

## Supplementary Figures

### DRUGGING HIJACKED KINASE PATHWAYS IN PEDIATRIC ONCOLOGY: OPPORTUNITIES AND CURRENT SCENARIO

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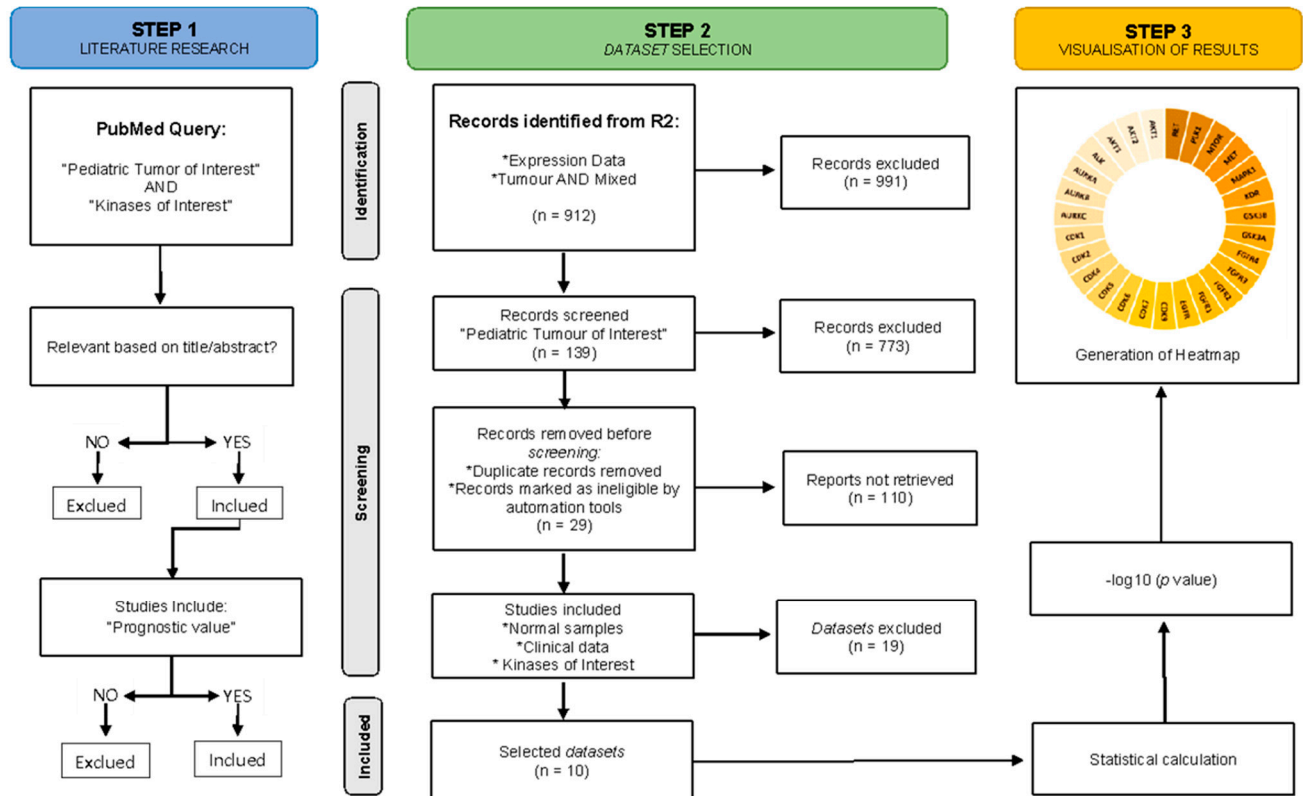
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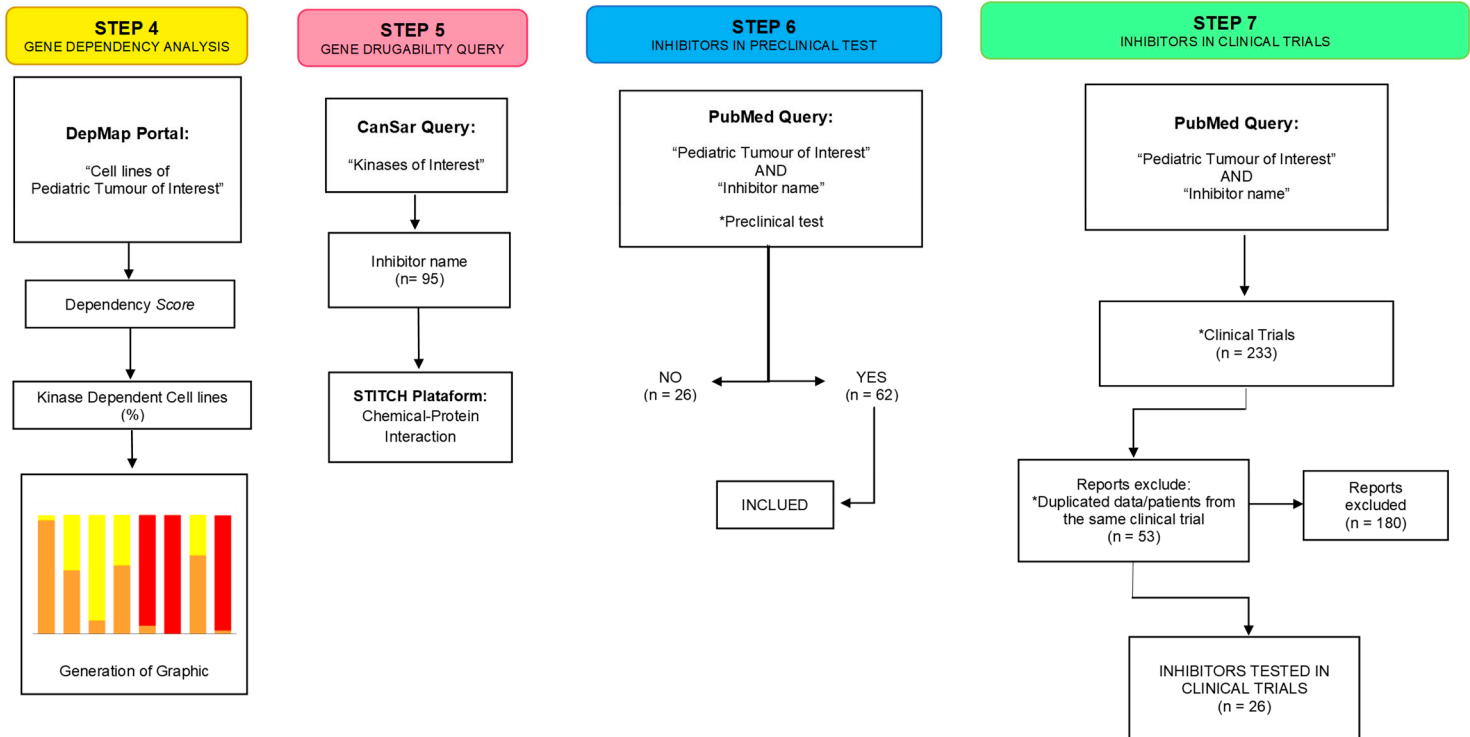
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*Adapted from:* Page MJ, McKenzie JE, Bossuyt PM, Boutron I, Hoffmann TC, Mulrow CD, et al. The PRISMA 2020 statement: an updated guideline for reporting systematic reviews. *BMJ* 2021;372:n71. doi: 10.1136/bmj.n71. For more information, visit: <http://www.prisma-statement.org/>



**Supplementary Figure S2:** Flowchart representing kinases of interest analysis in cell line dependency score and the identification of inhibitors, preclinical studies and clinical test describing the number originally identified, included and excluded, and the reasons for exclusions.



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**Supplementary Figure S3:** Schematic illustrations of kinases druggability identified by the CanSAR database in the other kinase families, including the total number of compounds with predicted interaction capacity with each kinase, as well as FDA-approved drugs, and clinical candidates. Interaction networks of kinase inhibitors and associated binding proteins according to STITCH ('search tool for interactions of chemicals'). Compounds are represented as pill-shaped nodes, while proteins are shown as spheres. Small nodes represent proteins of unknown 3D structures, while large nodes show proteins with known or predicted structures. Nodes that are associated to each other are linked by an edge: thicker lines represent stronger binding affinities. Networks were constructed considering a minimum required interaction score of 0.700, and based on associations reported in Curated Databases (gray lines), or on both Databases and Experimental/Biochemical Data (green lines). Purple lines represent functional links between proteins.

PI3K/AKT/mTOR inhibitors

Compounds

Clinical promise

FDA approved

mTOR	6188	15	2
GSK3A	3291	0	0
GSK3B	7610	2	0
AKT1	6134	4	0
AKT2	2756	0	0
AKT3	1622	0	0

A network diagram illustrating the interactions between various proteins and drugs in the PI3K/AKT/mTOR pathway. Proteins shown include GSK3B, AKT1, AKT2, PIK3CA, PIK3CG, MTOR, EIF4E, AZD8055, OSI-027, INK-128, CPT1A, CPT2, CYP2D6, perhexiline, PKI-179, PKI-587, Apitolisib, MK-2206 dihydr., LY2090314, GDC-0068, tricinibine, NVP-BEZ235, XL765, NVP-BGT226, everolimus, and PDGFRB. Drugs are represented by colored circles, and proteins by green circles. Lines indicate interactions between them.

MAPK inhibitors

Compounds

Clinical promise

FDA approved

MAPK1	7872	0	0
MAPK3	2718	0	0
RAF1	4764	3	4
PLK1	3242	5	0

A network diagram illustrating the interactions between various proteins and drugs in the MAPK pathway. Proteins shown include FLT4, FLT1, PDGFRA, PDGFRB, KDR, BRAF, RAF1, RET, KIT, FLT3, sorafenib, regorafenib, vemurafenib, and dabrafenib. Drugs are represented by colored circles, and proteins by green circles. Lines indicate interactions between them.

Cell cycle inhibitors

Compounds

Clinical promise

FDA approved

PLK1	3242	5	0
AURKA	5927	0	0
AURKB	4558	0	0
AURKC	1167	0	0
CDK1	4509	8	0
CDK2	9410	12	0
CDK4	4244	7	4
CDK5	3829	4	0
CDK6	4244	1	4
CDK7	1929	4	0
CDK9	4973	7	0

A network diagram illustrating the interactions between various proteins and drugs in the cell cycle pathway. Proteins shown include CDK7, CDK6, CDK4, CDK5, CDK2, CDK1, PLK1, CHEK1, PDPK1, Sns-032, AT7519, roscovitine, 7-hydroxystaur., y/benzamide, NMS-P937, volasertib, BI 2536, GSK461364A, milciclib, palbociclib, SU9516, SB1317/TG02, Ag-24322, and terameprocol. Drugs are represented by colored circles, and proteins by green circles. Lines indicate interactions between them.