

David E Root

List of Publications by Year in descending order

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Version: 2024-02-01

51
papers

23,392
citations

101543

36
h-index

182427

51
g-index

55
all docs

55
docs citations

55
times ranked

36837
citing authors

| # | ARTICLE | IF | CITATIONS |
|----|---|------|-----------|
| 1 | Genetic barcoding systematically compares genes in del(5q) MDS and reveals a central role for <i>CSNK1A1</i> in clonal expansion. <i>Blood Advances</i> , 2022, 6, 1780-1796. | 5.2 | 7 |
| 2 | PPM1D mutations are oncogenic drivers of de novo diffuse midline glioma formation. <i>Nature Communications</i> , 2022, 13, 604. | 12.8 | 22 |
| 3 | Systematic identification of biomarker-driven drug combinations to overcome resistance. <i>Nature Chemical Biology</i> , 2022, 18, 615-624. | 8.0 | 14 |
| 4 | Phosphate dysregulation via the XPR1-KIDINS220 protein complex is a therapeutic vulnerability in ovarian cancer. <i>Nature Cancer</i> , 2022, 3, 681-695. | 13.2 | 21 |
| 5 | Allosteric inhibition of PPM1D serine/threonine phosphatase via an altered conformational state. <i>Nature Communications</i> , 2022, 13, . | 12.8 | 15 |
| 6 | Structure-function analysis of the SHOC2-MRAS-PP1C holophosphatase complex. <i>Nature</i> , 2022, 609, 408-415. | 27.8 | 28 |
| 7 | Progression signature underlies clonal evolution and dissemination of multiple myeloma. <i>Blood</i> , 2021, 137, 2360-2372. | 1.4 | 26 |
| 8 | Noncanonical open reading frames encode functional proteins essential for cancer cell survival. <i>Nature Biotechnology</i> , 2021, 39, 697-704. | 17.5 | 85 |
| 9 | <i>LKB1</i> Is a Tumor Suppressor in the Progression of Myeloproliferative Neoplasms. <i>Cancer Discovery</i> , 2021, 11, 1398-1410. | 9.4 | 29 |
| 10 | Selective Modulation of a Pan-Essential Protein as a Therapeutic Strategy in Cancer. <i>Cancer Discovery</i> , 2021, 11, 2282-2299. | 9.4 | 21 |
| 11 | Paralog knockout profiling identifies DUSP4 and DUSP6 as a digenic dependence in MAPK pathway-driven cancers. <i>Nature Genetics</i> , 2021, 53, 1664-1672. | 21.4 | 61 |
| 12 | Defining the landscape of ATP-competitive inhibitor resistance residues in protein kinases. <i>Nature Structural and Molecular Biology</i> , 2020, 27, 92-104. | 8.2 | 30 |
| 13 | Acquired FGFR and FGF Alterations Confer Resistance to Estrogen Receptor (ER) Targeted Therapy in ER+ Metastatic Breast Cancer. <i>Clinical Cancer Research</i> , 2020, 26, 5974-5989. | 7.0 | 87 |
| 14 | A Genome-scale CRISPR Screen Identifies the ERBB and mTOR Signaling Networks as Key Determinants of Response to PI3K Inhibition in Pancreatic Cancer. <i>Molecular Cancer Therapeutics</i> , 2020, 19, 1423-1435. | 4.1 | 14 |
| 15 | A genome-wide gain-of-function screen identifies CDKN2C as a HBV host factor. <i>Nature Communications</i> , 2020, 11, 2707. | 12.8 | 11 |
| 16 | A dominant-negative effect drives selection of <i>TP53</i> missense mutations in myeloid malignancies. <i>Science</i> , 2019, 365, 599-604. | 12.6 | 265 |
| 17 | Neuronal differentiation and cell-cycle programs mediate response to BET-bromodomain inhibition in MYC-driven medulloblastoma. <i>Nature Communications</i> , 2019, 10, 2400. | 12.8 | 37 |
| 18 | The landscape of cancer cell line metabolism. <i>Nature Medicine</i> , 2019, 25, 850-860. | 30.7 | 350 |

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|----|--|------|-----------|
| 19 | A Functional Landscape of Resistance to MEK1/2 and CDK4/6 Inhibition in NRAS-Mutant Melanoma. <i>Cancer Research</i> , 2019, 79, 2352-2366. | 0.9 | 34 |
| 20 | WRN helicase is a synthetic lethal target in microsatellite unstable cancers. <i>Nature</i> , 2019, 568, 551-556. | 27.8 | 253 |
| 21 | Agreement between two large pan-cancer CRISPR-Cas9 gene dependency data sets. <i>Nature Communications</i> , 2019, 10, 5817. | 12.8 | 160 |
| 22 | Cells Lacking the <i>RB1</i> Tumor Suppressor Gene Are Hyperdependent on Aurora B Kinase for Survival. <i>Cancer Discovery</i> , 2019, 9, 230-247. | 9.4 | 119 |
| 23 | Pooled Lentiviral Delivery Genetic Screens. <i>Current Protocols in Molecular Biology</i> , 2018, 121, 32.1.1-32.1.21. | 2.9 | 20 |
| 24 | Orthologous CRISPR-Cas9 enzymes for combinatorial genetic screens. <i>Nature Biotechnology</i> , 2018, 36, 179-189. | 17.5 | 216 |
| 25 | Improved estimation of cancer dependencies from large-scale RNAi screens using model-based normalization and data integration. <i>Nature Communications</i> , 2018, 9, 4610. | 12.8 | 290 |
| 26 | Mutational processes shape the landscape of TP53 mutations in human cancer. <i>Nature Genetics</i> , 2018, 50, 1381-1387. | 21.4 | 334 |
| 27 | Selective gene dependencies in MYCN-amplified neuroblastoma include the core transcriptional regulatory circuitry. <i>Nature Genetics</i> , 2018, 50, 1240-1246. | 21.4 | 199 |
| 28 | The Canonical Wnt Pathway Drives Macropinocytosis in Cancer. <i>Cancer Research</i> , 2018, 78, 4658-4670. | 0.9 | 75 |
| 29 | Complementary information derived from CRISPR Cas9 mediated gene deletion and suppression. <i>Nature Communications</i> , 2017, 8, 15403. | 12.8 | 93 |
| 30 | Computational correction of copy number effect improves specificity of CRISPR-Cas9 essentiality screens in cancer cells. <i>Nature Genetics</i> , 2017, 49, 1779-1784. | 21.4 | 1,436 |
| 31 | Defining a Cancer Dependency Map. <i>Cell</i> , 2017, 170, 564-576.e16. | 28.9 | 1,794 |
| 32 | A Next Generation Connectivity Map: L1000 Platform and the First 1,000,000 Profiles. <i>Cell</i> , 2017, 171, 1437-1452.e17. | 28.9 | 2,281 |
| 33 | CRISPR-Cas9 screen reveals a MYCN-amplified neuroblastoma dependency on EZH2. <i>Journal of Clinical Investigation</i> , 2017, 128, 446-462. | 8.2 | 117 |
| 34 | Phenotypic Characterization of a Comprehensive Set of MAPK1 /ERK2 Missense Mutants. <i>Cell Reports</i> , 2016, 17, 1171-1183. | 6.4 | 119 |
| 35 | High-throughput Phenotyping of Lung Cancer Somatic Mutations. <i>Cancer Cell</i> , 2016, 30, 214-228. | 16.8 | 171 |
| 36 | A Genome-wide CRISPR Death Screen Identifies Genes Essential for Oxidative Phosphorylation. <i>Cell Metabolism</i> , 2016, 24, 875-885. | 16.2 | 244 |

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|----|--|------|-----------|
| 37 | Optimized sgRNA design to maximize activity and minimize off-target effects of CRISPR-Cas9. <i>Nature Biotechnology</i> , 2016, 34, 184-191. | 17.5 | 3,168 |
| 38 | <i>MTAP</i> deletion confers enhanced dependency on the PRMT5 arginine methyltransferase in cancer cells. <i>Science</i> , 2016, 351, 1214-1218. | 12.6 | 396 |
| 39 | A Functional Landscape of Resistance to ALK Inhibition in Lung Cancer. <i>Cancer Cell</i> , 2015, 27, 397-408. | 16.8 | 150 |
| 40 | Csnk1a1 inhibition has p53-dependent therapeutic efficacy in acute myeloid leukemia. <i>Journal of Experimental Medicine</i> , 2014, 211, 605-612. | 8.5 | 79 |
| 41 | Genetic modifiers of EGFR dependence in non-small cell lung cancer. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 18661-18666. | 7.1 | 46 |
| 42 | Genome-Scale CRISPR-Cas9 Knockout Screening in Human Cells. <i>Science</i> , 2014, 343, 84-87. | 12.6 | 4,210 |
| 43 | Rational design of highly active sgRNAs for CRISPR-Cas9-mediated gene inactivation. <i>Nature Biotechnology</i> , 2014, 32, 1262-1267. | 17.5 | 1,351 |
| 44 | KRAS and YAP1 Converge to Regulate EMT and Tumor Survival. <i>Cell</i> , 2014, 158, 171-184. | 28.9 | 608 |
| 45 | Parallel genome-scale loss of function screens in 216 cancer cell lines for the identification of context-specific genetic dependencies. <i>Scientific Data</i> , 2014, 1, 140035. | 5.3 | 328 |
| 46 | A melanocyte lineage program confers resistance to MAP kinase pathway inhibition. <i>Nature</i> , 2013, 504, 138-142. | 27.8 | 401 |
| 47 | A Genome-Scale RNA Interference Screen Implicates NF1 Loss in Resistance to RAF Inhibition. <i>Cancer Discovery</i> , 2013, 3, 350-362. | 9.4 | 299 |
| 48 | A public genome-scale lentiviral expression library of human ORFs. <i>Nature Methods</i> , 2011, 8, 659-661. | 19.0 | 477 |
| 49 | Systematic investigation of genetic vulnerabilities across cancer cell lines reveals lineage-specific dependencies in ovarian cancer. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 12372-12377. | 7.1 | 383 |
| 50 | COT drives resistance to RAF inhibition through MAP kinase pathway reactivation. <i>Nature</i> , 2010, 468, 968-972. | 27.8 | 1,325 |
| 51 | Identification of RPS14 as a 5q- syndrome gene by RNA interference screen. <i>Nature</i> , 2008, 451, 335-339. | 27.8 | 850 |