Acrivon Therapeutics

ACRIVON PREDICTIVE PRECISION PROTEOMICS (AP3): DRUG-TAILORED PATIENT SELECTION FOR CLINICAL SUCCESS

INVESTOR EVENT

MAY 01, 2023

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.

You are cautioned not to place undue reliance on these forward-looking statements, which are made only as of the date of this presentation. We undertake no obligation to update any forward-looking statements or to reflect new information or the occurrence of unanticipated events, except as required by law.

OUTLINE

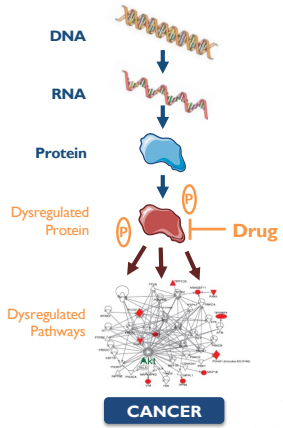
- Company overview
- Acrivon Predictive Precision Proteomics (AP3) platform update
- Preclinical pipeline update
- Clinical trial enrollment progress
- Corporate updates
- Q & A

ACRIVON THERAPEUTICS: DRUG-TAILORED PATIENT SELECTION

AIMING TO OVERCOME THE KEY ATTRITION FACTOR PREVENTING CLINICALLY ACTIVE DRUGS FROM REACHING MARKET

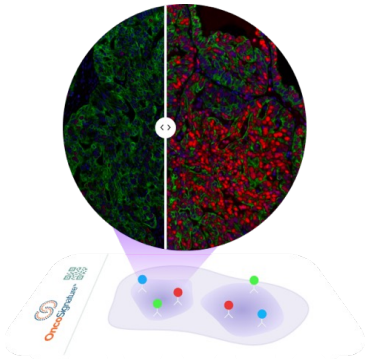
AP3 Platform

- Acrivon's proprietary proteomics-based predictive precision medicine platform
- Applied where NGS/genetics is insufficient and for our internal pipeline



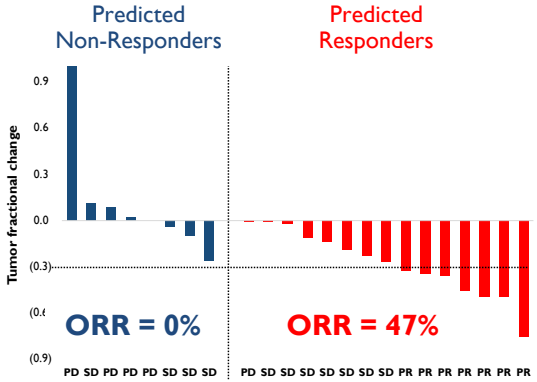
OncoSignature®

- Our proprietary predictive drug-tailored biopsy test
- Extensively evaluated in prospective preclinical studies, including prediction on blinded pretreatment tumor biopsies from past trials resulting in ORR 47% and 58%



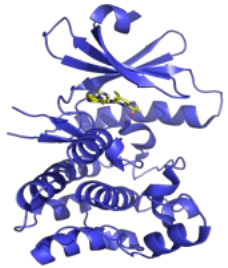
ACR-368 (Prexasertib)

- Clinically active (15-20% ORR) Phase 2 DNA Damage Response (DDR) inhibitor licensed from Eli Lilly & Co.
- Now being developed with OncoSignature patient selection for increased ORR with registrational intent

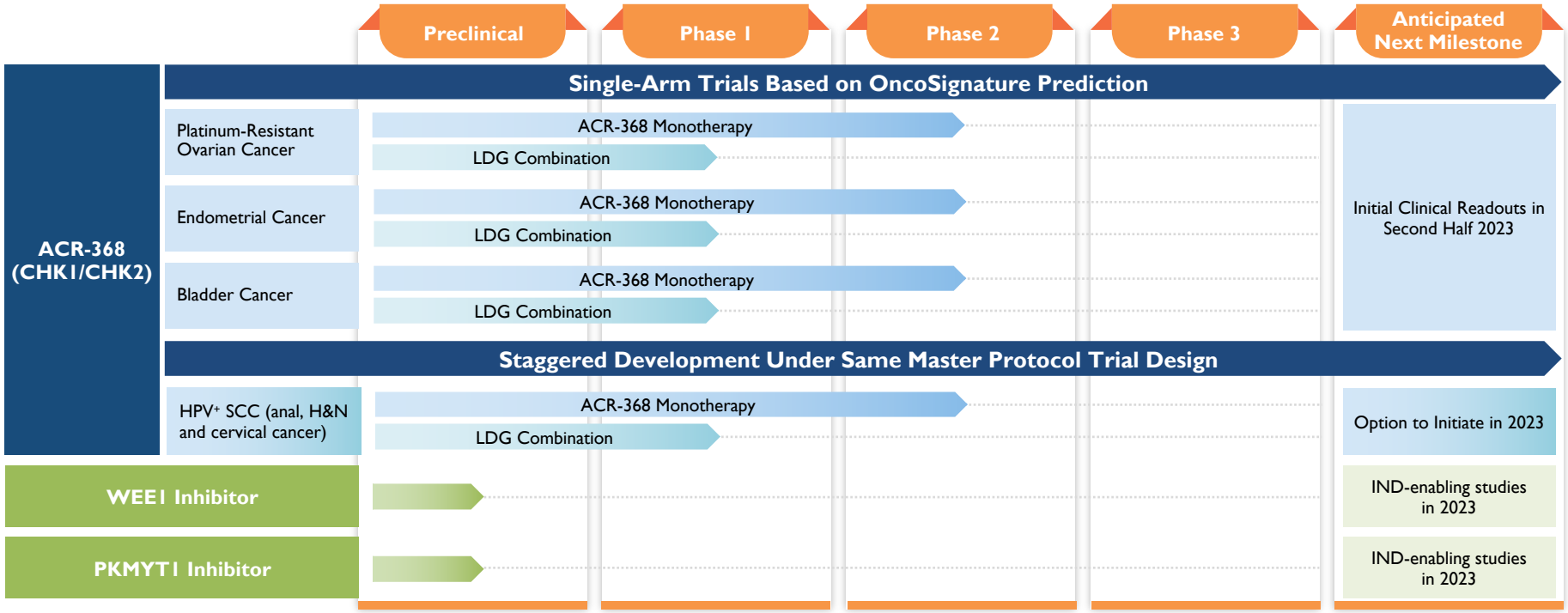


Pipeline

- Two co-crystallography- and AP3-driven preclinical programs targeting WEE1 and PKMYT1, proximal and redundant DDR nodes
- Single digit nM inhibitors, wholly-owned, opportunity for AP3 patient selection and pipeline combinations



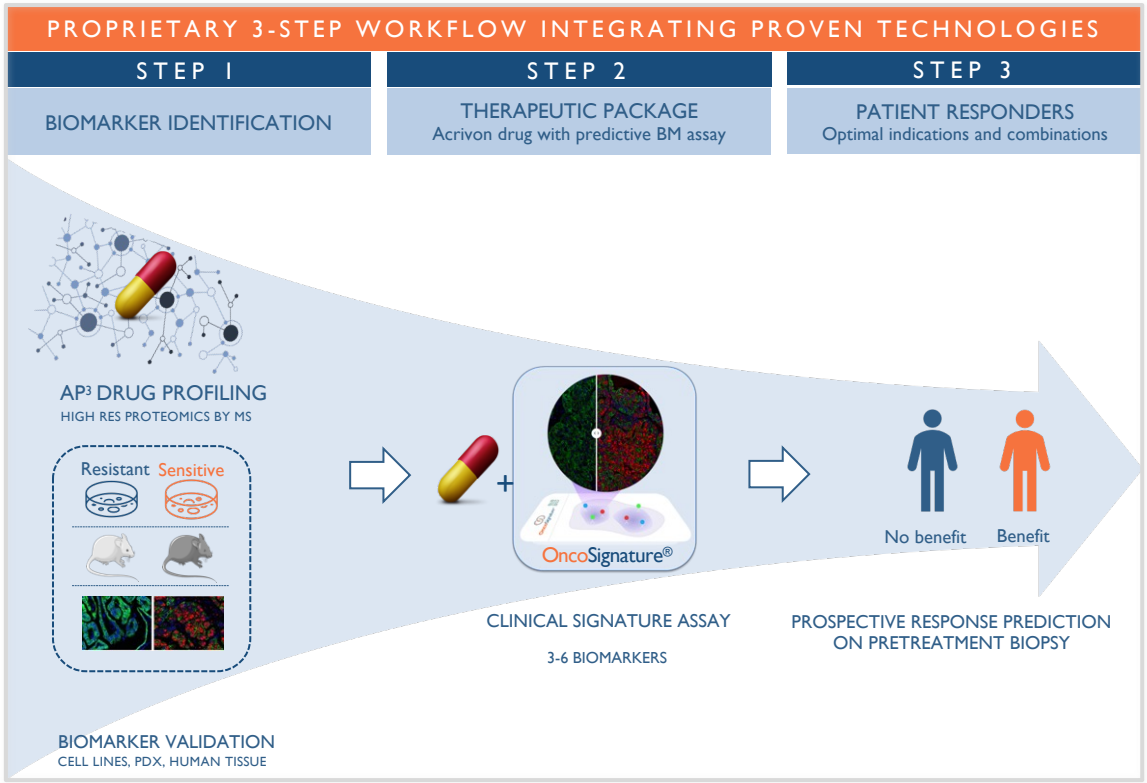
ACRIVON PIPELINE

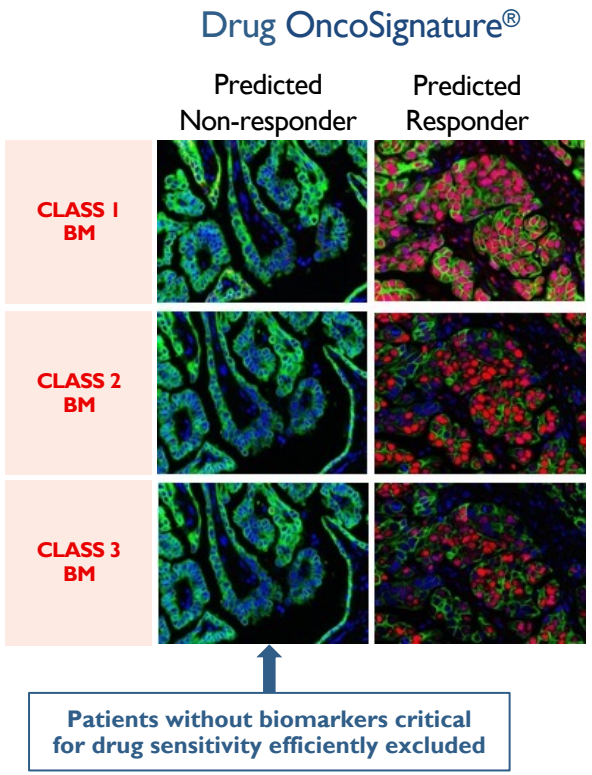


Notes

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

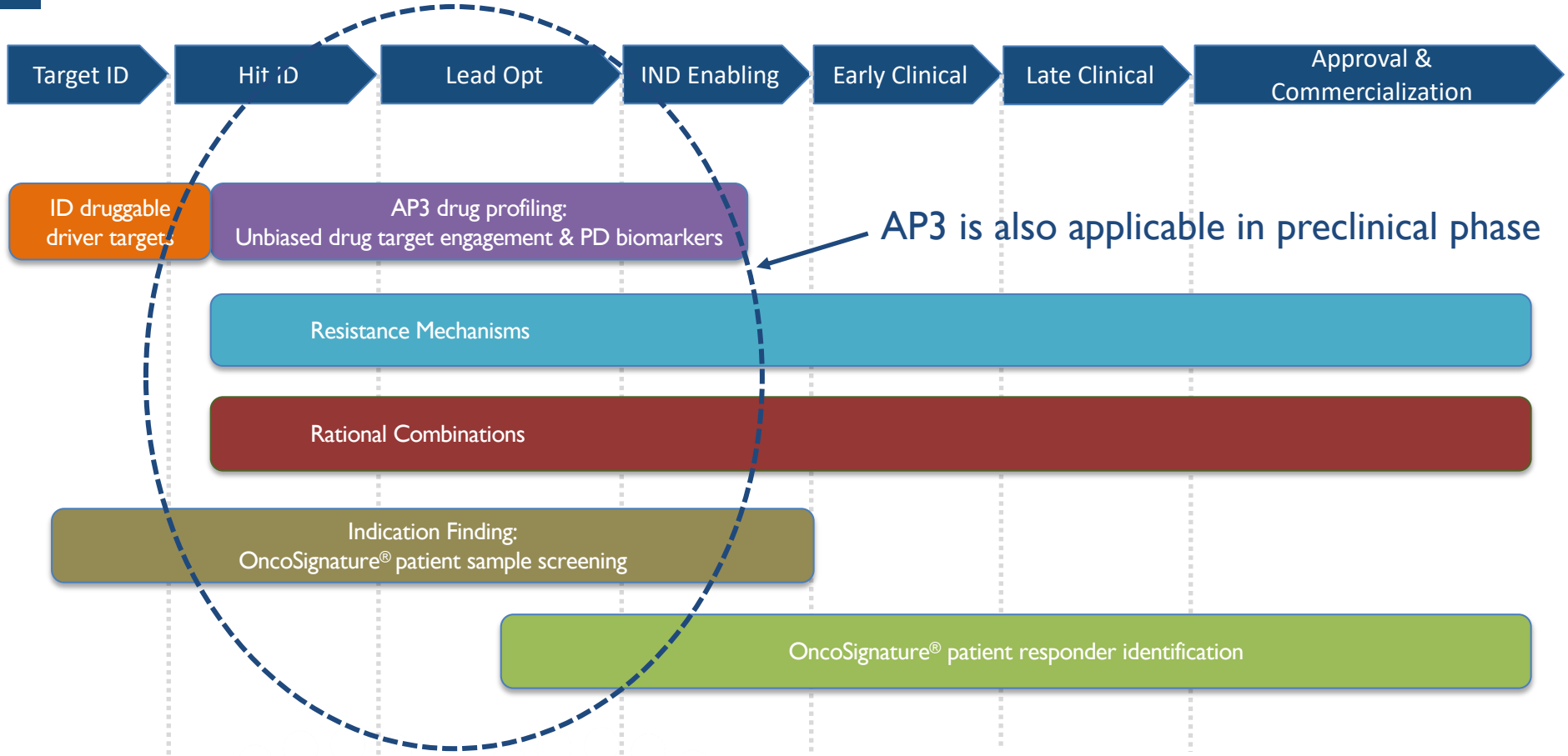
AP3 PLATFORM: DRUG RESPONSE PREDICTION IN INDIVIDUAL PATIENTS





"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*

AP3 IS APPLICABLE ACROSS DRUG DEVELOPMENT STAGES



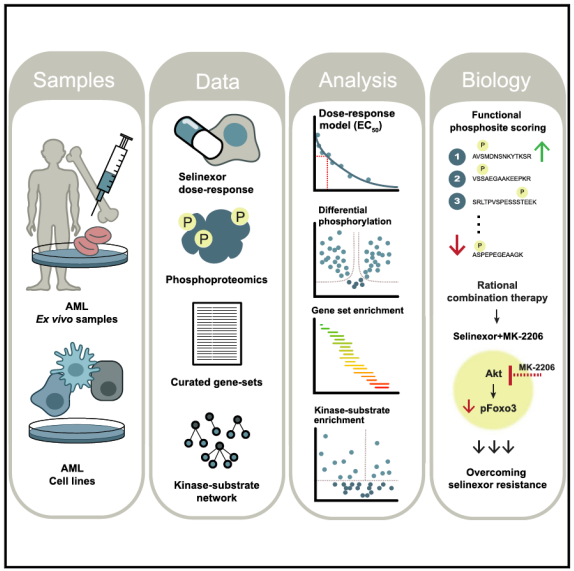
AP3 REVEALS SINGLE AGENT SENSITIVITY CONTEXT AND RATIONAL DRUG COMBINATIONS INDEPENDENT OF GENETIC INFORMATION

Article

Cell Reports

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

Graphical abstract



Authors

Kristina B. Emdal, Nicolàs Palacio-Escat, Caroline Wigerup, ..., Kristina Masson, Peter Blume-Jensen, Jesper V. Olsen

Correspondence

pub.saez@uni-heidelberg.de (J.S.-R.), kmasson@acrivon.com (K.M.), pblumejensen@acrivon.com (P.B.-J.), jesper.olsen@cpr.ku.dk (J.V.O.)

In brief

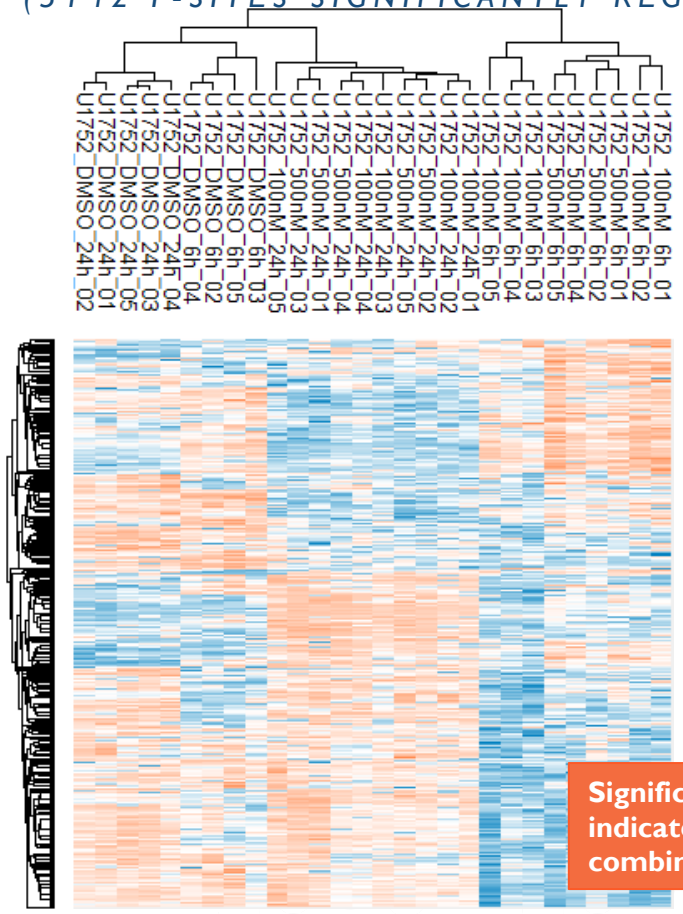
Emdal et al. combine phosphoproteomics of samples from patients with AML and functional phosphosite scoring to uncover clinically actionable molecular context for selinexor efficacy. Sensitivity to selinexor correlates with functional p53 and is enhanced with nutlin-3a, while resistance is associated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

EXAMPLE: DRUGGABLE CDC7 INHIBITOR RESISTANCE MECHANISM

(5142 P-SITES SIGNIFICANTLY REGULATED)



Enriched kinase motif	p-value
CDK1,2,4,6 kinase substrate motif	1.65E-08
Cdc2 kinase substrate motif	8.29E--09
CDK kinase substrate motif	9.99E-07
Calmodulin-dependent protein kinase II alpha substr.	7.71E-05

Enriched kinase motif	p-value
Calmodulin-dependent protein kinase II alpha substr.	3.20E-29
14-3-3 domain binding motif	9.73E-26
PKC kinase substrate motif	2.11E-25
PKC epsilon kinase substrate motif	3.87E-23
PAK2 kinase substrate motif	5.40E-23
PKA kinase substrate motif	5.01E-19
Phosphorylase kinase substrate motif	2.07E-14
MAPKAPK1 kinase substrate motif	3.48E-10
Akt kinase substrate motif	1.25E-10
p70 Ribosomal S6 kinase substrate motif	1.57E-07
Calmodulin-dependent protein kinase IV substr.	2.27E-07
Aurora-A kinase substrate motif	3.95E-07
Chk1 kinase substrate motif	1.77E-06
Pim1 kinase substrate sequence	1.94E-06

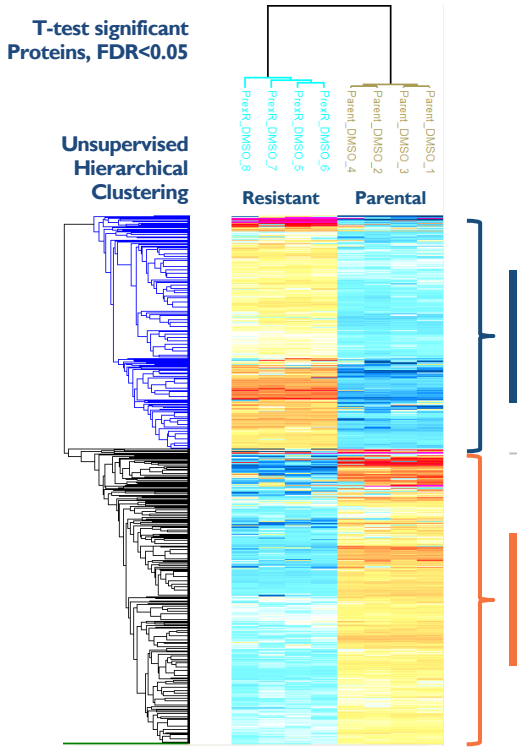
Enriched kinase motif	p-value
GSK-3, ERK1, ERK2, CDK5 substrate motif	4.53E-07
WW domain binding motif	4.53E-07

Enriched kinase X motif	p-value
	1.04E-50
	2.14E-50
	1.98E-38

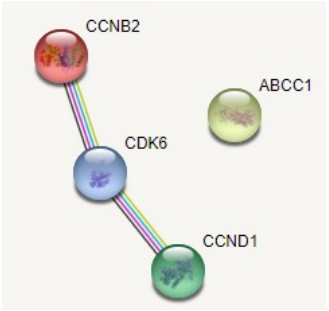
Enriched kinase motif	p-value
ERK1,2 kinase substrate motif	7.59E-08

Significant Kinase X response/cell cycle arrest after 24h in the non-responders indicate a CDC7i resistance mechanism that could be targeted with X-inhibitor combinations

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

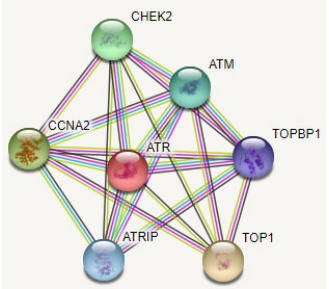


Upregulated in ACR-368 Resistant Cells



G1/S CELL CYCLE

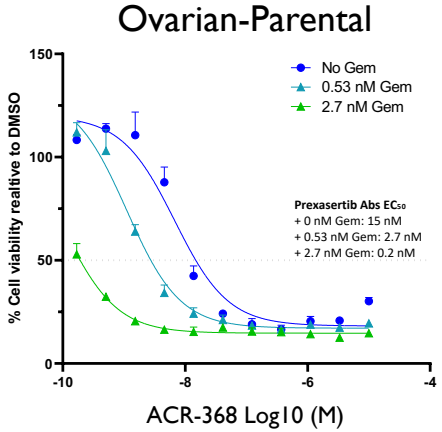
Downregulated in ACR-368 Resistant Cells

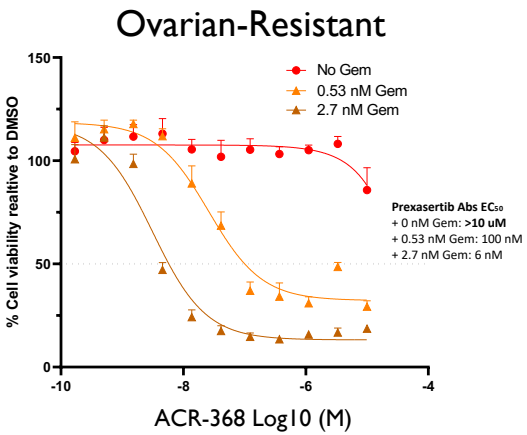


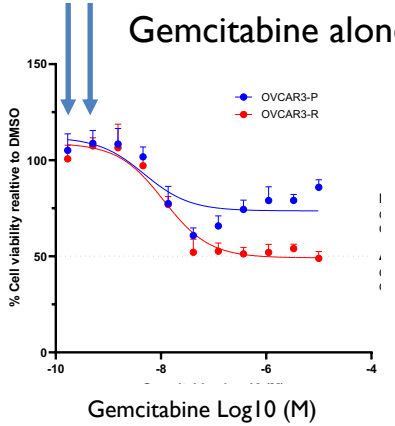
DNA DAMAGE REPAIR

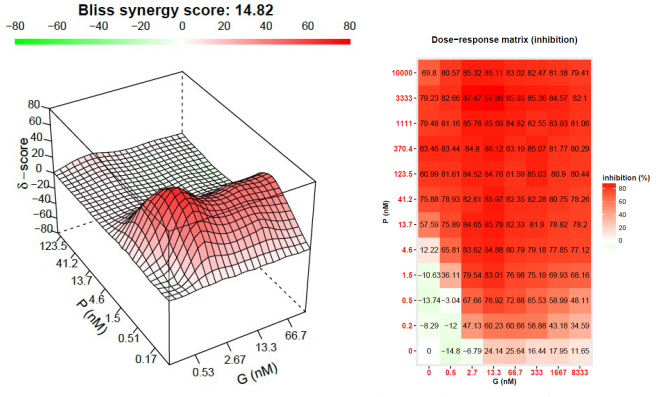
Data suggest that gemcitabine might be a rational combination to overcome DDR suppression

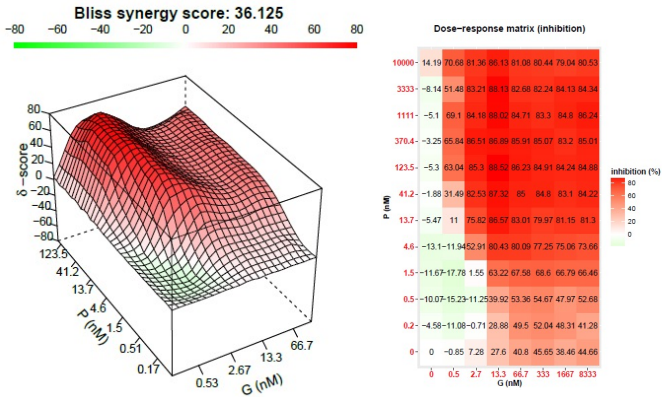
ULTRA-LOW DOSE GEMCITABINE SENSITIZES OVARIAN CANCER CELL LINES TO ACR-368











Bliss Synergy score:

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

INTERNAL PIPELINE: WEE1 AND PKMYT1 - LEVERAGING AP3

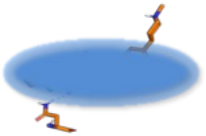
Rationale

- *Complement to in-licensing, leveraging our AP3 patient selection platform for high clinical POS*
- *Potential within DDR drug target class to pursue combinations (ACR-368, WEE1, and PKMYT1 inhibitors)*

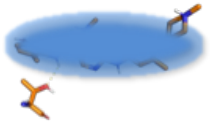
WEE1 and PKMYT1 programs

Lead optimization ongoing in several prioritized series based on high resolution co-crystals (WEE1: 1.5-2.6 Å; PKMYT1: 1.65-2.1 Å)

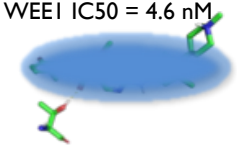
- Potent target inhibition (IC_{50}<10 nM)
- Confirmed target engagement in cells
- Multiple novel structural series
- Kinase selectivity (IVKA and AP3 profiling)
- PK studies ongoing



WEE1 IC50 = 4.6 nM



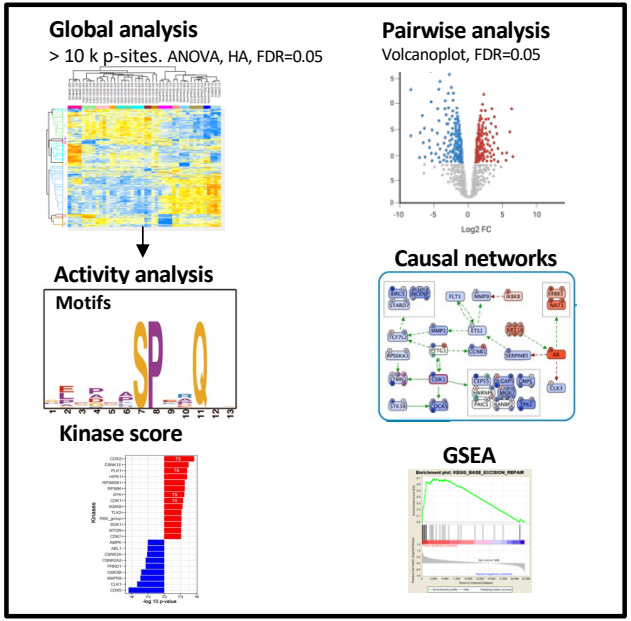
PKMYT1 IC50 = 2.4 nM



PKMYT1 IC50 = 10 nM

PKMYT1 co-crystallized with a candidate compound

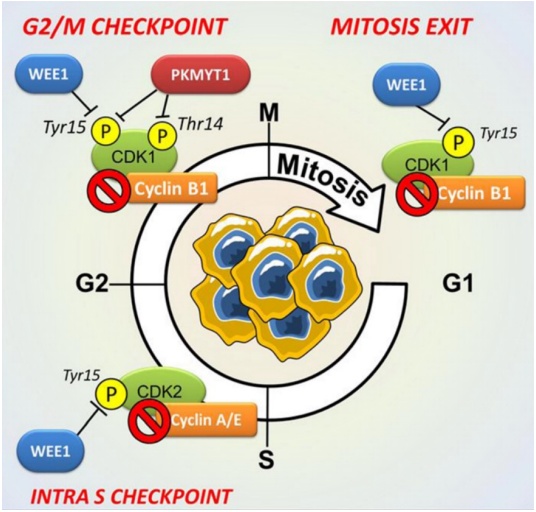
High throughput AP3 profiling



AP3 used for biologically relevant selectivity profiling

WEE1 AND PKMYT1 PROGRAMS: IDEAL FOR AP3 APPROACH

- WEE1 and PKMYT1 regulate S and G2-M cell cycle checkpoints to ensure proper DNA replication and mitotic completion through phosphorylation and inhibition of CDK2 and CDK1 and CDK1, respectively
- WEE1 inhibition propagates genomic instability by premature DNA replication and cell cycle progression, resulting in mitotic catastrophe
- PKMYT1 inhibition results in premature mitotic entry and cell death
- Strong preclinical data and emerging clinical data:
  - AZD1775/MK1775/adavosertib (AstraZeneca)
  - Debio0123 (Debiopharm)
  - ZN-c3 (Zentalis Pharmaceuticals)
  - SGR-XXX (preclinical, Schrödinger)
  - RP-6306 (Repare Therapeutics)



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

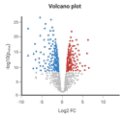
- ✓ Clinical activity (WEE1 single agent)
- ✓ Correlation with genetic alterations challenging, CCNE1 association being explored
- ✓ Acrivon intends to leverage OncoSignature® for optimal patient selection

DEVELOPMENT OF AP3-BASED PATIENT SELECTION ONCOSIGNATURE® TESTS

P-proteomics

Quantitative mapping >20,000 p-sites; 25% drug-related

Drug-regulated phospho-sites and biological processes

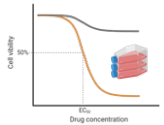


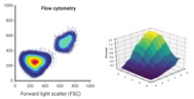
Pathway visualization and reconstitution

Literature and database mining

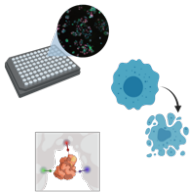
Cellular MOA

Dose response, knockdowns, drug combinations



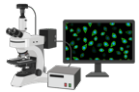


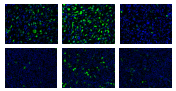
Target engagement, cell assays, imaging

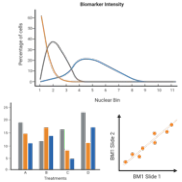


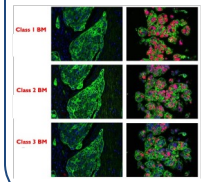
Technical Validation (Intended use tissue)

BM antibody validation by quantitative IF on human and PDX samples

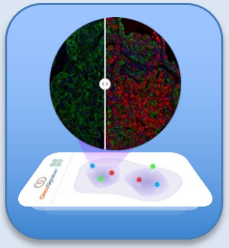






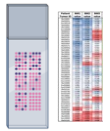


Final OncoSignature® Assay

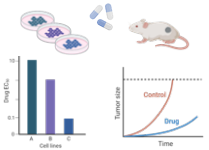


Functional Validation (Intended use tissue)

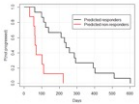
Human cancer screening: ID of drug-sensitive cancers and proportions of responders



Prediction of drug sensitivity in cancer cell lines and PDX models



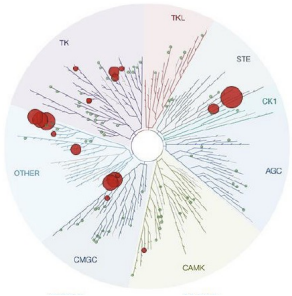
Patient responder prediction on pre-treatment tumor biopsies

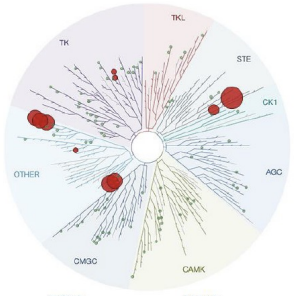


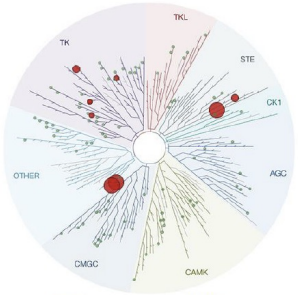
PROFILES OF BENCHMARK WEE1 AND PKMYT1 INHIBITORS

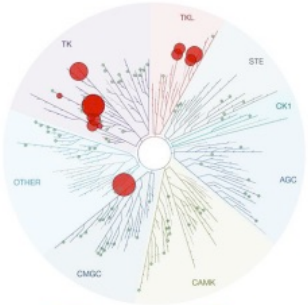
Assays	WEE1 inhibitor A	WEE1 inhibitor B	WEE1 inhibitor C	PKMYT1 inhibitor
Target IC50	1.2 nM	2.0 nM	1.0 nM	9.8 nM
Target Engagement IC50	18.6 nM	15.9 nM	109.0 nM	10 nM
Cell Viability IC50	31.9 nM	49.2 nM	318.0 nM	87 nM
Kinome Selectivity Score @ 1uM	0.172	0.101	0.082	0.121

Eurofins Discovery panel
(106 kinases)



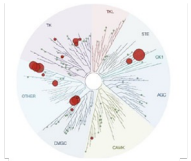




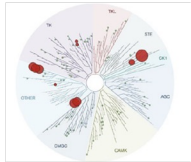


Traditional drug discovery profiling methods yield limited information

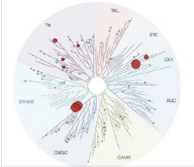
IN VITRO KINASE PROFILING DOES NOT NOT PREDICT DRUG-REGULATED KINASE ACTIVITY IN INTACT CELLS



Compound 1

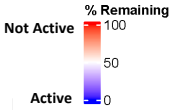


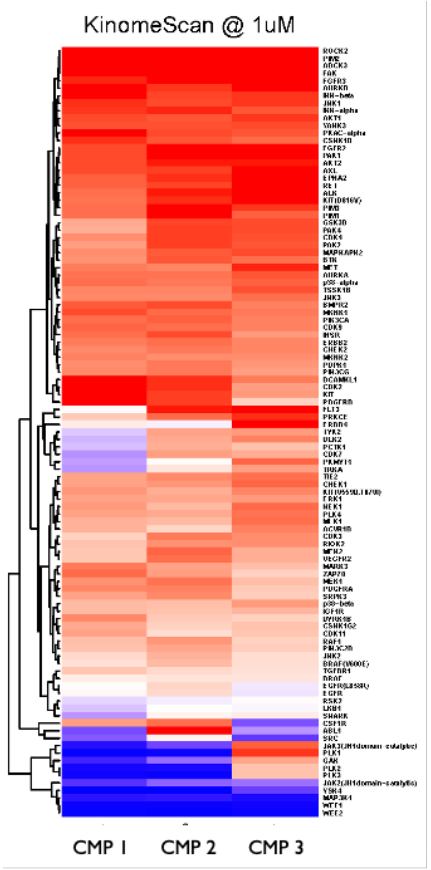
Compound 2



Compound 3

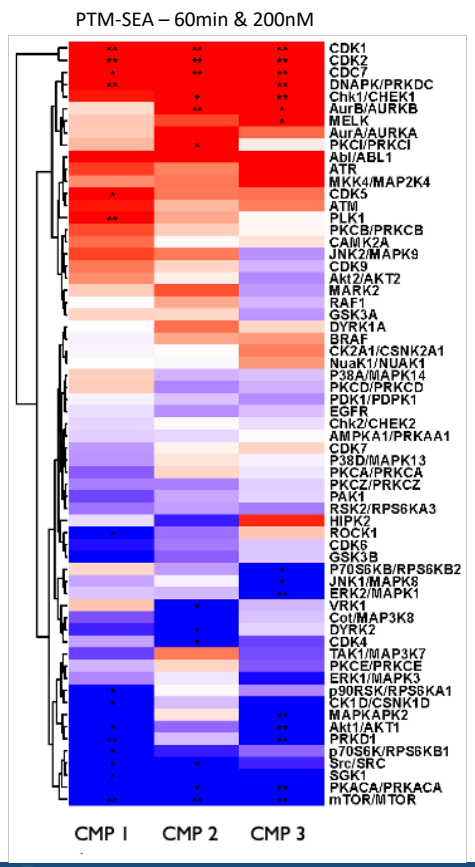
KinomeScan

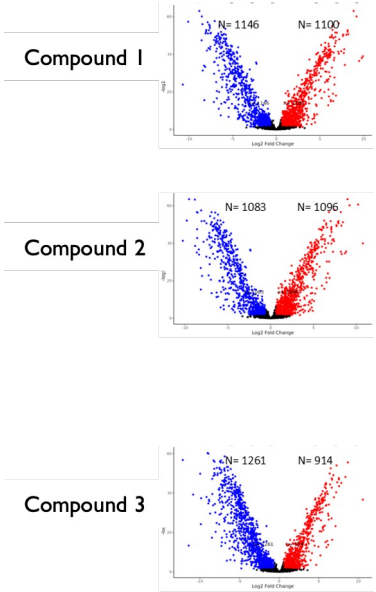




Eurofins Discovery KinomeScan

Kinase Activity*





Time : 60 minutes
Dose : 200 nM

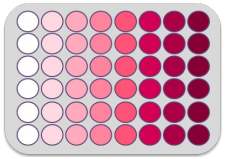
PROPRIETARY PIPE FOR AUTOMATED AP3 DATA ANALYSES

Proprietary machine learning algorithms applied to state-of-the-art AP3 MS-based phosphoproteomics for all compound projects

High throughput MS

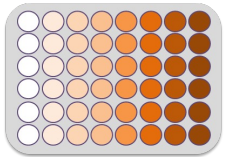
- deep, multi-parameter analyses (time, dose, cell type)

Plate 1 – Compound 1



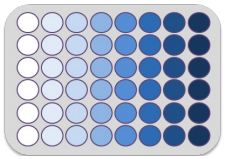
0 0.32 1.6 8 40 200 1000 5000 nM

Plate 2 – Compound 2



0 0.32 1.6 8 40 200 1000 5000 nM

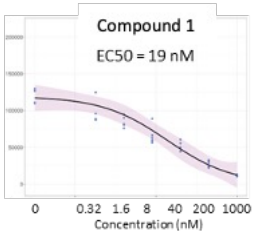
Plate 3 – Compound 3

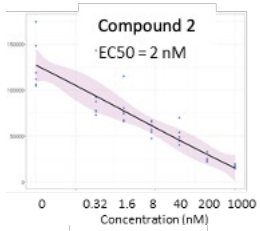


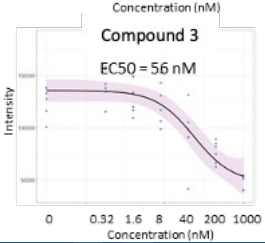
0 0.32 1.6 8 40 200 1000 5000 nM

Dose-response of target engagement

- Ex: Phosphorylation of CDK1 Y15

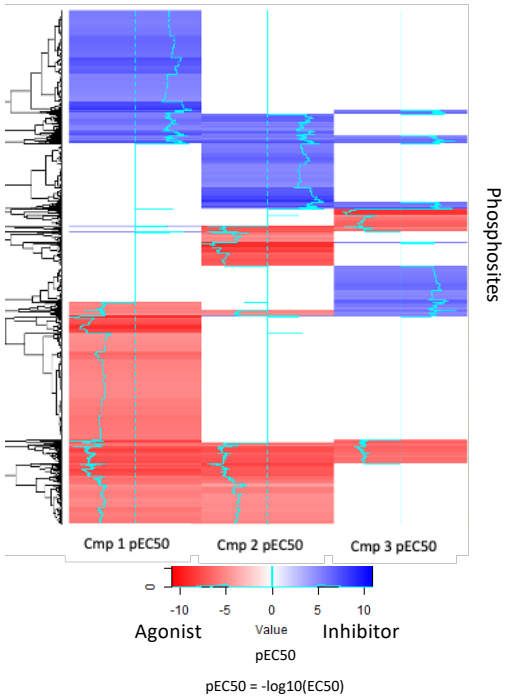






AP3 profiles of WEE1 inhibitors

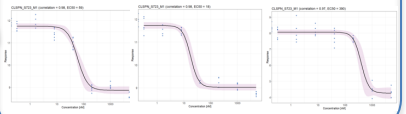
- WEE1 inhibitors are very differentiated



pEC50 = -log10(EC50)

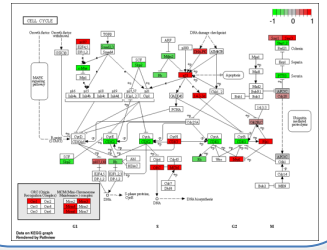
Unbiased PD marker identification

- Automated quantitation of EC50s for 5-6,000 PD markers in each MS run



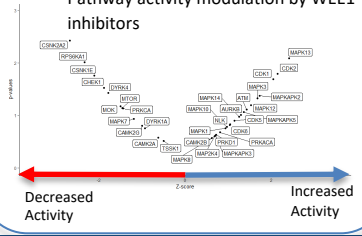
Pathway mapping

- Unbiased compound-specific effects on disease-driving signaling pathways



Mechanism of action

- Pathway activity modulation by WEE1 inhibitors



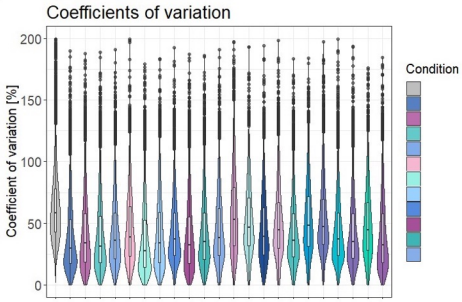
TIGHT, HIGH-RESOLUTION DATA WITH DEEP COVERAGE

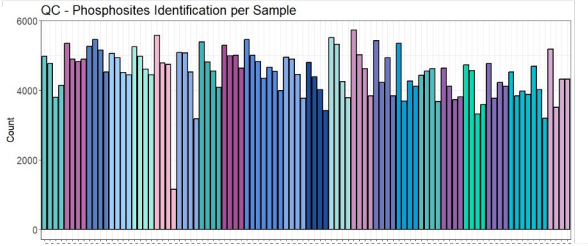
25,800 p-sites

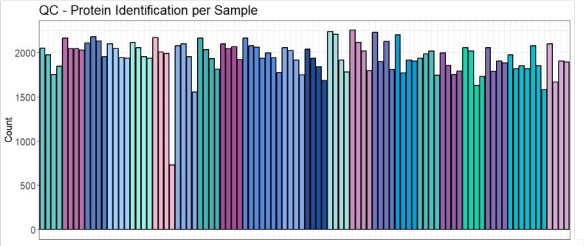
16,456 p-sites

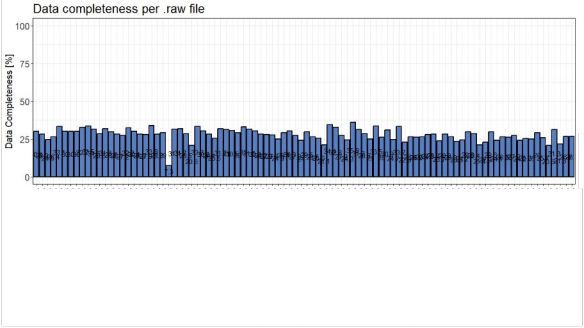
QC MS Data → Data Clean Up → QC Processed Data → Volcano Plots → Hierarchical Clustering → Consensus Sequence Motif → Kinase Inference → Pathway Enrichment → Functional Annotation → Network Mapping → Biomarkers

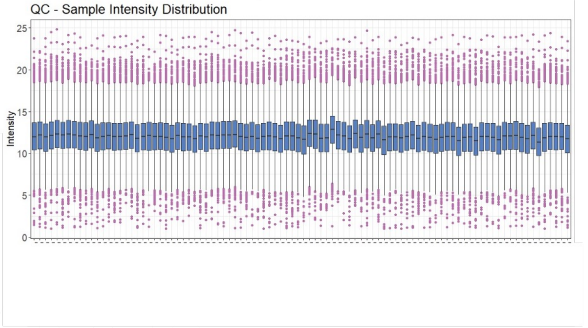
- Filter >60% in at least on condition
- Normalization: LOESS
- Imputation: SLSA

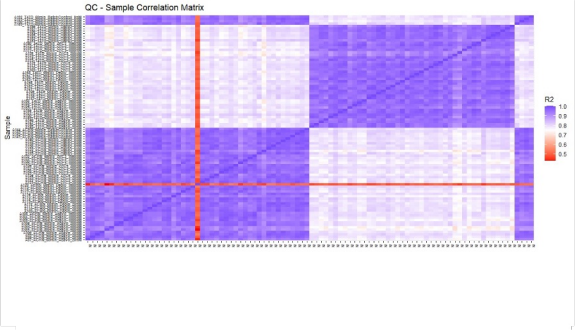






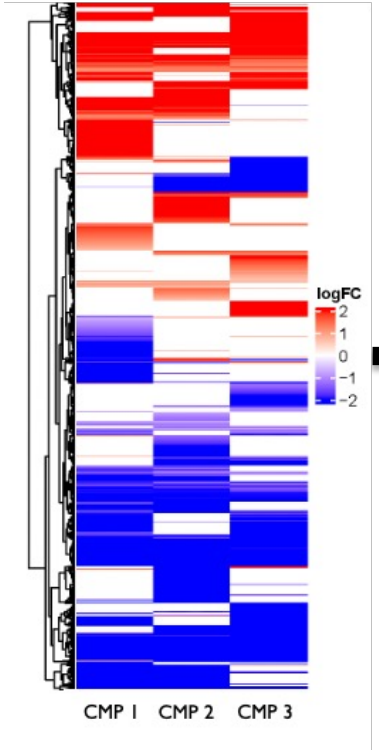




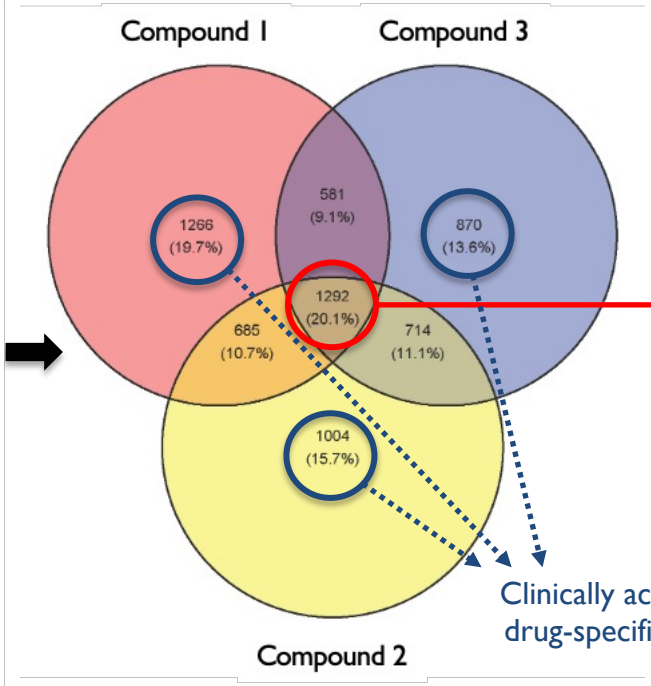


WEE1 INHIBITORS ARE MORE DIFFERENT THAN SIMILAR

Drug-regulated phosphorylation sites (unsupervised hierarchical cluster)



Unique and shared drug-regulated sites

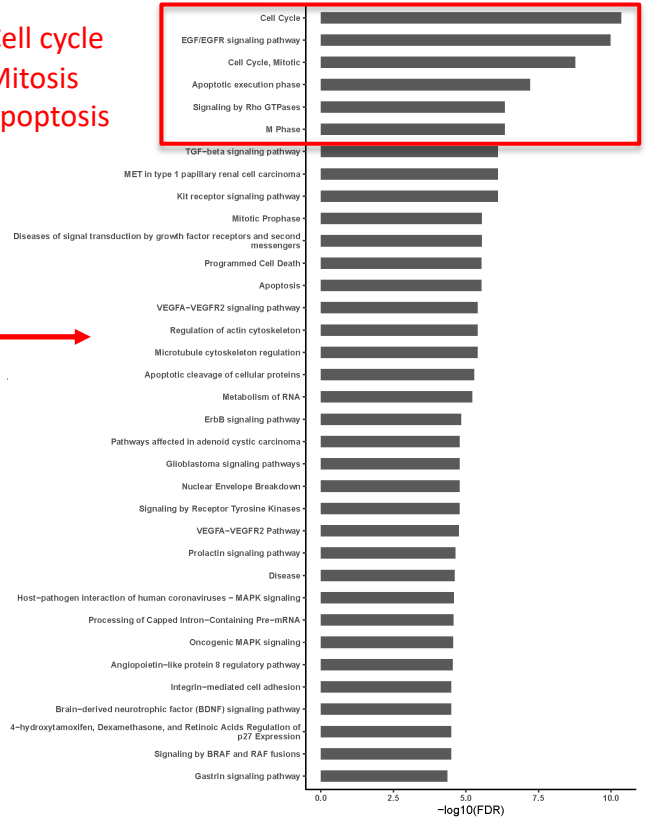


Shared on target mechanisms

Clinically actionable drug-specific effects

Pathway enrichment analysis

Cell cycle
Mitosis
apoptosis

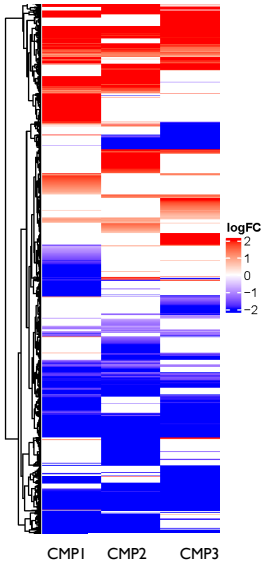


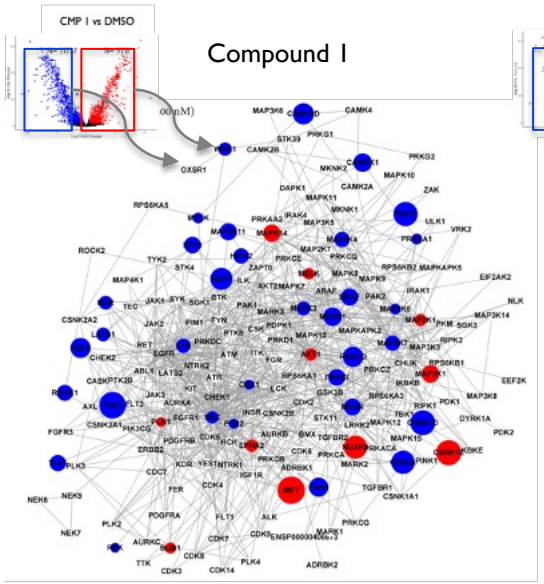
FDR < 0.5 & abs(Fold Change) > 1.5; Time : 60 minutes; Dose : 200 nM

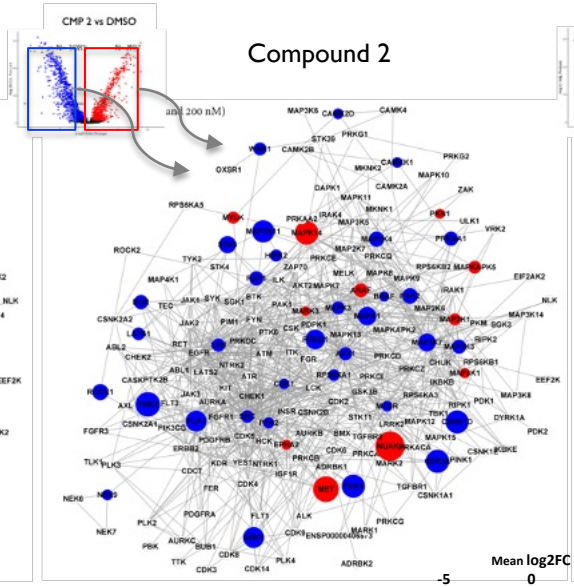
Pathway over-representation analysis: Wikipathway and Reactome; FDR < 0.00005; Significance = -log10(FDR)

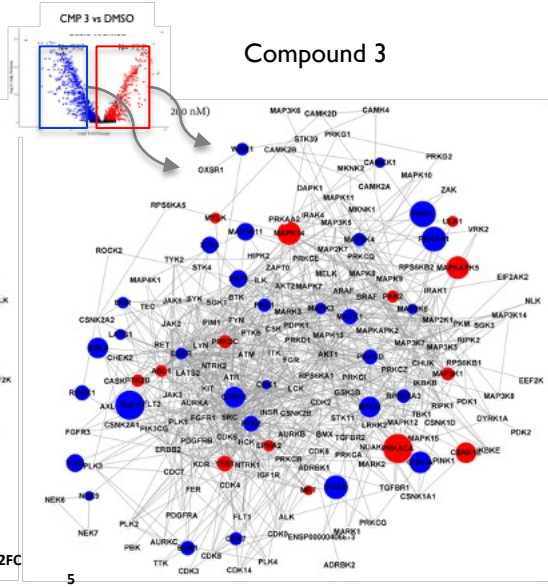
WEE1 INHIBITOR-REGULATED GLOBAL PHOSPHOPROTEOME REVEAL HIGHLY DIFFERENTIATED EFFECTS

Drug-regulated phosphosites







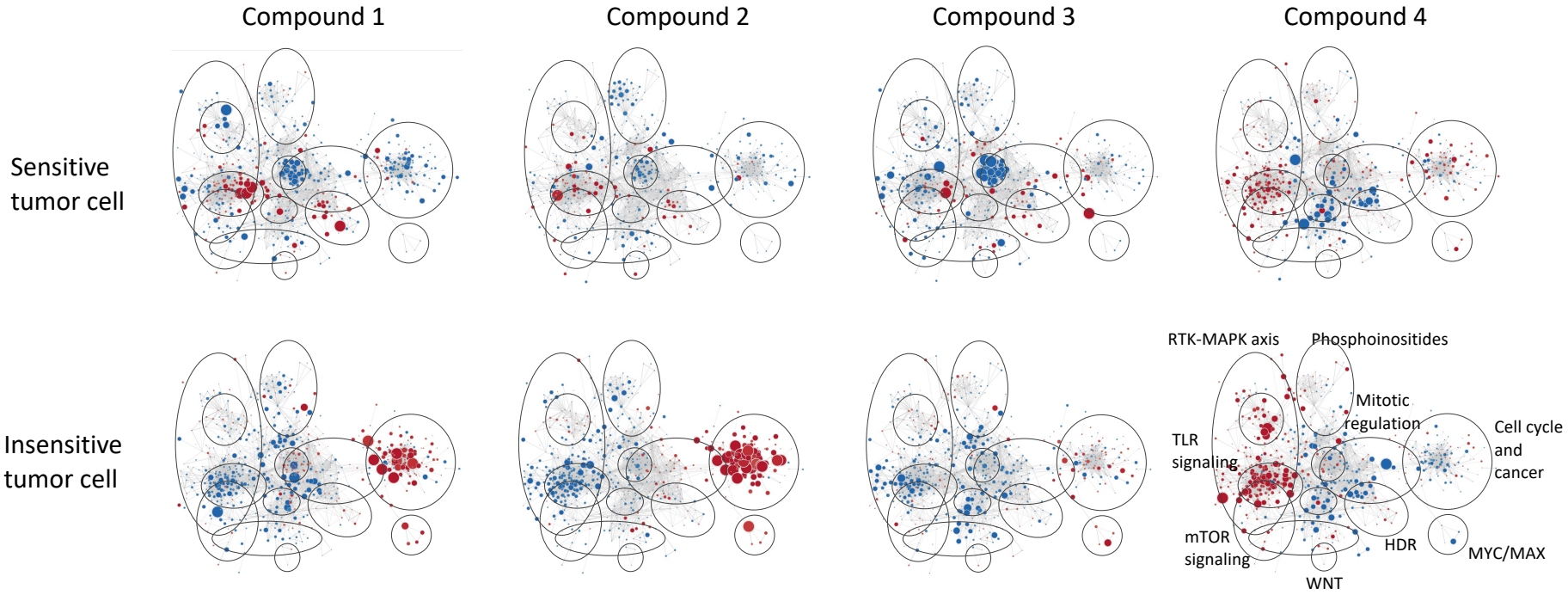


FDR < 0.5 & abs(Fold Change) > 1.5

Differentiated WEE1 inhibitor-specific effects provide opportunity for tailored patient responder identification

Time : 60 minutes; Dose : 200 nM

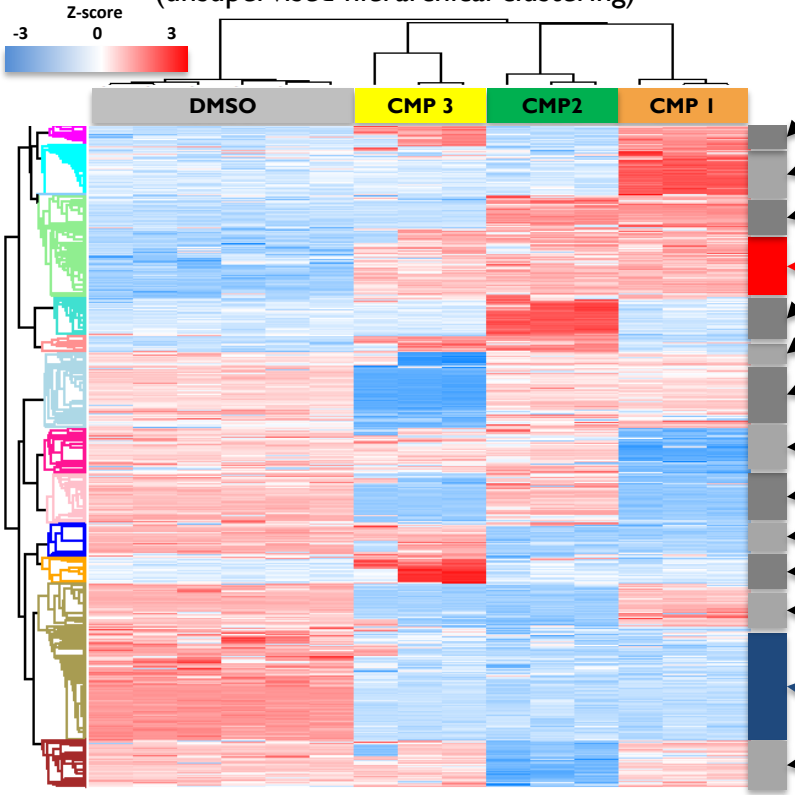
FUNCTIONAL PATHWAY NETWORK EFFECTS BY WEE1 AND PKMYT1 INHIBITORS ARE HIGHLY DISTINCT



Compounds 1 and 4 demonstrate opposite effects on HDR in sensitive cells

BENCHMARK WEE1 INHIBITORS HAVE DIFFERENTIATED COMPOUND-SPECIFIC DISEASE PATHWAY MODULATION

Drug-regulated phosphorylation sites
(unsupervised hierarchical clustering)



Drug regulation of **pathway activity states**
(substrate consensus motif enrichment analysis)

Pathway	Pvalue
Cdc2 kinase substrate motif	3.3E-10
CDK kinase substrate motif	6.7E-10
CDK1,2,4,6 kinase substrate motif	3.3E-09

positive regulation of sequestering of triglyceride	2.4E-11
RNA splicing, via transesterification reactions with bulged adenosine as nucleophile	9.8E-11
nuclear mRNA splicing, via spliceosome	9.8E-11

Cell Cycle	1.8E-11
Cell Cycle, Mitotic	3.2E-09
Regulation of TP53 Activity	8.5E-09

RIG-I-like receptor signaling pathway	1.1E-09

Signaling by Rho GTPases	1.2E-13
Cell Cycle	1.2E-11
SUMO E3 ligases SUMOylate target proteins	1.2E-11
TGF-beta signaling pathway	2.4E-11
Cell Cycle, Mitotic	1.4E-10

Apoptotic cleavage of cellular proteins	1.0E-09
Apoptotic execution phase	1.0E-09

MAPKAPK1 kinase substrate motif	1.9E-08

Nuclear Envelope Breakdown	2.7E-08
SUMO E3 ligases SUMOylate target proteins	2.7E-08
Mitotic Prophase	2.7E-08

Signaling by Rho GTPases	5.3E-10
Cell Cycle	1.1E-08
Membrane Trafficking	2.6E-08
Androgen receptor signaling pathway	4.7E-08
Brain-derived neurotrophic factor (BDNF) signaling pathway	4.7E-08

Cell Cycle, Mitotic	1.9E-09
Mitotic Prometaphase	2.3E-08
GSK-3, ERK1, ERK2, CDK5 substrate motif	3.1E-05
Mitotic Anaphase	2.3E-05
Resolution of Sister Chromatid Cohesion	1.1E-04
SUMOylation of DNA replication proteins	1.4E-04

Shared upregulated

WW domain binding motif	3.1E-45
GSK-3, ERK1, ERK2, CDK5 substrate motif	3.1E-45
Cdc2 kinase substrate motif	1.6E-28
CDK1,2,4,6 kinase substrate motif	1.6E-28
ERK1,2 kinase substrate motif	1.3E-22
CDK kinase substrate motif	2.0E-16
CDK5 kinase substrate motif	1.2E-13
Cell Cycle	2.3E-12
Cell Cycle, Mitotic	3.6E-11
M Phase	3.5E-07

Angiopoietin-like protein 8 regulatory pathway	3.1E-09
ATM signaling in development and disease	1.9E-08
Integrated breast cancer pathway	2.0E-08
4-hydroxytamoxifen, Dexamethasone, and Retinoic Acids Regulation of p27 Expression	2.0E-08
Target of rapamycin (TOR) signaling	2.2E-08

Pathways affected in adenoid cystic carcinoma	4.1E-07
Cell Cycle	4.3E-07
Signaling by Rho GTPases	4.3E-07
Chromatin modifying enzymes	4.3E-07
Apoptotic execution phase	4.8E-07

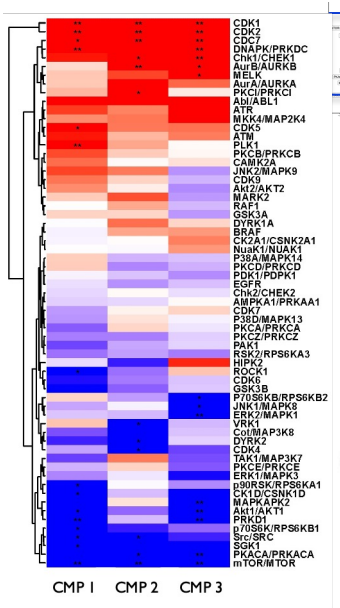
Shared downregulated

EGF/EGFR signaling pathway	3.5E-10
VEGFA-VEGFR2 signaling pathway	1.2E-07
MET in type 1 papillary renal cell carcinoma	2.2E-07
ErbB signaling pathway	2.9E-07
Signaling by Rho GTPases	3.0E-07

DIFFERENTIAL WEE1 INHIBITOR-REGULATED PATHWAY ACTIVITY

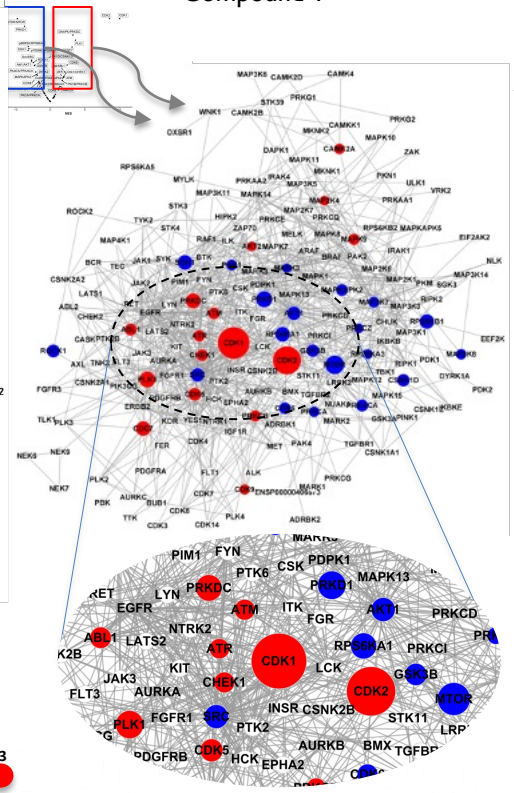
Shared on target CDK1/2 activation and compensatory activation of CHK1 and ATR

Substrate motif-inferred kinase activities

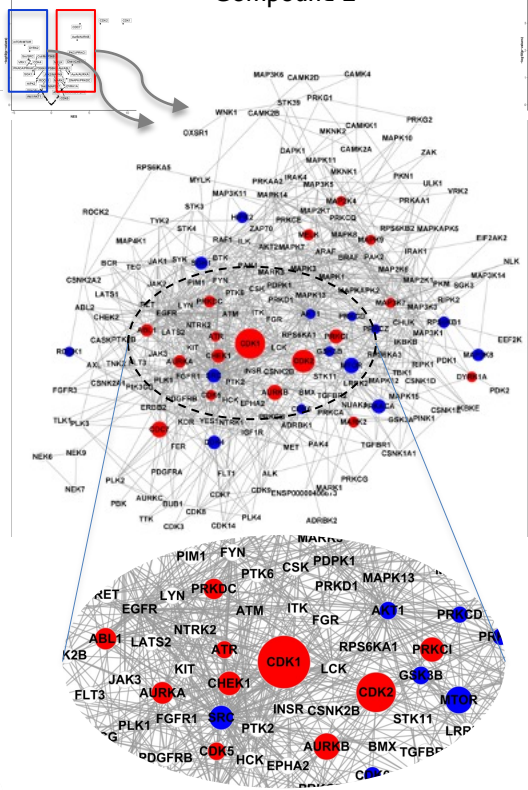


Time : 60 minutes
Dose : 200 nM

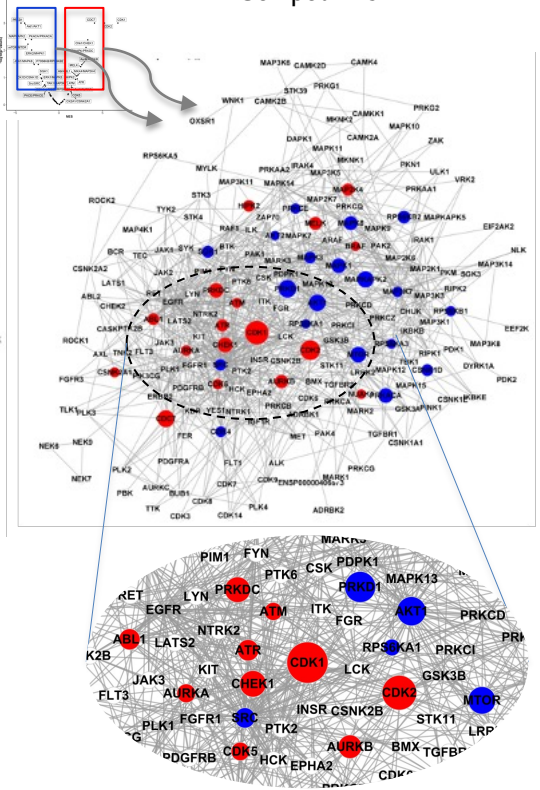
Compound 1



Compound 2

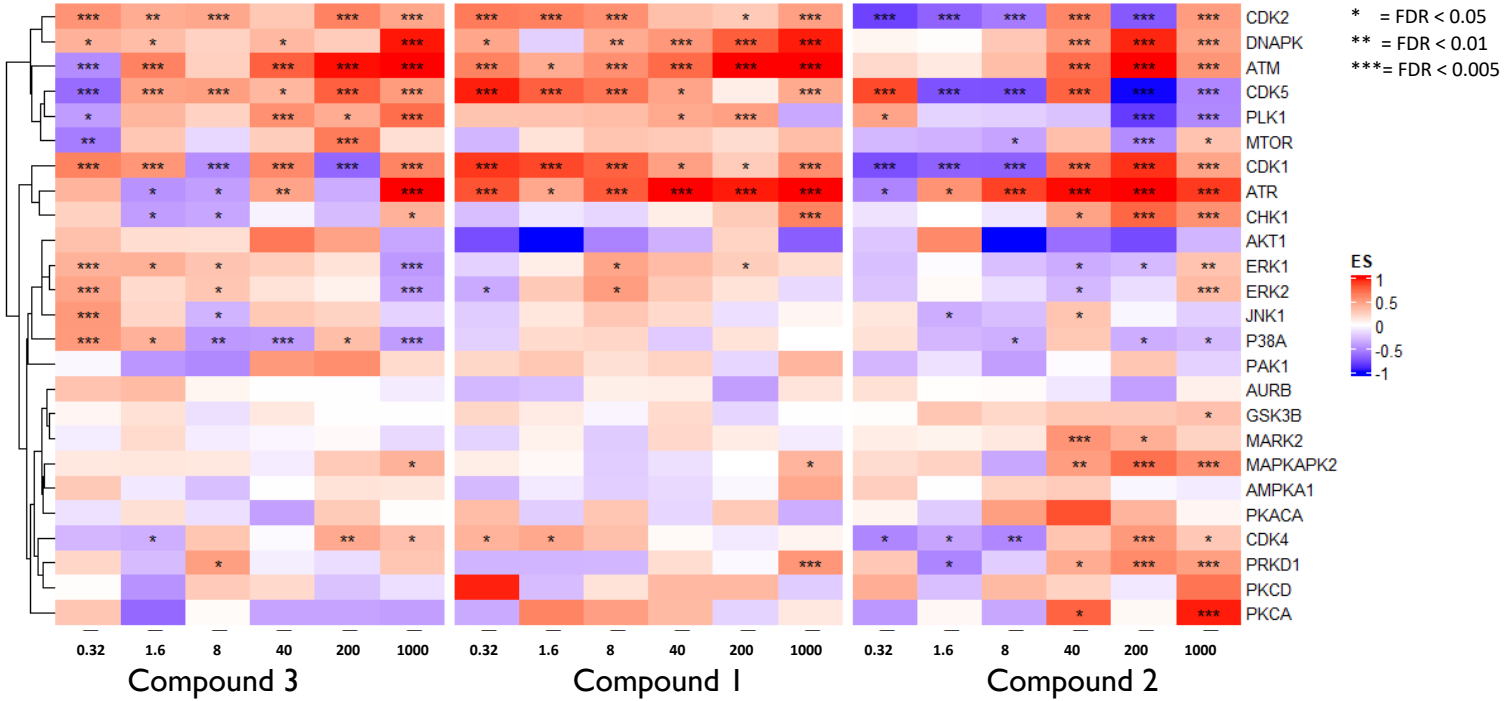


Compound 3



WEE1 INHIBITOR REGULATION OF PATHWAY ACTIVITY (4H)

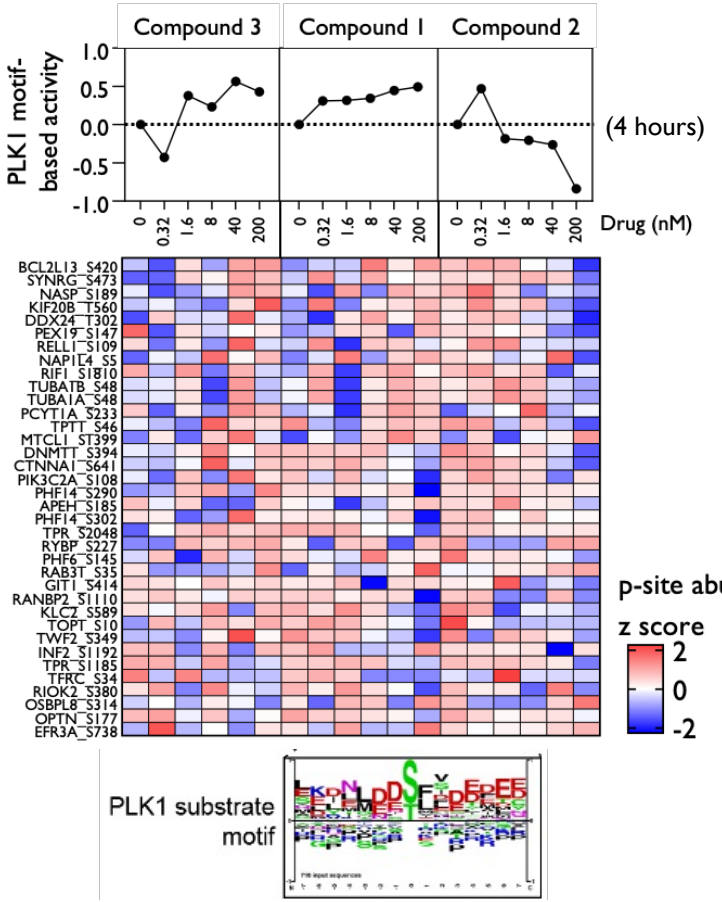
Drug-regulated kinase activities calculated based on consensus motif enrichment analysis

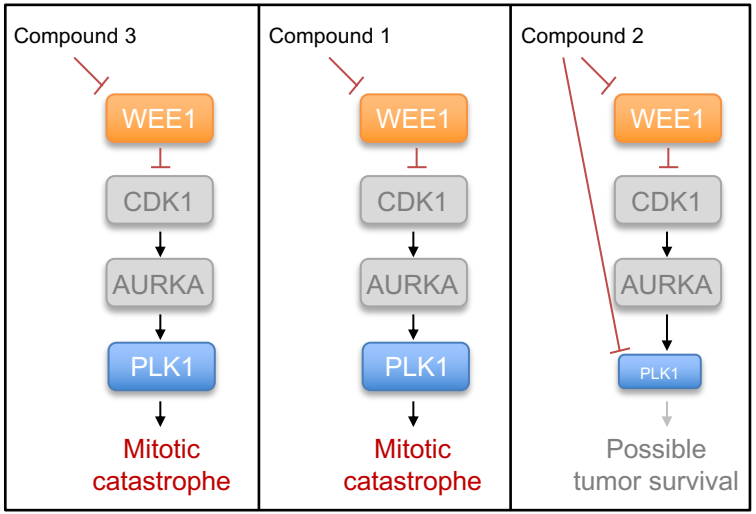


Compound 2 shows possible PLK1 inhibition and less pronounced CDK activation: Could counteract mitotic catastrophe
Compound 3 shows upregulation of MAPK and PI3K: Could be single agent resistance mechanisms

Upregulated kinase activities are color-coded in red with the corresponding false discovery rate (FDR) denoted with "*"

DIFFERENTIAL REGULATION OF PLK1 ACTIVITY – POTENTIAL IMPACT ON PATIENT TREATMENT OUTCOME

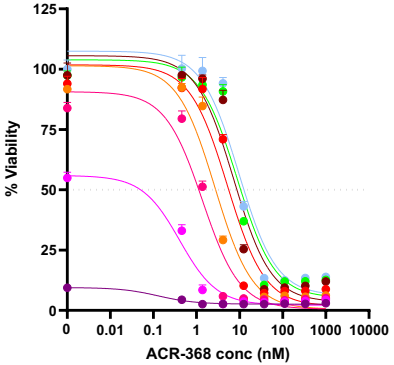


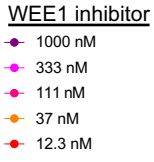


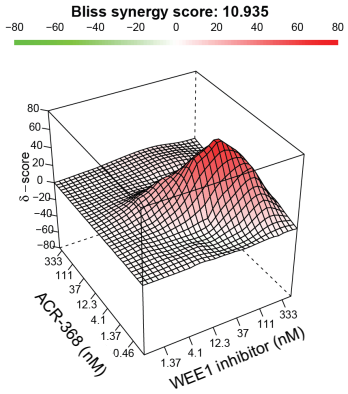
PLK1 inhibition might counteract mitotic catastrophe and has been associated with adverse events

ACR-368 IS SYNERGISTIC WITH AND OVERCOMES RESISTANCE TO WEE1 INHIBITOR

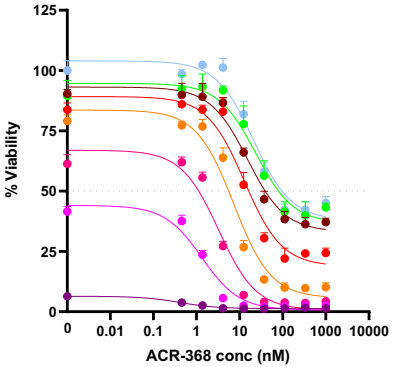
Human endometrial tumor cell line

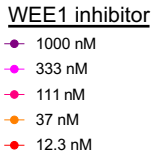


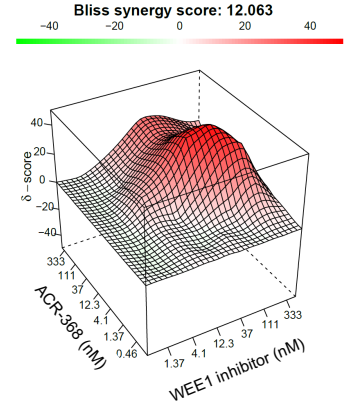


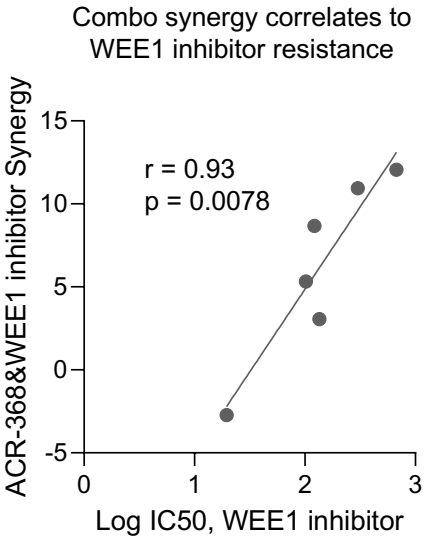


Human ovarian tumor cell line







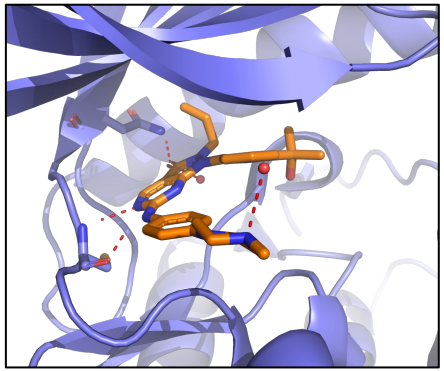


ACTIONABLE FINDINGS AND CONCLUSIONS

- AP3 enables unbiased measurement of compound-specific on- and off-target effects
- WEE1 inhibitors all demonstrate activation of CDK1/2 and cell cycle machinery
- Benchmark WEE1 inhibitor AP3 profiles can be leveraged for rational drug design and SAR ('dialing' in and out wanted and unwanted pathway effects)
- Differential actionable resistance mechanisms, e.g. WEE1 and CHK combination
- WEE1 inhibitor-treated patients predicted to still be sensitive to ACR-368

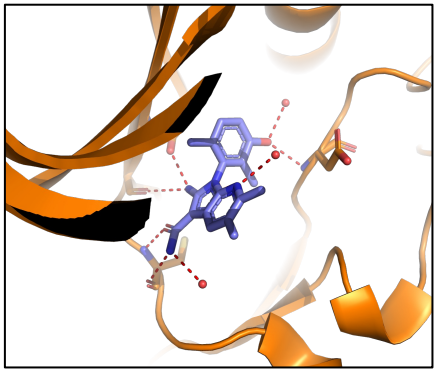
WEE1 AND PKMYT PROGRAM STATUS

- Hundreds of compounds designed and synthesized across multiple lead series
- High resolution co-crystal structures generated for >30 compounds in complex with Wee1 or PKMYT1 (resolution from about 1.5Å to <3Å)



Crystal structure of adavosertib:Wee1

Zhu et al, J. Med. Chem. 2017 60:7863–7875 (PDP: 5V5Y)



Crystal structure of RP-6306:PKMYT1

Szychowski et al, J. Med. Chem. 2022; 65:10251–10284 (PDP 8D6E)

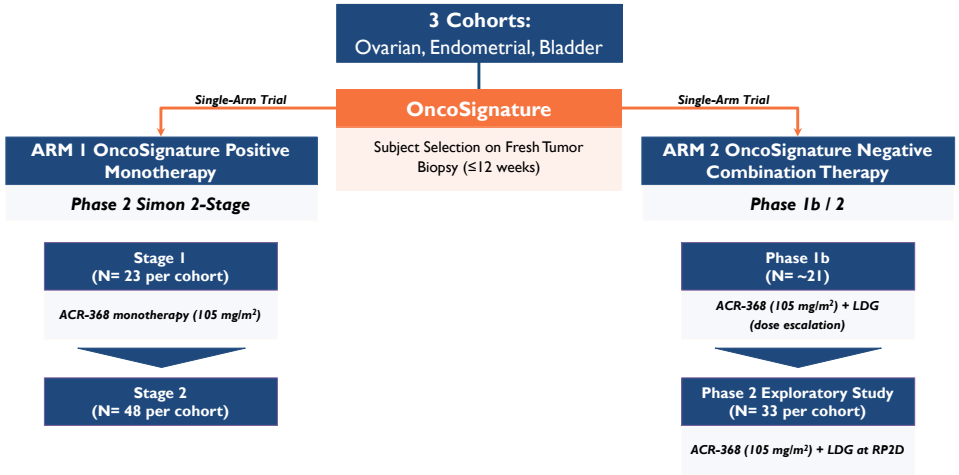
EXEMPLARY PKMYT1 AND WEE1 AND DUAL-SELECTIVE LEAD COMPOUND PROFILES

Compound	CMPD-2655	CMPD-2714	CMPD-2707	CMPD-2743 (A)
Wee1 IC_{50}	451 nM	251 nM	410 nM	1.3 nM
PKMYT1 IC_{50}	6.5 nM	2.9 nM	1.8 nM	20.6 nM
TE EC_{50}	118 nM (PKMYT1)	47.1 nM (PKMYT1)	56 nM (PKMYT11)	17 nM (Wee1) 233 nM (PKMYT1)
hERG IC_{50} (in vitro)	TBD	>100 µM	760 µM	1.4 µM
Hu microsomal Clint (µl/min/mg)	17	13	<10	102
Rat microsomal Clint (µl/min/mg)	17	16	<10	TBD
Mu t½ (IV); Vdss (L/kg); %F	0.9 hr; 2.71; 50%	1.8 hr; 3.19; 75%	0.9; 1.43; 64%	1.5 hr; 4.4; 25.3%

Compound	CMPD-2743	CMPD-2736	CMPD-2804	CMPD-2858
Wee1 IC_{50}	1.3 nM	1.25 nM	2.5 nM	2.1 nM
PKMYT1 IC_{50}	20.6 nM	45.8 nM	91% @ 10 µM	84% @ 10 µM
TE EC_{50}	17 nM (Wee1)	15 nM (Wee1)	9.9 nM (Wee1)	47.9 (Wee1)
Cell viability IC_{50}	25 nM	33 nM	N.D.	N.D.
hERG IC_{50} (in vitro)	1.4 µM	>100 µM	3.0 µM	4.0 µM
Rat microsomal Clint (µl/min/mg)	TBD	<10	-	TBD
Rat PO AUC/dose (h/L*kg)	0.185	0.05	0.09	0.21
Mu t½ (IV); Vdss (L/kg); %F	1.5 hr; 4.4; 25.3	N.D.	N.D.	N.D.

ACR-368 CLINICAL TRIAL

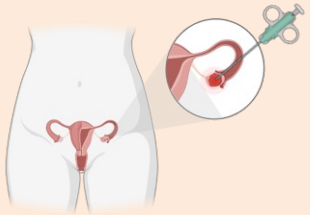
- We reconfirm our guidance and timeline of initial clinical readouts of our Phase 2 and Phase 1b/2 clinical trial in H2 2023
- Enrolling and dosing patients at the RP2D of ACR-368 based on predicted sensitivity using our ACR-368 OncoSignature Assay run by our CDx partner
- 19 sites currently activated[1]
- Key opinion leaders with extensive experience using ACR-368 from previous trials are actively participating



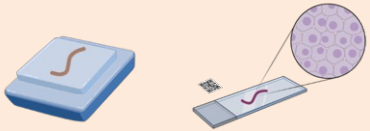
[1]https://clinicaltrials.gov/ct2/show/NCT05548296

ONCOSIGNATURE® TESTS: USAGE IN THE CLINIC

Pretreatment tumor biopsy

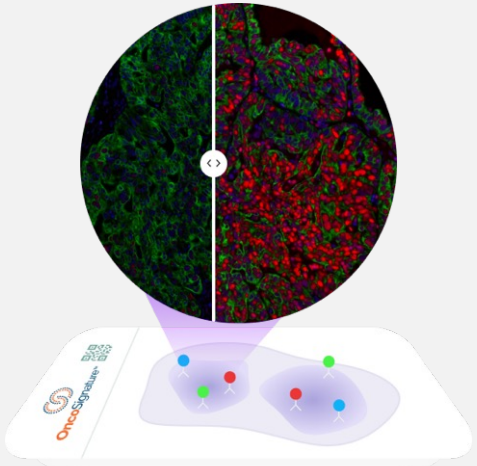


Sample processing



Biopsy in FFPE block

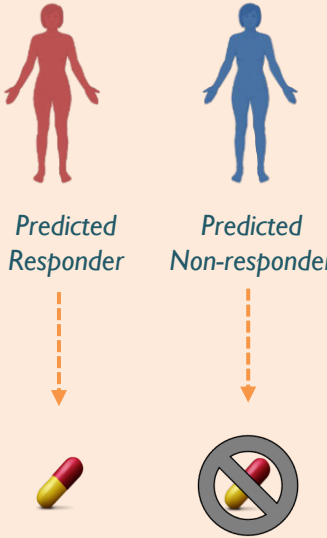
Automated tumor Region-of-Interest biomarker scoring



OncoSignature® test

- 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



Predicted Responder

Predicted Non-responder

FINANCIAL HIGHLIGHTS

Cash and marketable securities

$159.5M

Balance sheet 31-March-2023

Projected runway at least into

Q4'24

Current operating plan, assuming no additional financing

Fully Diluted Shares Outstanding

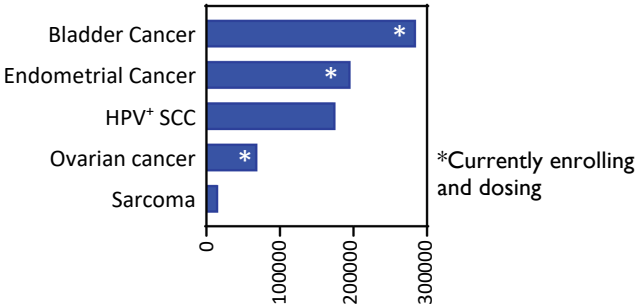
27.0M

Shares and equity grants outstanding 31-March-2023

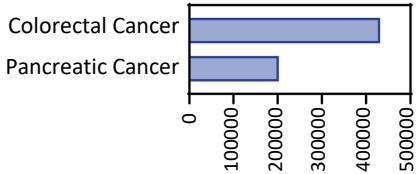
Unaudited.

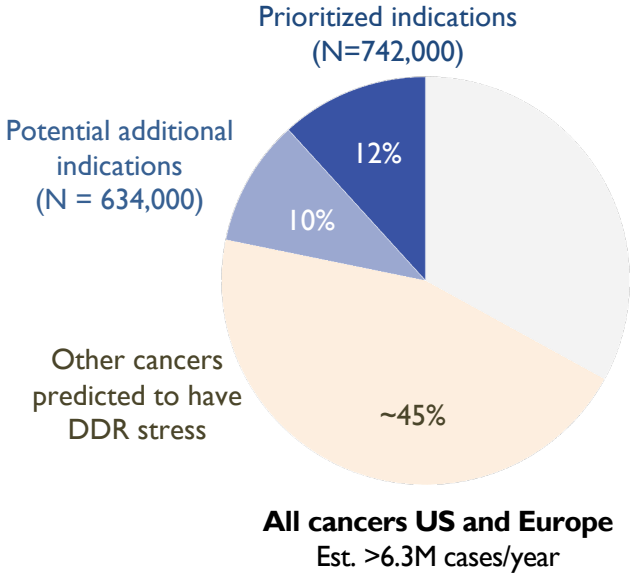
ACRIVON ADDRESSABLE MARKETS (US & EU INCIDENCE)

Prioritized indications for single agent ACR-368



Potential additional indications for single agent ACR-368





- ~30% (N = 223,000) of prioritized indications predicted sensitive to single agent ACR-368
- WEE1 and/or PKMYT1 inhibitor combinations with ACR-368 might further expand addressable fraction within sensitive tumor types

US cancer stats are based on ACS 2022 publication and subtype estimation from literature; EU cancer stats are based on IARC 2020 publication and subtype estimation from literature.
Cancers with DDR stress are estimated to be 67% which is calculated from MSK-IMPACT patient samples with DDR relevant mutations and CNVs, such as TP53, KRAS, CCNE1, etc.

THE AP3 APPROACH IS MODALITY AND DISEASE AGNOSTIC

Therapeutic modalities

Therapeutic areas