Cancer Therapeutics Response Portal

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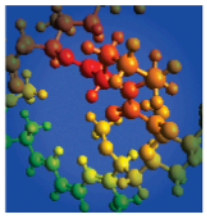
Profiling cancer cell-line sensitivities with small molecules

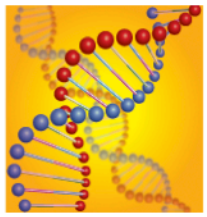
an NCI CTD^2 Network project

Several protein kinase-targeting drugs are yielding high clinical response rates when matched to cancer patients with specific genomic alterations in their cancers. Several other cancer drugs yield similarly high response rates within a particular cancer lineage. These clinical successes have prompted our efforts to identify more systematically additional genetic and lineage context-dependent small-molecule sensitivities.

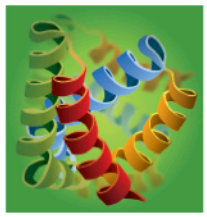
We have generated a novel 'Informer Set' of small-molecule probes and drugs that each selectively target a distinct node in cell circuitry and that collectively modulate a broad array of cell processes. By profiling the impact of this small-molecule collection on a panel of cancer cell lines for which extensive genetic characterizations are publicly available, we have generated a dataset that can be used to identify comprehensively relationships between genetic and lineage features of human cancer cell lines and small-molecule sensitivities.



Small Molecules



Enriched Features



Targets

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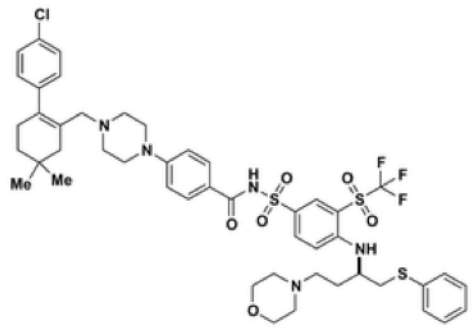
navitoclax

General | Enrichment Analysis



Target:	inhibitor of BCL2, BCL-xL and BCL-W
PubChem:	Search in PubChem for navitoclax
DrugBank:	Search in DrugBank for navitoclax

Additional compound information

Additional compound information is provided by the Broad computational chemical biology research group

Alternative name(s)

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navitoclax

General | Enrichment Analysis

▶ Cell Line Subset ? reset | all

- [x] all CCL types
- [ ] endometrium CCLs
- [ ] hematopoietic CCLs
- [ ] colon CCLs
- [ ] lung CCLs
  - [ ] adenocarcinomas
  - [ ] large cell carcinomas
  - [ ] non-small-cell carcinomas

▶ Dataset ? reset | all

cell lineage

- [ ] lineage type
- [ ] lineage sub-type

Oncomap data

- [x] Oncomap mutation calls
- [ ] Oncomap mutation combinations

hybrid-capture data

- [ ] targeted exome sequencing (TES)

▶ Cell Line Exclusion ? reset | all

- [x] exclude no CCL subset
- [ ] exclude frequently sensitive CCLs
- [ ] exclude highly mutated CCLs
- [x] exclude hematopoietic CCLs
- [x] exclude suspension CCLs

Enrichment Analysis

area under concentration-response curve

sensitive — *unresponsive*

Vertical gray bars indicate CCLs belonging to lineage (lineage as a feature) or mutated in gene (gene as a feature).

Show 10 entries

Feature	Enrichment	FDR q value	Direction	
CTNNB1		2.5000e-5	sensitive	all CCL types exclude suspension CCLs Oncomap mutation calls
CTNNB1		3.9500e-5	sensitive	all CCL types exclude hematopoietic CCLs Oncomap mutation calls
CTNNB1		2.2650e-4	sensitive	all CCL types exclude no CCL subset Oncomap mutation calls

Showing 1 to 3 of 3 entries — First | Previous | 1 | Next | Last