



Selectivity Matters and Pan-Mutant Allosteric Inhibition Delivers

July 15, 2026



Legends

Forward-Looking Statements

This presentation contains forward-looking statements that involve substantial risks and uncertainties. All statements other than statements of historical facts contained in this presentation are forward-looking statements. Such forward-looking statements include, among other things, statements regarding the potential of, and expectations regarding, OnKure's product candidates and programs, including OKI-355 and OKI-345; OnKure's ability to advance additional programs; expected milestones and the timing of such milestones, the submission of IND applications for OKI-355 and OKI-345; and statements regarding OKI-345 and OKI-355 as best-in-class. In some cases, you can identify forward-looking statements by terminology such as "expect," "estimate," "intend," "may," "plan," "potentially," "will" or the negative of these terms or other similar expressions.

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Agenda

Topic	Presenter
Welcome & Introduction	Nicholas Saccomano, Ph.D. <i>President & Chief Executive Officer of OnKure</i>
OnKure: A Differentiated Portfolio	
Targeting Cryptic Allosteric Pockets	Benjamin Cravatt, Ph.D. <i>Prof. of Chemistry and Norton B. Gilula Chair of Chemical Biology, Scripps Research</i>
The Pursuit of PI3K α Therapeutic Selectivity	Robert Abraham, Ph.D. <i>Chief Scientific Officer at Engine Biosciences</i>
OnKure's Pipeline Strategy & Portfolio Overview	Nicholas Saccomano, Ph.D. <i>President & Chief Executive Officer of OnKure</i>
Q&A	

Today's Guest KOLs



Benjamin F. Cravatt, Ph.D.

Professor of Chemistry and the Norton B. Gilula Chair of Chemical Biology at Scripps Research. A pioneer in chemical biology and proteomics, he has developed transformative technologies for protein and drug discovery and co-founded several biotechnology companies, including Vividion Therapeutics. He is a member of the National Academy of Sciences, and the recipient of the 2022 Wolf Prize in Chemistry.



Robert T. Abraham, Ph.D.

Chief Scientific Officer of Engine Biosciences and former head of Oncology R&D at Pfizer, where his teams advanced multiple clinical candidates and contributed to 11 FDA-approved oncology drugs. A pioneer in PI3K/mTOR biology, he has authored more than 230 scientific publications and serves as an advisor to leading biotechnology companies and Google Ventures.

OnKure is Developing a Differentiated Portfolio

OnKure Therapeutics

- **Developing PI3K α PAN-mutant Inhibitors** with the highest known selectivity across helical and kinase mutations
- Two distinct candidates designed for **Vascular Anomalies & Cancer**
- Experienced R&D team to support portfolio expansion and application to vascular anomalies beyond PI3K α inhibition

Portfolio

Two Lead PI3K α ^{PAN} Programs

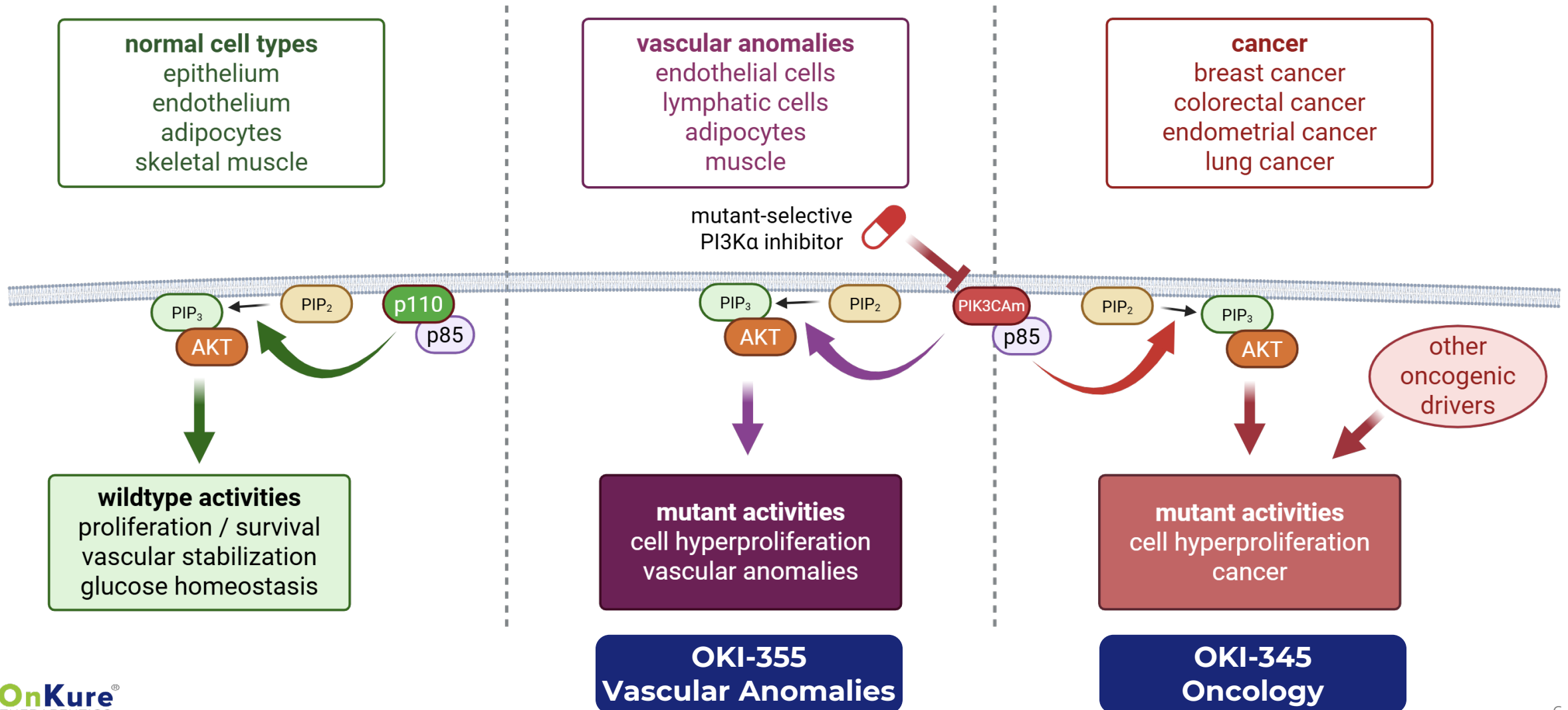
- OKI-355 in Vascular Anomalies
- OKI-345 in Cancer
 - ✓ PI3K α PAN-mut-selective inhibitors
 - ✓ Best-in-class drug properties
 - ✓ INDs expected 1H 2027

Discovery Programs

- Novel target(s) beyond PI3K α in Vascular Anomalies

PI3K α Pathway is Pleiotropic: Central to Normal & Disease Signaling

Disrupted cellular homeostasis due to mutant PI3K α drives cancers & vascular anomalies



A Differentiated Portfolio

Program	Initial Indication	Discovery	Preclinical	Clinical	Program Status	Next Anticipated Milestone
OKI-355 PI3Kα^{PAN} mutant-selective inhibitor	Vascular Anomalies				IND-Enabling Studies Ongoing	IND (1H 2027)
OKI-345 PI3Kα^{PAN} mutant-selective inhibitor	Breast Cancer				IND-Enabling Studies Ongoing	IND (1H 2027)
Discovery Target(s) to be announced; systemic and topical	Vascular Anomalies				Active Discovery	To be announced

Candidate Profile for Potential BIC PI3K α Pan-Inhibitors

Discovering pan-mutant inhibitors vs. the current landscape

Selectivity

At least 10X cellular selectivity in cell lines with major hotspot mutations in PI3K α

Efficacy

Potential Best-in-class anti-tumor activity in PI3K α mutant HR+ BC and Vascular Anomalies models

Safety

Best-in-class avoidance of wild-type PI3K α and associated toxicities

Coverage

Broad mutant coverage with brain penetration to maximize depth and durability of response

Comparison of cellular selectivity of OnKure vs. competitor pan-mutant PI3K α inhibitors

Compound	PI3K α Mutation		
	H1047R	E545K	E542K
Alpelisib	1x	1x	2x
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Combinability

Minimal DDI risk enables broad combination use & supports potential use in adjuvant settings

Mutation Resistance

Active against on-target resistance mutants, enabling treatment after PI3K α i relapse

Diverse IP

Protects assets and disables competition

Candidates

Two development candidates: HR+ Breast Cancer and VA

All cellular selectivity values were determined by OnKure. Cellular potency for each compound was determined in cell lines with specific PI3K α mutations shown in parentheses: T47D (H1047R), MCF7 (E545K), BT483 (E542K). Selectivity was derived from the ratio of the potency in a mutant cell line to the wild-type PI3K α SKBR3 cell line. [#]OKI-345 is under development in breast cancer; [‡]OKI-355 is under development in vascular anomalies



Benjamin Cravatt, Ph.D.

Characteristics of High-Value Allosteric Pockets

Not all allosteric pockets are equally druggable—successful targets share common features

Desirable Properties

Rare Cryptic State Stabilization

Ligand binding modulates protein activity through allosteric communication networks, leveraging local structural flexibility to enable induced-fit binding and stabilize transient functional conformations that are inaccessible to orthosteric inhibitors

Desirable Outcomes

Accessible Cryptic State

Pocket naturally samples an open conformation, enabling ligand binding without major unfolding

High Druggability

Enclosed geometry with hydrophobic hot spots, H-bonding opportunities, and displaceable waters supports potent small molecules

Target-Specific Pocket Architecture

Enables selective inhibition with reduced off-target activity

Cryptic Allosteric Pockets: A New Path to Better Drugs

Differentiated biology translates into differentiated therapeutics

Traditional Active Site	Cryptic Allosteric Pocket
Conserved across paralogs (<i>i.e.</i> , 500+ kinases)	Often target-specific
Competition with natural substrate (<i>i.e.</i> , ATP)	Unimpeded access to the cryptic allosteric pocket; higher potency potential
Resistance-prone	Orthogonal resistance mechanisms
Heavily mined target space	Expands druggable proteome by revealing hidden binding sites

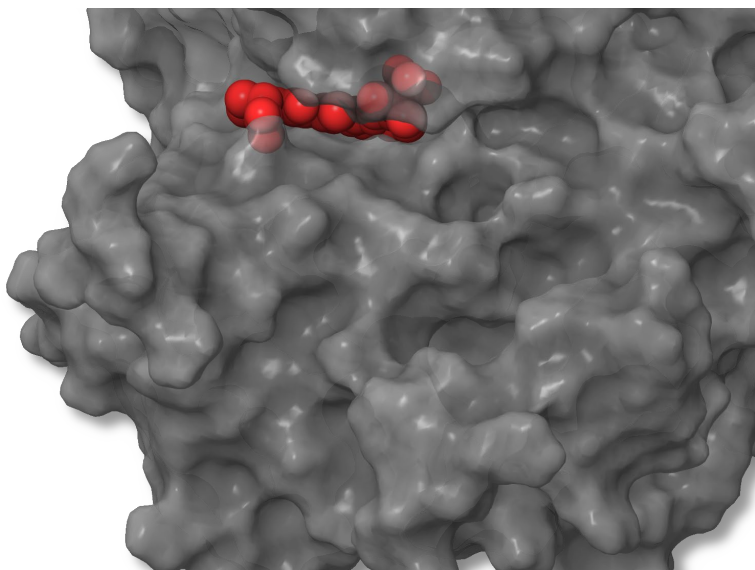
Key Value Drivers

- ✓ Access previously "undruggable" targets
- ✓ Improve selectivity versus orthosteric inhibitors
- ✓ Enable novel mechanisms of action
- ✓ Potential for mutant durable pharmacology
- ✓ Prolonged benefit for patients with resistance to active site drugs
- ✓ Opportunity for best-in-class therapeutics

Cryptic Allosteric: A New Path to Better Drugs for PI3K

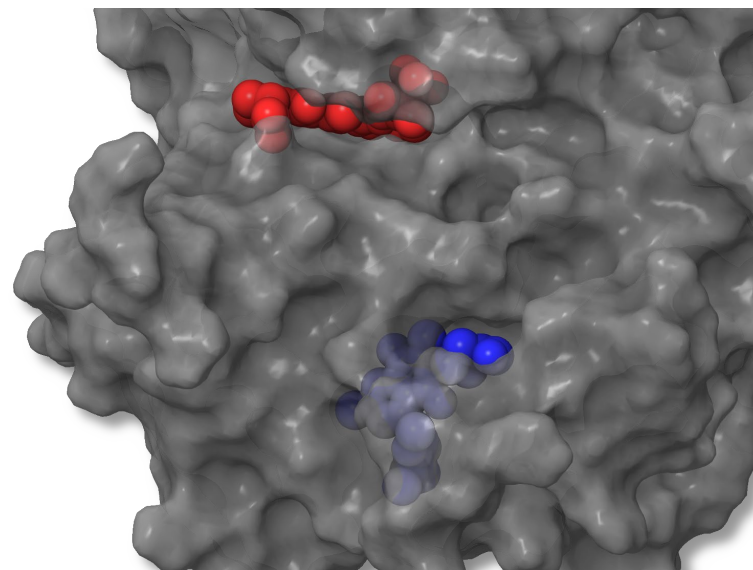
Differentiated biology translates into differentiated therapeutics

Traditional Active Site Alpelisib: Orthosteric Inhibitor



- Highly conserved binding site
- Competitive orthosteric inhibition
- Limited selectivity; resistance-prone

Cryptic Allosteric Pocket OKI: Allosteric Inhibitor



- Often target-specific pocket
- Modulates conformational equilibrium
- Higher selectivity; expands druggable proteome

Allosteric Inhibition Proven in Ph+ CML

SCEMBLIX® (asciminib) establishes clinical validation

Mechanistic Rationale

- Targets a **site other than** the ATP binding pocket
- Enables **high selectivity** vs. conserved kinase domains
- **Avoids direct competition** with high intracellular ATP levels
- Allows **fine-tuned modulation** of protein function
- Reduces risk of **off-target toxicity**
- Creates opportunity for **orthogonal combination strategies**



Clinical Validation

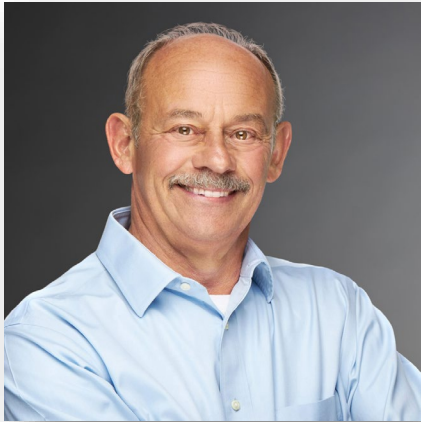
- First-in-class **inhibitor** targeting the ABL myristoyl pocket
- Designed to **overcome** resistance to ATP-competitive TKIs
- Demonstrates activity in **heavily pre-treated CML patients**
- Effective against **T315I & other resistant mutations**
- Improved **safety profile** vs. earlier-generation TKIs
- Validated via **regulatory approval and commercial uptake**

Sequential Innovation Creates Durable Competitive Advantage

Best-in-class franchises emerge from iterative gains in potency, selectivity, resistance coverage, & safety

Franchise	1 st Gen First-in-Class	2 nd Gen Higher Potency, Enhanced Selectivity	3 rd Gen Mutant Target Coverage	4 th Gen Improved Therapeutic Index
BCR-ABL	Target validation in CML imatinib	Faster, deeper response dasatinib, nilotinib	Covers T315I gatekeeper ponatinib	Allosteric (STAMP) inhibition asciminib
ALK	First-in-class ALK TKI crizotinib	CNS-active alectinib	Drug resistant mutations lorlatinib	Ongoing Research
EGFR	First EGFR TKIs gefitinib, erlotinib	Irreversible 2G potency afatinib, dacomitinib	Covers T790M osimertinib	Ongoing Research
PI3K	Isoform-selective idelalisib, alpelisib	Orthosteric BIC inavolisib	Wild-type-sparing Allosteric mutant-selective (STX-478 & RLY-2608)*	Allosteric pan-mutant selective OKI-345* & OKI-355*

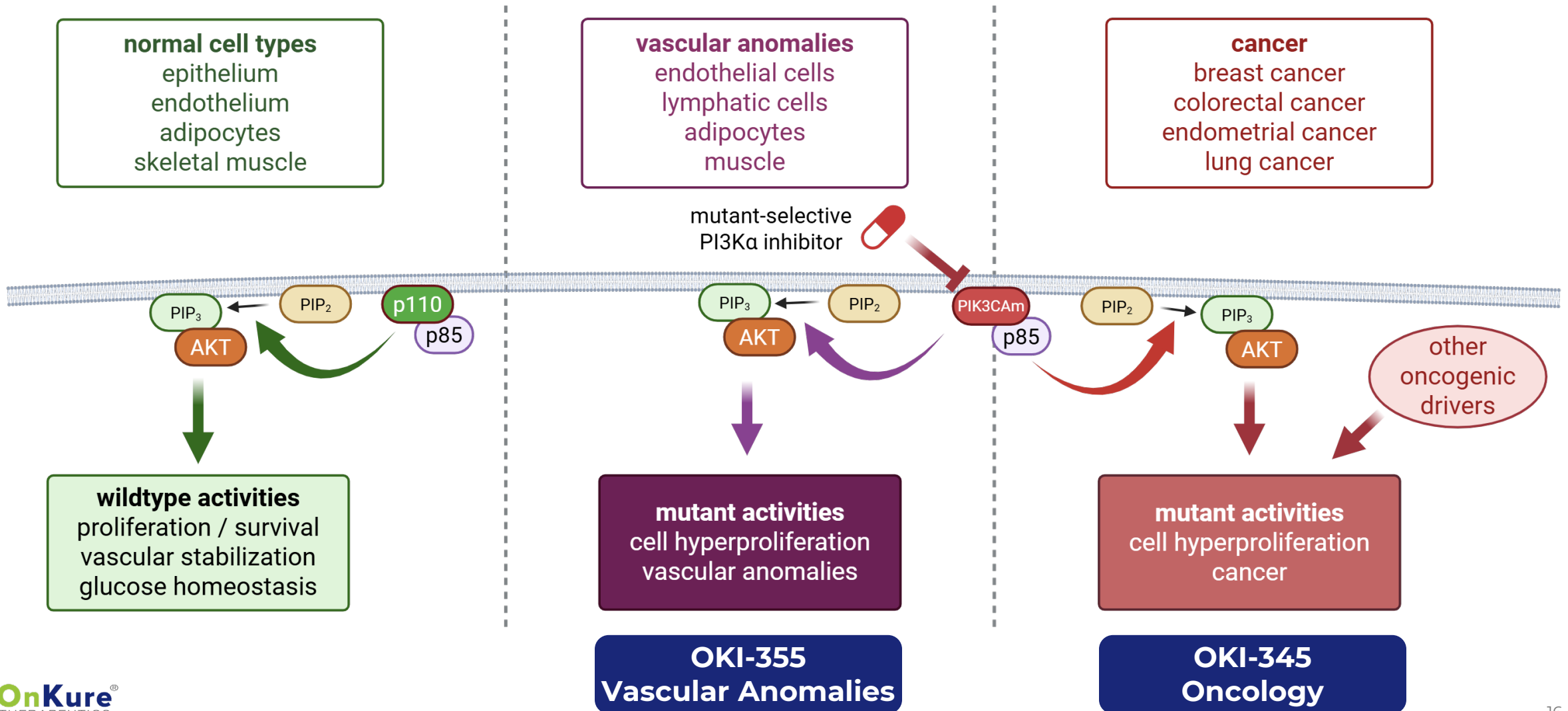
Sustained value is driven by repeatedly innovating against proven targets — not stopping at the first successful asset



Robert T. Abraham, Ph.D.

PI3K α Pathway is Pleiotropic: Central to Normal & Disease Signaling

Disrupted cellular homeostasis due to mutant PI3K α drives cancers & vascular anomalies



PI3K α : From Target Discovery toward Mutant-Selective Medicines

PI3K α mutations occur in major subset of vascular anomalies and ~15% of all cancers

1983–2000

Target Discovery

- Studies of a viral oncogene identify **PI3K α as a driver of carcinogenesis**
- Discovery of oncogenic PTEN & PI3K α mutations further validated the pathway
- PI3K pathway identified as a key regulator of cell growth, metabolism, and survival

2014–2019

Clinical Validation

- **Alpelisib became the first PI3K α -selective therapy approved for PI3K α -mutant solid tumors**

Next Generation

The Emerging Opportunity

- **Pan-mutant PI3K α inhibitors**
- Potential to spare wild-type PI3K α
- Improved therapeutic index & resistance coverage
- Greater combination flexibility

2000–2013

Target Validation

- **PI3K α confirmed as the most clinically relevant oncology target**
- **PI3K α mutation shown to drive vascular anomalies**
- Early inhibitors (wortmannin, LY294002) demonstrated PI3K α druggability
- Development shifted toward isoform-selective inhibition

2022

Clinical Approval in PROS

- **Alpelisib approved for PIK3CA-related overgrowth spectrum (PROS), a subset of vascular anomalies**

Challenges in Drugging PI3K α

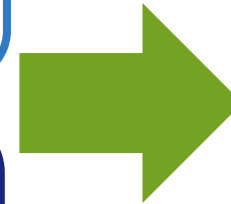
Next-generation mutant-selective inhibitors aim to preserve efficacy while reducing wild-type inhibition & metabolic toxicity

Chemistry Challenges

- Development of a pan-mutant inhibitor that targets the ATP binding site (orthosteric) will be extremely challenging
- Discovery & progression of molecules with >10X selectivity to avoid chronically emergent, clinically relevant wild-type derived toxicities

Clinical Challenges

- Use in combination regimens will be required
- Chronic dosing demands improved therapeutic window
 - Wild-type PI3K α plays key roles in normal cell growth & insulin function
 - On-target toxicities limit dosing: hyperglycemia, rash, diarrhea, stomatitis



The Path Forward

- Mutant-selective inhibition allows dose-intense therapy
- Increased probability of single-agent cytotoxicity
- Sparing of wild-type PI3K α improves the therapeutic window
- Reduces need for dose reductions or discontinuations due to unacceptable toxicity
- Enables development of 2- and 3-drug combinations to maximize efficacy



OnKure's Programs



Therapeutic Selectivity & Clinical Performance

Superior selectivity has translated into improved clinical outcomes

Ideal Performance

- Improved target coverage
- Better safety
- Greater combination potential
- Improved patient adherence
- Overall clinical benefit

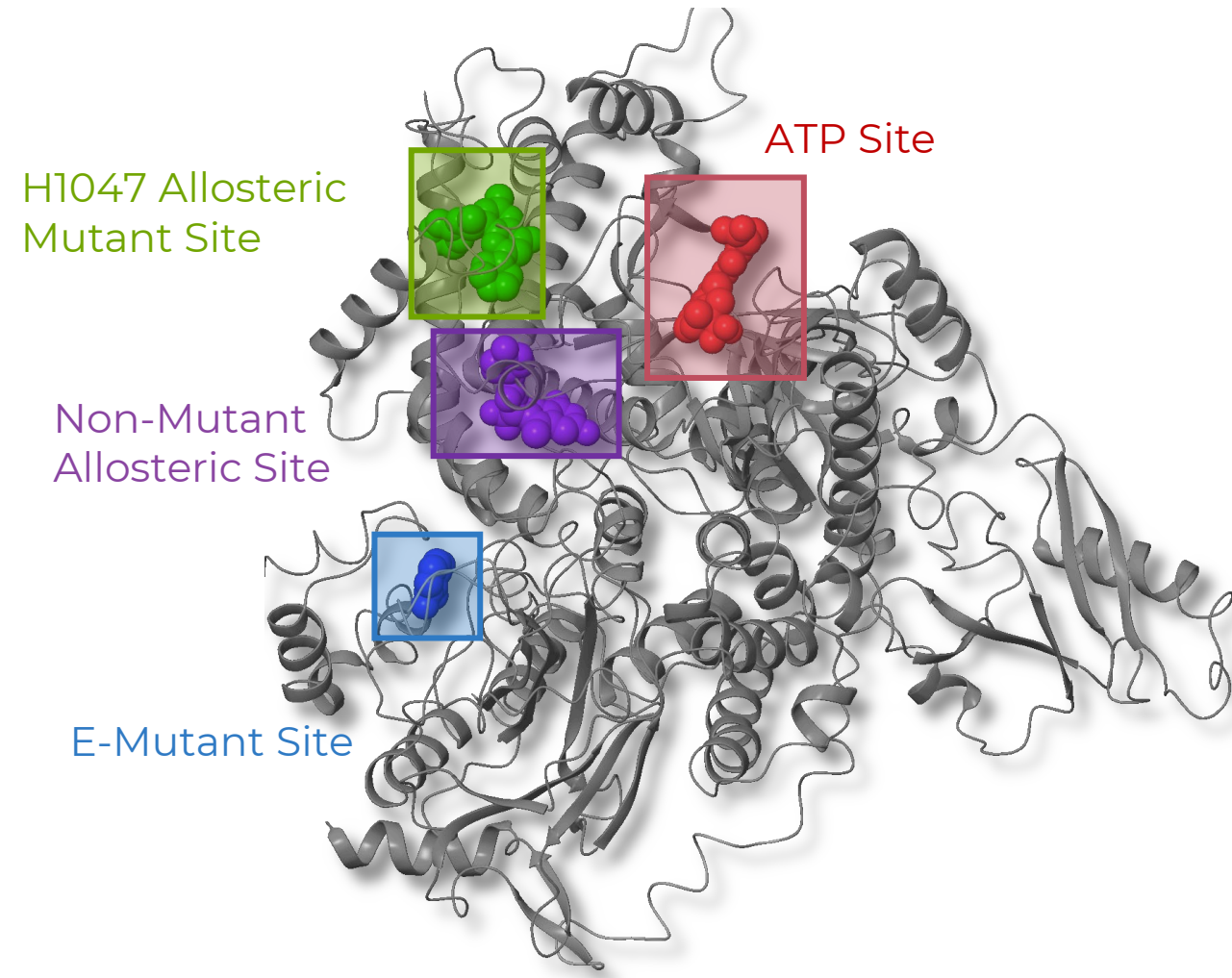
OnKure's Program Goals

- Minimize wild-type PI3K α inhibition
- Maximize PI3K α mutant inhibition
- Reduce systemic toxicity
- Establish best-in-class backbone medicine

OnKure's Structure-Based Drug Design Platform Enables Discovery of Allosteric PI3K α Pan-Mutant Inhibitors

Allosteric pan-inhibitor design

- Targeting regions proximal to PI3K α mutations:
 - **H1047 allosteric mutant site** (lead)
 - OnKure-discovered **E-mutant site** (proprietary)
- Designed to inhibit both kinase & helical domain mutants (H1047X, E542K, & E545K)
- Targets key regulatory regions driving mutant PI3K α activation
- Potential to overcome on-target resistance from prior therapies (**orthosteric: alpelisib and inavolisib; non-mutant allosteric: STX-478 and RLY-2608**)



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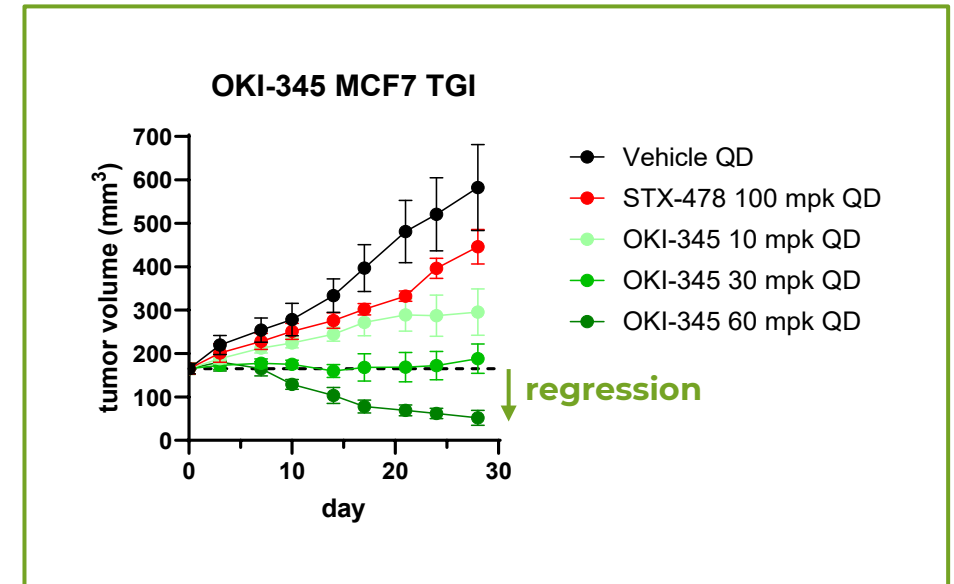
Selectivity Provides Deeper Responses when Dosed to MTD

A wider therapeutic window allows for greater mutant target coverage

Cellular Selectivity vs. SK-BR-3 WT

selectivity range	compound	PI3K α Mutation		
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>10x	OKI-345	58x	18x	10x
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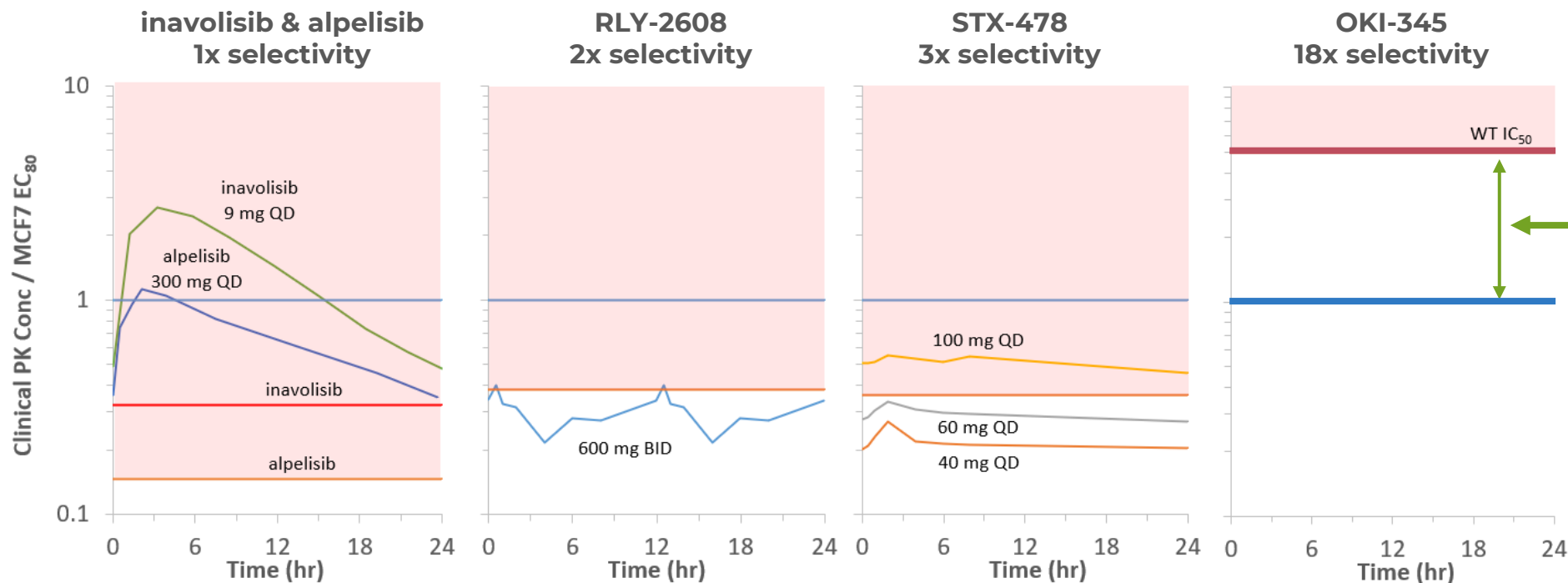
OKI-345 Drives Regressions in MCF7 Helical (E545K) Domain Mutant Xenograft Model



OKI-345 Greater Selectivity Leads to Superior Target Coverage and Efficacy over the Competition

The MCF-7 xenograft is ER+/PR+, HER2- and PI3K α **helical-domain hotspot mutant (E545K)** breast cancer. STX-478 was tested at the published dose in mice (Buckbinder et al., 2023)

OnKure's Thesis: Best-in-Class Selectivity Enables Greater Target Coverage to Unlock an Expanded Therapeutic Index



Greater **separation** between the red & blue lines reflects an **expanded** therapeutic window

Clinical¹ C_p / MCF7 EC₈₀ plots demonstrate that OKI-345 is expected to engage mutant PI3K α well below the WT IC₅₀, whereas the competitors will risk hyperglycemia/hyperinsulinemia

- Values > 1 (blue line) indicate clinically relevant target inhibition
- Values > WT PI3K α EC₅₀ (pink shaded area) indicate risk of hyperglycemia

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Portfolio

Two Lead PI3K α ^{PAN} Programs

- OKI-355 in Vascular Anomalies
- OKI-345 in Cancer
 - ✓ PI3K α PAN-mut-selective inhibitors
 - ✓ Best-in-class drug properties
 - ✓ INDs expected 1H 2027

Discovery Programs

- Novel target(s) beyond PI3K α in Vascular Anomalies

Q&A





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