 2A.

1.2. Action of WEE1 Kinase. Human WEE1 freezes the cell cycle at the G2-M and G1-S checkpoints by inhibiting the CDKs via phosphorylation at Y15. As a result, the formed homodimer cyclin B/A-pCDK1 complex, also called MPF (mitosis promoting factor), is inactive at the G2-M checkpoint, and the cell cycle is ceased. At the G1-S checkpoint, the inactive cyclin A/E-pCDK2 complex that forms stalls the cell cycle. WEE1 is found to act only if CDKs are bound to their respective cyclins in subsequent studies (Figure 2B,C).³² In normal cells, WEE1-mediated G2-M arrest ensures the maturation of daughter cells. Moreover, in cells with DNA damage, it ensures DNA repair. Therefore, loss of WEE1 action results in abnormally small-sized daughter cells and loss of genetic integrity, ultimately leading to mitotic catastrophe.⁹ WEE1 also phosphorylates HSP90 (Heat Shock Protein 90) on Y38, disrupting its chaperon and ATPase activity.^{33,34} Additionally, WEE1 is an “Epigenic modifier” that inhibits histone H2B (pY37), blocks histone transcription, and ensures appropriate stoichiometry between histones and DNA (Figure 2C).^{35,36} Moreover, it also interacts, phosphorylates, and inhibits SKP2/FBXL1 (S-Phase Kinase Associated Protein 2/F-box and Leucine-Rich Repeat Protein 1) (pS99), an E3 ubiquitin ligase responsible for degrading P21 and P27 (CDK inhibiting proteins), resulting in inhibited cell cycle progression.³⁷ Furthermore, it protects the replication forks by direct or indirect regulation of endonucleases, MUS81/EME1 (essential meiotic structure-specific endonuclease 1) via CDK1 inactivation.^{38–40}

1.3. Regulation of WEE1 Kinase. In the cell cycle, during the S and G2-phases, where the mitotic delay is a prerequisite, WEE1 is highly expressed and tightly shielded. During interphase, S642 is phosphorylated and bound by 14-3-3, stabilizing and protecting WEE1 from degradation.^{41–43}

Additionally, HSP90 also contributes to WEE1 stability, and its substrate, survivin, inhibits caspase-3 and, in turn, protects WEE1 from degradation.^{33,44,45} MIG6 (mitogen-inducible gene 6) binds at the kinase domain of WEE1 and physically obstructs and prevents WEE1 degradation.⁴⁶ WEE1 is transactivated by c-Fos/AP1 (c-Fos/activator protein 1) during the G1-S phase.⁴⁷ However, after cell maturation or patching the damaged DNA, the cell cycle should proceed into mitosis (M-phase). CDC25 controls the entry into mitosis by removing the inhibitory phosphate group on CDK1/2, thus setting it free to act.^{48,49} The cells proceed with mitosis only if WEE1 is nonfunctional. Hence, WEE1 sheds its armor and is ready for negative regulation by different mechanisms (inactivation and degradation).²⁶ Upon G2-M propagation, inactivation of WEE1 is a result of phosphorylation of WEE1 by NIM1/CDR1 (nonexpresser of PR genes1/cerebellar degeneration related protein 1, on the N-terminal catalytic domain),^{50–52} BRSK1/2 (BR serine/threonine kinase 1/2, at S642, that regulates differentiation of neurons),^{53,54} and CDK1/2-cyclin A (at T239).²⁸ During M-phase, ubiquitin-dependent protein degradation is responsible for the downfall of WEE1. Initially, during the G2-M transition, PLK1, CDK1, and CK2 phosphorylation at S53, S123, and S121 residues generate phosphodegrons (PDs), and CDC34 ubiquitination of WEE1 allows SCF (skp1/cul1/F-box) β -TrCP (β -transduction repeat-containing protein), Tome-1 (trigger-of-mitotic-entry 1), Smurf1 (Smad ubiquitination regulatory factor1), and Pof1/3 (Promoter of Filamentation1/3) (in fission yeast) mediated WEE1 degradation.^{55–61} However, in a later study, WEE1 was found to interact with the β -subunit of CK2, but this interaction showed no remarkable influence on WEE1 kinase activity.⁶² Another mechanism reported is the nuclear export of WEE1. (1) AKT (Protein Kinase B) phosphorylates WEE1 at S642, which promotes nuclear export via 14-3-3 Θ binding.⁶³ (2) A CRM1-dependent nuclear export may occur via phosphorylation of S/TX residues (CDK2-cyclin A) near the RxL1 motif embedded in NES.²⁸ During the onset of a new cycle, WEE1 is positively regulated via increased synthesis and dephosphorylation (FCP1 on T239).⁶⁴ In *Xenopus* WEE1, phosphorylation of T186 (human T329 equiv) of WEE box creates a pS/TP binding motif for PIN1 (peptidyl-prolyl cis-trans isomerase NIMA-interacting 1) that inhibits WEE1 activity during M-phase.⁶⁵ Zhu et al. recently identified WEE1 as an inactive endogenous homodimer forming intermolecular H-bonds between NRD (K177, H176, and T178) and KD (D405) of WEE1.³¹ These interactions are disrupted by the acetylation of K177 by GCN5 (General Control Non-Depressible 5) after pS642 by CHK1 due to DNA damage, which induces depolymerization and WEE1 activation. This action is reversed after DNA repair when SIRT1 (sirtuin 1) binds and flings the acetyl group off K177.³¹ WEE1 expression also tightly follows the circadian rhythm.⁶⁶ A summary of the phosphorylation pathways of WEE1 is illustrated in Figure 3.

1.4. WEE1 and Cancer. In most cancer cells, the tumor-suppressor TP53 is nonfunctional, and the G1/S checkpoint is inoperative. Hence, the cells lose the ability to mend DNA before replication in S-phase and are thus allowed to carry mutations. Therefore, the G2/M checkpoint shoulders the responsibility for patching the DNA by employing cell cycle arrest and mending the DNA just enough to dodge apoptosis.^{2,67} Thus, getting rid of the restriction on the G2/M checkpoint will have a massive impact on the cancer cells.

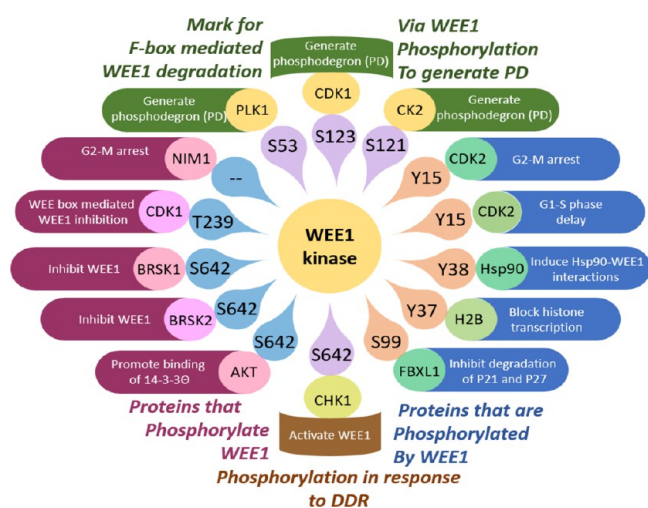


Figure 3. Proteins phosphorylation “of WEE1 and by WEE1”.

Apparently, WEE1 expression is highly elevated in many TP53 mutant cancer types like ovarian cancer, carcinomas, gliomas, leukemia, melanoma, breast cancer, medulloblastoma, etc., which further emphasizes its role in TP53 mutant onco-cell survival and growth. Moreover, WEE1 also regulates the G1/S checkpoint, so its inhibition not only disposes the cell cycle arrest at the G2/M gate but also at the G1/S gate, which further elevates γ -H2AX (histone family protein X) levels that imply DNA damage (double-strand breaks) and eventually cause mitotic catastrophe.² Furthermore, a functional P21, the downstream regulator of P53, apparently shields the cancer cells from WEE1 inhibition-induced DNA damage and cell death during the S-phase, thus further supporting the notion that TP53 mutants are more susceptible to WEE1 inhibition.⁶⁸ Later studies, however, unveiled that WEE1 inhibition is relatively less but productive on wild TP53 onco-cells. Further, AZD1775 radio-sensitizes oral tongue squamous cell carcinoma, irrespective of TP53 status.⁶⁹

In contrast, the WEE1 gene was less expressed in colon cancer, non-small cell lung cancer (NSCLC), prostate cancer, and stromal breast cancer, which are associated with lamentable prognosis.^{67,70,71} Cancers lacking WEE1 expression are prone to genetic abnormalities and may be sensitive to DNA-damaging agents (DDAs), and treating with these agents induces WEE1 expression.² Cells that either overexpress WEE1 or are induced to express WEE1, either way, depend on the G2/M checkpoint for escaping the mitotic catastrophe; thereby, inhibition of WEE1 provides a chance to treat both types of cancers.^{2,70} Additionally, monotherapy with WEE1 inhibitors (WEE1i) is effective against cells with active chromosomal instability (CIN), but a combination with DDAs is preferable for CIN-inactive cells.⁶⁷ Targeting WEE1 also shows promising results in cancer types with BRCA (breast cancer), RAS (Rat Sarcoma virus), ATRX (ATP-dependent helicase ATRX, X-linked helicase II), EGFR (Epidermal Growth Factor Receptor) mutants, and CCNE1 (Cyclin E1)-amplified cancer types.^{72–78}

PARP [poly(ADP-ribose) polymerase] is an essential target in tackling ovarian cancer, breast, pancreatic, and prostate cancers, including BRCA mutants. However, these cancers developed resistance to PARP inhibitors (PARPi) that undermined the therapeutic effects. The combination of PARPi with checkpoint regulating kinase inhibitors like

WEE1i is a rather commendable strategy.^{79,80} Additionally, combination therapy of WEE1i with PARPi is in clinical trials for refractory, relapsed, and recurrent tumors (NCT02511795, NCT02576444, and NCT03579316, etc.). Moreover, exceptional synergistic cytotoxicity is observed when WEE1 and CHK1 are simultaneously inhibited. The cytotoxicity is due to the increased loading of CDC45 (the kinase responsible for replication initiation) caused by CHK1 inhibition, which causes unscheduled DNA replication and thus increased DNA damage, along with an increase in CDK activity due to WEE1 inhibition that further impairs DNA. Additionally, in small cell lung cancer (SCLC) with acquired resistance to CHK1i, WEE1 is overexpressed. Hence, simultaneous inhibition of WEE1 and CHK1 is a promising strategy.^{81,82} Inhibition of ATR, the upstream regulator of CHK1, with WEE1, also elevates cytotoxicity due to elevated replication stress in acute myeloid leukemia (AML) and triple-negative breast cancer (TNBC), in addition to the antimetastatic effect. Thus, clinical trials (NCT03330847) using combination therapies provide a therapeutic advantage due to the lower toxicity profile of ATR inhibitors (ATRi) compared to CHK1 inhibitors (CHK1i).^{83–85} However, this combination has dissimilar effects on different cancer cells; hence, further development may be restricted.⁸⁶ Inhibiting WEE1 and RAD51 (responsible for repairing double-strand breaks of DNA) together also offers increased genotoxicity in a similar mechanism.⁸⁷

HDAC (histone deacetylase) inhibition restrains the action of CHK1 and expression of c-MYC, and simultaneous inhibition of WEE1 results in elevated DNA damage and ultimately causes cell death, irrespective of TP53 status. This combination is in clinical trials (NCT02381548) and is effective against FLT3 mutants.^{88,89} Furthermore, c-MYC is an upregulated gene in many cancers, and such cancers get addicted to its presence, so suppressing MYC is a sound strategy. However, MYC is mostly considered nondruggable, but targeting its allies is feasible enough. Therefore, the above strategy to inhibit HDAC and WEE1 is productive.^{90,91} HSP90 is an essential chaperone and a potential target in cancer cells because it ensures proper folding of oncoproteins and protects them from degradation. However, HSP90 inhibitors (HSP90i) are not cytotoxic but cytostatic, thereby limiting their application, but WEE1 inhibition sensitizes oncocells to HSP90i. This combined inhibition lowers the expression of both WEE1 and survivin, clients of HSP90, along with the inactivation of AKT in both *in vivo* and *in vitro* studies, which contributes to the exceptional cytotoxicity.^{44,92} WEE1 inhibition has also elevated the expression of STAT1-mediated IFN- γ and PD-L1 (programmed cell death ligand 1) in SCLCs, thus combined WEE1 and PD-L1 may open a new path.⁹³ Figure 4 illustrates all the possible proteins that proffer a sound strategy when inhibited alongside WEE1 in combination therapy.

1.5. Kinase Inhibitors in the Market. Kinase-mediated signaling pathways in many cancers have emerged as hallmark targets for anticancer agents, and the FDA has approved more than 70 drugs to date.⁹⁴ Most kinases are essential for vital cellular functions such as cell cycle progression, angiogenesis, cellular transport, cell adhesion, and signaling.³ Several kinase inhibitors on the market and clinical candidates have been targeting the phosphorylation site of kinase enzymes. The medicinal scaffolds such as aminopyrimidine, aminopyridine, fused pyrimidine, aminopyrazine, pyrazolopyrimidine, anthranilamide, thienopyridine, benzopyrimidine, quinoline, bipyr-

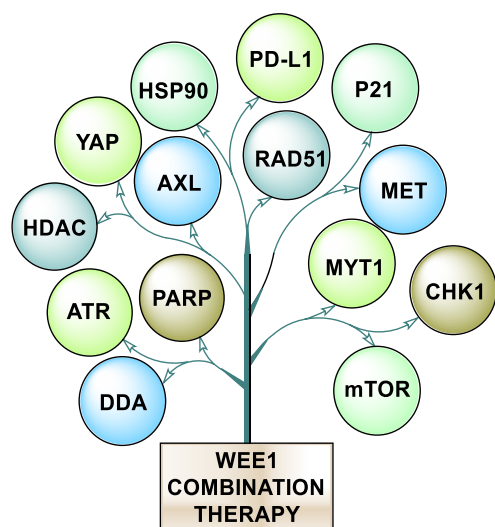


Figure 4. All the possible proteins that proffer sound strategy when inhibited alongside WEE1 in combination therapy.

idine, pyralopyrimidine, benzopyrazole, imidazopyrimidine, aminothiazole, pyralopyridine, pyridopyrimidine, pyrazotriazine, benzimidazole, indalopyrimidine, pyrazopyridine, pyrazolopyridine, quinazoline, and other miscellaneous heterocycles exist in the marketed drugs.

2. SMALL MOLECULE INHIBITORS OF WEE1 KINASE

WEE1 inhibitors are ATP competitive binders that bind in the ATP binding pocket of the kinase and prevent the ATP from binding, thus prohibiting WEE1 activation. Like all other kinase inhibitors, most WEE1i retain the pyrimidine core (I–XVI) and include scaffolds like pyridopyrimidines (VI–VIII), pyrazolopyrimidines (IV), pyrrolopyrimidines (III), pyrimidopyrimidines (X), and pyrimidine-based tricyclics (XI) and other micromolar scaffolds. Apart from these, WEE1i also include nonclassic kinase inhibitors like pyrrolocarbazoles (XVII), vanillates (4), pyrazoles (3), thiazoles (XIX), etc. Being a kinase, WEE1 also accommodates other kinase inhibitors in its ATP binding pocket, including bosutinib (7) and its isomer (8), PF03814735 (6), etc. Figure 5 summarizes all the scaffolds displaying WEE1 inhibition, including classic pyrimidine-based WEE1 kinase inhibitors, and other kinase inhibitors showing WEE1 inhibition. This review describes the above WEE1i, their binding modes, and synthesis procedures to provide an exemplar for the design and development of novel, more ideal WEE1i.

2.1. Pyridopyrimidine. Wang et al. identified PD0166285 (pyridopyrimidine) (10, Figure 6) as the first WEE1i through rapid screening of a chemical library. It is an ATP-competitive inhibitor of WEE1 and MYT1 with an IC_{50} value of 24 nM and 72 nM, respectively. It prevents phosphorylation of deactivation P-sites on CDK1 and abrogates the G2 checkpoint.⁹⁵ This ligand has also shown activity against other kinases or off-targets like c-Src (IC_{50} = 0.009 μ M), PDGFRB (IC_{50} = 0.1 μ M), FGFR (0.43 μ M), CDK1 (0.1 μ M), EGFR (0.35 μ M), and PF3D7 (0.35 μ M). In 2004, Mizenina and Moasser et al. identified two c-Src kinase inhibitors, PD179483 (11) and PD166326 (12), as *in vitro* WEE1i that blocked S-phase.⁹⁶ Some analogues and their activity values are mentioned in Table 1, and Figure 6A illustrates the structures of the very first WEE1 inhibitors.

2.1.1. Structure–Activity Relationship and Optimization Approaches of Pyridopyrimidines. The 2-aminopyrimidine ring of this scaffold acts like the adenine ring of ATP by forming 2 H-bond interactions (one pyrimidine “N” and 2-amino group) with backbone C376 of the hinge region and π – π interactions with F433 (Figures 6B–D).⁹⁷ The aromatic substitution at position-6 remains perpendicular to the core moiety and forms catalytic π -interactions with K328 and H350 (Figure 6D).⁹⁷ 2',6'-Disubstituted aromatic rings increase activity; however, the 2',6'-dichloro group is optimal.⁹⁸ 3'-OH or 3'-NH₂ groups are tolerated but not bulkier groups since they clash with E346.^{97,98} Similarly, small electronegative groups on 4'-position like –OH and –NH₂ associate with D463 and contribute to increased activity.⁹⁷ N-Phenyl and its substitutions (R group from Table 1) protrude from the binding pocket and are solvent-exposed regions. Bulky hydrophilic substitutions with moderate length are highly sought after.⁹⁷ Alkyl substitution on position-5 increases selectivity against c-Src (the alkyl group sterically clashes with T338 residue); however, this selectivity comes at the expense of potency.⁹⁸ In the case of 8N-pyridopyrimidines, pyridine’s “N” (position-8) substituted with small alkyl groups like methyl or ethyl are more active, and these substituents are sandwiched in the cavity between F433 and V331; however, basic groups like amines are not tolerated.⁹⁹ On the other hand, 6N-pyridopyrimidines show no significant difference in activity profile. In either case, position-5 carbonyl, if present, interacts with N376, the gatekeeper residue.⁹⁹ Despite tremendous efforts, the optimization of this scaffold has yet to yield a WEE1i with high selectivity, restricting its clinical applications.

2.1.2. Synthesis of 8N-Pyridopyrimidine Core (VI, VII). The substituted 8N-pyridopyrimidine (VII) scaffold can be made by a method in which 4-chloro-2-(methylthio)pyrimidine-5-carbonyl chloride (13) is reacted with Grignard reagent or aryl zinc halide. In the case of the Grignard reagent, low temperature is maintained in THF. In contrast, aryl zinc halide is first treated to a mixture of CuCN:2LiCl and then reacted with 13 in THF at low temperature to give keto aryl intermediate 14. In the first case, 14 reacts with an alkyl amine at high temperature in isopropanol and generates 15. Bicyclic intermediate 18 is cyclized, when intermediate 15 reacts with another alkyl amine along with N,N-dimethylformidimidethylacetal (DMF-DMA) at high temperature in a microwave reactor. In the second case, intermediate 14 is converted into bicyclic core 18 upon reaction with N-alkyl-substituted amide 19 in the presence of the (Pd₂(dba)₃) catalyst, xantphos ligand, and Ce₂CO₃ at high temperature in dioxane. Another route to generate 18 is when an amide 16 is reacted with 14 and affords 17, which in turn generates 18 when reacted with alkyl boronic acid at ambient temperature in a base Et₃N and solvent CH₂Cl₂. The resultant product 18 is first oxidized with *m*-CPBA in acetonitrile and trifluoroacetic acid, followed by a reaction with aryl amines at elevated temperatures to give VI core (Table 1, Scheme 1).¹⁰⁰

Scaffold VII can be synthesized by reacting 20 with an alkyl amine in a basic medium, followed by reduction with lithium aluminum hydride (LAH) to produce an alcohol intermediate oxidized with MnO₂ to give the corresponding aldehyde 21. Condensation of aldehyde 21 with aryl acetonitrile in a basic medium at 105 °C gives a cyclized imine 22, which, when undergoes acetylation, hydrolysis, followed by oxidation and

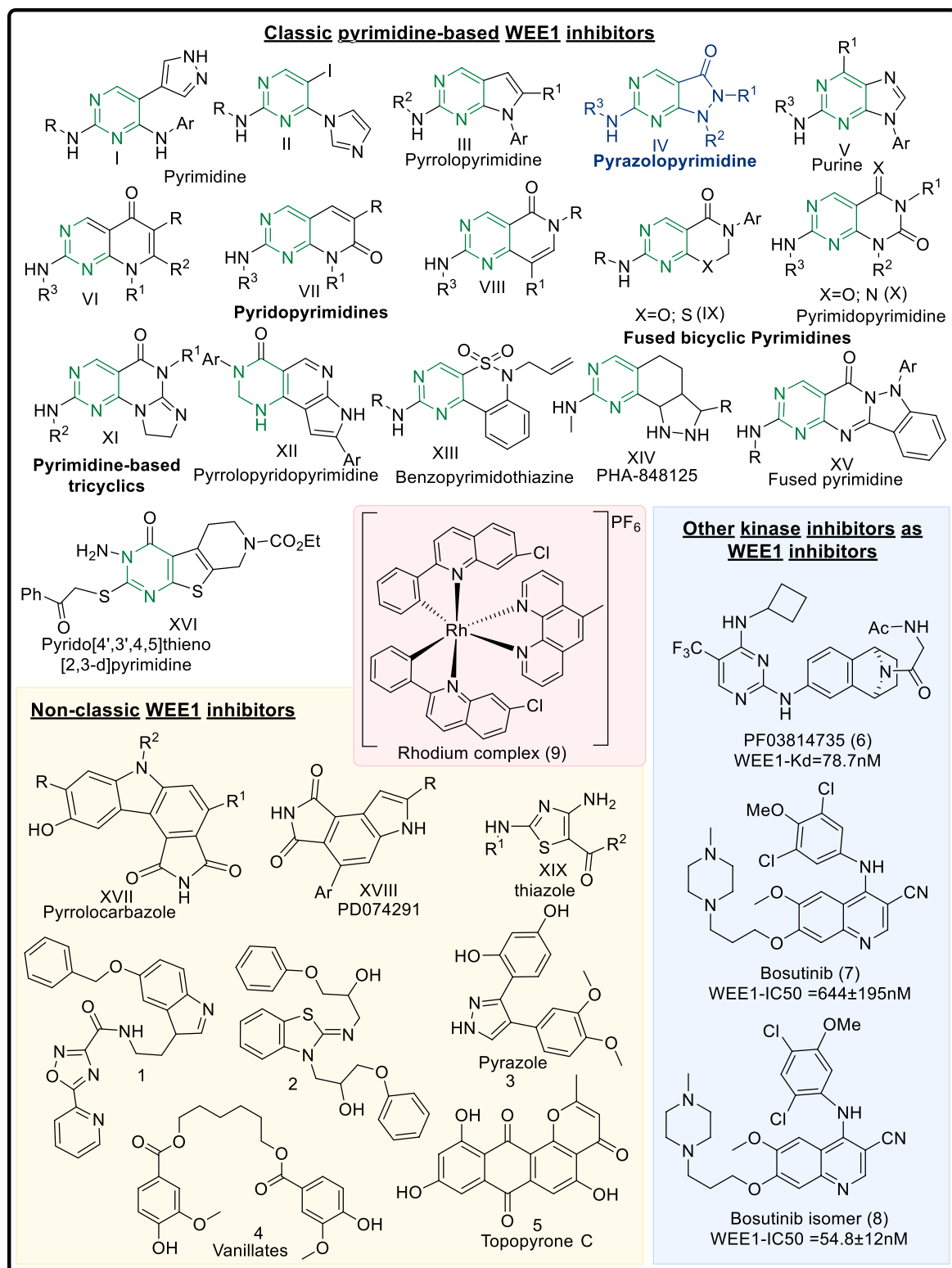


Figure 5. WEE1 kinase inhibitors from different heterocyclic scaffolds.

amination, gives the 8*N*-pyridopyrimidine (**VII**) core (Table 1, Scheme 2).¹⁰¹

2.1.3. Synthesis of 6*N*-Pyridopyrimidine Core. When treated with 1,1-dimethoxy-*N,N*-dimethylmethanamine (**24**), ester **23** transforms into dimethyl analogue **25** at elevated temperatures, initially reacting with ammonia in an acidic condition with EtOH as a solvent gives a cyclized intermediate

26, which upon alkylation with an alkyl halide produces 6*N*-substituted intermediate **27**. Dimethyl analogue **25** can also cyclize into **27** directly by reacting with a substituted amine in acidic media. Upon bromination of **27**, **28** is produced, which undergoes Suzuki coupling and gives the arylated core **29** (Scheme 3).¹⁰²

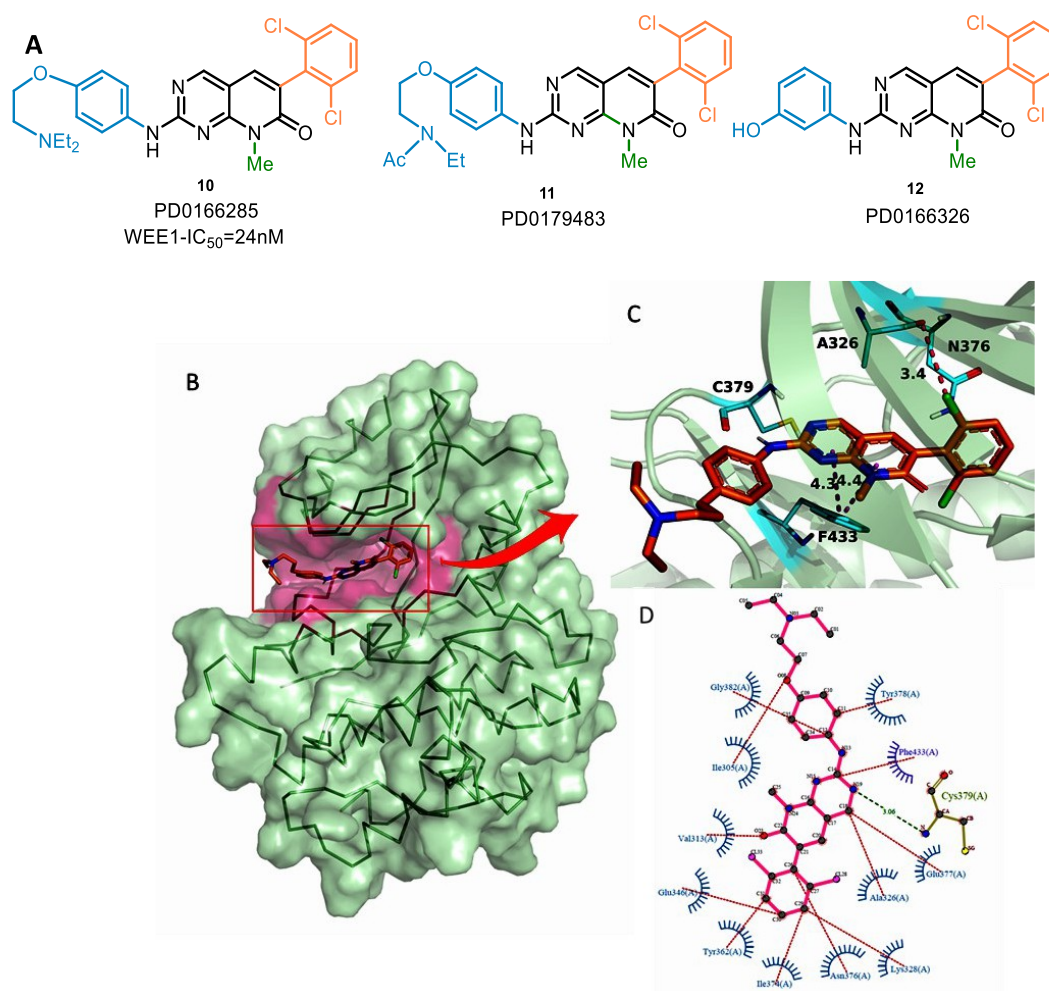


Figure 6. (A) Pyridopyrimidine analogues, (B) PD0166285 (**10**) in ATP binding pocket, and (C,D) PD0166285 (**10**) interaction profile in 3D and 2D, respectively (PDB ID: 5VC5).

Table 1. Some Pyridopyrimidine Analogues^a

| structure | comp | R | R ¹ | R ² | R ³ | IC ₅₀ (μM) |
|-----------|------|----------------------|--------------------|----------------|---|-----------------------|
| VI | 35 | 2',6'-diCl, 3'-OH Bn | Me | H | 3-phenoxypropanoic acid | 0.04 |
| VI | 36 | 2'-Cl Bn | Me | Me | <i>N,N</i> -diethyl-2-phenoxyethan-1-amine | 0.55 |
| structure | comp | R | R ¹ | R ² | R ³ | K _i (nM) |
| VII | 37 | 2',6'-diCl Bn | Me | – | 1-phenylpiperazine | 0.3 |
| VII | 38 | 2',6'-diCl Bn | Me | – | <i>N</i> -methyl-1,2,3,4-tetrahydroisoquinoline | 0.2 |
| VIII | 39 | 2',6'-diCl Bn | CH ₂ OH | – | 2,4,4-trimethyl-1,2,3,4-tetrahydroisoquinoline | 0.3 |
| VIII | 40 | 2',6'-diCl Bn | Me | – | 1-methyl-4-phenylpiperazine | 0.5 |

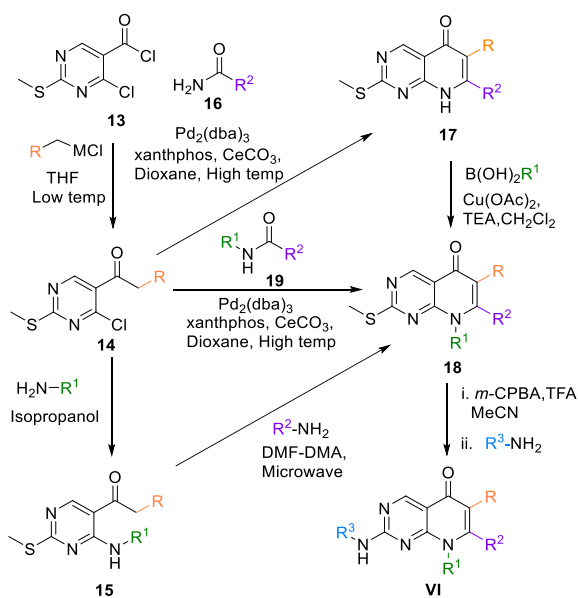
^aBn stands for benzene.

Similarly, **29** can also be generated when aqueous LiOH in THF and MeOH mixture hydrolyses the ester **30** to acid **31**, which is converted into its respective amide **32** when reacted with thionyl chloride in DMF and dioxane to get an acid chloride that is then allowed to react with a substituted amine. The amide **32** is then reacted with (chloromethylene)-dimethyliminium chloride (**33**) in DMF, which gives **29**. Additionally, in an alternate method, key ester **30** is reacted with **24**, and gives dimethylamine intermediate **34**, which, upon reaction with an aryl amine, produces **29** (Scheme 4).¹⁰²

The resultant arylated **29** upon oxidation by *m*-CPBA and reaction with another aromatic amine yields 6*N*-pyridopyrimidine core (**VIII**) (Table 1, Scheme 5).¹⁰²

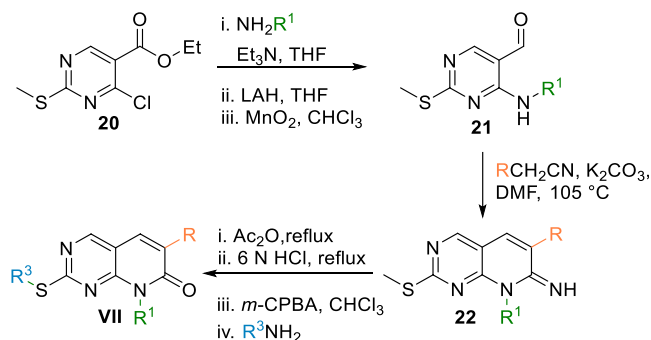
2.2. Pyrrolocarbazole. Pyrrolocarbazoles (**XVII**) were first synthesized and tested for WEE1 inhibition by Booth et al. in 2003, which exhibited IC₅₀ < 1 μM, including activity against CHK1 and PKC (Protein kinase C).¹⁰³ Squire et al. in 2005, described the human WEE1 structure with respect to the CHK1 structure using the PDB ID: 1X8B (a cocrystal structure of WEE1 complexed with Booth et al.'s pyrrolocarbazole, PD0407824 (**41**)).¹⁶ Later, Palmer et al. in 2006 confirmed PD0407824 (**41**) showing potent WEE1 inhibition (IC₅₀ = 97 nM) in a high-throughput screening (HTS) program and proposed its structure–activity relationship (Figure 7).¹⁰⁴ All analogues of **41** bind in the ATP binding pocket of WEE1 as shown in Figure 8A,D in the ATP competitive manner. Additionally, **41** displayed potent CHK1

Scheme 1. Synthesis of 8*N*-Pyridopyrimidine (VI) Analogues^a



^aAdapted from Mastracchio et al.¹⁰⁰

Scheme 2. Synthesis of 8*N*-Pyridopyrimidine (VII) Analogues^a

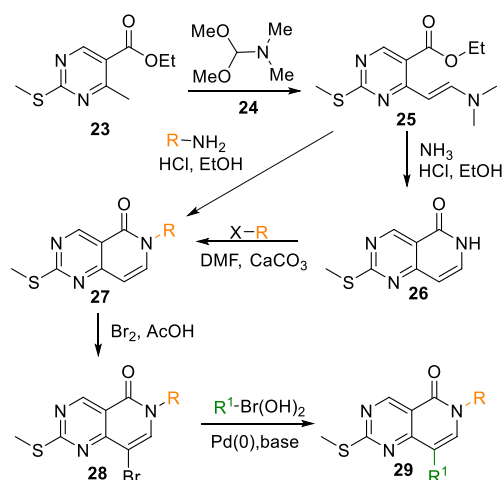


^aAdapted from Klutchko et al.¹⁰¹

inhibition ($IC_{50} = 47$ nM) due to its similar structure to the indolocarbazole scaffold of CHK1i. Despite systematic optimization to achieve selectivity, this scaffold displayed a broad-spectrum of kinase inhibition, which may have been the reason not to consider it for clinical trials. A few pyrrolocarbazole analogues are tabulated in Table 2, along with their IC_{50} values.

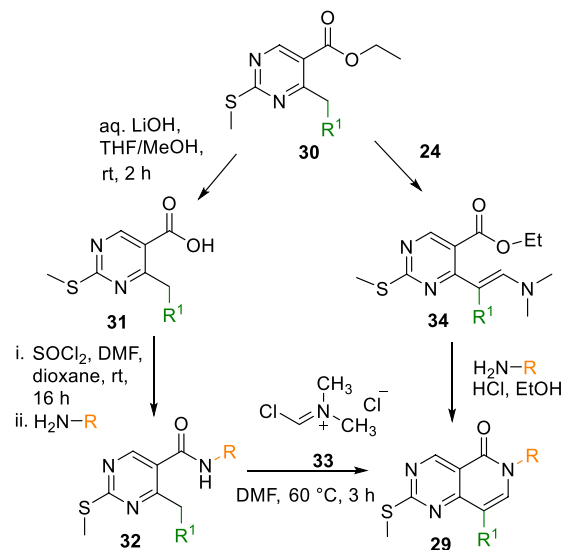
2.2.1. Structure–Activity Relationship and Optimization Approaches of Pyrrolocarbazoles. Palmer et al. proposed that the pyrrolo group is essential as 1-CO forms an H-bond with the –NH of C379 while the other 3-CO interacts with the gatekeeper residue N376 and a water molecule through H-bonding (Figure 8A–H).¹⁰⁴ Additionally, pyrrolo 2-NH acts as a HBD (hydrogen bond donor) to E377. The following two rings form π – π stacking interactions with F433 (Figures 8 and 9).¹⁰⁴ The presence of 9-OH facilitates the formation of H-bond with C379, G382, and occasionally with Y378; this results in a stronger binding affinity to the protein; hence, other substituents are not tolerated (Figure 8).¹⁰⁴ The 2'-position of the aryl prefers "Cl" but can tolerate other substitutions with zero to little decline in activity while

Scheme 3. Synthesis of 6*N*-Pyridopyrimidine Core and Crucial Intermediate 29^a



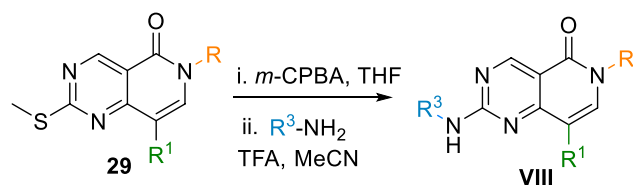
^aAdapted from Penning et al.¹⁰²

Scheme 4. Synthesis of Key Intermediate 29^a



^aAdapted from Penning et al.¹⁰²

Scheme 5. Synthesis of 6*N*-Pyridopyrimidine Analogues from 29^a



^aAdapted from Penning et al.¹⁰²

elevating selectivity (Figure 8E–H). However, 2',6'-dichloro or 2',6'-dimethyl increases potency and selectivity (Figure 7).¹⁰⁴ 5-Me substitution increases selectivity against CHK1, but alkanes larger than methyl are not tolerated. The carbazole "6*N*" interacts with S383 via three ordered water molecules. However, "N" can be replaced with either "S" or "O". This replacement shows no significant change in WEE1 activity but

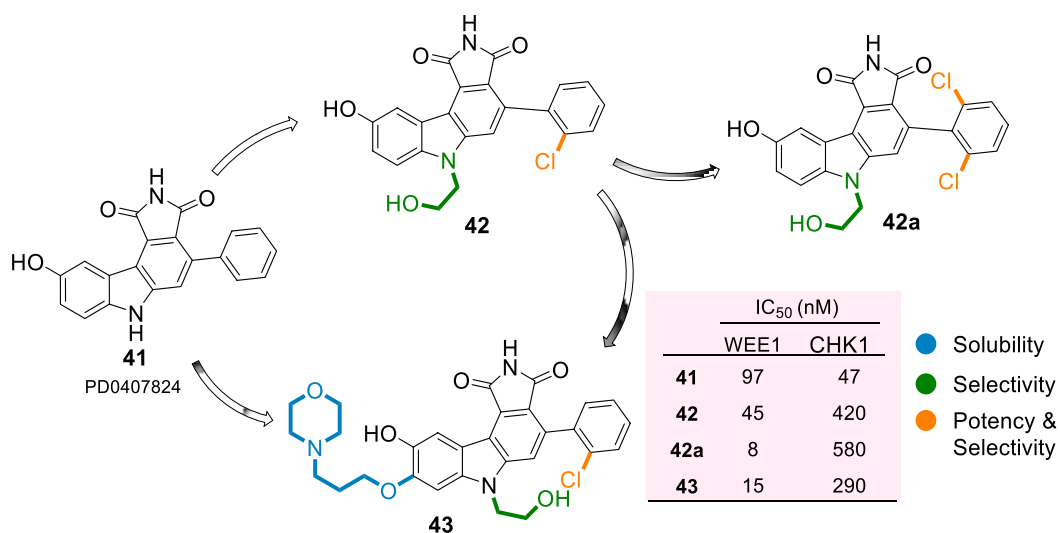


Figure 7. Optimization of PD0407824 (41) to enhance selectivity, potency, and solubility (adopted from Palmer et al.;¹⁰⁴ Smail, Baker et al.;¹⁰⁵ and Smail, Lee et al.¹⁰⁶).

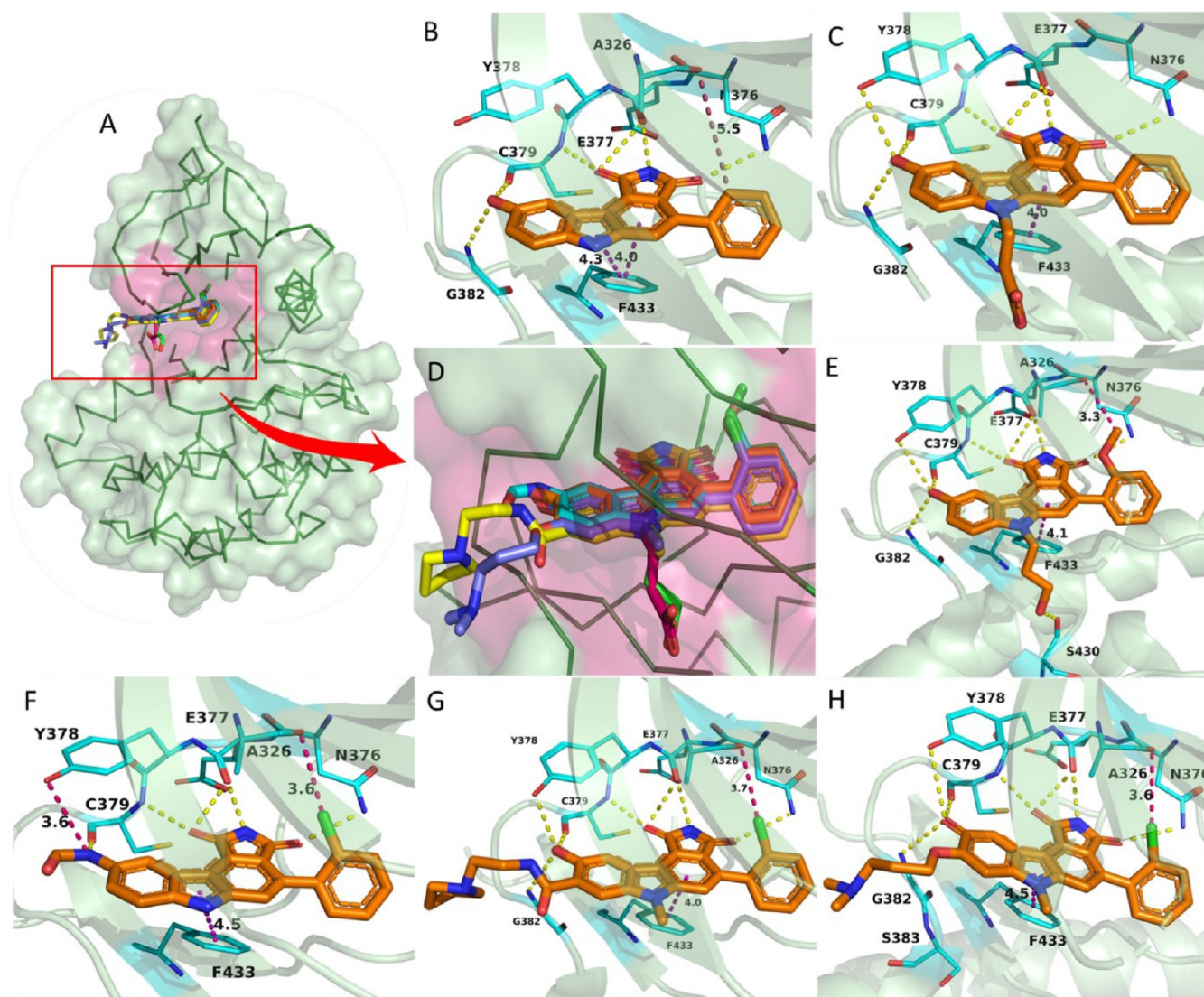


Figure 8. Pyrrolocarbazoles (XVII)-Pyrrolocarbazoles-WEE1 interaction profile in 3D. (A) Pyrrolocarbazoles and their binding modes in the WEE1 kinase pocket, (B) PDB ID: 1X8B, (C) PDB ID: 2NI6, (D) insight of overlapped poses of pyrrolocarbazoles, (E) PDB ID: 2IO6, (F) PDB ID: 2Z2W, (G) PDB ID: 3BI6, and (H) PDB ID: 3BIZ.

Table 2. Pyrrolocarbazole Analogues (XVII)^a

| comp | R | R ¹ | R ² | IC ₅₀ (nM) |
|------|--|----------------|---|-----------------------|
| 44 | H | Ph | H | 130 |
| 45 | H | 2-Cl Bn | H | 11 |
| 46 | H | 2,6-diCl Bn | H | 28 |
| 47 | H | 2-Cl Bn | (CH ₂) ₃ OH | 9 |
| 48 | H | 2-Cl Bn | (CH ₂) ₂ CONH ₂ | 6 |
| 49 | (CH ₂) ₄ NMe ₂ | 2-Cl Bn | H | 49 |
| 50 | O(CH ₂) ₃ Nmorph | 2-Cl Bn | (CH ₂) ₂ OH | 15 |

^aBn stands for benzene, Ph for phenyl, and morph for morpholine.

increases selectivity if replaced with “O”.¹⁰⁴ Smail and Baker et al. introduced 6*N*-substitutions that can influence WEE1 and CHK1 selectivity, and slightly bulkier acidic groups increased selectivity and WEE1 potency; however, neutral polar groups like alcohols and amides are dual-specific inhibitors of WEE1 and CHK1 with elevated potencies (Figure 8C,E).¹⁰⁵ Smail and Lee et al. added bulky side chains containing amines like pyrrolidine at position-8 of 6*N*-methyl or 6*N*-alcohols to increase solubility with a slight increase in WEE1 potency (Figure 8G,H).¹⁰⁶ The 4-aryl remains perpendicular to the pyrrolocarbazole moiety and fits into a small lipophilic cavity beside the gatekeeper (N376) (Figure 9A–F). A hydrophobic substitution at the 2'- position of the aryl enables an appropriate orientation to fit in the small pocket while forming a halogen bond with A326. Thus, this substitution, if absent, significantly reduces the potency of the inhibitor.

2.2.2. Synthesis of Pyrrolocarbazoles. Pyrrolocarbazoles (XVII) are synthesized by performing Wittig reactions of substituted 6-methoxy-1*H*-indole-2-carbaldehyde (51) with aryltriphenylphosphonium salt to give the corresponding 2-substituted dienes 52. Moreover, obtained diene 52 undergoes *N*-alkylation by an alkyl halide in the presence of NaH to give *N*-substituted diene 53 that is then reacted with 1*H*-pyrrole-2,5-dione or maleimide (54) at 175 °C directly to perform a Diels–Alder reaction or SnCl₂ in toluene can also be used to form key cyclic compound 55. Aromatization of 55 using DDQ or MnO₂ in dioxane followed by demethylation BBr₃ in CH₂Cl₂ produce the pyrrolocarbazole moiety (XVII). Skipping *N*-alkylation produces XVII, where R² = H (Table 2, Scheme 6).¹⁰⁴

XVII can also be prepared by reacting the aldehyde 51 with Ph₃PCHCOOBn to give a diene ester 56, which undergoes a Diels–Alder reaction with maleimide (54) to give the cyclic intermediate 57. Oxidation and reduction followed by amination of 57 give a free amine 58, which upon treatment with NaNO₂ in an acidic medium followed by iodination with KI and CuI give iodo-analogue 59. Reduction by PyHCl followed by Suzuki coupling of 59 gives a R¹-substituted intermediate, which upon alkylation with R²X in basic medium gives XVII (Table 2, Scheme 7).¹⁰⁴

Another method to prepare the pyrrolocarbazole moiety is using a Grignard reagent to add alkyl or aryl to the aldehyde 51 to generate substituted alcohol 60. The corresponding alcohol 60 is oxidized with MnO₂ to form a ketone, which upon reacting with alkyl or aryl phosphonium, the Wittig reagent gives the corresponding diene 61. XX can be generated when the diene 61 reacts with maleimide (54) at 180 °C for 40 min, followed by oxidation with MnO₂, then demethylation by BBr₃ (Scheme 8).¹⁰⁴

Palmer et al. also provided an alternate method of synthesis where diene 52 reacted with maleic anhydride 62 gives the

carbazole intermediate 63, which upon reaction with 2, 4-dimethoxybenzylamine (64) in the presence of acetic acid forms 65. Oxidation of benzylated analogue 65 with MnO₂ followed by reaction with R²X in basic media gives the aromatic compound 66, which reacts with TFA in anisole then demethylation by BBr₃ in DCM produces XVII (Table 2, Scheme 9).¹⁰⁴

2.3. Pyrazolopyrimidine. Sagara et al. patented pyrazolopyrimidine (IV) analogues in 2007 as WEE1i.¹⁰⁷ In 2009, high-throughput screening of a small chemical library discovered an initial hit, which was used to develop MK-1775 (67, Figure 13), a pyrazolopyrimidine, the first most potent and selective WEE1 kinase inhibitor with an IC₅₀ value of 5.2 nM and an EC₅₀ value of 49 nM (WiDr cells).¹⁰⁸ MK-1775, later renamed AZD1775 or Adavosertib, was quickly promoted into phase-I, II clinical trials for monotherapy and combination therapies. It sensitizes the onco-cells to genotoxic agents like radiation, including antimetabolites (Gemcitabine, 5-Fluoro-uracil, Pemetrexed, and Capecitabine), alkylating agents (like Cis-platin, Temozolomide, and Carboplatin), antimicrotubular agent (like Paclitaxel and Docetaxel), and topoisomerase inhibitors (like Doxorubicin, Irinotecan, and Topotecan). And it has indeed reinforced carboplatin's efficiency in TP53 mutants, including those with refractory or resistant ovarian cancer.¹⁰⁹ Additionally, nonchemotherapeutic agents like PARPi (Olaparib) and ATRi (Ceralasertib) provide a better alternative for combinational therapy.¹¹⁰ HDAC inhibitor (Belinostat) and monoclonal antibodies (Durvalumab) are also studied with AZD1775. However, AZD1775 in combination therapy displayed fatigue, nausea, vomiting, diarrhea, thrombocytopenia, and neutropenia.^{110,111} As a single agent, AZD1775 initiates premature mitotic entry by WEE1 inhibition, but Guertin et al. stated that its cytotoxicity is a major consequence of AZD1775-induced DNA damage. Additionally, Guertin et al. reported AZD1775's adverse events, including gastrointestinal disorders like diarrhea, vomiting, nausea, and hematologic toxicities (myelosuppression).¹¹² Do et al. in 2015 also found myelosuppression and tachyarrhythmia as dose-limiting toxicities, limiting its clinical development.¹¹³ Later, Wright et al. discovered AZD1775's equipotent PLK1 inhibitory action (WEE1, K_d = 3.2 nM; PLK1, K_d = 3 nM), and the binding mode is depicted in Figure 10. Though PLK1 is a negative regulator of WEE1, it regulates many pathways like FOXO, ATR signaling, FOXM1 pathways, APC/C-mediated degradations, etc.¹¹⁴ Therefore, off-target PLK1 inhibition by AZD1775 disrupts these pathways and might cause AZD1775's cytotoxicity, including its adverse effects and toxicity profile.¹¹⁴ Moreover, AZD1775 also targets JAK2/3 (Janus kinase 2/3), ABL1, YES1, MAP3K4 (mitogen-activated protein kinase kinase kinase 4), etc. Hence, there is a need for new, more selective inhibitors.

Some studies have observed the waning cytotoxicity of AZD1775. This phenomenon is not due to mutations in WEE1 but other mechanisms. Sen et al. identified a new pathway in SCLC that induces acquired resistance to WEE1i where AXL (AXL receptor tyrosine kinase) is overexpressed and so is its downstream protein mTOR (mechanistic target of rapamycin kinase), in addition to CHK1 activation that paves an alternate pathway to deactivate CDK1. Moreover, pS6 (phosphorylated ribosomal protein S6) and MET (mesenchymal–epithelial transition kinase) upregulation also desensitize SCLC cells to AZD1775.^{115,116} Lewis et al. observe that prolonged inhibition

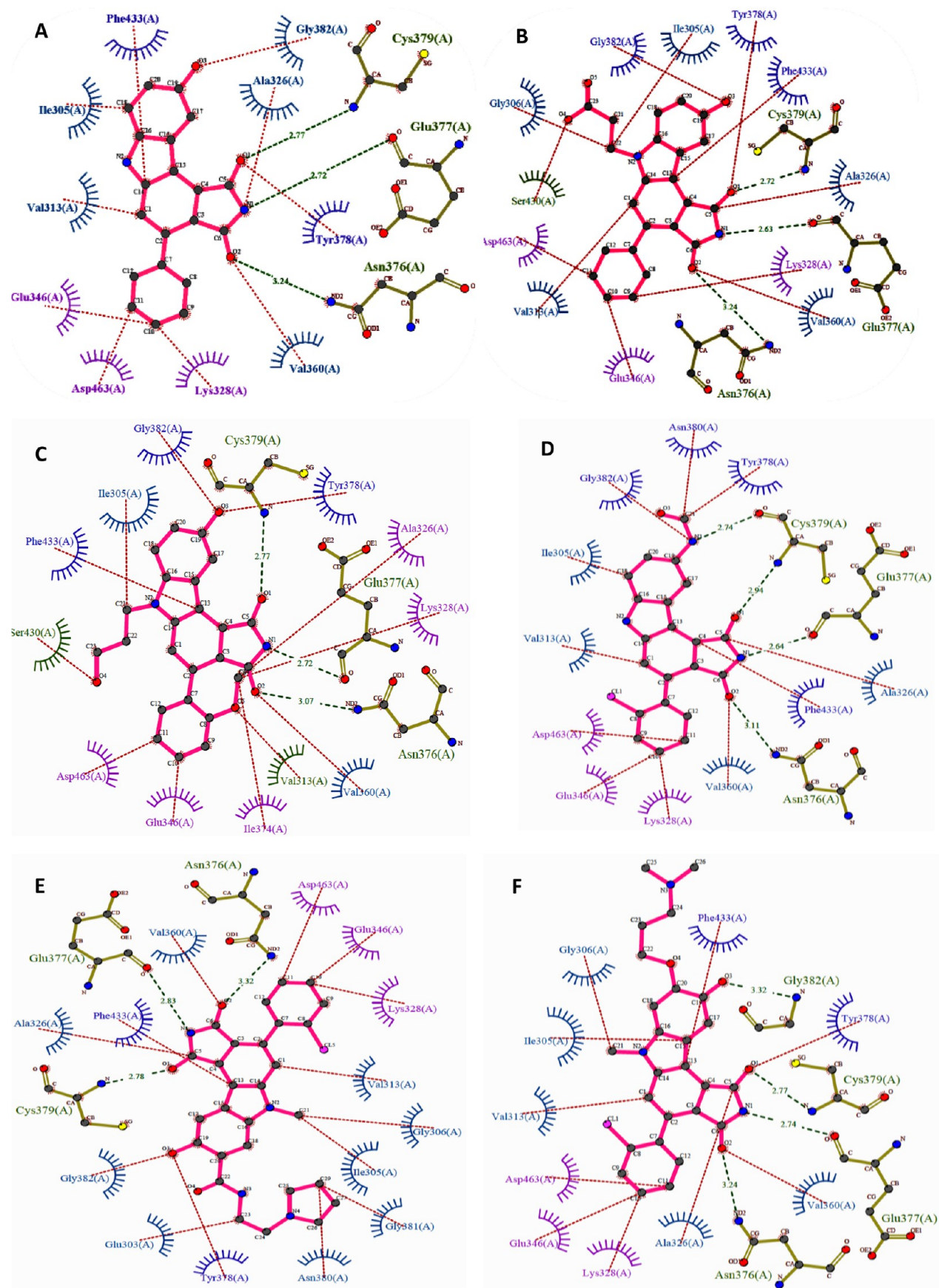
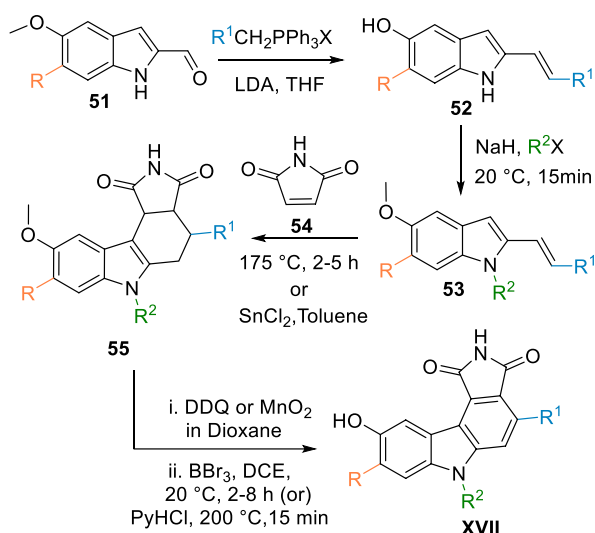


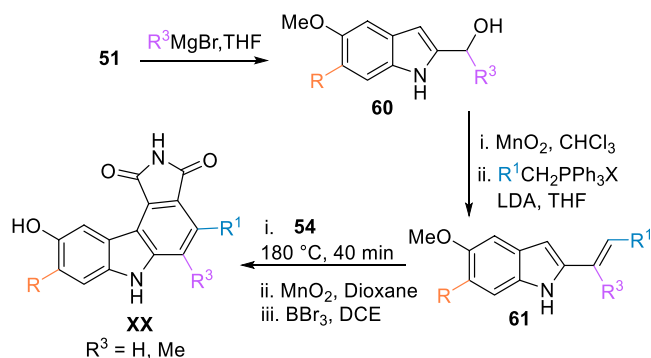
Figure 9. Pyrrolocarbazoles (XVII)-WEE1 interaction profile. (A) PDB ID: 1X8B, (B) PDB ID: 2NI6, (C) PDB ID: 2IO6, (D) PDB ID: 2Z2W, (E) PDB ID: 3BI6, and (F) PDB ID: 3BIZ.

Scheme 6. Synthesis of Maleimide-Based Pyrrolo-carbazole Analogues^a

^aAdapted from Palmer et al.¹⁰⁴

of WEE1 by AZD1775 promotes acquired resistance in HeLa cells due to overexpression of MYT1 (an alternate CDK1 regulator), and eliminating MYT1 has resensitized cells to AZD1775.¹¹⁷ Furthermore, in leukemia cells, HDAC activity is increased, which further increases *c*-MYC expression and confers acquired resistance to WEE1 inhibition.¹¹⁸ Additionally, Yes-associated protein (YAP) triggers the Fanconi anemia (FA) pathway and the corresponding transcriptional regulator, E2F1, which repair DNA damage and contribute to resistance. Further, the coinhibition of WEE1 and YAP with Dasatinib has sensitized the OVCAR-8 ovarian cancer cell line to AZD1775.¹¹⁹ Therefore, a parallel inhibition of WEE1 and CHK1, mTOR, AXL, HDAC, and YAP offers a good enough strategy to overcome the resistance (Figure 3).

Apart from AZD1775, ZN-c3, or Azenosertib (71), another pyrazolopyrimidine developed by Zentaris, is in phase-I, II trials in monotherapy for treating triple-negative breast cancer, ovarian cancer (NCT05368506), solid tumors (NCT04158336, NCT04972422), malignant tumors (NCT05128825), and uterine serous carcinoma (NCT04814108). In combination

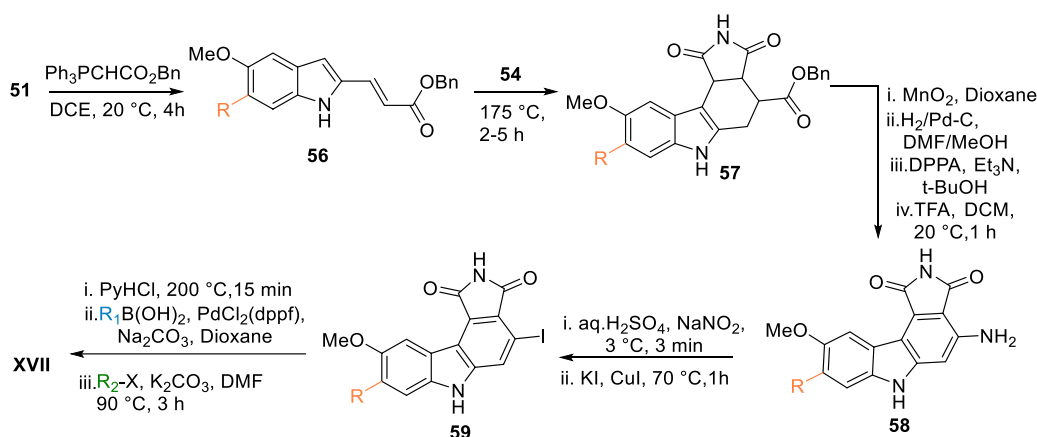
Scheme 8. Synthesis of Maleimide-Based Multi-Substituted Pyrrolo-carbazole Analogues^a

^aAdapted from Palmer et al.¹⁰⁴

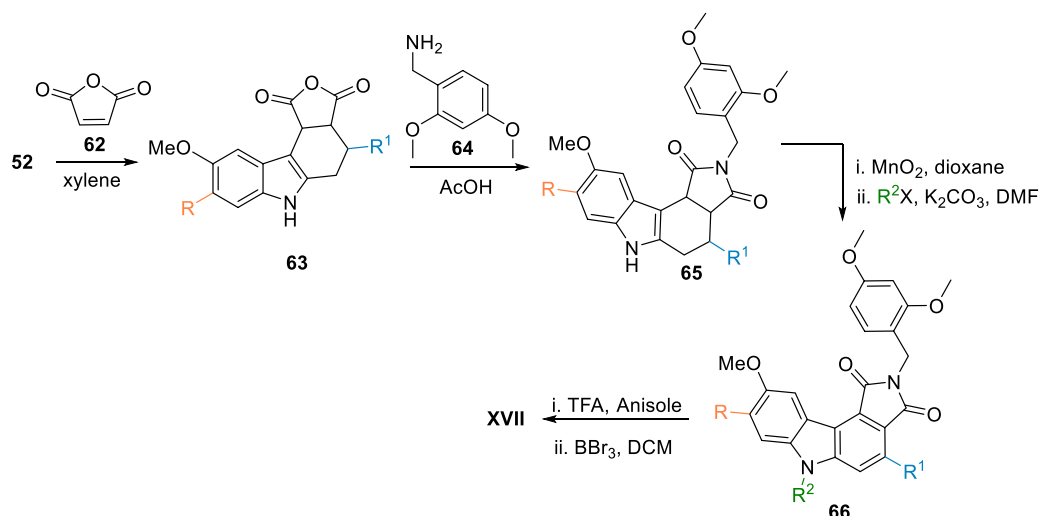
therapy, ZN-c3 is used to treat osteosarcoma with Gemcitabine (NCT04833582), Pt-resistant ovarian cancer along with PARPi (Niraparib; NCT05198804), and Carboplatin, Pegylated liposomal Doxorubicin, Paclitaxel, and Gemcitabine (NCT04516447); acute myeloid leukemia (AML) with Bcl2 inhibitor (ZN-d5; NCT05682170); and metastatic colorectal cancer with BRAF (Encorafenib) and EGFR (Cetuximab) kinase inhibitors.

A monotherapy trial observed that ovarian cancer with amplified CCNE1 gene is hypersensitive to ZN-c3 in both *in vitro* and *in vivo* studies. Hypersensitivity toward ZN-c3 is also observed in combination therapies with chemotherapeutics like Paclitaxel.¹²⁰ Nevertheless, another phase-I study (NCT05431582) is withdrawn due to lack of participants. Another analogue, SC0191 (70), demonstrated WEE1 inhibition and antiproliferative activity in TP53 mutant cells.¹²¹ The progress of detailed clinical trials of AZD1775 as monotherapy or in combination with other potential anticancer agents is provided in Table 3.

2.3.1. Structure–Activity Relationship and Optimisation Approaches of Pyrazolopyrimidine. Pyrazolopyrimidines (IV) are Type-I kinase inhibitors that contain a 2-amino-pyrimidine ring where 2-amino and 1N form an H-bond with C379 of WEE1 kinase. 6-carbonyl “O” also interacts with the N376 residue.¹²² The allyl attached to 5N is an important auxiliary group that enhances the interactions of carbonyl “O”

Scheme 7. Another route to synthesise maleimide-based pyrrolo-carbazole analogues^a

^aAdapted from Palmer et al.¹⁰⁴

Scheme 9. Synthesis of Maleic Anhydride-Based Multi-Substituted Pyrrolocarbazole Analogues^{4f}

^{4f}Adapted from Palmer et al.¹⁰⁴

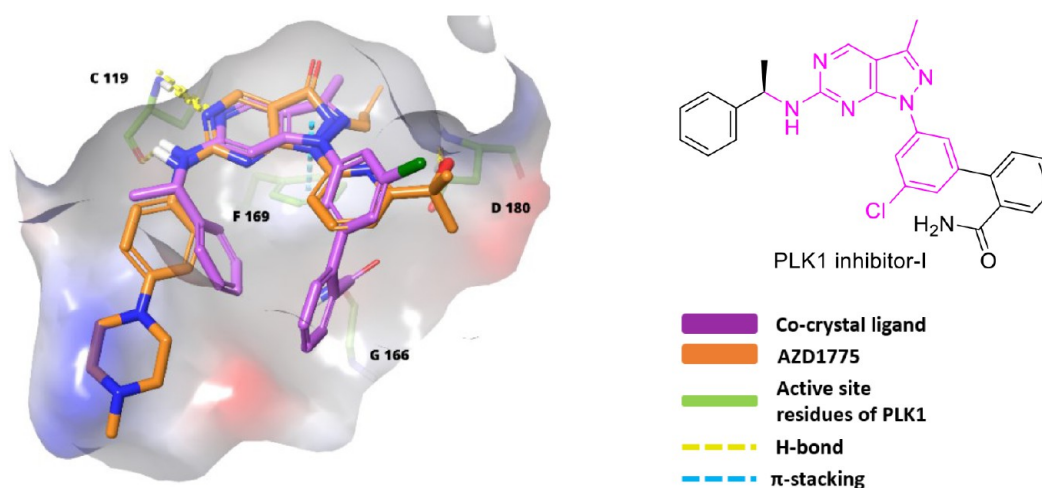


Figure 10. Overlapping of AZD1775 and PLK1 inhibitor-I in the active site of PLK1 (PDB ID: 3DBD).

with the gatekeeper. In addition, it may associate with K328 as it is within Vander Waals' radii (Figures 11A-I and 12A-E). Allyl, when replaced with -Me and methoxybenzyl showed a significant reduction and complete loss of activity, respectively. Further, eliminating this group has resulted in an inactive inhibitor.¹²³ The 4N is substituted with a 3'-isopropanol-substituted aromatic ring where the -OH group is necessary as it bonds with the D463 residue. The methyl groups, on the other hand, play a supporting role to lock the -OH group in an appropriate conformation.¹²⁴ At last, the pyrazolopyrimidine ring forms π - π interactions with the F433 residue.¹²⁴ Matheson et al. investigated the role of 2-amine substitutions that are solvent exposed, then proposed CM061 (68), and stated that substitution on the piperazine ring reduces toxicity while retaining its activity.¹²⁴ Additionally, the presence of a flexible alkyl amine substitution on the para-position of the aniline (69) contributes to increased potency as a result of the induced H-bond with D386/E303.¹²³ Despite enhanced potency and selectivity, 68 and 69 showed diminished cell viability and cytotoxicity, verifying that AZD1775's cytotoxicity is not a product of WEE1 inhibition alone. Figure 13 illustrates the optimization of AZD1775.

Huang et al. investigated the effect of altering the 2-amino substitutions and pyridine group of AZD1775 on its selectivity, potency, and acceptable ADMET and PK properties. Introducing bicyclic substitutions on 2-amine has indelibly increased its potency but at the expense of intrinsic microsomal clearance with no significant increase in its selectivity.¹²⁵ On the other hand, introducing a cyclopentapyridyl with a 3°-OH has indeed increased potency and selectivity while maintaining excellent druglike properties, including low intrinsic clearance.¹²⁵ Additionally, the (*R*)-enantiomer of 3°-OH is more potent relative to its counterpart as the (*R*)-alcohol interacts with D463 (Figure 12D,E). Moreover, an ethyl group on cyclopentapyridyl (71) is more beneficial than the methyl group, while other bulkier alkyl groups showed a drastic decrease in potency (Figures 13 and 14A,B). Furthermore, modifications to the allyl group had a detrimental effect on activity, further validating the importance of this group. Eventually, ZN-c3 (71) was proposed, which is highly selective (IC₅₀: WEE1 = 3.8 nM, PLK1 = 227 nM) and also shows sound cytotoxicity in H23 cell lines (IC₅₀: ZN-c3 = 103 nM, AZD1775 = 122 nM).¹²⁵ Moreover, cyclized AZD1775 has retained its allyl group as well as its *tert*-alcohol;

Table 3. Clinical Trials of AZD1775 and Their Status, Purpose, and Conditions^a

| S. no. | NCT number | status | therapy | drugs | phase | conditions | purpose |
|--------|-------------|--------|---------|--|-------|---|---|
| 1 | NCT02508246 | C | CT | AZD1775, CDDP, Docetaxel | 1 | HNSCC | side effects and the best dose of AZD1775 in combination with CDDP, Docetaxel |
| 2 | NCT02666950 | C | MT, CT | AZD1775, AraC | 2 | advanced acute myeloid leukemia and myelodysplastic syndrome | competency of AZD1775 with and without Cytarabine |
| 3 | NCT02196168 | T | CT | CDDP, AZD1775 | 2 | recurrent or metastatic squamous cell cancer of the head and neck | competency of AZD1775 with and without CDDP |
| 4 | NCT02194829 | A | CT | AZD1775, Gemcitabine Hydrochloride, Nab-paclitaxel | 1 | metastatic adenocarcinoma of the pancreas | side effects and best dose of AZD1775 in combination with Nab-paclitaxel, Gemcitabine Hydrochloride |
| 5 | NCT02381548 | T | CT | AZD1775, Belinostat | 1 | relapsed and refractory myeloid malignancies and acute myeloid leukemia | side effects and best dose of AZD1775 and Belinostat |
| 6 | NCT01164995 | A | CT | AZD1775, Carboplatin | 2 | epithelial ovarian cancer | proof of concept (POC) study to prove WEE1 inhibition as an effective treatment in TP53 mutants |
| 7 | NCT02906059 | C | CT | AZD1775, Irinotecan | 1 | RAS or BRAF mutated metastatic colorectal cancer | safety and effectiveness in RAS or BRAF mutants |
| 8 | NCT03028766 | C | CT | AZD1775, CDDP, radiotherapy | 1 | head and neck cancer | best dose of AZD1775 in combination with CDDP |
| 9 | NCT02101775 | A | CT | AZD1775, Gemcitabine Hydrochloride | 2 | recurrent, platinum resistant epithelial ovarian, primary peritoneal, or fallopian tube cancers | comparing gemcitabine monotherapy to gemcitabine in combination with AZD 1775 |
| 10 | NCT02037230 | C | CT | AZD1775, Gemcitabine, radiotherapy | 1, 2 | adenocarcinoma of the pancreas | maximum tolerated dose (MTD) of AZD1775 |
| 11 | NCT04460937 | S | CT | AZD1775, radiotherapy | 1 | esophageal and gastroesophageal junction cancer | maximally tolerated dose (MTD) of AZD1775 |
| 12 | NCT01748825 | C | MT | AZD1775 | 1 | advanced refractory solid tumors | safety, tolerability, and PK |
| 13 | NCT03253679 | S | MT | AZD1775 | 2 | advanced malignant solid neoplasm and refractory malignant solid neoplasm | objective response rate (ORR) to AZD1775 |
| 14 | NCT03668340 | R | MT | AZD1775 | 2 | uterine cancer | safety and effectiveness of AZD1775 |
| 15 | NCT03315091 | C | MT | AZD1775 | 1 | solid tumors | effect of food on the pharmacokinetics (PK) |
| 16 | NCT02207010 | C | MT | AZD1775 | 0 | glioblastoma multiforme (GBM) | CNS penetration |
| 17 | NCT02688907 | T | MT | AZD1775 | 2 | small cell lung cancer | competency of AZD1775 in MYC family amplification or CDKN2A mutation in TP53 mutants |
| 18 | NCT02593019 | C | MT | AZD1775 | 2 | small cell lung cancer | competency of AZD1775 in TP53 mutants |
| 19 | NCT02585973 | C | CT | AZD1775, CDDP, intensity modulated radiotherapy | 1b | carcinoma, squamous cell of head and neck | dose-escalation trial |
| 20 | NCT02791919 | W | CT | AZD1775, AraC, Fludarabine Phosphate | 1 | relapsed or refractory acute myeloid leukemia | dose-escalation trial, toxicity, PK |
| 21 | NCT03385655 | R | CT | AZD1775, Savolitinib, Darolutamide, CFI-400945, Ipatasertib, Durvalumab, and Tremelimumab, Carboplatin | 2 | prostate cancer | DNA abnormalities or biomarkers |
| 22 | NCT03313557 | C | MT | AZD1775 | 1 | solid tumors | safety and tolerability |
| 23 | NCT03333824 | C | CT | AZD1775, caffeine (CYP1A2), omeprazole (CYP2C19), midazolam (CYP3A), granisetron | 1 | advanced solid tumors | effect of AZD1775 on PK of other drugs |
| 24 | NCT03345784 | A | CT | AZD1775, CDDP, external beam radiation therapy | 1 | cervical, upper vaginal, and uterine cancers | recommended phase-II dose (RP2D) and safety profile of AZD1775 |
| 25 | NCT02610075 | C | MT | AZD1775 | 1 | solid tumors | determine maximum tolerated dose (MTD) |
| 26 | NCT02482311 | C | MT | AZD1775 | 1 | solid tumors | safety, tolerability, and PK |
| 27 | NCT02511795 | C | CT | AZD1775, Olaparib | 1 | refractory solid tumors and SCLC | dose-escalation trial |
| 28 | NCT02087176 | T | CT | AZD1775, antimetabolic agent, Pegfilgrastim | 2 | previously treated SCLC | comparative study of AZD1775+antimetabolic agent with placebo |
| 29 | NCT02341456 | C | MT, CT | AZD1775, Paclitaxel, Carboplatin | 1 | advanced solid tumors | multicenter study in adult asian patients |
| 30 | NCT02513563 | W | CT | AZD1775, Paclitaxel, Carboplatin | 1 | lung cancer | effects of AZD1775 |

Table 3. continued

| S. no. | NCT number | status | therapy | drugs | phase | conditions | purpose |
|--------|-------------|--------|---------|---|-------|--|--|
| 31 | NCT02087241 | T | CT | AZD1775, Pemetrexed, Carboplatin | 2 | advanced NSCLC | comparative study of chemotherapy with and without AZD1775 |
| 32 | NCT03718143 | T | MT, CT | AZD1775, AraC | 2 | myelofibroses, acute myeloid leukemia, myelodysplastic syndromes | effects of AZD1775 as a single agent and in combination with AraC |
| 33 | NCT03012477 | C | CT | AZD1775, CDDP | 2 | breast cancer | effects of AZD1775 |
| 34 | NCT01047007 | T | MT, CT | AZD1775, CDDP, S-FU | 1 | solid tumors | safety and MTD of AZD1775 |
| 35 | NCT02448329 | C | CT | AZD1775, Paclitaxel | 2 | advanced gastric adenocarcinoma | effects of AZD1775 |
| 36 | NCT04462952 | C | MT | AZD1775 | 1 | advanced solid tumors | safety, tolerability, pharmacokinetics (PK), and antitumor activity |
| 37 | NCT04439227 | A | MT | AZD1775 | 2 | lymphoma, neoplasm, myeloma | effect of AZD1775 on BRCA mutants |
| 38 | NCT01076400 | T | CT | AZD1775, Topotecan, CDDP | 1, 2 | cervical cancer | safety and MTD of AZD1775 |
| 39 | NCT01357161 | C | CT | AZD1775, Paclitaxel, CDDP | 2 | ovarian cancer | safety and efficacy of AZD1775 |
| 40 | NCT00648648 | C | CT | AZD1775, CDDP, Carboplatin, Gemcitabine | 1 | solid tumors | dose-escalation trial |
| 41 | NCT03284385 | A | MT | AZD1775 | 2 | SETD2-deficient solid tumors | effect of AZD1775 on SETD2 mutants |
| 42 | NCT04197713 | S | CT | AZD1775, Olaparib | 1 | solid tumors | side effects and best dose of AZD1775 |
| 43 | NCT02095132 | A | CT | AZD1775, Irinotecan | 1, 2 | solid tumors | side effects and best dose of AZD1775 |
| 44 | NCT01922076 | C | CT | AZD1775, radiotherapy | 1 | diffuse intrinsic pontine gliomas | side effects and best dose of AZD1775 |
| 45 | NCT01849146 | A | CT | AZD1775, radiotherapy, Temozolomide | 1 | glioblastoma | side effects and best dose of AZD1775 |
| 46 | NCT03579316 | R | MT, CT | AZD1775, Olaparib, Ceralasertib | 2 | recurrent fallopian tube, ovarian, primary peritoneal carcinomas | comparative study of AZD1775 with and without PARP inhibitors |
| 47 | NCT05008913 | T | MT | AZD1775 | 1 | advanced solid tumors | ADME study |
| 48 | NCT04949425 | T | MT | AZD1775 | 1 | advanced solid tumors | safety and tolerability study |
| 49 | NCT04590248 | A | MT | AZD1775 | 2 | uterine serous carcinoma | safety and efficacy of AZD1775 |
| 50 | NCT05212025 | W | CT | AZD1775, Gemcitabine | 2 | pancreatic cancer | safety and efficacy of the combination |
| 51 | NCT02546661 | A | MT, CT | AZD1775, AZD4547, MEDI4736, Olaparib, Vistusertib, AZD9150, Selumetinib | 1 | muscle invasive bladder cancer | safety, tolerability, pharmacokinetics (PK), and antitumor activity |
| 52 | NCT02937818 | A | CT | AZD1775, CBDP | 2 | platinum refractory extensive-stage SCLC | efficacy, safety, and tolerability effects of AZD1775 |
| 53 | NCT02659241 | A | MT | AZD1775 | 1 | peritoneal carcinomas | efficacy and safety |
| 54 | NCT02272790 | A | CT | AZD1775, CBDP, Paclitaxel, PLD, Gemcitabine | 2 | advanced fallopian tube, ovarian, primary peritoneal carcinomas | safety and efficacy of Olaparib in combination with AZD1775 and Ceralasertib |
| 55 | NCT03330847 | A | CT | AZD1775, Olaparib, Ceralasertib | 2 | ovarian, fallopian tube, peritoneal cancer breast cancer | molecular profiling-based assignment of cancer therapy |
| 56 | NCT01827384 | C | CT | AZD1775, Carboplatin, Everolimus, Temozolomide, Trameetinib Veliparib | 2 | advanced malignant solid neoplasm | genetic testing for targeted therapy |
| 57 | NCT02465060 | A | CT | AZD1775, target-oriented inhibitors | 2 | solid tumors, lymphomas | |

^aC, completed; R, recruiting; A, active; S, suspended; T, terminated; W, withdrawn; CT, combination therapy; and MT, monotherapy.

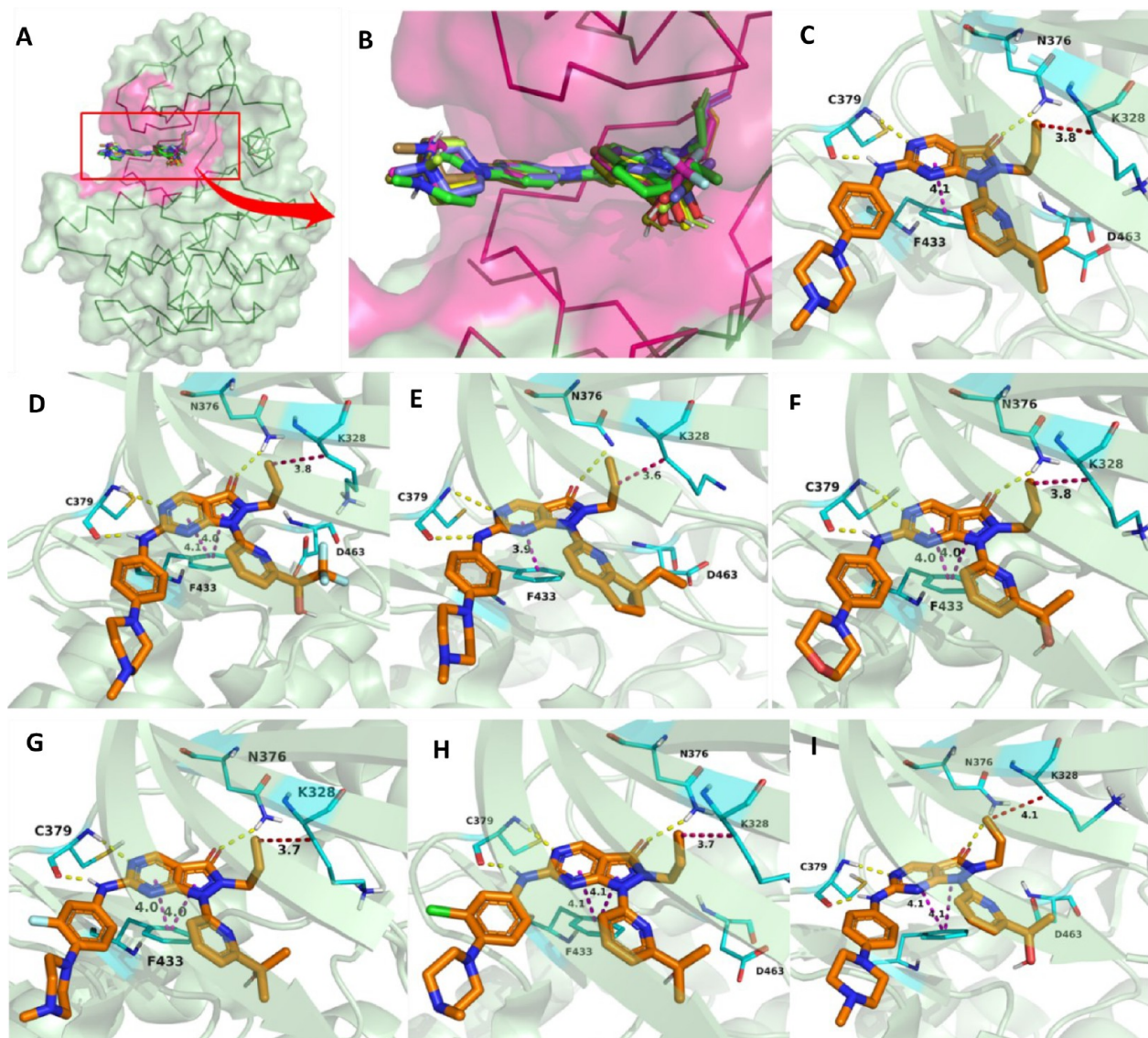


Figure 11. Pyrazolopyrimidine (IV)-WEE1 interaction profile in 3D; (A) Pyrazolopyrimidine and their binding modes in WEE kinase pocket; (B) insights of overlapped poses of Pyrazolopyrimidines, (C) PDB ID: 5V5Y, (D) PDB ID: SVD4, (E) PDB ID: 7N3U and (F) PDB ID: SVD5, (G) PDB ID: SVD7, (H) PDB ID: SVD8, (I) PDB ID: SVD9.

hence, its binding mode ought to be similar to that of AZD1775. However, cyclization-associated intramolecular adjustments might restrain its binding efficiency in the WEE1 pocket. The cyclization approach may also disrupt the π - π stackings of SC0191 (70) with key F433. The cyclization of AZD1775 may improve the lipophilicity of the analogue, which might play a critical role in the determination of binding free energy (Figure 14C).

A recent study by Guler et al. investigated the selectivity associated with the allyl group of AZD1775. In PLK1, the cavity accommodating the allyl group is narrower as the gatekeeper is L130. Therefore, the bulkier groups are not tolerated. Cyclic alkenes (67a) retained WEE1 activity while improving selectivity against PLK1. Other unsaturated and saturated groups displayed decreased WEE1 activity.¹²⁶ Furthermore, this study determined myelosuppression as an on-target consequence (independent of PLK1 inhibition) of WEE1 inhibition using the Colony forming unit-megakaryocyte assay (CFU-Mk).¹²⁶ Thus, this study offers a new scope for further optimization. A few analogues of pyrazolopyr-

imidine (80–83) and pyrrolopyrimidine (84, 85), along with their inhibitory constant values, are incorporated in Figure 15.

2.3.2. Synthesis of Pyrazolopyrimidine Analogues. Alkyl hydrazine, when reacted with the ester 20 in the presence of a base like DIPEA (*N,N*-diisopropylethylamine) in THF results in the formation of an intermediate, which is reacted with EtOH to undergo cyclization in the basic medium to give the pyrazolopyrimidine moiety 72. Intermediate 72 is oxidized by PPMS (potassium peroxydisulfate complex salt) in acetonitrile to give sulfoxide 73. In turn, 73 is reacted with an aryl-substituted amine in a basic medium, followed by a reaction with an aryl or alkyl bromide via Cu-catalyzed Ullman coupling or Chanlam coupling to give MK1775 analogues (IV) (Scheme 10).¹²⁷

Another method to synthesize IV is by coupling the ester 20 with an alkyl bromide, which gives disubstituted intermediate 74, and copper acetate and K_2CO_3 in dioxane catalyze the reaction. Intermediate 74 undergoes oxidation by PPMS in acetonitrile to produce NA = not available, which in the

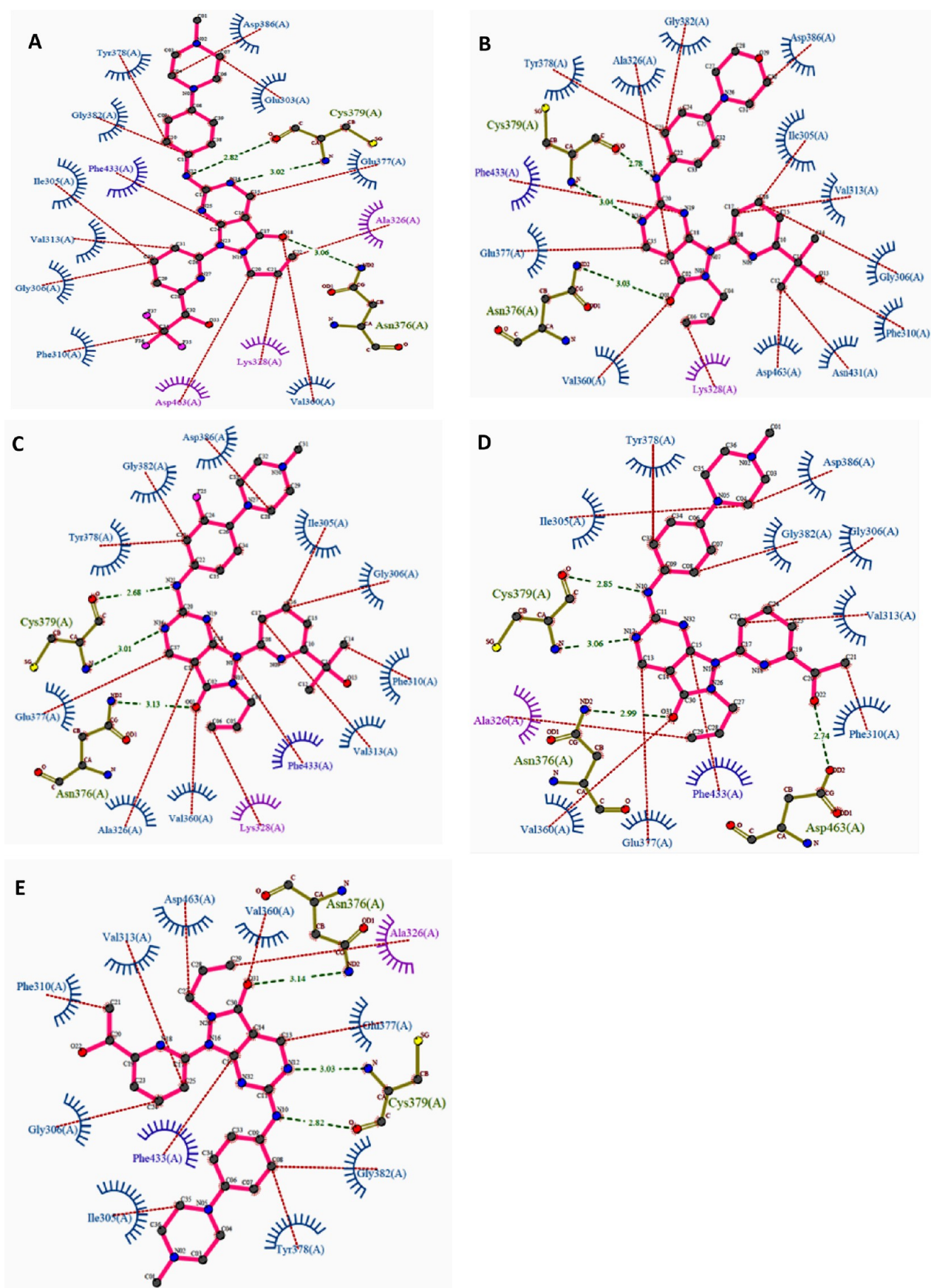


Figure 12. Pyrazolopyrimidine-WEE1 interaction profile in 2D. (A) PDB ID: 5VD4, (B) PDB ID: 5VD5, (C) PDB ID: 5VD7, (D) PDB ID: 5VD9, and (E) PDB ID: 5VDA.

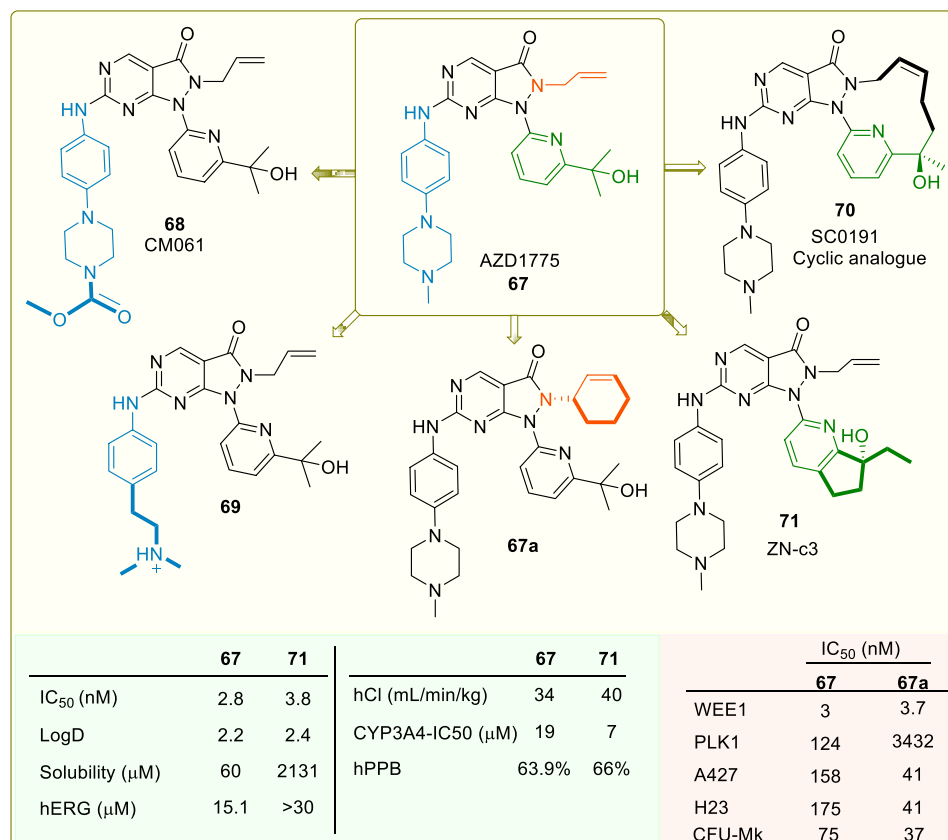


Figure 13. Optimization of AZD1775-based analogues (adopted from Matheson et al.;^{123,124} Qian et al.;¹²¹ Huang et al.;¹²⁵ and Guler et al.¹²⁶).

presence of a base like DIPEA in toluene reacts with an aryl amine to form **IV** (Scheme 11).¹²⁷

Yu et al. patented a new synthesis method for the preparation of AZD1775. Here, the ester **20** is reacted with hydrazine; then an aryl is substituted at “N” to give mono aryl substituted intermediate **76**, which is reacted with an allyl halide followed by oxidation and *N*-alkylation to produce AZD1775 (**67**) (Scheme 12).¹²⁸

Allyl pyrazolopyrimidine (**77**) is substituted with pyridinyl-hexenol (**78**) in the presence of 1,2-dimethylethylenediamine, methyl acetate, and potassium carbonate in dioxane to give **79**. Alkene metathesis using Grubbs second generation catalyst in toluene, oxidation of the methylthio group, followed by reaction with methylphenylpiperazine in DIPEA generated the macrocyclic analogue, SC0191 (**70**) of AZD1775 (Scheme 13).¹²⁹

2.4. Pyrrolopyrimidine Analogues. The significant binding of AZD1775, a pyrazolopyrimidine class of analogue, with ATP binding residues via H-bond formation with C379 and N379, as well as a hydrophobic network with pocket residues like I305, F443, and V313, led to the design of another series of WEE1 kinase inhibitors, pyrrolo[2,3-*d*]pyrimidine scaffold (**XXI** and **XXII**) (Figure 16). The pyrrolo[2,3-*d*]pyrimidine core proved to be a preferential scaffold with micromolar potency against WEE1 inhibition in biological enzyme assays and cellular anticancer screening methods.¹³⁰ A few analogues (**84** and **85**) are shown in Figure 15.

2.4.1. Structure–Activity Relationship and Optimization Approaches of Pyrrolopyrimidines. SAR studies with various chemical modifications are being investigated following the

optimization of the pyrrolo[2,3-*d*]pyrimidine scaffold as a potential WEE1i.¹³⁰ WEE1 inhibition and anticancer activity of isopropyl and the effect of the sulfoximine group was investigated as fundamental in retaining the efficacy.

Also, isosterically similar alkyl, cyclopropyl, and alkoxy chains on pyrrolo[2,3-*d*]pyrimidines and piperazine incorporation, along with their potencies, were monitored (Figures 15, 16).¹³⁰ Later, it was discovered that the fluoro-group adjacent to the alkyl chain on the core scaffold showed weak WEE1i (**XXI**) and loss of anticancer activity in the NCI-H1299 cell line. The design strategy, optimization of the pyrrolo[2,3-*d*]pyrimidine core as an emerging scaffold, and SAR studies against WEE1 kinase inhibition showed that the propyl alcohol and sulfoximine moieties on the pyridine (**XXII**) were crucial in imparting the anticancer activity, whereas the fluoro-group on the optimized core reduced the anticancer effect. Additionally, the pirazinyl and piperazinyl substituted amines occupy the hydrophobic cavity formed by I305, F443, and V313 residues of WEE1 kinase and furnish the H-bonds as well as charged interactions through the quaternary system, which is not seen in the case of morpholines/spiro system.¹³⁰ Pyrrolopyrimidines retain the aminopyrimidine ring of pyrazolopyrimidines, and thus the interactions with C379 are preserved. However, removing carboxyl group has resulted in a loss of interaction with the N376 residue, contributing to its decreased potency. On the other hand, the fluoro-substitution further reduced the potency due to harmful interactions with N376 and its surrounding residues. Replacing the isopropanol substitution on pyridine with iminodimethylsulfanone has decreased the potency because the bad interactions eclipse the

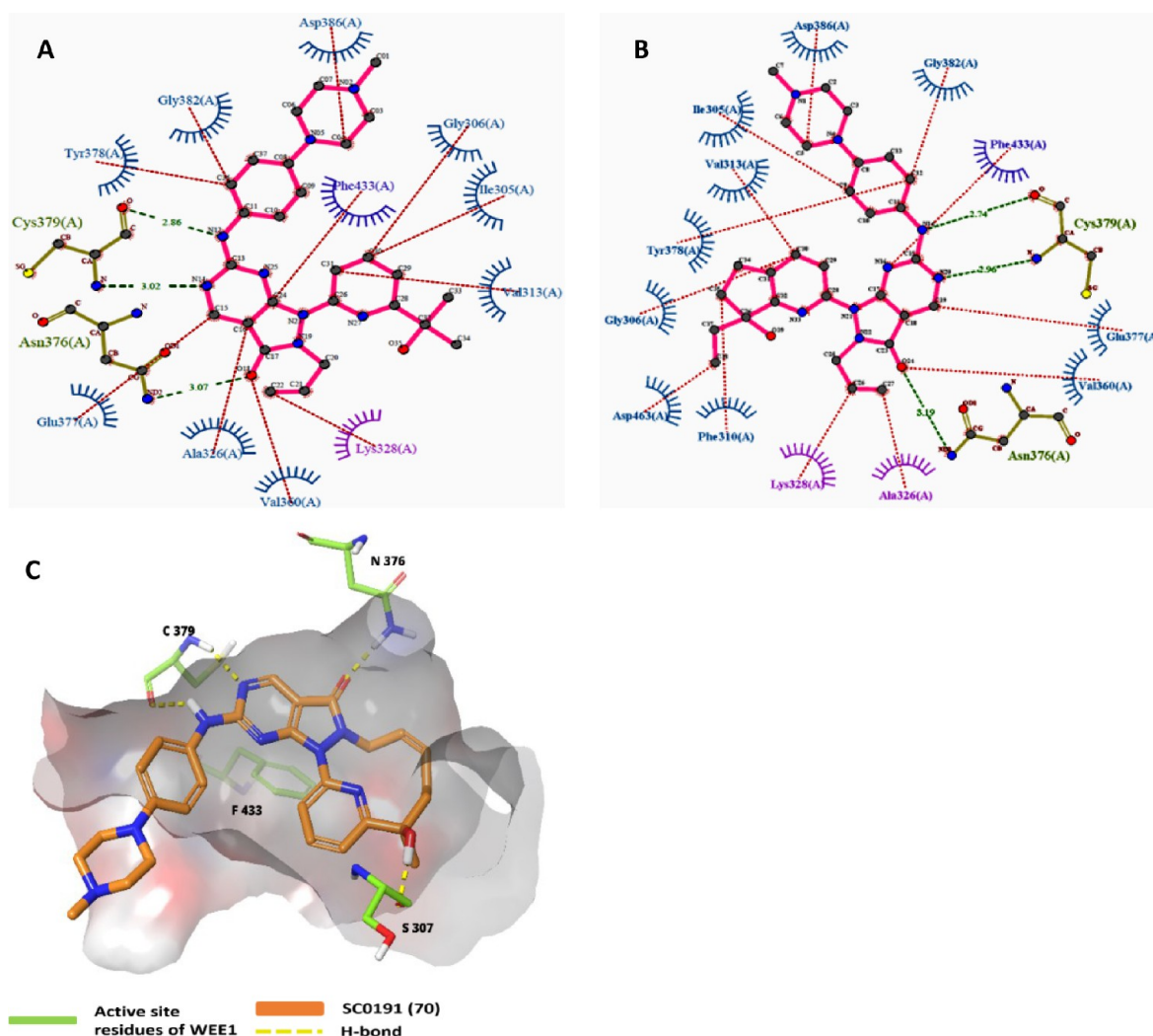


Figure 14. (A) 2D Interaction profile of AZD1775 (67) (PDB ID: 5V5Y), (B) ZN-c3 (71) (PDB ID: 7N3U), respectively, and (C) interaction profile of SC0191 (70) with WEE1's active site residues.

good interactions with D463, K328, and other neighboring residues (Figure 17).¹³⁰

2.4.2. Synthesis of Pyrrolopyrimidine analogues. The chemical synthesis of the pyrrolo[2,3-*d*]pyrimidine scaffold (XXI) involves the reaction of dichloro-substituted pyrimidine 86 and 2-amino-6-substituted (propyl alcohol or sulfoximine) pyridine 87 under reflux conditions to yield intermediate 88. The pyrimidine intermediate 88 upon CuI and Pd catalyzed reaction with an alkyne undergoes cyclization to afford desired scaffold 89, which on subsequent reaction with *N*-methylpiperazinyl amine afforded the pyrrolo[2,3-*d*]pyrimidine class (XXI) of WEE1 kinase inhibitor with either propyl alcohol and sulfoximine substitution (Scheme 14).¹³⁰

Fluorination of key pyrrolopyrimidine intermediate 89 using Selectfluor afforded the fluorinated derivative 90 and which, upon subsequent coupling with 4-(4-methylpiperazin-1-yl)-aniline, afforded the weak WEE1 kinase inhibitor XXII (Scheme 15).¹³⁰

2.5. Pyrimidopyrimidine. Pyrimidopyrimidine scaffold (Xb) was first mentioned in a patent as a WEE1i by Bamba et al. (2008).¹³¹ Later, other analogues of this scaffold were synthesized and tested for WEE1 inhibitory action (Figure 18). Additionally, Debio-0123 (91) (WEE1: IC₅₀ = 41 nM, PLK1: IC₅₀ = >10,000 nM) of this series is a potent and selective

WEE1i from Debiopharm. It is in phase-I clinical trials for monotherapy (NCT05109975) and combination therapy with Carboplatin (NCT03968653) against advanced solid tumors.

Debio-0123 (91) showed excellent target engagement with dose and time-dependent increase in γ H2AX and histone H3 concentrations (indicating DNA damage). Though all tested doses were well tolerated, studies on various cell lines and animal species recommended a dosage of 30 mg/kg.¹³² Another study on debio-0123 combined with carboplatin and etoposide observed an increase in apoptosis and a decline in tumor growth in SCLC *in vitro* and *in vivo*. Moreover, the study concluded that debio-0123 sensitizes SCLC tumors to the corresponding DDAs.¹³³ Lately, a new phase-I, II trial is launched to identify its recommended phase-II dose (RP2D), safety, tolerability, and efficacy in combination with Temozolomide and radiation against Glioblastoma (IDH wild type) and grade-III Astrocytoma (NCT05765812). This study deduced debio-0123 as an effective agent against glioblastoma *in vitro*. Furthermore, as a monotherapy, the oral administration of debio-0123 penetrated blood-brain barrier and inhibited tumor growth *in vivo* exceptionally well, thus highlighting debio-0123's therapeutic potential.¹³⁴

2.5.1. Synthesis of Pyrimidopyrimidine. Aryl-isocyanate is added to a mixture of the amine 98 and NaH in DMF at room

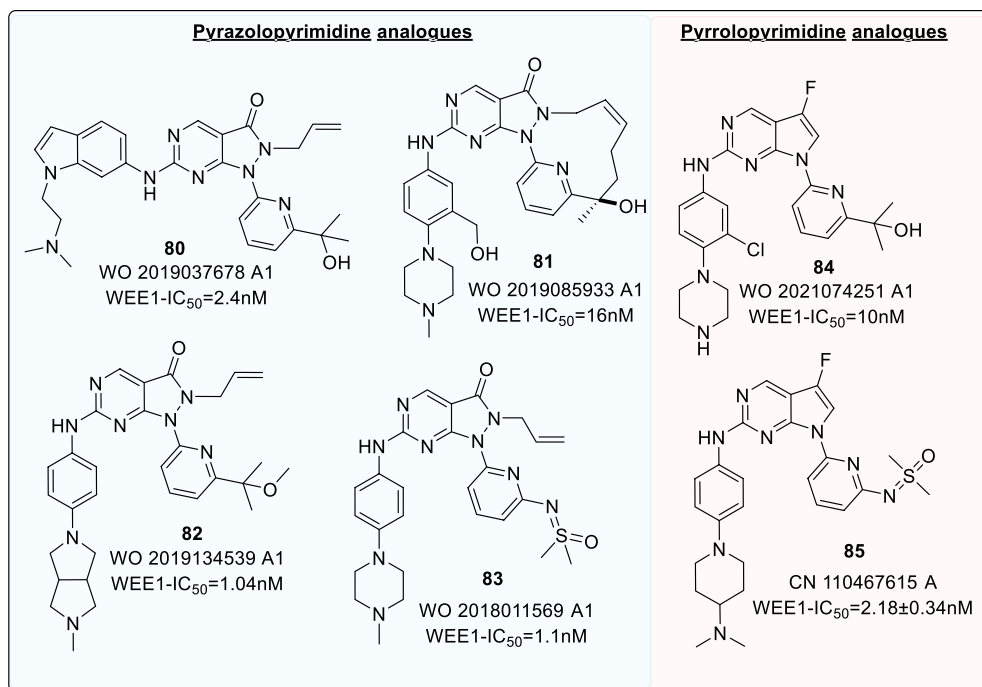
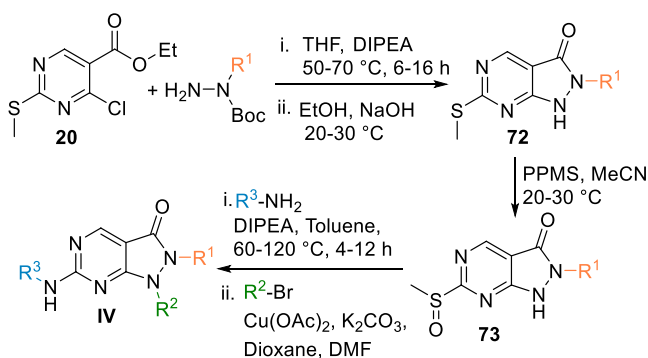


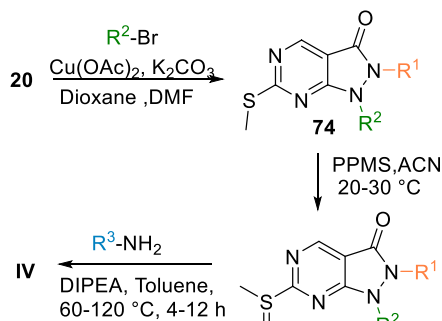
Figure 15. Pyrazolopyrimidine (80–83) and pyrrolopyrimidine (84 and 85) analogues.

Scheme 10. Synthesis of Pyrazolopyrimidines (IV)^a



^aAdapted from Minh Pham et al.¹²⁷

Scheme 11. Synthesis of Pyrazolopyrimidines^a



^aAdapted from Minh Pham et al.¹²⁷

temperature and stirred to produce a 6*N*-aryl pyrimidopyrimidine-2,4-dione moiety **99**. In the first route, **99** is oxidized by *m*-CPBA, followed by reacting with an aryl amine in the presence of the base to give **102** via the formation of an intermediate **100**. 4*N*-alkylation by an alkyl halide in

diazabicycloundecene (DBU) gives **Xa**. In another route, **99** first undergoes 4*N*-alkylation to give **101**, followed by oxidation with *m*-CPBA, then reacted with an aryl amine in the presence of DIPEA to produce **Xa**. Intermediate **101** can also be synthesized by reacting **20** with an alkyl amine in the basic environment, followed by reacting with aryl isocyanide (Scheme 16).¹³⁵

Analogues of **93** (**Xb**) can be synthesized by reacting 4-amino-2-chloropyrimidin-5-carbonitrile (**103**) with isocyanate in base (NaH). This reaction gives imino-pyridopyrimidine moiety **104**, which undergoes 4*N*-alkylation by alkyl halide to generate a disubstituted intermediate **105**, then undergoes amination by reacting with tosylate monohydrate to produce **Xb** (Scheme 17).¹³⁶

4-Amino-2-methylsulfanyl-pyrimidin-5-carbonitrile (**106**) first reacts with an aryl amine to give 2°-aminopyrimidine **107**, which is first oxidized by *m*-CPBA, then reacts with an aryl amine under basic conditions to give 2-aryl substituted pyrimidine **108**. **Xb** is produced when **108** is allowed to react with isocyanate (Scheme 18).¹³⁶

2.6. Pyrimidine-Based Tricyclics: De Novo Design and Optimization.

However, *de novo* design and optimization of the pyrimidopyrimidine scaffold afforded the pyrimidine-based tricyclic (PBT) scaffold (**XI**, Figure 19). A 5-membered heterocyclic ring is fused to the pyrimidopyrimidine ring, which is confined between V313 and F433 like the pyridine ring of AZD1775, and these analogues (PBT) exhibit good potency, PK properties, and oral antitumor efficacy when tested in murine xenograft models.¹³⁷ This series offered IMP7068 (**95**) from Impact Therapeutics, a potential phase-I clinical candidate against advanced solid tumors in monotherapy (NCT04768868). The trial so far recommends doses up to 160 mg to observe sound preliminary antitumor activities and pharmacodynamics; additionally, well-tolerated treatment-related toxicity profile with negligible dose-limiting toxicities was observed.¹³⁸

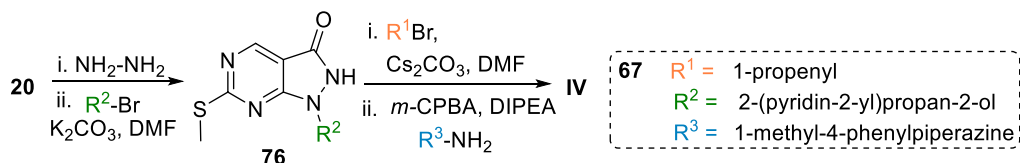
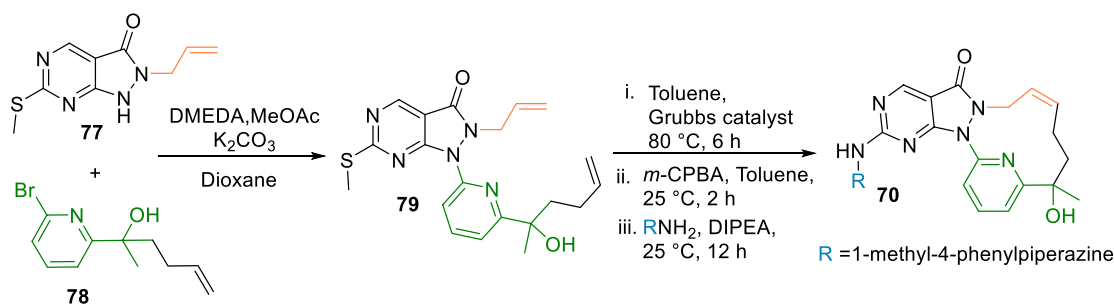
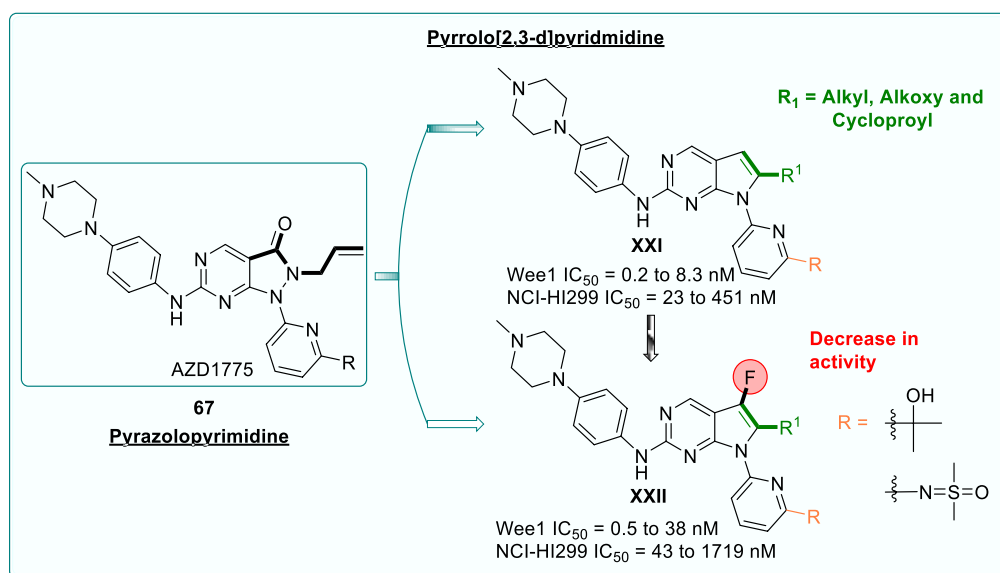
Scheme 12. Synthesis of AZD1775^a^aAdapted from Yu et al.¹²⁸Scheme 13. Synthesis of Macrocyclic Analogue of AZD1775 (70)^a^aAdapted from Qian et al.¹²⁹

Figure 16. Optimization of the pyrrolo[2,3-d]pyrimidine scaffold as WEE1 kinase inhibitors (adopted from Chen et al.¹³⁰).

2.6.1. *Structure–Activity Relationship and Optimization Approaches of Pyrimidine-Based Tricyclics.* 2-Amino and the 3N of the pyrimidine ring are associated with C379 through H-bonds. While the 5-carbonyl ‘O’ interacts with the N376-gatekeeper residue.¹³⁷ The 2-amino substitutions extend out of the pocket and are solvent-exposed. The aryl substitution on the 2-amino group is very essential as it is sandwiched between I305 and G382 and forms π – σ interactions.¹³⁷ The 6N-substituted benzene remains perpendicular to the tricyclic ring and fits into the lipophilic pocket beside the gatekeeper. Similar to pyrrolocarbazoles, these tricyclic compounds also prefer a 2’-Cl, but a 2’-Cl, 6’-F substitution resulted in increased potency (Figure 19).¹³⁷ The substitutions to aniline must contain at least one ‘N’. However, as shown in Figure 19, tetrahydroisoquinoline with *gem*-dimethyl or cyclopropyl

elevates the activity.¹³⁷ Figure 20 shows the overlap image of pyrimidopyrimidine and pyridine-based tricyclic analogues in the ATP pocket of WEE1.

2.6.2. *Synthesis of Pyrimidine-Based Tricyclics.* The pyrimidine-based tricyclic core (XI) is synthesized from the key intermediate 99 when treated with phosphorus oxychloride (POCl_3) in DIPEA, followed by a reaction with 2,2-dimethoxyethanamine (112) in acetonitrile at elevated temperature, then treated with acids like conc. HCl to give the key tricyclic intermediate 113. Another method of synthesizing 113 is by reacting 99 with either sodium azide at elevated temperature in DIPEA or by reaction with formyl hydrazine in acetonitrile. Moreover, reacting the ester 20 with 1-(2-aminoethyl)-3-alkyl urea 114 in the presence of DIPEA in acetonitrile and then treating with POCl_3 also gives the

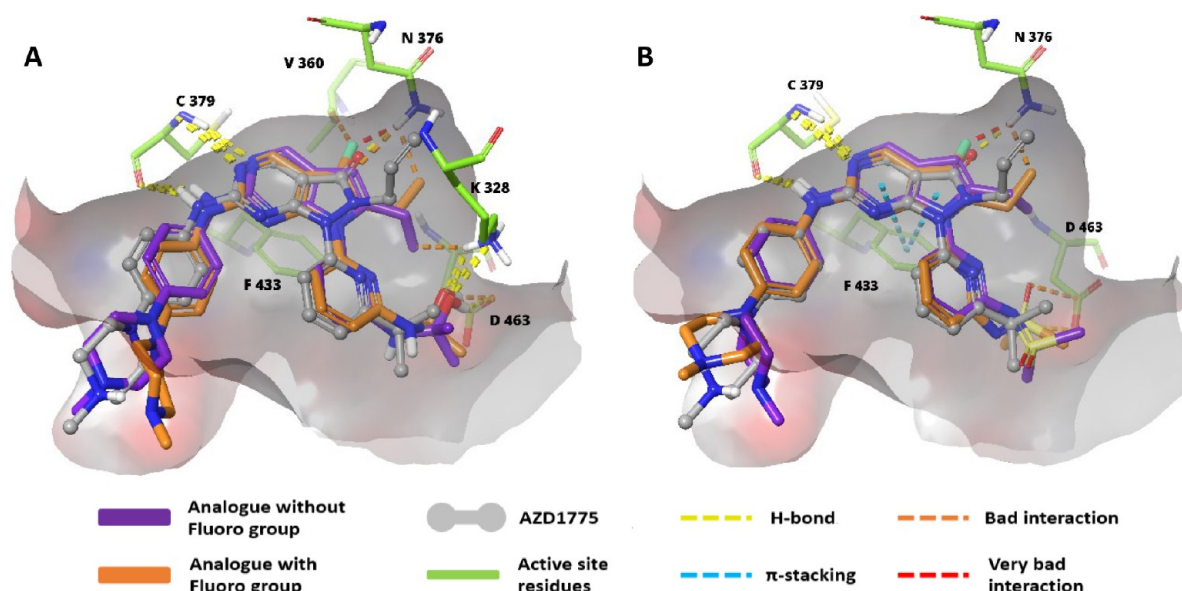
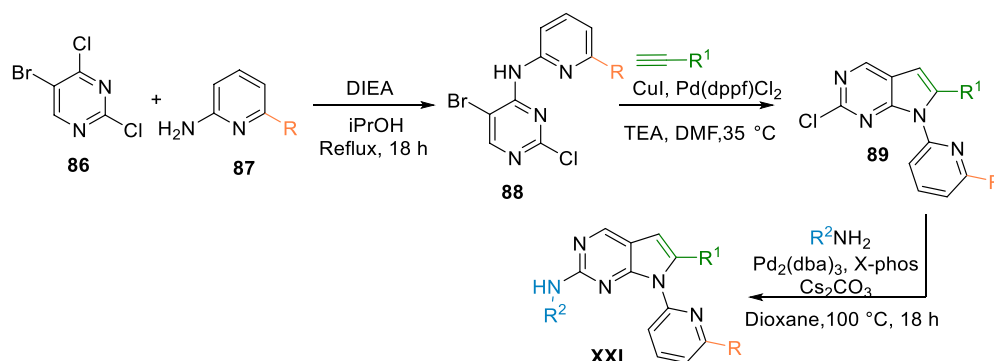


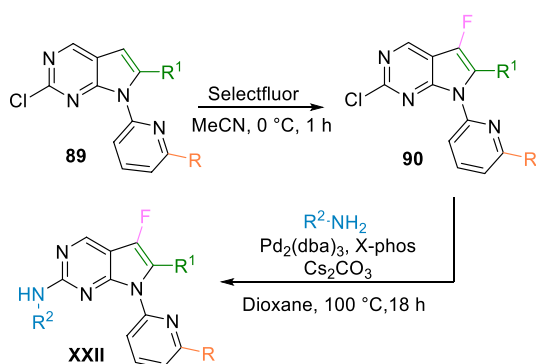
Figure 17. Relative interaction profile of pyrrolopyrimidine scaffolds (XXI and XXII) and AZD1775. (A) Pyrrolopyrimidine scaffolds with 3°-alcohol substituted pyridine and (B) pyrrolopyrimidine scaffolds with iminodimethylsulfanone-substituted pyridine.

Scheme 14. Synthesis of Pyrrolopyrimidines (XXI)^a



^aAdapted from Chen et al.¹³⁰

Scheme 15. Synthesis of Fluoro-Pyrrolopyrimidines (XXII)^a



^aAdapted from Chen et al.¹³⁰

tricyclic core **113**. The prepared **113** is then oxidized with *m*-CPBA and then amination by reacting with an aryl amine in DIPEA to produce PBT analogues (**XI**) (Scheme 19).^{139,140}

2.7. Other Scaffolds and Their Synthetic Schemes. Later in 2019, via ensemble docking of 20 WEE1 crystal structures, two new ligands **1** and **2** (Figure 5) were

identified.¹⁴¹ In the same year, Hu et al. screened the ZINC database via ligand-based pharmacophore modeling and identified eight potential ligands with new scaffolds, which were further subjected to QSAR, ADMET, and binding free energy studies followed by molecular dynamics (MD) simulations and ultimately proposed **3** (Figure 5) as a potent WEE1i.¹⁴² Furthermore, vanillates (**4**) (Figure 5) have also exhibited micromolar WEE1 inhibition and were initially treated as an important class of WEE1i.¹⁴³ Conversely, patent literature has also provided new scaffolds worth investigating. Shouyao Holdings' SY-4835 (confidential structure) is a phase-I WEE1i being tested against advanced solid tumors to evaluate the pharmacokinetics, safety, tolerability, and anticancer activity (NCT05291182). Yang et al. were the first to identify the rhodium(III) complex **9**, which induces mitotic catastrophe via induced DNA damage, as a potent single agent WEE1i in TP53 mutant (MDA-MB-231) cells.¹⁴⁴ Olawale et al. performed *in silico* studies using FDA-approved drugs and proposed Dasatinib and Cangrelor as potential repurposed WEE1i.¹⁴⁵

PF03814735 (**6**) is an Aurora kinase inhibitor in clinical trials. It showed nanomolar WEE1 inhibition (IC₅₀ = 78.7 nM). It can be synthesized by reacting trifluoro-methylpyr-

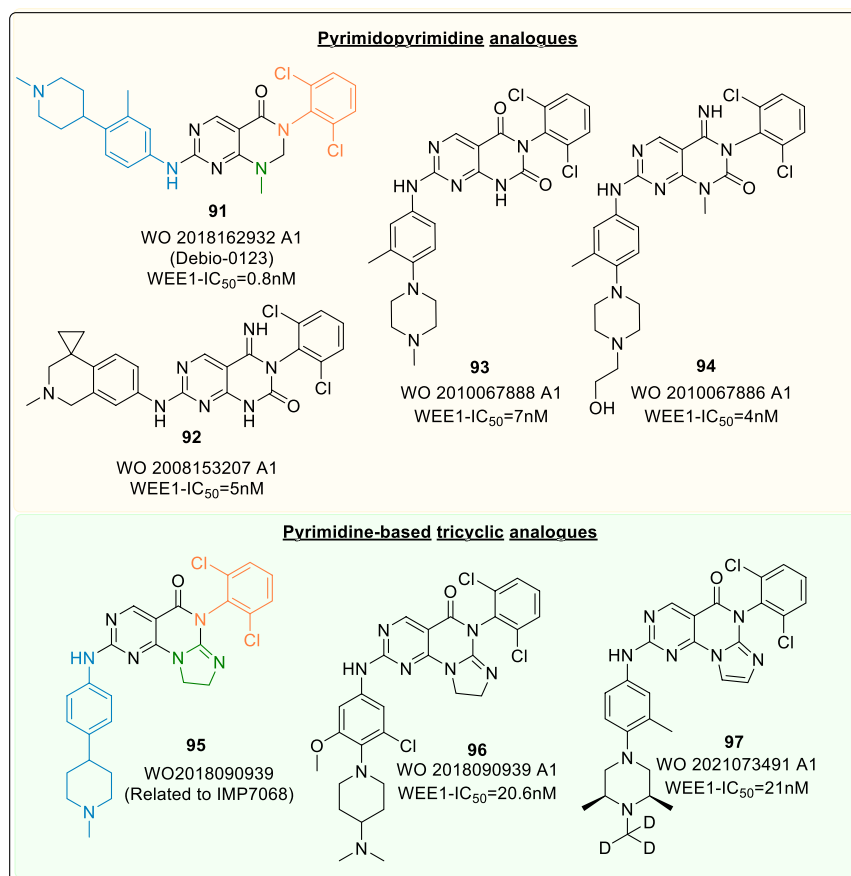
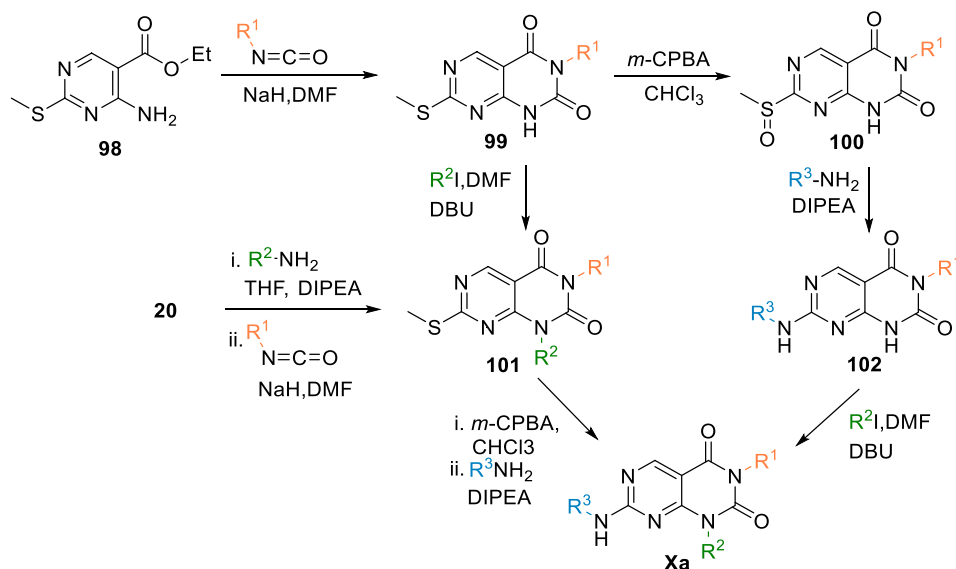


Figure 18. Pyrimidopyrimidine analogue and pyrimidine-based tricyclic analogue.

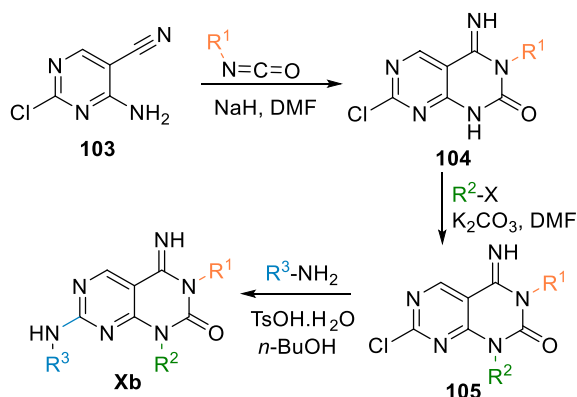
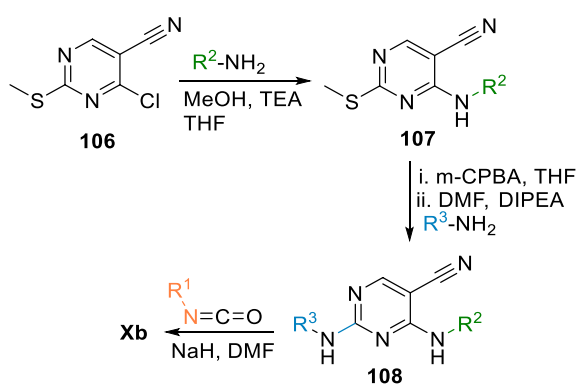
Scheme 16. Synthesis of Pyrimidopyrimidine (Xa)^a



^aAdapted from Bamba et al.¹³⁵

imidine (**115**) with the amine **116** in the presence of ZnCl₂ in ether, then treated with TEA in *t*-butanol and ethylene dichloride (DCE), followed by *N*-deprotection to give aminopyridine intermediate **117**, which is first reacted with the carboxylic acid **118**, then substituted with cyclopropylamine to produce PF03814735 (**6**) (Scheme 20).¹⁴⁶

Bosutinib (**7**) is a tyrosine kinase (Abl and Src) inhibitor used for treating chronic myelogenous leukemia. It showed IC₅₀ = 644 ± 195 nM against WEE1 kinase. Its isomer (**8**) is also a dual Abl and Src inhibitor displayed IC₅₀ = 54.8 ± 12 nM against WEE1.¹⁴⁷ Both isomers can be synthesized by reacting chloroquinoline **119** with their respective dichloro-

Scheme 17. Synthesis of Pyrimidopyrimidine (Xb)^a^aAdapted from Yoshizumi et al.¹³⁶Scheme 18. Synthesis of Pyrimidopyrimidine^a^aAdapted from Yoshizumi et al.¹³⁶

openylamine positional isomers **120** and **121** in pyrimidine hydrochloride and 2-methoxyethanol followed by reacting with *N*-methylpiperazine in KI (Scheme 21).¹⁴⁸

An alkyl/aryl amine is substituted on pyrimidine **122** in the presence of a base like DIPEA to give **123**, which in the presence of the palladium catalyst reacts with pyrazole **124** when exposed to microwaves giving pyrimidine-based inhibitor (**I**) (Scheme 22).¹⁴⁹

The reaction of imidazolyl pyrimidine **125** and an aryl amine is catalyzed by palladium catalyst and X-Phos, which generates the arylamine-substituted imidazolyl pyrimidine (**II**) (Scheme 23).¹⁵⁰

The amide **126** reacts with diiodomethane in a basic medium and undergoes cyclization to form an intermediate **127** which, when oxidized and reacted with an amine, gives the product pyrimidothiazenes (**IXa**) or pyrimidooxazines (**IXb**) (Scheme 24).¹⁵¹

Benzothiazineonedioxide **128** is initially reacted with *N,N*-dimethoxytrimethylamine and then reacted with *S*-methyl thiourea (initially treated with acetic acid) to produce pyrimidobenzothiazineonedioxide **129** which, when oxidized and reacted with an aryl-substituted amine, gives **XIII** (Scheme 25).¹⁵²

Li et al. in 2018 performed pharmacophore modeling, docking, and MD simulations and identified a new scaffold (**XVI**) having an IC₅₀ value of 22.32 μM against WEE1 and an IC₅₀ value of 17.8 μM when tested against A-549 cell lines.¹⁵³ Pyridothienopyrimidine (**XVI**) is synthesized by cyclization of pyridothiophene **130** with hydrazine, followed by reacting with bromophenylethanone (**132**) via forming an intermediate **131** (Scheme 26).¹⁵⁴

2.7.1. Hybrid WEE1 Kinase Inhibitor and Its Synthesis. The hybrid set of new compounds (**XV**) comprises the essential structural and pharmacophore features of promising WEE1i (**XI** and **IV**) that were designed and synthesized (Figure 21). The kinase inhibition profile of hybrid analogues targeting WEE1 kinase provided a potential framework for developing of novel anticancer agents.

Aminoindazole **133** is substituted to ethyl 4-chloro-2-(methylthio)pyrimidine-5-carboxylate (**134**) in the presence of a base like DIPEA to give the amino indazole-substituted

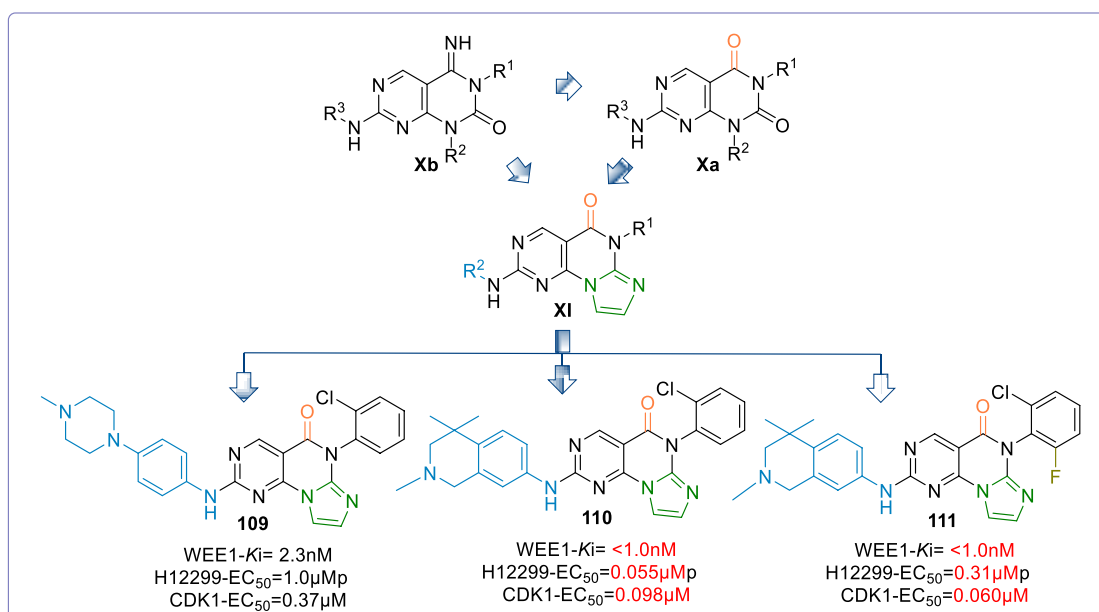


Figure 19. Optimization of PBT (adapted from Tong et al.¹³⁷).

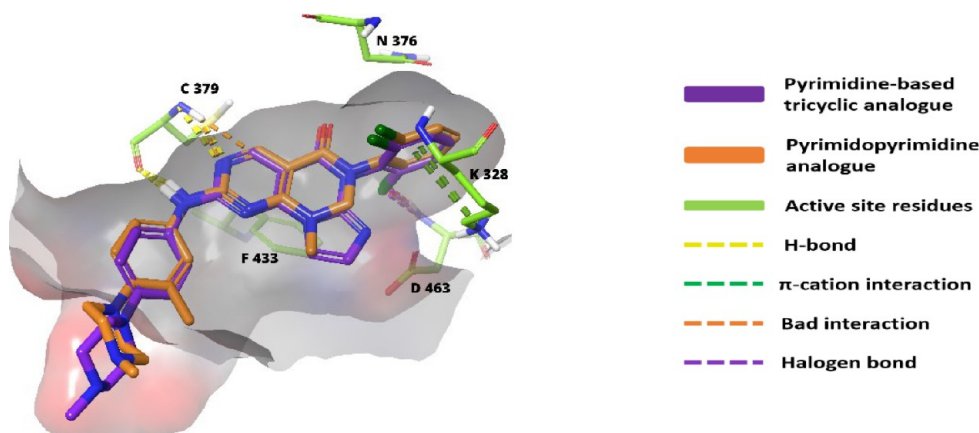
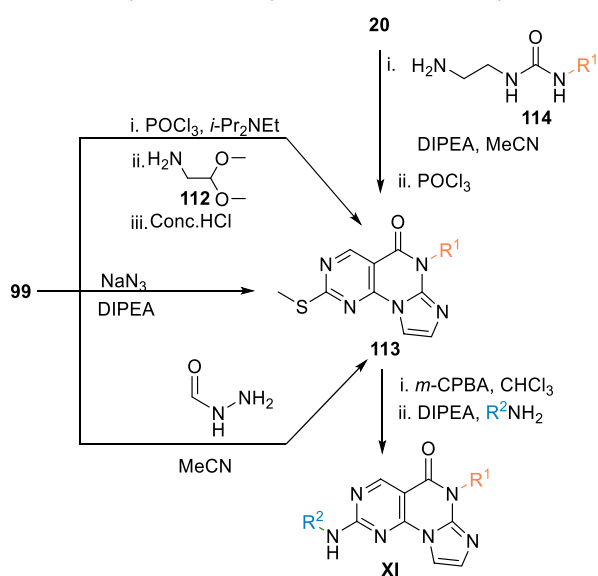


Figure 20. Pyrimidopyrimidine (91) and pyrimidine-based tricyclic scaffold (95) interactions with WEE1 kinase residues.

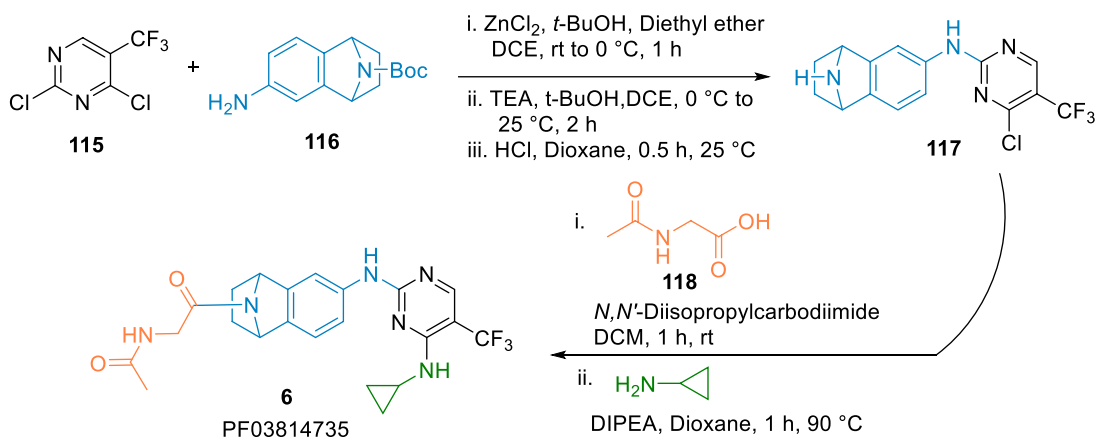
Scheme 19. Synthesis of Pyrimidine-Based Tricyclics (XI)^a



^aFrom 99 to 113 (adapted from Woods et al.¹³⁹) and from 20 to 113 (adapted from Tian et al.¹⁴⁰).

ethyl(methylthio)pyrimidine carboxylate (135), which is *N*-alkylated by bromo alkyl or aryl in basic medium to give 136.

Scheme 20. Synthesis of PF03814735 (6)^a

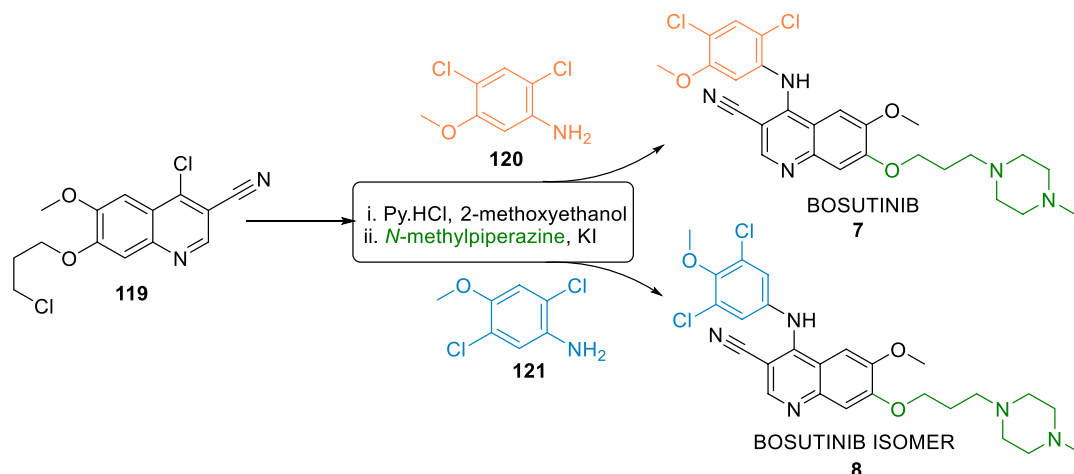
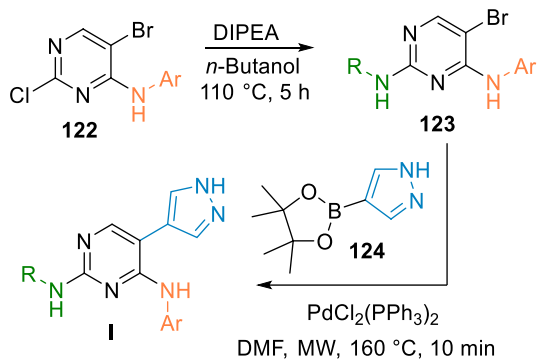
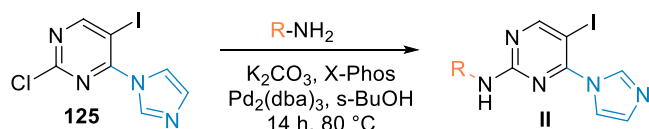
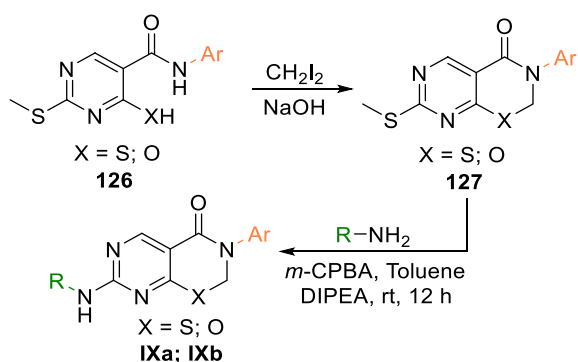
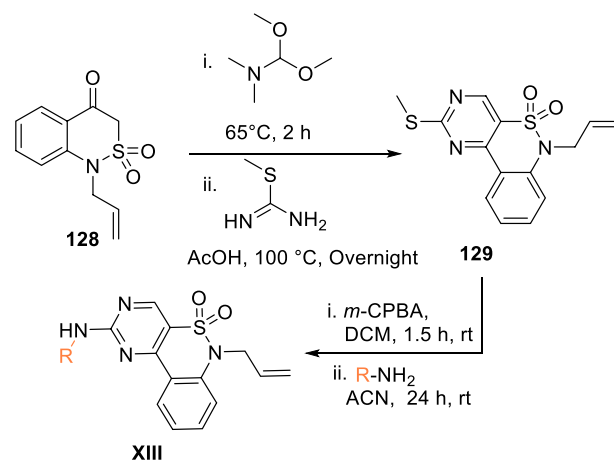
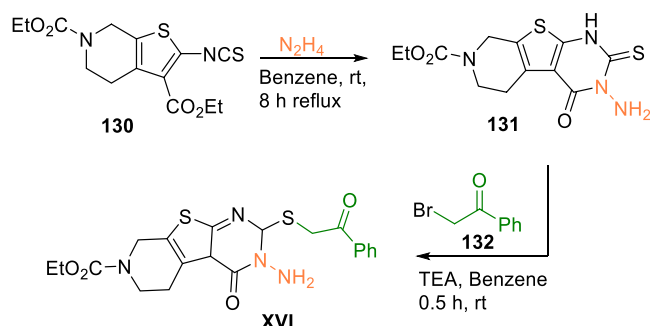


^aAdapted from Arcari et al.¹⁴⁶

Base-catalyzed hydrolysis of 136 (an ester) gives an acid 137. Cyclization of obtained acid 137 catalyzed by hydroxybenzotriazole gives basic designed core 138. Oxidation followed by amination of 138 produces the hybrid scaffold XV (Scheme 27).¹⁵⁵

3. DEGRADERS OF WEE1 KINASE

WEE1i known so far are also off-target binders, i.e., apart from WEE1, they also interact with other kinases. Therefore, selective degradation of the protein using PROTACs (proteolysis targeting chimeras) is another strategy to explore.¹⁵⁶ PROTACs are chemical chimera degraders that take over natural protein control systems. PROTACs contain three components. (1) The warhead or target binder agents that bind with the protein, (2) the E3 ligase binding moiety (EBM) that binds with a component of the protein control system (PCS), and (3) the linker that joins the warhead and the EBM.¹⁵⁷ The PROTACs anchor the target and the component of PCS (E3 ligase), ease ubiquitination, and mark the protein for recognition by proteasomes or autophagosomes, which degenerate the target proteins.¹⁵⁷ As PROTACs recruit the proteasomes, they are specific and selective, though the warhead is nonselective.¹⁵⁸ Additionally, after degradation of the target protein, the released PROTACs continue degrading another target protein; thus, the PROTACs have relatively high potency. The efficiency of PROTACs is a

Scheme 21. Synthesis of Bosutinib (7) and Its Isomer (8)^a^aAdapted from Wang et al.¹⁴⁸Scheme 22. Synthesis of Pyrimidine-Based inhibitor (I)^a^aAdapted from Reid et al.¹⁴⁹Scheme 23. Synthesis of Pyrimidine Inhibitors (II)^a^aAdapted from Choi et al.¹⁵⁰Scheme 24. Synthesis of Pyrimidothiazenes (IXa) and Pyrimidooxazines (IXb)^a^aAdapted from Kumar et al.¹⁵¹Scheme 25. Synthesis of XIII^a^aAdapted from Miyashiro et al.¹⁵²Scheme 26. Synthesis of Pyridothienopyrimidine (XVI)^a^aAdapted from Ahmed et al.¹⁵⁴

product of inhibition and degradation of the target protein. The increase in selectivity and potency is also observed in WEE1 PROTACs.¹⁵⁹ Li et al. constructed the first WEE1 PROTAC, ZNL-02-096 (142), by anchoring the E3 ubiquitin ligase recruiter pomalidomide (139), a cereblon binding ligand to AZD1775, which showed ten times more potency. Though

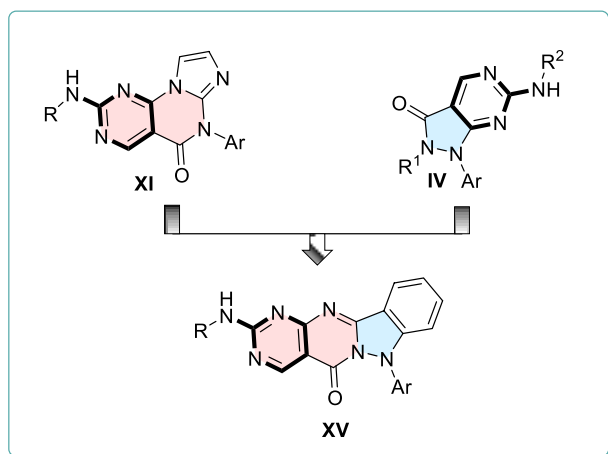


Figure 21. Hypothetical design strategy of XV.

it inhibits both WEE1 and PLK1 *in vitro*, it only degrades WEE1 in cells with maximal degradation at 100 nM.¹⁶⁰

Aublette et al. linked VH032 (**140**) and pomalidomide analogues (**139**) that bind to VHL (Von Hippel-Lindau) E3 ligase and CRBN (Cereblon) E3 ligase, respectively, to AZD1775 using different linkers and proposed the SAR of WEE1 PROTAC degraders. According to him, the linker length and nature determine the efficiency of the degrader. He proposed using either shorter or longer linkers but not intermediate ones. The proposed degraders MA055 (**143**) and MA071 (**145**) have indeed shown increased selectivity but no apparent change in apoptosis or antiproliferative effects compared to AZD1775.¹⁵⁶ Similar results were obtained by Zhu et al. in *in vitro* studies of **144**, a PROTAC degrader constructed using AZD1775 and CRBN E3 ligase recruiter and *in vivo* studies using MV-4–11 cells showed good WEE1 degradation in the target site after 3 h treatment.¹⁵⁹ Compound **144** has displayed sound pharmacokinetic properties in *in vitro* and *in vivo* studies. Moreover, one excess carbon in the linker of **144** contributed to an increase in WEE1 degradation compared to **142**, accentuating the importance of linkers' length to a PROTAC degrader.¹⁵⁹ In contrast, compound libraries containing glutarimide-structural frag-

ments were synthesized and screened for compounds promoting the ubiquitination of WEE1. WX106 (**141**), a CRBN competitive binder, induced the desired proteasome-dependent degradation of WEE1 and is effective against 18 cell lines tested.¹⁶¹ The toxicity of AZD1775 is a result of off-target and on-target inhibition, but the corresponding PROTACs offer ample selectivity and probably no off-target toxicity and tolerable on-target toxicity. Figure 22 depicts the components of PROTAC degraders and summarizes the PROTAC degraders of WEE1 kinase.

3.1. Synthesis of E3 Ligase Recruiters and Their Corresponding Degraders.

3.1.1. Synthesis of E3 Ligase Recruiters.

Scheme 28 depicts the preparation of the VH032 analogue **150**, a VHL E3 ligase recruiter. In the first step, *p*-bromobenzonitrile (**147**) reacted with 4-methylthiazole (**148**) in the presence of palladium acetate, KOAc, and dimethylacetamide (DMAc). Next, it is treated with NaBH₄, cobalt(II)-chloride in MeOH followed by reaction with Boc-Hyp-OH in DMF, then later DIPEA is added, followed by HATU to give **149**. Deprotection of Boc by TFA and DCM followed by the addition of Boc-*L*-tert-leucine when treated with DIPEA, HATU in DMF generate **150** (Scheme 28).¹⁵⁶

On the other hand, pomalidomide analogue **153** is obtained by reacting 3-fluoro-phthalic anhydride (**151**) with 3-amino-2,6-piperidindionhydrobromide salt (**152**), when dissolved in acetic acid and heated with KOAc (Scheme 29).¹⁵⁶

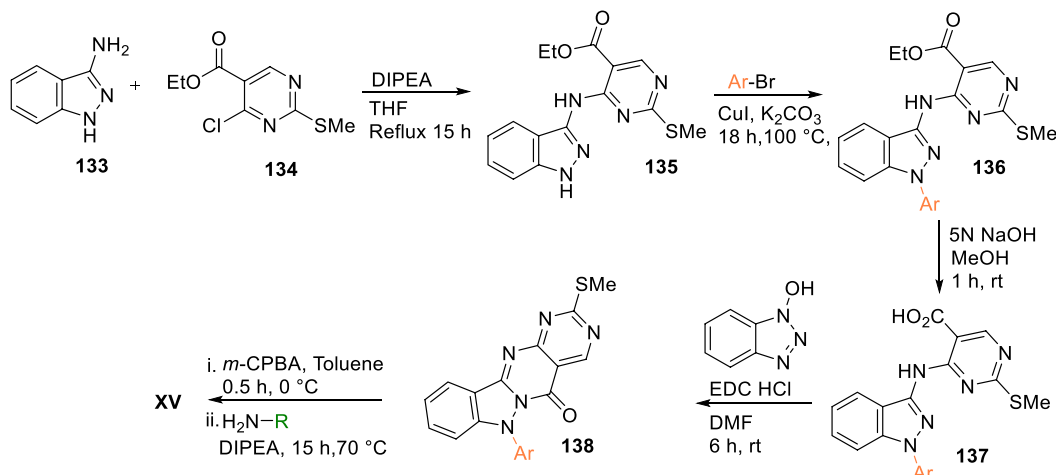
3.1.2. Synthesis of Degraders.

MA055 (**143**), a VHL-derived PROTAC, is produced when Boc deprotected VH032 analogue **150** undergoes amide formation with MK1775 acid analogue **154** (Scheme 30).¹⁵⁶

Li et al. in 2020 synthesized the first series of WEE1 PROTAC degraders where MK1775's analogue **155** was coupled with Boc-linker **156** in basic medium to generate Boc-substituted MK1775's analogue **157**, when treated with TFA and DCM to remove Boc and give an amine **158**. By substitution of the amine **158** to the pomalidomide analogue **153** in DIPEA and DMSO, alkyl-linked **142** and **144** can be synthesized (Scheme 31).¹⁶⁰

Moreover, CRBN PROTAC degrader is synthesized in two steps. First, the pomalidomide analogue **153** and diamine linker **159** are reacted in the presence of DIPEA and

Scheme 27. Synthesis of Hybrid Scaffold (XV)^a



^aAdapted from Takahashi et al.¹⁵⁵

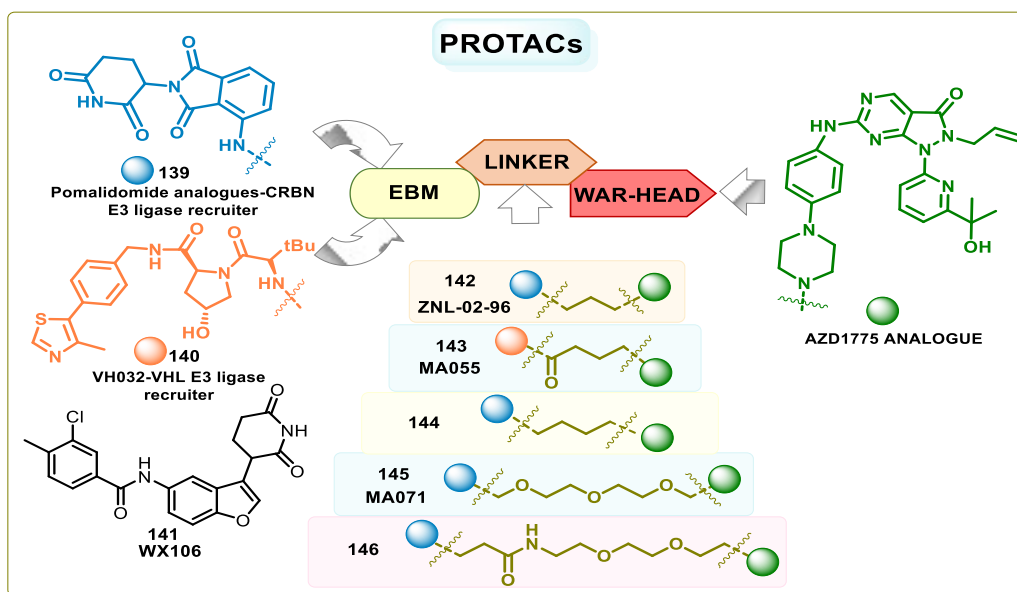
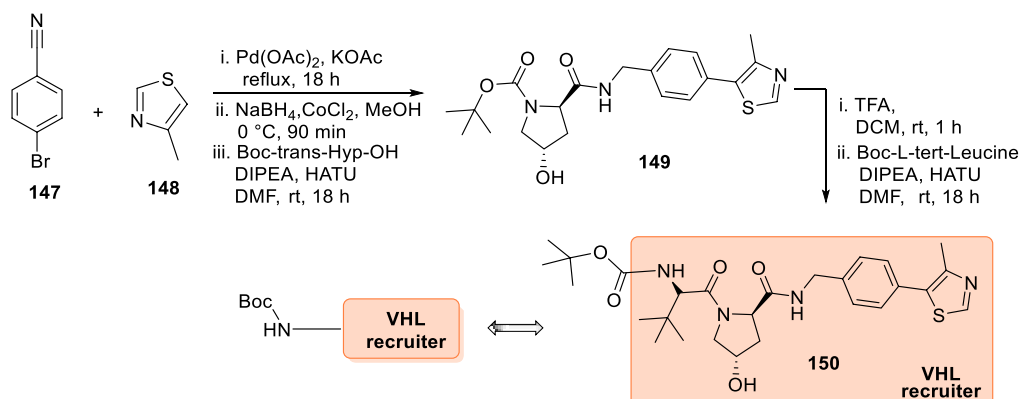


Figure 22. Structure of WEE1 PROTACs containing AZD1775 as a warhead, E3 ligase binding moieties, and various linkers (adopted from Li et al.,¹⁶⁰ Aublette et al.,¹⁵⁶ and Zhu et al.)¹⁵⁹.

Scheme 28. Synthesis of VHL Recruiter 150^a



^aAdapted from Aublette et al.¹⁵⁶

dimethylacetamide to generate the Boc-protected intermediate **160**, which undergoes deprotection followed by base-catalyzed amide formation with **154** to produce MA071 (**145**) (Scheme 32).¹⁵⁶

CRBN recruiter **153** is substituted with an amine linker **161** and then hydrolyzed to acid **162** that is condensed with MK1775's amine analogue **158** to give the degrader **146** containing an amide linker (Scheme 33).¹⁶⁰

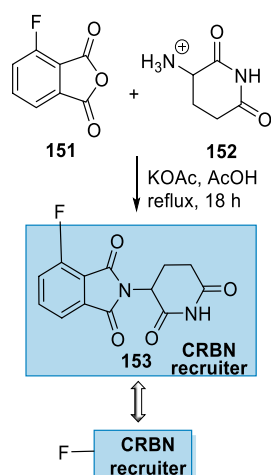
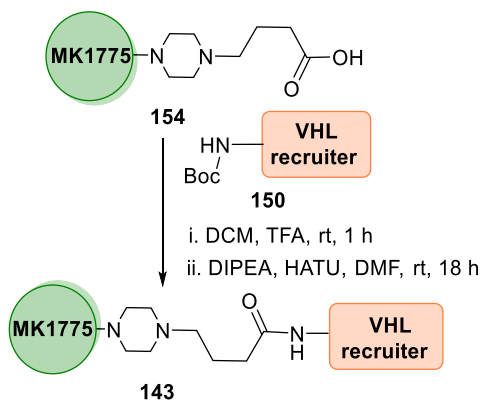
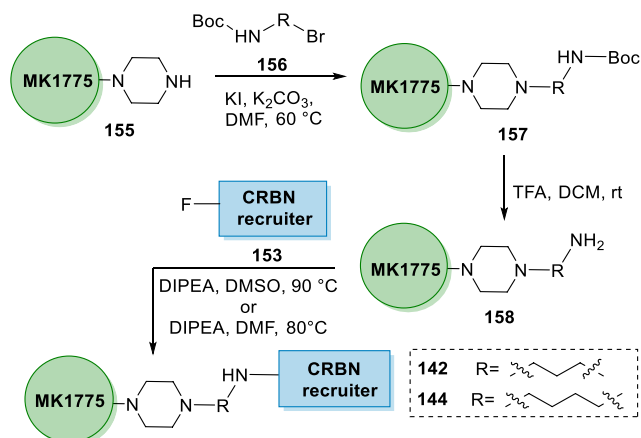
4. OTHER MECHANISMS OR STRATEGIES OF WEE1 DOWNREGULATION

Modulation of WEE1 expression in tumor cells using miRNAs (microRNAs), siRNAs (small-interference or silencing RNAs), and lncRNAs (long noncoding RNAs) is another ingenious strategy. MicroRNAs (miR- or miRNAs) are small, noncoding single-stranded RNAs that target mRNA and prevent protein synthesis by recognizing and binding to the 3'UTR (3' untranslated region).¹⁷¹ lncRNAs, on the other hand, act as miRNA sponges that regulate miRNA levels through actions indirectly regulating gene expression. Table 4 shows some of the lncRNAs and their target miRNAs that regulate WEE1,

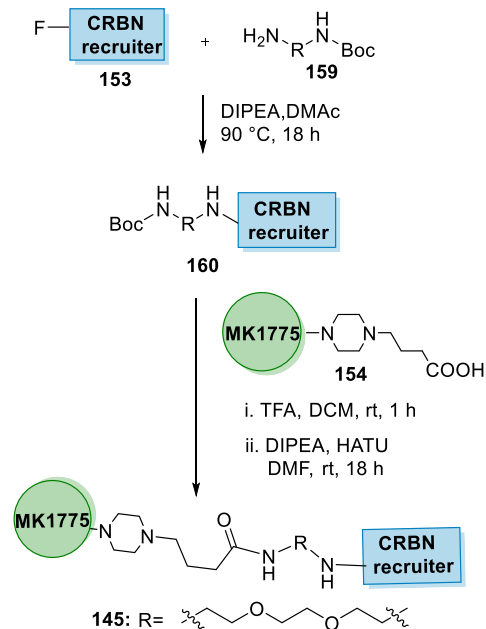
while miRNAs targeting WEE1 are tabulated in Table 5. Additionally, siRNAs targeting WEE1 are constructed.¹⁷² The silencing of WEE1 by siRNA has demonstrated increased chemosensitization in many cancers.⁷⁰

5. ADVERSE EVENTS OF EXISTING CLINICAL CANDIDATES

The first clinical candidate AZD1775 has undergone many clinical trials as a single agent and in combination with radiotherapy and diverse chemotherapeutics. These trials unveiled AZD1775's noxious toxicity profile.¹¹⁰ Most studies, be it monotherapy or combination therapy identified treatment emergent adverse events (TEAEs), drug-related adverse events (DRAEs), and dose-limiting toxicities (DLTs), including \geq grade 3 myelosuppression and grade 1–3 gastrointestinal (GI) toxicity.¹¹⁰ Excruciating grade 4 or 3 myelosuppression is observed in almost all trials, limiting AZD1775's potential as an ideal candidate.¹¹⁰ Initially, the toxicity profile of AZD1775 was inseparable from its off-target activity against PLK1, but recent studies and trials using more selective analogue ZN-c3 also showed treatment-related adverse events, including all

Scheme 29. Synthesis of Pomalidomide Analogue 153, a CRBN Recruiter^a^aAdapted from Aublette et al.¹⁵⁶Scheme 30. Synthesis of Degradier 143^a^aAdapted from Aublette et al.¹⁵⁶Scheme 31. Synthesis of Degradier^a^aAdapted from Li et al.¹⁶⁰ and Zhu et al.¹⁵⁹

grades of GI toxicities, \geq grade 3 neutropenia, and other hematological toxicities.^{186,187} Additionally, a 2023 study to optimize selective AZD1775 analogues identified thrombocytopenia as an inevitable consequence of WEE1 inhibition and

Scheme 32. Synthesis of Degradier 145^a^aAdapted from Aublette et al.¹⁵⁶

not PLK inhibition, asserting thrombocytopenia as an on-target toxicity.¹²⁶ On the other hand, IMP7068 exhibited negligible DLTs and treatment-related adverse events (TRAEs), including grade 1/2 increased levels of alanine aminotransferase (ALT) and aspartate aminotransferase (AST) and grade 1/2 diarrhea, which are tolerable.¹³⁸ Other candidate Debio-0123 is currently tested against advanced solid tumors (NCT05109975, NCT03968653) in phase-I and glioblastoma (NCT05765812) phase-I, II in monotherapy and combination therapy with manageable toxicity profile.¹³² SY-4835 is also in phase-I trial against advanced solid tumor (NCT05291182), and its toxicity profile is not yet determined. Table 6 summarizes the adverse events exhibited by clinical candidates.

6. DISCUSSION

WEE1 is a CDK inhibition kinase with three family members: WEE1/WEE1A, WEE2/WEE1B, and MYT1/PKMYT1. This family of kinases inhibits CDKs by phosphorylating inhibitory P-sites (T14 and/or Y15), resulting in cell cycle arrest. WEE1, the mitotic regulator, mainly ensures the generation of mature daughter cells. Loss of WEE1 action results in abnormally small-sized daughter cells, ultimately leading to mitotic catastrophe. The somatic WEE1/WEE1A contains the classic kinase structure and is equipped with NLS, NES, AcM, and three PEST regions. It conserves the HxD, DxG, and AxE motifs and four RxL motifs and is furnished with P-sites at S642, T239, S123, S121, and S53, as well as other auto-P-sites, besides an acetylation site K177 enclosed within NES that regulates WEE1 activation. Additionally, binding consensus for 14-3-3, cyclin A-CDK complex, CRK, and CRM1 are present.

In addition to being a mitotic regulator, WEE1 is an epigenetic modifier that inhibits H2B and blocks histone transcription. During the S and G2 phases, WEE1 is highly expressed and tightly shielded by the individual and combined efforts of 14-3-3, HSP90, and MIG6. In contrast, WEE1 is depressed during the initiation of the M-phase as it loses its shields and is

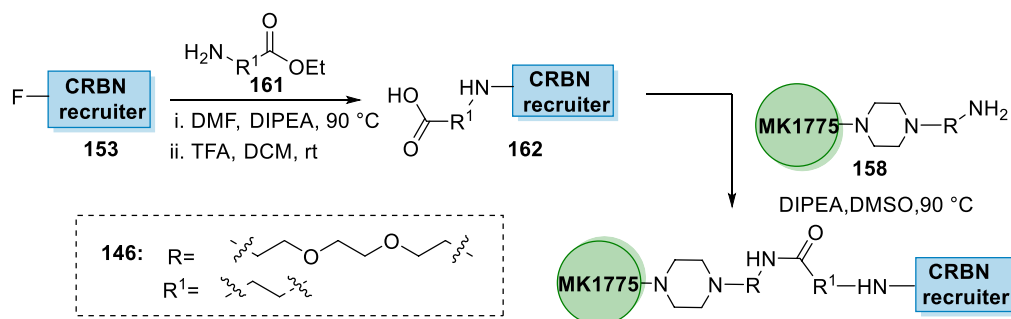
Scheme 33. Synthesis of Degraders^a^aAdapted from Li et al.¹⁶⁰

Table 4. WEE1/miRNA/lncRNA Axis

| S. no. | lncRNA | miRNA | refs |
|--------|------------------|------------|------|
| 1 | lncRNA DLX6-AS1 | miR-424-5p | 162 |
| 2 | lncRNA VIM-AS1 | miR-105-5p | 163 |
| 3 | lncRNA XIST | miR-16-5p | 164 |
| 4 | lncRNA FGD5-AS1 | miR-140-5p | 165 |
| 5 | lncRNA SNHG3 | miR-384 | 166 |
| 6 | lncRNA NEAT1_2 | miR-101-3p | 167 |
| 7 | circZNF91 | miR-1283 | 168 |
| 8 | lncRNA FOXD3-AS1 | miR-128-3p | 169 |
| 9 | circSNAP47 | miR-625-5p | 170 |

Table 5. miRNA Regulating WEE1

| S. no. | year | miRNA | cancer cells | refs |
|--------|------|------------------------------------|--|------|
| 1 | 2009 | miR-195 | human embryonic stem cells (hESCs) | 173 |
| 2 | 2010 | miR-516a-3p miR-128a miR-155 | pituitary adenomas | 174 |
| 3 | 2011 | miR-17 miR-20a miR-106b | unrestricted somatic stem cells from human cord blood (USSC) | 175 |
| 4 | 2011 | miR-128 | glioma cells | 176 |
| 5 | 2013 | miR-497 | neuroblastoma cells | 177 |
| 6 | 2013 | miR-424 | renal cancer cells | 178 |
| 7 | 2013 | miR-381 | | |
| 8 | 2015 | miR-17-92 cluster | leukemia | 179 |
| 9 | 2016 | miR-219-5p | RAW264.7 cells | 180 |
| 10 | 2017 | miR-503 | laryngeal carcinoma | 181 |
| 11 | 2017 | miR-194 | laryngeal squamous cell carcinoma (LSCC) | 182 |
| 12 | 2019 | miR-526b-3p | glioma cells | 183 |
| 13 | 2019 | miR-384 | laryngeal carcinoma cells | 166 |
| 14 | 2019 | miR-101-3P | HCC | 167 |
| 15 | 2020 | miR-140-5p | NSCLC | 165 |
| 16 | 2020 | miR-105-5p | glioma cells | 163 |
| 17 | 2021 | miR-16-5p | NSCLC | 184 |
| 18 | 2022 | miR-138-5P | glioma cells | 185 |

subjected to hyperphosphorylation by PLK1, CDK1, and CK2 to generate phosphodegrons (PDs), which is then degraded by F-box proteins like SCF β -TrCP, Tome-1, Smurf1, and Pof1/3 during the M-phase. Additionally, WEE1 is subjected to inhibitory phosphorylation by NIM1/CDR1, BRSK1/2, and

Table 6. Toxicity profile of clinical candidates^a

| candidate | toxicities | grade |
|------------|------------------|----------|
| AZD1775 | myelosuppression | ≥ 3 |
| | GI toxicities | 1–3 |
| | fatigue | 3 |
| ZN-c3 | GI toxicities | all |
| | neutropenia | ≥ 3 |
| IMP7068 | increased ALT | 1 or 2 |
| | increased AST | 1 or 2 |
| | diarrhea | 1 or 2 |
| Debio-0123 | NA | NA |
| SY-4835 | NA | NA |

^aNA = not available.

CDKs. WEE1 is highly expressed in many cancer types. Hence, suppressing WEE1 has a massive impact.

WEE1 inhibition sensitizes tumor cells to chemotherapy and radiotherapy while enhancing the antitumor activities of other kinase inhibitors. WEE1 suppression can be achieved by small molecule ATP competitive binders/WEE1i, PROTAC degraders, and noncoding RNAs. WEE1i are broadly classified as pyridopyrimidines, pyrrolocarbazoles, pyrazolopyrimidines, pyrimidopyrimidine, pyrimidine-based tricyclics (derived from pyrimidopyrimidine), and pyrrolopyrimidines, and their synthesis strategies are provided. Pyridopyrimidines and pyrrolocarbazoles exhibited a broad spectrum of kinase activity and were thus eliminated from the course of preclinical studies. The pyrazolopyrimidines series, however, offers two clinical candidates in phase-I, II, namely, AZD1775/MK1775/Adavosertib and ZN-c3/Azenosertib. Additionally, Debio-0123 (pyrimidopyrimidine), IMP7068 (PBT), and SY-4835 (confidential structure) are in phase-I clinical trials. All series bind to C379, N376, and F433 residues. 2-Amine substitutions are solvent-exposed (except pyrrolocarbazoles), and the other aromatic ring substitutions fill a small hydrophobic pocket near N376; this ring prefers 2'-Cl or 2',6'-dichloro substitution (except pyrazolopyrimidines). The literature and patent study also unveiled other scaffolds showing WEE1 inhibition. On the other hand, PROTACs are selective degraders constructed using an AZD1775 analogue as the warhead, and the constructed PROTACs displayed better selectivity, potency, and anticancer activity than AZD1775. Hence, PROTACs may be a better option. Additionally, the ncRNAs like miRNAs, lncRNAs, and siRNAWEE1 also modulate WEE1 expression but absence of suitable vectors hampers their applications.

Many RNAi screening studies showed WEE1 as a better target to combat cancer, and the clinical candidate AZD1775,

the most selective and most studied WEE1i, displayed adverse events in clinical studies, limiting its development. Additionally, some cancers acquired resistance against AZD1775 due to overexpression of other kinases like MYT1, YAP, etc. This resistance can be restricted by using a variety of kinase inhibitors alongside WEE1i as a form of combination therapy. However, ZN-c3, an analogue of AZD1775, is relatively selective for WEE1 and is in phase-I, II clinical trials. Nevertheless, it is in its early stages and cannot be considered a better alternative. Like ZN-c3, other clinical candidates, SY-4835, IMP7068, and Debio-0123, are in the early stages; thus, a relative best pick is not possible. Hence, further studies of existing WEE1 clinical candidates, optimization of WEE1i, and the design of new inhibitors may boost this strategy to new heights.

7. CHALLENGES

WEE1 has become a promising anticancer target, and many inhibitors are being discovered and constructed. (i) WEE1, being a kinase, is a tricky target. (ii) WEE1i bind in the ATP binding pocket of WEE1. However, all kinases have ATP binding pockets; hence, WEE1i are less likely to be selective. (iii) WEE1i are also highly nonspecific (off-target). (iv) Acquired resistance against WEE1i due to mechanisms other than mutations in the WEE1 protein. (v) Eradication of on-target myelosuppression.

8. OPINION OF INTEREST

WEE1 is one of the checkpoint kinases responsible for the mitotic delay. WEE1 has two functions: (1) to ensure the maturation of daughter cells before mitosis and (2) to ensure DNA repair before mitosis. Its absence causes mitotic catastrophe. In an account of its mitotic regulatory function, WEE1 is highly expressed in many types of cancers, displaying its role in cancer cell survival and growth. Therefore, targeting WEE1 is a promising strategy in the battle against cancer. Since the discovery of the first WEE1i PD0166285 in 2001, WEE1 inhibitory effects in cancer cells have been studied, and satisfactory anticancer effects have been observed. Many RNAi kinome screenings have also identified WEE1 as a better target. Moreover, AZD1775, the most studied clinical candidate, shows many adverse effects in monotherapy and combination therapy. Additionally, in monotherapy desensitization of cancers to AZD1775 is seen; thus, combination therapy is a better option.

Besides boosting anticancer activity, combination therapy also enhances potency that might reduce dose-limiting toxicities. In addition to DNA-damaging agents, WEE1 is also combined with PARP and ATR inhibitors. However, the G2-M checkpoint is not single-handedly regulated by WEE1, but MYT1 also plays a key role. Hence, combined WEE1 and MYT1 inhibition may be a better option, given MYT1's overexpression in some WEE1i-resistant cancers. However, these kinases are equally important in normal cells with high replication; thus, their inhibition may be counterproductive as inhibition of WEE1 alone resulted in more severe myelosuppression. Additionally, WEE1i, along with mTOR, MYC, YAP, MET, and HDAC inhibition, offers an alternate method that is effective against the acquired resistance to WEE1i. Furthermore, simultaneous inhibition of WEE1 and HSP90/HDAC/ATR may be a good approach as they directly or indirectly regulate other checkpoint kinases, enhancing the cytotoxicity

even in cancers resistant to WEE1i. Nevertheless, it is uncertain if these combinations result in a tolerable toxicity.

On the other hand, PROTACs may be a better alternative to inhibitors as they significantly enhance potency and selectivity, which might reduce off-target and dose-limiting toxicities. However, the studies have been limited in this direction. Additionally, gene-silencing therapies with RNAi are also effective, but ideal vectors are not available, thus limiting their application. To enhance WEE1 inhibition, compromising its stability is also an alternative. WEE1 stabilizers like MIG6 and 14-3-3, if inhibited, may contribute to the cause. Additionally, investigating the relationship between PD-L1 and WEE1 has opened a new path to treat SCLC, and ongoing clinical trials could afford possibilities. However, choosing precise WEE1i and PD-L1 inhibitors (either MAB or small molecule) as a combination therapy in the clinical investigation is a complicated task.

9. FUTURE PERSPECTIVES

This review presents a diverse range of compounds exhibiting potent WEE1 inhibition. Among these molecules, certain compounds have been discontinued or advanced through clinical trials, while most of the inhibitors have not been progressed beyond initial testing. Consequently, there is a need for additional studies aimed at identifying and optimizing novel lead compounds from existing but not yet fully evaluated inhibitors. Notably, the extensively studied clinical candidate, AZD1775, was abandoned due to its dire toxicity profile. However, its more selective derivative, ZN-c3, demonstrated a superior preclinical profile. Nonetheless, its clinical data is sparse, including information on its toxicity profile. The other clinical candidates, IMP7068 and Debio-123, are also at the premium with limited data. A recent study however, identified the most alarming toxicity, myelosuppression as a consequence of WEE1 inhibition. However, adequate studies are to be conducted to authenticate this notion. Therefore, additional fugitive trials followed by comprehensive long-term studies are warranted. PROTACs are peerless in terms of their potency and selectivity, presenting an opportunity for WEE1 degradation with little or no off-target clinical toxicity. However, this potential needs to be confirmed. While miRNA therapy has shown promising results, further investigations in this direction are needed before a cancer therapeutic can be developed. Conversely, emerging concerns regarding WEE1i resistance have become apparent. Therefore, additional studies aiming to deepen our understanding of WEE1-associated pathways are needed. Furthermore, it has been substantiated that cancer types with TP53 mutations are more liable to WEE1 inhibition. However, other cancer types also exhibit sensitivity to WEE1 inhibition, while certain TP53 mutant types have developed resistance. Thus, an exhaustive analysis and systematic categorization of patient profiles are imperative to identify the beneficiary of this inhibition.

10. CONCLUSION

WEE1, the mitotic regulator and epigenetic modifier, is elected as a prime anticancer target. It is a typical kinase that is highly expressed and stabilized during the G2 and S-phases and suppressed during the M-phase, contributing to its mitotic regulatory function. Currently, WEE1i, in combination with PARP and ATM inhibitors, is in clinical trials. Other proteins like HDAC, HSP90, and CHK1 inhibitors, etc. are other

proposed combinations to curb WEE1i resistance. Clinical studies on AZD1775, including monotherapy and combination therapy with DNA damaging agents, including radiation, showed adverse effects with remarkable anticancer activity. Hence, understanding the biology of WEE1 and concept of design and discovery of WEE1i may lead to the development of better candidates. Thus, this broad-spectrum multidisciplinary overview of WEE1i unveils benefits toward the design of new focused libraries against WEE1 kinase for further investigations.

AUTHOR INFORMATION

Corresponding Author

Surender Singh Jadav – Department of Natural Products and Medicinal Chemistry, CSIR-Indian Institute of Chemical Technology Tarnaka, Hyderabad 500037, India; Academy of Scientific and Innovative Research (AcSIR), Ghaziabad 201002, India; orcid.org/0000-0002-5397-8956; Email: surenderjs@iict.res.in

Authors

Vidya Jyothi Alli – Department of Natural Products and Medicinal Chemistry, CSIR-Indian Institute of Chemical Technology Tarnaka, Hyderabad 500037, India

Pawan Yadav – Department of Natural Products and Medicinal Chemistry, CSIR-Indian Institute of Chemical Technology Tarnaka, Hyderabad 500037, India

Vavilapalli Suresh – Department of Organic Synthesis and Process Chemistry, CSIR-Indian Institute of Chemical Technology Tarnaka, Hyderabad 500037, India; Academy of Scientific and Innovative Research (AcSIR), Ghaziabad 201002, India

Complete contact information is available at:
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Notes

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ABBREVIATIONS AND ACRONYMS

| | |
|-------------|--|
| DDRs | DNA damage responses |
| ATR | Ataxia-Telangiectasia mutated and Rad3-related, single-strand DNA breakage |
| ATM | Ataxia-Telangiectasia mutated, double-strand DNA breakage |
| CHK1/2 | checkpoint kinase 1/2 |
| CDC kinases | cell division cycle kinase |
| CDK1/2 | cell division kinases 1/2 |
| S/T kinases | Serine/threonine kinases |
| PDB | protein data bank |
| NRD | N-terminal regulatory domain |
| KD | central kinase domain |
| CRD | C-terminal regulatory domain |
| P-site | phosphorylation site |
| PLK1 | Polo-like kinase 1 |
| NLS | nuclear localization signal |

| | |
|----------------|--|
| CK2 | casein kinase 2 |
| NTD | N-terminal domain |
| CTD | C-terminal domain |
| BRSK1/2 | BR serine/threonine kinase 1/2 |
| AKT | AKT kinase or Protein Kinase B |
| CRM1 | chromosomal maintenance 1 or exportin-1 |
| NES | nuclear export signal |
| CRK | CRK adaptor protein |
| AcM | acetylation motif |
| MPF | mitosis promoting factor |
| pCDK | phosphorylated CDK |
| HSP90 | heat shock protein 90 |
| SKP2 | S-phase kinase associated protein 2 |
| FBXL1 | F-box and leucine-rich repeat protein 1 |
| EME1 | essential meiotic structure-specific endonuclease 1 |
| MIG6 | mitogen-inducible gene 6 |
| c-Fos/AP1 | c-Fos/Activator Protein 1 |
| NIM1 | nonexpresser of PR genes 1 |
| CDR1 | cerebellar degeneration Related Protein 1 |
| SCF | skp1/cul1/F-box |
| β -TrCP | β -transduction repeat-containing protein |
| Tome-1 | trigger-of-mitotic-entry 1 |
| Smurf1 | Smad ubiquitination regulatory factor 1 |
| Pof1/3 | promoter of filamentation 1/3 |
| PIN1 | peptidyl-prolyl cis–trans isomerase NIMA-interacting 1 |
| GCN5 | general control non-depressible 5 |
| SIRT1 | sirtuin 1 |
| γ -H2AX | histone family protein X |
| CCNE1 | cyclin E1 |
| NSCLC | nonsmall cell lung cancer |
| DDAs | DNA damaging agents |
| WEE1i | WEE1 inhibitors |
| CIN | chromosomal instability |
| BRCA | breast cancer gene |
| RAS | rat sarcoma virus gene |
| ATRX | ATP-dependent helicase ATRX, X-linked helicase II |
| EGFR | epidermal growth factor receptor |
| PARP | poly (ADP-ribose) polymerase |
| PARPi | PARP inhibitors |
| CHK1i | CHK1 inhibitors |
| AML | acute myeloid leukemia |
| TNBC | triple-negative breast cancer |
| ATRi | ATR inhibitors |
| HDAC | histone deacetylase |
| HSP90i | HSP90 inhibitors |
| c-MYC | cellular-myelocytomatosis gene |
| PD-L1 | programmed cell death ligand 1 |
| SCLC | small cell lung cancer |
| c-Src | cellular-sarcoma gene |
| THF | tetrahydrofuran |
| DMF-DMA | N,N-dimethylformidedimethylacetal |
| m-CPBA | m-chloroperoxybenzoic acid |
| LAH | lithium aluminum hydride |
| DMF | N,N-dimethylformamide |
| HBD | hydrogen bond donor |
| DDQ | 2,3-dichloro-5,6-dicyano-1,4-benzoquinone |
| TFA | trifluoroacetic acid |
| PKC | protein kinase C |
| FOXO | Forkhead box protein O |
| FOXM1 | Forkhead box protein M1 |

| | |
|----------------|---|
| APC/C | anaphase-promoting complex |
| JAK2/3 | Janus kinase 2/3 |
| MAP3K4 | mitogen-activated protein kinase kinase kinase 4 |
| ABL1 | tyrosine-protein kinase ABL1 |
| YES1 | proto-oncogene tyrosine-protein kinase YES1 |
| AXL | AXL receptor tyrosine kinase |
| mTOR | mechanistic target of Rapamycin kinase |
| pS6 | phosphorylated ribosomal protein S6 |
| MET | mesenchymal–epithelial transition kinase |
| YAP | yes-associated protein |
| FA | fanconi anemia |
| CDDP | cis-diaminodichloroplatinum(II) or cis-platin |
| AraC | cytarabine |
| HNSCC | head and neck squamous cell carcinoma |
| PK | pharmacokinetics |
| MTD | maximum tolerant dose |
| ADMET | absorption, distribution, metabolism, excretion, and toxicity |
| CBDP | cannabidiol |
| DIPEA | <i>N,N</i> -diisopropylethylamine |
| PPMS | potassium peroxydisulfate complex salt |
| DBU | diazabicycloundecene |
| PBT | pyrimidine-based tricyclics |
| QSAR | quantitative structure–activity relationships |
| MD simulations | molecular dynamics simulations |
| DCE | dichloroethane |
| PROTACs | proteolysis-targeting chimeras |
| EBM | E3 ligase binding moiety |
| PCS | protein control system |
| VHL E3 ligase | Von Hippel-Lindau E3 ligase |
| CRBN E3 ligase | Cereblon E3 ligase |
| SAR | structure–activity relationship |
| DMAc | dimethylacetamide |
| HATU | hexafluorophosphate azabenzotriazole tetramethyl uranium |
| DCM | dichloromethane |
| DMSO | dimethyl sulfoxide |
| miRNAs or miR | microRNAs |
| siRNAs | small-interference or silencing RNAs |
| lncRNAs | long noncoding RNAs |
| 3'UTR | 3' untranslated region |
| hESCs | human embryonic stem cells |
| LSCC | laryngeal squamous cell carcinoma |
| HCC | hepatocellular carcinoma |

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