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Optimization of potent and selective dual mTORC1 and mTORC2 inhibitors: The discovery of AZD8055 and AZD2014

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ABSTRACT

The optimization of a potent and highly selective series of dual mTORC1 and mTORC2 inhibitors is described. An initial focus on improving cellular potency whilst maintaining or improving other key parameters, such as aqueous solubility and margins over hERG IC_{50} , led to the discovery of the clinical candidate AZD8055 (14). Further optimization, particularly aimed at reducing the rate of metabolism in human hepatocyte incubations, resulted in the discovery of the clinical candidate AZD2014 (21).

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The mammalian target of rapamycin (mTOR) is a key target in the development of antitumor therapies.¹ Activated by growth factor/mitogenic stimulation activation of the phosphatidylinositol 3-kinase (PI3K)/Akt signaling pathway mTOR is a central regulator of cell growth and proliferation. This PI3K–Akt–mTOR pathway is one of the most frequently dysregulated pathways in cancer.² mTOR, a serine/theronine kinase of approximately 289 kDa in size, is a member of the evolutionary conserved eukaryotic PI3K like kinase (PIKK) family of proteins, for example DNA dependent protein kinase (DNA-PK) and Ataxia-telangiectasia mutated (ATM).^{3–5}

The known mTOR inhibitor Rapamycin and its analogues (RAD001, CCI-779, AP23573) bind to the FKBP12/rapamycin complex binding domain (FRB), resulting in suppression of signaling to the downstream targets p70S6K and 4E-BP1.^{6,7} The potent but non-specific inhibitors of PI3K, LY294002 and wortmannin, have also been shown to inhibit the kinase function of mTOR; however, in this case the catalytic domain of the protein is targeted.⁸

Recently it has been shown that mTOR can exist in an alternative, rapamycin insensitive, complex that signals to Akt.⁹ The existence of both a rapamycin sensitive complex (mTORC1) and a rapamycin insensitive complex (mTORC2) may provide an explanation for the differences observed in the earlier work of Brunn et al.⁸ and Edinger et al.¹⁰ Rapamycin and its analogues have been shown to activate AKT signaling as a consequence of inhibition of the negative feedback loop downstream of mTORC1.¹¹ Moreover, this is associated with a shorter time to progression in glioblastoma patients treated with rapamycin suggesting that dual mTORC1 and 2 inhibitors that inhibit AKT signaling could offer greater clinical benefit compared with rapalogues.¹² In addition, dual mTORC1 and mTORC2 inhibitors may exhibit a broader spectrum of clinical activity.

We have previously described the identification of compound **1** from a screening campaign and the subsequent optimization of the scaffold resulting in the discovery of Ku-0063794 (Fig. 1).¹³

Ku-0063794 is a potent inhibitor of mTOR kinase (IC₅₀ = 0.0025 μ M) and displays a high level of selectivity against other members of the PIKK family (IC₅₀ against PI3K isoforms α , β , γ , δ = 8.9, >30, >30 and 5.3 μ M, respectively).¹⁴ Ku-0063794 also showed a high level of general kinase selectivity and was inactive against a panel of over 200 kinases when tested at 10 μ M. In cells



Figure 1. The structures of 1 and Ku-0063794.



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Table 1

The introduction of basic groups to the C7 aryl substituent



Compd No.	R	pAKT (S ⁴⁷³) IC ₅₀ (μM)	Solubility (µM)	hERG IC ₅₀ (µM)
Ku-0063794	OH O	0.24	2.4	8.3
2	HO NH	0.062	>1100	27.5
3	HO	0.137	>2000	13.0
4	N H	0.303	>1400	17.4
5	N I	>2.43	_	_

Ku-0063794 has been shown to modulate downstream markers of mTORC1 (inhibition of pS6 at Ser^{235/236} IC₅₀ = 0.66 μ M) and mTORC2 (inhibition of pAKT at Ser⁴⁷³ IC₅₀ = 0.24 μ M).¹⁵ Ku-0063794 has been shown to be active in mouse xenograft models.¹⁶

Despite the high affinity of Ku-0063794 for mTOR kinase the moderate cellular potency was felt to offer scope for further improvement. Data generated on Ku-0063794 and close analogues highlighted the similar cellular potencies and structure-activity relationship (SAR) seen with both the pS6 (S^{235/236}) and the pAKT (S⁴⁷³) measures. As a result a simplified cascade with the pAKT (S⁴⁷³) cellular measure as the primary assay was introduced. Enzyme data and pS6 (S^{235/236}) cellular data was generated on compounds of interest only. In addition, a relatively low aqueous solubility $(2.4 \,\mu\text{M})^{17,18}$ and relatively high potency against the hERG (human ether-a-go-go-related gene) ion channel $(IC_{50} = 8.3 \mu M)^{19}$ may also present problems for the long term clinical development of Ku-0063794. Consequently, further optimization was initiated to identify highly selective compounds with increased cellular potency, improved aqueous solubility and an improved margin to the hERG IC₅₀.

Our initial strategy to improve aqueous solubility was the introduction of basic functionality, thereby giving a charged molecule at physiological pH. Previous studies had shown that the pendant aryl ring at the C7-position of the Pyridopyrimidine core could tolerate a variety of substituents, although the presence of the benzyl alcohol H-bond donor was known to be advantageous. With this in mind we looked to replace the benzyl alcohol with a range of secondary benzyl amines (Table 1). Such compounds were generally well tolerated with certain examples (e.g., 2) showing improved potency. As anticipated these compounds showed a dramatic improvement in solubility and a reduction in hERG potency was also observed. Removal of the methoxy group, 3, did give a slight reduction in potency but excellent solubility was retained. Attempts to introduce tertiary amines in this position resulted in a significant reduction in potency (5 cf 4) highlighting the importance of an H-bond donor in that region of the molecule.



Figure 2. The structures of **6** (pAKT IC₅₀ = 2.92 μ M) and **7** (pAKT IC₅₀ = 0.026 μ M).

Despite the improved cellular potency and solubility, **2** showed little oral exposure presumably due to compromised permeability and higher efflux. The apparent permeability (Papp), as measured in MDCKII cells, for Ku-0063794 and **2** in both the A–B and B–A directions are 26/453 nm/s and 150/166 nm/s, respectively.^{20,21}

The oxygen of the C4-morpholine has been established as a key pharmacophoric element for this series¹³ with attempts to remove this causing a considerable reduction in potency (e.g., **6**). Analogies to other known PIKK family inhibitors would suggest that this oxygen participates in a key interaction with the hinge region of the kinase. However, conservative changes in this region are tolerated, and in particular the 3S-methyl morpholine containing compound, **7**, was identified as having significantly improved cellular potency (Fig. 2). Interestingly, a modest increase in solubility was also observed for this compound (16 μ M).

The impact of replacing the C4-morhpoline with a 3S-methyl morpholine has been examined across a range of analogues. An analysis of matched pairs (Fig. 3) shows a consistent improvement in cellular potency with an average increase of 0.73 ± 0.11 in pIC₅₀. A similar analysis also highlights a trend for improved solubility, on average between 5- and 10-fold; however, no assessment of the solid state properties of these compounds has been made. These observations are consistent with the 3S-methyl group either locking the morpholine ring in a more favorable conformation for binding or accessing a small lipophilic pocket upon binding. The increase in solubility may reflect a lowering in crystal lattice energy due to disrupted crystal packing upon the addition of the methyl group. Similar SAR regarding the hinge binding morpholine has recently been described for other PIKK inhibitors although the observations are subtly different between series.²²

Aqueous solubility is often negatively correlated with lipophilicity, hence another strategy adopted was to reduce the lipophilic-



Figure 3. Matched pairs plot highlighting the impact of switching from a morpholine to a 3S-methyl morpholine on both cellular pIC_{50} and solubility.

Table 2





8	0.094	4.14	3.75	66	4.0
9	0.103	3.40	>4.0	13	13.2
·	D. 1	· •	,	•	

ity of the core. Pteridine analogues (e.g., **9**) were tolerated; however, the anticipated reduction in lipophilicity (based on ClogPprediction)²³ was not reflected in the measured log*D* values¹⁸ and indeed a reduction in solubility was observed (Table 2).

We next focused our attention on the C2 substituent. A wide range of amines were tolerated including non-morpholine substituents, basic amines and acyclic amines (8–12) as were aromatic substituents, such as compound 13; however, when assessing the overall balance of properties the 3S-methyl morpholine analogue, 14, appeared optimal (Table 3).

Compound **14** is a potent inhibitor of mTOR kinase (IC₅₀ = 0.00013 µM) and displays a high level of selectivity against other members of the PIKK family (IC₅₀ against PI3K isoforms α , β , γ , δ = 3.6, 19, 3.2 and 15 µM, respectively) and was inactive against a general panel of over 200 kinases when tested at 10 µM. Unlike rapamycin, **14** inhibits both mTORC1 and mTORC2 in cells with similar potencies (pS6 (S^{235/236}) IC₅₀ = 0.027 µM, pAKT (S⁴⁷³) IC₅₀ = 0.024 µM). Compound **14** also demonstrates a more complete inhibition of phosphorylation of mTORC1 substrate 4E-BP1 (Thr^{37/46}) compared to rapamycin in MCF-7 cells and was also shown to inhibit pAKT (S⁴⁷³) in this cell line whereas rapamycin treatment resulted in an activation of AKT as a consequence of inhibition of a negative feedback loop.²⁴ Compound **14** has been shown to modulate substrates of both mTORC1 and 2 in vivo and

Table 3

Modifications to the C2 amine

Compd No.	R	pAKT (S ⁴⁷³) IC ₅₀ (μM)	Solubility (µM)	hERG IC ₅₀ (µM)		
8	N N N N N N N N N N	0.094	66	4.0		
10	`Nон	0.060	13	8.0		
11	NNN	0.166	>1200	>32		
12	ŇH ∣ ↓ 0	0.061	170	17.0		
13	`N [≪] N	0.141	26	>32		
14		0.024	30	30.4		

Table 4

Modifications to the C7 benzyl amine functionality



Compd No.	R	pAKT (S ⁴⁷³) IC ₅₀ (μM)	Solubility (µM)	hERG IC ₅₀ (µM)	Hu Heps (μL/min/ 10 ⁶ cells)
15	OH MeO	0.090	160	>32	37.8
16	H ₂ N MeO	0.017	>690	>32	33.2
17	O N H MeO	0.009	44	>32	14.3
18	N MeO	2.83	>640	>32	4.3

Table 5

Modifications to the C7 methoxy and amide substituents

$R \stackrel{(0)}{\longrightarrow} N \stackrel{(1)}{\longrightarrow} N$						
Compd No.	R	pAKT (S ⁴⁷³) IC ₅₀ (μM)	Solubility (µM)	hERG IC ₅₀ (µM)	Hu Heps (µL/min/ 10 ⁶ cells)	
19	N H F F	0.026	190	24.2	14.9	
20		0.358	110	>32	176.4	
21	N H	0.080	>600	47.5	<4.2	
22	HO NH	0.041	>870	>32	<5.4	

delivers a dose-dependent tumor growth inhibition in mouse xenograft models.²⁴ Compound **14** was subsequently selected for clinical development and referred to as AZD8055.

Despite its promising profile in preclinical disease models, AZD8055 was found to exhibit high turnover in human hepatocytes ($36.4 \mu L/min/10^6$ cells) and also showed lower bioavailability in rat compared with mouse (12% cf 81%). The high turnover of AZD8055 in human hepatocytes, combined with inconsistent rodent pharmacokinetics (PK), was felt to constitute a considerable

risk when trying to predict clinical exposure and hence optimization was continued to identify compounds with an increased confidence of achieving the required clinical exposure.

The metabolism of functional groups such as benzyl alcohols and aryl-methyl ethers is well precedented and were postulated as potential metabolic liabilities in AZD8055. Steric crowding of the benzyl alcohol, such as in compound 15, had little impact on human hepatocyte metabolism (Table 4). A primary amide could be used to replace the benzyl alcohol generating a potent compound with a dramatically increased aqueous solubility (16), although the rate of human hepatic turnover remained high. Substitution on the amide, 17, did reduce the rate of turnover in human hepatocytes and generally maintained the excellent properties of the molecule, albeit with a reduction in aqueous solubility. A further reduction in hepatic turnover was observed for the tertiary amide **18**: however, this change was associated with a significant reduction in potency again highlighting the importance of an H-bond donor in this vicinity. Limited attempts were made to replace the C7 phenyl ring with aromatic heterocycles but such compounds lost activity (data not shown).

Strategies to reduce potential metabolism of the methoxy group, such as difluorination (**19**) or cyclisation (**20**), were broadly tolerated but failed to deliver a reduction in hepatic turnover (Table 5). Removal of the methoxy group (**21**), however, did result in a compound with good cellular potency and low hepatic turnover. Compound **21** showed excellent aqueous solubility, margin to the hERG IC₅₀ and was shown to have good oral exposure in both rat and mouse. Variation of the amide substituent did result in modest improvements in potency with compound **22**, in particular, showing an attractive in vitro profile. However, **22** failed to deliver oral exposure in rodents.

Compound **21** is a potent inhibitor of mTOR kinase (IC₅₀ = 0.0028 µM) and displays a high level of selectivity against other members of the PIKK family (IC₅₀ against PI3K isoforms α , β , γ , δ = 3.8, >30, >30 and >29 µM, respectively) and was inactive against a general panel of over 200 kinases when tested at 10 µM. Compound **21** inhibits both mTORC1 and mTORC2 in vitro (pS6 (S^{235/236}) IC₅₀ = 0.2 µM, pAKT (S⁴⁷³) IC₅₀ = 0.08 µM) and has shown dose-dependent tumor growth inhibition in a mouse MCF7 xenograft model alongside modulation of mTORC1 and mTORC2 biomarkers.²⁵ Compound **21** shows consistent exposure in rodents and a low turnover in human hepatocyte incubations and was subsequently selected for clinical development and referred to as AZD2014. A comparison of key in vitro parameters, including potency, solubility, protein binding²⁶ and rodent PK,²⁷ for Ku-0063794, AZD8055 and AZD2014 is given in Table 6.

The general synthesis of compounds 2-5 is shown in Scheme 1.²⁸ Reaction of 2,6-dichloronicotinic acid (**23**) with liquid ammo-

Table 6				
Comparison	of key	pre-clinical	parameters	

	Ku-0063794	AZD8055	AZD2014
mTOR IC50 (µM)	0.0025	0.00013	0.0028
pAKT (S ⁴⁷³) IC ₅₀ (μM)	0.24	0.024	0.080
pS6 (S ^{235/236}) IC ₅₀ (µM)	0.66	0.027	0.2
logD	3.25	3.23	3.16
Solubility (µM)	2.4	30	>600
f _u (Mouse)	0.01	0.04	0.05
f _u (Rat)	0.15	0.08	0.09
$f_{\rm u}$ (Human)	0.08	0.13	0.05
Hu Heps (µL/min/10 ⁶ cells)	-	36.4	<4.2
Mouse clearance (mL/min/kg)	3.1	42.8	10.4
Mouse bioavailability	61%	81%	>100%
Rat clearance (mL/min/kg)	35.8	36.6	12.6
Rat bioavailability	33%	12%	40%
hERG IC ₅₀ (μ M)	8.3	30.4	47.5



Scheme 1. Reagents and conditions: (a) (i) NH₃(liq), 18 bar, 130 °C, 90%; (ii) SOCl₂, THF, rt; (iii) NH₃(g), THF, rt, 92% over 2 steps; (b) (COCl₂, toluene, 115 °C, 95%; (c) POCl₃, Hünigs base, toluene, 100 °C, 48%; (d) morpholine, Hünigs base, CH₂Cl₂, 0 °C- rt, 92%; (e) 2,6-dimethylmorpholine, Hünigs base, DMA, 70 °C, 45%; (f) [2-methoxy-5-(4,4,5,5-tetramethyl-1,3,2-dioxaborolan-2-yl)phenyl]methanol, Pd(PPh₃)₄, Na₂CO₃, toluene/ethanol, 140 °C, 75%; (g) (i) MsCl, Et₃N, CH₂Cl₂, rt, 99%; (ii) selected amine, K₂CO₃, Et₃N, DMF, 40 °C.

nia at elevated temperature and pressure results in the selective introduction of an amino group into the C2 position and subsequent conversion of the carboxylic acid to the primary amide, via the acyl chloride intermediate, generates **24** which can then be cyclised with oxalyl chloride to complete the Pyridopyrimidine scaffold (**25**). Chlorination with phosphorous oxychloride results in the trichloro intermediate **26** and selective installation of the C4 amine is achieved by reaction with the desired amine at low temperature (**27**). Reaction with a second amine at elevated temperature is then used to install the C2 amine functionality (**28**). Finally, the C7 aryl substituent can be installed using palladium mediated cross couplings with desired boronic ester to give Ku-0067394. Conversion of the benzyl alcohol to a benzyl chloride and subsequent displacement with the desired amine generates compounds **2–5**.

The general synthesis of compounds **14–22** is shown in Scheme 2.²⁹ 3S-Methylmorpholine is installed sequentially at the C4 then C2 positions of trichloro intermediate **26** to generate **29** which can then be reacted with a range of boronic esters using palladium mediated cross couplings to generate compounds **14–22**. Analogous procedures were used to deliver compounds **6–8** and compounds **10–13**. Pteridine compound **9** was synthesized from the commercially 7-phenylpteridine-2,4-diol using chemistry analogous to that described in Scheme 1.



Scheme 2. Reagents and conditions: (a) (i) 3S-Methylmorpholine, Hünigs base, CH₂Cl₂, 0 °C-rt, 87%; (ii) 3S-methylmorpholine, Hünigs base, DMA, 70 °C, 71%; (b) selected boronic ester, Pd(PPh₃)₄, Na₂CO₃, toluene/ethanol, 140 °C or selected boronic ester, Pd(PPh₃)₄, K₂CO₃, MeCN/water, 150 °C.

In summary, we have shown how iterative SAR investigations have been used to optimize the cellular potency, aqueous solubility and hERG potency of lead compound Ku-0063794 to deliver the clinical candidate AZD8055. Further optimization focused on reducing turnover in human hepatocytes and resulted in the identification of the clinical candidate AZD2014, which was believed to offer a reduced human PK risk compared to AZD8055. AZD8055 and AZD2014 are potent and selective dual mTORC1 and mTORC2 inhibitors which show a differentiation from rapamycin in vitro and have demonstrated dose-dependent tumor growth inhibition in mouse xenograft models. AZD8055 was evaluated in a phase I clinical study in patients with advanced tumors but is no longer in clinical development. AZD2014 is currently in phase I.

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the lipid PIP2 as substrate. More detailed description of the assay conditions are described in Ref. $^{\rm 24}$

- 15. MDA-MB-468 cells were exposed for 2 h to increasing concentrations of compound. At the end of the incubation period cells were fixed, washed and probed with antibodies against S⁴⁷³ pAKT or against S^{235/236} phosphorylated S6 (pS6). Levels of phosphorylation were assessed using an Acumen laser scanning cytometer (TTP Labtech). Figures quoted are the mean of at least 3 determinations and the standard error in the mean (pIC₅₀) was <0.3.</p>
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