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Discovery and characterization of selective, FGFR1 sparing, inhibitors of FGFR2/3 oncogenic mutations for the treatment of cancers

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Expanding the Reach of Precision Medicine Through the Development of Novel MasterKey Therapies



Addressing significant unmet need for novel precision oncology therapies for patients

Uniquely de-orphaning oncogenic mutations to develop single therapies designed to inhibit specific mutation families

Our proprietary computational Mutation Allostery Pharmacology (MAP) drug discovery engine is designed to develop a spectrum-selective (MasterKey) small molecule therapy

Robust pipeline of oral, potent and selective small molecule kinase inhibitors across a range of indications and target groups including EGFR, HER2, BRAF and FGFR

FGFR2 and FGFR3: Important Oncogenic Drivers in Solid Tumors, Poorly Served by Available Therapies





NATIONAL CANCER

INSTITUTE

Current drugs limited by lack of selectivity & FGFR2/3: potent oncogenic drivers across human tumors poor resistance profile Prevalence of FGFR2/3 mutations and fusions 1. Approved pan-FGFR inhibitors suffer from FGFR1-mediated in Solid Tumors hyperphosphatemia leading to frequent dose interruptions or reductions and limited efficacy. Bladder 20-25% **Endometrial** Secondary resistance mutations, at key residues within the 10-15% 2. kinase domain, emerge following treatment. Melanoma 10% Hepatobiliary 7-8% **Black Diamond Approach** CRC 4-5% Cancer of Unknown Primary 4-5% Target spectrum of High barrier to drug Esophagogastric 3-4% FGFR2 alterations resistant mutations Cervical 3-4% H&N 3-4% Optimization CNS & Brain 3-4% Strategy FGFR2 Mut. and Fusions NSCLC 2-3% FGFR3 Mut. and Fusions Ovarian 2-3% Spare FGFR1 for wide Target spectrum of FGFR3 alterations therapeutic window Breast 2-3%

MAP platform reveals FGFR2/3 oncogenic mutations and resolves structural differences vs FGFR1 to support drug discovery





MAP platform identifies novel, clinically relevant and actionable FGFR2/3 allosteric mutations





Mutation-Allostery-Pharmacology (MAP) platform is a genomic and proteomic ruledbased algorithm that reveals allosteric oncogenes:

- Revealing the topography of oncogenic mutation hotpots
- Increasing oncogenicity prediction
- Aggregating spectrum of mutations to be drugged by a single compound

MAP platform coupled with proprietary X-Ray crystal structure and MD simulation reveal actionable differences between FGFR1 and FGFR2/3



Goals: Reveal the structural differences in the active site between FGFR1 and FGFR2/3.

Approach: All-atom MD simulations and study of proprietary the x-ray crystal structure.

Results: Structural differences in FGFR3 vs FGFR1 active sites revealed





BDTX FGFR2/3 Leads Differentiated by Broad Selectivity Profile While Sparing Wild Type FGFR1 and Potency Against Key Resistance Mutations





BDTX FGFR2/3 Leads Demonstrate In-vivo Efficacy While Limiting FGFR1-related Toxicity







The future of cancer therapy





Repeat dosing in Rats at

Erdafitinib			
Source	Species	Dose	Unbound AUClast (h·µM) (M/F)
BDTX	Mouse	30 mpk PO-QD	0.252
	Rat	50 mpk PO- QD	0.344
NDA [NME] 212018	Human	8 mg/day	0.394
		BDTX-A	
Source	Species	Dose	Unbound AUClast (h·µM)
BDTX	Mouse	150 mpk PO- QD	4.29
	Rat	30 mpk IP-QD	4.44

 In mouse and rat models, while Erdafitinib promote hyperphosphatemia, BDTX compounds, dosed at efficacious exposure, don't promote hyperphosphatemia.

Black Diamond to Deliver the Next Generation of Oncogenic FGFR Inhibitors





