

Acrivon

Therapeutics



*ACRIVON PREDICTIVE PRECISION PROTEOMICS (AP3)
OVERCOMING LIMITATIONS OF GENETICS-BASED PRECISION MEDICINE*

CORPORATE PRESENTATION

AUGUST 2024

FORWARD-LOOKING STATEMENTS

Certain information contained in this presentation includes forward-looking statements within the meaning of the Private Securities Litigation Reform Act of 1995 regarding our future results of operations or financial condition, business strategy and plans and objectives of management for future operations. In some cases, you can identify forward-looking statements because they contain words such as “anticipate,” “believe,” “contemplate,” “continue,” “could,” “estimate,” “expect,” “intend,” “may,” “plan,” “potential,” “predict,” “project,” “should,” “target,” “will,” or “would” or the negative of these words or other similar terms or expressions. Our forward-looking statements are based primarily on our current expectations and projections about future events and trends that we believe may affect our business, financial condition and results of operations. The outcome of the events described in the forward-looking statements is subject to risks and uncertainties, including the factors described in our filings with the U.S. Securities and Exchange Commission. New risks and uncertainties emerge from time to time, and it is not possible for us to predict all risks and uncertainties that could have an impact on the forward-looking statements contained in this presentation. The results, events, and circumstances reflected in the forward-looking statements may not be achieved or occur, and actual results, events, or circumstances could differ materially from those described in the forward-looking statements.

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CRITICAL CHALLENGES FACING BIOPHARMA INDUSTRY

Challenge

Acrivon Predictive Precision Proteomics (AP3)



Discovering **potent** compounds suitable for **clinical monotherapy**

Optimal target/pathway selectivity for rapid generation of single agent active compounds



Determining **which patients will benefit from** those drugs

Identification of drug-sensitive indications and patients for actionable precision medicine



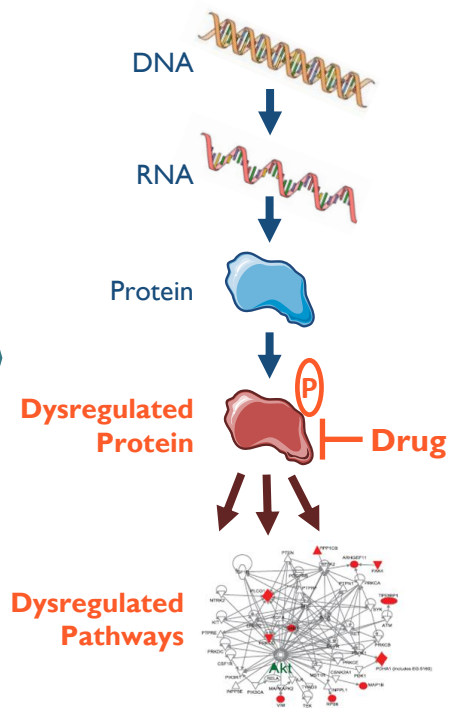
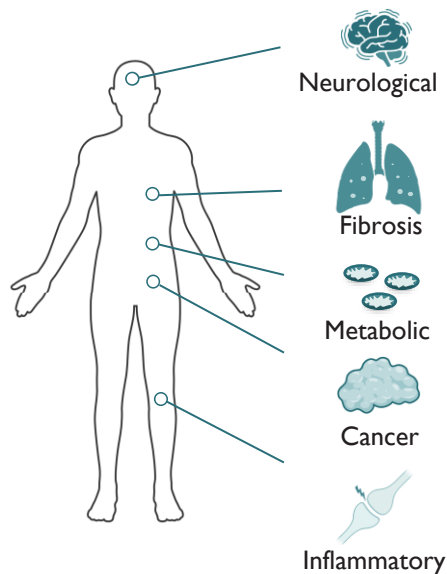
Preventing or reducing resistance to **maximize response durability**

Ability to rapidly identify and overcome resistance mechanisms



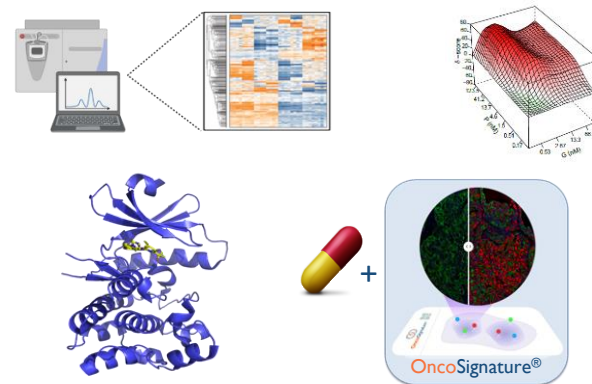
AP3 is a proprietary, machine learning-enabled internal R&D engine that effectively addresses these challenges, driving rapid advancement of our pipeline

ACRIVON THERAPEUTICS – A NEXT-GENERATION PRECISION MEDICINE COMPANY



Acrivon Predictive Precision Proteomics (AP3)

- Enables an exact match between the disease-driving, dysregulated pathways with a drug's mechanism of action (Acrivon meaning \approx exact, accurate)
- Broadly applicable in R&D (biological SAR, resistance, patient responders); leveraged for internal pipeline

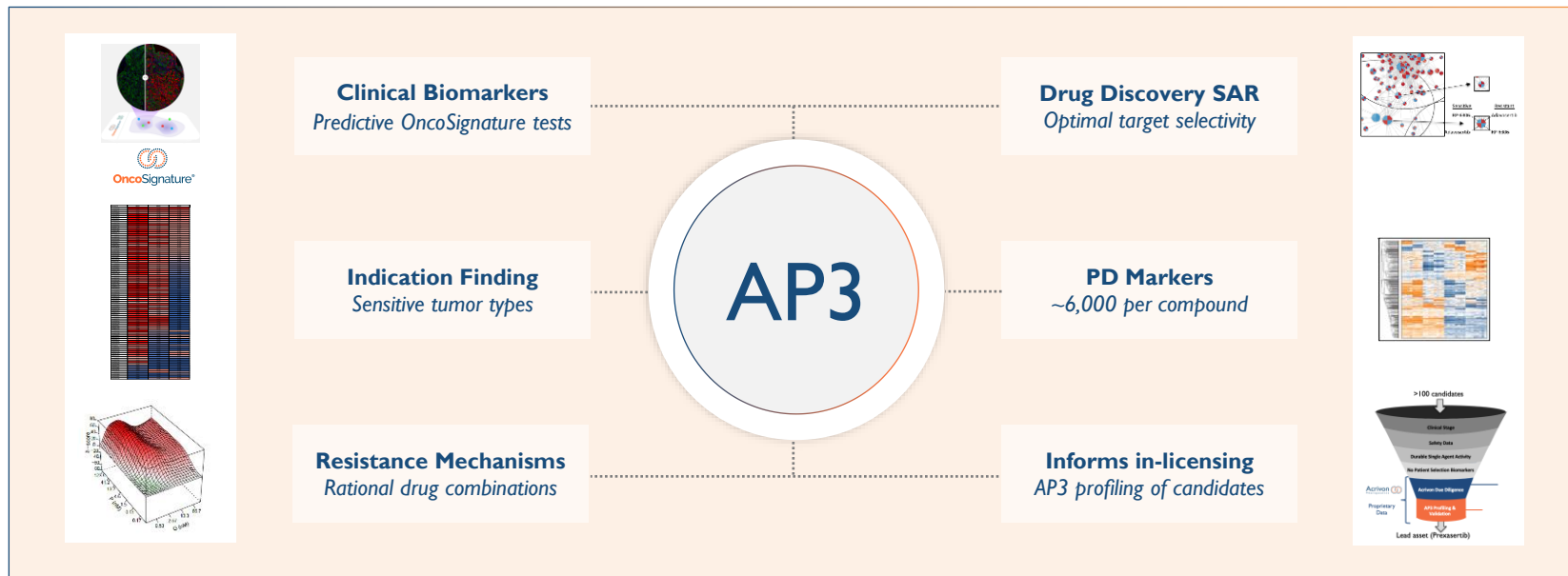


Blume-Jensen, P & Hunter, T: Oncogenic kinase signaling *Nature* (2001)

Olsen, JV et al: Global, in vivo, and site-specific phosphorylation dynamics in signaling networks *Cell* (2006);

Andersen, JN et al: Pathway-based identification of biomarkers for targeted therapeutics: personalized oncology with PI3K pathway inhibitors *Sci Transl Med* (2010)

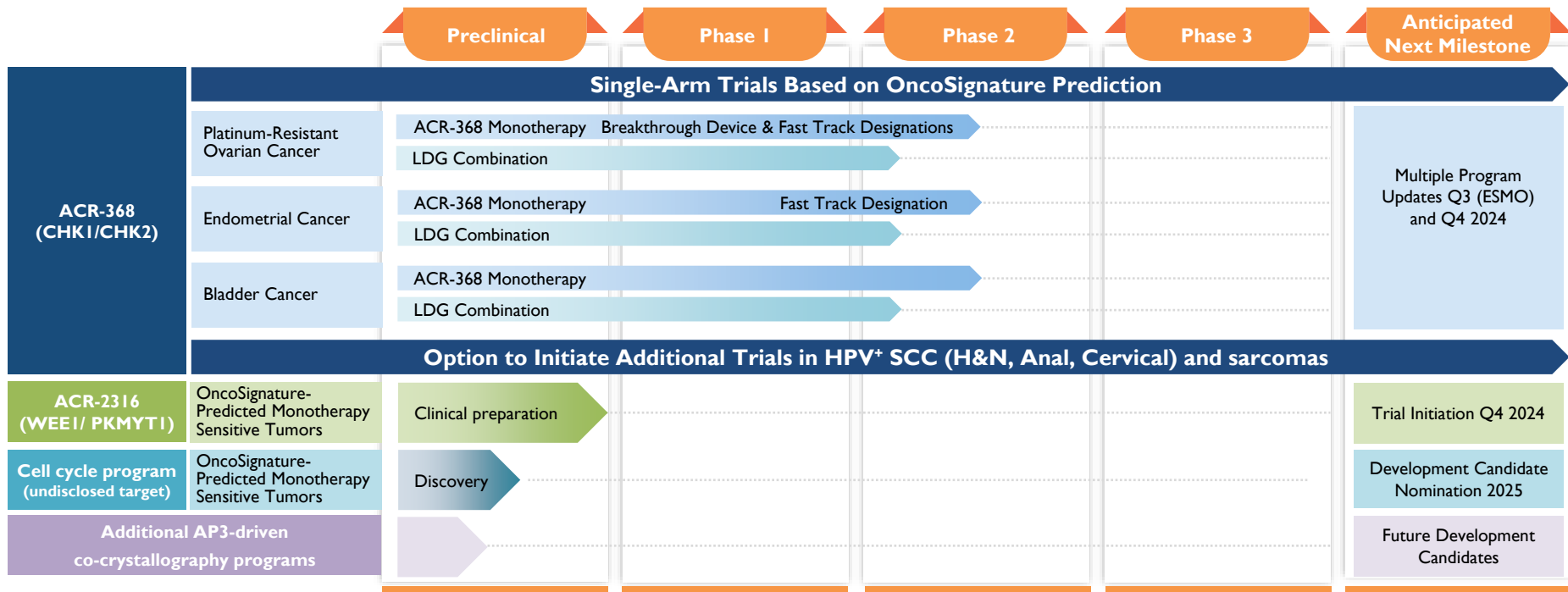
AP3: HIGHLY DIFFERENTIATED - MULTIPLE R&D DELIVERABLES



Intellectual Property
De novo exclusivity & protection against generics



ACRIVON PIPELINE



Notes

ACR-368 Monotherapy

Registrational intent Phase 2 single arm trials based on predicted sensitivity to ACR-368 monotherapy in OncoSignature-positive patients

LDG Combination

Exploratory Phase 1b/2 single arm trials of ACR-368 in combination with low dose gemcitabine, or LDG, in OncoSignature-negative patients

ACRIVON THERAPEUTICS FOUNDATION

Development Site (Boston)

- Drug and clinical biomarker assay development
- Clinical trials
- Market access pending approval

HQ LOCATED IN BOSTON - ACCESS TO LEADING DRUG DISCOVERY, BIOTECH, AND PHARMA



Peter Blume-Jensen
CEO, President,
Co-Founder



Kristina Masson
EVP, Bus Ops,
Site Head and
Co-Founder



Jesper V. Olsen
Academic Co-Founder,
Novo-Nordisk Foundation
Protein Center, Cph.

Precision-Proteomics Site (Lund/Copenhagen)

- Early pipeline drug programs
- **BM** identification and drug profiling
- Mass spectrometry

PROTEOMIC HUB LOCATED IN MEDICON VALLEY - NORTHERN EUROPE'S LEADING LIFE SCIENCE CLUSTER



Founded 2018, IPO November 2022 (NASDAQ:ACRV)

For more information, please visit <https://acrivon.com>

ACCOMPLISHED LEADERSHIP TEAM



Peter Blume-Jensen, M.D., Ph.D.
CEO, President, Founder

- Executive Serono, Merck & Co., Daiichi Sankyo
- CSO Metamark - Marketed prostate proteomic test ProMark®
- Inventor Acrivon Predictive Precision Proteomics (AP3)



Rasmus Holm-Jorgensen
Chief Financial Officer

- Novo Nordisk Finance and IR
- Synageva pipeline expansion and \$9bn sale to Alexion
- Kiniksa founding team, IPO and commercial launch



Kristina Masson, Ph.D., M.B.A
Site Head Acrivon AB, Co-Founder
EVP Business Operations

- Cross-functional Leadership Merrimack Pharmaceuticals, MIT/BROAD
- Founder and CEO, OncoSignature AB (acquired by Acrivon Therapeutics)



Jean-Marie Cuillerot, M.D.
Chief Medical Officer

- Chief Medical Officer, Agenus, Dragonfly
- Global head of clinical development in immuno-oncology at EMD Serono
- Clinical development leadership roles at BMS and Novartis



Eric Devroe, Ph.D.
Chief Operating Officer

- Founder and CEO, Opsonix
- Business executive MD Anderson Cancer Center and Metamark
- EIR Wyss Institute, Harvard
- Associate, Flagship Pioneering



Erick Gamelin, M.D., Ph.D.
Chief Development Officer

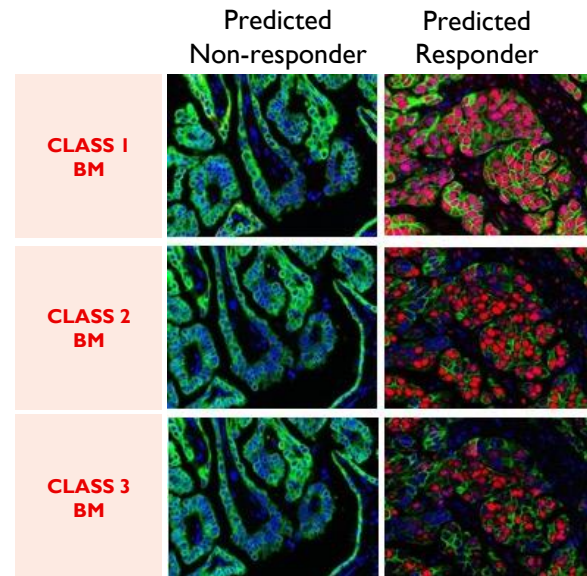
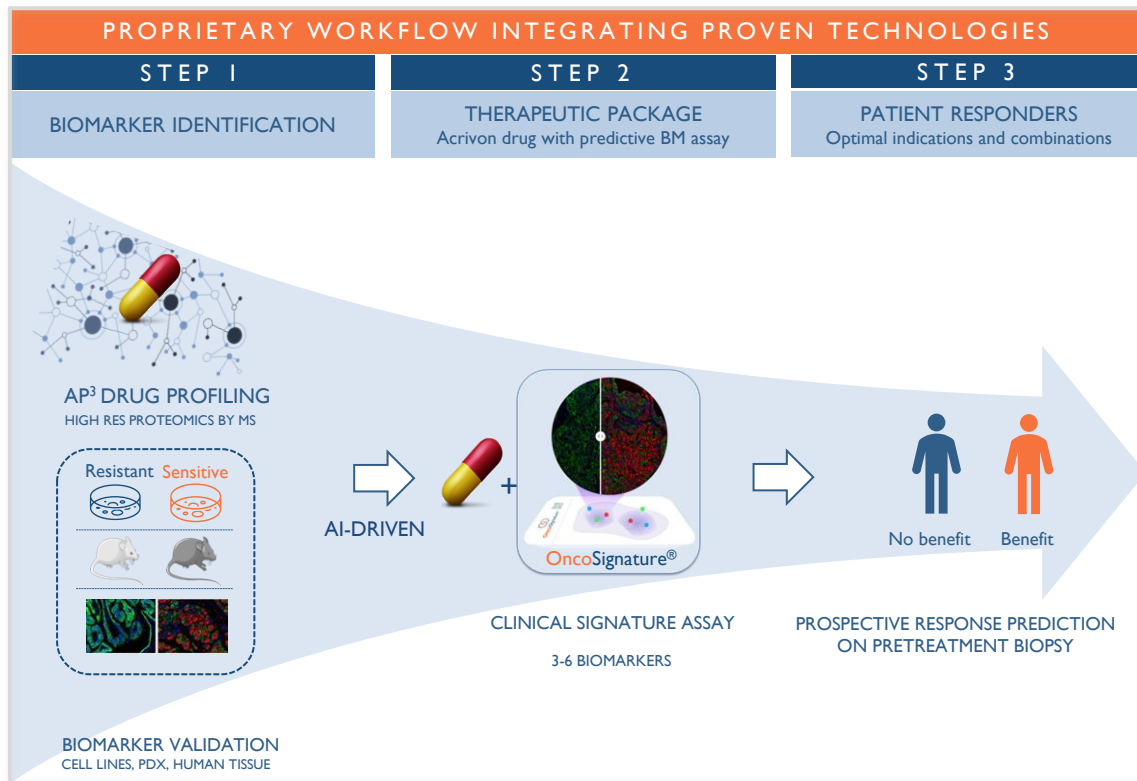
- Professor, CEO, large national cancer center and hospital
- Executive Amgen, Pfizer, Dynavax, MacroGenics; CMO STEP Pharma
- >100 ph I-3 oncology trials



Mary-Alice Miller, J.D.
Chief Legal Officer

- Over 20 years corporate legal experience
- Served as general counsel of 2 companies taken public
- Boston Business Journal "40 Under 40"

AP3 PLATFORM: DRUG RESPONSE PREDICTION IN INDIVIDUAL PATIENTS

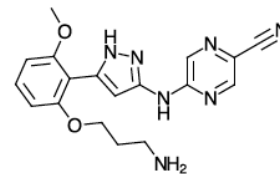


Patients without biomarkers critical for drug sensitivity efficiently excluded

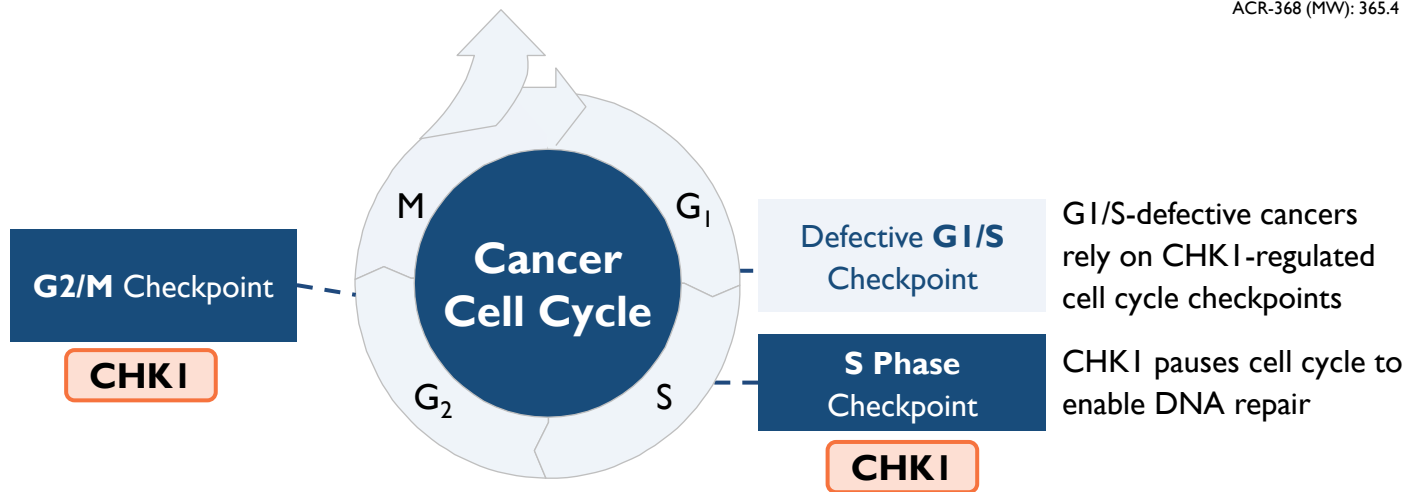
"Disease Pathway-Based Method to Generate Biomarker Panels Tailored to Specific Therapeutics for Individualized Treatments": EP 2 229 589, issued June 10, 2015; US2017/0067877A9, pending. OncoSignature® is a Registered Trademark: US Reg. No. 5,718,472; Int. Cl. 5, 42. Intl. Reg. 1382289

ACR-368: A CLINICALLY ACTIVE PHASE 2 CHK1/2 INHIBITOR

- ATP-competitive inhibitor of CHK1 (0.9 nM) and CHK2 (8 nM)
- Good ADME properties, minimal drug-drug interaction (DDI) potential
- Discovered by Array Biopharma, acquired by Eli Lilly & Company
- CoM patent exp. Oct., 2030; Salt-form exp. Apr., 2037



ACR-368 (MW): 365.4



- **Durable monotherapy activity:** Platinum-resistant ovarian and squamous cell cancers (Anal and H&N)
- **Large safety database, favorable safety profile:** > 1,000 patients treated (~50% mono, ~50% in combination)
- **Ideal for AP3 method:** Proven clinical activity, but requires patient responder identification to achieve sufficient ORR

CLINICAL OVERVIEW OF PAST LILLY-SPONSORED MULTI-CENTER ACR-368 MONOTHERAPY STUDIES

Indication	Trial	ORR [#] (confirmed)	Median DoR ^o	Reference
HGSOC* (BRCA wild type and mutant; platinum-resistant and refractory)	Phase 2 (46-center, 8-country study)	12.1% (platinum-resistant)	5.6 months	Konstantinopoulos et al; Gynec. Oncol.: 2022
Squamous cell cancer (anal cancer, head & neck cancer [H&N])	Phase 1b multi-center	19% HPV+ H&N 15% anal cancer	7 months (HPV+ H&N) 12 months anal cancer	Hong et al, CCR, 2018

Dosing and Administration

- IV q14d (RP2D = 105 mg/m²)

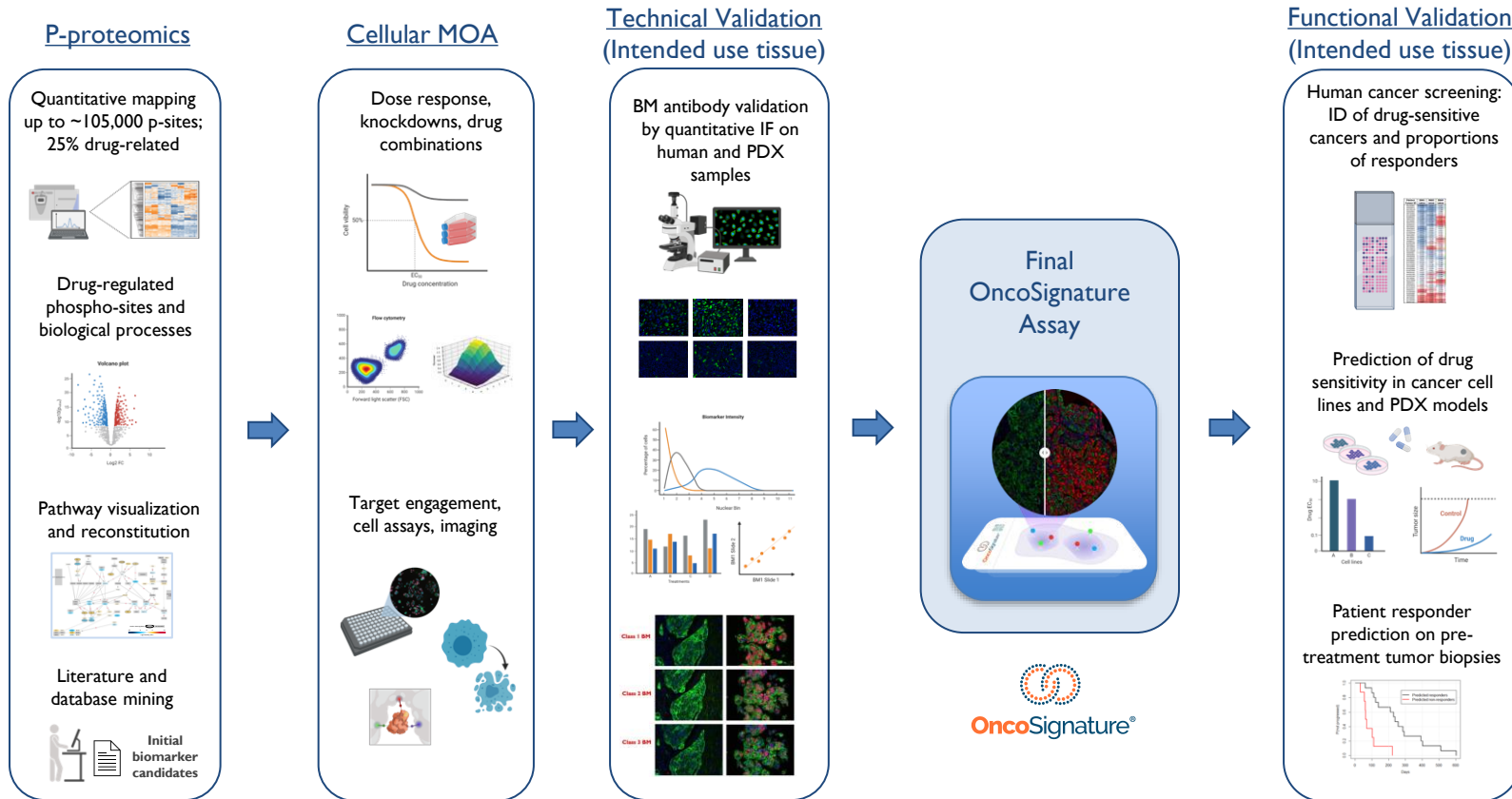
Safety summary

- Acceptable safety profile in >1,000 patients
 - No clinical or regulatory holds imposed across all clinical studies to date
- Primary adverse events ≥ grade 3 were hematological (manageable neutropenia and thrombocytopenia)
- Limited ≥ grade 3 non-hematological toxicities (≤7% for all AEs)
- Drug-related discontinuations <1-2%

Despite significant efforts, no predictive biomarkers were identified, need for alternative biomarker approach

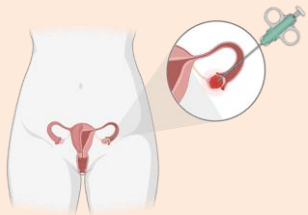
*High grade serous ovarian cancer; # Overall response rate; ^oDuration of Response

DEVELOPMENT OF AP3-BASED PATIENT SELECTION ONCOSIGNATURE TESTS



ACR-368 ONCOSIGNATURE TEST: USAGE IN THE CLINIC

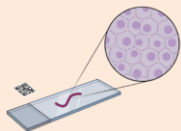
Pretreatment tumor biopsy



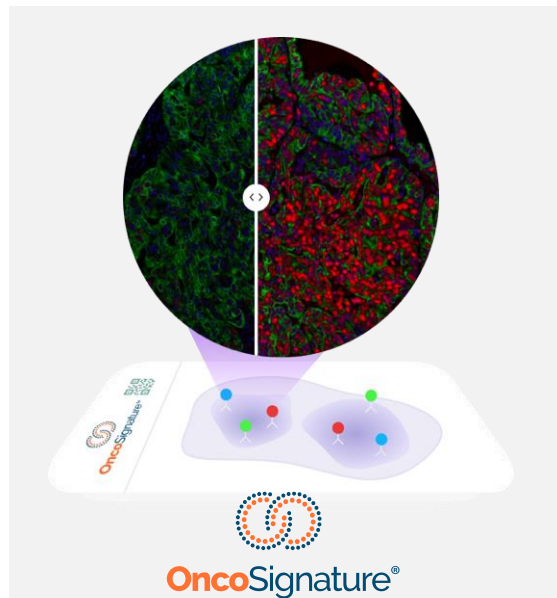
Sample processing



Biopsy in
FFPE
block



Automated tumor
Region-of-Interest
biomarker scoring



- Pretreatment tumor biopsy test
- Compatible with 5 business days turn-around
- Offered by CDx partner under exclusive license from Acrivon

Treatment decision based on patient stratification



OncoSignature-
positive



OncoSignature-
negative



ACR-368
monotherapy

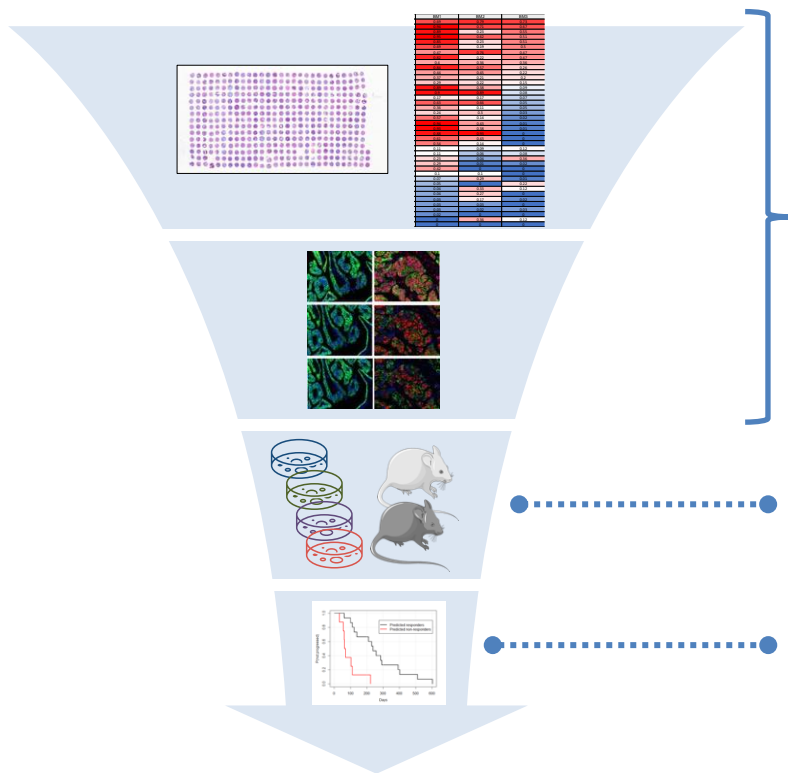


ACR-368 + LDG
combination

CONSISTENT ACR-368 ONCOSIGNATURE PERFORMANCE ACROSS PRECLINICAL STUDIES

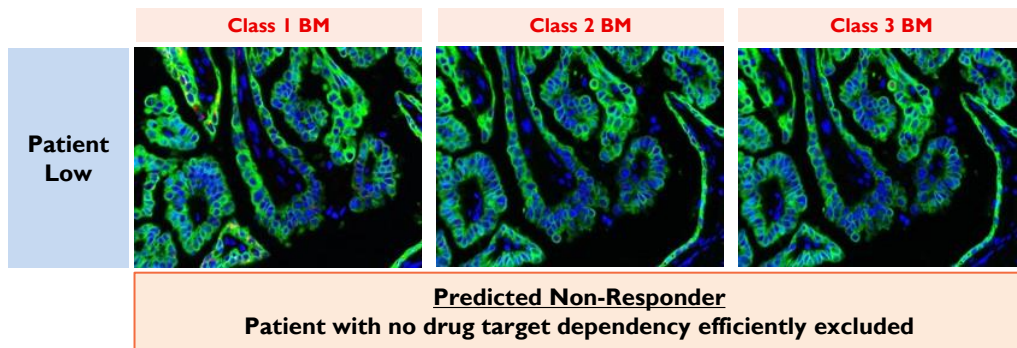
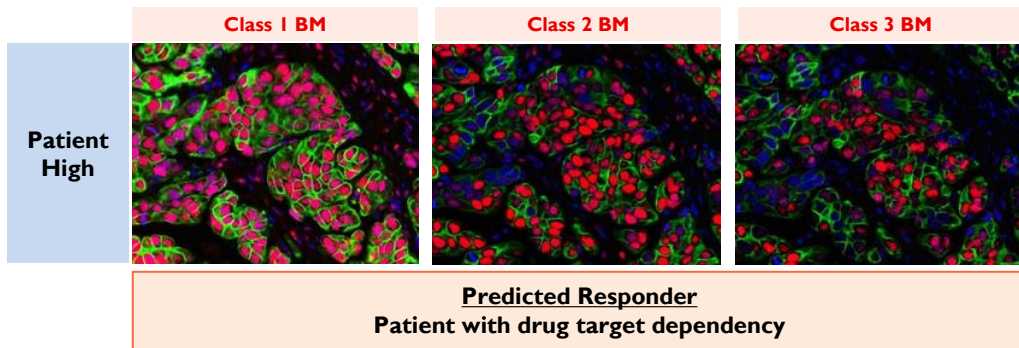


OncoSignature®



- Prediction of the fraction of human tumors sensitive to single agent ACR-368
 - Selection rate 30-40% across lead indications
- Identification of additional human tumor types predicted sensitive to single agent ACR-368
 - Endometrial and bladder cancer
- Prediction of treatment outcome in human PDX models
 - ORR enrichment to ≥ 55%; AUC of 0.88 and 0.9
- Two separate, prospectively designed, blinded studies of biopsies from past Phase 2 trials with ACR-368 in patients with platinum-resistant ovarian cancer
 - ORR enrichment to 47% (NCI) and 58% (Lilly multi-center)

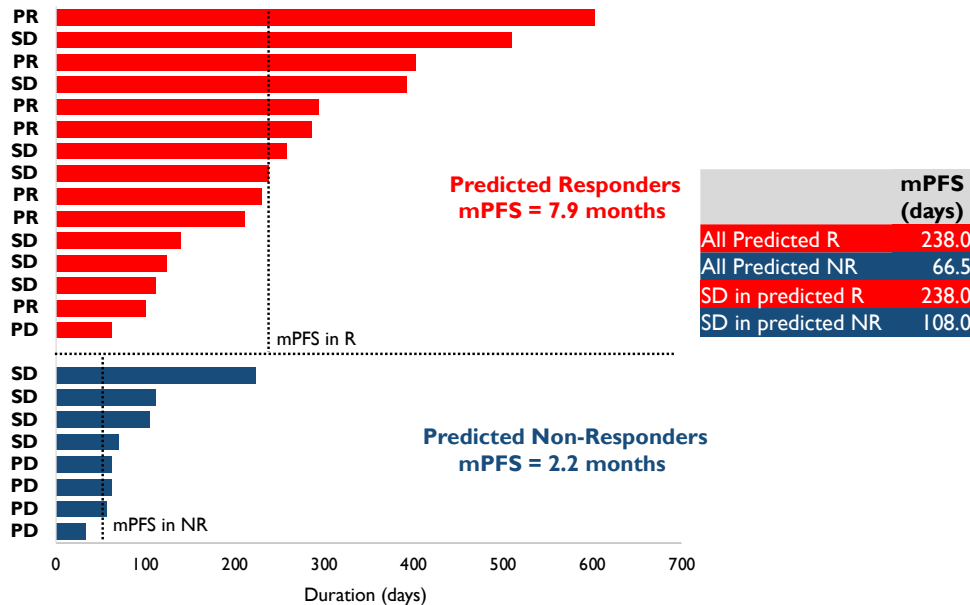
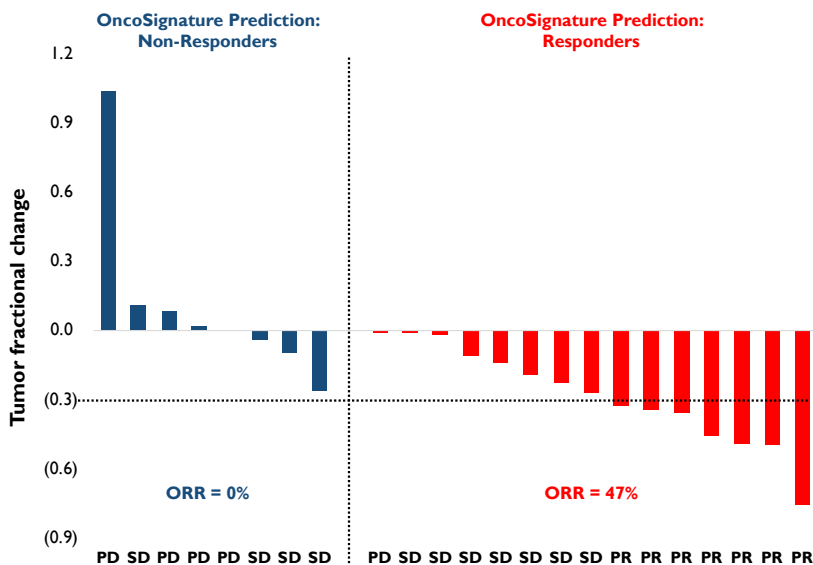
ACR-368 ONCOSIGNATURE PREDICTION OF DRUG SENSITIVITY: BIOMARKER QUANTITATION ACROSS HUMAN CANCER PATIENT SAMPLES



Tissue ID.	BM1	BM2	BM3
Fov060265	0.69	0.79	0.73
Fov050855	0.94	0.71	0.67
Fov041300	0.89	0.23	0.55
Fov060380	0.95	0.62	0.51
Fov060050	0.85	0.23	0.51
Fov041285	0.69	0.19	0.5
Fov100142	0.47	0.76	0.47
Fov050764	0.82	0.22	0.47
Fov041267	0.4	0.36	0.36
Fov100146	0.84	0.57	0.26
Fov060382	0.44	0.45	0.22
Fov041269	0.37	0.21	0.2
Fov060302	0.29	0.22	0.15
Fov020067	0.89	0.38	0.09
Fov100003	0.9	0.89	0.08
Fov050700	0.17	0.17	0.07
Fov050139	0.63	0.66	0.05
Fov041138	0.36	0.11	0.05
Fov060152	0.24	0.3	0.03
Fov030062	0.57	0.14	0.02
Fov060133	0.94	0.43	0.01
Fov050666	0.93	0.38	0.01
Fov060371	0.88	0.93	0
Fov020497	0.61	0.43	0
Fov010706	0.54	0.14	0
Fov020386	0.11	0.09	0.12
Fov050734	0.11	0.06	0.08
Fov040872	0.23	0.04	0.36
Fov050659	0.29	0.01	0.02
Fov060293	0.42	0	0
Fov060210	0.1	0.1	0
Fov050840	0.07	0.29	0.01
Fov040855	0.05	0	0.22
Fov050816	0.04	0.33	0.12
Fov060355	0.04	0.27	0
Fov010252	0.03	0.17	0.02
Fov010682	0.03	0.03	0
Fov060553	0.03	0.02	0.03
71768C3	0.02	0	0
Fov150230	0	0.36	0.12
Fov060308	0	0	0

BIOPSY STUDY I: SUBSTANTIAL RESPONSE AND PFS BENEFIT IN PREDICTED RESPONDERS (BLINDED, PROSPECTIVELY DESIGNED STUDY)

- Available pretreatment tumor biopsies from past phase 2 trials at NCI with ACR-368 in platinum-resistant ovarian cancer were obtained
- OncoSignature scores were generated **blinded to treatment outcome** at Acrivon and analyzed by **3rd party biostatistician** in **prospectively designed study**

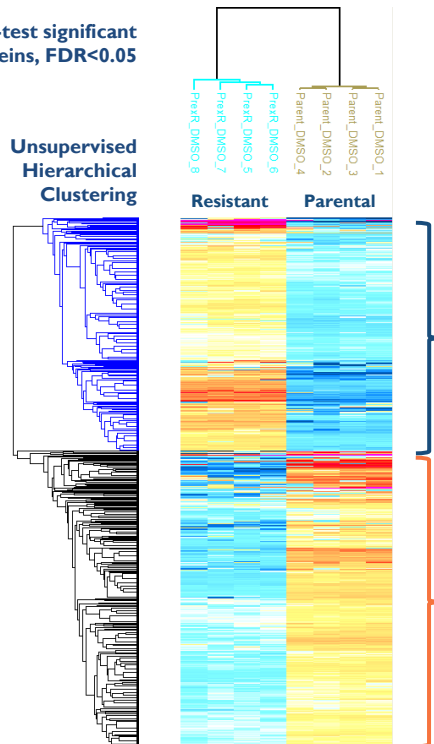


Result: ORR ~47%; mPFS = 7.9 months

AP3 UNCOVERS ACTIONABLE ACR-368 RESISTANCE MECHANISMS UNBIASED AND INDEPENDENT OF GENETIC INFORMATION

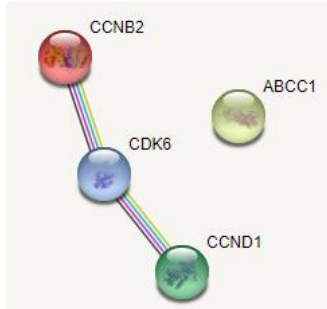
T-test significant
Proteins, FDR<0.05

Unsupervised
Hierarchical
Clustering

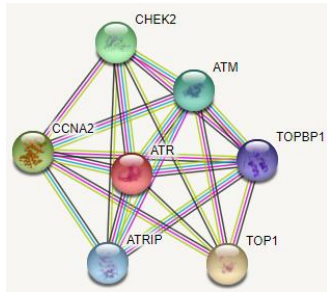


Upregulated in
ACR-368 Resistant Cells

Downregulated in ACR-
368 Resistant Cells



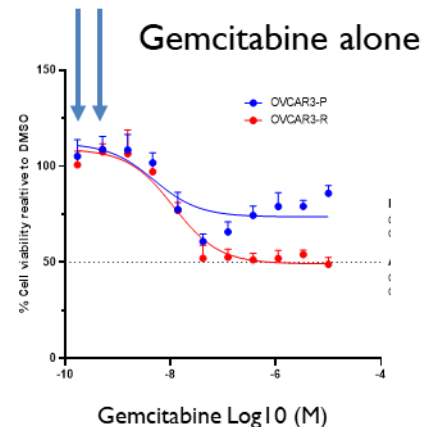
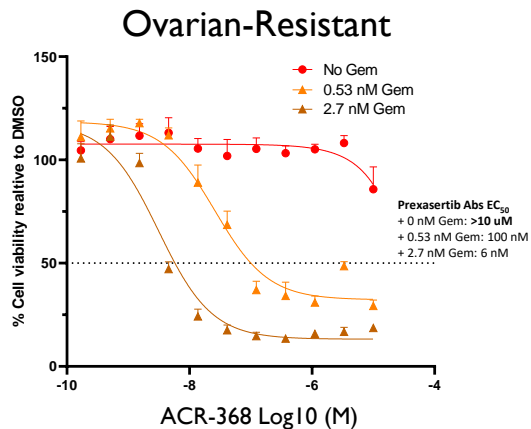
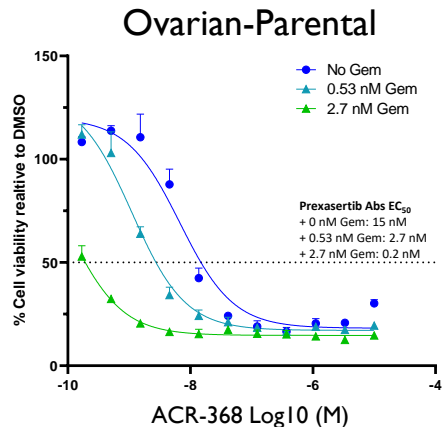
G1/S CELL CYCLE



DNA DAMAGE REPAIR

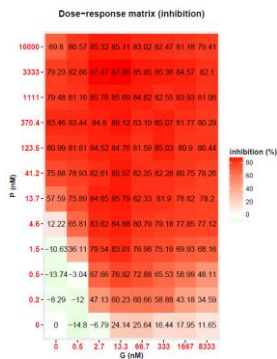
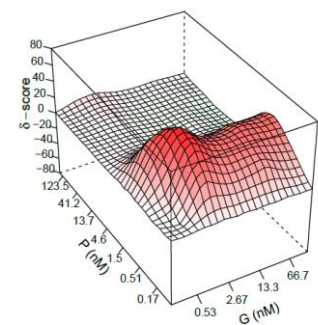
Data suggest that gemcitabine might be a rational combination to overcome DDR suppression

LOW DOSE GEMCITABINE SENSITIZES OVARIAN CANCER CELL LINES TO ACR-368



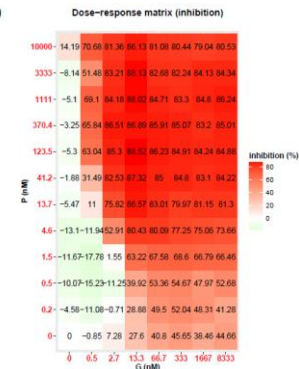
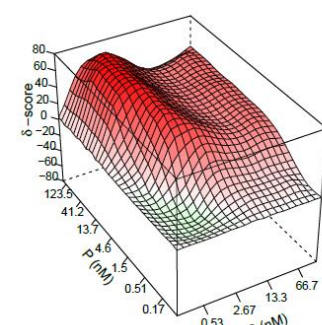
Bliss synergy score: 14.82

-80 -60 -40 -20 0 20 40 60 80



Bliss synergy score: 36.125

-80 -60 -40 -20 0 20 40 60 80



Bliss Synergy score:

- <-10: Drug interaction is likely antagonistic
- -10 to 10: Drug interaction is likely additive
- >10: Drug interaction is likely synergistic

THERAPEUTIC BAR FOR HIGH GRADE PLATINUM-RESISTANT OVARIAN AND ENDOMETRIAL CANCER NEW APPROVALS

- Platinum-resistant ovarian cancer: $\geq 2^{\text{nd}}$ line SOC* ~12% ORR, mDoR 3.7 – 5.7 months
 - Mirvetuximab: Post 1-3 prior lines, FRa-high PROC (~35% of patients; ORR ~35%, PFS = 5.6 months)
 - ~85% of patients with PROC do not benefit from mirvetuximab
- High grade endometrial cancer: $\geq 3^{\text{rd}}$ line SOC** ~9% ORR, mDoR 3.1 months
- ACR-368 clinical activity (without patient selection) in past platinum-resistant ovarian trials: ~12% ORR, mDoR >5.6 months
 - (BRCA-mutant and BRCA wild type patients regardless # lines of prior therapy; Lilly-sponsored 46-center, 8-country, N=169 patient study)^

- TPP - high grade PROC: $\geq 25\%$ ORR with CI lower bound >15%
- TPP - high grade endometrial cancer: $\geq 20\text{-}25\%$ ORR with CI lower bound >15%

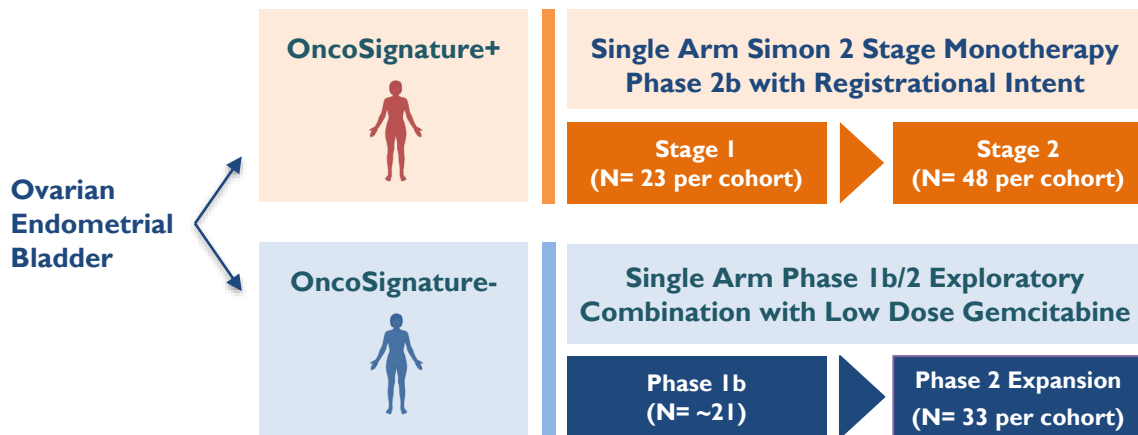
* Aurelia trial: Pujade-Lauraine E et al, JCO (2014); Corail trial: Gaillard S et al, JCO (2016)

** Ray-Coquard I et al, BJC (2013)

^ Konstantinopoulos P et al, Gyn Oncol. (2022)

ENROLLING AND DOSING ACR-368 IN THREE HIGH UNMET NEED INDICATIONS: OVARIAN, ENDOMETRIAL AND BLADDER CANCER

- RP2D of ACR-368 based on predicted sensitivity using our ACR-368 OncoSignature Assay run by our CDx partner
- 68 sites activated¹
- Key opinion leaders, some with extensive experience using ACR-368 from previous trials are actively participating



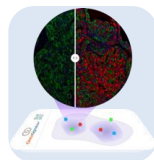
- FDA Fast Track Designation granted May 8, 2023 for ACR-368 monotherapy in OncoSignature-positive patients with Platinum-Resistant Ovarian Cancer and Endometrial Cancer
- FDA Breakthrough Device Designation granted November 16, 2023 for ACR-368 OncoSignature Assay for the identification of ovarian cancer patients who may benefit from treatment with ACR-368

¹<https://clinicaltrials.gov/ct2/show/NCT05548296>

ACR-368-201 STATUS – OVARIAN AND ENDOMETRIAL (LOCKED ONCOSIGNATURE THRESHOLDS, PROSPECTIVE TRIAL)

OncoSignature-positive
ACR-368 RP2D (105 mg/m²)

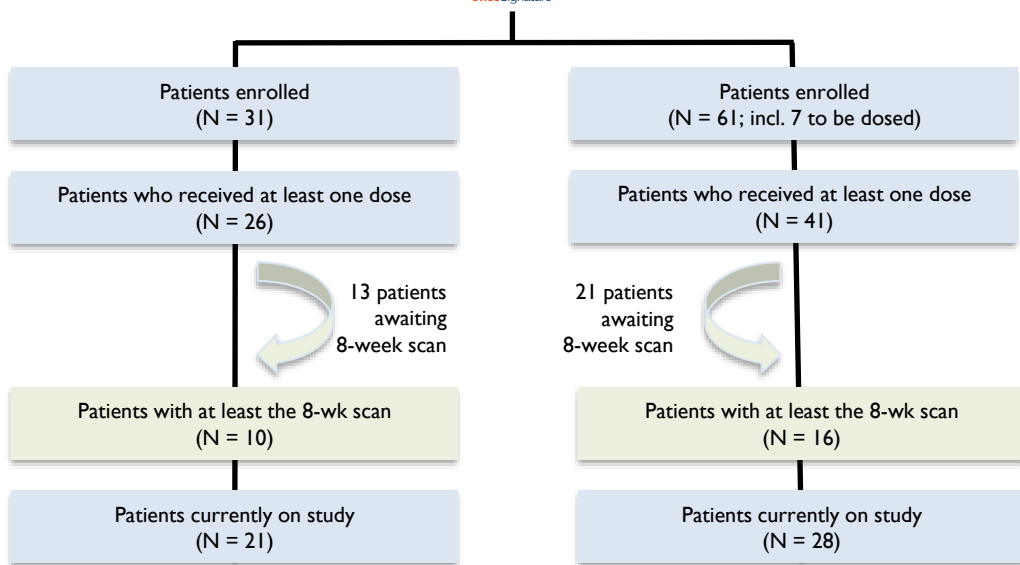
Registrational intent Phase 2



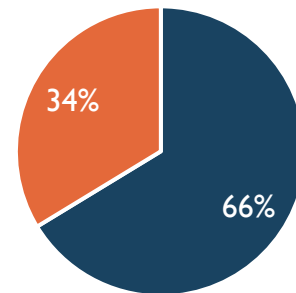
OncoSignature

OncoSignature-negative
ACR-368 RP2D (105 mg/m²) + ULDG RP2D (10 mg/m²)

Exploratory Phase 1B/2

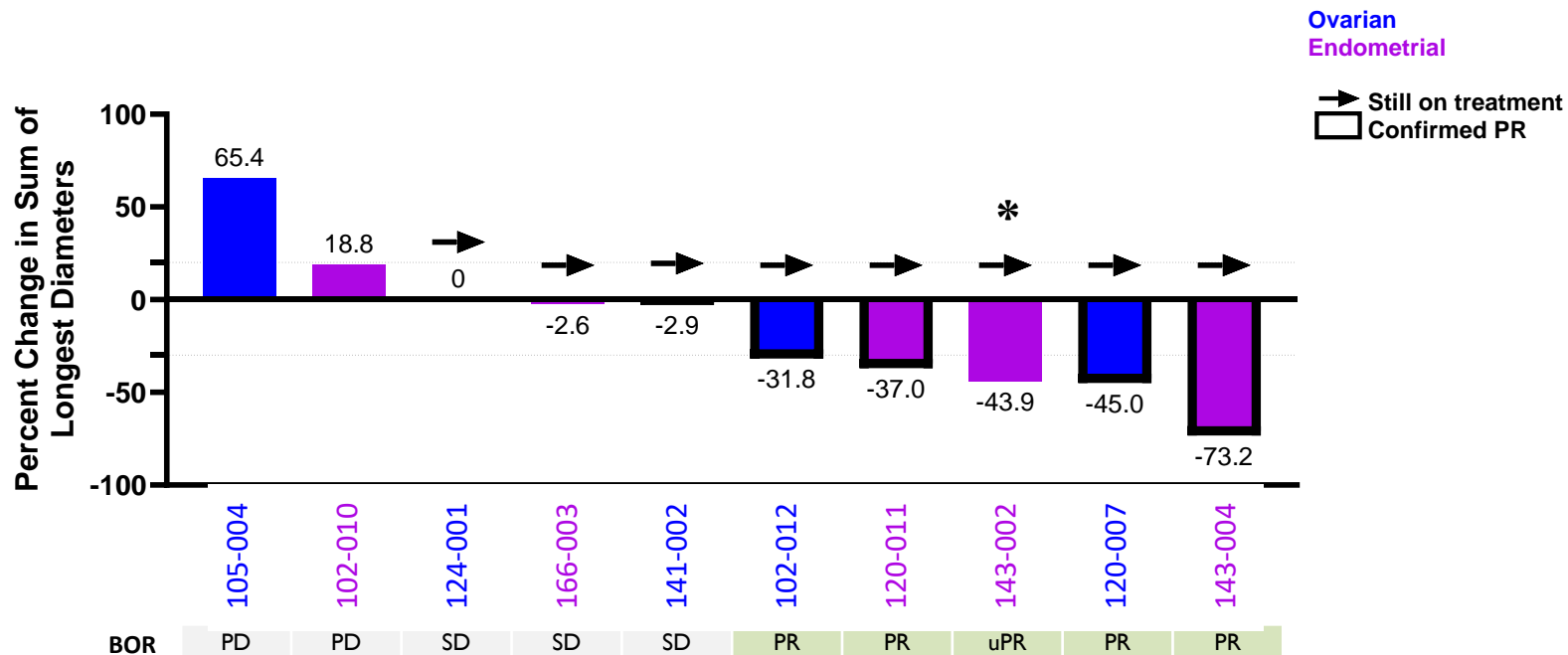


- OncoSignature-Negative
- OncoSignature-Positive



OncoSignature-positive rate =34%, consistent with predicted ~35% based on patient tumor sample OncoSignature screening prior to clinical trial

ONCOSIGNATURE+ GYN PATIENTS – TUMOR SHRINKAGE (LOCKED THRESHOLDS, PROSPECTIVE EVALUATION PER PROTOCOL)



*Since data cut off, the one unconfirmed PR has been confirmed bringing the total confirmed PRs to 5

BOR = Best overall response

Data cut as of April 1, 2024

ONCOSIGNATURE-POSITIVE PHASE 2 MONOTHERAPY GYN SUMMARY- PROSPECTIVE DATA WITH LOCKED THRESHOLDS

	Ovarian	Endometrial	Total
OncoSignature Positive (Arm 1)			
PR (confirmed)	2	3	5
SD	2	1	3
PD	1	1	2
Total	5	5	10
ORR	40%	60%	50%

-Ovarian: The 95% CI[^] for ORR = (12%, 77%). For reference, ovarian SOC ~12%.

-Endometrial: The 95% CI[^] for ORR = (23%, 88%). For reference, endometrial SOC ~ 9%

All 5 confirmed responders on treatment; median DoR not reached

[^] Agresti-Coull

ACR-368 ONCOSIGNATURE PROSPECTIVELY PREDICTS SENSITIVITY TO MONOTHERAPY IN ONGOING PHASE 2 TRIAL

ORR	BM+ (ARM 1) ACR-368 monotherapy	BM- (ARM 2) ACR-368 + ULDG	Patients (N)
Ovarian	40% (2/5)	0% (0/11)	16
Endometrial	60% (3/5)	0% (0/5)	10
Combined	50% (5/10)	0% (0/16)	26

P value (confirmed PRs) = 0.0038

Notes:

- (non-parametric bootstrap simulation and Fisher test BM+ vs BM-)
- **ORR in ovarian all-comer = 12.5%, which is consistent with JTJN study (12%)**

Data cut as of April 1, 2024

ENDOMETRIAL CANCER IS AN AP3-PREDICTED TUMOR TYPE

ACR-368 OncoSignature-based indication finding prior to trial entry

Sq. NSCLC

Sample ID	BM1	BM2	BM3
h001812	0.12	0.26	0.26
h001813	0.09	0.06	0.06
h001814	0.26	0.06	0.06
h001815	0.26	0.06	0.06
h001816	0.26	0.06	0.06
h001817	0.26	0.06	0.06
h001818	0.26	0.06	0.06
h001819	0.26	0.06	0.06
h001820	0.26	0.06	0.06
h001821	0.26	0.06	0.06
h001822	0.26	0.06	0.06
h001823	0.26	0.06	0.06
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h001825	0.26	0.06	0.06
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h001828	0.26	0.06	0.06
h001829	0.26	0.06	0.06
h001830	0.26	0.06	0.06
h001831	0.26	0.06	0.06
h001832	0.26	0.06	0.06
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h001844	0.26	0.06	0.06
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h001854	0.26	0.06	0.06
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Endometrial cancer

Sample ID	BM1	BM2	BM3
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h001932	0.26	0.06	0.06
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h001936	0.26	0.06	0.06
h001937	0.26	0.06	0.06
h001938	0.26	0.06	0.06
h001939	0.26	0.06	0.06
h001940	0.26	0.06	0.06
h001941	0.26	0.06	0.06
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h001945	0.26	0.06	0.06
h001946	0.26	0.06	0.06
h001947	0.26	0.06	0.06
h001948	0.26	0.06	0.06
h001949	0.26	0.06	0.06
h001950	0.26	0.06	0.06

OncoSignature-positive = 0%
(ORR in past trial: 0%)

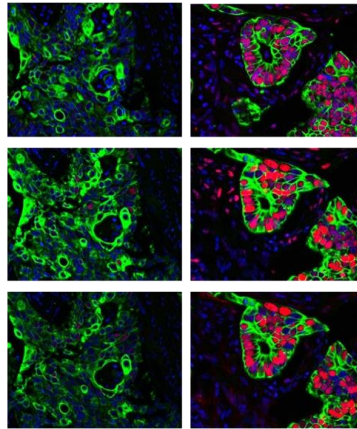
OncoSignature-positive = 30-40%

ACR-368 OncoSignature imaging demonstrates addition to CHK1/2 DDR axis

Endometrial patient samples

Patient 1 LOW

Patient 2 HIGH

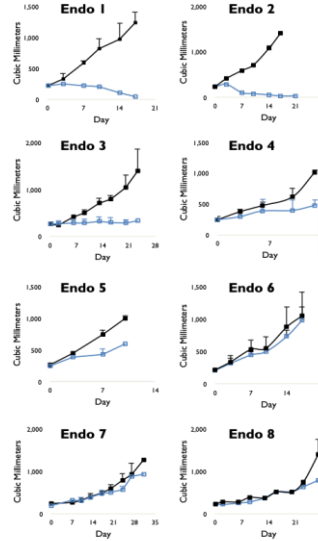


Predicted Non-Responders

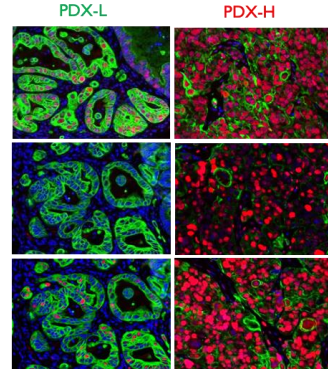
Predicted Responders

Confirmation of predicted sensitivity in genetically non-modified PDX models

Endometrial PDX



Confirmation of ACR-368 OncoSignature prediction in PDX tumor tissues pretreatment



Predicted Non-Responders

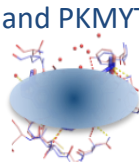
Predicted Responders

in >1,000 cancer patients treated with ACR-368 in Lilly-sponsored trials, endometrial cancer was not tested

INTERNAL PIPELINE: ADVANCING DEVELOPMENT CANDIDATE ACR-2316 AND OTHER PROGRAMS - LEVERAGING AP3

ACR-2316 and DDR programs

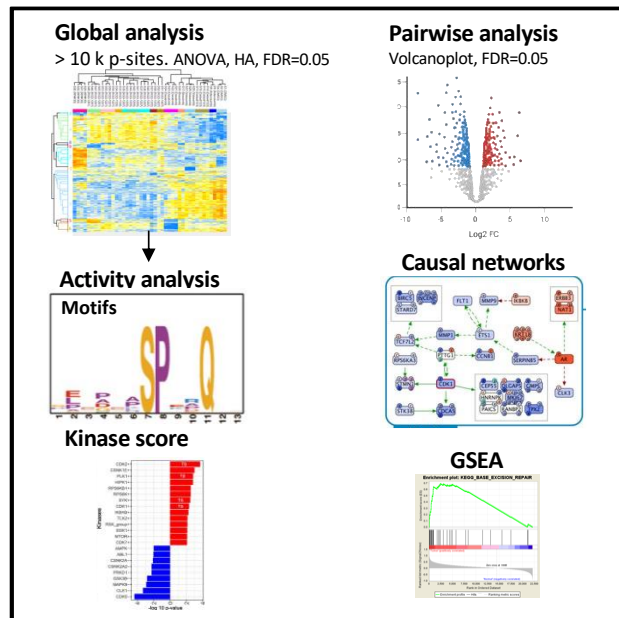
- >40 high resolution co-crystals (1.5-3.1 Å) and novel WEE1- and PKMYT1-selective structural series and lead candidates
- ACR-2316 a novel, potent, selective dual inhibitor
- Designed by AP3 to overcome WEE1 and PKMYT1 single inhibitor resistance
- IND target date Q3 2024 and trial initiation Q4 2024



Cell cycle inhibitor program with undisclosed target

- Anticipated development candidate 2025

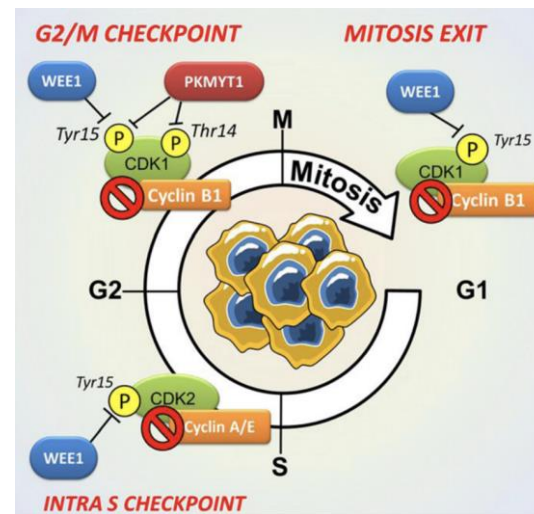
High throughput AP3 profiling



AP3 used for biologically relevant selectivity profiling

WEE1 AND PKMYT1 ARE ATTRACTIVE CANCER TARGETS: IDEAL FOR AP3 APPROACH

- WEE1 and PKMYT1 regulate S and G2-M cell cycle checkpoints to ensure proper DNA replication and mitotic completion
- Defective DNA repair is highly prevalent in cancers, creating a dependency on checkpoint proteins
- WEE1 inhibition propagates genomic instability by premature DNA replication and cell cycle progression
- PKMYT1 inhibition results in premature mitotic entry



Ghelli Luserna di Rorà et al. J. Hematol Oncol, 2020

- Several WEE1 inhibitors and a PKMYT1 inhibitor have demonstrated anti-tumor activity in clinical trials across solid tumor types
- Current clinical agents challenged by lack of predictive biomarkers and narrow therapeutic index, limiting safety and efficacy

ACR-2316 –UNIQUELY ENABLED BY AP3 TO OVERCOME LIMITATIONS OF CURRENT WEE1 AND PKMYT1 INHIBITORS

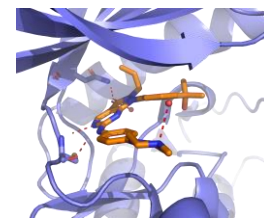
Program goals:

- **Superior single agent activity (AP3)**
 - AP3-guided design to overcome WEE1 and PKMYT1 single inhibitor resistance through balanced dual inhibition
- **High selectivity and potency (co-crystallography)**
 - Structure-guided design to limit adverse events (AEs) to be on-target, transient, mechanism-based
- **Streamlined clinical development (ACR-2316 OncoSignature)**
 - To identify/prioritize sensitive indications prior to clinical start and for drug target engagement-based dose optimization

ACR-2316: Rationally designed WEE1/PKMYT1 development candidate

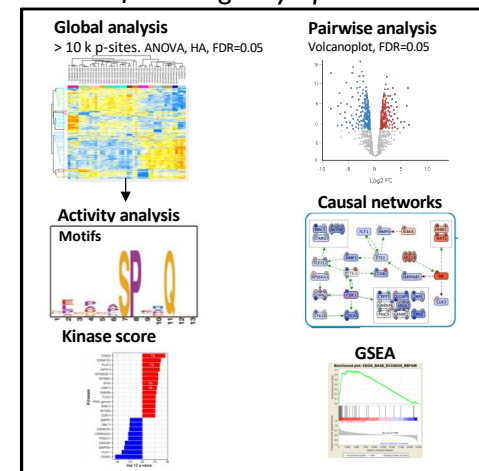
- ✓ 5-20-fold more potent in preclinical models than clinical benchmarks
- ✓ Superior anti-tumor efficacy with complete tumor regression across models
- ✓ High selectivity ensures transient, short-lived, mild AEs
- ✓ Potent WEE1 inhibition, balanced PKMYT1 inhibition, overcomes resistance

Co-crystallography for drug design and selectivity



Zhu et al, J. Med. Chem. (2017)

AP3 used for biologically optimal SAR



ACR-2316 IS A POTENTIALLY BEST-IN-CLASS AGENT RATIONALLY DESIGNED USING ACRIVON'S AP3 PLATFORM

Program Goals

- 1 Superior single agent activity
- 2 High selectivity and potency
- 3 Favorable safety profile
- 4 Streamlined clinical development

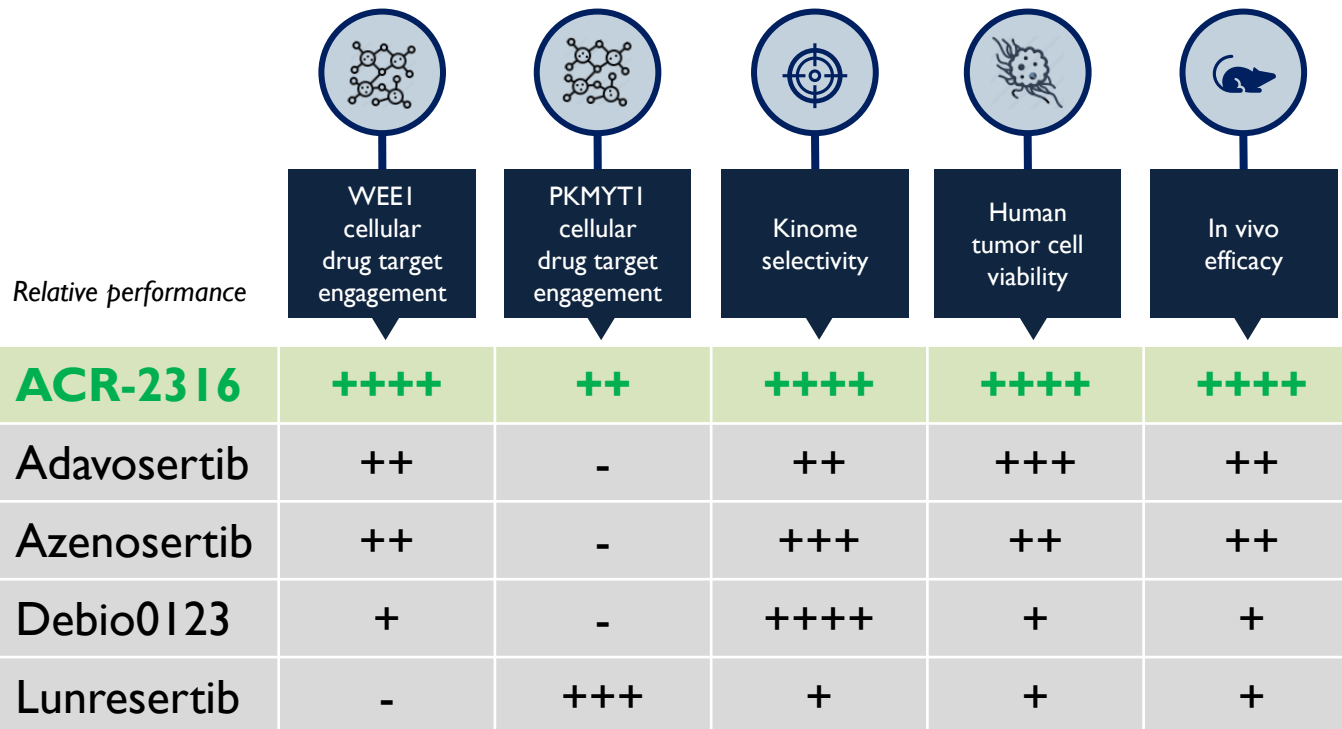
AP3-Enabled SAR

Demonstrated Preclinical Results

- Superior* single agent anti-tumor activity through robust CDKI, CDK2, and PLKI activation and elimination of dominant resistance mechanisms through balanced WEE1 and PKMYT1 inhibition
- 5-20-fold more potent* in preclinical models than clinical benchmarks
- High selectivity results in adverse events limited to transient, short-lived, mechanism-based, reversible
- Broad preclinical therapeutic index and anti-tumor activity across dosing regimens
- AP3-based identification of PD biomarkers and prioritization of promising indications

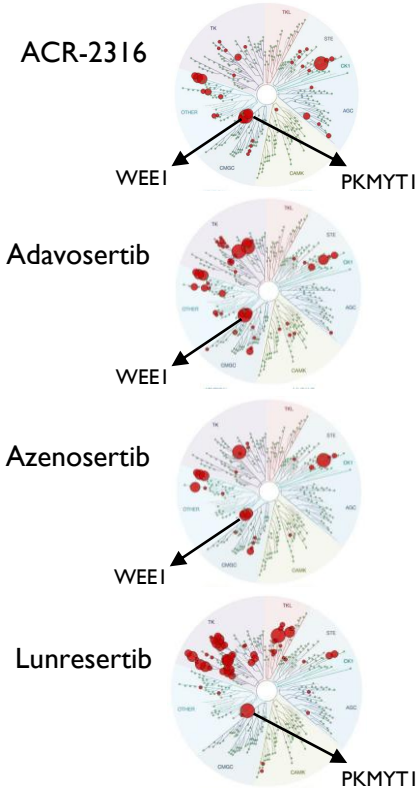
*Head-to-head preclinical studies against benchmarks with clinical data

ACR-2316 SHOWS ATTRACTIVE PROFILE IN ONGOING PRECLINICAL STUDIES

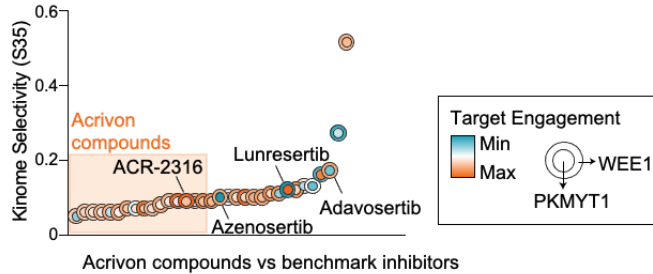


DUAL WEE1/PKMYT1 INHIBITOR ACR-2316 DEMONSTRATES STRONG POTENCY AND SELECTIVITY

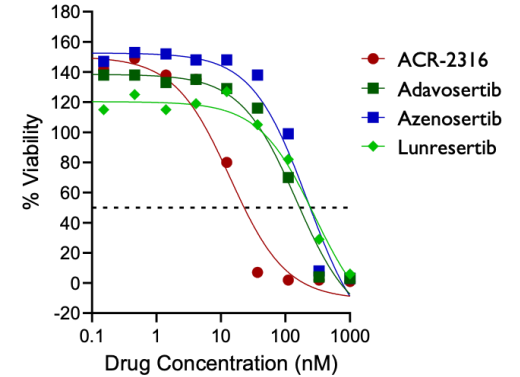
KinomeScan (468 kinases @ 1 μ M)



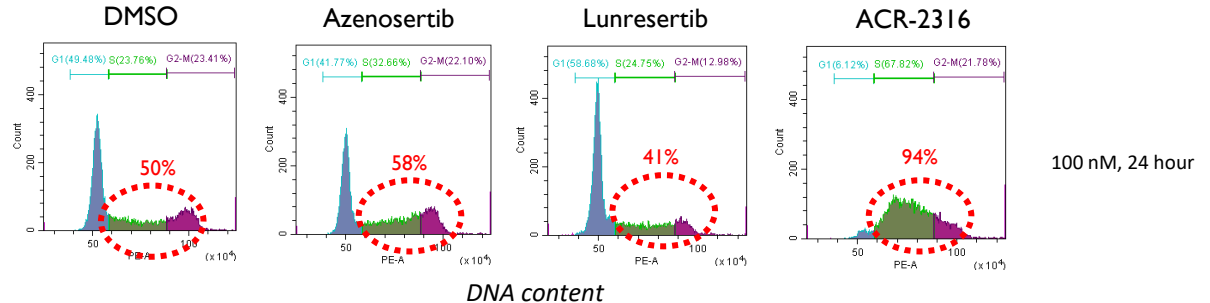
ACR-2316 is highly selective (KinomeScan)



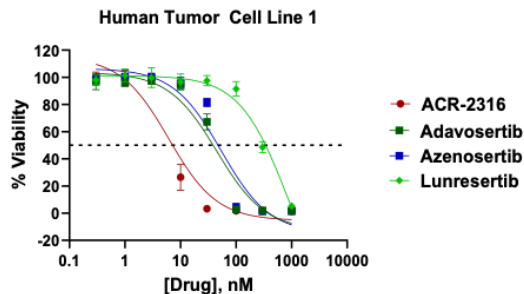
ACR-2316 potently inhibits cancer cell viability



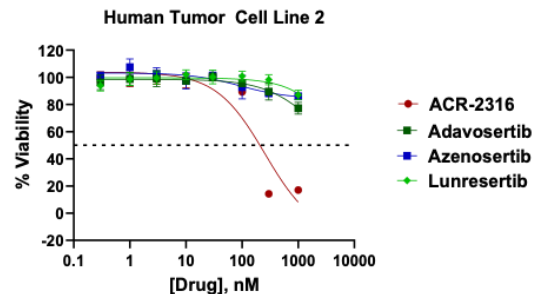
ACR-2316 exerts potent cell cycle effects with pronounced S-G2/M accumulation



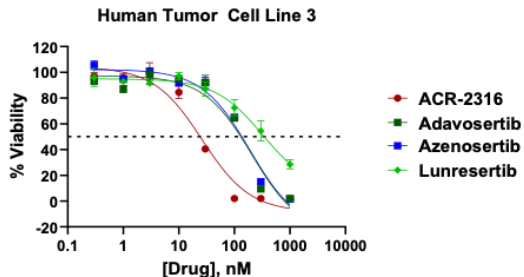
ACR-2316 SHOWS SUPERIOR ACTIVITY VS BENCHMARKS ACROSS ALL HUMAN TUMOR CELL LINES TESTED



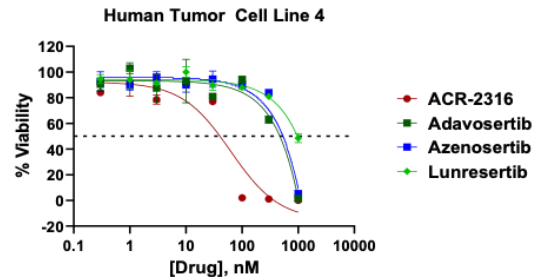
ACR-2316 IC50 (nM)	Adavosertib IC50 (nM)	Azenosertib IC50 (nM)	Lunresertib IC50 (nM)
7	39	47	340



ACR-2316 IC50 (nM)	Adavosertib IC50 (nM)	Azenosertib IC50 (nM)	Lunresertib IC50 (nM)
207	> 1000	> 1000	> 1000



ACR-2316 IC50 (nM)	Adavosertib IC50 (nM)	Azenosertib IC50 (nM)	Lunresertib IC50 (nM)
24	130	136	345



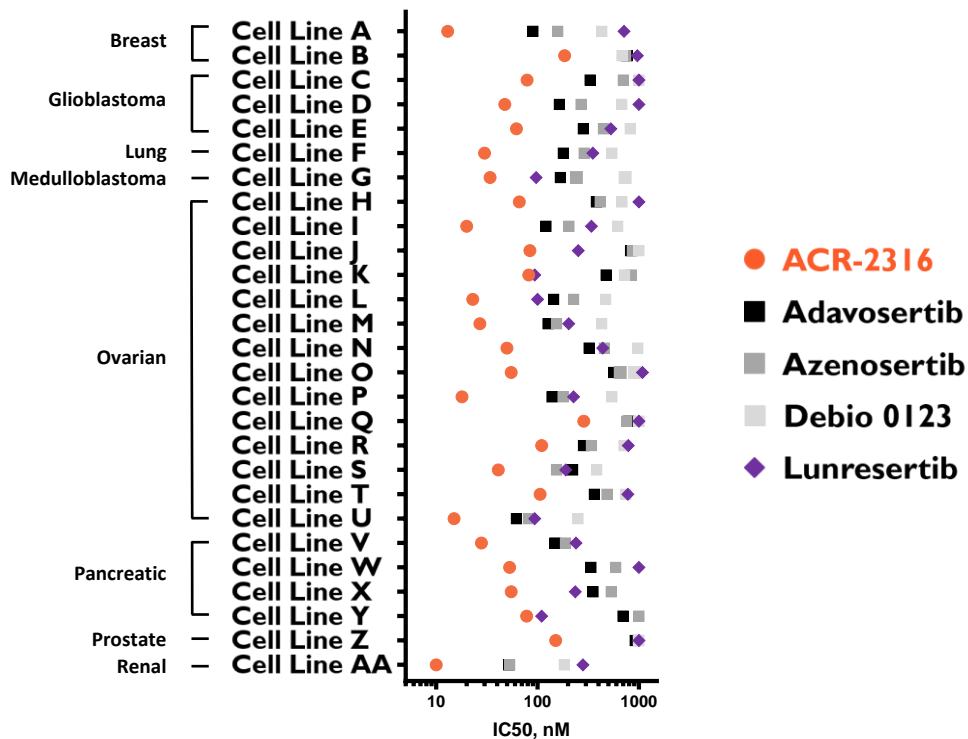
ACR-2316 IC50 (nM)	Adavosertib IC50 (nM)	Azenosertib IC50 (nM)	Lunresertib IC50 (nM)
40	471	533	967

Example: Ovarian human cancer cell lines

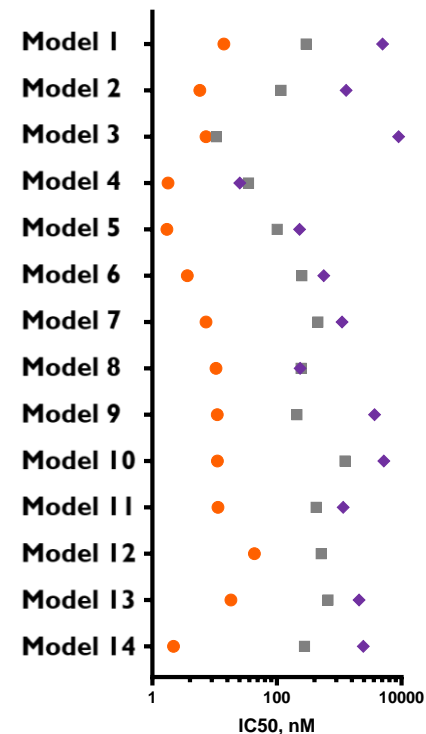
19 ovarian and other human tumor cell lines tested to date

ACR-2316 IS HIGHLY POTENT ACROSS HUMAN TUMOR CELL LINES AND PATIENT-DERIVED *EX VIVO* TUMOR MODELS

Human tumor cell lines

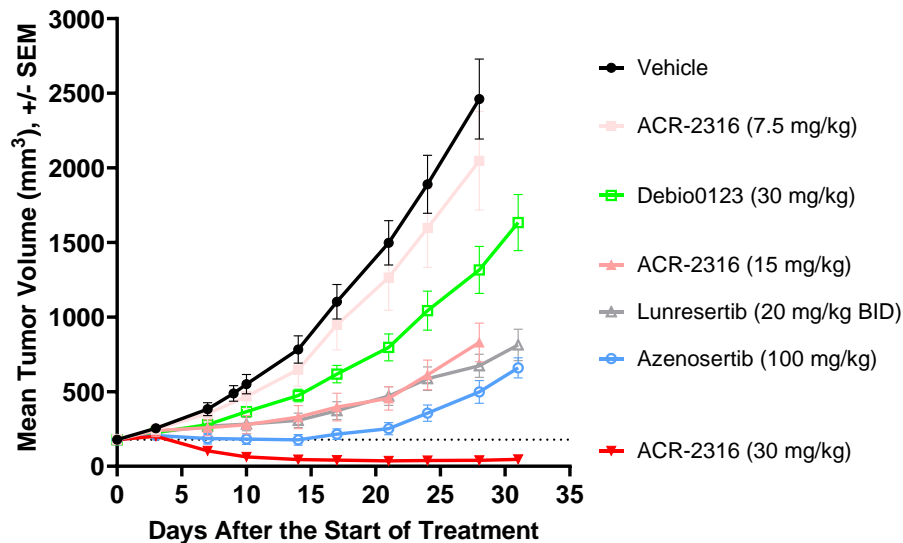


Patient-derived ex vivo tumor models

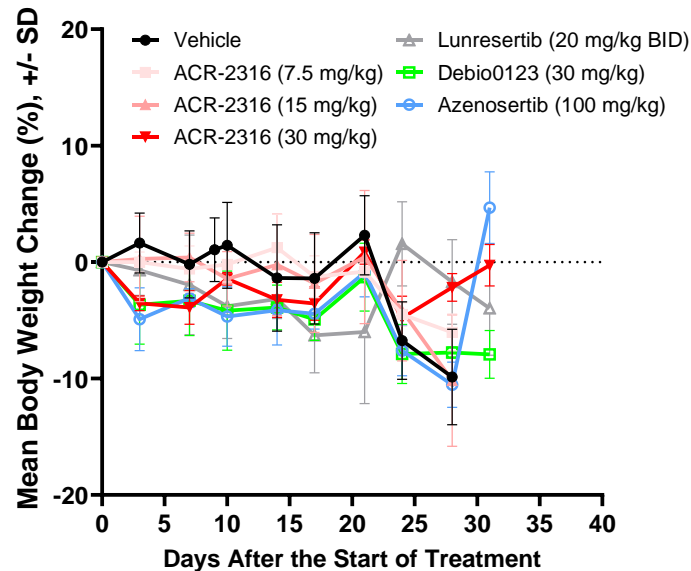


ACR-2316 SHOWS POTENT ANTI-TUMOR ACTIVITY COMPARED TO CLINICAL WEE1 OR PKMYTI INHIBITORS – MODEL 1

Efficacy (5d on/2d off)

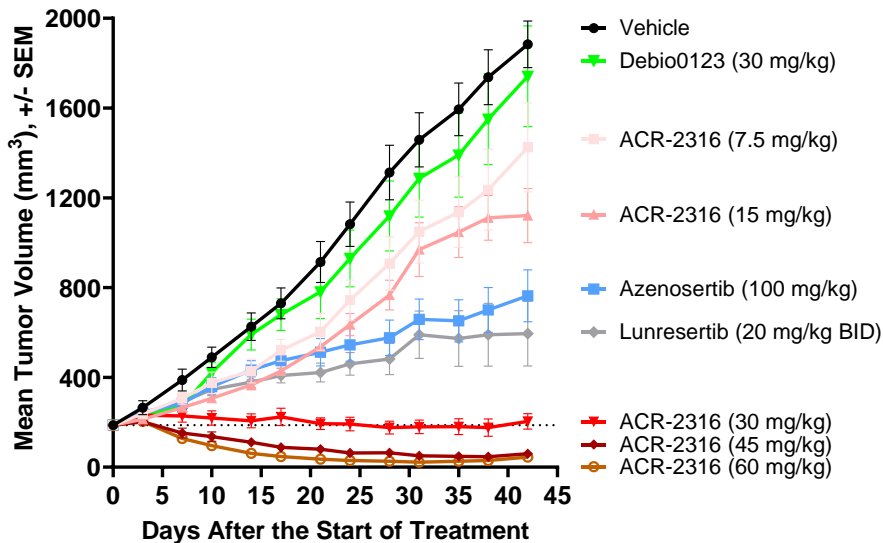


Tolerability (5d on/2d off)

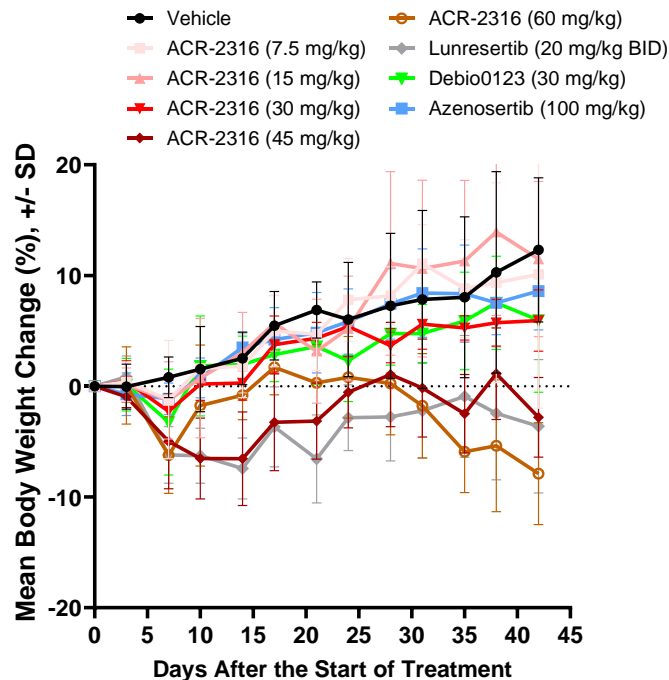


ACR-2316 SHOWS POTENT ANTI-TUMOR ACTIVITY COMPARED TO CLINICAL WEE1 OR PKMYTI INHIBITORS – MODEL 2

Efficacy (5d on/2d off)

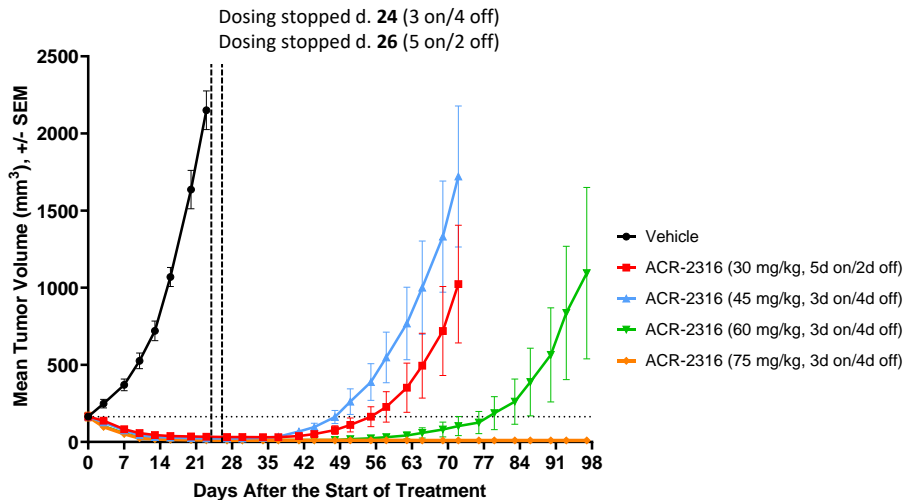


Tolerability (5d on/2d off)

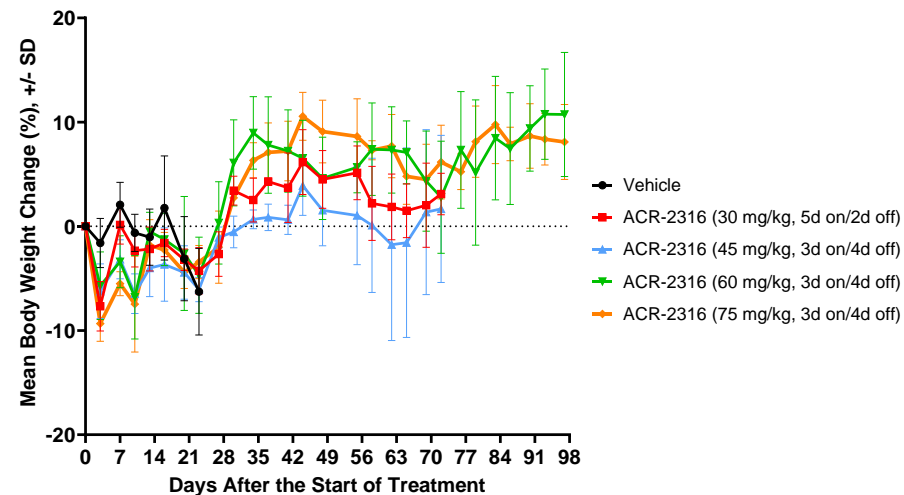


ACR-2316 LEADS TO POTENT AND DURABLE TUMOR REGRESSION

Efficacy

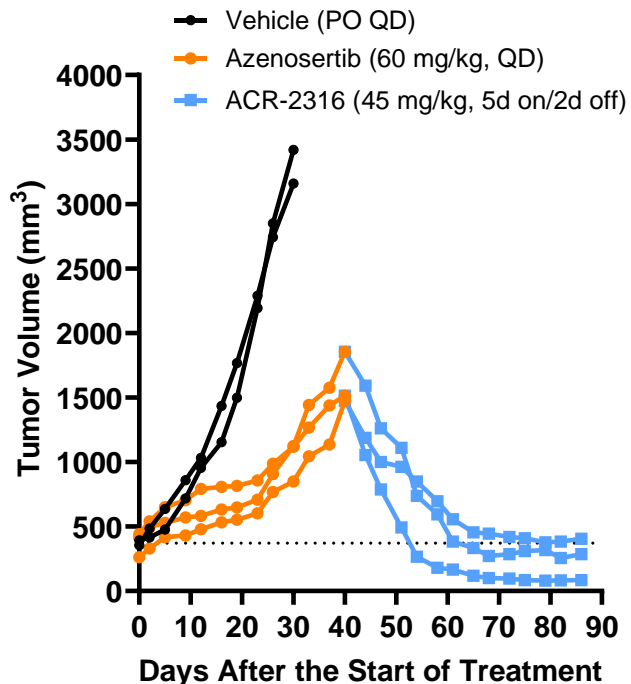


Tolerability

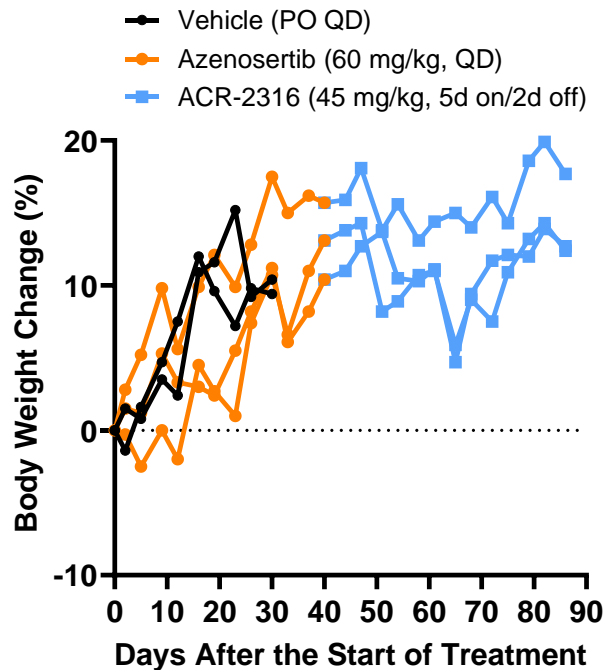


ACR-2316 SHOWS DEEP REGRESSION IN TUMORS PROGRESSING ON A BENCHMARK WEE1 INHIBITOR

Anti-tumor activity

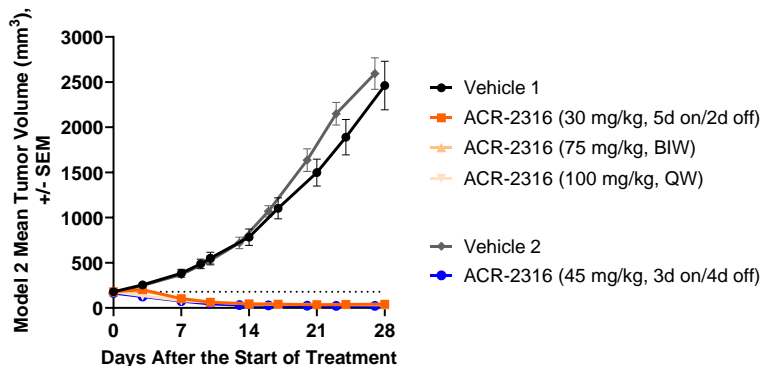
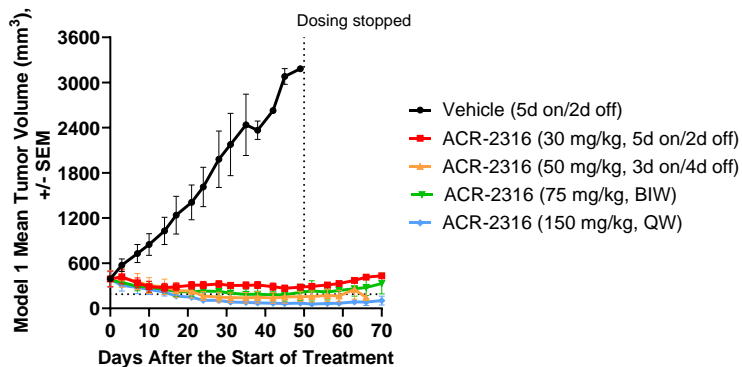


Tolerability

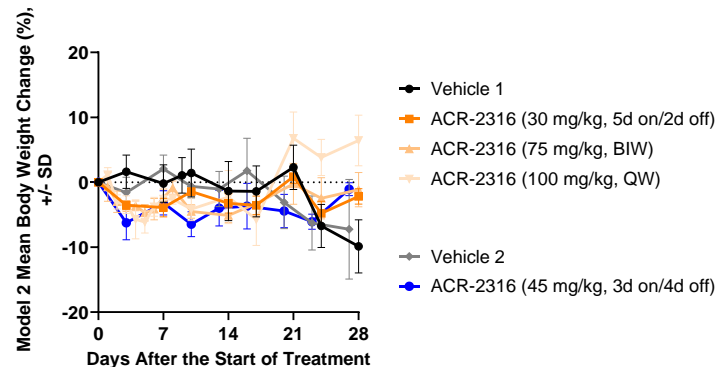
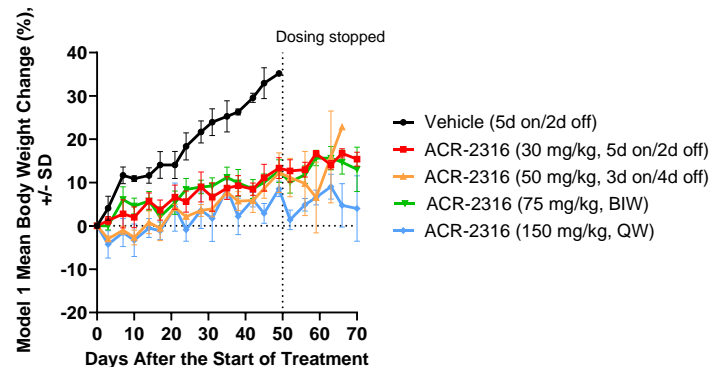


STRONG ACR-2316 EFFICACY DEMONSTRATED ACROSS BROAD RANGE OF DOSING REGIMENS AND MODELS

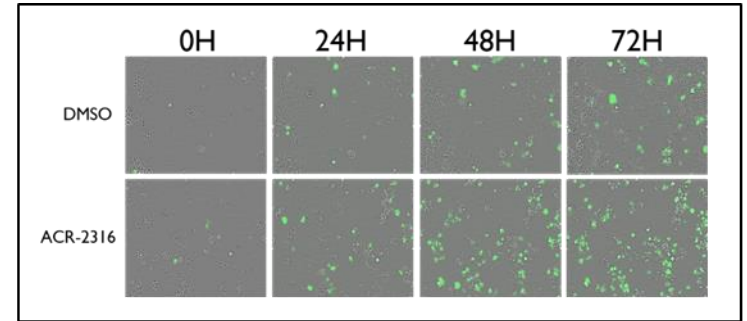
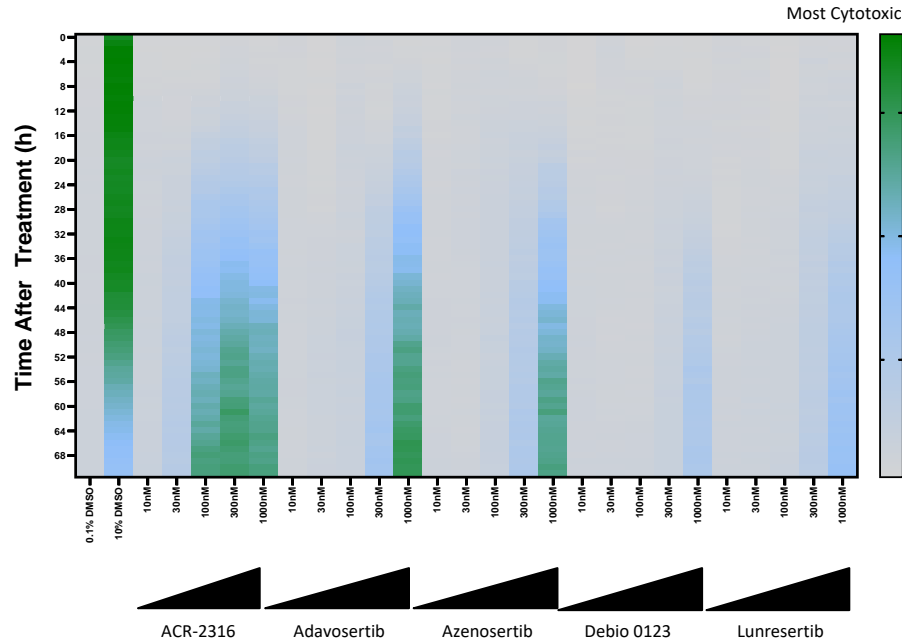
Efficacy



Tolerability



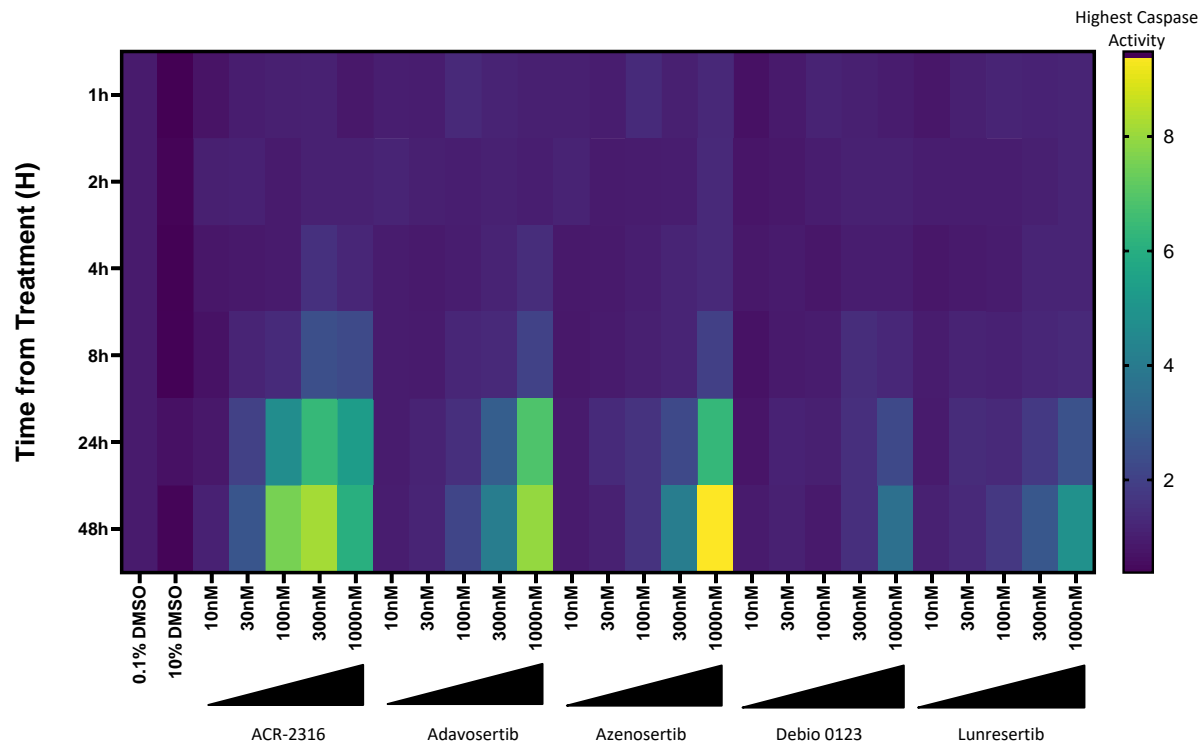
ACR-2316 INDUCES POTENT CELL DEATH COMPARED TO BENCHMARK WEE1 AND PKMYTI INHIBITORS



Representative images of OVCAR3 cells treated with 0.1% DMSO or 100 nM ACR-2316 (green fluorescence = dead cells)

CellTox-Green Assay

ACR-2316 INDUCES POTENT CASPASE 3/7 CLEAVAGE COMPARED TO BENCHMARK WEE1 OR PKMYTI INHIBITORS



Caspase 3/7-Glo Assay (OVCAR3 Cells)

ACR-2316 - FAVORABLE PRECLINICAL SAFETY PROFILE

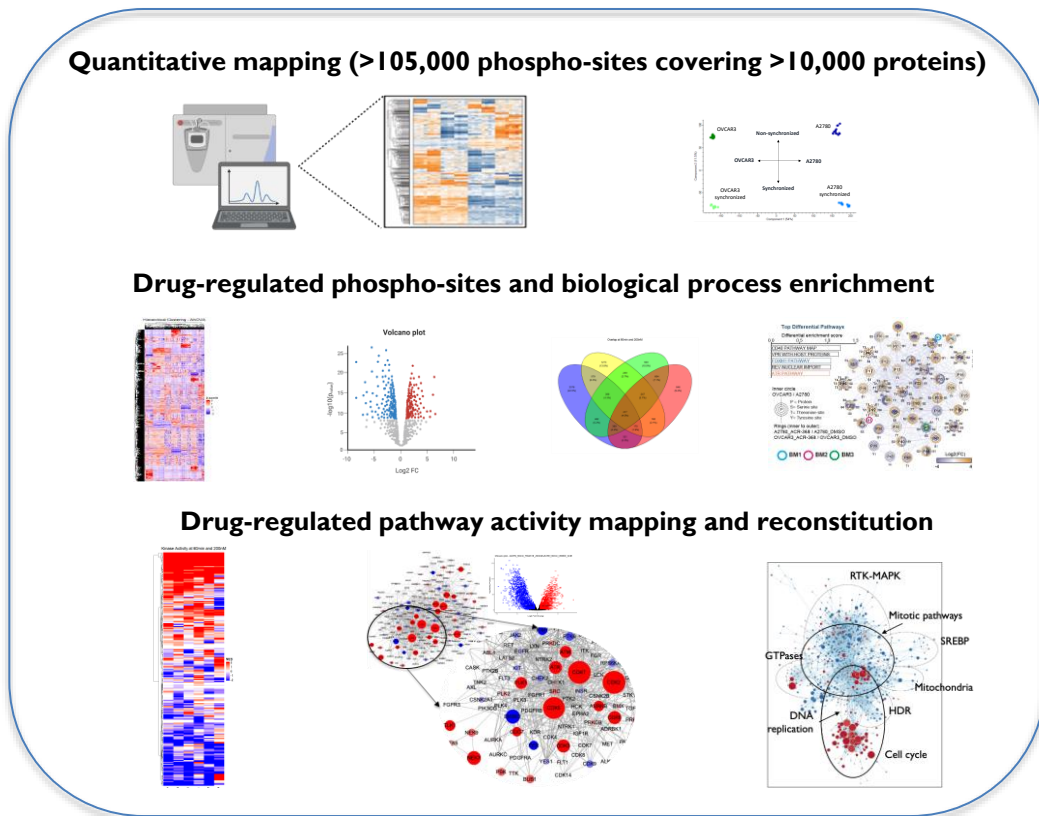
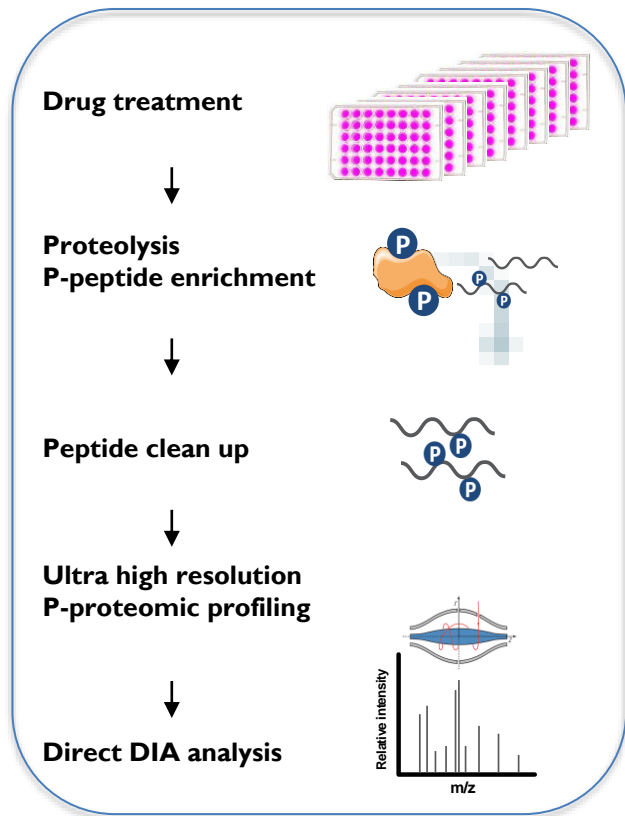
Mice:

- ACR-2316 is well-tolerated, resulting in tumor regression in xenograft mouse models at multiple dosing regimens (qw, 2qw, 3d on/4d off, 5d on/2d off, and qd)
- Transient, reversible, mechanism-based hematological adverse events

Rat and dog MTD, DRF, and GLP tox studies:

- MTD \geq 30 mg/kg in both species (single dose)
- GLP tox studies (31 days) completed in rat and dog with the planned human dosing regimen achieving exposure required for tumor regression
- Minimal hematological effects in rats, except for mechanism-based transient, fully reversible reticulocytopenia between dosing cycles
- Mechanism-based, reversible food/GI effect in dogs, not impeding weight gain

STREAMLINED AP3-BASED BIOLOGICAL SAR OPTIMIZATION FOR SINGLE AGENT ACTIVITY OF PRECLINICAL PROGRAMS



High resolution and throughput MS-based P-proteomics

Proprietary pipe for automated AP3 analyses with actionable results

AP3: TIGHT, HIGH-RESOLUTION DATA WITH DEEP COVERAGE

35388 p-sites

15733 p-sites

QC MS Data

Data Clean Up

QC Processed Data

Volcano Plots

Hierarchical Clustering

Consensus Sequence Motif

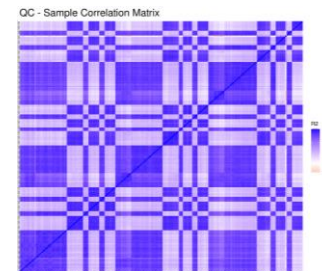
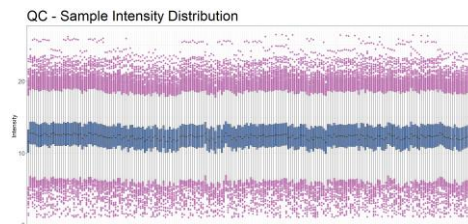
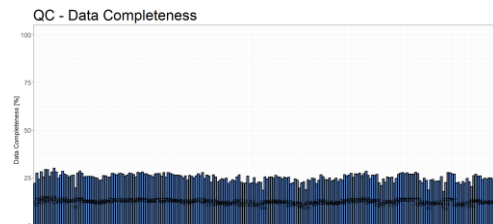
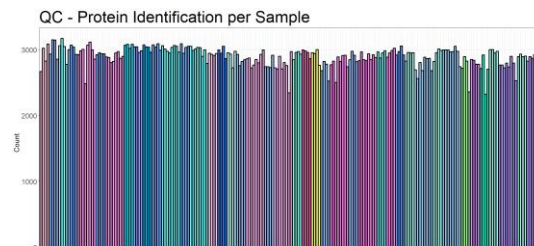
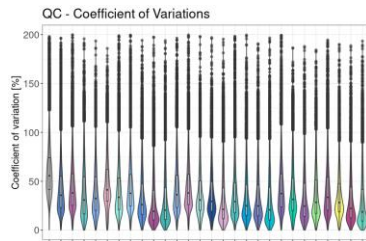
Kinase Inference

Pathway Enrichment

Functional Annotation

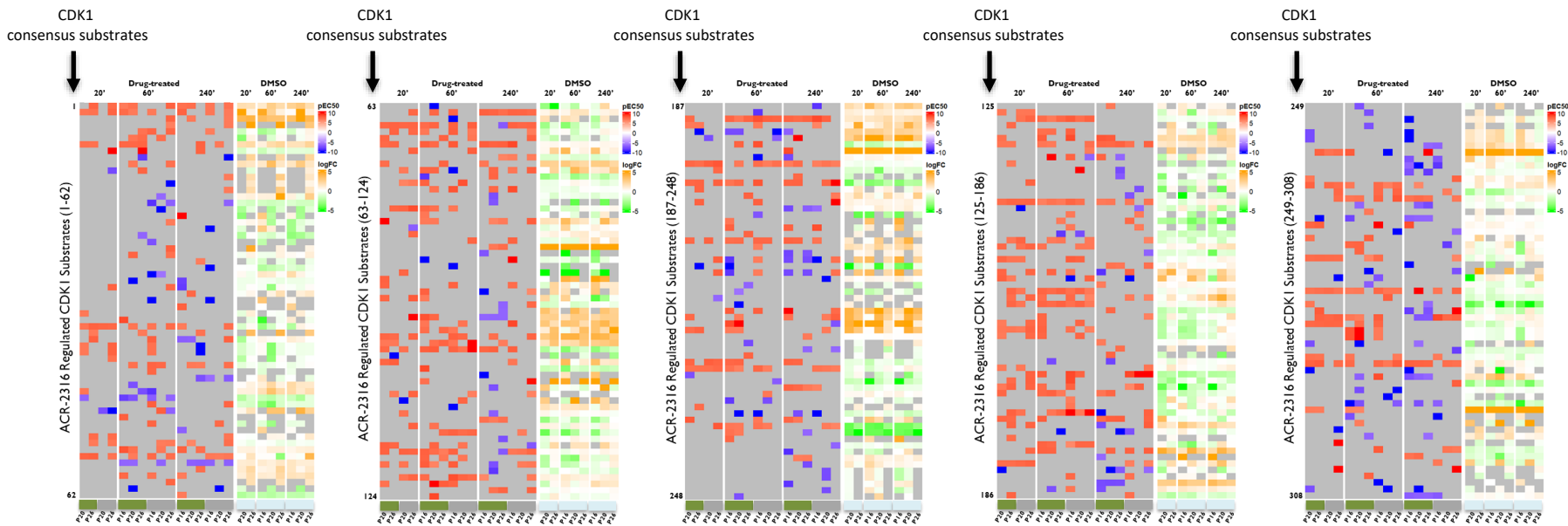
Network Mapping

Biomarkers



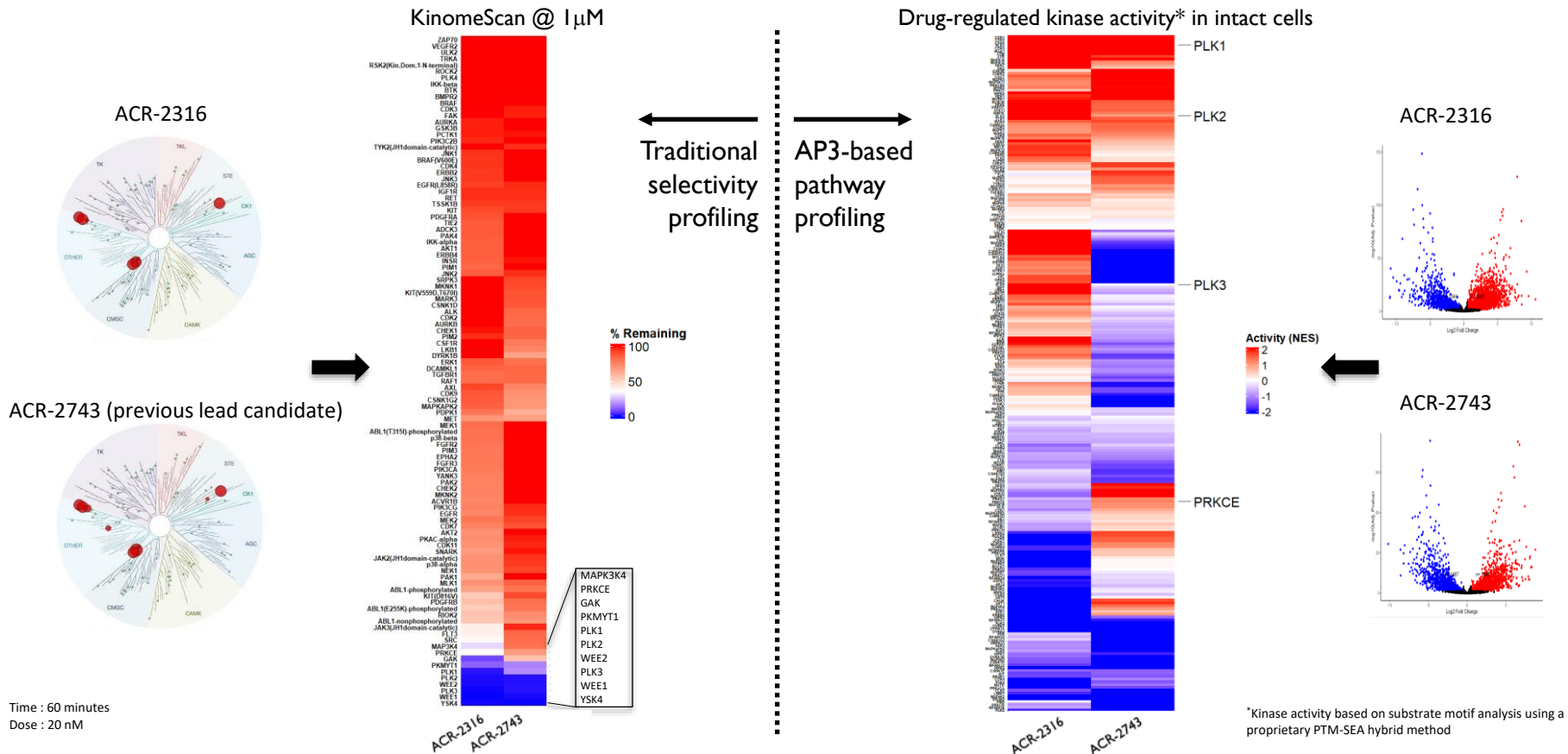
- ✓ Acrivon proprietary compound data (~50 million data points per experiment); dozens of compounds profiled
- ✓ Miniaturized, high throughput, scalable: <2 weeks turn-around, automated AI computational analyses in 1 day
- ✓ Actionable results: Resistance mechanisms, rational combinations, drug-tailored OncoSignature patient selection

ACR-2316 RESULTS IN STRONG ACTIVATION OF CDK1 ACROSS CELL LINES



- Unbiased quantitation of ACR-2316-regulated CDK1 substrate p-sites (308) in intact cells based on CDK1 consensus recognition motif (Acrivon proprietary hybrid database approach) across multiple experiments
- Actionable insight into drivers of mitotic catastrophe and on-target CDK1-driven pathways

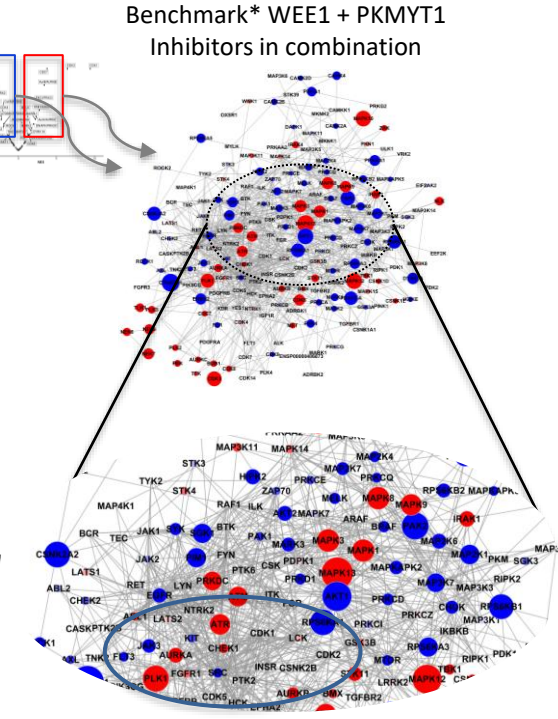
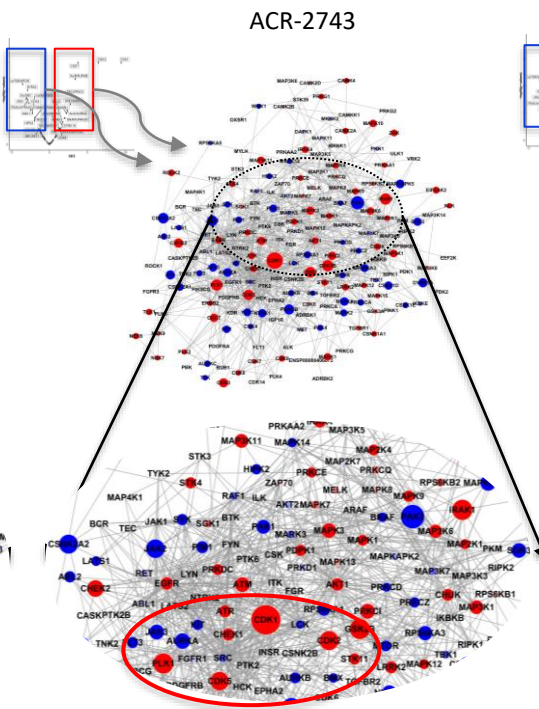
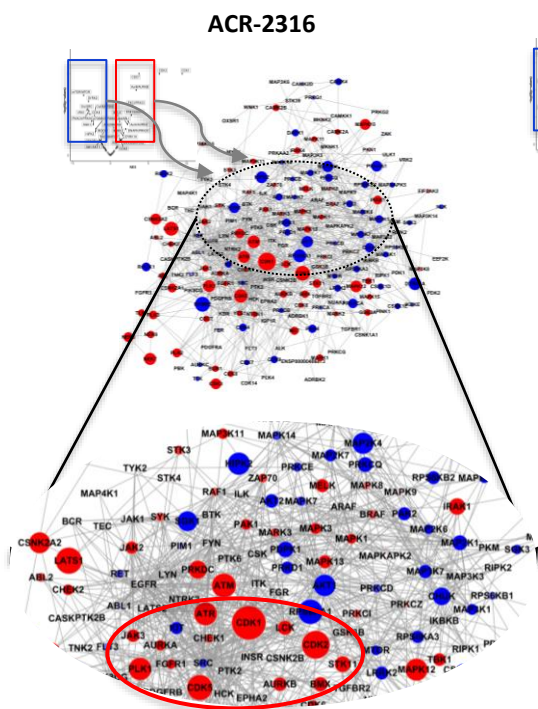
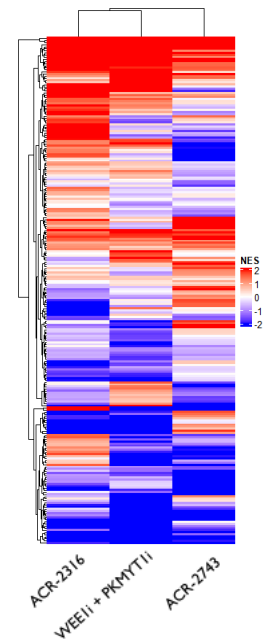
AP3 REVEALS DRUG-REGULATED KINASE ACTIVITY IN INTACT CELLS NOT DETECTABLE BY STANDARD METHODS



OPTIMIZED DUAL INHIBITORS SHOW DESIRABLE PATHWAY EFFECTS

Optimized dual WEE1 and PKMYT1 inhibitors affect cell cycle and canonical MAPK pathways in desirable manner

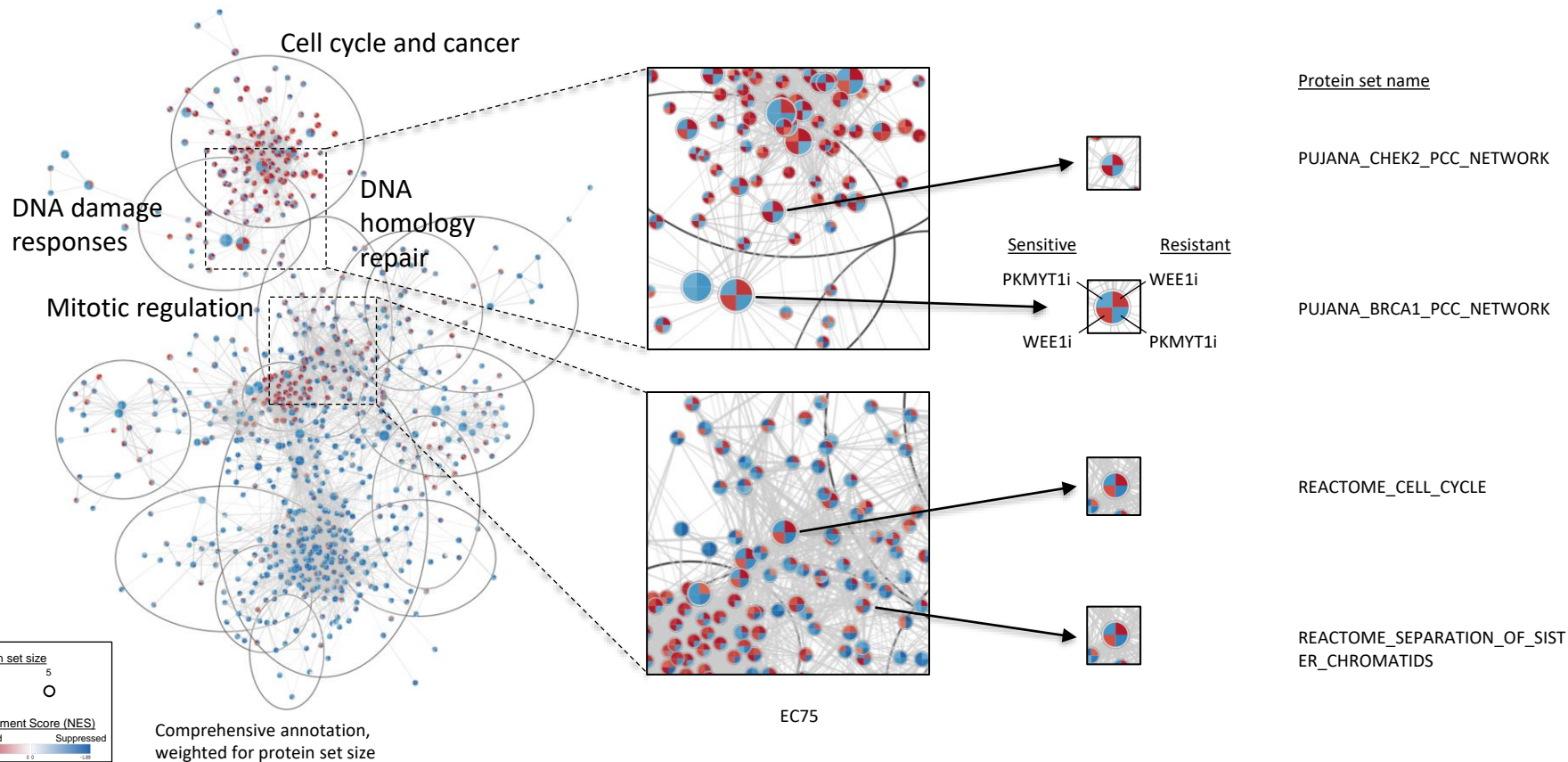
Substrate motif-inferred kinase activities



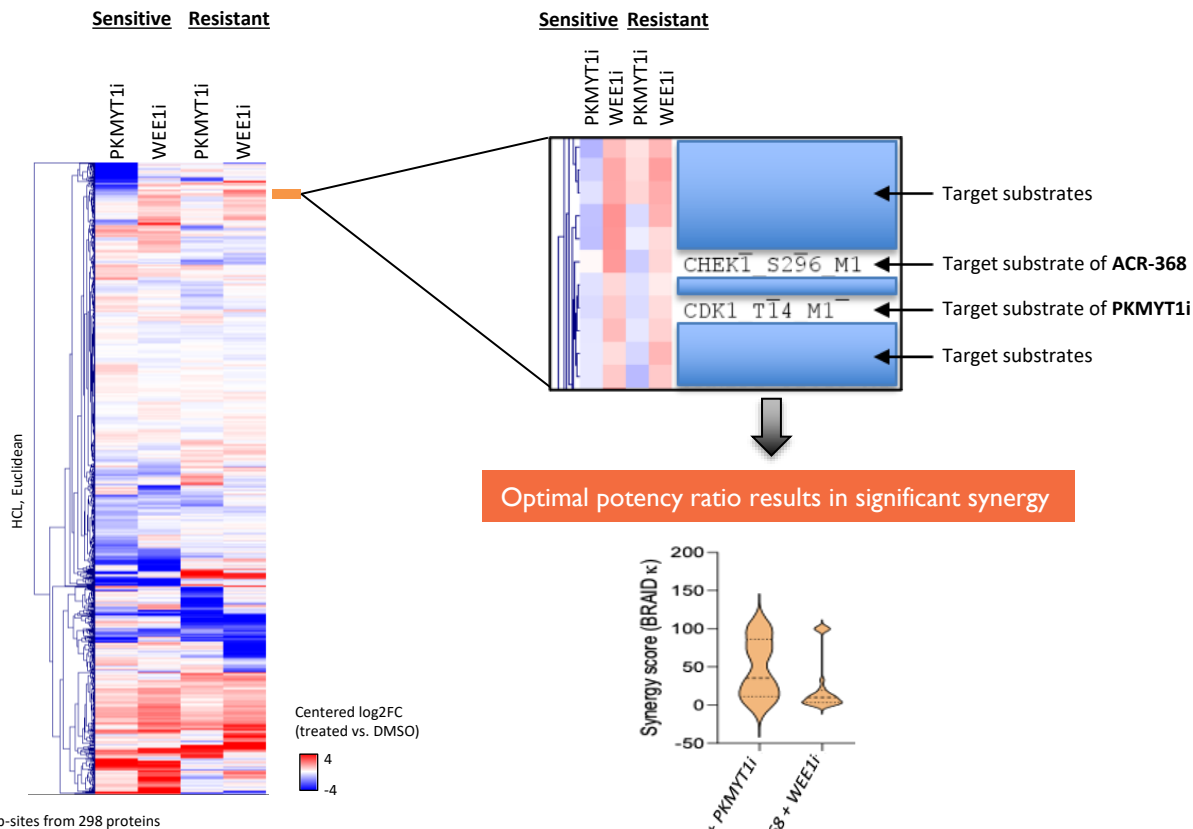
Kinase activity based on proprietary PTM-SEA-based hybrid workflow and analyses

*Clinical-stage selective WEE1 and PKMYT1 inhibitors

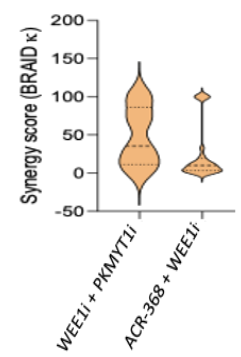
AP3-DERIVED DUAL POTENCY OPTIMIZATION TO OVERCOME WEE1 INHIBITOR RESISTANCE: RECIPROCAL QUENCHING



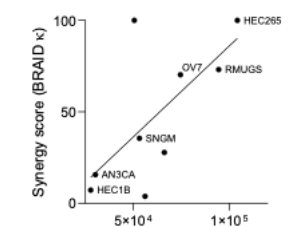
AP3 RECIPROCAL QUENCHING REVEALS OPTIMAL TARGET POTENCY PROFILE FOR DUAL WEE1/PKMYT1 INHIBITOR



Optimal potency ratio results in significant synergy

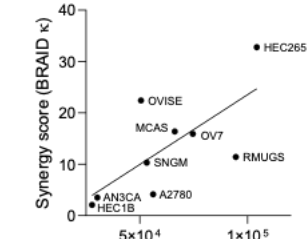


WEE1i and PKMYT1i dual inhibition synergy



WEE1 inhibitor sensitivity (Mean AUC)
Pearson $r = 0.68$
p value = 0.0459

WEE1i and ACR-368



WEE1 inhibitor sensitivity (Mean AUC)
Pearson $r = 0.71$
p value = 0.0324

EXPEDITING ACR-2316 TOWARDS CLINICAL MONOTHERAPY DEVELOPMENT

A novel, AP3-enabled, internally discovered dual WEE1 / PKMYTI inhibitor

Rational Design



- Optimized via AP3
- AP3-enabled design for optimized single agent activity

Superior Profile



- Potent anti-tumor activity across human tumor cell lines and in tumor-bearing mice vs benchmarks

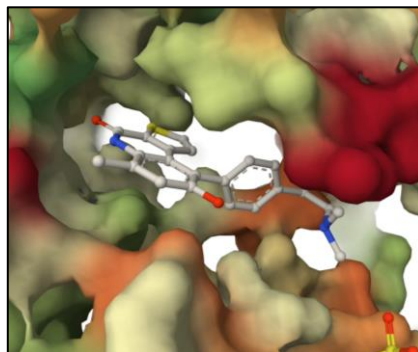
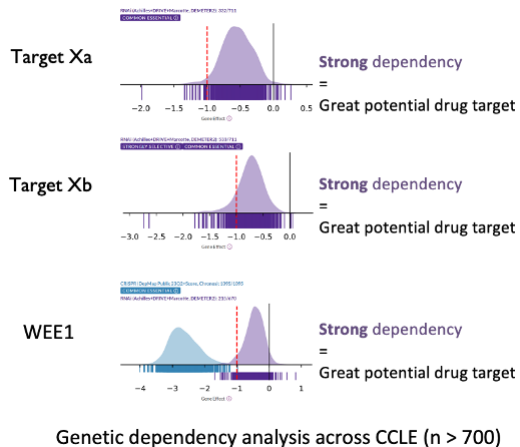
Streamlined Development



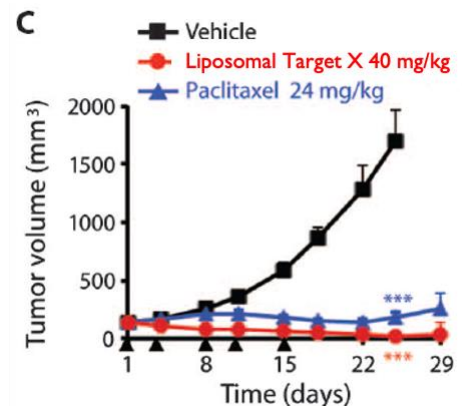
- Rapidly advancing towards IND in Q3 2024, aiming for monotherapy development
- OncoSignature development for indication finding
- Dose optimization to be guided by drug target engagement (BM2)

CELL CYCLE REGULATORY PIPELINE PROGRAM (UNDISCLOSED TARGET)

- Target X – an exciting cancer drug target, no/minimal competitor programs, perfectly suited for AP3 platform
- DepMap data suggest suggest target X is an essential gene for cancer cell viability
- Strong mechanistic target rationale for role in oncogenesis
- Highly selective tool compound shows strong anti-tumor efficacy in rodent models
- Tool compound AP3 profiling supports selectivity
- New preclinical program leveraging co-crystallography and AP3 infrastructure successfully built for ACR-2316



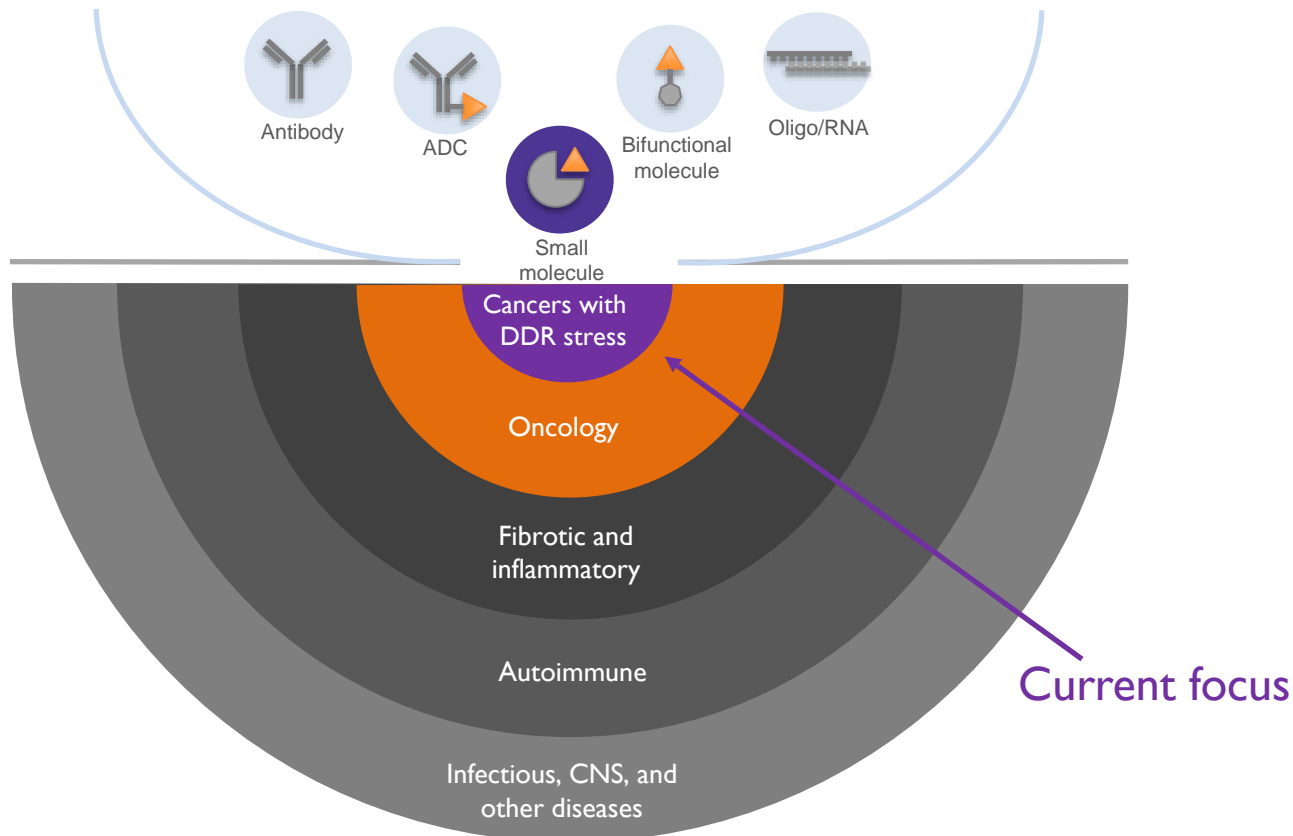
Tool compound is a selective target X inhibitor (originally believed to be inhibitor for another target)



Development candidate 2025

THE AP3 APPROACH IS MODALITY AND DISEASE AGNOSTIC

Therapeutic modalities



FINANCIAL HIGHLIGHTS

Cash and marketable securities

\$220.4M

Balance sheet
30-June-2024

Projected runway into

H2'26

Current operating plan, assuming
no additional financing

Fully Diluted Shares Outstanding

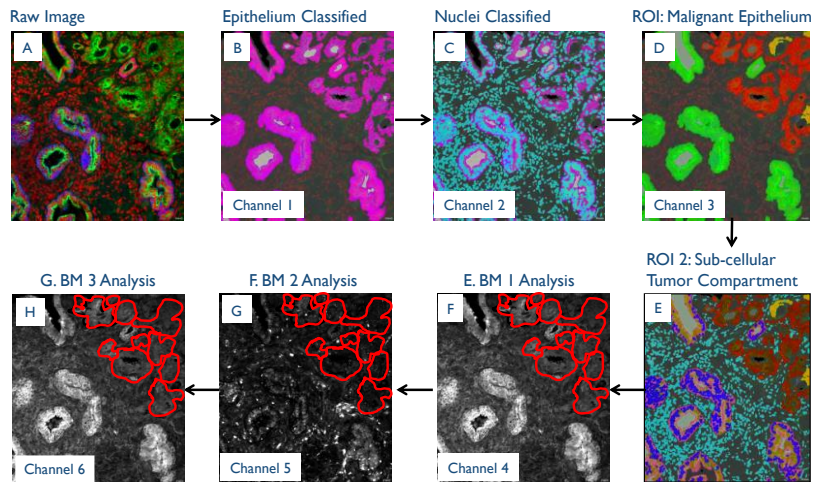
43.9M

Including shares, pre-funded
warrants and equity grants
outstanding 30-June-2024

APPENDIX

TEAM HAS PIONEERED OUTCOME-PREDICTIVE QUANTITATIVE PROTEOMIC MULTIPLEX IN SITU TEST

Prostate cancer 8-marker biopsy test developed and launched by Founding team



- **ProMark®:** Marketed, automated *in situ* proteomic test for human outcome prediction included under NCCN guidelines
- **Founding team:** Has pioneered p-proteomics and quantitative multiplex imaging including double-blinded clinical validation*

Ideal test	Protein multiplex <i>in situ</i> test	Current CDx tests
Quantitative and automated	✓	(✓)
Validated Abs and reagents	✓	(✓)
Drug target and pathway activation context	✓	
Biomarkers measured in relevant region on tumor biopsy	✓	
Imaging algorithm (tissue pattern)	✓	
Addresses tumor heterogeneity	✓	
Double-blinded, prospective validation	✓	(✓)

*Blume-Jensen et al: Development and clinical validation of an *in situ* biopsy-based multimarker assay for risk stratification in prostate cancer. Clinical Cancer Research (2015)

PROOF-OF-CONCEPT FOR PROTEIN BIOMARKER SIGNATURE: MARKETED, OUTCOME-PREDICTIVE MULTIPLEX CANCER TEST

Biology of Human Tumors

Clinical
Cancer
Research

Development and Clinical Validation of an *In Situ* Biopsy-Based Multimarker Assay for Risk Stratification in Prostate Cancer

(2015)

Peter Blume-Jensen¹, David M. Berman², David L. Rimm³, Michail Shipitsin¹, Mathew Putzi⁴, Thomas P. Nifong¹, Clayton Small¹, Sibgat Choudhury¹, Teresa Capela¹, Louis Coupal⁵, Christina Ernst¹, Aeron Hurley¹, Alex Kaprelyants¹, Hua Chang¹, Eldar Giladi¹, Julie Nardone¹, James Dunyak¹, Massimo Loda⁶, Eric A. Klein⁷, Cristina Magi-Galluzzi⁸, Mathieu Latour⁹, Jonathan I. Epstein¹⁰, Philip Kantoff⁶, and Fred Saad⁹

- Third-party blinded clinical validation, bioinformatic analysis (U. Montreal)
- Validation of locked ProMark™ test on single institution biopsy cases (N=274)
- Secondary validation on multi-center biopsy cohort (N=359) for clinical use indication
- Marketed test included under NCCN Guidelines and Medicare coverage

PIONEERING PHOSPHO-PROTEOMICS STUDY IDENTIFIES NOVEL PI3'K PATHWAY INHIBITOR BIOMARKERS

Science
Translational
Medicine



Sci Transl Med
2: 1-14 (2010)

RESEARCH ARTICLE

CANCER DRUG DEVELOPMENT

Pathway-Based Identification of Biomarkers for Targeted Therapeutics: Personalized Oncology with PI3K Pathway Inhibitors

Jannik N. Andersen,^{1*} Sriram Sathyanarayanan,^{1*} Alessandra Di Bacco,¹ An Chi,¹ Theresa Zhang,¹ Albert H. Chen,¹ Brian Dolinski,¹ Manfred Kraus,¹ Brian Roberts,¹ William Arthur,² Rich A. Klinghoffer,^{1†} Diana Gargano,^{1‡} Lixia Li,¹ Igor Feldman,¹ Bethany Lynch,¹ John Rush,³ Ronald C. Hendrickson,^{4§} Peter Blume-Jensen,^{1§||} Cloud P. Paweletz¹

Editorial Highlights:

VOLUME 28 NUMBER 10 OCTOBER 2010 NATURE BIOTECHNOLOGY

Tracing cancer networks with phosphoproteomics

David B Solit & Ingo K Mellinghoff

A mass-spectrometry approach for identifying downstream events in cancer signaling pathways may help to tailor therapies to individual patients.

Science
Translational
Medicine



TOWARD CUSTOMIZING TUMOR TREATMENT

Just as our view of Earth has become increasingly global, cells are now seen as complex networks of interacting and intersecting signaling pathways rather than a collection of regulated genes.

Nature Reviews Cancer | AOP, published online 19 August 2010; doi:10.1038/nrc2922



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A discovery strategy for novel cancer biomarkers

OLSEN LAB-EXAMPLES OF DEEP PROTEOMICS DRUG PROFILING

Science Signaling (2018)

ALK-i: LDK378, TAE684, crizotinib, lorlatinib.

SCIENCE SIGNALING | RESEARCH RESOURCE

CANCER

Integrated proximal proteomics reveals IRS2 as a determinant of cell survival in ALK-driven neuroblastoma

Kristina B. Emdal^{1,2}, Anna Kathrine Pedersen^{1,2}, Doris B. Bekker-Jensen¹, Alicia Lundby^{1,3}, Shara Chappell⁴, Kåre De Preter⁵, Chiara Francavilla^{1,6,7}, Jesper V. Olsen^{1,8}

Cell Reports (2018)

SHP2-i: SHP099 -allosteric inhibitor.

Large-Scale Phosphoproteomics Reveals Shp-2 Phosphatase-Dependent Regulators of Pdgfr Receptor Signaling

Tawee S. Bath^{1,2}, Moreno Pagani^{1,2}, Anamaria Pfeiffer¹, Maxim A.X. Tollemars¹, Chiara Francavilla^{1,3,4} and Jesper V. Olsen^{1,5,6}

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³Center for Chromosome Stability and Center for Health Aging, Institute for Cellular and Molecular Medicine, Faculty of Health and Medical Sciences, University of Copenhagen, 2200 Copenhagen, Denmark
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⁷Correspondence: chiara.francavilla@proteinresearch.au.dk (C.F.), jesper.olse@proteinresearch.au.dk (J.V.O.)
⁸https://doi.org/10.1016/j.celrep.2018.02.038

Cell Reports (2017)

CHK1-i: SCH900776, ATM-i: KU55933

Proteomics Reveals Global Regulation of Protein SUMOylation by ATM and ATR Kinases during Replication Stress

Stephanie Munk^{1,2,3,4}, Jin Ohi⁵, Sagarin⁶, Zhenguo Xiao^{1,2}, Tamara Singh Bath¹, Giulia Franciosa¹, Louisa von Stechow¹, Andres Jaegerin Lopez-Contreras¹, Alfred Cornelis Ots Verhoog^{1,2,3,4} and Jesper Velgaard Olsen^{1,4,5,6}

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³Department of Molecular Cell Biology, Leiden University Medical Center, 2300 RC Leiden, the Netherlands
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⁶Correspondence: s.v.ohi@uhasselt.be (J.O.V.), jesper.olse@proteinresearch.au.dk (J.V.O.)
⁷https://doi.org/10.1016/j.celrep.2017.09.058

Cell Reports (2017)

CDK7-i: THZ-1
Phosphoproteomics of Primary Cells Reveals Druggable Kinase Signatures in Ovarian Cancer

Chiara Francavilla^{1,2,3,4}, Michela Lupia^{1,2}, Kalligoi Tsibou^{1,2,3,4}, Alessandro Villa^{1,2}, Katarzyna Kowalczyk^{1,2}, Rina Rakwiewicze-Janus-Christiansen¹, Giovanni Bertoni¹, Stefano Costantini¹, Sven Brannk¹, Lars J. Jensen¹, Ugo Ciovanni^{1,2,3,4} and Jesper V. Olsen^{1,2,3,4,5,6}

¹Proteomics Program, Novo Nordisk Foundation Center for Protein Research, Faculty of Health and Medical Sciences, University of Copenhagen, Blegdamsvej 3B, 2200 Copenhagen, Denmark
²Unit of Cytopathological Oncology Research, Program of Cytopathological Oncology, European Institute of Oncology, Via Risparzonzi 485, 20143 Milan, Italy
³Research Systems Biology Program, Novo Nordisk Foundation Center for Protein Research, Faculty of Health and Medical Sciences, University of Copenhagen, Blegdamsvej 3B, 2200 Copenhagen, Denmark
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¹²https://doi.org/10.1016/j.celrep.2017.03.075

Cell Systems (2017)

Deepest proteome resolution of a human cell to date

An Optimized Shotgun Strategy for the Rapid Generation of Comprehensive Human Proteomes

Doris B. Bekker-Jensen¹, Christian D. Kelstrup^{1,2}, Tawee S. Bath¹, Sara C. Larsen¹, Christa Hedrup¹, Jesper B. Brannsek¹, Karina D. Sørensen¹, Soren Hoyer¹, Torben F. Omholt¹, Claus L. Andersen¹, Michael L. Nielsen¹ and Jesper V. Olsen^{1,3,4}

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³Institute of Pathology, Aarhus University Hospital, Palle Juul-Jensens Boulevard 99, 8000 Aarhus, Denmark
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⁶Correspondence: christian.kelstrup@rtpor.au.dk (C.D.K.), jesper.olse@proteinresearch.au.dk (J.V.O.)
⁷https://doi.org/10.1016/j.celsys.2017.09.009

Cell (2019)

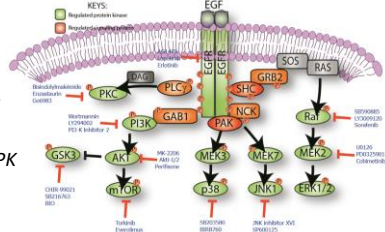
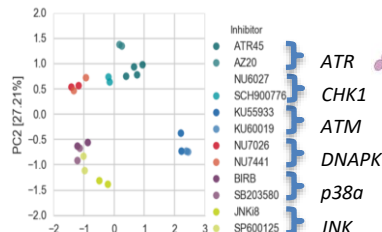
Functional mapping of differential signaling by RPTK mutants

Oncogenic Mutations Rewire Signaling Pathways by Switching Protein Recruitment to Phosphotyrosine Sites

Alicia Lundby^{1,2,3}, Giulia Franciosa¹, Kristina B. Emdal¹, Jan C. Refsgaard¹, Sebastian P. Gnosa¹, Doris B. Bekker-Jensen¹, Anna Secher¹, Svetlana R. Maurya¹, Indrani Paul¹, Bianca L. Mendez¹, Christian D. Kelstrup¹, Chiara Francavilla¹, Maria Kvelborg¹, Guillermo Montoya¹, Lars J. Jensen¹, and Jesper V. Olsen^{1,2,3,4}

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⁶https://doi.org/10.1016/j.cell.2019.08.009

ONGOING (MULTICENTER): Profiling of DDR and core kinase pathway inhibitors (>45)



Nature Communications (2020)

Highest throughput, sensitivity, and scalability to date

ARTICLE

<https://doi.org/10.1038/s41467-020-16691-9> OPEN

Rapid and site-specific deep phosphoproteome profiling by data-independent acquisition without the need for spectral libraries

Doris B. Bekker-Jensen¹, Oliver M. Bernhardt², Alexander Hogrebe³, Ana Martinez-Val⁴, Lynn Verbeke⁵, Tejas Gandhi⁶, Christian D. Kelstrup¹, Lukas Reiter⁷ & Jesper V. Olsen^{1*}

Nature Communications (2021)

Subcellular compartmental proteomics

ARTICLE

<https://doi.org/10.1038/s41467-021-27899-y> OPEN

Spatial-proteomics reveals phospho-signaling dynamics at subcellular resolution

Ana Martinez-Val¹, Doris B. Bekker-Jensen^{1,2}, Sophia Steigerwald³, Claire Koenig⁴, Ole Ostergaard⁵, Adil Mehta⁶, Trung Tran⁷, Krzysztof Sikorski⁸, Estefania Torres-Vega⁹, Ewa Kwasniewic⁹, Solveig Hlin Brynjólfsson⁹, Lisa B. Franke¹⁰, Rasmus Kjaebsted¹⁰, Nicola Krogh¹¹, Alicia Lundby¹⁵, Simon Bekker-Jensen⁹, Frigjof Lund-Johansen^{4,12} & Jesper V. Olsen^{1,13}

Nature Communications (2021)

Clinically actionable resistance mechanisms

ARTICLE

<https://doi.org/10.1038/s41467-021-27781-9> OPEN

Proteomics of resistance to Notch1 inhibition in acute lymphoblastic leukemia reveals targetable kinase signatures

Giulia Franciosa¹, Jos G. A. Smits^{2,3}, Sonia Minuzzo³, Ana Martinez-Val¹, Stefano Indraccolo^{3,4} & Jesper V. Olsen^{1,5}

ADVISORS AND COLLABORATORS

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Cancer Institute & Ludwig
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Adj. Prof. UCSD

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Queen's Cancer Res. Inst.,
Ontario Canada

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- Expert on protein biomarkers and quantitative tissue imaging
- Academic lead on ProMark®



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Academic Co-Founder
Professor, Novo-Nordisk
Foundation Protein
Center, Cph. University

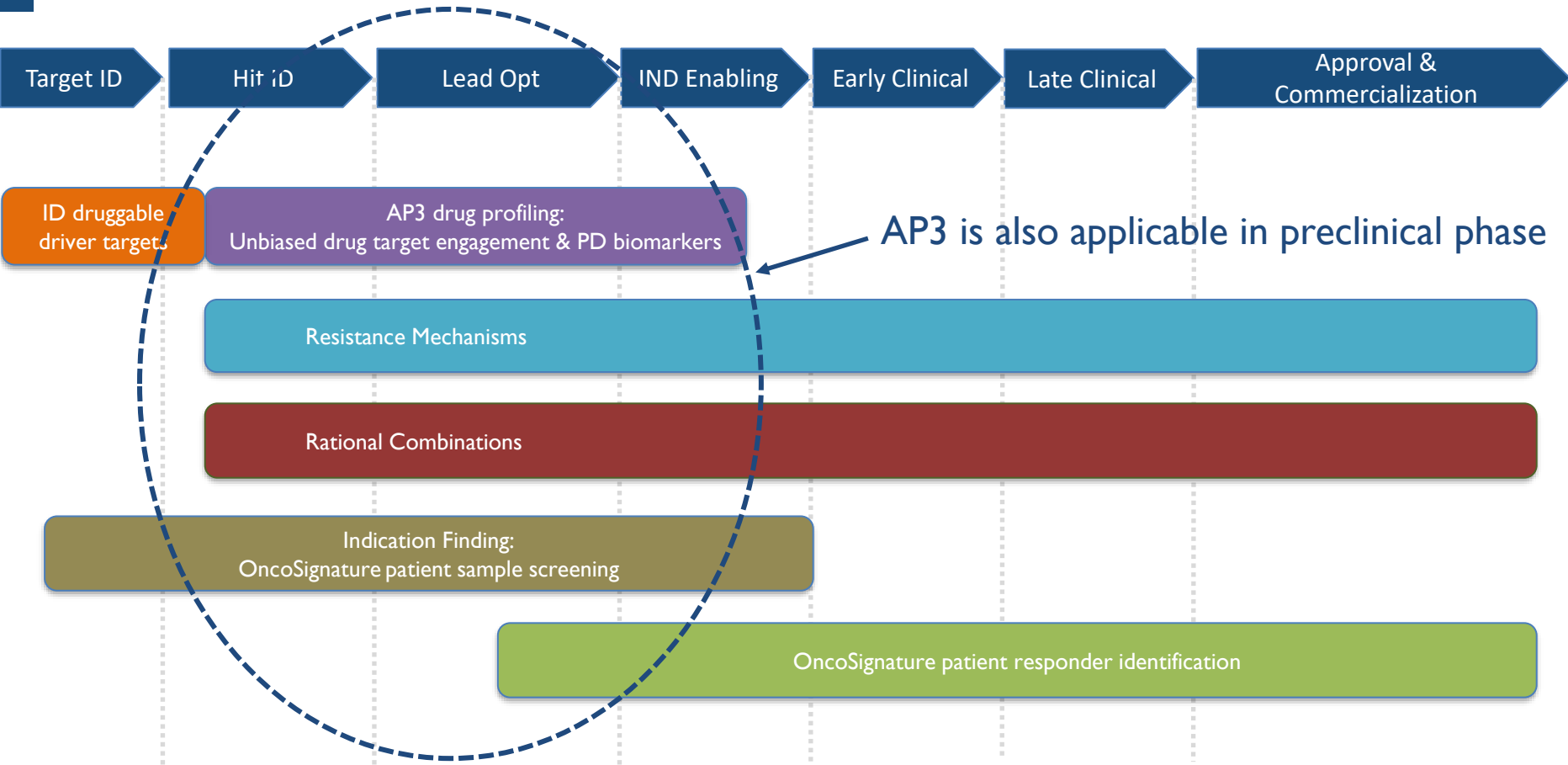
- Recognized pioneer and leading authority in phosphoproteomics and proteomic systems analyses
- Top 0.1% most cited scientist in protein sciences



Jung-Min Lee, M.D.
NCI Collaborator
Investigator, Lasker
Clinical Research
Scholar, NCI

- Expert on women's cancers and DNA damage response (DDR)
- Lead and co-PI on numerous HGSOC & TNBC trials
- Lead PI on ACR-368 platinum-resistant ovarian trials

AP3 IS APPLICABLE ACROSS DRUG DEVELOPMENT STAGES



ACR-2316 MEETS PRE-SPECIFIED DEVELOPMENT CANDIDATE CRITERIA

	Target	ACR-2316
MOA	<ul style="list-style-type: none"> AP3 phosphoproteomics-based, optimized MOA; selective, dual WEE1/PKMYT1 inhibition 	✓
Potency	<ul style="list-style-type: none"> In vitro kinase activity, $IC_{50} \leq 10$ nM Potent <i>in cell</i> target engagement in optimized ratio Activity across sensitive human tumor cell lines, $IC_{50} < 20$ nM 	✓ ✓ ✓
Selectivity	<ul style="list-style-type: none"> Kinase panel profiling – highly selective (kinome selectivity) AP3 profiling confirms desirable CDK and PLK activation for mitotic catastrophe/apoptosis 	✓ ✓
ADME/PK	<ul style="list-style-type: none"> Orally bioavailable $T_{1/2}$ suitable for once/day dosing 	✓ ✓
In vitro safety	<ul style="list-style-type: none"> Low in vitro hERG (>10 μM) and CYP inhibition and induction (>1 μM) 	✓
Solubility	<ul style="list-style-type: none"> > 50 μM for active compounds 	✓
PPB	<ul style="list-style-type: none"> $< 90\%$ 	✓
In vivo efficacy	<ul style="list-style-type: none"> Demonstrated potent target engagement intratumorally in vivo Potent single agent activity in CDX models 	✓ ✓

KEY DATA: ACR-2316 VERSUS BENCHMARKS

	Assay	ACR-2316	Adavosertib	Azenosertib	Debio 123	Lunresertib
Biochemical	Wee1 Binding IC ₅₀	1 nM	1 nM	2 nM	1 nM	31 nM
	PKMYT1 Binding IC ₅₀	27 nM	155 nM	337 nM	2 μM	10 nM
Cellular Target Engagement	WEE1 EC ₅₀ (Y15)	2 nM	19 nM	16 nM	109 nM	>10 μM
	PKMYT1 EC ₅₀ (T14 AlphaLISA)	145 nM	4 μM	2 μM	>10 μM	11 nM
In Vitro Cancer Cell Viability	Human cancer cell viability IC ₅₀	11 nM (cell line 1) 17 nM (cell line 2) 21 nM (cell line 3)	52 nM (cell line 1) 127 nM (cell line 2) 96 nM (cell line 3)	48 nM (cell line 1) 111 nM (cell line 2) 128 nM (cell line 3)	165 nM (cell line 1) 338 nM (cell line 2) 94 nM (cell line 3)	372 nM (cell line 1) 400 nM (cell line 2) 173 nM (cell line 3)
	Human PDX (CTG-3226) viability IC ₅₀	0.011 μM	N/A	0.209 μM	N/A	3.69 μM
Selectivity	Kinome selectivity: S(35) / S(10)	0.091 / 0.071	0.172 / 0.101	0.101 / 0.071	0.062 / 0.03	0.121 / 0.101
In Vivo Efficacy	CDX model 1 efficacy [T/C (%) / dose mg/kg (frequency)]	0.6 % / 45 mg/kg (QD)	23 % / 60 mg/kg (QD)	26.8 % / 100 mg/kg (QD)	66.4 % / 30 mg/kg (QD)	33 % / 20 mg/kg (BID)
	CDX model 2 efficacy [T/C (%) / dose mg/kg (frequency)]	1.7 % / 60 mg/kg (QD)	N/A	41 % / 100 mg/kg (QD)	87 % / 30 mg/kg (QD)	36 % / 20 mg/kg (BID)
	Ovarian PDX model Efficacy [T/C (%) / dose mg/kg (frequency)]	20 % / 45 mg/kg (QD)	N/A	116 % / 60 mg/kg (QD)	N/A	122 % / 18 mg/kg (BID)

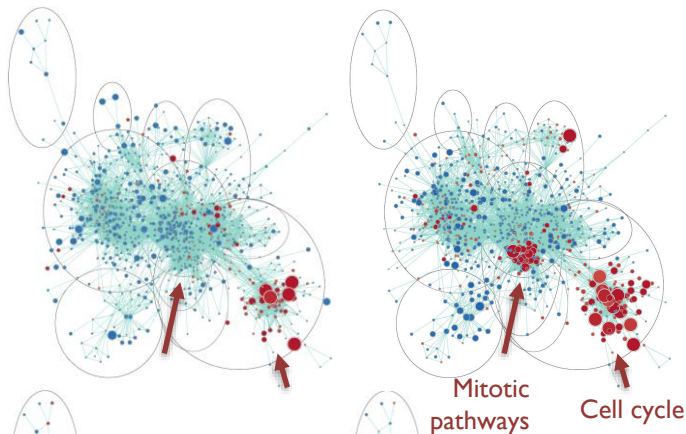
AP3 ANALYSIS: ACR-2316 REGULATES CELL CYCLE AND MITOSIS MORE POTENTLY THAN BENCHMARK WEE1 INHIBITOR

60min
200nM

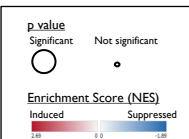
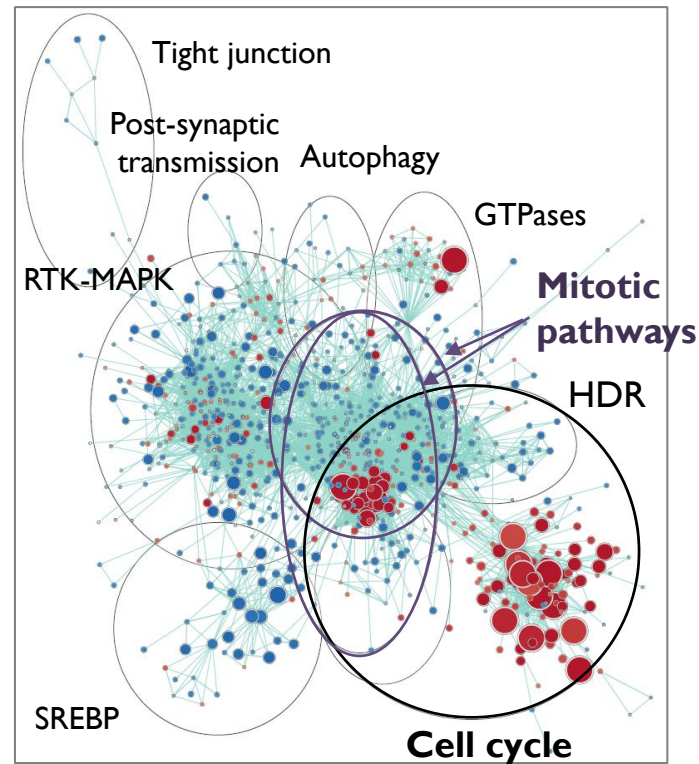
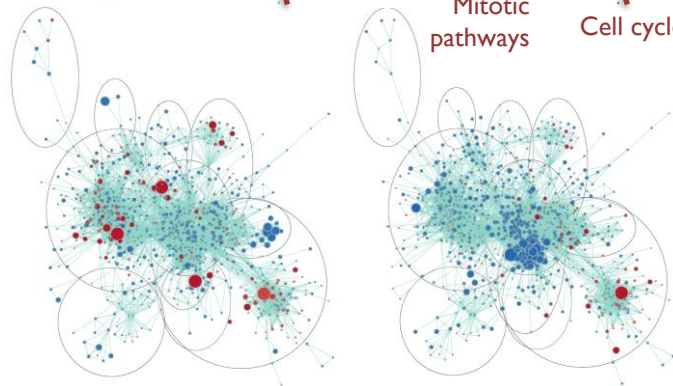
WEE1 inhibitor

ACR-2316

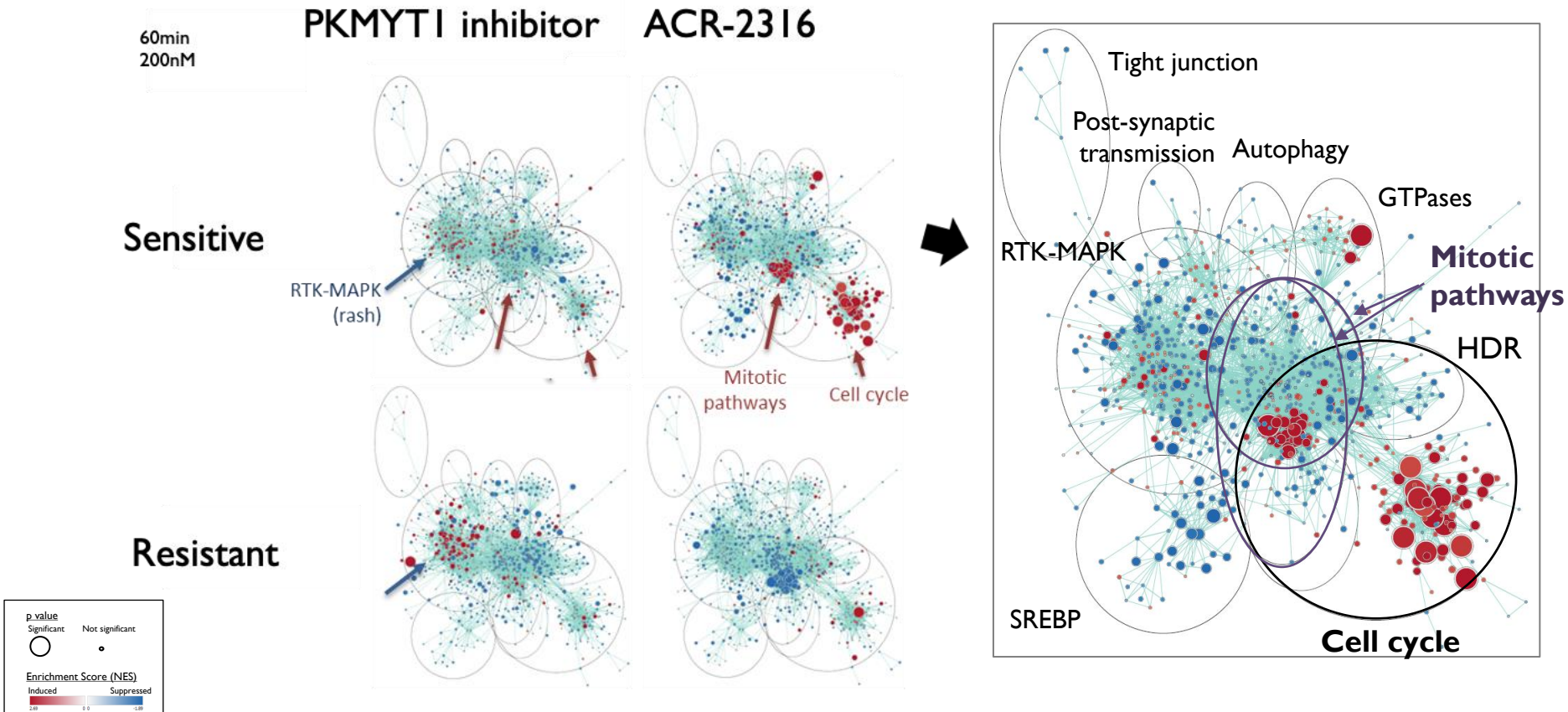
Sensitive



Resistant

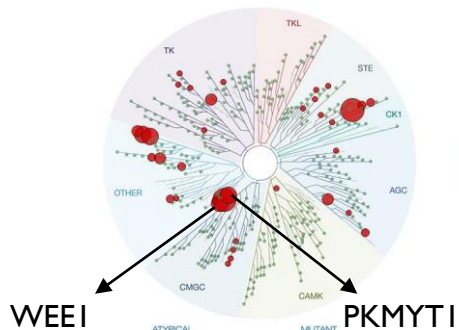


AP3 ANALYSIS: ACR-2316 REGULATES CELL CYCLE AND MITOSIS MORE POTENTLY THAN BENCHMARK PKMYTI INHIBITOR

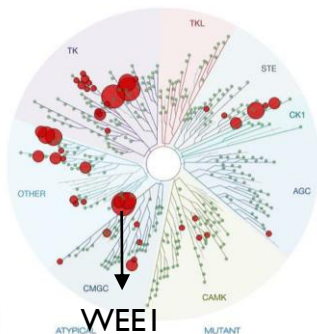


COMPREHENSIVE KINOME SELECTIVITY PROFILING

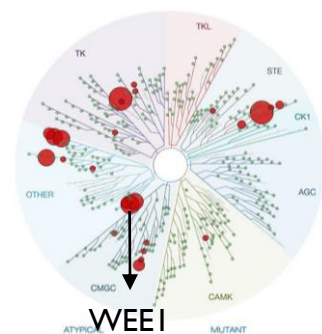
ACR-2316



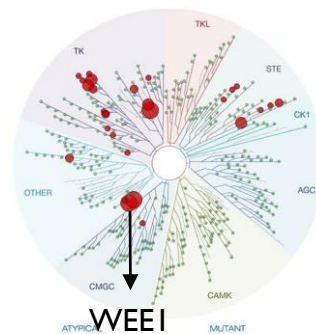
Adavosertib



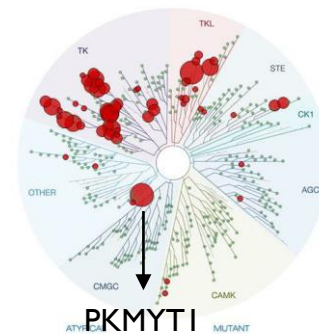
Azenosertib



Debio0123



Lunresertib



468 kinases
@ 1 μ M

Percent Control
 ● 0%
 ● 0.1%
 ● 0.1-1%
 ● 1-5%
 ● 5-10%
 ● 10-35%
 ● > 35%

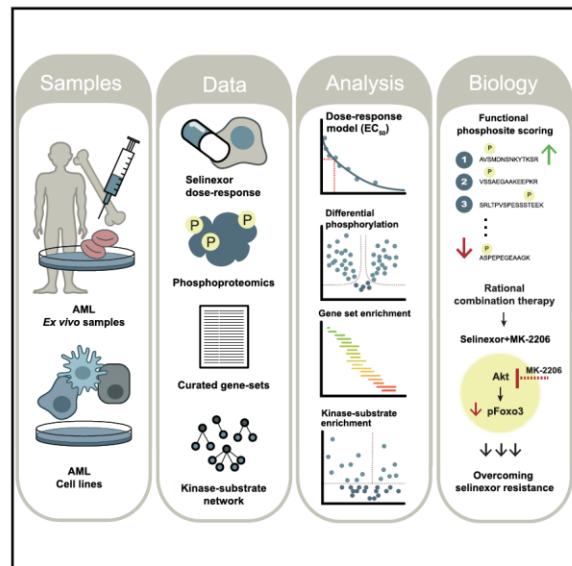
KinomeScan

Cell Reports

Article

Phosphoproteomics of primary AML patient samples reveals rationale for AKT combination therapy and p53 context to overcome selinexor resistance

Graphical abstract



Authors

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In brief

Emdal et al. combine phosphoproteomics of samples from patients with AML and functional phosphosite scoring to uncover clinically actionable molecular context for selinexor efficacy. Sensitivity to selinexor correlates with functional p53 and is enhanced with nutlin-3a, while resistance is associated with dysregulated AKT-FOXO3 signaling and overcome by combining with MK-2206.

Using spatial phosphoproteomics (*Nat. Commun.*, 2021) Acrivon's AP3 platform can uncover single agent sensitivity and rational drug combinations for targets with complicated mechanism of action

Cell Reports, August 9, 2022

ELI LILLY ACR-368 HIGH LEVEL LICENSE TERMS (RIGHT OF FIRST NEGOTIATION)

- In-licensing completed 27 January 2021
 - WW exclusive rights with rights to sub-license
 - \$5M up front and low single digit percentage equity subject to ordinary dilution going forward
 - Aggregate development and commercial milestone payments of up to \$168M, of which \$5M is due prior to NDA
 - Tiered percentage royalty on annual net sales ranging from low single-digit up to a maximum of 10% subject to certain specified reductions
 - Drug product as well as drug substance sufficient to treat several hundred patients
 - Limited right of first negotiation expiring 45 days upon completion of certain clinical milestones