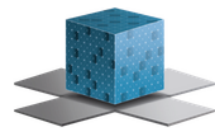


A novel platform to identify synergistic drug combination to combat cancer recurrence and prolong clinical efficacy

ChemAxon User Meeting, Cambridge MA, March 25-26 2019

Stephan Schürer

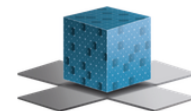
Department of Molecular and Cellular Pharmacology, Department of Psychiatry, Sylvester Comprehensive Cancer Center, Center for Molecular Therapeutics, Center for Computational Science, BD2K LINCS Data Coordination and Integration Center, University of Miami, Miami, FL, USA



BD2K-LINCS
DATA COORDINATION AND
INTEGRATION CENTER



Acknowledgements



BD2K-LINCS
DATA COORDINATION AND
INTEGRATION CENTER

- **Amar Koleti**
 - Dušica Vidović
 - John Turner
 - Tanya Kelley
 - Afoma Umeano
 - Derek Essegian
 - **Vasileios Stathias**
 - Caty Chung
 - Daniel Cooper
 - Rimpi Khurana
- Avi Ma'ayan
 - Mario Medvedovic
 - Stephan Schürer
- **Nagi Ayad**

<http://bd2k-lincs.org/#/about#team>

sschurer@miami.edu

BD2K-LINCS DCIC U54 HL127624



NIH LINCS
PROGRAM



ChemAxon

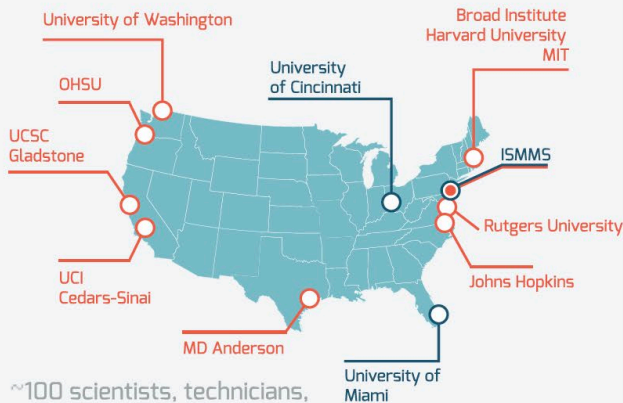


UNIVERSITY
OF MIAMI

LINCS

BY THE NUMBERS

15 INSTITUTIONS



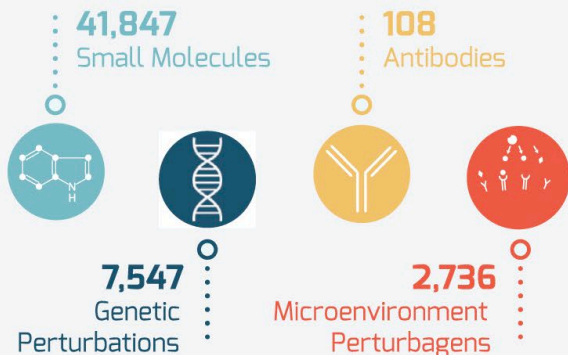
Data Coordination and Integration Center

BD2K-LINCS | ISMMS | University of Miami | University of Cincinnati

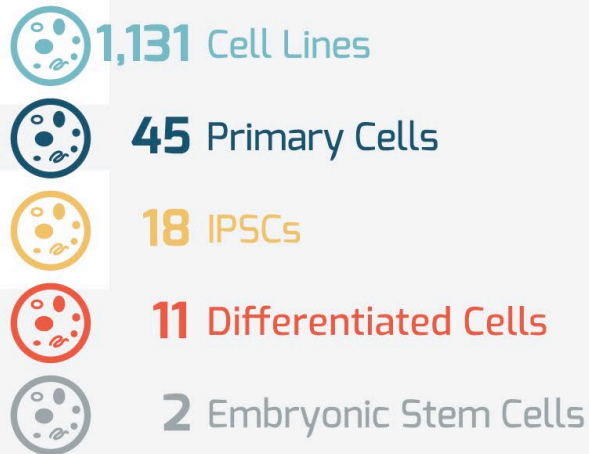
Data and Signature Generation Centers

| NeuroLINCS | MEP LINCS | DToxS | PCCSE |
|--|---------------------|---|--|
| UCI Cedars-Sinai Gladstone Johns Hopkins MIT | OHSU MD Anderson | ISMMS Rutgers University | Broad Institute University of Washington MIT |
| HMS LINCS Harvard University UCSC | | Broad Transcriptomics Broad Institute | |

4 PERTURBATION TYPES



5 CELL TYPES



5 SIGNATURE TYPES

Transcriptomics



Proteomics



Binding



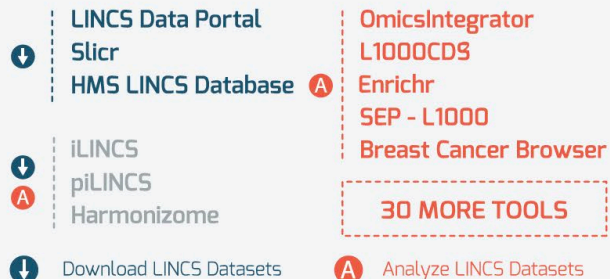
Epigenomics



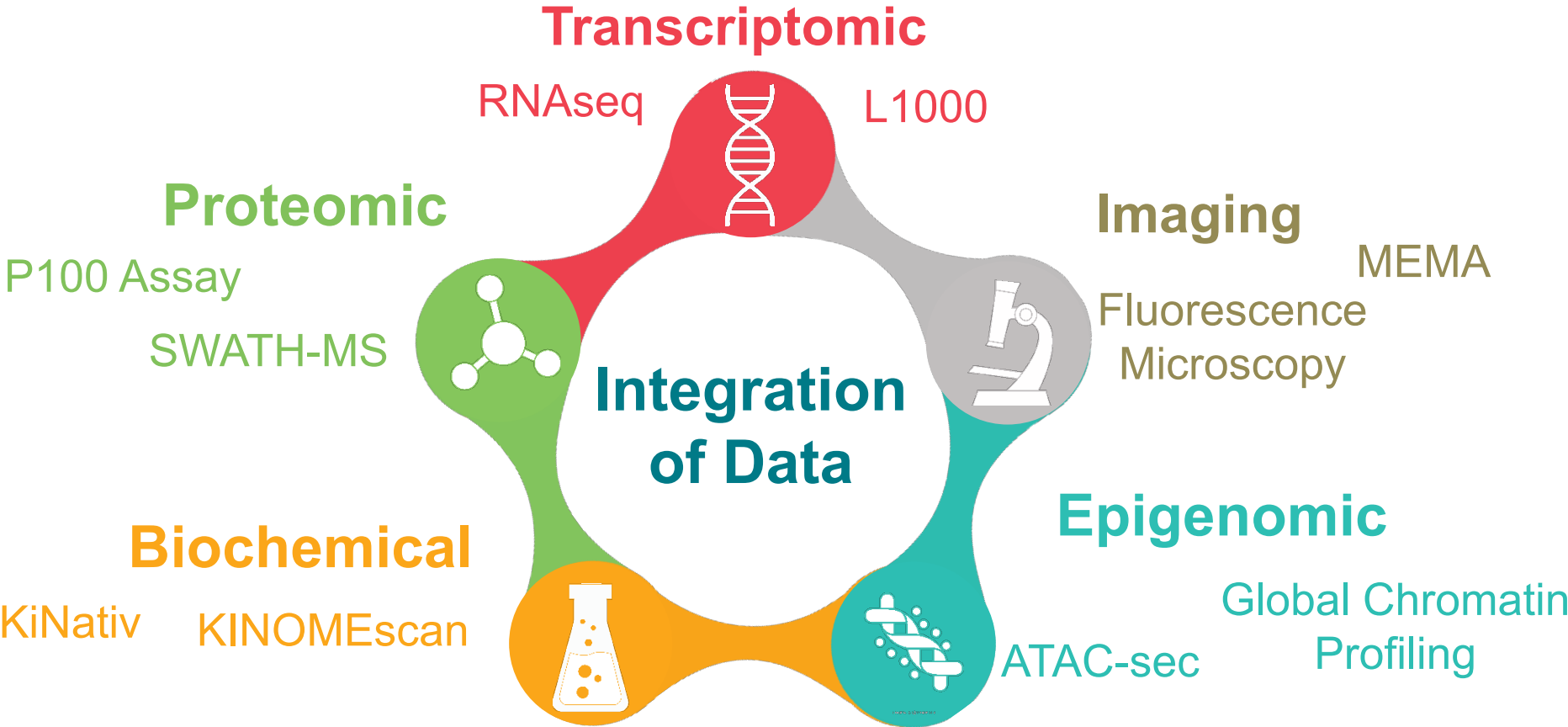
Imaging



FEATURED LINCS TOOLS

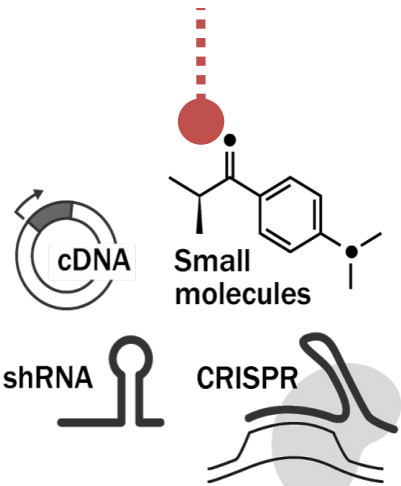


LINCS Project generates diverse multidimensional data

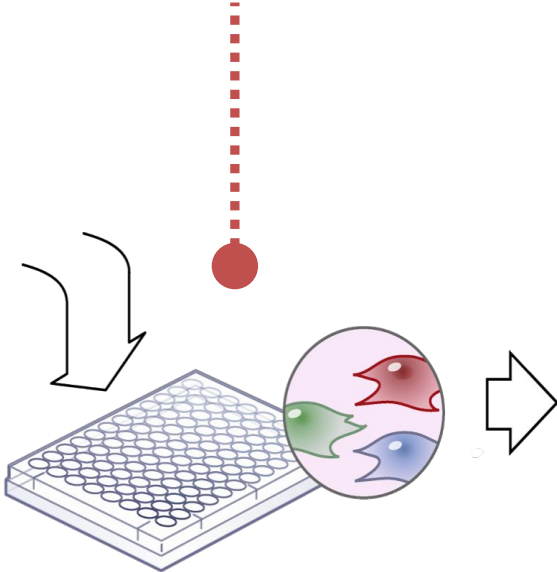


LINCS Signatures characterize diverse cellular responses upon perturbation

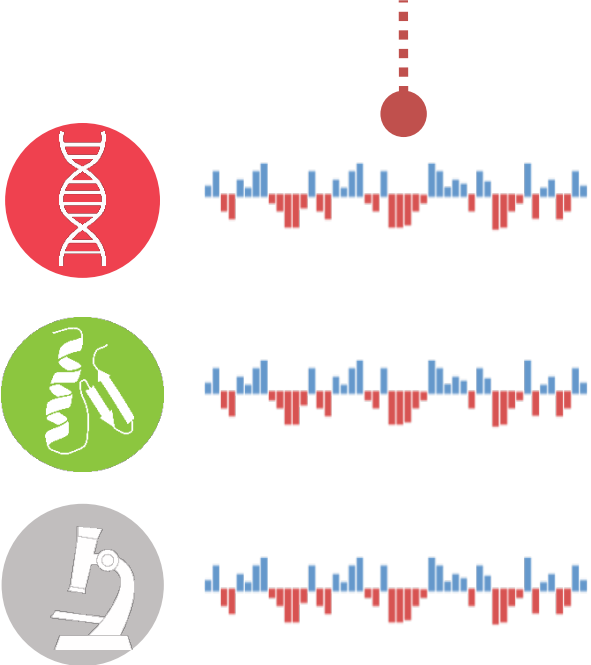
Perturbations



Cell Lines



Signatures



LINCS Data Portal - Home Page



381 Datasets



41847 Small Molecules



1127 Cells



978 Genes



1469 Proteins /155 Peptide Probes



8 Antibodies

14 Methods

06 Subject Areas

12 Centers

06 Projects

11 Biological Processes

Binding

Imaging

Transcriptomics

Proteomics

Epigenomics

Metabolomics

201 Datasets

85 Datasets

12 Datasets

9 Datasets

4 Datasets

1 Datasets

KINOMEScan kinase-small molecule binding assay

163 Datasets

KiNativ kinase-small molecule binding assay

30 Datasets

Bead-based immunoassay for protein state

3 Datasets

ELISA protein secretion profiling assay

3 Datasets

ELISA protein state assay

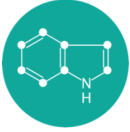
2 Datasets

KINOMEScan kinase-small molecule binding assay

Assay Overview

Compounds that bind the kinase active site and directly (sterically) or indirectly (allosterically) prevent kinase binding to the immobilized ligand, will reduce the amount of kinase captured on the solid support (Panels A & B). Conversely, test molecules that do not bind the kinase have no effect on the amount of kinase captured on the solid support (Panel C). Screening hits are identified by

LINCS Data Portal - <http://lincsportal.ccs.miami.edu/>



Small Molecules

Accelerate the discovery of novel therapeutics for precision medicine by unravelling LINCS small molecules annotations for approved drugs, clinical phase and chemical probes.

Search assays, cell lines, and perturbagens...

[Browse](#) | [Structure Search](#) | [About](#) | [Help](#)

Search for Small Molecule

Search LINCS small molecules by generic names, synonyms, trade names and explore across LINCS datasets, model systems and annotations.

Example search for [Seliciclib](#) can query using either "[Roscovitine](#)" or "[CYC-202](#)". A comprehensive list of generic names and synonyms are also stored and can be used as search terms.

Explore Annotations

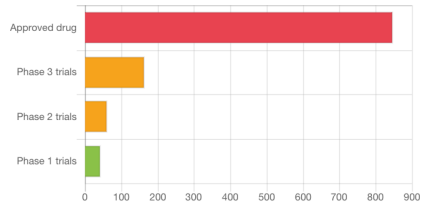
Search can be performed by a wide set of annotations such as mechanism of actions [Cyclin-dependent kinase 2 inhibitor](#), MESH terms [CARCINOMA](#), EFO terms [CYSTIC FIBROSIS](#) and cells [MCF7](#).

Advanced Search

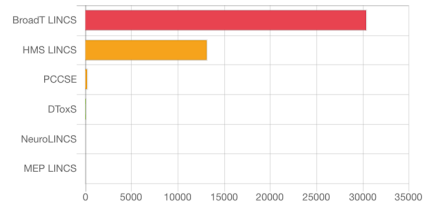
Search also facilitates AND , OR , NOT queries. Some examples 1) find Small Molecules that are used in KINOMEScan and L1000 assays. 2) Find Small Molecules that have annotated as Cyclin-dependent inhibitor or kinase inhibitor.

Statistics

Small Molecules by FDA PHASE



Small Molecules by Source



Cells

Accelerate the discovery of novel therapeutics for precision medicine by unravelling LINCS cells annotations.

Search assays, cell lines, and perturbagens...

[Browse](#) | [About](#) | [Help](#)

Search for Cells

Search LINCS cells by generic names, synonyms, diseases and explore across LINCS datasets, perturbagens and annotations.

Example search for [MCF7](#) or explore more details through the Cell Landing Pages "[MCF7](#)". A comprehensive list of generic names and synonyms are also stored and can be used as search terms.

Explore Annotations

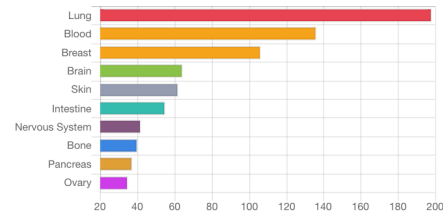
Search can be performed by a wide set of annotations such as organs [Breast](#), Diseases [Melanoma](#), Assays [Fluorescence imaging cell growth inhibition assay](#) and Small Molecules [Enzastaurin](#).

Advanced Search

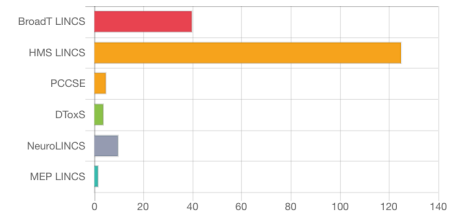
Search also facilitates AND , OR , NOT queries. Some examples 1) find cells that are used in P100 and L1000 assays. 2) Find cells that are derived from Lung.

Statistics

Cells by Organ



Cells by Center



L1000 Dataset -small molecule perturbagens- LINCS Phase 2 (June 2015) (LDG-1227: LDS-1273, LDS-1274, LDS-1275, LDS-1233)



Description **Metadata** Download Analysis Tools Visualize Community

LINCS ID LDG-1227: LDS-1273, LDS-1274, LDS-1275, LDS-1233

Center: Todd Golub, Aravind Subramanian: L1000 Dataset -small molecule perturbagens- LINCS Phase 2 (June 2015), 2015, LINCS (collection), <http://identifiers.org/lincs.data/LDG-1227>, retrieved: Oct 20, 2017.

Description: Data measured for 978 representative genes in 15 cell lines treated with 241 small molecules.

Data Source <http://www.ncbi.nlm.nih.gov/g>

Release Date Jun 30, 2015

Processing Pipeline <https://github.com/cmap/11k>

Citation *To cite a specific dataset*

Export:

Assay Name L1000 mRNA profiling assay

Assay Description L1000 is a bead-based, high-throughput chemical and genetic perturbation assay. The data is processed through a computational pipeline to generate expression signatures. The data contains a fluorescence intensity per 1,000 genes after deconvolution of the directly measured landmark transcripts. Level 4 scores for each profile relative to the control.

Assay Protocol

Keywords

L1000 Dataset -small molecule perturbagens- LINCS Phase 2 (June 2015) (LDG-1227: LDS-1273, LDS-1274, LDS-1275, LDS-1233)



Description **Metadata** Download Analysis Tools Visualize Community

277 Small molecules

5 Cell lines

Small molecules

| Name | LINCS ID | Center Sample ID | Provider | Provider Catalog ID |
|------------------------|----------|------------------------|--|----------------------|
| NU-7441 | LSM-1061 | BRD-K00337317-001-05-8 | Shanghai Haoyuan Chemexpress Co., Ltd. | HY-11006 |
| BRD-K00337317-001-05-8 | LSM-1061 | BRD-K00337317-001-05-8 | Shanghai Haoyuan Chemexpress Co., Ltd. | XMD11-50; LRRK2-in-1 |
| BRD-K00337317-001-05-8 | LSM-1061 | BRD-K00337317-001-05-8 | Shanghai Haoyuan Chemexpress Co., Ltd. | HY-12041 |
| BRD-K00337317-001-05-8 | LSM-1061 | BRD-K00337317-001-05-8 | Shanghai Haoyuan Chemexpress Co., Ltd. | HY-10162 |
| BRD-K00337317-001-05-8 | LSM-1061 | BRD-K00337317-001-05-8 | Shanghai Haoyuan Chemexpress Co., Ltd. | HY-10162 |

Showing 1 to 5 of 277 small molecules

L1000 Dataset -small molecule perturbagens- LINCS Phase 2 (June 2015) (LDG-1227: LDS-1273, LDS-1274, LDS-1275, LDS-1233)



Description **Metadata** Download Analysis Tools Visualize Community

| Data Level | Data Description | Dataset ID | Version | Size | Download | Cite |
|------------|------------------|-----------------------|---------|-------------|---|---|
| 1 | LDS-1273 | Raw dataset | 1.0 | 51736.33 MB | <input type="button" value="Download"/> | <input type="button" value="Cite"/> <input type="button" value="Export"/> |
| 2 | LDS-1274 | Processed raw dataset | 1.0 | 372.90 MB | <input type="button" value="Download"/> | <input type="button" value="Cite"/> <input type="button" value="Export"/> |
| 3 | LDS-1275 | Normalized dataset | 1.0 | 11294.75 MB | <input type="button" value="Download"/> | <input type="button" value="Cite"/> <input type="button" value="Export"/> |
| 4 | LDS-1233 | Signature dataset | 1.0 | 9769.81 MB | <input type="button" value="Download"/> | <input type="button" value="Cite"/> <input type="button" value="Export"/> |

| Provider | Provider Catalog ID |
|---|-----------------------|
| ATCC Own, Mario Niepel (Harvard Medical School) | null, æHTB-22, HTB-22 |
| | CCL-185 |
| | CRL-4010 |
| Institute | contact provider |
| The Broad Institute, æThe Broad Institute | contact provider, N/A |

Showing 1 to 5 of 277 small molecules

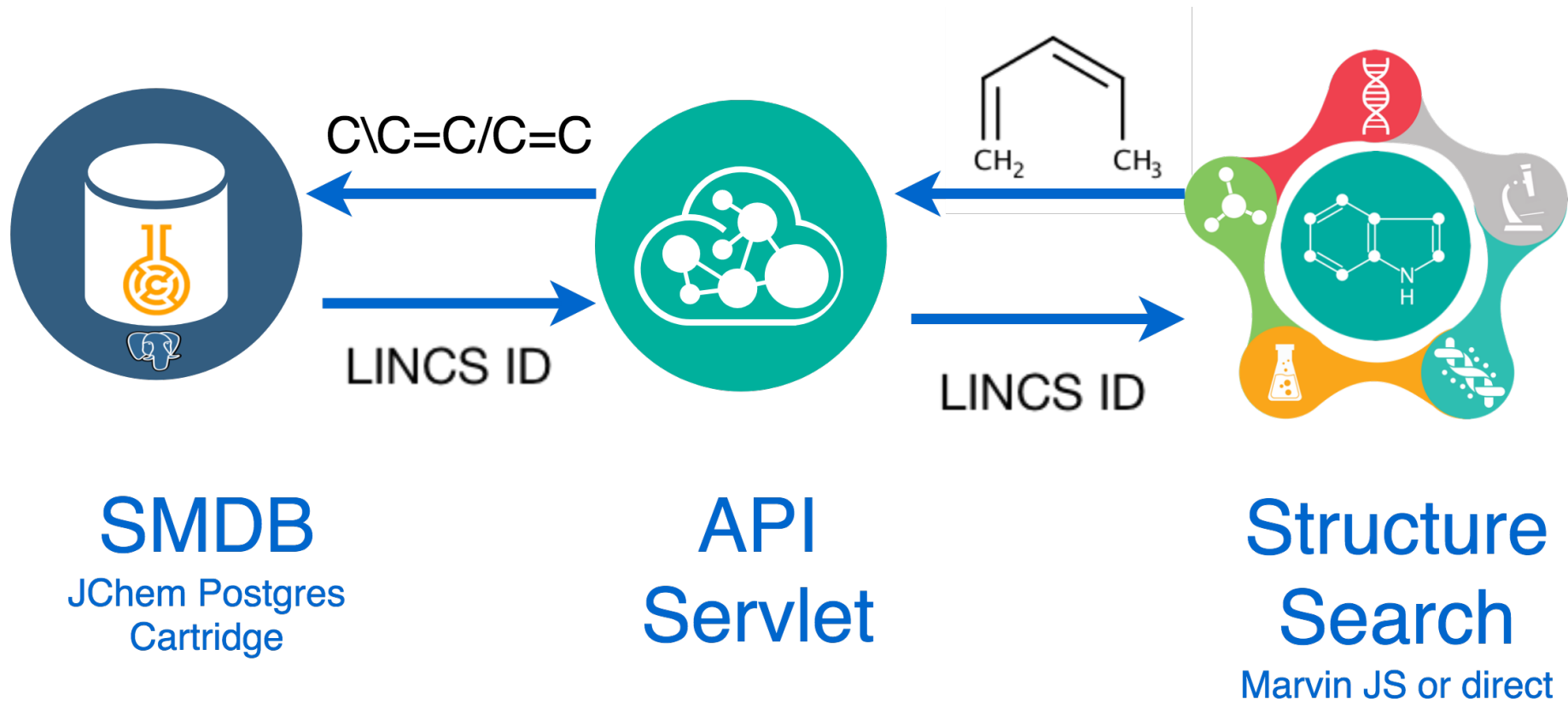


The image shows a chemical structure editor window. In the center, a chemical structure is displayed: a pyridine ring (a six-membered aromatic ring with two nitrogen atoms) is connected at its 2-position to an amine group (-NH-), which is in turn connected to a benzene ring. The interface includes a toolbar at the top with icons for file operations (save, undo, redo, delete, copy, paste, zoom, settings, help) and navigation (left and right arrows). On the left side, there is a vertical toolbar with icons for selecting, drawing lines, rings, and adding/removing atoms. On the right side, there is a vertical element palette listing atoms: H, C, N, O, S, F, P, Cl, Br, I, and a dot representing a radical. At the bottom of the editor, there are icons for drawing various rings (square, pentagon, hexagon, heptagon, octagon) and zoom controls.

Provide Feedback

Substructure Search Similarity Search

LDP Chemical Structure Search Engine



OR

LINCS Center

- BroadT LINCS 67
- HMS LINCS 48

[+ More](#)

Bioassay Type

- L1000 mRNA profiling assay 68
- KINOMEScan kinase-small molecule binding assay 39

[+ More](#)

Clinical Phase

- Approved drug 7
- Phase 2 trials 7

[+ More](#)

Pharmacological Classification

- Tyrosine kinase inhibitors 9
- Protein kinase inhibitors 6

[+ More](#)

Mechanism of Action

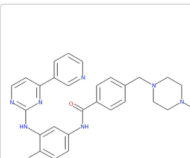
- Epidermal growth factor receptor erbB1 inhibitor 2
- Focal adhesion kinase 1 inhibitor 2

[+ More](#)

Search assays, cell lines, and perturbagens...

Filtered by: [LSM-15449](#) OR [LSM-21027](#) OR [LSM-24505](#) OR [LSM-1459](#) OR [LSM-18669](#) OR [LSM-4750](#) OR [LSM-36387](#) O ([Incidentifier](#)) [clear all](#)

Total Small Molecules: 93



Imatinib

Synonyms: GGP-57148B; Gleevec; Glivec; Imatinib; IMATINIB (352474); Imatinib Mesilate; Imatinib Mesylate; IMATINIB (STI571); STI-571

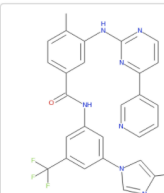
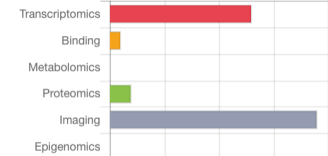
Max Phase: Approved drug

Mechanism of Action: Platelet-derived growth factor receptor beta inhibitor; Stem cell growth factor receptor inhibitor; Tyrosine-protein kinase ABL inhibitor [Explore](#)

Pharmacological Classification: Tyrosine kinase inhibitors; Protein kinase inhibitors [Explore](#)

Model Systems: 669 cell-lines used [Show](#) [Explore](#)

Datasets: Used in 32 Datasets [Show](#) [Explore](#)

[List view](#) [Table view](#) [Download](#)


Nilotinib

Synonyms: AMN-107; Nilotinib; NILOTINIB (AMN-107); Nilotinib Hydrochloride Monohydrate; Tasigna

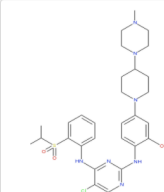
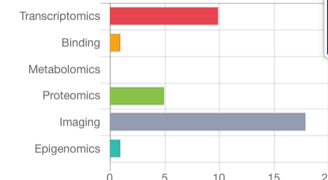
Max Phase: Approved drug

Mechanism of Action: Tyrosine-protein kinase ABL inhibitor [Explore](#)

Pharmacological Classification: Tyrosine kinase inhibitors; Protein kinase inhibitors [Explore](#)

Model Systems: 162 cell-lines used [Show](#) [Explore](#)

Datasets: Used in 31 Datasets [Show](#) [Explore](#)

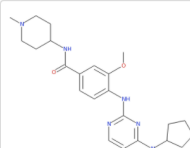
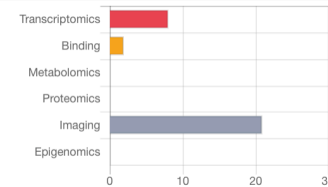


TAE-684

Synonyms: NVP-TAE684

Model Systems: 637 cell-lines used [Show](#) [Explore](#)

Datasets: Used in 28 Datasets [Show](#) [Explore](#)



BI-2536

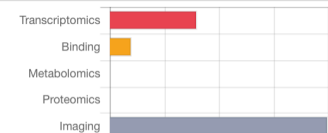
Synonyms: BI 2536; BI-2536; NPK33-1-98-1

Max Phase: Phase 2 trials

Mechanism of Action: Serine/threonine-protein kinase PLK1 inhibitor [Explore](#)

Model Systems: 644 cell-lines used [Show](#) [Explore](#)

Datasets: Used in 27 Datasets [Show](#) [Explore](#)



Profile Feedback

OR

LINCS Center

- BroadT LINCS 6
- HMS LINCS 5

[+ More](#)

Bioassay Type

- L1000 mRNA profiling assay 6
- KINOMEScan kinase-small molecule binding assay 5

[+ More](#)

Clinical Phase

- Approved drug 7
- Phase 2 trials 7

[+ More](#)

Pharmacological Classification

- Protein kinase inhibitors 5
- Tyrosine kinase inhibitors 4

[+ More](#)

Mechanism of Action

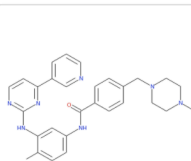
- Human immunodeficiency virus type 1 reverse transcriptase inhibitor 2
- Stem cell growth factor receptor inhibitor 2

[+ More](#)

Search assays, cell lines, and perturbagens...

Filtered by: [LSM-15449](#) OR [LSM-21027](#) OR [LSM-24505](#) OR [LSM-1459](#) OR [LSM-18669](#) OR [LSM-4750](#) OR [LSM-36387](#) O ([lincsidentifier](#)) ✕ [Approved drug \(FDA_PHASE\)](#) ✕ [clear all](#) ✕

Total Small Molecules: 7

[List view](#) [Table view](#) [Download](#)


Imatinib

Synonyms: CGP-57148B; Gleevec; Glivec; Imatinib; IMATINIB (3524741); Imatinib Mesilate; Imatinib Mesylate; IMATINIB (STI571); STI-571

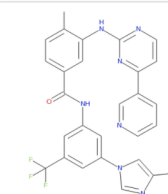
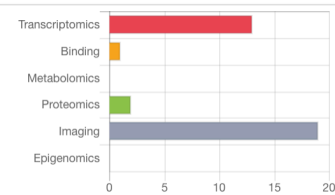
Max Phase: Approved drug

Mechanism of Action: Platelet-derived growth factor receptor beta inhibitor; Stem cell growth factor receptor inhibitor; Tyrosine-protein kinase ABL inhibitor [Explore](#)

Pharmacological Classification: Tyrosine kinase inhibitors; Protein kinase inhibitors [Explore](#)

Model Systems: 669 cell-lines used [Show](#) [Explore](#)

Datasets: Used in 32 Datasets [Show](#) [Explore](#)



Nilotinib

Synonyms: AMN-107; Nilotinib; NILOTINIB (AMN-107); Nilotinib Hydrochloride Monohydrate; Tasigna

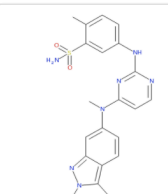
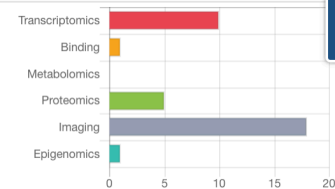
Max Phase: Approved drug

Mechanism of Action: Tyrosine-protein kinase ABL inhibitor [Explore](#)

Pharmacological Classification: Tyrosine kinase inhibitors; Protein kinase inhibitors [Explore](#)

Model Systems: 162 cell-lines used [Show](#) [Explore](#)

Datasets: Used in 31 Datasets [Show](#) [Explore](#)



Pazopanib

Synonyms: 635702-64-6; GW786034; GW786034B; Pazopanib; Pazopanib HCl; Pazopanib Hydrochloride; Votrient

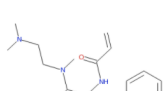
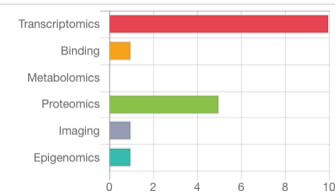
Max Phase: Approved drug

Mechanism of Action: Fibroblast growth factor receptor 3 inhibitor; Macrophage colony stimulating factor receptor inhibitor; Tyrosine-protein kinase LCK inhibitor; Tyrosine-protein kinase ITK/TSK inhibitor; Vascular endothelial growth factor receptor inhibitor; Stem cell growth factor receptor inhibitor; Platelet-derived growth factor receptor inhibitor; Fibroblast growth factor receptor 1 inhibitor [Explore](#)

Pharmacological Classification: Angiogenesis inhibitors; Protein kinase inhibitors [Explore](#)

Model Systems: 1115 cell-lines used [Show](#) [Explore](#)

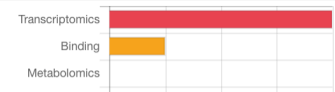
Datasets: Used in 13 Datasets [Show](#) [Explore](#)



Osimertinib

Synonyms: AZD-9291; AZD-9291 MESYLATE; HG-14-8-02; Osimertinib; Osimertinib Mesylate; Tagrisso

Max Phase: Approved drug



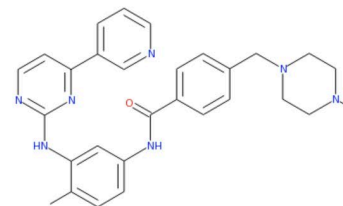


Imatinib (LSM-1023)

[Description](#) [Datasets](#) [Curated Data](#)

Compound Information

| | |
|-------------------|---|
| Name | Imatinib |
| LINCS (ID) | LSM-1023 |
| PubChem (CID) | 5291 |
| ChEBI (ID) | 31690 , 45783 |
| ChEMBL (ID) | CHEMBL1642 , CHEMBL2386595 , CHEMBL941 |
| Alternative Names | CGP-57148B; Gleevec; Glivec; Imatinib; IMATINIB (3524741); Imatinib Mesilate; Imatinib Mesylate; IMATINIB (STI571); STI-571 |
| SMILES | Show |
| InChI | Show |



Find Similar Structures

Similarity Search

POWERED BY ChemAxon

- 95% Similar Molecules
- 90% Similar Molecules
- 80% Similar Molecules

Related LINCS Compounds by chemical structure (similarity ≥ 0.9)

| |
|---------------------------|
| LSM-43288 |
| LSM-45329 |
| LSM-44525 |

Predicted Physicochemical Properties

| | |
|-------------------|-------------|
| Molecular formula | C29H31N7O |
| Molecular weight | 493.60g/mol |
| Lipinski 3 | Fail |
| Lipinski 5 | Pass |
| Bioavailability | Pass |
| Lead likeliness | Fail |

| | |
|------------------|-------|
| cLogP | 4.38 |
| Rotatable bonds | 7 |
| H bond acceptors | 7 |
| H bond donors | 2 |
| TPSA | 86.28 |
| QED | 0.40 |



OR

LINCS Center

- BroadT LINCS 3
- HMS LINCS 3

+ More

Bioassay Type

- KINOMEScan kinase-small molecule binding assay 3
- L1000 mRNA profiling assay 3

+ More

Clinical Phase

- Approved drug 1

+ More

Pharmacological Classification

- Protein kinase inhibitors 1
- Tyrosine kinase inhibitors 1

+ More

Mechanism of Action

- DNA topoisomerase II alpha inhibitor 1

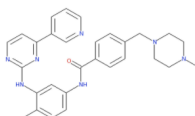
- Less

Search assays, cell lines, and perturbagens...

Filtered by: LSM-45329* OR *LSM-43288* OR *LSM-1023* OR *LSM-44525 (lincidentifer) x clear all x

Total Small Molecules: 4

List view Table view Download



Imatinib

Synonyms: CGP-57148B; Gleevec; Glivec; Imatinib; IMATINIB (3524741); Imatinib Mesilate; Imatinib Mesylate; IMATINIB (STI571); STI-571

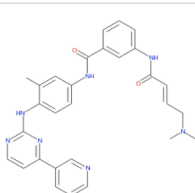
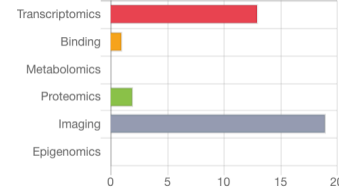
Max Phase: Approved drug

Mechanism of Action: Platelet-derived growth factor receptor beta inhibitor; Stem cell growth factor receptor inhibitor; Tyrosine-protein kinase ABL inhibitor [Explore](#)

Pharmacological Classification: Tyrosine kinase inhibitors; Protein kinase inhibitors [Explore](#)

Model Systems: 669 cell-lines used [Show](#) [Explore](#)

Datasets: Used in 32 Datasets [Show](#) [Explore](#)

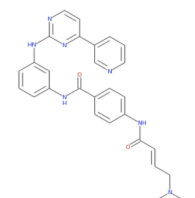
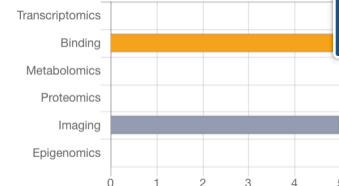


JNK-IN-8

Synonyms:

Model Systems: 14 cell-lines used [Show](#) [Explore](#)

Datasets: Used in 10 Datasets [Show](#) [Explore](#)

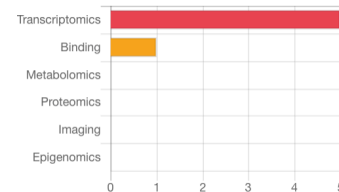


JNK-IN-2

Synonyms: ZG-10

Model Systems: 93 cell-lines used [Show](#) [Explore](#)

Datasets: Used in 6 Datasets [Show](#) [Explore](#)



Provide Feedback

Glioblastoma Multiforme (GBM)



- Most **common** and **aggressive** adult brain tumor
- Occurs primarily in ages of 45-70 years



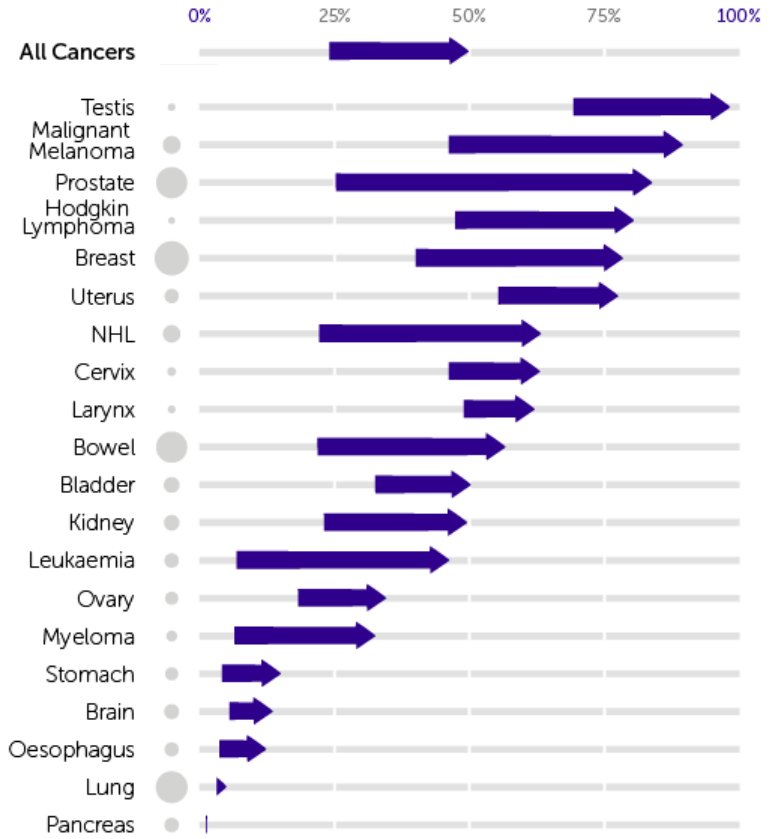
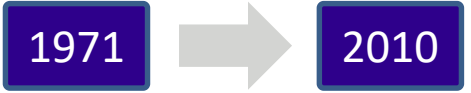
- Surgical resection followed by radiotherapy and temozolamide chemotherapy



- Annual incidence: 1 / 19,000
- 5-years survival rate **< 9.8%**

Little progress has been made in the survival of brain cancer patients

Changes in the 10-year survival



Little progress has been made in the survival of brain cancer patients

Changes in the 10-year survival

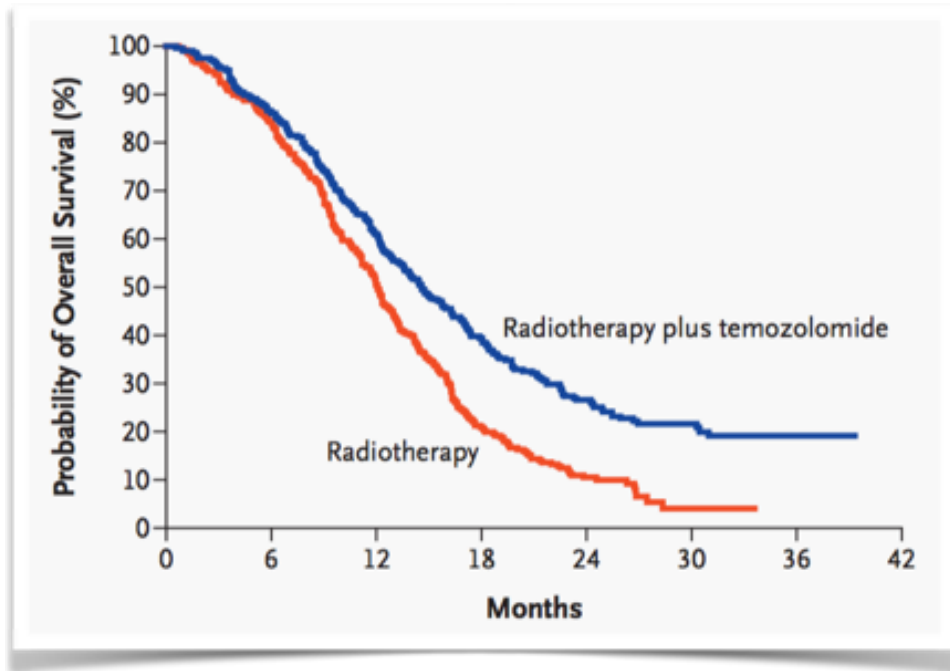
1971 → 2010



Brain Cancer



Current GBM Treatment is Ineffective



Standard of Care

1. Maximal surgical resection
2. Radiotherapy
3. Temozolomide (TMZ) treatment

No early detection Biomarker

Temozolomide (2005)

2.5 month increase in survival
(14.6 vs 12.1 months)

Stupp et al. 2005

Targeted phase III trials have failed to improve overall survival of Glioblastoma patients

VEGF



Avastin



Cediranib



Enzastaurin

MGMT



O⁶-BG

EGFR



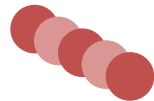
Nimotuzumab



Erlotinib



Gefitinib



Rindopepimut

ITGAV



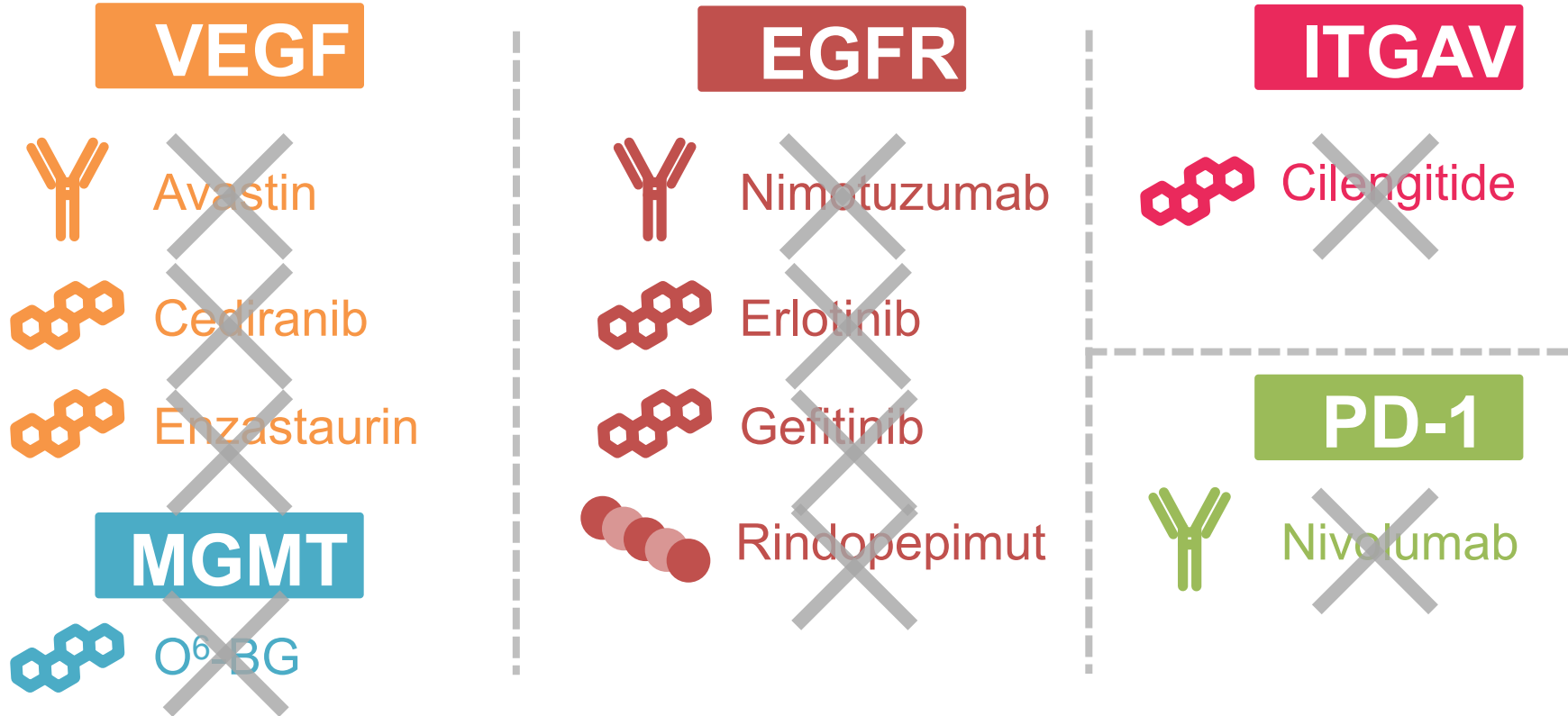
Cilengitide

PD-1



Nivolumab

Targeted phase III trials have failed to improve overall survival of Glioblastoma patients

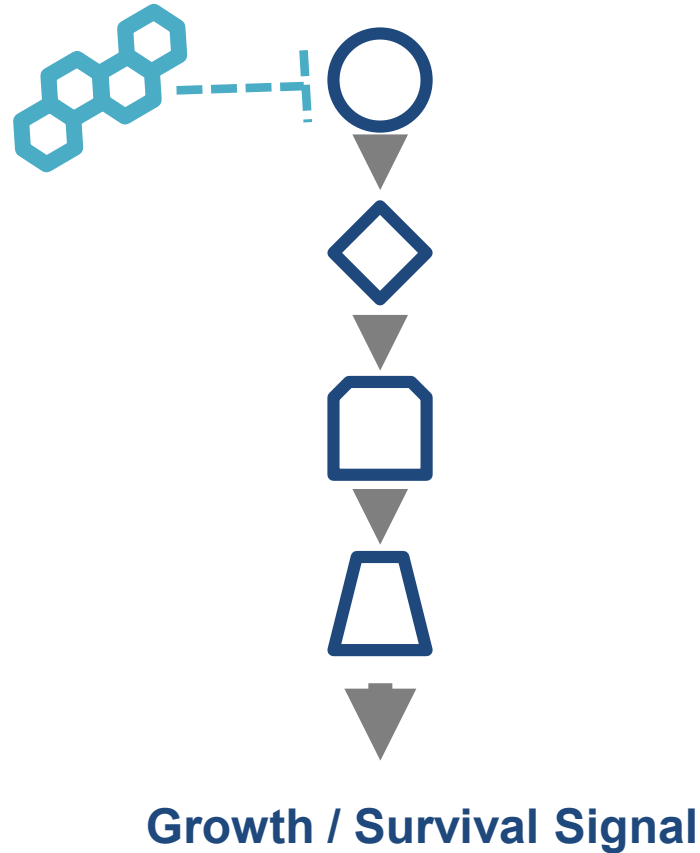


Tumors can adapt to targeted therapy by reprogramming signaling pathways resulting in resistance

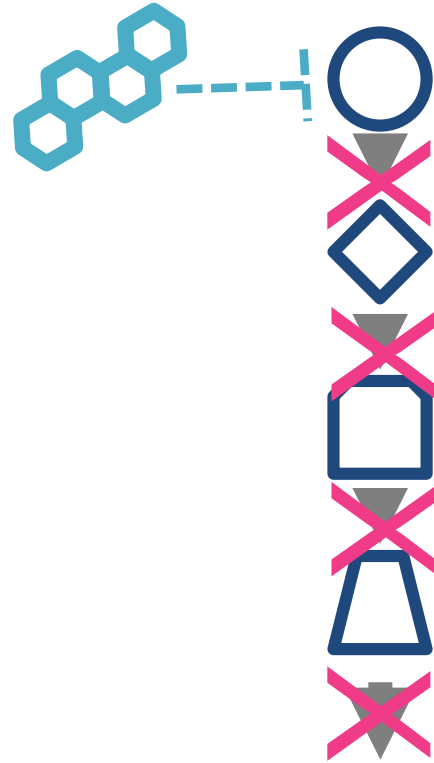


Growth / Survival Signal

Tumors can adapt to targeted therapy by reprogramming signaling pathways resulting in resistance

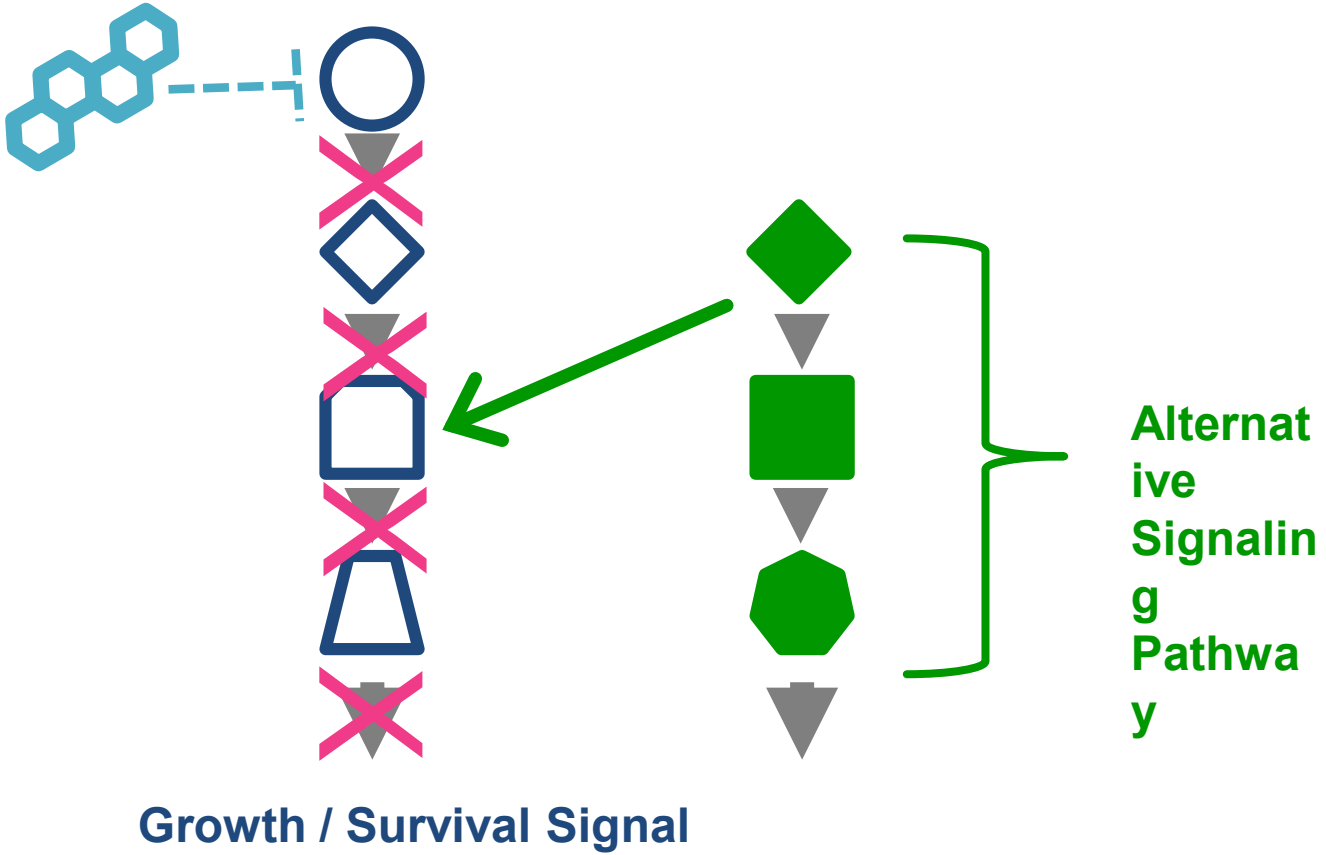


Tumors can adapt to targeted therapy by reprogramming signaling pathways resulting in resistance

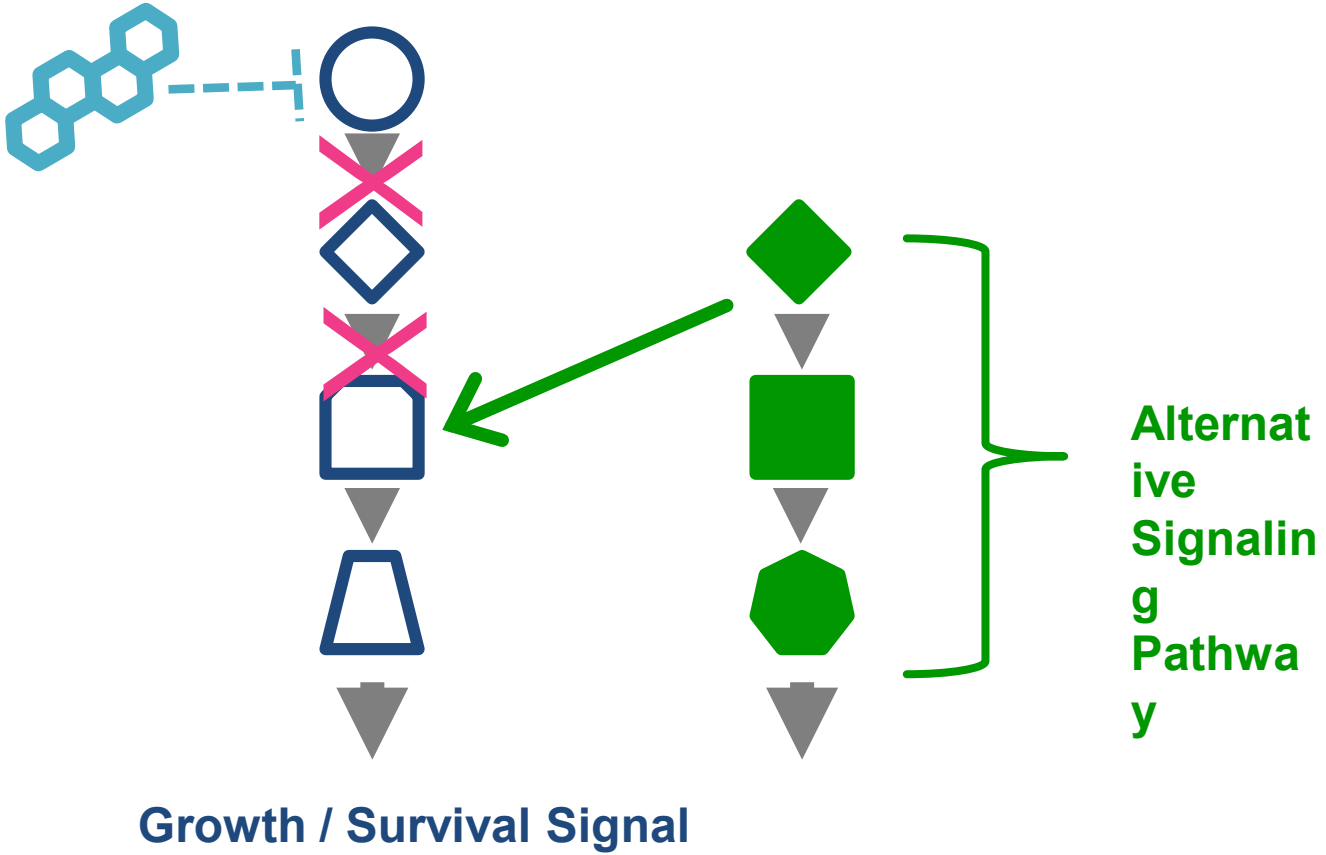


Growth / Survival Signal

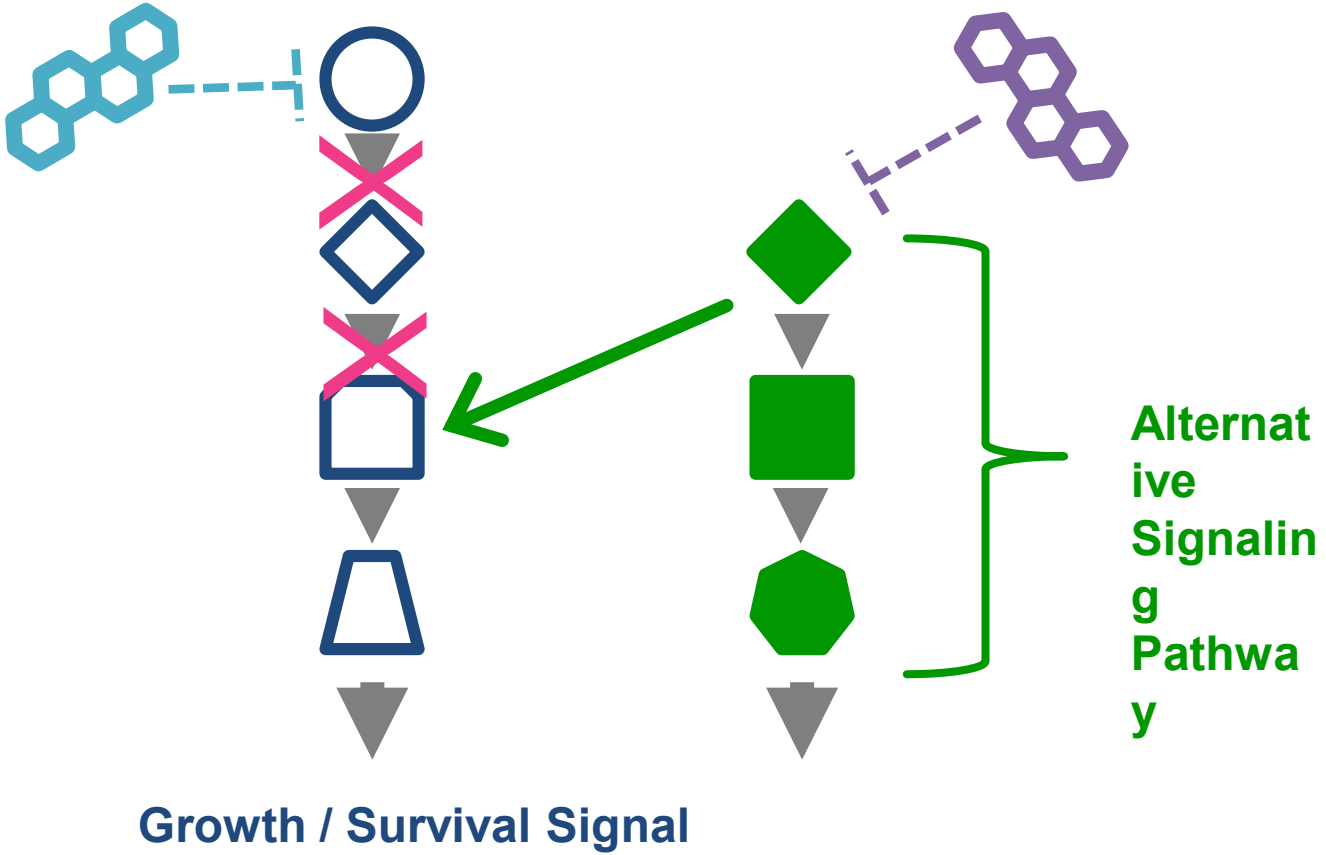
Tumors can adapt to targeted therapy by reprogramming signaling pathways resulting in resistance



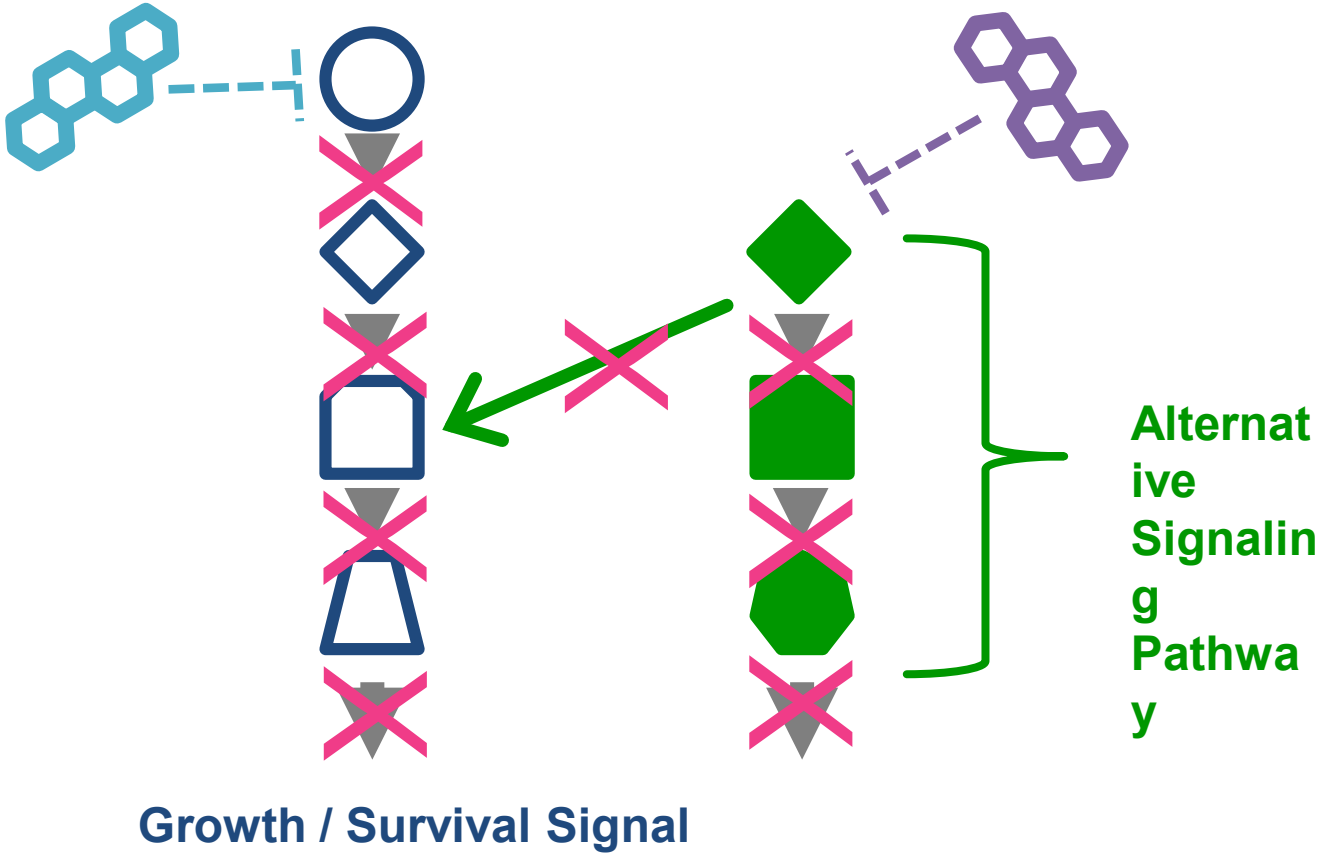
Tumors can adapt to targeted therapy by reprogramming signaling pathways resulting in resistance



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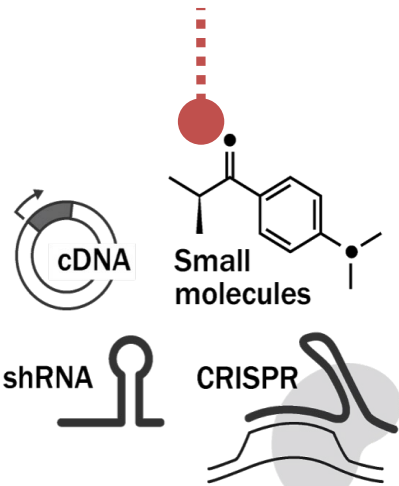


Tumors can adapt to targeted therapy by reprogramming signaling pathways resulting in resistance

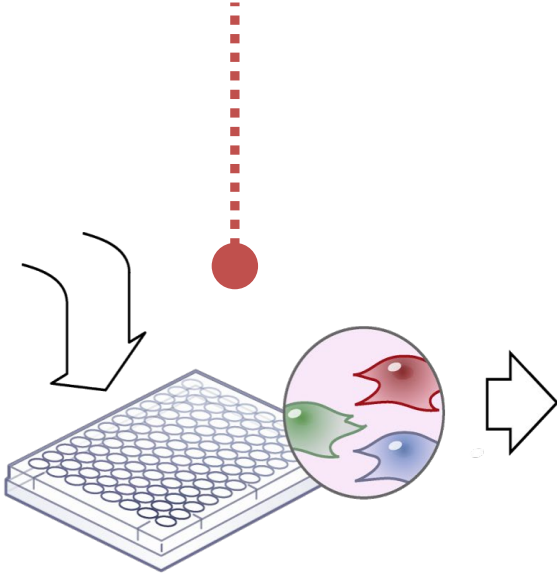


LINCS Signatures characterize diverse cellular responses upon perturbation

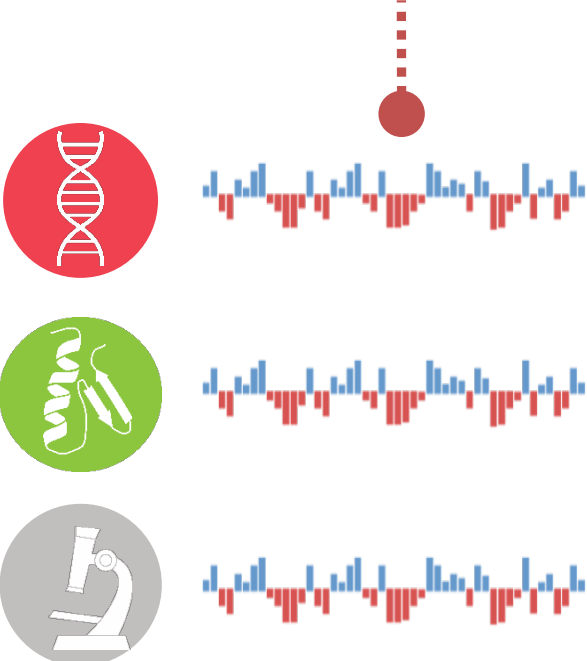
Perturbations



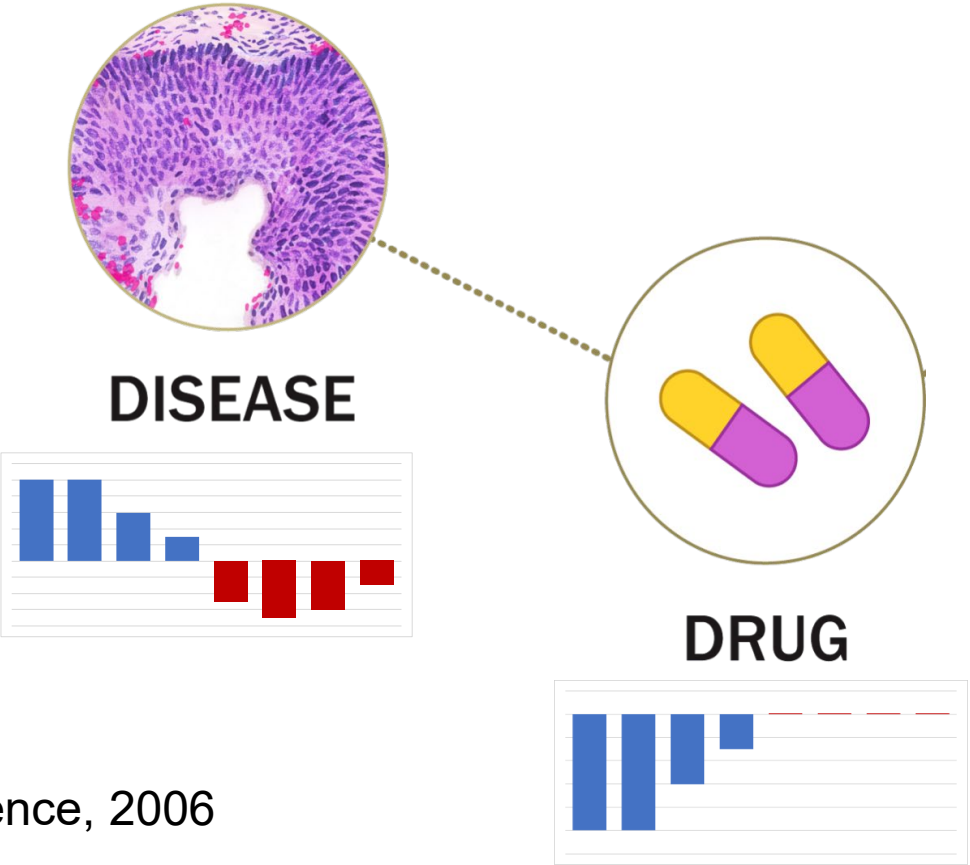
Cell Lines



Signatures



CMap concept: linking diseases to therapeutics



Lamb et al. Science, 2006

ARTICLE

Received 7 Dec 2016 | Accepted 17 May 2017 | Published 12 Jul 2017

DOI: [10.1038/ncomms16022](https://doi.org/10.1038/ncomms16022)

[OPEN](#)

Reversal of cancer gene expression correlates with drug efficacy and reveals therapeutic targets

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SCIENCE TRANSLATIONAL MEDICINE | RESEARCH ARTICLE

CANCER

Systems biology–based drug repositioning identifies digoxin as a potential therapy for groups 3 and 4 medulloblastoma

Lei Huang^{1*}, Sarah Garrett Injac^{2,3*}, Kemi Cui¹, Frank Braun², Qi Lin², Yuchen Du², Huiyuan Zhang², Mari Kogiso², Holly Lindsay^{2,3}, Sibao Zhao^{2,3}, Patricia Baxter^{2,3}, Adesina Adekunle⁴, Tsz-Kwong Man³, Hong Zhao¹, Xiao-Nan Li^{2,3†}, Ching C. Lau^{3†§}, Stephen T. C. Wong^{1†}

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SCIENTIFIC REPORTS

Personalised drug repositioning for Clear Cell Renal Cell Carcinoma using gene expression

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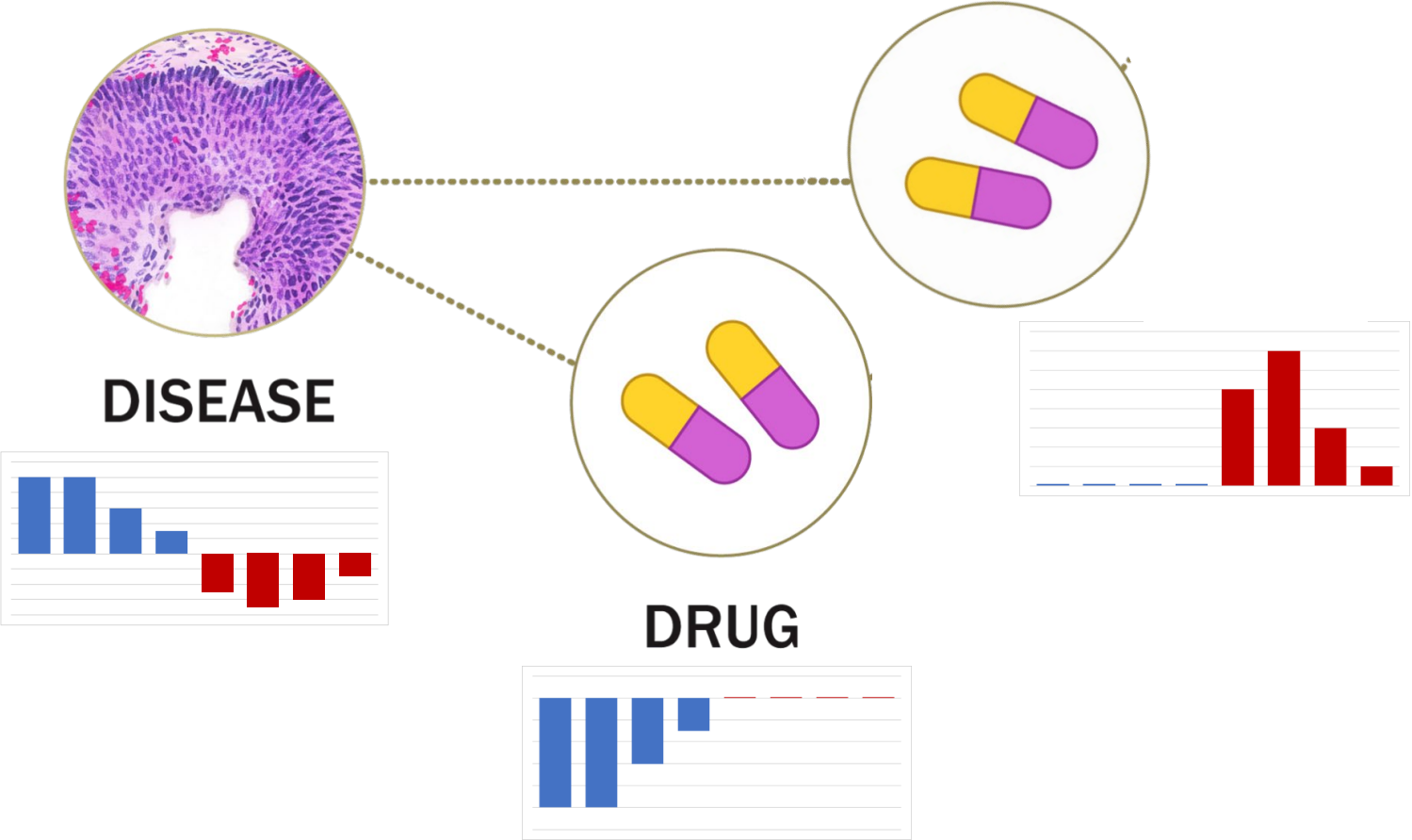
Integrated Systems and Technologies

Novel Drug Candidates for the Treatment of Metastatic Colorectal Cancer through Global Inverse Gene-Expression Profiling

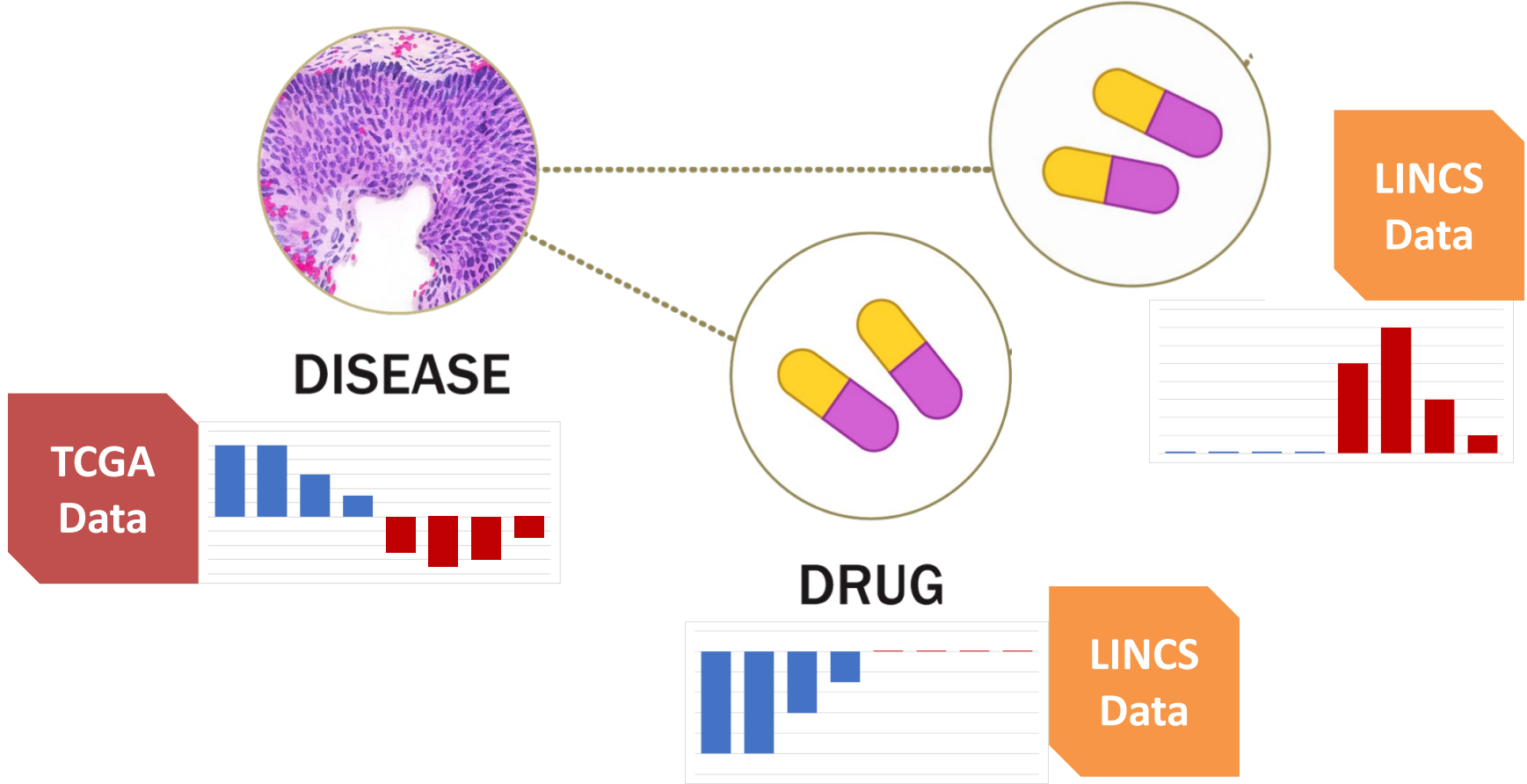
Vera van Noort^{1,2}, Sebastian Schölch³, Murat Iskar¹, Georg Zeller¹, Kristina Ostertag⁴, Christine Schweitzer³, Kristin Werner³, Jürgen Weitz³, Moritz Koch³, and Peer Bork^{1,5}

Cancer
Research

Similar approach for combination therapies



Similar approach for combination therapies



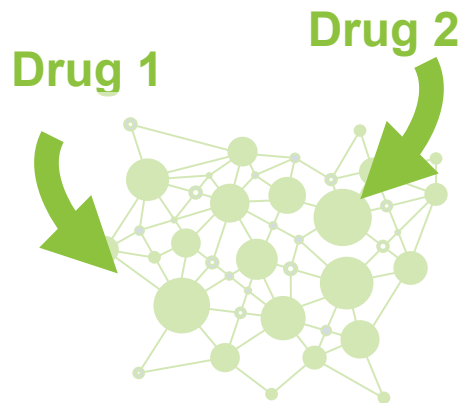
1

One Signature
per Compound



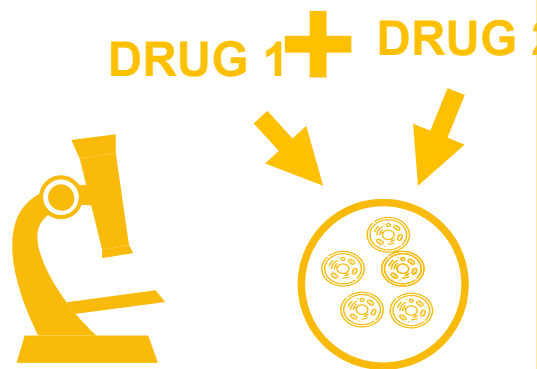
2

Identify Drug
Combinations



3

Validate
in vitro /
in vivo



1

One Signature
per Compound



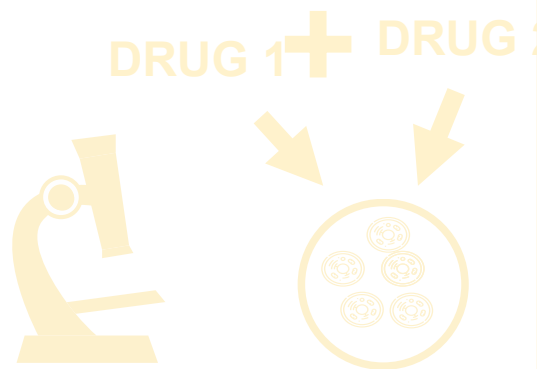
2

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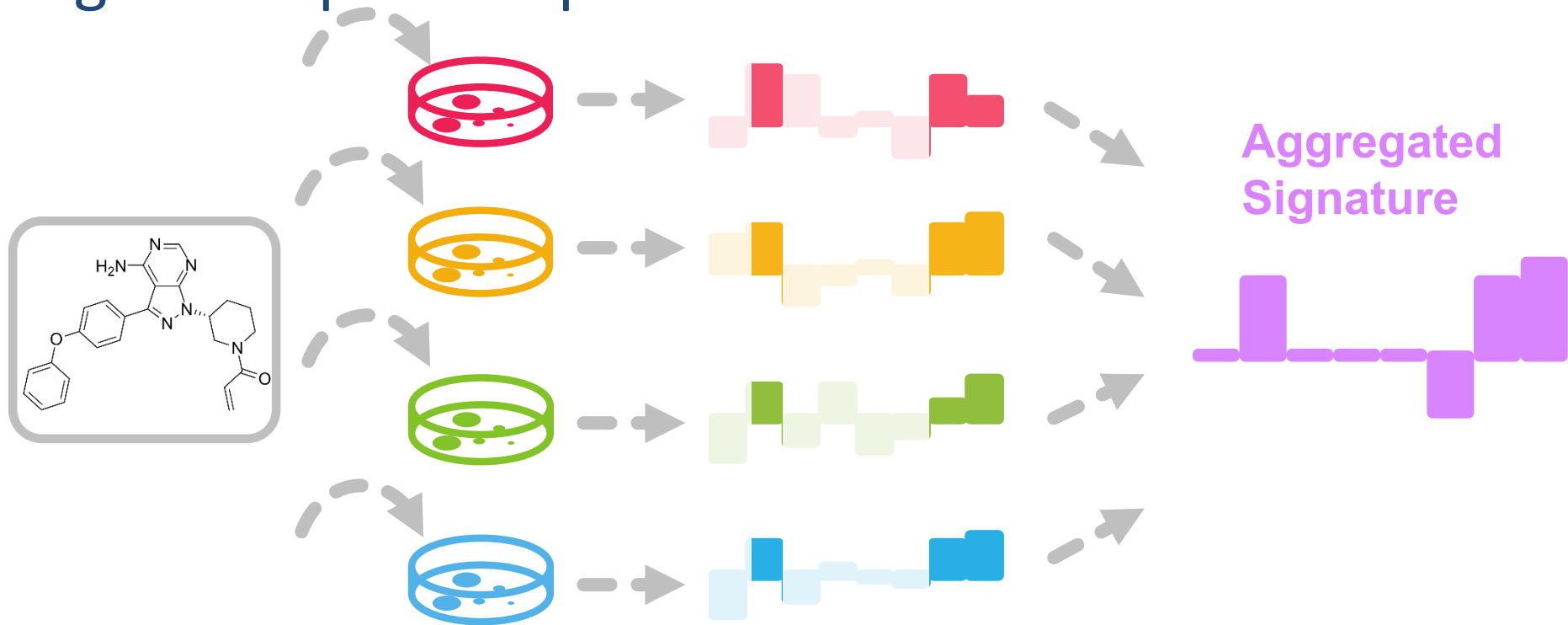


3

Validate
in vitro /
in vivo

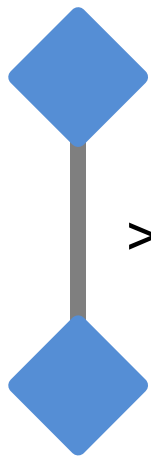


Collapse the gene expression profiles into one signature per compound



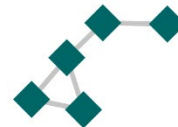
Compounds with same Mechanism of Action form distinct networks

Small Molecule 1

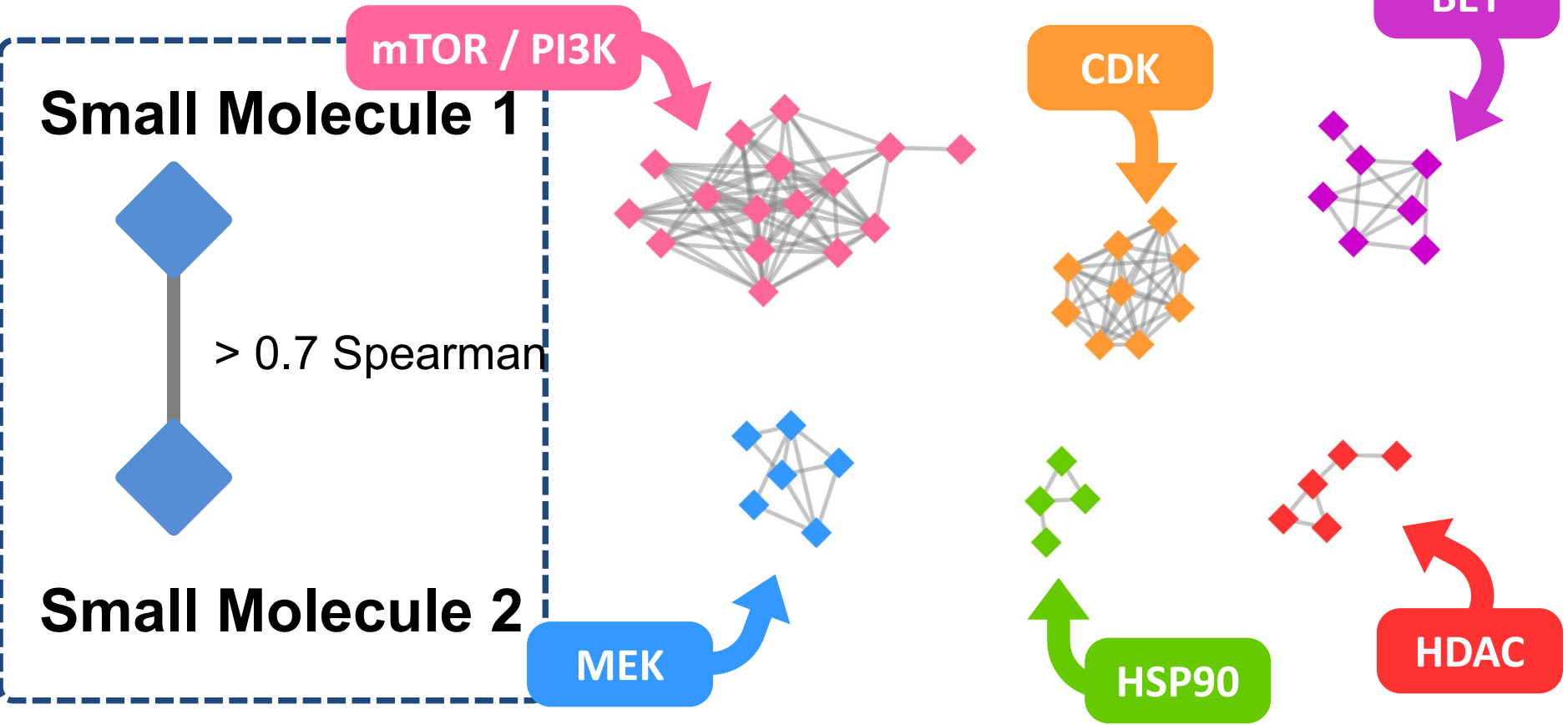


> 0.7 Spearman

Small Molecule 2



Compounds with same Mechanism of Action form distinct networks



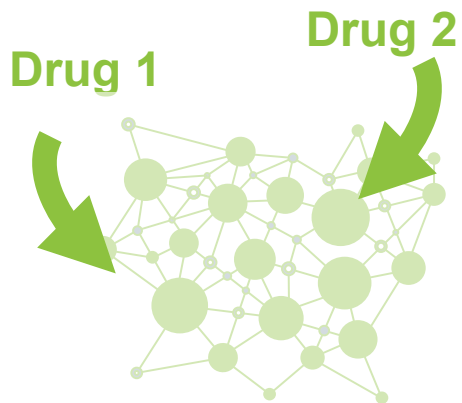
1

One Signature
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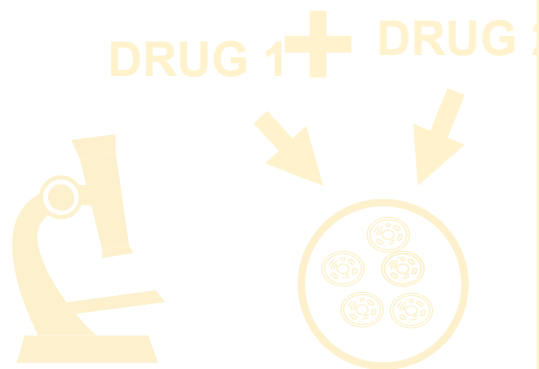
2

Identify Drug
Combinations

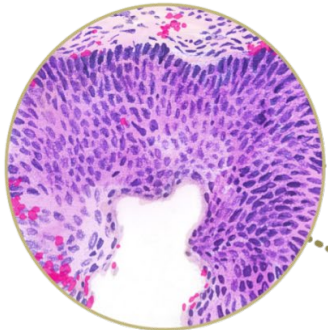


3

Validate
in vitro /
in vivo

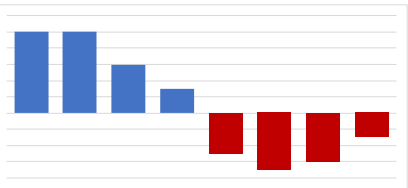


Glioblastoma disease signature from TCGA

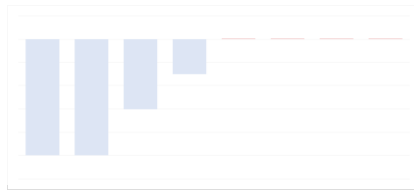


DISEASE

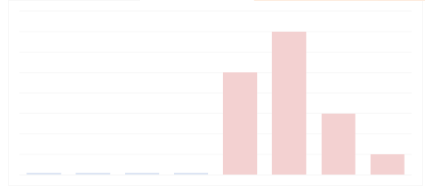
**TCGA
Data**



DRUG

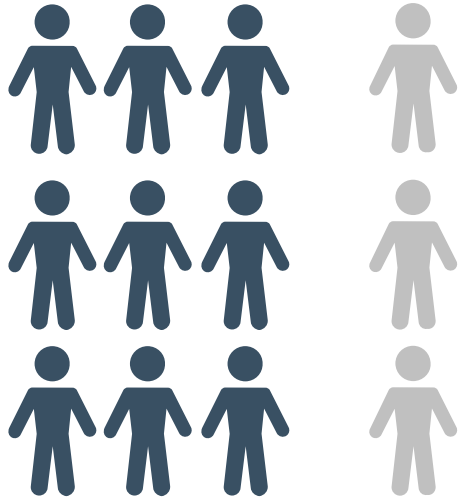


**LINCS
Data**



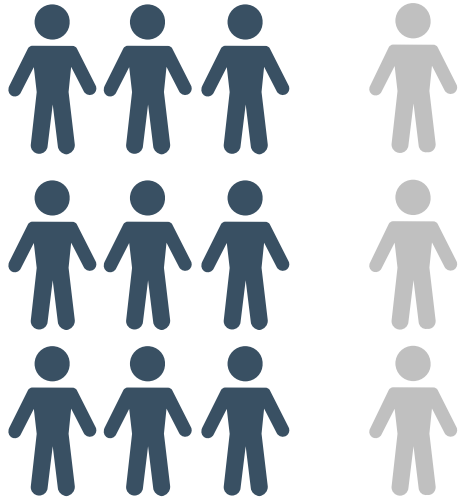
**LINCS
Data**

Identify Differentially Expressed Genes in Glioblastoma Samples

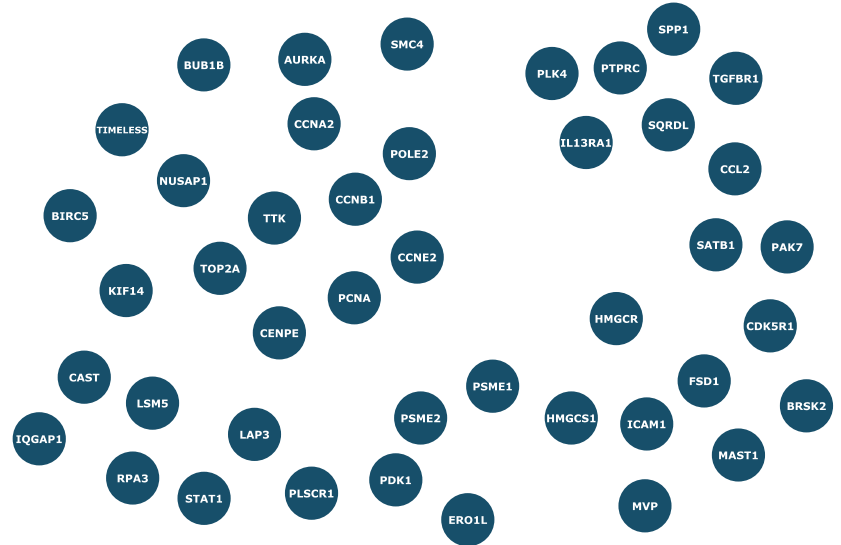
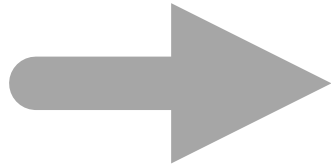


**Glioblastoma Samples
and Controls**
(from TCGA)

Identify Differentially Expressed Genes in Glioblastoma Samples



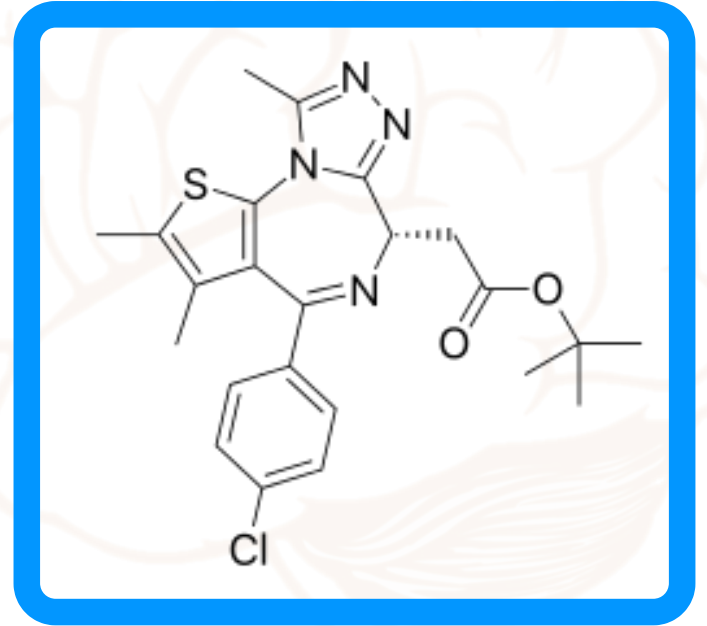
**Glioblastoma Samples
and Controls
(from TCGA)**



**Differentially Expressed Genes
in Glioblastoma**

JQ1 is a potent Bromodomain inhibitor

- JQ1 reduces proliferation and survival of glioblastoma PDXs
- Bromodomains:
Readers of lysine acetylation
- Many cancers are sensitive to bromodomain inhibitors



Resistance after Bromodomain inhibition emerges in multiple cancer types

Breast Cancer

Response and resistance to BET bromodomain inhibitors in triple-negative breast cancer

Shaokun Shu^{1,2*}, Charles Y. Lin^{1,2*}, Housheng Hansen He^{1,2,3,4,5*}, Robert M. Witwicki^{1,2*}, Doris P. Tabassum¹, Justin M. Roberts¹, Michalina Janiszewska^{1,2}, Sung Jin Huh^{1,2}, Yi Liang¹, Jeremy Ryan^{1,2}, Ernest Doherty^{1,2}, Hisham Mohammed², Hao Guo¹, Daniel G. Stover^{1,2}, Muhammad B. Ekram^{1,2}, Guillermo Peluffo^{1,2}, Jonathan Brown^{1,2}, Clive D'Santos¹, Ian E. Krop^{1,2}, Deborah Dillon^{1,2}, Michael McKeown^{1,2}, Christopher Ott^{1,2}, Jun Qi^{1,2}, Min Ni^{1,2}, Prakash K. Rao⁹, Melissa Duarte², Shwu-Yuan Wu^{1,6}, Cheng-Ming Chiang^{1,2}, Lars Anders¹, Richard A. Young¹, Eric P. Winer^{1,2}, Antony Letal^{1,2}, William T. Barry^{2,3}, Jason S. Carroll⁷, Henry W. Long^{1,2,9}, Myles Brown^{1,2,3}, X. Shirley Liu^{1,2,9,12}, Clifford A. Meyer¹, James E. Bradner^{1,2,12} & Kornelia Polyak^{1,2,9,12}

Colorectal Cancer

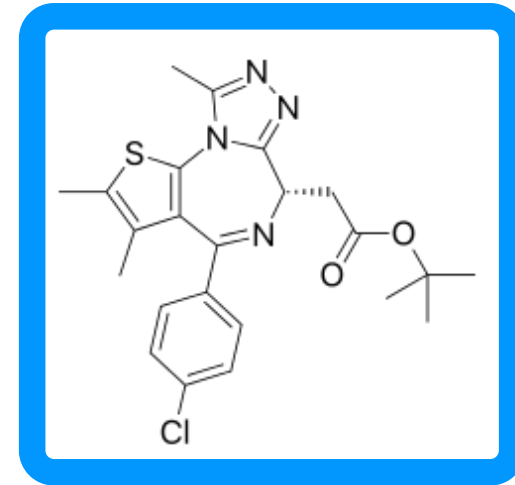
Loss of TRIM33 causes resistance to BET bromodomain inhibitors through MYC- and TGF- β -dependent mechanisms

Xiarong Shi⁸, Valia T. Mihaylova⁸, Leena Kuruvilla⁸, Fang Chen⁸, Stephen Viviano⁸, Massimiliano Baldassarre⁸, David Sperandio⁸, Ruben Martinez⁸, Peng Yue⁸, Jamie G. Bates⁸, David G. Breckenridge⁸, Joseph Schlessinger^{8,9}, Benjamin E. Turk^{8,1}, and David A. Calderwood^{8,1}

Leukemia

BET inhibitor resistance emerges from leukaemia stem cells

Chun Yew Fong^{1,2,3}, Omer Ghan^{1,2}, Enid Y. N. Lam¹, Alan F. Rubin^{4,5}, Sarah Ftouni¹, Dean Tyler^{1,2}, Kym Stanley¹, Devbarna Sinha¹, Paul Yeh^{1,2,3}, Jessica Morison⁶, George Giotopoulos⁶, Dave Lugo¹, Philip Jeffrey⁷, Stanley Chun-Wei Lee⁸, Christopher Carpenter⁹, Richard Gregory⁷, Robert G. Ramsay^{1,2}, Steven W. Lane¹⁰, Omar Abdel-Wahab⁸, Tony Kouzarides¹, Ricky W. Johnstone^{1,2}, Sarah-Jane Dawson^{1,2}, Brian J. P. Huntly⁶, Rab K. Prinjha¹, Anthony T. Papenfuss^{1,2,4,5} & Mark A. Dawson^{1,2,3}



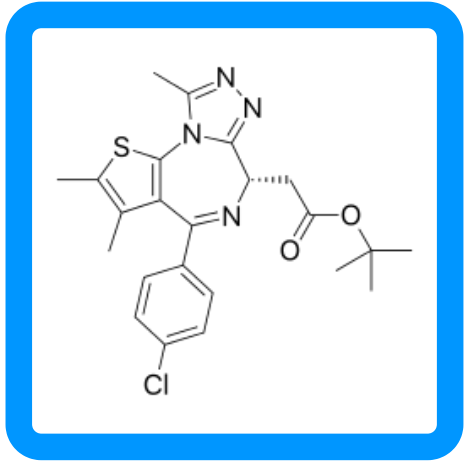
JQ1

Ovarian Cancer

Resistance to BET Bromodomain Inhibitors Is Mediated by Kinome Reprogramming in Ovarian Cancer

Ailison M. Kurimchak¹, Claude Shelton¹, Kelly E. Duncan¹, Katherine J. Johnson¹, Jennifer Brown¹, Shane O'Brien², Rashid Gabbasov^{2,4}, Lauren S. Fink¹, Yuesheng Li¹, Nicole Lounsbury³, Magid Abou-Gharbia³, Wayne E. Childers³, Denise C. Connolly², Jonathan Chernoff¹, Jeffrey R. Peterson¹, and James S. Duncan^{1,5}

Identify a small molecule that would be effective in combination with JQ1

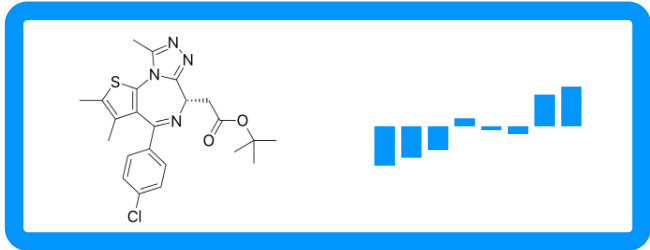


JQ1

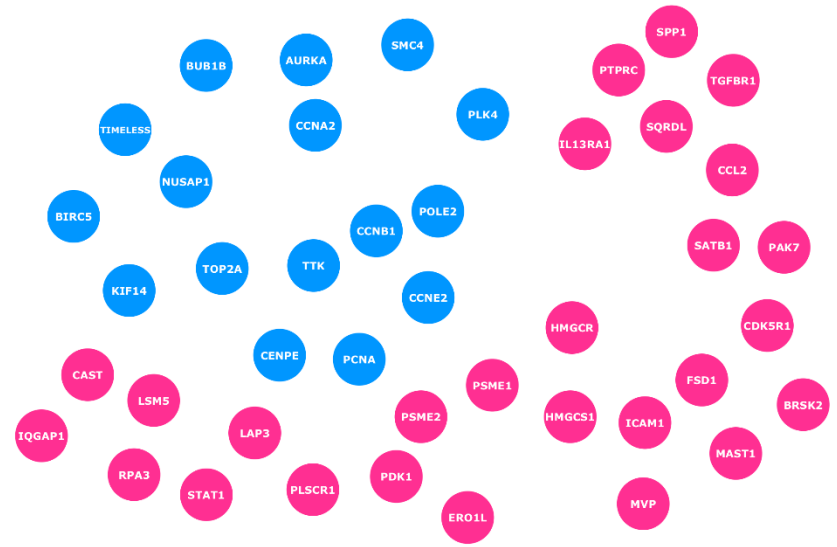
+



Identify compounds that induce orthogonal gene expression

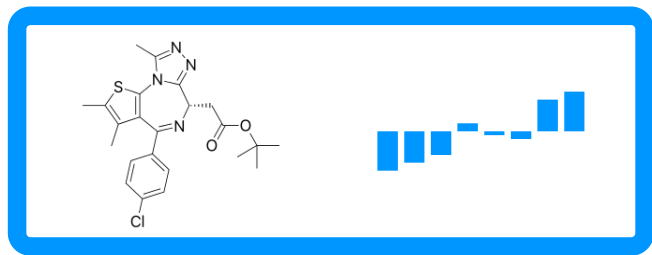


JQ1



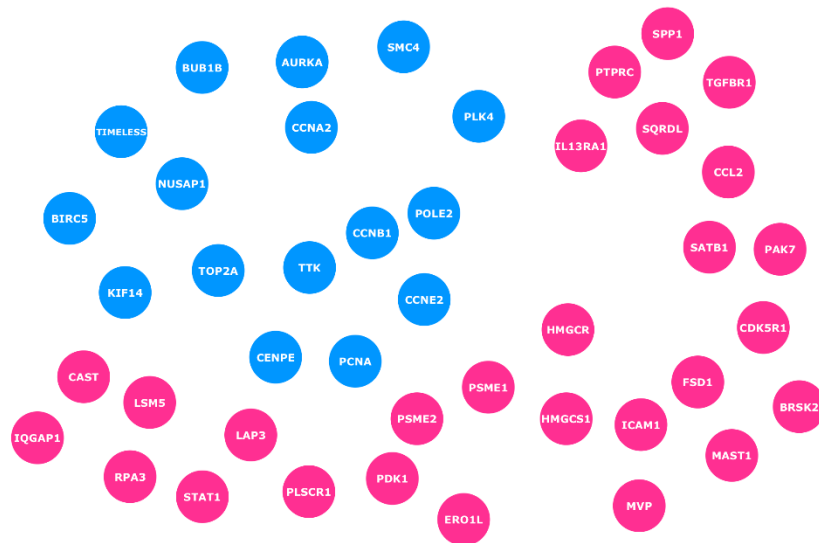
Differentially Expressed Genes in Glioblastoma

Identify compounds that induce orthogonal gene expression



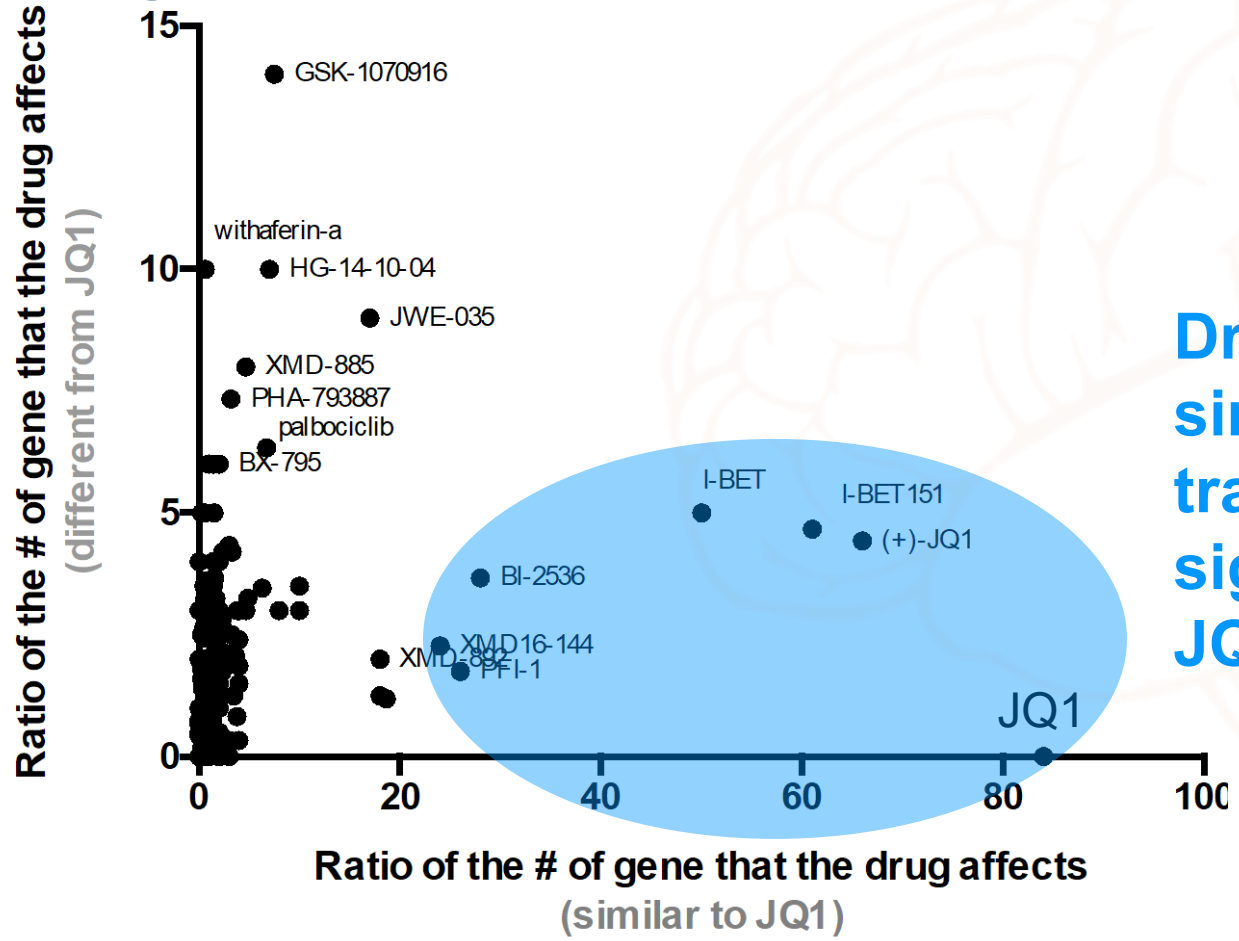
JQ1

Compound



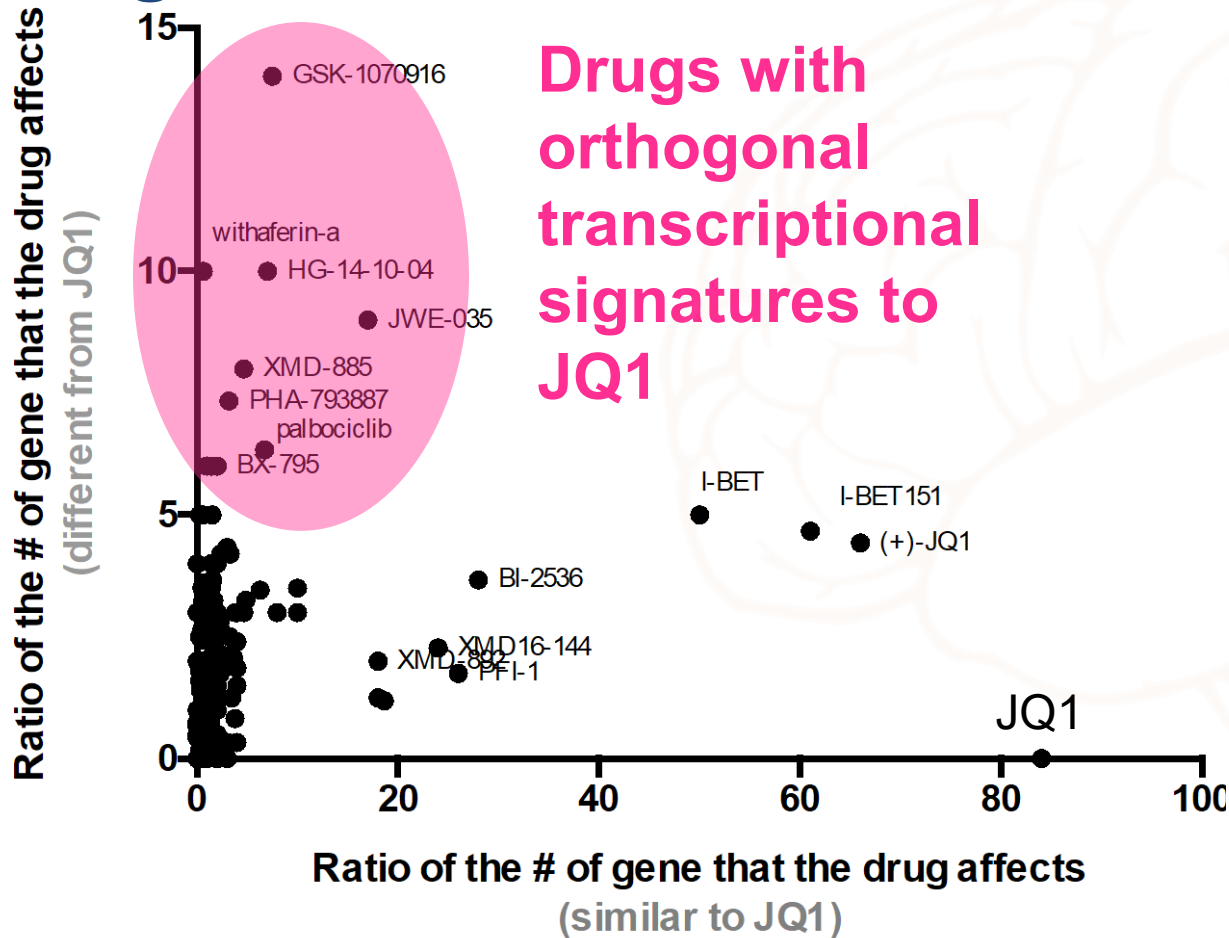
Differentially Expressed Genes
in Glioblastoma

All Drugs were ranked based on similarity to JQ1

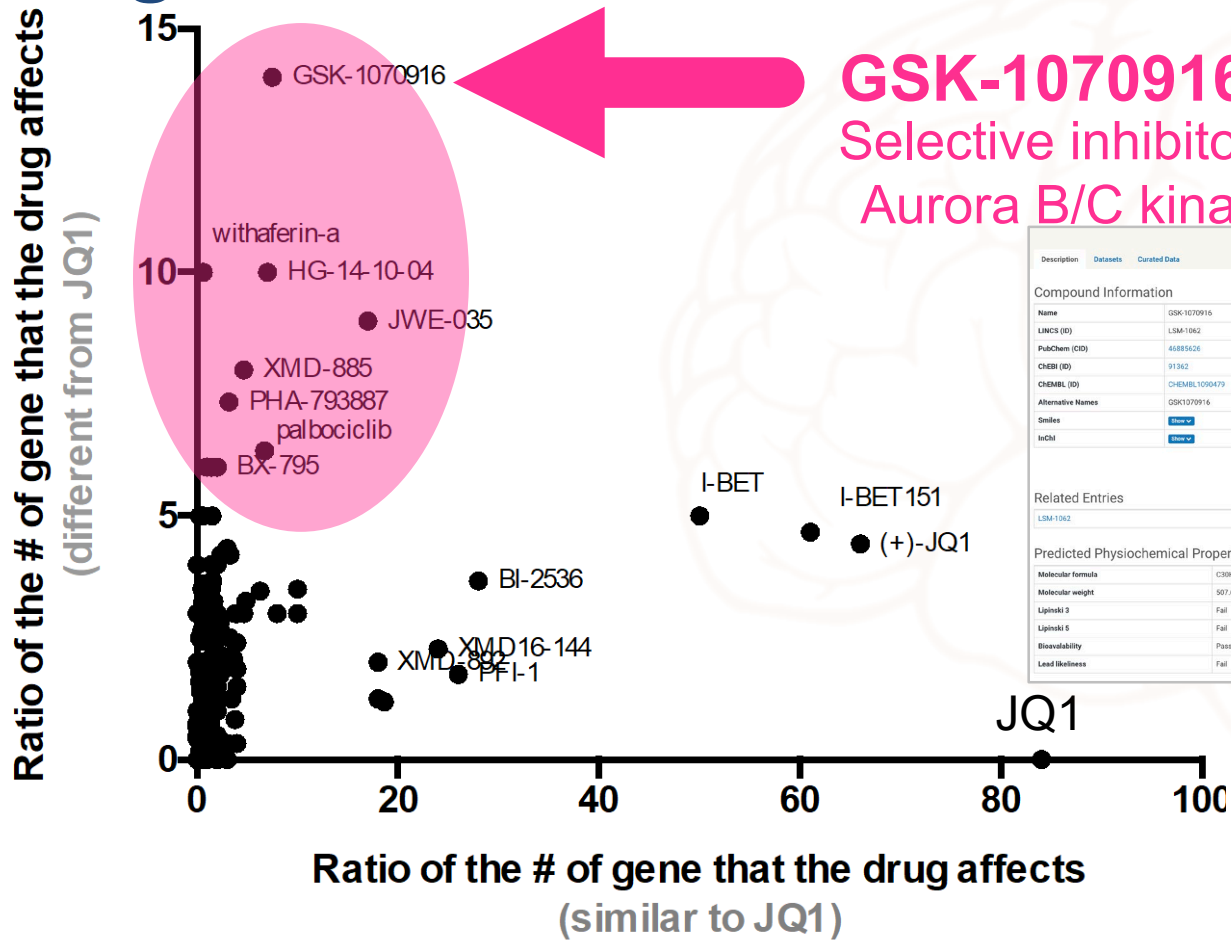


Drugs with similar transcriptional signatures to JQ1

All Drugs were ranked based on similarity to JQ1



All Drugs were ranked based on similarity to JQ1



GSK-1070916
Selective inhibitor of
Aurora B/C kinase

GSK-1070916 (LSM-1062)

Description Datasets Curated Data

Compound Information

| | |
|-------------------|----------------------|
| Name | GSK-1070916 |
| LINCS (ID) | LSM-1062 |
| PubChem (CID) | 4688426 |
| CHEBI (ID) | 91362 |
| CHEMBL (ID) | CHEMBL1090479 |
| Alternative Names | GSK1370916 |
| Smiles | View |
| InChI | View |

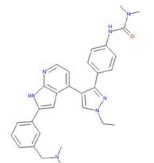
Find Similar Structures [Similarity Search](#)

Related Entries

LSM-1062

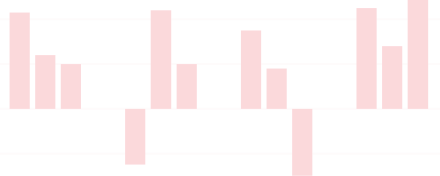
Predicted Physicochemical Properties

| | | | |
|-------------------|-----------|------------------|-------|
| Molecular Formula | C30H32N2O | ctLogP | 4.55 |
| Molecular weight | 507.63 | Rotatable bonds | 7 |
| Lipinski 3 | Fail | H bond acceptors | 4 |
| Lipinski 5 | Fail | H bond donors | 2 |
| Bioavailability | Pass | TPSA | 82.08 |
| Lead likeness | Fail | QED | 0.33 |



1

One Signature
per Compound



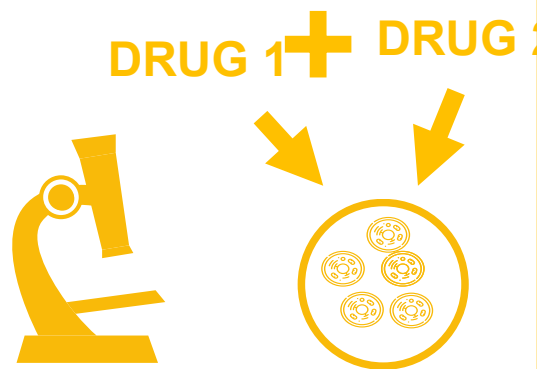
2

Identify Drug
Combinations



3

Validate
in vitro /
in vivo



Treat Glioblastoma PDX cells with JQ1 and / or GSK-1070916

JQ1

AND / OR

GSK1070916

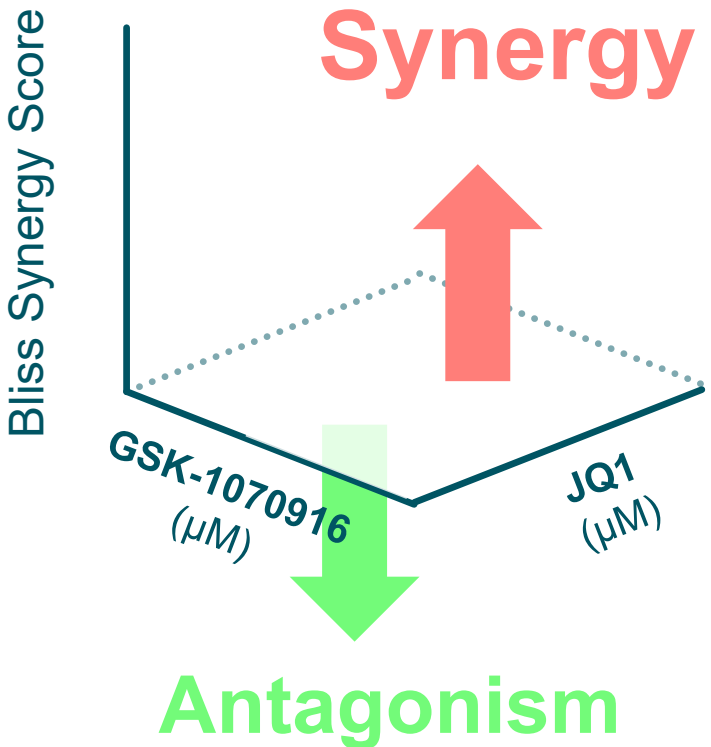
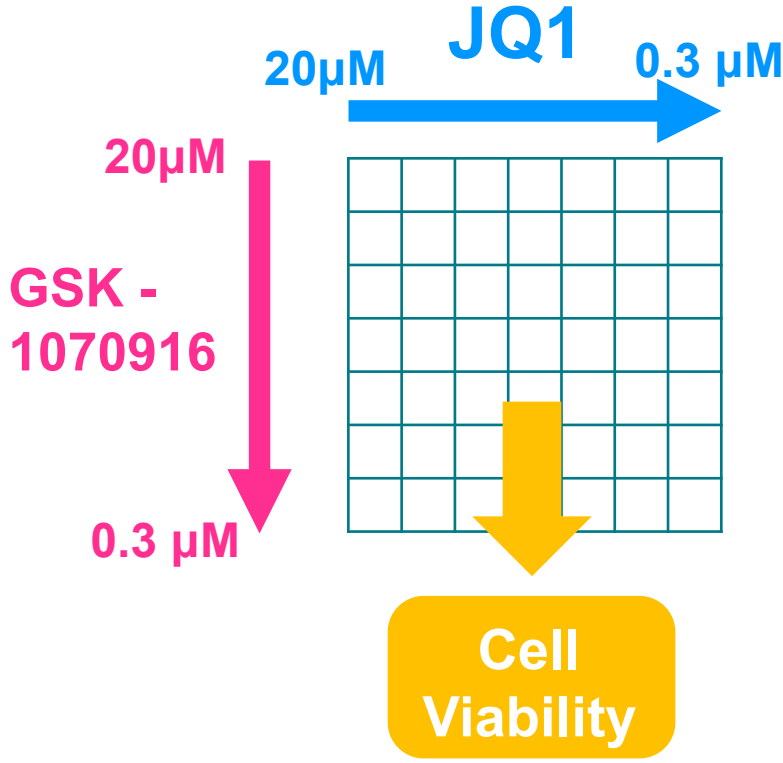


Quantify
ATP

(Cell Titer Glo)

Glioblastoma PDXs

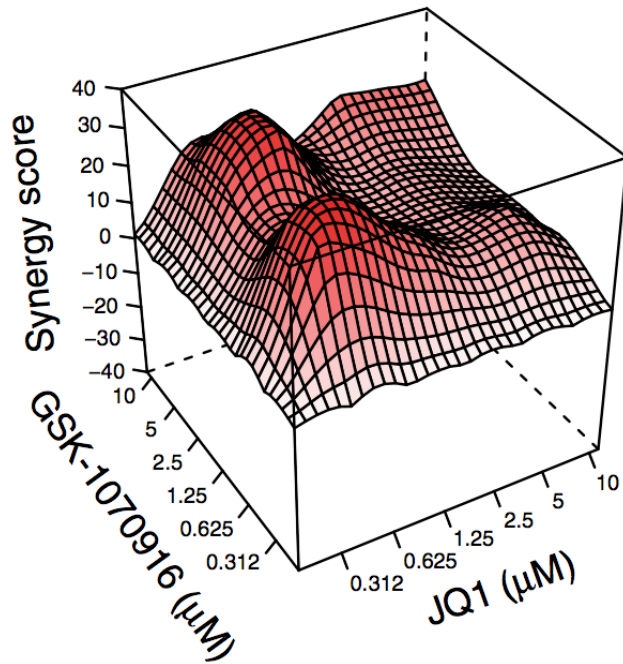
Bliss independence analysis of cell- viability combination response



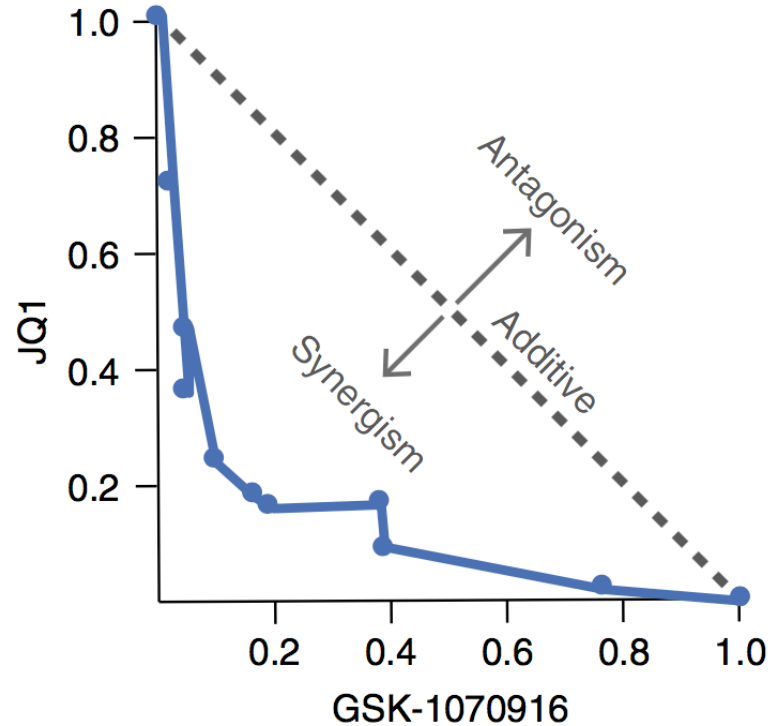
JQ1 + GSK-1070916 synergize in reducing cell viability

GBM39, CellTiter-Glo®

Bliss synergy score: 17.484



Average loewe CI: 0.59

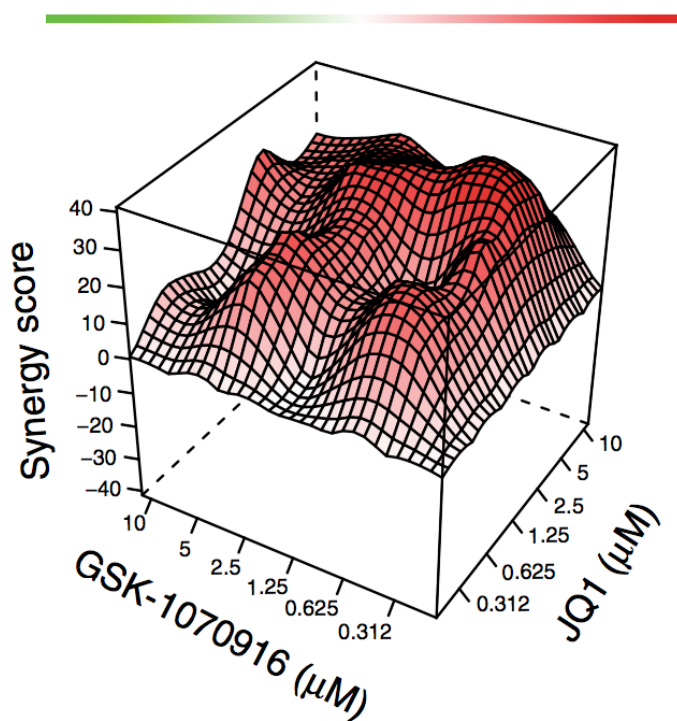


JQ1 + GSK-1070916 synergize in Glioblastoma cell death

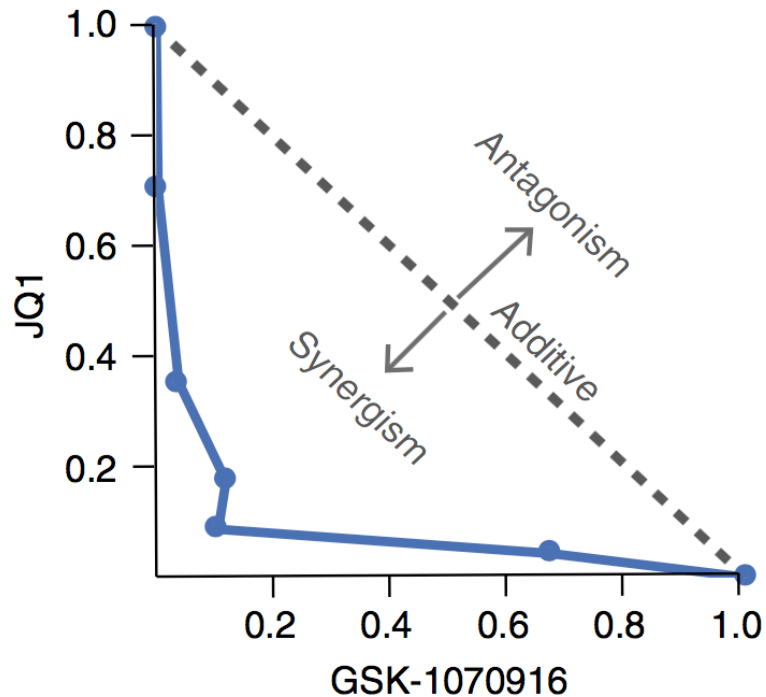
GBM39, Caspase-Glo®

Bliss synergy score: 20.445

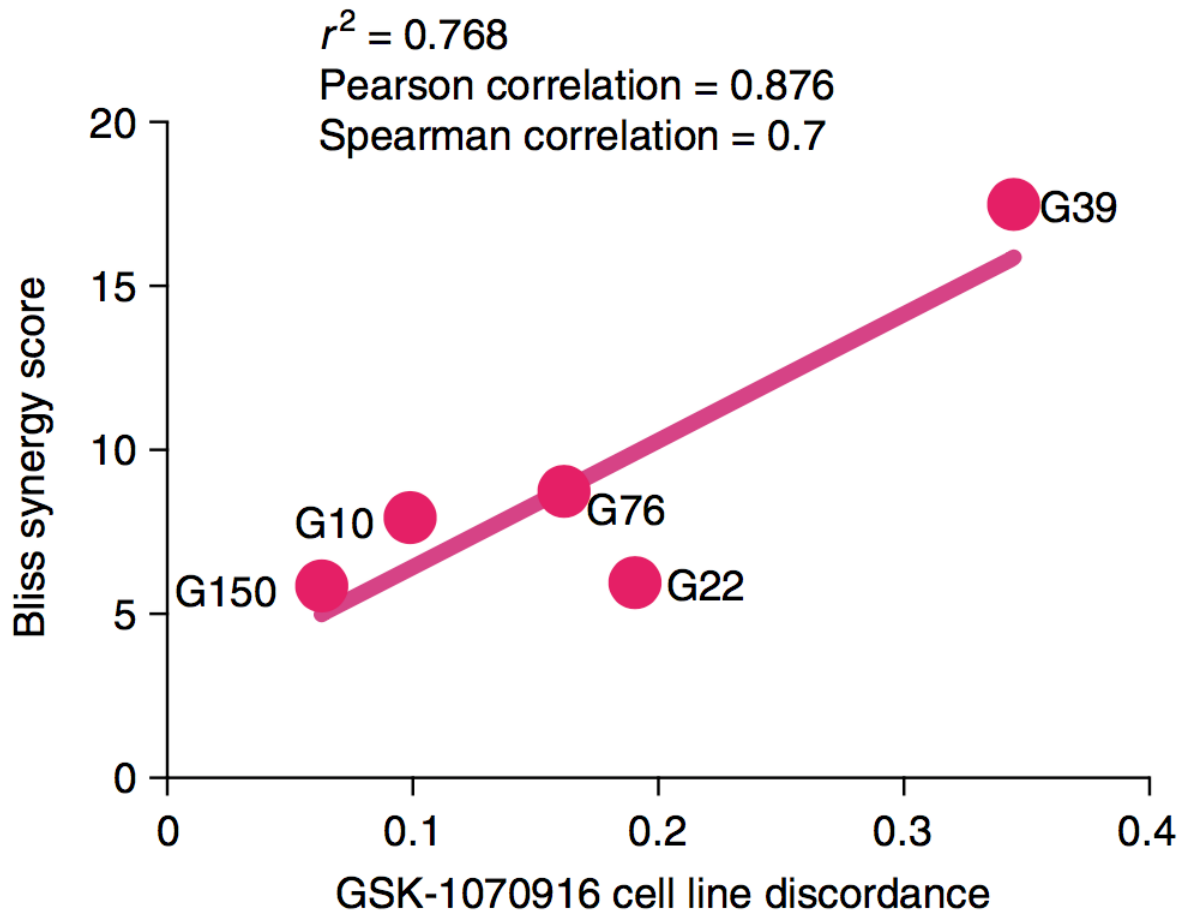
-40 -30 -20 -10 0 10 20 30 40



Average loewe CI: 0.61



Synergistic response correlates with discordance





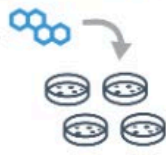
1 Calculate Disease Signature

Differentially Expressed Genes between TCGA tumor samples and same-tissue controls

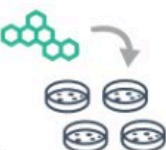
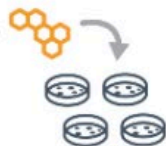


2 Calculate Transcriptional Response Signatures

Reference Small Molecule



LINCS L1000 Small Molecules



3 Calculate Overlap between Reference Small Molecule and Disease Signature

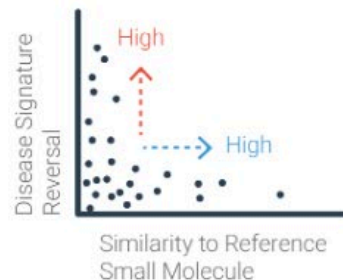


4 Score L1000 Small Molecules to maximize the reversal of the Disease Signature



5 Rank LINCS L1000 small molecules based on their similarity to the Reference Compound and the reversal of the Disease Signature

● = LINCS Small Molecule





Download Synergy Plot Data

Download Drug Signatures

| Drug | Disease_Same | Disease_Opp | Disease_Discordance | Reference_Drug_Orthogonality | Drug_Repurposing_Hub | CLUE | Manual |
|--------------|--------------|-------------|---------------------|------------------------------|-------------------------|--------------------------------------|------------------------------------|
| GSK-1070916 | 0.07 | 1.00 | 1 | 0.0892857142857143 | Aurora kinase inhibitor | Aurora kinase inhibitor | N/A |
| HG-14-10-04 | 0.07 | 0.71 | 0.714285714285714 | 0.0833333333333333 | N/A | N/A | potent and specific ALK inhibitor |
| JWE-035 | 0.07 | 0.64 | 0.642857142857143 | 0.202380952380952 | N/A | Aurora kinase inhibitor | N/A |
| palbociclib | 0.21 | 1.36 | 0.452380952380952 | 0.0803571428571429 | CDK inhibitor | CDK inhibitor | N/A |
| PHA-793887 | 0.21 | 1.57 | 0.523809523809524 | 0.0378787878787879 | CDK inhibitor | CDK inhibitor | N/A |
| withaferin-a | 0.07 | 0.71 | 0.714285714285714 | 0.0076530612244898 | N/A | N/A | Inhibits NF- κ B activation |
| XMD-885 | 0.07 | 0.57 | 0.571428571428571 | 0.0555555555555556 | MAP kinase inhibitor | Leucine rich repeat kinase inhibitor | N/A |

PDX GBM Group 3

PDX GBM Group 4

| | | | |
|--------|-----|-------------------------|-----------------------------------|
| 333333 | N/A | N/A | potent and specific ALK inhibitor |
| 80952 | N/A | Aurora kinase inhibitor | N/A |



Drug and disease signature integration identifies synergistic combinations in glioblastoma

Vasileios Stathias, Anna M. Jermakowicz, Marie E. Maloof, Michele Forlin, Winston Walters, Robert K. Suter, Michael A. Durante, Sion L. Williams, J. William Harbour, Claude-Henry Volmar, Nicholas J. Lyons, Claes Wahlestedt, Regina M. Graham, Michael E. Ivan, Ricardo J. Komotar, Jann N. Sarkaria, Aravind Subramanian, Todd R. Golub, Stephan C. Schürer & Nagi G. Ayad

Nature Communications **9**, Article number: 5315 (2018) | [Download Citation](#)

Abstract

Glioblastoma (GBM) is the most common primary adult brain tumor.



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3
Citations

11
Altmetric

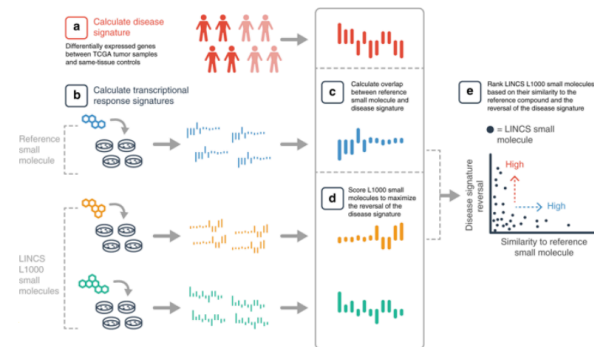
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Figures

References

Fig. 1



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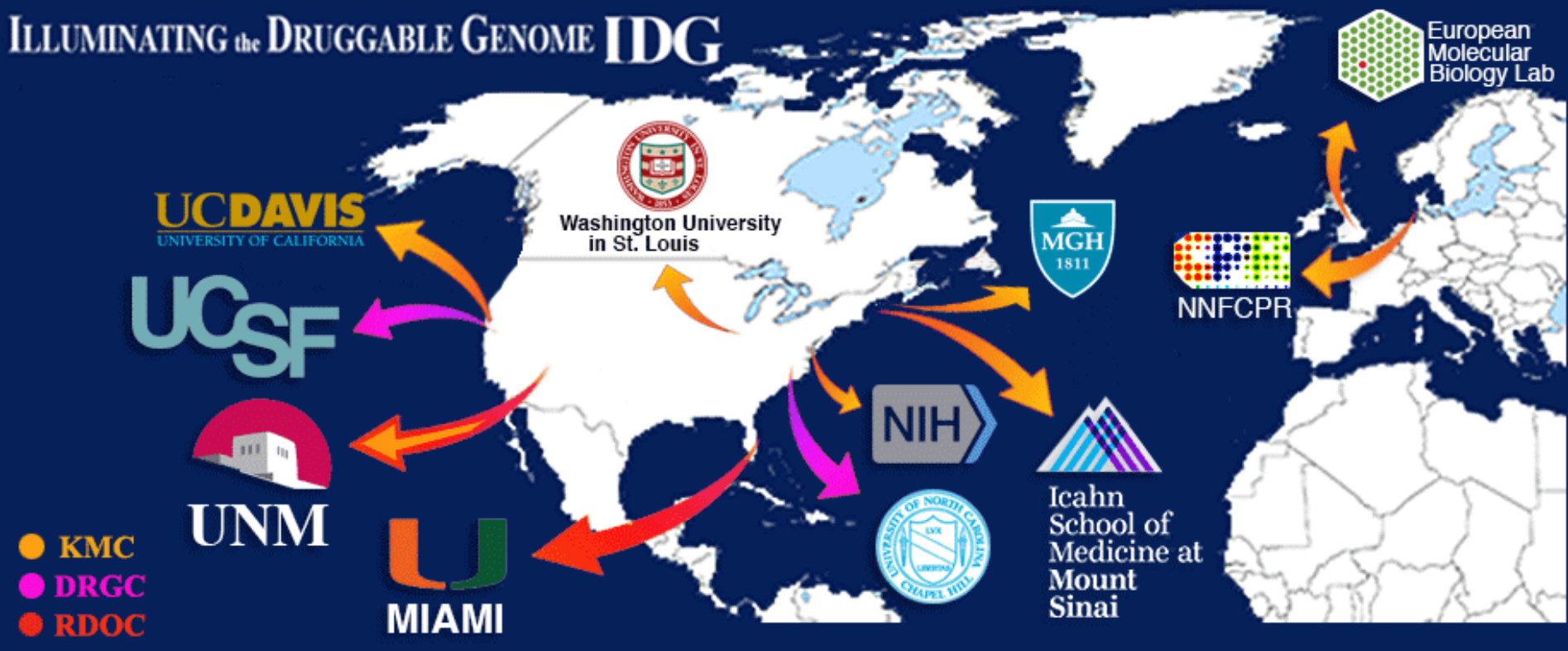
[Full size image >>](#)

Take away (why did I show this)

- Use LINCS data (<http://lincsportal.ccs.miami.edu>)
- Representation of chemical structures by transcriptional consensus signatures
- Systems-level data driven approach – vs target-driven approach
- Current work: combining transcriptional signatures with with chemical structure-based signatures

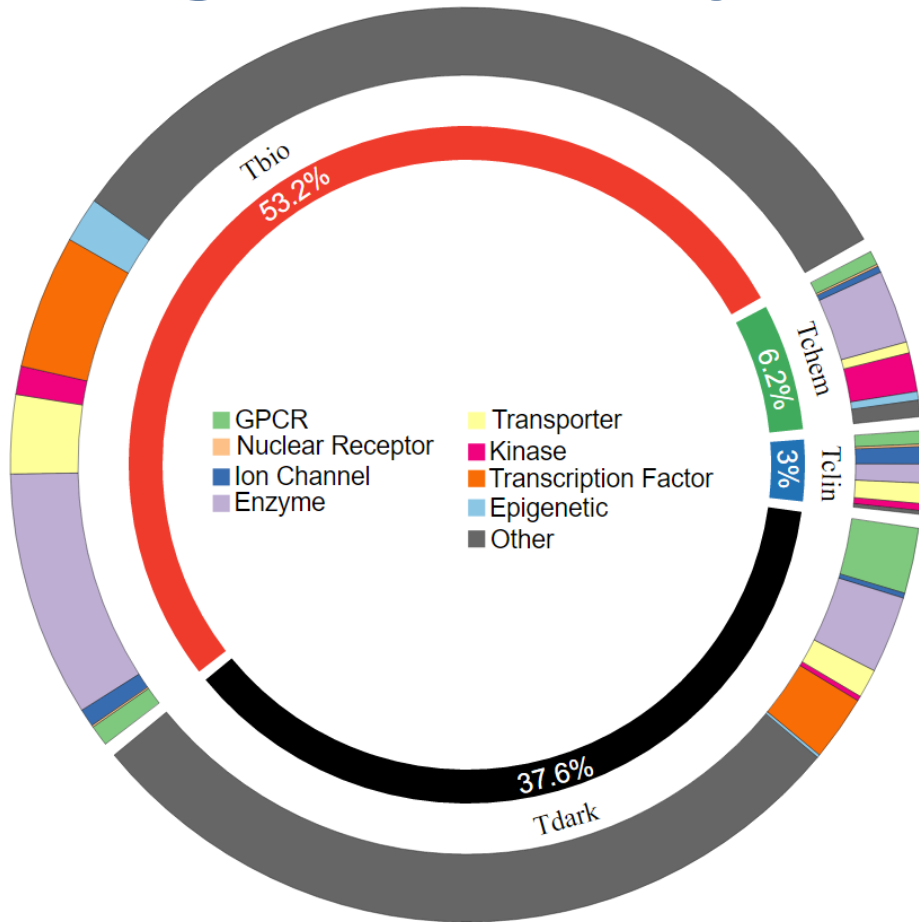
Illuminating the Druggable Genome (IDG)

ILLUMINATING the DRUGGABLE GENOME IDG



<http://druggablegenome.net>

Target Development Level (TDL)




- Most protein classification schemes are based on structural and functional criteria.
- For therapeutic development, it is useful to understand how much and what types of data are available for a given protein, thereby highlighting well-studied and understudied targets.
- Proteins annotated as drug targets are **Tclin**
- Proteins for which *potent* small molecules are known are **Tchem**
- Proteins for which biology is better understood are **Tbio**
- Proteins that lack antibodies, publications or Gene RIFs are **Tdark**







Analysis | Published: 23 March 2018

Unexplored therapeutic opportunities in the human genome

Tudor I. Oprea , Cristian G. Bologa, Søren Brunak, Allen Campbell, Gregory N. Gan, Anna Gaulton, Shawn M. Gomez, Rajarshi Guha, Anne Hersey, Jayme Holmes, Ajit Jadhav, Lars Juhl Jensen, Gary L. Johnson, Anneli Karlson, Andrew R. Leach, Avi Ma'ayan, Anna Malovannaya, Subramani Mani, Stephen L. Mathias, Michael T. McManus, Terrence F. Meehan, Christian von Mering, Daniel Muthas, Dac-Trung Nguyen, John P. Overington, George Papadatos, Jun Qin, Christian Reich, Bryan L. Roth, Stephan C. Schürer, Anton Simeonov, Larry A. Sklar, Noel Southall, Susumu Tomita, Ilinca Tudose, Oleg Ursu, Dušica Vidović, Anna Waller, David Westergaard, Jeremy J. Yang & Gergely Zahoránszky-Köhalmi - Show fewer authors

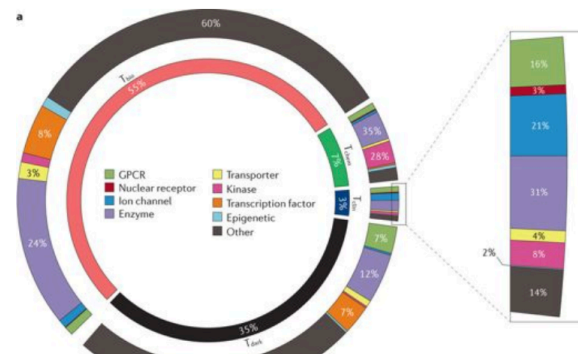
Nature Reviews Drug Discovery **17**, 317–332 (2018) | [Download Citation](#) 

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9 Citations | 210 Altmetric | [Article metrics >>](#)

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- Figures**
- References

Figure 1: Target development level categories applied to the human proteome.



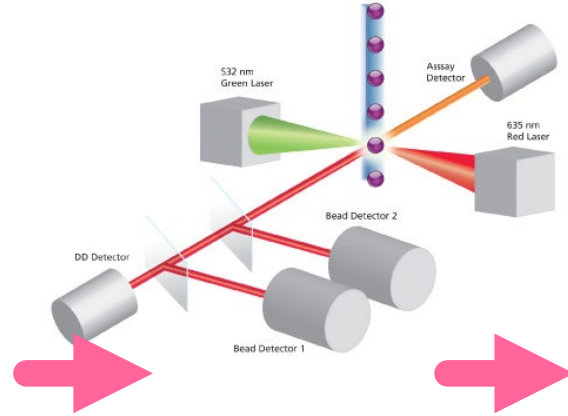
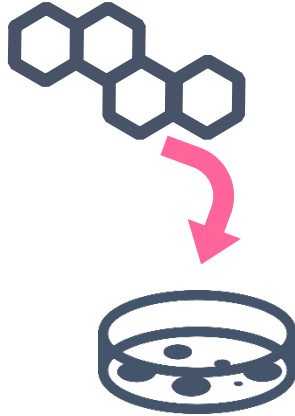
Additional slides

L1000 Gene Expression Platform

 1753 Compounds

 >50 Cell Lines

 2 Timepoints

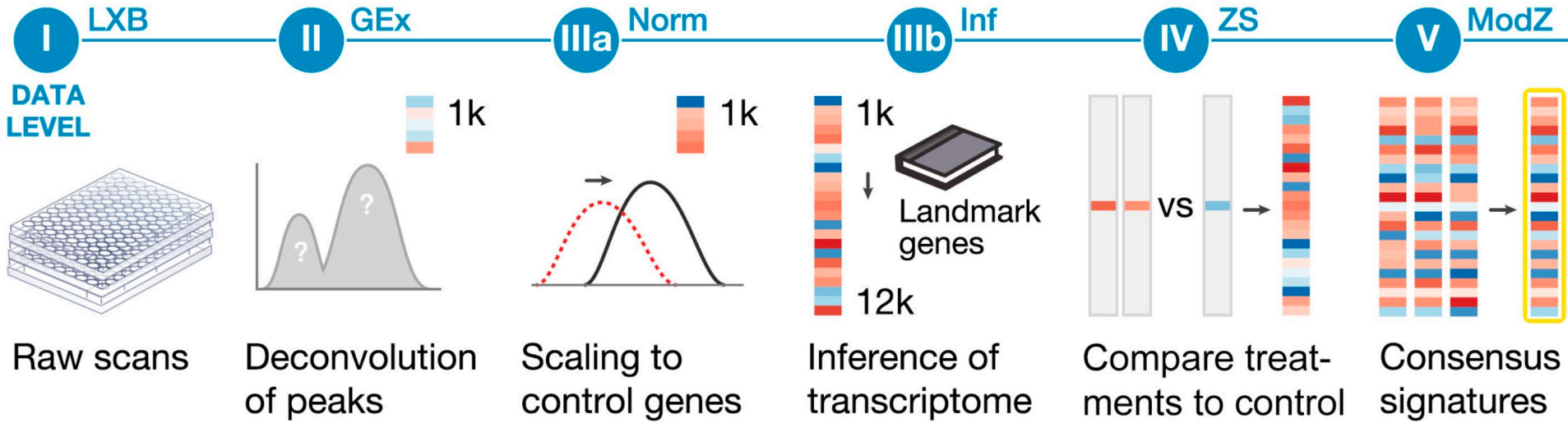



978

Luminex Reader

Aravind Subramanian et al, Cell, 2017

L1000 Computational Processing Pipeline



t-SNE Clustering of 4515 TCGA RNA-seq tumor samples

Cancer Subtype

- BRCA
- COAD
- GBM
- HNSC
- KIRC
- LUAD
- LUSC
- READ
- UCEC
- OV

Head and neck
squamous cell carcinoma

Lung adenocarcinoma

Lung squamous cell carcinoma

