Precision medicine: NGS variant analysis and interpretation for translational research

PanDrugs: Matching mutations with therapies

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Predisposition



Actionable genomic alterations

Prognosis









Diagnosis

Treatment



Predisposition



Prognosis

It's bad, Bad, Bad, Bad, Met good, Bad, Octhosk is grim. Poor for grown prognessis. Bad, Very bad, Basaodd!

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Genomic alterations

Diagnosis

Pharmacogenomics

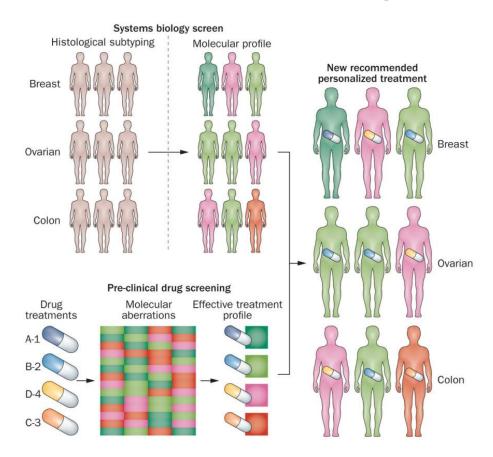
Treatment





Pharmacogenomics

Studies the effect of the genomic alterations in the drug response.



- Breaks the rule"one size fits all"
- Individual variation predicts:
 - Response
 - No response
 - Side effects
- Tailors a suitable treatment for a stratified patient

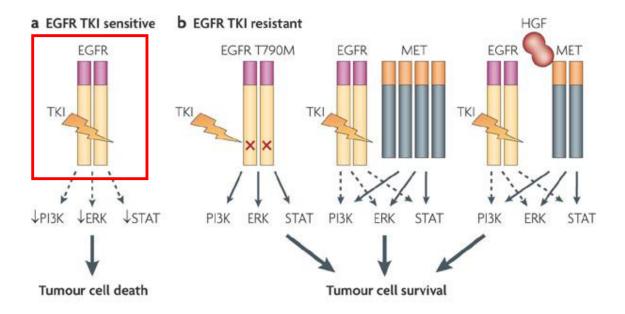
Werner, H. M. J. et al. (2014) Cancer Systems Biology: a peek into the future of patient care?Nat. Rev. Clin. Oncol. doi:10.1038/nrclinonc.2014.6

Gene-drug considerations

Target/Biomarker

Target & marker genes

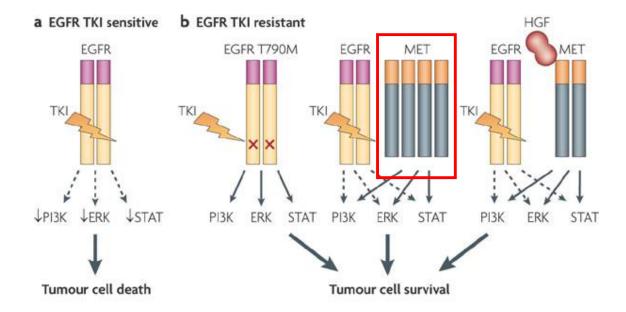
TARGET human gene that contributes to a disease phenotype and can be targeted directly by a drug (small molecule, monoclonal antibody, ...)



Target & marker genes

TARGET human gene that contributes to a disease phenotype and can be targeted directly by a drug (small molecule, monoclonal antibody, ...)

MARKER its **genetic status** is associated with a drug response by **clinical or experimental** evidences

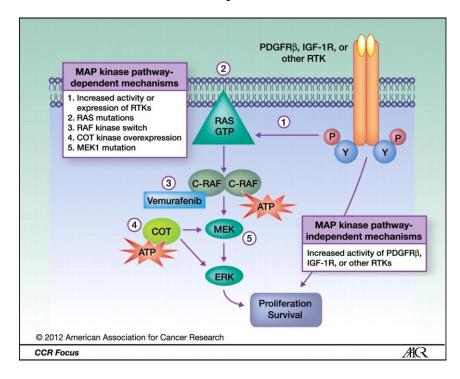


Gene-drug considerations

Target/Biomarker

• Sensitivity/Resistance

Sensitivity vs Resistance



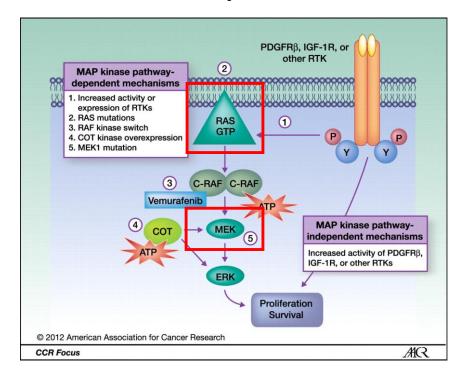
Melanoma treatment with BRAF mutation

VEMURAFENIB



Advanced or metastatic pancreatic cancer

Sensitivity vs Resistance



Melanoma treatment with BRAF mutation





Advanced or metastatic pancreatic cancer



Gene-drug considerations

Target/Biomarker

• Sensitivity/Resistance

• Type of event in drug response

Gene-drug considerations

Target/Biomarker

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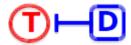
Type of event in drug response

Direct/Indirect drug action

Direct/Indirect associations

DRUG-GENE DIRECT ASSOCIATIONS

The altered gene is the target or biomarker of the drug



DRUG-GENE INDIRECT ASSOCIATIONS

The drug has as a target a gene related to the altered one



D Drug

T Altered target gene

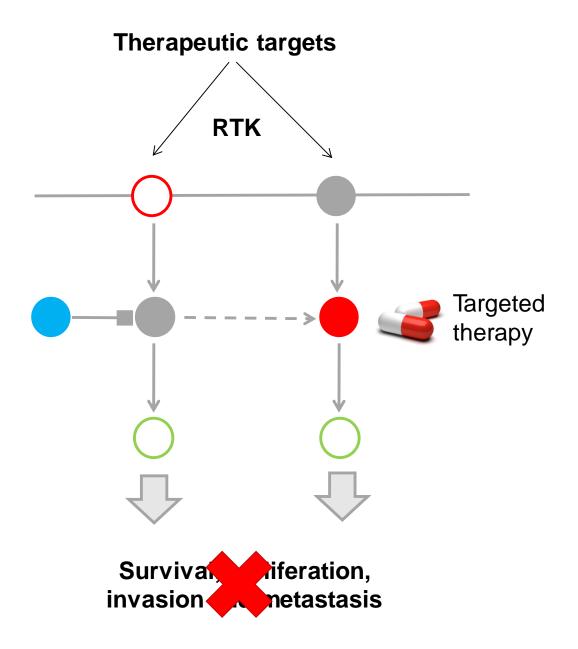
G Altered non target gene

T Wild type target gene

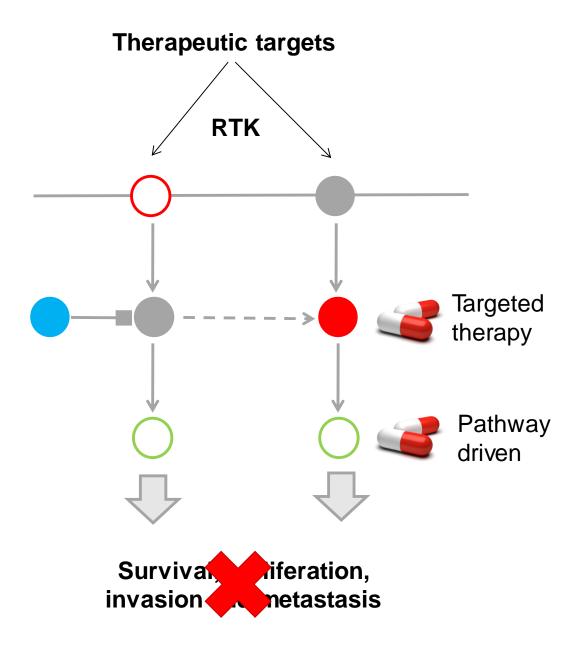
Therapeutic targets **RTK**

Survival, proliferation, invasion and metastasis

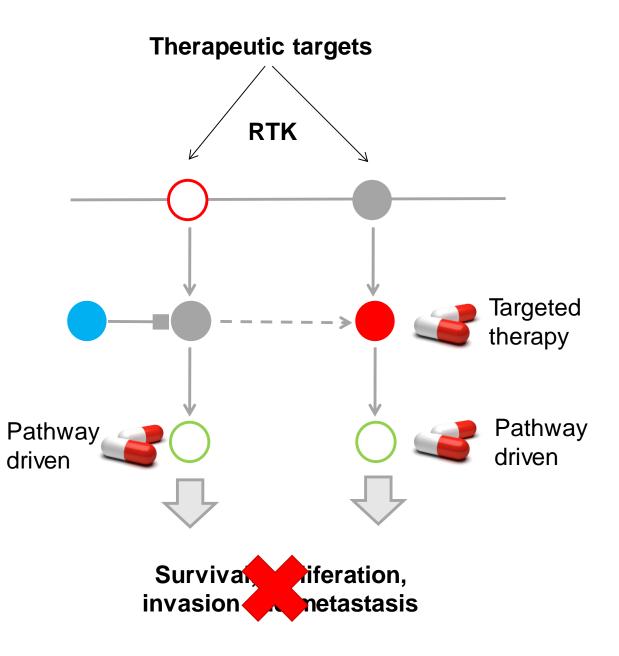
- Actionable
- Wild-type or No Actionable
- Tumor suppressor gene mutated
- Oncogene mutated
- Druggable



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- 3 Indirect pharmacological assignation driven by a tumor suppressor

Drug considerations

Approval Status

Approval status

Approved

Same condition Other







Clinical trials

Same condition clinical trials Other

Repurposing





Experimental

Withdrawn

Drug considerations

Approval Status

Classifications

Target-based classification of drugs



Anatomical Therapeutical Chemical (ATC) classification of drugs



Mechanism of Action (MOA) classification of drugs



Drug considerations

Approval Status

Classifications

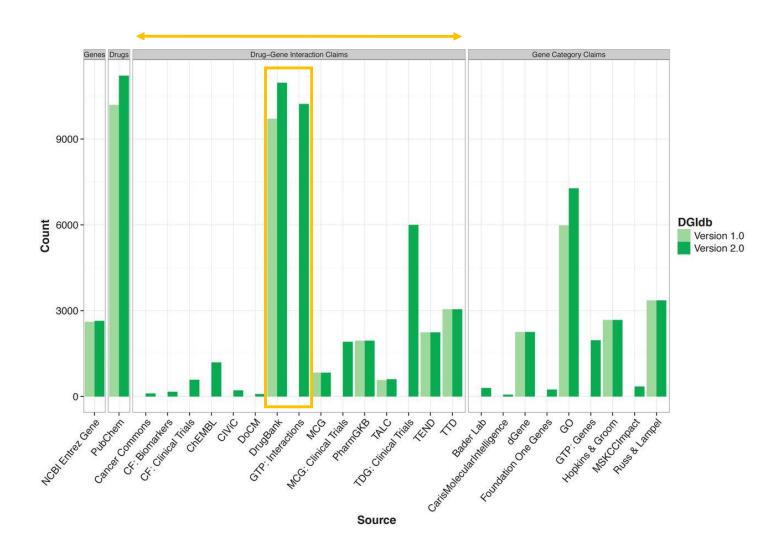
Nomenclature

- Chemical names (IUPAC, SMILES) e.g. 2-acetyloxybenzoicacid (IUPAC)
- Code Identifiers (CAS) e.g. 50-78-2
- Generic or nonproprietary names (INN) e.g. acetylsalicylic acid
- Trade names e.g. Aspirin





Drug-gene association resources: DGIdb



Cancer Commons: drugs approved or undergoing clinical trials for use in lung, prostate and skin cancer Clearity Foundation Biomarkers: biomarkers that predict response to selected drugs in ovarian tumors Clearity Foundation Clinical Trials: clinical trials records based on their relevance to breast and ovarian cancer

DrugBank: large resource detailing drugs and drugtarget information

My Cancer Genome: with interactions of specific mutations and therapies

My Cancer Genome Clinical Trials: My Cancer Genome interactions obtained from clinical trials **PharmGKB:** with potentially clinically actionable drug-gene associations

TALC: targeted agents in lung cancer

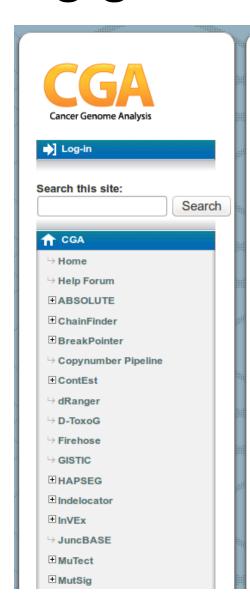
TEND: manual curation of FDA approved drugs and

their targets from DrugBank

TTD: therapeutic targets and corresponding drugs

Alex H. Wagner et al. (2016) Nucleic Acids Research

Drug-gene association resources: TARGET



Home >

TARGET

What is TARGET?

TARGET (tumor alterations relevant for genomics-driven therapy) is a database of genes that, when somatically altered in cancer, are directly linked to a clinical action. TARGET genes may be predictive of response or resistance to a therapy, prognostic, and/or diagnostic.

TARGET is intended to be a community resource for translational oncology. To maintain relevance and keep pace with new preclinical and clinical discoveries, it is updated quarterly.

How do I get the TARGET database?

TARGET is available for download as an Excel spreadsheet.

TARGET_db_v3_02142015.xlsx

TARGET db v2 05042014.xlsx

TARGET db v1 07012013.xlsx

With a specific drug name Additional information about:

- sensitivity / resistance
- target / marker gene
- genomic alteration

How can I contribute to the TARGET database?

If you would like to nominate a particular gene for inclusion as being clinically relevant, please complete this survey.

If your submission is selected for inclusion, you will be notified. Furthermore, if you would like to be acknowledged as the expert for that submission, you will be attributed in future editions of TARGET.

Drug-gene association resources: Monoclonal antibodies

- Highly selective
- Successful treatment in several diseases as rheumatoid arthritis, multiple sclerosis, cancer
 - eg. Rituximab in B-cell lymphoma (CD20 (MS4A1)) Cetuximab in colon cancer (EGFR)

https://en.wikipedia.org/wiki/List_of_therapeutic_monoclonal_antibodies

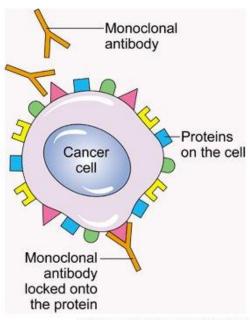
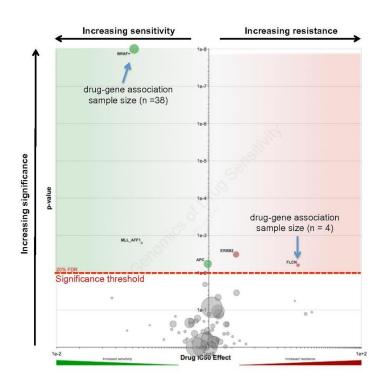


Diagram showing a monoclonal antibody attached to a cancer cell © CancerHelp UK

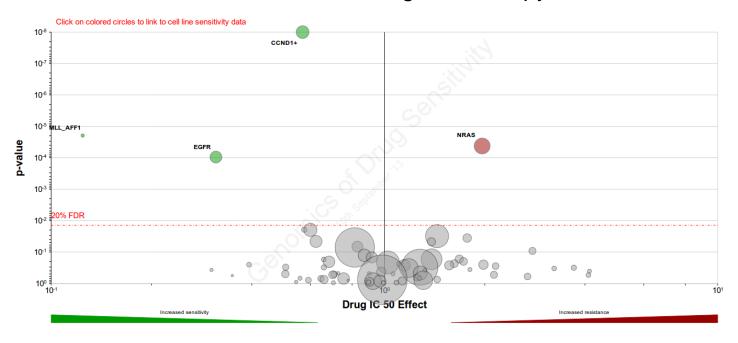
Drug-gene association resources: GDSC

http://www.cancerrxgene.org/

~ 1000 cancer cell lines mutations, amplifications, deletions, expression data 140 compounds



Gefitinib: EGFR targeted therapy



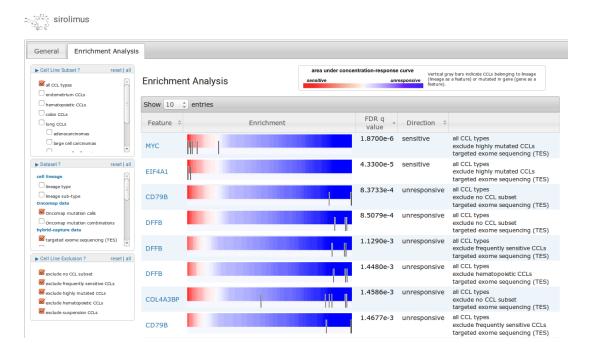
	Gene	Effect	P-value	No. of mutations
CCND1		0.568	6.56e-11	29
MLL_AFF1		0.124	0.0000196	2
NRAS		1.96	0.0000422	45
EGFR		0.312	0.0000950	25
<u>KIT</u>		0.574	0.0195	5
SMAD4		0.600	0.0198	31
KRAS		1.44	0.0313	95
MET		1.77	0.0359	13
FBXW7		0.623	0.0461	26

Drug-gene association resources: CTRP



http://www.broadinstitute.org/ctrp/

860 cancer cell lines mutations, CNV, expression data 481 small molecules



PANDRUGS

Cancer-oriented computational approach to prioritize and select therapies based on genomic data.

- Definition of a comprehensive catalogue of drugs associated with alterations at gene level.
- A variant/gene prioritization system according to the biological relevance.
- A prioritization system of therapy assignations according to their therapeutic utility in a specific genomic context.

PANDRUGS





What is PanDrugs?

PanDrugs provides a platform to guide the selection of therapies from the results of genome-wide studies in cancer disease.

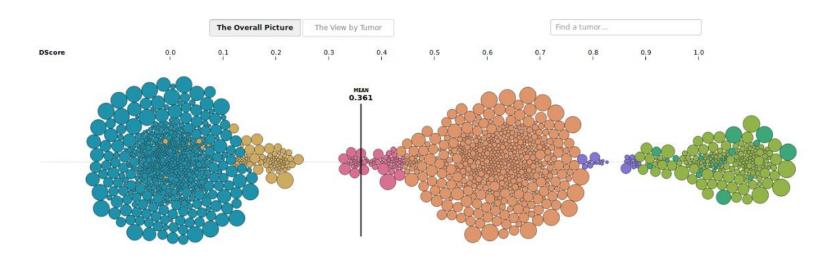
Using 4 alternative inputs (e.g. standard VCF files, RNK files, gene list and drug query), PanDrugs identify actionable molecular alterations and prioritize drugs by calculating gene-drug scores which takes into account: i) genomic feature evidence by mutation impact score; ii) target pathway context; iii) drug approval status (FDA, clinical trial or experimental small molecule inhibitors) and iv) manually-curated pharmacological information retrieved from the literature.

PanDrugs scores combines biological and clinical relevance of the genes and their susceptibility to be targeted reflecting the strength or evidence level of the gene-drug association in order to assist the clinical decision

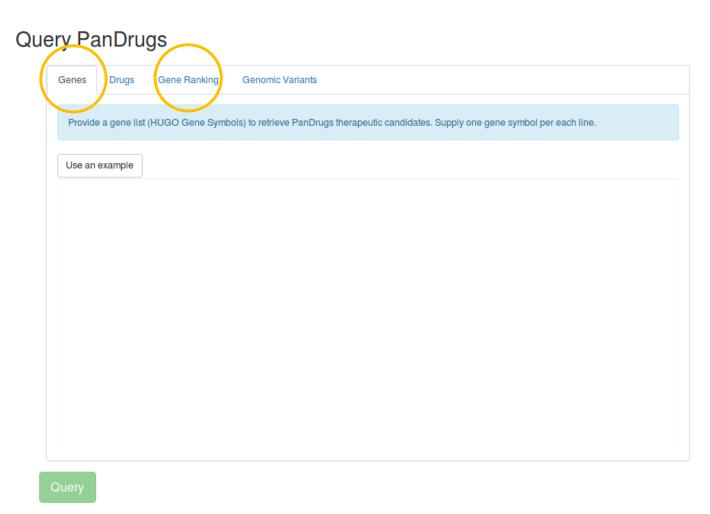
PanDrugs current version integrates data from 18 primary sources and supports ~50,000 drug-target associations obtained from ~6,000 genes and ~11,000 unique compounds.

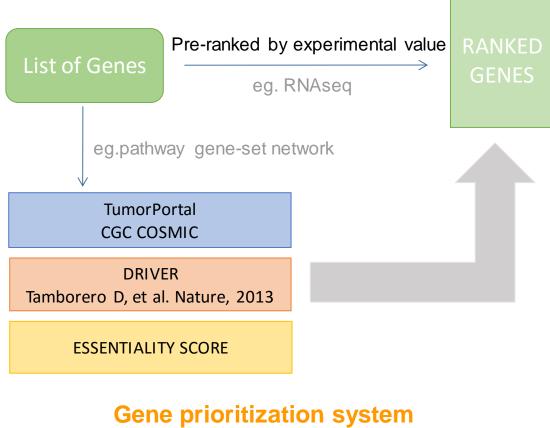
PanDrugs across TCGA tumoral landscape (by Drugs Genes)

This plot shows the percentage of patients in different tumor types from TCGA study that would be treated according to PanDrugs suggestions based on punctual genetic alterations. Each bubble represents a treatment with a particular drug and the drug score is the highest one among the computed for each patient that could be treated with that compound. Only alterations with a gene score greater or equal than 0.6 are considered.



Input options

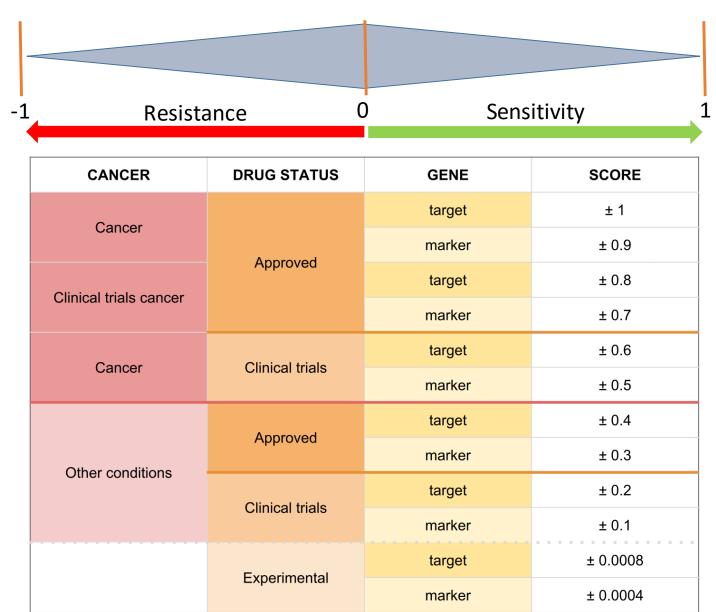




Gene Score (GScore) calculation

Drug Relevance (DScore)

0



Pre-calculated values

Drug Relevance (DScore)

Approved and Clinical trials:

Gene factor = # genes (max. 9) - 1 (if indirect and no marker evidence)
Source factor = # expert curated sources (max 9)

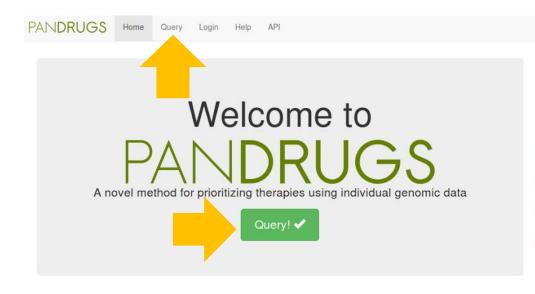
DScore = Pre-computed value - 0.1 + (0.01 * Gene Factor) + 0.001 + (0.001 * Source Factor)

Experimental:

DScore = Pre-computed value - 0.0002 (if indirect)

INDIRECT assignations will have a lower DScore unless a marker evidence supports the association.

If one drug has a sensitivity response due to one gene, but a resistance response due to another one, the drug assignation is updated as RESISTANCE and the score turn into negative.



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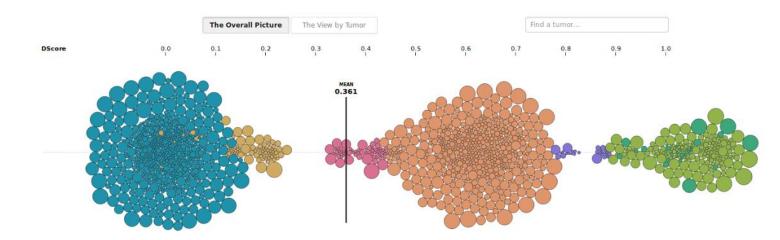
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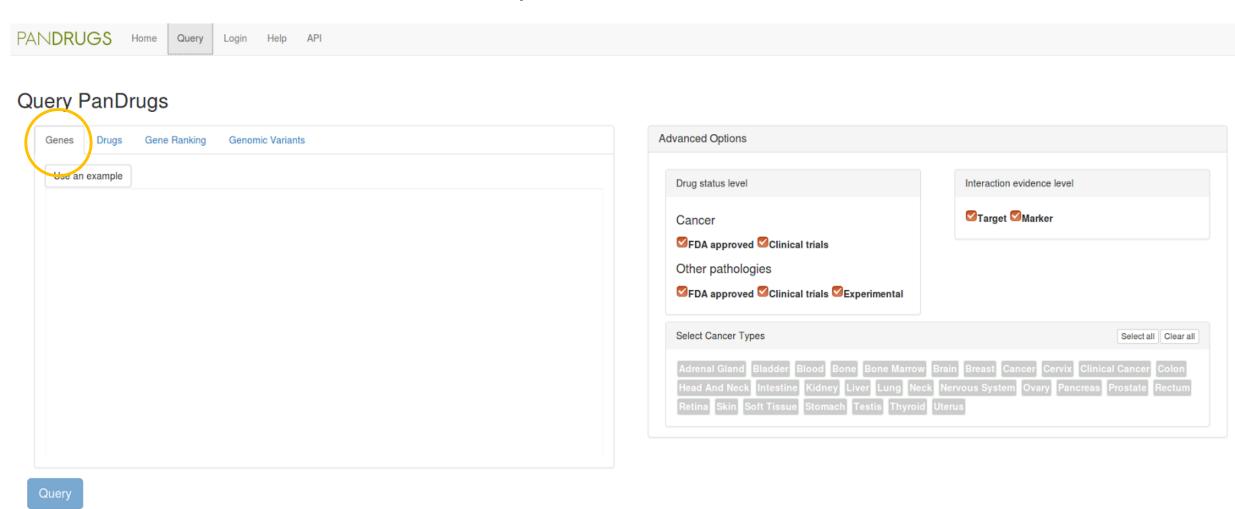
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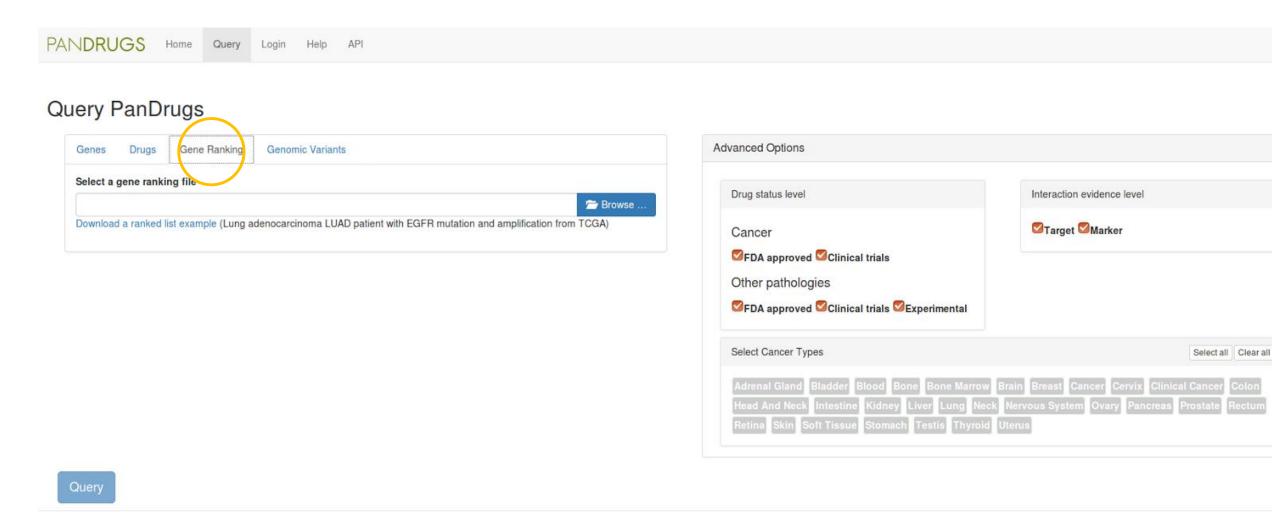
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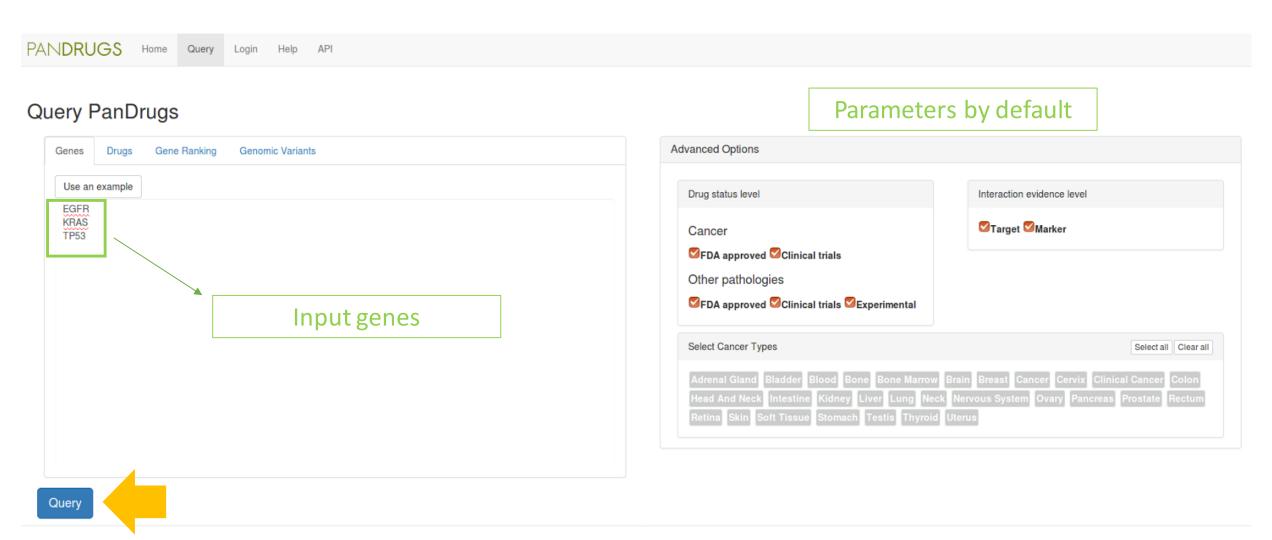
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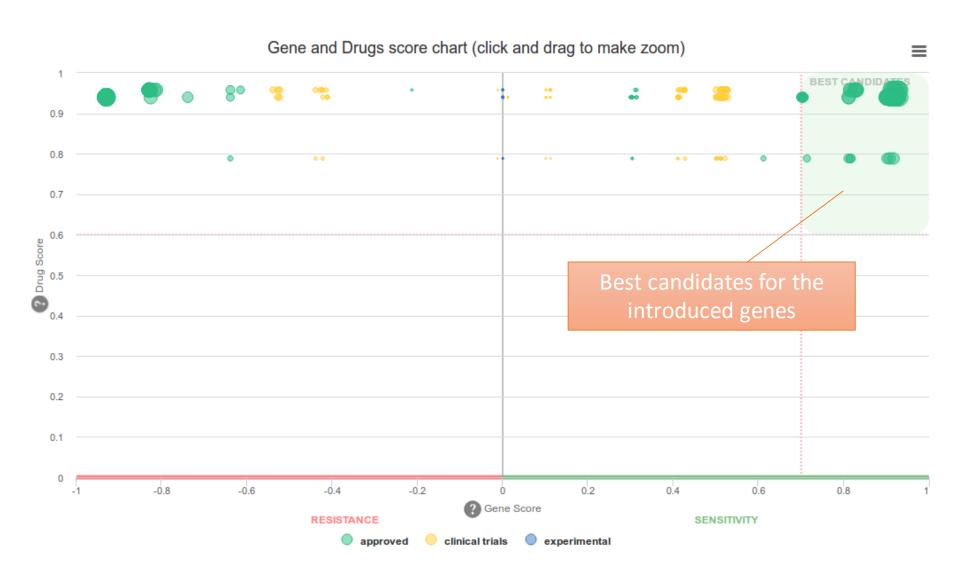
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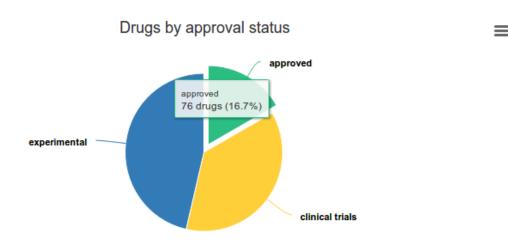


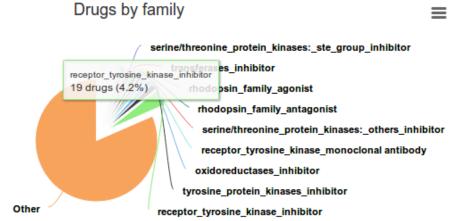




Gene and Drugs score chart (click and drag to make zoom)







								Down	Download as CSV	
Actions	Gene(s)	Drug O	Family ②	Source(s)	Drug status 😱	Type of therapy 🚱	Interaction	▼ DScore ②	GScore (2)	
+	EGFR and KRAS	TRAMETINIB	serine/threonine_protein_kinases:_ste_group_inhibitor	CIV CC CFB DoCM DB GIPI MCG MCGCT TALC	Approved for skin cancer	Targeted therapy	⑥→ ⑦ ⊢□	0.9300	0.9577	
+	EGFR and KRAS	CETUXIMAB	receptor_tyrosine_kinase_monoclonal antibody	CIV CC CFB DoCM DB GtPI MCG PGKB TALC TCGA TEND TTD TCT moAb	Approved for colon and rectum cancer	Targeted therapy	⊕ □	0.9300	0.9577	
+	EGFR and KRAS	COBIMETINIB	Other	CC CFB DB MCG MCGCT TALC TCT	Approved for skin cancer	Targeted therapy	⑥→ ⑦⊢ □	0.9270	0.9577	
+	EGFR and KRAS	REGORAFENIB	receptor_tyrosine_kinase_inhibitor	DB GtPI MCG MCGCT TALC TCT	Approved for colon, intestine, rectum and stomach cancer	Targeted therapy	⑥→ ⑦⊢ □	0.9260	0.9577	
+	EGFR	TRASTUZUMAB	receptor_tyrosine_kinase_monoclonal antibody	CIV CFB CFCT DoCM DB GtPI MCG PGKB TALC TCGA TEND TTD TCT moAb	Approved for breast and stomach cancer	Targeted therapy	⊕ □	0.9200	0.9398	
+	EGFR	LAPATINIB	receptor_tyrosine_kinase_inhibitor	CIV CC CFB CFCT DoCM DB GDSC GiPI MCG PGKB TALC TCGA TEND TTD TCT	Approved for breast cancer	Targeted therapy	⊕ □	0.9200	0.9398	
+	EGFR and KRAS	SORAFENIB	receptor_tyrosine_kinase_inhibitor	CIV CFCT DoCM DB GDSC GIPI MCG MCGCT PGKB TALC TCGA TEND TTD TCT	Approved for kidney cancer	Targeted therapy	⑥→ ⑦⊢ □	0.9200	0.9577	
+	EGFR	PERTUZUMAB	receptor_tyrosine_kinase_monoclonal antibody	CFB DoCM DB GtPI MCG PGKB TALC TCGA TTD TCT moAb	Approved for breast cancer	Targeted therapy	⊕	0.9190	0.9398	
+	TP53	PACLITAXEL	rhodopsin_family_antagonist	CIV CFB CFCT DB GDSC GIPI PGKB TEND TTD	Approved for breast, lung, ovary and pancreas cancer	Chemotherapy	⑥→ ⑦ ⊢□	0.9170	0.7884	
+	EGFR	AFATINIB	receptor_tyrosine_kinase_inhibitor	CC DB GDSC GtPI MCG MCGCT TALC TTD TCT	Approved for lung cancer	Targeted therapy	⊕ □	0.9170	0.9398	

Actio	ons Gene(s) 🔞	Drug ②	Family ②	Source(s) ②	Drug status 😢	Type of therapy 👔	Interaction 🔞	▼DScore ?	GScore (2)
_	EGFR and KRAS	TRAMETINIB	serine/threonine_protein_kinases:_ste_group_inhibitor	CIV CC CFB DoCM DB GtPI MCG MCGCT TALC TCT	Approved for skin cancer	Targeted therapy	⑥→⑦⊢D	0.9300	0.9577
	as an inhibitor of MAI to EGFR and KRAS EGFR and KRAS Sensitivity: SENSITIV Alteration: WT (sensi (resistance)	P2K1, a protein downstream /ITY / RESISTANCE tivity) / Missense_mutation RAMETINIB"+"MAP2K1" in:	serine/threonine_protein_kinases:_ste_group_inhibitor	CIVIC, CancerCommons, ClearityFoundationBiomarkers, DoCM, DrugBank, GuideToPharmacologyInteractions, MyCancerGenome, MyCancerGenomeClinicalTrial, TALC, TdgClinicalTrial			G→ T ⊢D See pathways	0.9300	0.9577
	response to TRAMET FDA KRAS Sensitivity: SENSITIV Alteration: Missense_	mutation RAMETINIB"+"KRAS" in:	serine/threonine_protein_kinases:_ste_group_inhibitor	CIVIC, CancerCommons, ClearityFoundationBiomarkers, DoCM, DrugBank, GuideToPharmacologyInteractions, MyCancerGenome, MyCancerGenomeClinicalTrial, TALC, TdgClinicalTrial			⑦D	0.8300	0.9577