Doron Lipson

List of Publications by Year
in descending order

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153 papers	18,058 citations	28242 55 h-index	17580 121 g-index
155 all docs	155 docs citations	155 times ranked	29613 citing authors

#	Article	IF	Citations
1	GOrilla: a tool for discovery and visualization of enriched GO terms in ranked gene lists. BMC Bioinformatics, 2009, 10, 48.	1.2	3,032
2	Development and validation of a clinical cancer genomic profiling test based on massively parallel DNA sequencing. Nature Biotechnology, 2013, 31, 1023-1031.	9.4	1,785
3	Blood-based tumor mutational burden as a predictor of clinical benefit in non-small-cell lung cancer patients treated with atezolizumab. Nature Medicine, 2018, 24, 1441-1448.	15.2	936
4	Identification of new ALK and RET gene fusions from colorectal and lung cancer biopsies. Nature Medicine, 2012, 18, 382-384.	15.2	782
5	Discovering Motifs in Ranked Lists of DNA Sequences. PLoS Computational Biology, 2007, 3, e39.	1.5	633
6	Activation of MET via Diverse Exon 14 Splicing Alterations Occurs in Multiple Tumor Types and Confers Clinical Sensitivity to MET Inhibitors. Cancer Discovery, 2015, 5, 850-859.	7.7	632
7	Two-State Allosteric Behavior in a Single-Domain Signaling Protein. Science, 2001, 291, 2429-2433.	6.0	574
8	Emergence of Constitutively Active Estrogen Receptor-Î± Mutations in Pretreated Advanced Estrogen Receptorâ€“Positive Breast Cancer. Clinical Cancer Research, 2014, 20, 1757-1767.	3.2	529
9	Oncogenic and drug-sensitive NTRK1 rearrangements in lung cancer. Nature Medicine, 2013, 19, 1469-1472.	15.2	526
10	Kinase fusions are frequent in Spitz tumours and spitzoid melanomas. Nature Communications, 2014, 5, 3116.	5.8	521
11	Aberrant Overexpression of Satellite Repeats in Pancreatic and Other Epithelial Cancers. Science, 2011, 331, 593-596.	6.0	452
12	Response to Cabozantinib in Patients with RET Fusion-Positive Lung Adenocarcinomas. Cancer Discovery, 2013, 3, 630-635.	7.7	438
13	Targeted Next-generation Sequencing of Advanced Prostate Cancer Identifies Potential Therapeutic Targets and Disease Heterogeneity. European Urology, 2013, 63, 920-926.	0.9	379
14	New Routes to Targeted Therapy of Intrahepatic Cholangiocarcinomas Revealed by Next-Generation Sequencing. Oncologist, 2014, 19, 235-242.	1.9	371
15	Comparative genomic hybridization using oligonucleotide microarrays and total genomic DNA. Proceedings of the National Academy of Sciences of the United States of America, 2004, 101, 17765-17770.	3.3	336
16	Inflammatory Myofibroblastic Tumors Harbor Multiple Potentially Actionable Kinase Fusions. Cancer Discovery, 2014, 4, 889-895.	7.7	334
17	The distribution of <scp>BRAF</scp> gene fusions in solid tumors and response to targeted therapy. International Journal of Cancer, 2016, 138, 881-890.	2.3	248
18	Integrated genomic DNA/RNA profiling of hematologic malignancies in the clinical setting. Blood, 2016, 127, 3004-3014.	0.6	244

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19	Genomic and functional analysis of leukemic transformation of myeloproliferative neoplasms. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, E5401-10.	3.3	238
20	Broad, Hybrid Captureâ€"Based Next-Generation Sequencing Identifies Actionable Genomic Alterations in Lung Adenocarcinomas Otherwise Negative for Such Alterations by Other Genomic Testing Approaches. Clinical Cancer Research, 2015, 21, 3631-3639.	3.2	236
21	A computational approach to distinguish somatic vs. germline origin of genomic alterations from deep sequencing of cancer specimens without a matched normal. PLoS Computational Biology, 2018, 14, e1005965.	1.5	191
22	Targeted next-generation sequencing of head and neck squamous cell carcinoma identifies novel genetic alterations in HPV+ and HPV- tumors. Genome Medicine, 2013, 5, 49.	3.6	188
23	Quantification of the yeast transcriptome by single-molecule sequencing. Nature Biotechnology, 2009, 27, 652-658.	9.4	172
24	BRAF Fusions Define a Distinct Molecular Subset of Melanomas with Potential Sensitivity to MEK Inhibition. Clinical Cancer Research, 2013, 19, 6696-6702.	3.2	160
25	Comprehensive Genomic Profiling of Pancreatic Acinar Cell Carcinomas Identifies Recurrent RAF Fusions and Frequent Inactivation of DNA Repair Genes. Cancer Discovery, 2014, 4, 1398-1405.	7.7	151
26	Fluorescence In Situ Hybridization, Immunohistochemistry, and Next-Generation Sequencing for Detection of EML4-ALK Rearrangement in Lung Cancer. Oncologist, 2015, 20, 316-322.	1.9	151
27	Analytical Validation of a Hybrid Captureâ€"Based Next-Generation Sequencing Clinical Assay for Genomic Profiling of Cell-Free Circulating Tumor DNA. Journal of Molecular Diagnostics, 2018, 20, 686-702.	1.2	149
28	Global organization of replication time zones of the mouse genome. Genome Research, 2008, 18, 1562-1570.	2.4	148
29	Efficient Calculation of Interval Scores for DNA Copy Number Data Analysis. Journal of Computational Biology, 2006, 13, 215-228.	0.8	132
30	Next-Generation Sequencing Identifies and Immunohistochemistry Confirms a Novel Crizotinib-Sensitive ALK Rearrangement in a Patient with Metastatic Nonâ€"Small-Cell Lung Cancer. Journal of Thoracic Oncology, 2012, 7, e14-e16.	0.5	124
31	Relapsed Classic E-Cadherin (CDH1)â€"Mutated Invasive Lobular Breast Cancer Shows a High Frequency of HER2 (ERBB2) Gene Mutations. Clinical Cancer Research, 2013, 19, 2668-2676.	3.2	122
32	Advanced urothelial carcinoma: next-generation sequencing reveals diverse genomic alterations and targets of therapy. Modern Pathology, 2014, 27, 271-280.	2.9	122
33	A High Frequency of Activating Extracellular Domain ERBB2 (HER2) Mutation in Micropapillary Urothelial Carcinoma. Clinical Cancer Research, 2014, 20, 68-75.	3.2	120
34	Comprehensive Genomic Profiling Identifies a Subset of Crizotinib-Responsive ALK-Rearranged Non-Small Cell Lung Cancer Not Detected by Fluorescence In Situ Hybridization. Oncologist, 2016, 21, 762-770.	1.9	119
35	Virtual terminator nucleotides for next-generation DNA sequencing. Nature Methods, 2009, 6, 593-595.	9.0	113
36	Clinical nextâ€generation sequencing successfully applied to fineâ€needle aspirations of pulmonary and pancreatic neoplasms. Cancer Cytopathology, 2013, 121, 688-694.	1.4	110

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37	Gene expression and amplification in breast carcinoma cells with intrinsic and acquired doxorubicin resistance. Oncogene, 2001, 20, 1300-1306.	2.6	104
38	Profiling of 149 Salivary Duct Carcinomas, Carcinoma Ex Pleomorphic Adenomas, and Adenocarcinomas, Not Otherwise Specified Reveals Actionable Genomic Alterations. Clinical Cancer Research, 2016, 22, 6061-6068.	3.2	99
39	New class of gene-termini-associated human RNAs suggests a novel RNA copying mechanism. Nature, 2010, 466, 642-646.	13.7	98
40	Protocol Dependence of Sequencing-Based Gene Expression Measurements. PLoS ONE, 2011, 6, e19287.	1.1	97
41	EGFR Kinase Domain Duplication (EGFR-KDD) Is a Novel Oncogenic Driver in Lung Cancer That Is Clinically Responsive to Afatinib. Cancer Discovery, 2015, 5, 1155-1163.	7.7	94
42	High-Throughput Genomic Profiling of Adult Solid Tumors Reveals Novel Insights into Cancer Pathogenesis. Cancer Research, 2017, 77, 2464-2475.	0.4	93
43	Characterization of Clinical Cases of Collecting Duct Carcinoma of the Kidney Assessed by Comprehensive Genomic Profiling. European Urology, 2016, 70, 516-521.	0.9	90
44	Characterization of Clinical Cases of Advanced Papillary Renal Cell Carcinoma via Comprehensive Genomic Profiling. European Urology, 2018, 73, 71-78.	0.9	87
45	Identification of Recurrent FGFR3â€“TACC3 Fusion Oncogenes from Lung Adenocarcinoma. Clinical Cancer Research, 2014, 20, 6551-6558.	3.2	85
46	Comprehensive Genomic Profiling of Advanced Esophageal Squamous Cell Carcinomas and Esophageal Adenocarcinomas Reveals Similarities and Differences. Oncologist, 2015, 20, 1132-1139.	1.9	84
47	RICTOR Amplification Defines a Novel Subset of Patients with Lung Cancer Who May Benefit from Treatment with mTORC1/2 Inhibitors. Cancer Discovery, 2015, 5, 1262-1270.	7.7	84
48	Comprehensive genomic profiling of 295 cases of clinically advanced urothelial carcinoma of the urinary bladder reveals a high frequency of clinically relevant genomic alterations. Cancer, 2016, 122, 702-711.	2.0	81
49	Genomic Profiling of a Large Set of Diverse Pediatric Cancers Identifies Known and Novel Mutations across Tumor Spectra. Cancer Research, 2017, 77, 509-519.	0.4	75
50	Nonamplification ERBB2 genomic alterations in 5605 cases of recurrent and metastatic breast cancer: An emerging opportunity for antiâ€HER2 targeted therapies. Cancer, 2016, 122, 2654-2662.	2.0	71
51	Oncogenic Alterations in ERBB2/HER2 Represent Potential Therapeutic Targets Across Tumors From Diverse Anatomic Sites of Origin. Oncologist, 2015, 20, 7-12.	1.9	69
52	Comprehensive Genomic Profiling of Advanced Penile Carcinoma Suggests a High Frequency of Clinically Relevant Genomic Alterations. Oncologist, 2016, 21, 33-39.	1.9	69
53	Evaluation of 122 advancedâ€stage cutaneous squamous cell carcinomas by comprehensive genomic profiling opens the door for new routes to targeted therapies. Cancer, 2016, 122, 249-257.	2.0	67
54	Prospective Comprehensive Genomic Profiling of Advanced Gastric Carcinoma Cases Reveals Frequent Clinically Relevant Genomic Alterations and New Routes for Targeted Therapies. Oncologist, 2015, 20, 499-507.	1.9	64

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55	Genomic Profiling of Advanced-Stage, Metaplastic Breast Carcinoma by Next-Generation Sequencing Reveals Frequent, Targetable Genomic Abnormalities and Potential New Treatment Options. Archives of Pathology and Laboratory Medicine, 2015, 139, 642-649.	1.2	63
56	Comprehensive Genomic Profiling of Relapsed and Metastatic Adenoid Cystic Carcinomas by Next-generation Sequencing Reveals Potential New Routes to Targeted Therapies. American Journal of Surgical Pathology, 2014, 38, 235-238.	2.1	57
57	Comprehensive genomic profiling of extrahepatic cholangiocarcinoma reveals a long tail of therapeutic targets. Journal of Clinical Pathology, 2016, 69, 403-408.	1.0	56
58	Identifying In-Trans Process Associated Genes in Breast Cancer by Integrated Analysis of Copy Number and Expression Data. PLoS ONE, 2013, 8, e53014.	1.1	54
59	A Novel Translocation Breakpoint within the BPTF Gene Is Associated with a Pre-Malignant Phenotype. PLoS ONE, 2010, 5, e9657.	1.1	53
60	Individualized Molecular Analyses Guide Efforts (IMAGE): A Prospective Study of Molecular Profiling of Tissue and Blood in Metastatic Triple-Negative Breast Cancer. Clinical Cancer Research, 2017, 23, 379-386.	3.2	50
61	A Comparison of Single Molecule and Amplification Based Sequencing of Cancer Transcriptomes. PLoS ONE, 2011, 6, e17305.	1.1	48
62	Response of an ERBB2-Mutated Inflammatory Breast Carcinoma to Human Epidermal Growth Factor Receptor 2â€“Targeted Therapy. Journal of Clinical Oncology, 2014, 32, e88-e91.	0.8	44
63	Comprehensive Genomic Profiling of Clinically Advanced Medullary Thyroid Carcinoma. Oncology, 2016, 90, 339-346.	0.9	43
64	Tumor-specific HSP90 inhibition as a therapeutic approach in JAK-mutant acute lymphoblastic leukemias. Blood, 2015, 126, 2479-2483.	0.6	36
65	Comprehensive Genomic Profiling Identifies Frequent Drug-Sensitive EGFR Exon 19 Deletions in NSCLC not Identified by Prior Molecular Testing. Clinical Cancer Research, 2016, 22, 3281-3285.	3.2	33
66	Durable Response to Crizotinib in a MET-Amplified, KRAS-Mutated Carcinoma of Unknown Primary. Case Reports in Oncology, 2014, 7, 503-508.	0.3	32
67	Single-Molecule Sequencing. Methods in Enzymology, 2010, 472, 407-430.	0.4	31
68	Single-step capture and sequencing of natural DNA for detection of BRCA1 mutations. Genome Research, 2012, 22, 340-345.	2.4	30
69	Distinct age-associated molecular profiles in acute myeloid leukemia defined by comprehensive clinical genomic profiling. Oncotarget, 2018, 9, 26417-26430.	0.8	25
70	RET Fusion Lung Carcinoma: Response to Therapy and Clinical Features in a Case Series of 14 Patients. Clinical Lung Cancer, 2017, 18, e223-e232.	1.1	24
71	Error Tolerant Indexing and Alignment of Short Reads with Covering Template Families. Journal of Computational Biology, 2010, 17, 1397-1411.	0.8	23
72	Antitumor Response of an ERBB2 Amplified Inflammatory Breast Carcinoma With EGFR Mutation to the EGFR-TKI Erlotinib. Clinical Breast Cancer, 2014, 14, e14-e16.	1.1	22

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73	Joint Analysis of DNA Copy Numbers and Gene Expression Levels. Lecture Notes in Computer Science, 2004, , 135-146.	1.0	20
74	MSI-H testing via hybrid capture based NGS sequencing of liquid biopsy samples.. Journal of Clinical Oncology, 2019, 37, 504-504.	0.8	19
75	Comprehensive genomic profiling of biliary tract cancers to reveal tumor-specific differences and frequency of clinically relevant genomic alterations.. Journal of Clinical Oncology, 2015, 33, 4009-4009.	0.8	18
76	MDM2 amplification (Amp) to mediate cabozantinib resistance in patients (Pts) with advanced RET-rearranged lung cancers.. Journal of Clinical Oncology, 2016, 34, 9068-9068.	0.8	15
77	Comprehensive genomic profiling of biliary tract cancers to reveal tumor-specific differences and genomic alterations.. Journal of Clinical Oncology, 2015, 33, 231-231.	0.8	14
78	Optimization of probe coverage for high-resolution oligonucleotide aCGH. Bioinformatics, 2007, 23, e77-e83.	1.8	13
79	Extended Antitumor Responseof a BRAF V600E Papillary Thyroid Carcinoma to Vemurafenib. Case Reports in Oncology, 2014, 7, 343-348.	0.3	13
80	R269C variant of ESR1: high prevalence and differential function in a subset of pancreatic cancers. BMC Cancer, 2020, 20, 531.	1.1	12
81	Circulating Tumor DNA and Biomarker Analyses From the LOTUS Randomized Trial of First-Line Ipatasertib and Paclitaxel for Metastatic Triple-Negative Breast Cancer. JCO Precision Oncology, 2020, 4, 1012-1024.	1.5	11
82	NTRK1 gene fusions as a novel oncogene target in lung cancer.. Journal of Clinical Oncology, 2013, 31, 8023-8023.	0.8	11
83	Identifying ALK rearrangements that are not detected by FISH with targeted next-generation sequencing of lung carcinoma.. Journal of Clinical Oncology, 2014, 32, 8049-8049.	0.8	11
84	RNA Sequencing and Quantitation Using the Helicos Genetic Analysis System. Methods in Molecular Biology, 2011, 733, 37-49.	0.4	9
85	A metastatic colon adenocarcinoma harboring BRAF V600E has a durable major response to dabrafenib/trametinib and chemotherapy. OncoTargets and Therapy, 2015, 8, 3561.	1.0	9
86	Framework for Identifying Common Aberrations in DNA Copy Number Data. , 2007, , 122-136.		8
87	Hybrid Capture-Based Comprehensive Genomic Profiling Identifies Lung Cancer Patients with Well-Characterized Sensitizing Epidermal Growth Factor Receptor Point Mutations That Were Not Detected by Standard of Care Testing. Oncologist, 2018, 23, 776-781.	1.9	8
88	Use of the FoundationOne next-generation sequencing (NGS) assay to detect actionable alterations leading to clinical benefit of targeted therapies for relapsed and refractory breast cancer.. Journal of Clinical Oncology, 2013, 31, 1009-1009.	0.8	8
89	Use of next-generation sequencing (NGS) to detect a novel ALK fusion and a high frequency of other actionable alterations in colorectal cancer (CRC).. Journal of Clinical Oncology, 2012, 30, 3533-3533.	0.8	7
90	Durable clinical benefit to trastuzumab and chemotherapy in a patient with metastatic colon adenocarcinoma harboring ERBB2 amplification. Oncoscience, 2015, 2, 581-584.	0.9	6

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91	Frequency of MET amplification determined by comprehensive next-generation sequencing (NGS) in multiple solid tumors and implications for use of MET inhibitors.. Journal of Clinical Oncology, 2013, 31, 11068-11068.	0.8	6
92	Comprehensive genomic profiling of clinically advanced colorectal carcinoma to reveal frequent opportunities for targeted therapies.. Journal of Clinical Oncology, 2015, 33, 3553-3553.	0.8	5
93	Patient Derived Xenograft (PDX) Models Recapitulate the Genomic-Driver Composition of Acute Leukemia Samples. Blood, 2014, 124, 286-286.	0.6	4
94	Discovery of recurrent KIF5B-RET fusions and other targetable alterations from clinical NSCLC specimens.. Journal of Clinical Oncology, 2012, 30, 7510-7510.	0.8	4
95	Use of next-generation sequencing (NGS) to identify actionable genomic alterations (GA) in diverse solid tumor types: The Foundation Medicine (FMI) experience with 2,200+ clinical samples.. Journal of Clinical Oncology, 2013, 31, 11020-11020.	0.8	4
96	Clinical next generation sequencing (NGS) to reveal high frequency of alterations to guide targeted therapy in lung cancer patients.. Journal of Clinical Oncology, 2013, 31, 8020-8020.	0.8	4
97	Genomic alterations (GA) predicted to confer lack of benefit from trastuzumab in advanced esophagogastric cancers (EGC): Analysis of 527 HER2-amplified (HER2amp) cases.. Journal of Clinical Oncology, 2018, 36, 44-44.	0.8	4
98	Comprehensive genomic profiling of ctDNA in patients with colon cancer and its fidelity to the genomics of the tumor biopsy.. Journal of Clinical Oncology, 2018, 36, 569-569.	0.8	4
99	Profiling Genomic Alterations Of Diffuse Large B-Cell Lymphoma (DLBCL) At Diagnosis, Relapse, and Transformation, Using a Novel Clinical Diagnostic Targeted Sequencing Platform. Blood, 2013, 122, 1761-1761.	0.6	3
100	Next-generation sequencing of FFPE solid tumor specimens for clinical use.. Journal of Clinical Oncology, 2012, 30, 10524-10524.	0.8	3
101	Next-generation sequencing (NGS) to identify actionable genomic changes in common and rare solid tumors: The FMI experience with the initial 50 consecutive patients.. Journal of Clinical Oncology, 2012, 30, 10590-10590.	0.8	3
102	Potentially actionable kinase fusions in inflammatory myofibroblastic tumors.. Journal of Clinical Oncology, 2013, 31, 10513-10513.	0.8	3
103	Unique genomic features in adolescent and young adult, as compared to older adult, nonâ€Hodgkin lymphoma and potential therapeutic targets. British Journal of Haematology, 2017, 178, 640-642.	1.2	2
104	Patient Derived Xenograft (PDX) Models Faithfully Recapitulate The Genetic Composition Of Primary AML. Blood, 2013, 122, 1328-1328.	0.6	2
105	Identification Of Actionable Genomic Alterations In Hematologic Malignancies By a Clinical Next Generation Sequencing-Based Assay. Blood, 2013, 122, 230-230.	0.6	2
106	Extensive High-Depth Sequencing Of Longitudinal CLL Samples Identifies Frequent Mutations In MAP Kinase Signaling and Novel Mutations Activating Notch and Beta-Catenin. Blood, 2013, 122, 2858-2858.	0.6	2
107	Novel Chromatin Modifying Gene Alterations and Significant Survival Association of ATM and P53 in Mantle Cell Lymphoma. Blood, 2014, 124, 3033-3033.	0.6	2
108	Clinical Relevant Alterations Identified By Comprehensive Genomic Profiling Can Potentially Improve Therapeutic Option and Change Prognosis in Hematologic Malignancies. Blood, 2016, 128, 5109-5109.	0.6	2

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109	Next-generation sequencing of genomic and cDNA to identify a high frequency of kinase fusions involving ROS1, ALK, RET, NTRK1, and BRAF in Spitz tumors.. Journal of Clinical Oncology, 2013, 31, 9002-9002.	0.8	2
110	Clinical application of comprehensive next-generation sequencing-based genomic profiling for identification of actionable genomic alterations in pediatric solid tumors and hematolymphoid malignancies: The Foundation Medicine pediatric experience.. Journal of Clinical Oncology, 2014, 32, 10035-10035.	0.8	2
111	Comprehensive genomic profiling of solid tumors from 677 adolescents and young adults for revealing a distinct spectrum of targetable genomic alterations.. Journal of Clinical Oncology, 2014, 32, 11008-11008.	0.8	2
112	Analytic validation of a clinical circulating tumor DNA assay for patients with solid tumors.. Journal of Clinical Oncology, 2016, 34, e23049-e23049.	0.8	2
113	Integrated Genetic Profiling Of JAK2 Wildtype Chronic-Phase Myeloproliferative Neoplasms. Blood, 2013, 122, 1588-1588.	0.6	1
114	Pilot Study To Evaluate The Prevalence Of Actionable Oncogenic Mutations In Patients With Relapsed Refractory Multiple Myeloma. Blood, 2013, 122, 755-755.	0.6	1
115	Comprehensive Genomic Profiling (CGP) of Angioimmunoblastic T-Cell Lymphoma (AITL) to Prospectively Inform Diagnosis and Clinical Management. Blood, 2015, 126, 3898-3898.	0.6	1
116	An analysis of ERBB2 alterations (amplifications and mutations) found by next-generation sequencing (NGS) in 2000+ consecutive solid tumor (ST) patients.. Journal of Clinical Oncology, 2013, 31, 11000-11000.	0.8	1
117	Targeted next-generation sequencing (NGS) of carcinoma of unknown primary site (CUP): Actionable genomic alterations (GA) and new routes to targeted therapies.. Journal of Clinical Oncology, 2014, 32, 11048-11048.	0.8	1
118	Comprehensive genomic profiling (CGP) of cervical squamous cell carcinoma (cSCC) to identifiy targeted therapy options.. Journal of Clinical Oncology, 2015, 33, 5602-5602.	0.8	1
119	Comprehensive genomic profiling of 443 cases of renal cell carcinoma to reveal frequent clinically relevant genomic alterations.. Journal of Clinical Oncology, 2015, 33, 433-433.	0.8	1
120	Clinical next generation sequencing (NGS) of fine needle aspiration (FNA) biopsies in non-small cell lung (NSCLC) and pancreatic cancers.. Journal of Clinical Oncology, 2013, 31, 11100-11100.	0.8	1
121	Distinct age-associated genomic profiles in acute myeloid leukemia (AML) using FoundationOne heme.. Journal of Clinical Oncology, 2016, 34, 7041-7041.	0.8	1
122	A microarray analysis of differential gene expression associated with the development of doxorubicin resistance in breast carcinoma. , 2003, , 82-87.		0
123	Identifying cancer mutations in neuroendocrine prostate cancer (NEPC) through massively parallel DNA sequencing of formalin-fixed paraffin-embedded (FFPE) tissue.. Journal of Clinical Oncology, 2012, 30, 110-110.	0.8	0
124	Use of next-generation sequencing (NGS) to detect high frequency of targetable alterations in primary and metastatic breast cancer (MBC).. Journal of Clinical Oncology, 2012, 30, 10559-10559.	0.8	0
125	Targeted next-generation sequencing (NGS) of advanced prostate cancer (PCA) using formalin-fixed tissue.. Journal of Clinical Oncology, 2012, 30, 4649-4649.	0.8	0
126	Overview Of The Genomic Landscape Of High Risk Diffuse Large B-Cell Lymphoma Using Targeted DNA and RNA Sequencing. Blood, 2013, 122, 501-501.	0.6	0

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127	Mutational Profiling Of Myeloid Malignancies For Prediction Of Disease Relapse Following Allogeneic Stem Cell Transplantation. Blood, 2013, 122, 2096-2096.	0.6	0
128	Comprehensive Mutational Profiling In Myelodysplastic Syndromes Treated With Decitabine and Tretinoin. Blood, 2013, 122, 2791-2791.	0.6	0
129	High-Throughput Mutational Profiling Of Post-Myeloproliferative Neoplasm Acute Myeloid Leukemia Reveals Frequent Mutations In NRAS In JAK2V617F-Negative Post-MPN AML. Blood, 2013, 122, 4098-4098.	0.6	0
130	Rictor amplification to define a novel and unique subset of lung cancer patients.. Journal of Clinical Oncology, 2014, 32, 8027-8027.	0.8	0
131	Next-generation sequencing (NGS) to identify actionable genomic alterations (GA) in â€œpan-negativeâ€• lung adenocarcinomas (ADC) from patients with no smoking or a light smoking (NS/LS) history.. Journal of Clinical Oncology, 2014, 32, 8029-8029.	0.8	0
132	Next-generation sequencing (NGS)-based profiling of pancreatic acinar cell carcinoma for identification of a recurrent SND1-BRAF fusion.. Journal of Clinical Oncology, 2014, 32, 11029-11029.	0.8	0
133	Genomic Analysis of Serial Samples from CLL Patients Identifies Clonal Events Associated with Disease Progression. Blood, 2014, 124, 1954-1954.	0.6	0
134	Clinical Utility of Comprehensive Profiling of Genomic Alterations in Hematologic Malignancies. Blood, 2014, 124, 1072-1072.	0.6	0
135	Genomic Alterations of Histone Modification Genes Are Significantly Less Common in Non-Hodgkin Lymphomas of Adolescents and Young Adults Compared to Older Patients. Blood, 2014, 124, 1684-1684.	0.6	0
136	Utility of Combined DNA and RNA Next Generation Sequencing in Leukemias for Identification of Prognostic and Therapeutically Relevant Genomic Alterations in Clinical Practice. Blood, 2014, 124, 1039-1039.	0.6	0
137	Genomic Profiling Combining DNA and RNA Analysis of 112 Formalin-Fixed Paraffin-Embedded Diffuse Large B Cell Lymphoma Specimens Identifies a High Frequency of Clinically Relevant Genomic Alterations. Blood, 2014, 124, 704-704.	0.6	0
138	Comprehensive genomic profiling (CGP) of advanced stage esophageal squamous cell carcinomas (ESCC) and esophageal adenocarcinomas (EAC) to reveal similarities and differences.. Journal of Clinical Oncology, 2015, 33, 7-7.	0.8	0
139	Comprehensive genomic profiling of anal squamous cell carcinoma to reveal frequency of clinically relevant genomic alterations in the PI3K/mTOR pathway.. Journal of Clinical Oncology, 2015, 33, 3522-3522.	0.8	0
140	Amplification of CRKL in human cancer: A rare event associated with potential sensitivity to targeted therapy.. Journal of Clinical Oncology, 2015, 33, 1526-1526.	0.8	0
141	Comprehensive genomic profiling of 443 patients with advanced renal cell carcinoma (RCC) to reveal clinically relevant genomic alterations and to aid in classification of rare subtypes.. Journal of Clinical Oncology, 2015, 33, 4520-4520.	0.8	0
142	Intratumoral heterogeneity of cancer driver genomic alterations across several tumor types.. Journal of Clinical Oncology, 2015, 33, 1558-1558.	0.8	0
143	Comprehensive genomic profiling of advanced stage esophageal squamous cell carcinomas (ESCC) and esophageal adenocarcinomas (EAC).. Journal of Clinical Oncology, 2015, 33, 1535-1535.	0.8	0
144	Comprehensive genomic profiling identifies clinically relevant genomic alterations in relapsed and metastatic penile squamous cell carcinoma.. Journal of Clinical Oncology, 2015, 33, e15628-e15628.	0.8	0

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145	Comprehensive genomic profiling of 295 cases of clinically advanced urothelial carcinoma of the urinary bladder to reveal frequency of clinically relevant genomic alterations.. Journal of Clinical Oncology, 2015, 33, 4526-4526.	0.8	0
146	Comprehensive genomic profiling of salivary gland adenocarcinomas to reveal frequency of druggable targets.. Journal of Clinical Oncology, 2015, 33, 6040-6040.	0.8	0
147	Integrated DNA/RNA Profiling for Somatic Alterations in Adult B-Cell ALL. Blood, 2015, 126, 1422-1422.	0.6	0
148	Predictive and Prognostic Significance of Comprehensive Genomic Profiling in Patients with Diffuse Large B-Cell Lymphoma. Blood, 2015, 126, 2651-2651.	0.6	0
149	Comprehensive genomic profiling in colorectal cancer (CRC) to identify differing frequencies of clinically relevant genomic alterations (CRGA) in tumors of patients (pts) less than age 50 as compared to those of pts over age 65.. Journal of Clinical Oncology, 2016, 34, 570-570.	0.8	0
150	Comprehensive Clinical Genomic Profiling Defines Age-Associated Molecular Targets in Pediatric and Adult Acute Myeloid Leukemia. Blood, 2016, 128, 596-596.	0.6	0
151	Comprehensive genomic profiling (CGP) of esophageal and tubular GI tumors to identify frequencies of ErbB family member amplification with therapeutic implications.. Journal of Clinical Oncology, 2017, 35, 8-8.	0.8	0
152	Co-existing alterations in cell-cycle pathway genes and impact on benefit from trastuzumab in advanced esophagogastric cancers (EGC): Analysis of 527 Her2-amplified cases.. Journal of Clinical Oncology, 2018, 36, 4063-4063.	0.8	0
153	Landscape of kinase rearrangements (kRE) detected in circulating tumor DNA (ctDNA).. Journal of Clinical Oncology, 2018, 36, 12041-12041.	0.8	0