

# John N Weinstein

## List of Publications by Year in descending order

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Version: 2024-02-01

345  
papers

136,762  
citations

433

131  
h-index

114

342  
g-index

366  
all docs

366  
docs citations

366  
times ranked

119441  
citing authors

| #  | ARTICLE  | IF   | CITATIONS |
|----|--|------|-----------|
| 1  | The origin of bladder cancer from mucosal field effects. <i>IScience</i> , 2022, 25, 104551.   | 1.9  | 12        |
| 2  | Whole-genome characterization of lung adenocarcinomas lacking alterations in the RTK/RAS/RAF pathway. <i>Cell Reports</i> , 2021, 34, 108707.  | 2.9  | 16        |
| 3  | Compound NSC84167 selectively targets NRF2-activated pancreatic cancer by inhibiting asparagine synthesis pathway. <i>Cell Death and Disease</i> , 2021, 12, 693.  | 2.7  | 5         |
| 4  | A Consensus Molecular Classification of Muscle-invasive Bladder Cancer. <i>European Urology</i> , 2020, 77, 420-433.   | 0.9  | 741       |
| 5  | Urothelial-to-Neural Plasticity Drives Progression to Small Cell Bladder Cancer. <i>IScience</i> , 2020, 23, 101201.   | 1.9  | 18        |
| 6  | Retrospective evaluation of whole exome and genome mutation calls in 746 cancer samples. <i>Nature Communications</i> , 2020, 11, 4748.  | 5.8  | 27        |
| 7  | Mechanism of Catalysis by <i>L</i> -Asparaginase. <i>Biochemistry</i> , 2020, 59, 1927-1945.   | 1.2  | 36        |
| 8  | Assessment of Luminal and Basal Phenotypes in Bladder Cancer. <i>Scientific Reports</i> , 2020, 10, 9743.  | 1.6  | 83        |
| 9  | A user guide for the online exploration and visualization of PCAWG data. <i>Nature Communications</i> , 2020, 11, 3400.  | 5.8  | 23        |
| 10 | Reply To Kenneth B. Yatai, Mark J. Dunning, Dennis Wang. Consensus Genomic Subtypes of Muscle-invasive Bladder Cancer: A Step in the Right Direction but Still a Long Way To Go. <i>Eur Urol</i> 2020;77:434-438. <i>European Urology</i> , 2020, 77, 436-438. | 0.9  | 1         |
| 11 | Pan-cancer analysis of whole genomes. <i>Nature</i> , 2020, 578, 82-93.  | 13.7 | 1,966     |
| 12 | Comprehensive molecular characterization of mitochondrial genomes in human cancers. <i>Nature Genetics</i> , 2020, 52, 342-352.  | 9.4  | 256       |
| 13 | Integrated Analysis of TP53 Gene and Pathway Alterations in The Cancer Genome Atlas. <i>Cell Reports</i> , 2019, 28, 1370-1384.e5.   | 2.9  | 382       |
| 14 | Glutaminase Activity of <i>L</i> -Asparaginase Contributes to Durable Preclinical Activity against Acute Lymphoblastic Leukemia. <i>Molecular Cancer Therapeutics</i> , 2019, 18, 1587-1592.   | 1.9  | 46        |
| 15 | Dysregulation of EMT Drives the Progression to Clinically Aggressive Sarcomatoid Bladder Cancer. <i>Cell Reports</i> , 2019, 27, 1781-1793.e4.   | 2.9  | 102       |
| 16 | Response envelope analysis for quantitative evaluation of drug combinations. <i>Bioinformatics</i> , 2019, 35, 3761-3770.  | 1.8  | 3         |
| 17 | Integrated transcriptomic-genomic tool Texomer profiles cancer tissues. <i>Nature Methods</i> , 2019, 16, 401-404.   | 9.0  | 7         |
| 18 | Whole-Organ Genomic Characterization of Mucosal Field Effects Initiating Bladder Carcinogenesis. <i>Cell Reports</i> , 2019, 26, 2241-2256.e4.   | 2.9  | 31        |

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|----|---|------|-----------|
| 19 | ElemCor: accurate data analysis and enrichment calculation for high-resolution LC-MS stable isotope labeling experiments. BMC Bioinformatics, 2019, 20, 89. | 1.2  | 402       |
| 20 | Assessment of l-Asparaginase Pharmacodynamics in Mouse Models of Cancer. Metabolites, 2019, 9, 10.  | 1.3  | 11        |
| 21 | Interactive Clustered Heat Map Builder: An easy web-based tool for creating sophisticated clustered heat maps. F1000Research, 2019, 8, 1750.                | 0.8  | 31        |
| 22 | Interactive Clustered Heat Map Builder: An easy web-based tool for creating sophisticated clustered heat maps. F1000Research, 2019, 8, 1750.                | 0.8  | 31        |
| 23 | ZC3H12A Expression in Different Stages of Colorectal Cancer. Oncoscience, 2019, 6, 301-311.   | 0.9  | 10        |
| 24 | An Integrated TCGA Pan-Cancer Clinical Data Resource to Drive High-Quality Survival Outcome Analytics. Cell, 2018, 173, 400-416.e11.                        | 13.5 | 2,277     |
| 25 | Comprehensive Characterization of Cancer Driver Genes and Mutations. Cell, 2018, 173, 371-385.e18.  | 13.5 | 1,670     |
| 26 | Cell-of-Origin Patterns Dominate the Molecular Classification of 10,000 Tumors from 33 Types of Cancer. Cell, 2018, 173, 291-304.e6.                        | 13.5 | 1,718     |
| 27 | A Pan-Cancer Analysis of Enhancer Expression in Nearly 9000 Patient Samples. Cell, 2018, 173, 386-399.e12.  | 13.5 | 228       |
| 28 | Perspective on Oncogenic Processes at the End of the Beginning of Cancer Genomics. Cell, 2018, 173, 305-320.e10.  | 13.5 | 272       |
| 29 | Machine Learning Identifies Stemness Features Associated with Oncogenic Dedifferentiation. Cell, 2018, 173, 338-354.e15.                                    | 13.5 | 1,417     |
| 30 | Oncogenic Signaling Pathways in The Cancer Genome Atlas. Cell, 2018, 173, 321-337.e10.  | 13.5 | 2,111     |
| 31 | Pathogenic Germline Variants in 10,389 Adult Cancers. Cell, 2018, 173, 355-370.e14.   | 13.5 | 620       |
| 32 | Somatic Mutational Landscape of Splicing Factor Genes and Their Functional Consequences across 33 Cancer Types. Cell Reports, 2018, 23, 282-296.e4.         | 2.9  | 333       |
| 33 | Driver Fusions and Their Implications in the Development and Treatment of Human Cancers. Cell Reports, 2018, 23, 227-238.e3.                                | 2.9  | 407       |
| 34 | Genomic, Pathway Network, and Immunologic Features Distinguishing Squamous Carcinomas. Cell Reports, 2018, 23, 194-212.e6.                                  | 2.9  | 245       |
| 35 | Pan-Cancer Analysis of lncRNA Regulation Supports Their Targeting of Cancer Genes in Each Tumor Context. Cell Reports, 2018, 23, 297-312.e12.               | 2.9  | 205       |
| 36 | The Cancer Genome Atlas Comprehensive Molecular Characterization of Renal Cell Carcinoma. Cell Reports, 2018, 23, 313-326.e5.                               | 2.9  | 523       |

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|----|--|-----|-----------|
| 37 | Spatial Organization and Molecular Correlation of Tumor-Infiltrating Lymphocytes Using Deep Learning on Pathology Images. Cell Reports, 2018, 23, 181-193.e7.                          | 2.9 | 683       |
| 38 | The Immune Landscape of Cancer. Immunity, 2018, 48, 812-830.e14.   | 6.6 | 3,706     |
| 39 | Machine Learning Detects Pan-cancer Ras Pathway Activation in The Cancer Genome Atlas. Cell Reports, 2018, 23, 172-180.e3.   | 2.9 | 119       |
| 40 | Integrated Genomic Analysis of the Ubiquitin Pathway across Cancer Types. Cell Reports, 2018, 23, 213-226.e3.  | 2.9 | 83        |
| 41 | Genomic and Molecular Landscape of DNA Damage Repair Deficiency across The Cancer Genome Atlas. Cell Reports, 2018, 23, 239-254.e6.  | 2.9 | 801       |
| 42 | Molecular Characterization and Clinical Relevance of Metabolic Expression Subtypes in Human Cancers. Cell Reports, 2018, 23, 255-269.e4.   | 2.9 | 204       |
| 43 | Systematic Analysis of Splice-Site-Creating Mutations in Cancer. Cell Reports, 2018, 23, 270-281.e3.   | 2.9 | 177       |
| 44 | The Integrated Genomic Landscape of Thymic Epithelial Tumors. Cancer Cell, 2018, 33, 244-258.e10.  | 7.7 | 270       |
| 45 | Genomic Assessment of Muscle-Invasive Bladder Cancer: Insights from the Cancer Genome Atlas (TCGA) Project. Molecular Pathology Library, 2018, , 43-64.                                | 0.1 | 0         |
| 46 | Scalable Open Science Approach for Mutation Calling of Tumor Exomes Using Multiple Genomic Pipelines. Cell Systems, 2018, 6, 271-281.e7.   | 2.9 | 605       |
| 47 | Pan-cancer Alterations of the MYC Oncogene and Its Proximal Network across the Cancer Genome Atlas. Cell Systems, 2018, 6, 282-300.e2.   | 2.9 | 284       |
| 48 | lncRNA Epigenetic Landscape Analysis Identifies EPIC1 as an Oncogenic lncRNA that Interacts with MYC and Promotes Cell-Cycle Progression in Cancer. Cancer Cell, 2018, 33, 706-720.e9. | 7.7 | 400       |
| 49 | Genomic and Functional Approaches to Understanding Cancer Aneuploidy. Cancer Cell, 2018, 33, 676-689.e3.   | 7.7 | 750       |
| 50 | Comparative Molecular Analysis of Gastrointestinal Adenocarcinomas. Cancer Cell, 2018, 33, 721-735.e8.   | 7.7 | 396       |
| 51 | A Comprehensive Pan-Cancer Molecular Study of Gynecologic and Breast Cancers. Cancer Cell, 2018, 33, 690-705.e9.   | 7.7 | 478       |
| 52 | Global analysis of tRNA and translation factor expression reveals a dynamic landscape of translational regulation in human cancers. Communications Biology, 2018, 1, 234.              | 2.0 | 58        |
| 53 | A Pan-Cancer Analysis Reveals High-Frequency Genetic Alterations in Mediators of Signaling by the TGF- $\beta$ 2 Superfamily. Cell Systems, 2018, 7, 422-437.e7.                       | 2.9 | 134       |
| 54 | The chromatin accessibility landscape of primary human cancers. Science, 2018, 362, .  | 6.0 | 781       |

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|----|--|------|-----------|
| 55 | Integrative Molecular Characterization of Malignant Pleural Mesothelioma. <i>Cancer Discovery</i> , 2018, 8, 1548-1565.  | 7.7  | 422       |
| 56 | Comprehensive Molecular Characterization of the Hippo Signaling Pathway in Cancer. <i>Cell Reports</i> , 2018, 25, 1304-1317.e5.   | 2.9  | 329       |
| 57 | SoS Notebook: an interactive multi-language data analysis environment. <i>Bioinformatics</i> , 2018, 34, 3768-3770.  | 1.8  | 7         |
| 58 | Comprehensive Analysis of Alternative Splicing Across Tumors from 8,705 Patients. <i>Cancer Cell</i> , 2018, 34, 211-224.e6.   | 7.7  | 623       |
| 59 | Clinical significance of FBXO17 gene expression in high-grade glioma. <i>BMC Cancer</i> , 2018, 18, 773.   | 1.1  | 9         |
| 60 | Integrated Molecular Characterization of Testicular Germ Cell Tumors. <i>Cell Reports</i> , 2018, 23, 3392-3406.   | 2.9  | 324       |
| 61 | The Glutaminase Activity of L-Asparaginase Mediates Suppression of Asns Upregulation. <i>Blood</i> , 2018, 132, 3959-3959.   | 0.6  | 3         |
| 62 | Predicting high-risk endometrioid carcinomas using proteins. <i>Oncotarget</i> , 2018, 9, 19704-19715.   | 0.8  | 5         |
| 63 | Integrated genomic and molecular characterization of cervical cancer. <i>Nature</i> , 2017, 543, 378-384.  | 13.7 | 1,158     |
| 64 | Comprehensive Molecular Characterization of Pheochromocytoma and Paraganglioma. <i>Cancer Cell</i> , 2017, 31, 181-193.  | 7.7  | 532       |
| 65 | Expression of human endogenous retrovirus-K is strongly associated with the basal-like breast cancer phenotype. <i>Scientific Reports</i> , 2017, 7, 41960.  | 1.6  | 73        |
| 66 | Comprehensive and Integrative Genomic Characterization of Hepatocellular Carcinoma. <i>Cell</i> , 2017, 169, 1327-1341.e23.  | 13.5 | 1,794     |
| 67 | A Pan-Cancer Proteogenomic Atlas of PI3K/AKT/mTOR Pathway Alterations. <i>Cancer Cell</i> , 2017, 31, 820-832.e3.  | 7.7  | 433       |
| 68 | Integrated Molecular Characterization of Uterine Carcinosarcoma. <i>Cancer Cell</i> , 2017, 31, 411-423.   | 7.7  | 309       |
| 69 | Integrative Genomic Analysis of Cholangiocarcinoma Identifies Distinct IDH-Mutant Molecular Profiles. <i>Cell Reports</i> , 2017, 18, 2780-2794.   | 2.9  | 416       |
| 70 | Explore, Visualize, and Analyze Functional Cancer Proteomic Data Using the Cancer Proteome Atlas. <i>Cancer Research</i> , 2017, 77, e51-e54.  | 0.4  | 101       |
| 71 | Comprehensive Molecular Characterization of Muscle-Invasive Bladder Cancer. <i>Cell</i> , 2017, 171, 540-556.e25.  | 13.5 | 1,742     |
| 72 | <i>NSD1</i> Inactivation and <i>SETD2</i> Mutation Drive a Convergence toward Loss of Function of H3K36 Writers in Clear Cell Renal Cell Carcinomas. <i>Cancer Research</i> , 2017, 77, 4835-4845. | 0.4  | 40        |

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|----|---|------|-----------|
| 73 | Integrative Analysis Identifies Four Molecular and Clinical Subsets in Uveal Melanoma. <i>Cancer Cell</i> , 2017, 32, 204-220.e15.  | 7.7  | 642       |
| 74 | Integrated Genomic Characterization of Pancreatic Ductal Adenocarcinoma. <i>Cancer Cell</i> , 2017, 32, 185-203.e13.  | 7.7  | 1,428     |
| 75 | A Galaxy Implementation of Next-Generation Clustered Heatmaps for Interactive Exploration of Molecular Profiling Data. <i>Cancer Research</i> , 2017, 77, e23-e26.  | 0.4  | 32        |
| 76 | Comprehensive and Integrated Genomic Characterization of Adult Soft Tissue Sarcomas. <i>Cell</i> , 2017, 171, 950-965.e28.  | 13.5 | 738       |
| 77 | PathwaysWeb: a gene pathways API with directional interactions, expanded gene ontology, and versioning. <i>Bioinformatics</i> , 2016, 32, 312-314.  | 1.8  | 3         |
| 78 | Mutational Profiles Reveal an Aberrant TGF- $\beta$ 2-CEA Regulated Pathway in Colon Adenomas. <i>PLoS ONE</i> , 2016, 11, e0153933.  | 1.1  | 17        |
| 79 | Gene Expression Profile of the Clinically Aggressive Micropapillary Variant of Bladder Cancer. <i>European Urology</i> , 2016, 70, 611-620.   | 0.9  | 120       |
| 80 | Altered Expression and Splicing of <i>ESRP1</i> in Malignant Melanoma Correlates with Epithelial-Mesenchymal Status and Tumor-Associated Immune Cytolytic Activity. <i>Cancer Immunology Research</i> , 2016, 4, 552-561. | 1.6  | 50        |
| 81 | Comprehensive Pan-Genomic Characterization of Adrenocortical Carcinoma. <i>Cancer Cell</i> , 2016, 29, 723-736.   | 7.7  | 482       |
| 82 | Distinct patterns of somatic genome alterations in lung adenocarcinomas and squamous cell carcinomas. <i>Nature Genetics</i> , 2016, 48, 607-616.   | 9.4  | 933       |
| 83 | Meta-Analysis of the Luminal and Basal Subtypes of Bladder Cancer and the Identification of Signature Immunohistochemical Markers for Clinical Use. <i>EBioMedicine</i> , 2016, 12, 105-117.                              | 2.7  | 257       |
| 84 | Molecular Profiling Reveals Biologically Discrete Subsets and Pathways of Progression in Diffuse Glioma. <i>Cell</i> , 2016, 164, 550-563.  | 13.5 | 1,695     |
| 85 | TCGASpliceSeq a compendium of alternative mRNA splicing in cancer. <i>Nucleic Acids Research</i> , 2016, 44, D1018-D1022.   | 6.5  | 358       |
| 86 | Comprehensive Molecular Characterization of Papillary Renal-Cell Carcinoma. <i>New England Journal of Medicine</i> , 2016, 374, 135-145.  | 13.9 | 1,040     |
| 87 | A Patient-Derived, Pan-Cancer EMT Signature Identifies Global Molecular Alterations and Immune Target Enrichment Following Epithelial-to-Mesenchymal Transition. <i>Clinical Cancer Research</i> , 2016, 22, 609-620.     | 3.2  | 388       |
| 88 | Red Blood Cell-Encapsulation of L-Asparaginase Favorably Modulates Target Selectivity and Pharmacodynamics. <i>Blood</i> , 2016, 128, 1266-1266.  | 0.6  | 2         |
| 89 | The Cancer Genome Atlas Project on Muscle-invasive Bladder Cancer. <i>European Urology Focus</i> , 2015, 1, 94-95.  | 1.6  | 7         |
| 90 | Whole-genome and multisector exome sequencing of primary and post-treatment glioblastoma reveals patterns of tumor evolution. <i>Genome Research</i> , 2015, 25, 316-327.   | 2.4  | 343       |

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|-----|---|------|-----------|
| 91  | Genomic Classification of Cutaneous Melanoma. <i>Cell</i> , 2015, 161, 1681-1696.   | 13.5 | 2,562     |
| 92  | TANRIC: An Interactive Open Platform to Explore the Function of lncRNAs in Cancer. <i>Cancer Research</i> , 2015, 75, 3728-3737.  | 0.4  | 518       |
| 93  | Co-occurring Genomic Alterations Define Major Subsets of <i>KRAS</i> -Mutant Lung Adenocarcinoma with Distinct Biology, Immune Profiles, and Therapeutic Vulnerabilities. <i>Cancer Discovery</i> , 2015, 5, 860-877. | 7.7  | 696       |
| 94  | Comprehensive, Integrative Genomic Analysis of Diffuse Lower-Grade Gliomas. <i>New England Journal of Medicine</i> , 2015, 372, 2481-2498.  | 13.9 | 2,582     |
| 95  | The Molecular Taxonomy of Primary Prostate Cancer. <i>Cell</i> , 2015, 163, 1011-1025.  | 13.5 | 2,435     |
| 96  | TransVar: a multilevel variant annotator for precision genomics. <i>Nature Methods</i> , 2015, 12, 1002-1003.   | 9.0  | 67        |
| 97  | Invasive Bladder Cancer: Genomic Insights and Therapeutic Promise. <i>Clinical Cancer Research</i> , 2015, 21, 4514-4524.   | 3.2  | 110       |
| 98  | Comprehensive Molecular Portraits of Invasive Lobular Breast Cancer. <i>Cell</i> , 2015, 163, 506-519.  | 13.5 | 1,485     |
| 99  | Catalytic Role of the Substrate Defines Specificity of Therapeutic L-Asparaginase. <i>Journal of Molecular Biology</i> , 2015, 427, 2867-2885.  | 2.0  | 25        |
| 100 | Development of a robust classifier for quality control of reverse-phase protein arrays. <i>Bioinformatics</i> , 2015, 31, 912-918.  | 1.8  | 43        |
| 101 | Characterization of long non-coding RNA transcriptome in clear cell renal cell carcinoma by next-generation deep sequencing. <i>Molecular Oncology</i> , 2015, 9, 32-43.  | 2.1  | 75        |
| 102 | Long non-coding RNA profiling links subgroup classification of endometrioid endometrial carcinomas with trithorax and polycomb complex aberrations. <i>Oncotarget</i> , 2015, 6, 39865-39876.                         | 0.8  | 20        |
| 103 | Next-Generation Sequencing of Translocation Renal Cell Carcinoma Reveals Novel RNA Splicing Partners and Frequent Mutations of Chromatin-Remodeling Genes. <i>Clinical Cancer Research</i> , 2014, 20, 4129-4140.     | 3.2  | 117       |
| 104 | Genes suppressed by DNA methylation in non-small cell lung cancer reveal the epigenetics of epithelial-mesenchymal transition. <i>BMC Genomics</i> , 2014, 15, 1079.  | 1.2  | 45        |
| 105 | A curated census of autophagy-modulating proteins and small molecules. <i>Autophagy</i> , 2014, 10, 1316-1326.  | 4.3  | 29        |
| 106 | Integrated Genomic Characterization of Papillary Thyroid Carcinoma. <i>Cell</i> , 2014, 159, 676-690.   | 13.5 | 2,318     |
| 107 | Tumor Subtype-Specific Cancer-Testis Antigens as Potential Biomarkers and Immunotherapeutic Targets for Cancers. <i>Cancer Immunology Research</i> , 2014, 2, 371-379.  | 1.6  | 90        |
| 108 | The Somatic Genomic Landscape of Glioblastoma. <i>Cell</i> , 2014, 157, 753.  | 13.5 | 51        |

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|-----|---|------|-----------|
| 109 | PRADA: pipeline for RNA sequencing data analysis. <i>Bioinformatics</i> , 2014, 30, 2224-2226.  | 1.8  | 147       |
| 110 | Targeted metabolomic analysis of amino acid response to L-asparaginase in adherent cells. <i>Metabolomics</i> , 2014, 10, 909-919.  | 1.4  | 32        |
| 111 | Comprehensive molecular characterization of urothelial bladder carcinoma. <i>Nature</i> , 2014, 507, 315-322.   | 13.7 | 2,496     |
| 112 | The glutaminase activity of l-asparaginase is not required for anticancer activity against ASNS-negative cells. <i>Blood</i> , 2014, 123, 3596-3606.                      | 0.6  | 150       |
| 113 | An Artifact in LC-MS/MS Measurement of Glutamine and Glutamic Acid: In-Source Cyclization to Pyroglutamic Acid. <i>Analytical Chemistry</i> , 2014, 86, 5633-5637.        | 3.2  | 68        |
| 114 | Comprehensive molecular characterization of gastric adenocarcinoma. <i>Nature</i> , 2014, 513, 202-209.   | 13.7 | 5,055     |
| 115 | The Somatic Genomic Landscape of Chromophobe Renal Cell Carcinoma. <i>Cancer Cell</i> , 2014, 26, 319-330.  | 7.7  | 665       |
| 116 | Comprehensive molecular profiling of lung adenocarcinoma. <i>Nature</i> , 2014, 511, 543-550.   | 13.7 | 4,572     |
| 117 | Multiplatform Analysis of 12 Cancer Types Reveals Molecular Classification within and across Tissues of Origin. <i>Cell</i> , 2014, 158, 929-944.                         | 13.5 | 1,242     |
| 118 | Assessing the clinical utility of cancer genomic and proteomic data across tumor types. <i>Nature Biotechnology</i> , 2014, 32, 644-652.                                  | 9.4  | 257       |
| 119 | Squamous Cell Carcinoma of the Oral Tongue in Young Non-Smokers Is Genomically Similar to Tumors in Older Smokers. <i>Clinical Cancer Research</i> , 2014, 20, 3842-3848. | 3.2  | 124       |
| 120 | A pan-cancer proteomic perspective on The Cancer Genome Atlas. <i>Nature Communications</i> , 2014, 5, 3887.  | 5.8  | 456       |
| 121 | High Resolution Copy Number Variation Data in the NCI-60 Cancer Cell Lines from Whole Genome Microarrays Accessible through CellMiner. <i>PLoS ONE</i> , 2014, 9, e92047. | 1.1  | 36        |
| 122 | Tissue-specific isoform switch and DNA hypomethylation of the pyruvate kinase PKM gene in human cancers. <i>Oncotarget</i> , 2014, 5, 8202-8210.                          | 0.8  | 127       |
| 123 | Comprehensive analysis of long non-coding RNAs in human breast cancer clinical subtypes. <i>Oncotarget</i> , 2014, 5, 9864-9876.  | 0.8  | 188       |
| 124 | Genome-Wide Mapping and Subtype Classification of Long Non-Coding RNA in Acute Myeloid Leukemia. <i>Blood</i> , 2014, 124, 2355-2355.                                     | 0.6  | 0         |
| 125 | Measurement of DNA Concentration as a Normalization Strategy for Metabolomic Data from Adherent Cell Lines. <i>Analytical Chemistry</i> , 2013, 85, 9536-9542.            | 3.2  | 90        |
| 126 | The Somatic Genomic Landscape of Glioblastoma. <i>Cell</i> , 2013, 155, 462-477.  | 13.5 | 3,979     |



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|-----|---|------|-----------|
| 127 | Discrepancies in drug sensitivity. <i>Nature</i> , 2013, 504, 381-383.  | 13.7 | 39        |
| 128 | The Cancer Genome Atlas Pan-Cancer analysis project. <i>Nature Genetics</i> , 2013, 45, 1113-1120.  | 9.4  | 6,265     |
| 129 | VirusSeq: software to identify viruses and their integration sites using next-generation sequencing of human cancer tissue. <i>Bioinformatics</i> , 2013, 29, 266-267.  | 1.8  | 209       |
| 130 | An Epithelial-Mesenchymal Transition Gene Signature Predicts Resistance to EGFR and PI3K Inhibitors and Identifies Axl as a Therapeutic Target for Overcoming EGFR Inhibitor Resistance. <i>Clinical Cancer Research</i> , 2013, 19, 279-290. | 3.2  | 848       |
| 131 | Integrated genomic characterization of endometrial carcinoma. <i>Nature</i> , 2013, 497, 67-73.   | 13.7 | 4,075     |
| 132 | Genomic and Epigenomic Landscapes of Adult De Novo Acute Myeloid Leukemia. <i>New England Journal of Medicine</i> , 2013, 368, 2059-2074.   | 13.9 | 4,139     |
| 133 | TCPA: a resource for cancer functional proteomics data. <i>Nature Methods</i> , 2013, 10, 1046-1047.  | 9.0  | 446       |
| 134 | Tumor-Specific Isoform Switch of the Fibroblast Growth Factor Receptor 2 Underlies the Mesenchymal and Malignant Phenotypes of Clear Cell Renal Cell Carcinomas. <i>Clinical Cancer Research</i> , 2013, 19, 2460-2472.                       | 3.2  | 72        |
| 135 | Landscape of DNA Virus Associations across Human Malignant Cancers: Analysis of 3,775 Cases Using RNA-Seq. <i>Journal of Virology</i> , 2013, 87, 8916-8926.  | 1.5  | 187       |
| 136 | A survey of intragenic breakpoints in glioblastoma identifies a distinct subset associated with poor survival. <i>Genes and Development</i> , 2013, 27, 1462-1472.  | 2.7  | 74        |
| 137 | Integrative Genomic Characterization of Oral Squamous Cell Carcinoma Identifies Frequent Somatic Drivers. <i>Cancer Discovery</i> , 2013, 3, 770-781.   | 7.7  | 484       |
| 138 | Prognostically relevant gene signatures of high-grade serous ovarian carcinoma. <i>Journal of Clinical Investigation</i> , 2013, 123, 517-25.   | 3.9  | 462       |
| 139 | The Glutaminase Activity Of L-Asparaginase Is Not Required For Anticancer Activity Against Asns-Negative Cell Lines. <i>Blood</i> , 2013, 122, 4912-4912.   | 0.6  | 1         |
| 140 | Proteomic Profiling Identifies Dysregulated Pathways in Small Cell Lung Cancer and Novel Therapeutic Targets Including PARP1. <i>Cancer Discovery</i> , 2012, 2, 798-811.   | 7.7  | 432       |
| 141 | BreakFusion: targeted assembly-based identification of gene fusions in whole transcriptome paired-end sequencing data. <i>Bioinformatics</i> , 2012, 28, 1923-1924.   | 1.8  | 54        |
| 142 | SpliceSeq: a resource for analysis and visualization of RNA-Seq data on alternative splicing and its functional impacts. <i>Bioinformatics</i> , 2012, 28, 2385-2387.   | 1.8  | 231       |
| 143 | Identification of Common Prognostic Gene Expression Signatures with Biological Meanings from Microarray Gene Expression Datasets. <i>PLoS ONE</i> , 2012, 7, e45894.  | 1.1  | 18        |
| 144 | Cell lines battle cancer. <i>Nature</i> , 2012, 483, 544-545.   | 13.7 | 95        |

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|-----|---|------|-----------|
| 145 | AMPK± Modulation in Cancer Progression: Multilayer Integrative Analysis of the Whole Transcriptome in Asian Gastric Cancer. <i>Cancer Research</i> , 2012, 72, 2512-2521.                             | 0.4  | 91        |
| 146 | PurityEst: estimating purity of human tumor samples using next-generation sequencing data. <i>Bioinformatics</i> , 2012, 28, 2265-2266.   | 1.8  | 68        |
| 147 | Functional Categories Associated with Clusters of Genes That Are Co-Expressed across the NCI-60 Cancer Cell Lines. <i>PLoS ONE</i> , 2012, 7, e30317.   | 1.1  | 11        |
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