

22-24 April 2022 Poster #21

## AB521 is a Novel and Potent Clinical-stage HIF-2α Inhibitor for the Treatment of Renal Cell Carcinoma

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Background. The transcription factor Hypoxia-inducible Factor (HIF)-2α is an oncogenic driver in clear cell renal cell carcinoma (ccRCC). HIF-2α protein levels are regulated posttranslationally in an oxygen-dependent manner. Hypoxic or pseudohypoxic conditions promote HIF-2 $\alpha$  stabilization and transcription of pro-tumorigenic genes. Inhibition of HIF-2 $\alpha$ has significant potential to mitigate tumor growth, particularly in cancers like ccRCC that have a high prevalence of molecular alterations associated with pseudohypoxia, namely mutations or epigenetic silencing of the Von Hippel-Lindau (VHL) protein. Herein we report findings associated with bioinformatic gene signature analyses and characterize AB521, a novel small molecule HIF-2α inhibitor.

<u>Methods</u>. Published and novel gene signatures were applied to publicly available datasets. Potency and specificity of AB521 was evaluated using biochemical and cell-based assays. Efficacy, pharmacokinetics, and pharmacodynamics associated with AB521 were evaluated in preclinical species and a healthy volunteer study is on-going.

**Results.** Evaluated signatures related to hypoxia and HIF-2 $\alpha$  were associated with therapeutic response to HIF-2 $\alpha$  inhibition in preclinical models. Binding assays and crystal structure elucidation demonstrated that AB521 avidly binds the HIF-2α PAS-B domain. AB521 potently inhibited HIF-2α-dependent reporter transcription and VEGF protein secretion in 786-O cells. AB521 also selectively inhibited HIF-2 $\alpha$ -, but not HIF-1 $\alpha$ -, regulated gene expression in Hep3B hepatocellular carcinoma cells. In vivo, AB521 significantly regressed mouse ccRCC xenograft tumors and decreased on-target pharmacodynamic markers in a dose-dependent manner. Additionally, AB521 enhanced anti-tumor activity of a VEGF-targeting tyrosine kinase inhibitor. AB521 had a favorable pharmacokinetics (PK) in vitro and in vivo, resulting in a profile suitable for once-daily oral dosing in humans. Recent healthy volunteer data confirms both the predicted PK profile as well as modulation of erythropoietin (EPO) in a dose dependent manner.



Figure 2. AB521 alone or in combination with the tyrosine kinase inhibitor (TKI) cabozantinib (cabo), showed enhanced anti-tumor activity in the A498 ccRCC xenograft model. (A and B) Vehicle or AB521 administered once daily by oral gavage (PO QD) when tumors were ~300 mm<sup>3</sup>. (A) Group averages over time. (B) Pharmacodynamic changes in intratumoral gene expression (ccnd1 and vegfa) and plasma protein levels (VEGF) 24 hours after vehicle or 100 mg/kg AB521 treatment. (C) Vehicle, 100 mg/kg AB521, 30 mg/kg cabozantinib (cabo), or a combination of the two agents administered PO QD when tumors were ~500 mm<sup>3</sup>. Shown are group averages over time. Pharmacokinetic parameters in preclinical species, including mice, has been disclosed previously<sup>2</sup>. ns, not significant.

**Conclusions.** Transcriptional data can be further applied to understand the therapeutic potential of HIF-2α inhibition. AB521 is a novel and selective HIF-2α inhibitor with profound anti-tumor activity, and clinical evaluation of this molecule is underway.





Figure 1. HIF-2 $\alpha$  drives physiological changes to adapt to low oxygen that are **hijacked by the tumor.** HIF-2 $\alpha$  is a transcription factor comprised of two proteins: a stablyexpressed  $\beta$  subunit (HIF-1 $\beta$ /ARNT) and an oxygen-sensitive  $\alpha$  subunit (HIF-2 $\alpha$ ). In hypoxic or pseudohypoxic conditions, HIF-2 $\alpha$  is stabilized and drives transcriptional programs that promote tumor progression. AB521 is a novel, potent, and selective allosteric small molecule inhibitor that can prevent HIF-2α-dependent gene transcription and block tumor progression.

	In vitro Profile of AB521			
	Assay	AB521	<b>MK-6482</b> ª	
	HIF-2 $lpha$ 786-O Luc Reporter IC <sub>50</sub> (nM)	8.2 ± 2.5 (n = 24)	16.9 ± 10.1 (n = 8)	
_	Control 786-O Luc Reporter IC <sub>50</sub> (nM)	> 10,000 (n = 6)	> 10,000 (n = 7)	
ellula	HIF-2α 786-O Luc Reporter IC <sub>50</sub> (nM) [in 100% Serum]	46.5 ± 14.2 (n = 24)	61.8 ± 6.6 (n = 4)	
0	786-O VEGF AlphaLISA IC <sub>50</sub> (nM)	28.9 ± 3.6 (n = 11)	47.7 ± 30.8 (n = 4)	
	Hep3B <i>EPO</i> Transcript IC <sub>50</sub> (nM)	35.9 ± 5.0 (n = 3)	39.0 ± 9.7 (n = 3)	
a	HIF-2α TSA ΔT <sub>M</sub> (°C)	14.7 ± 0.6 (n = 14)	12.1 ± 0.3 (n = 4)	
emic	HIF-2 $\alpha$ MST $K_{\rm D}$ (nM)	2.4 ± 0.8 (n = 3)	15.4 ± 2.7 (n = 3)	
oche	HIF-2 $\alpha$ ITC $K_{\rm D}$ (nM)	53.6 ± 17.9 n = 3)	58.3 ± 19.3 (n = 3)	
Ö	HIF-2 $\alpha$ SPA IC <sub>50</sub> (nM)	16.6 ± 5.0 (n = 8)	22.3 ± 5.6 (n = 5)	

Table 1. Characterization of AB521 and MK-6482<sup>a</sup> in Arcus biochemical and cellbased assays. Cellular assays: HIF luciferase (Luc) reporter and VEGF secretion in 786-O ccRCC cells; erythropoietin (EPO) transcription in Hep3B hepatocellular carcinoma cells. Binding Assays performed with the HIF-2α PAS-B domain: TSA, Thermal Shift Assay; MST,

Figure 3. Arcus HIF-2α-dependent gene signatures are associated with responses in patient-derived xenograft (PDX) models and prognosis in sunitinib-treated ccRCC **patients.** (A) Hypoxia-driven genes downregulated by treatment with a HIF-2 $\alpha$  inhibitor (HIF2Ai) *in vitro* were used to derive cell type-specific HIF-2α signatures. Mac, macrophage; HIF2Ai, PT2385 synthesized at Arcus according to published methods<sup>9</sup>. (B) Arcus-derived signatures correlate with HIF-2 $\alpha$  protein better than EPAS1 RNA in VHL wild type ccRCC tumors<sup>3</sup>. (C) High expression of HIF-2 $\alpha$  signatures are associated with poorer progressionfree survival (PFS) in RCC<sup>4</sup>. (D) Expression of *EPAS1* and HIF-2α gene signatures are higher in HIF2Ai sensitive PDXs<sup>5</sup> compared to resistant PDXs (comparing vehicle groups) and downregulated upon treatment with HIF2Ai in sensitive PDXs. (E) Expression of EPAS1 and

30 mg AB521	-76
10 mg AB521	-41
3 mg AB521	3

Table 2. Average percent reduction in erythropoietin (EPO) levels observed at 24 hours after a single dose of AB521, relative to pre-dose, in each treatment cohort.

- ✤ AB521 has been extensively characterized in a suite of biochemical and cell-based assays and demonstrates a high affinity for the HIF-2a PAS-B domain and potent inhibition of HIF-
- ✤ In ccRCC xenograft models, AB521 significantly inhibits tumor growth, and enhanced antitumor activity was observed when administered in combination with the TKI cabozantinib
- Arcus-derived HIF-2α signatures are correlated with HIF-2α protein expression in VHL wild type ccRCC and high scores are associated with poorer PFS. PDX models sensitive to HIF-2α inhibition express higher signature scores and downregulate these signatures upon HIF-2α inhibition. ccRCC responding to sunitinib express higher levels of HIF-2α RNA and
- ↔ We project a dose of 45-60 mg once daily AB521 will match the potency-corrected exposure of 120 mg belzutifan and anticipate an ability explore higher doses without the PK saturation observed with belzutifan<sup>1</sup> (Figure 4).
- Significant modulation of EPO levels in healthy volunteers following administration of a single dose of AB521 has been observed (Table 2). Dose escalation continues in the ARC-14 healthy volunteer study and initiation of clinical trials in cancer patients is expected to begin in the latter half of 2022.

## Microscale Thermophoresis; ITC, Isothermal Calorimetry; SPA, Scintillation Proximity

Assay. <sup>a</sup>MK-6482/belzutifan was synthesized at Arcus according to published methods<sup>1</sup>.

HIF-2α gene signatures are higher in sunitinib-treated ccRCC responders<sup>7,8</sup>. CPM, counts per

million. ssGSEA, single sample gene set enrichment analysis.

6) Liberzon et al. 2015 Cell Sys; DOI: 10.1016/j.cels.2015.12.004

7) McDermott et al. 2018 Nat Med; DOI: 10.1038/s41591-018-0053-3

8) Rini et al. 2019 Lancet; DOI: 10.1016/S0140-6736(19)30723-8

9) When et al. 2018 J Med Chem; DOI: 10.1021/acs.jmedchem.8b01196

<sup>2019</sup> J Med Chem; DOI: 10.1021/acs.jmedchem.9b00719

Gauthier *et al.* 2021 Mol Cancer Ther; DOI: 10.1158/1535-7163.TARG-21-P206 (https://arcusbio.com/publications/`

<sup>2019</sup> Cell; DOI: 10.1016/j.cell.2019.10.007

<sup>4)</sup> The results shown here are in part based upon data generated by the TCGA Research Network: https://www.cancer.gov/tcga

<sup>5)</sup> Chen *et al.* 2016 Nat; DOI: 10.1038/nature19796