Roman Yelensky

List of Publications by Year
in descending order

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140 papers	14,975 citations	31976 53 h-index	26613 107 g-index
140 all docs	140 docs citations	140 times ranked	24915 citing authors

#	Article	IF	Citations
1	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.	3.2	191
2	Rucaparib in relapsed, platinum-sensitive high-grade ovarian carcinoma (ARIEL2 Part 1): an international, multicentre, open-label, phase 2 trial. Lancet Oncology, The, 2017, 18, 75-87.	10.7	975
3	Genomic profiling of ER ⁺ breast cancers after short-term estrogen suppression reveals alterations associated with endocrine resistance. Science Translational Medicine, 2017, 9, .	12.4	91
4	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.	2.5	2
5	Biological and clinical evidence for somatic mutations in BRCA1 and BRCA2 as predictive markers for olaparib response in high-grade serous ovarian cancers in the maintenance setting. Oncotarget, 2017, 8, 43653-43661.	1.8	85
6	Presence of both alterations in FGFR/FGF and PI3K/AKT/mTOR confer improved outcomes for patients with metastatic breast cancer treated with PI3K/AKT/mTOR inhibitors. Oncoscience, 2016, 3, 164-172.	2.2	34
7	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.	4.1	71
8	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.	4.1	81
9	Comprehensive Genomic Profiling of Clinically Advanced Medullary Thyroid Carcinoma. Oncology, 2016, 90, 339-346.	1.9	43
10	Cancer Therapy Directed by Comprehensive Genomic Profiling: A Single Center Study. Cancer Research, 2016, 76, 3690-3701.	0.9	203
11	Integrated genomic DNA/RNA profiling of hematologic malignancies in the clinical setting. Blood, 2016, 127, 3004-3014.	1.4	244
12	Clinical Actionability of Comprehensive Genomic Profiling for Management of Rare or Refractory Cancers. Oncologist, 2016, 21, 1315-1325.	3.7	64
13	The distribution of <scp>BRAF</scp> gene fusions in solid tumors and response to targeted therapy. International Journal of Cancer, 2016, 138, 881-890.	5.1	248
14	TP53 Alterations Correlate with Response to VEGF/VEGFR Inhibitors: Implications for Targeted Therapeutics. Molecular Cancer Therapeutics, 2016, 15, 2475-2485.	4.1	73
15	Triple-negative breast cancers with amplification of JAK2 at the 9p24 locus demonstrate JAK2-specific dependence. Science Translational Medicine, 2016, 8, 334ra53.	12.4	105
16	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.	4.1	67
17	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.	7.0	99
18	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.	3.7	119

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19	Comprehensive Genomic Profiling of Advanced Penile Carcinoma Suggests a High Frequency of Clinically Relevant Genomic Alterations. Oncologist, 2016, 21, 33-39.	3.7	69
20	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.	7.0	33
21	Characterization of Clinical Cases of Collecting Duct Carcinoma of the Kidney Assessed by Comprehensive Genomic Profiling. European Urology, 2016, 70, 516-521.	1.9	90
22	Evaluation of a Congenital Infantile Fibrosarcoma by Comprehensive Genomic Profiling Reveals an LMNA-NTRK1 Gene Fusion Responsive to Crizotinib. Journal of the National Cancer Institute, 2016, 108, .	6.3	68
23	Comprehensive genomic profiling of extrahepatic cholangiocarcinoma reveals a long tail of therapeutic targets. Journal of Clinical Pathology, 2016, 69, 403-408.	2.0	56
24	RAS/MAPK Activation Is Associated with Reduced Tumor-Infiltrating Lymphocytes in Triple-Negative Breast Cancer: Therapeutic Cooperation Between MEK and PD-1/PD-L1 Immune Checkpoint Inhibitors. Clinical Cancer Research, 2016, 22, 1499-1509.	7.0	428
25	Evaluation of microsatellite instability (MSI) status in gastrointestinal (GI) tumor samples tested with comprehensive genomic profiling (CGP).. Journal of Clinical Oncology, 2016, 34, 528-528.	1.6	6
26	Characterization of mutational load in patients with advanced urothelial cancer.. Journal of Clinical Oncology, 2016, 34, 460-460.	1.6	0
27	Comprehensive genomic profiling (CGP) to assess mutational load in gastric and esophageal adenocarcinomas: Implications for immunotherapies.. Journal of Clinical Oncology, 2016, 34, 66-66.	1.6	1
28	Genomic alterations in DNA repair and chromatin remodeling genes in estrogen receptor-positive metastatic breast cancer patients with exceptional responses to capecitabine. Cancer Medicine, 2015, 4, 1289-1293.	2.8	7
29	Durable clinical benefit to trastuzumab and chemotherapy in a patient with metastatic colon adenocarcinoma harboring ERBB2 amplification. Oncoscience, 2015, 2, 581-584.	2.2	6
30	A metastatic colon adenocarcinoma harboring BRAF V600E has a durable major response to dabrafenib/trametinib and chemotherapy. OncoTargets and Therapy, 2015, 8, 3561.	2.0	9
31	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.	9.4	632
32	Comprehensive Genomic Profiling of Carcinoma of Unknown Primary Site. JAMA Oncology, 2015, 1, 40.	7.1	199
33	Comprehensive Genomic Profiling of Advanced Esophageal Squamous Cell Carcinomas and Esophageal Adenocarcinomas Reveals Similarities and Differences. Oncologist, 2015, 20, 1132-1139.	3.7	84
34	RET Fusion as a Novel Driver of Medullary Thyroid Carcinoma. Journal of Clinical Endocrinology and Metabolism, 2015, 100, 788-793.	3.6	65
35	Lung Master Protocol (Lung-MAP)â€”A Biomarker-Driven Protocol for Accelerating Development of Therapies for Squamous Cell Lung Cancer: SWOG S1400. Clinical Cancer Research, 2015, 21, 1514-1524.	7.0	205
36	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.	2.5	63

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37	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.	3.7	64
38	Comparative analysis of primary tumour and matched metastases in colorectal cancer patients: Evaluation of concordance between genomic and transcriptional profiles. European Journal of Cancer, 2015, 51, 791-799.	2.8	83
39	Next generation sequencing of exceptional responders with BRAF-mutant melanoma: implications for sensitivity and resistance. BMC Cancer, 2015, 15, 61.	2.6	25
40	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.	9.4	84
41	Multiple gene aberrations and breast cancer: lessons from super-responders. BMC Cancer, 2015, 15, 442.	2.6	11
42	Loss of Heterozygosity at the CYP2D6 Locus in Breast Cancer: Implications for Germline Pharmacogenetic Studies. Journal of the National Cancer Institute, 2015, 107, .	6.3	37
43	Oncogenic Alterations in ERBB2/HER2 Represent Potential Therapeutic Targets Across Tumors From Diverse Anatomic Sites of Origin. Oncologist, 2015, 20, 7-12.	3.7	69
44	Comprehensive Genomic Profiling (CGP) of Angioimmunoblastic T-Cell Lymphoma (AITL) to Prospectively Inform Diagnosis and Clinical Management. Blood, 2015, 126, 3898-3898.	1.4	1
45	Comprehensive genomic profiling (CGP) of advanced cancers to identify MET exon 14 alterations that confer sensitivity to MET inhibitors.. Journal of Clinical Oncology, 2015, 33, 11007-11007.	1.6	5
46	Prospective study comparing outcomes in patients with advanced malignancies on molecular alteration-matched versus non-matched therapy.. Journal of Clinical Oncology, 2015, 33, 11019-11019.	1.6	8
47	Germline variants in cancer risk genes detected by NGS-based comprehensive tumor genomic profiling (CGP).. Journal of Clinical Oncology, 2015, 33, 11084-11084.	1.6	5
48	Comprehensive genomic profiling of clinically advanced colorectal carcinoma to reveal frequent opportunities for targeted therapies.. Journal of Clinical Oncology, 2015, 33, 3553-3553.	1.6	5
49	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.	1.6	18
50	Results of ARIEL2: A Phase 2 trial to prospectively identify ovarian cancer patients likely to respond to rucaparib using tumor genetic analysis.. Journal of Clinical Oncology, 2015, 33, 5508-5508.	1.6	60
51	Comprehensive genomic profiling of biliary tract cancers to reveal tumor-specific differences and genomic alterations.. Journal of Clinical Oncology, 2015, 33, 231-231.	1.6	14
52	Defects in DNA repair genes and sensitivity to cisplatin based neoadjuvant chemotherapy (NAC) for bladder cancer.. Journal of Clinical Oncology, 2015, 33, 320-320.	1.6	5
53	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.	1.6	1
54	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.	1.6	0

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55	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.	1.6	0
56	Tumor biopsies in high grade ovarian cancer: Clinical utility and challenges for biomarker-directed therapy.. Journal of Clinical Oncology, 2015, 33, 5539-5539.	1.6	0
57	Amplification of CRKL in human cancer: A rare event associated with potential sensitivity to targeted therapy.. Journal of Clinical Oncology, 2015, 33, 1526-1526.	1.6	0
58	Defects in DNA repair genes and sensitivity to cisplatin based neoadjuvant chemotherapy (NAC) for bladder cancer.. Journal of Clinical Oncology, 2015, 33, 4514-4514.	1.6	0
59	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.	1.6	0
60	Intratumoral heterogeneity of cancer driver genomic alterations across several tumor types.. Journal of Clinical Oncology, 2015, 33, 1558-1558.	1.6	0
61	Comprehensive genomic profiling of advanced stage esophageal squamous cell carcinomas (ESCC) and esophageal adenocarcinomas (EAC).. Journal of Clinical Oncology, 2015, 33, 1535-1535.	1.6	0
62	Comprehensive genomic profiling identifies clinically relevant genomic alterations in relapsed and metastatic penile squamous cell carcinoma.. Journal of Clinical Oncology, 2015, 33, e15628-e15628.	1.6	0
63	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.	1.6	0
64	Comprehensive genomic profiling of salivary gland adenocarcinomas to reveal frequency of druggable targets.. Journal of Clinical Oncology, 2015, 33, 6040-6040.	1.6	0
65	Kinase fusions are frequent in Spitz tumours and spitzoid melanomas. Nature Communications, 2014, 5, 3116.	12.8	521
66	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.	7.1	238
67	Triple-Negative Breast Cancer Patients Treated at MD Anderson Cancer Center in Phase I Trials: Improved Outcomes with Combination Chemotherapy and Targeted Agents. Molecular Cancer Therapeutics, 2014, 13, 3175-3184.	4.1	31
68	Molecular Profiling of the Residual Disease of Triple-Negative Breast Cancers after Neoadjuvant Chemotherapy Identifies Actionable Therapeutic Targets. Cancer Discovery, 2014, 4, 232-245.	9.4	413
69	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.	3.7	57
70	A High Frequency of Activating Extracellular Domain ERBB2 (HER2) Mutation in Micropapillary Urothelial Carcinoma. Clinical Cancer Research, 2014, 20, 68-75.	7.0	120
71	New Routes to Targeted Therapy of Intrahepatic Cholangiocarcinomas Revealed by Next-Generation Sequencing. Oncologist, 2014, 19, 235-242.	3.7	371
72	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.	9.4	151

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73	Advanced urothelial carcinoma: next-generation sequencing reveals diverse genomic alterations and targets of therapy. Modern Pathology, 2014, 27, 271-280.	5.5	122
74	Emergence of Constitutively Active Estrogen Receptor-Î± Mutations in Pretreated Advanced Estrogen Receptorâ€“Positive Breast Cancer. Clinical Cancer Research, 2014, 20, 1757-1767.	7.0	529
75	A Targeted Next-Generation Sequencing Assay Detects a High Frequency of Therapeutically Targetable Alterations in Primary and Metastatic Breast Cancers: Implications for Clinical Practice. Oncologist, 2014, 19, 453-458.	3.7	53
76	Concordance of Genomic Alterations between Primary and Recurrent Breast Cancer. Molecular Cancer Therapeutics, 2014, 13, 1382-1389.	4.1	104
77	Abstract 1893: A computational method for somatic versus germline variant status determination from targeted next-generation sequencing of clinical cancer specimens without a matched normal control. Cancer Research, 2014, 74, 1893-1893.	0.9	13
78	Patient Derived Xenograft (PDX) Models Recapitulate the Genomic-Driver Composition of Acute Leukemia Samples. Blood, 2014, 124, 286-286.	1.4	4
79	Novel Chromatin Modifying Gene Alterations and Significant Survival Association of ATM and P53 in Mantle Cell Lymphoma. Blood, 2014, 124, 3033-3033.	1.4	2
80	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.	1.6	2
81	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.	1.6	2
82	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.	1.6	1
83	Next-generation sequencing to identify molecular alterations in DNA repair and chromatin maintenance genes associated with pathologic complete response (pT0) to neoadjuvant accelerated methotrexate, vinblastine, doxorubicin, and cisplatin (AMVAC) in muscle-invasive bladder cancer (MIBC).. Journal of Clinical Oncology, 2014, 32, 4538-4538.	1.6	3
84	Analysis of candidate homologous repair deficiency genes in a clinical trial of olaparib in patients (pts) with platinum-sensitive, relapsed serous ovarian cancer (PSR SOC).. Journal of Clinical Oncology, 2014, 32, 5536-5536.	1.6	2
85	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.	1.6	11
86	Anastrozole and everolimus in advanced gynecologic and breast malignancies: activity and molecular alterations in the PI3K/AKT/mTOR pathway. Oncotarget, 2014, 5, 3029-3038.	1.8	40
87	Unique molecular signatures as a hallmark of patients with metastatic breast cancer: Implications for current treatment paradigms. Oncotarget, 2014, 5, 2349-2354.	1.8	54
88	PI3K/AKT/mTOR genomic alterations in 94 patients with metastatic breast cancer in the phase I clinic at MD Anderson: Prevalence and association with response.. Journal of Clinical Oncology, 2014, 32, 2606-2606.	1.6	0
89	Rictor amplification to define a novel and unique subset of lung cancer patients.. Journal of Clinical Oncology, 2014, 32, 8027-8027.	1.6	0
90	Estrogen receptor-positive (ER+) metastatic breast cancer (MBC) patients (pts) with extreme responses (ERs) to capecitabine having tumors with genomic alterations in DNA repair and chromatin remodeling genes.. Journal of Clinical Oncology, 2014, 32, 555-555.	1.6	0

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91	Therapeutic insights for malignant phyllodes from next-generation sequencing.. Journal of Clinical Oncology, 2014, 32, e22069-e22069.	1.6	0
92	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.	1.6	0
93	Evidence of PIK3CA and TP53 co-mutation in breast cancer identification on next-generation sequencing (NGS) of ERBB2 (HER2)-amplified residual disease following preoperative anti-HER2 therapy.. Journal of Clinical Oncology, 2014, 32, 625-625.	1.6	0
94	Genomic Analysis of Serial Samples from CLL Patients Identifies Clonal Events Associated with Disease Progression. Blood, 2014, 124, 1954-1954.	1.4	0
95	Clinical Utility of Comprehensive Profiling of Genomic Alterations in Hematologic Malignancies. Blood, 2014, 124, 1072-1072.	1.4	0
96	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.	1.4	0
97	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.	1.4	0
98	Clinical nextâ€generation sequencing successfully applied to fineâ€needle aspirations of pulmonary and pancreatic neoplasms. Cancer Cytopathology, 2013, 121, 688-694.	2.4	110
99	Development and validation of a clinical cancer genomic profiling test based on massively parallel DNA sequencing. Nature Biotechnology, 2013, 31, 1023-1031.	17.5	1,785
100	D538G Mutation in Estrogen Receptor-Î±: A Novel Mechanism for Acquired Endocrine Resistance in Breast Cancer. Cancer Research, 2013, 73, 6856-6864.	0.9	340
101	Next-Generation Sequencing Reveals High Concordance of Recurrent Somatic Alterations Between Primary Tumor and Metastases From Patients With Nonâ€“Small-Cell Lung Cancer. Journal of Clinical Oncology, 2013, 31, 2167-2172.	1.6	170
102	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.	8.2	188
103	Targeted Next-generation Sequencing of Advanced Prostate Cancer Identifies Potential Therapeutic Targets and Disease Heterogeneity. European Urology, 2013, 63, 920-926.	1.9	379
104	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.	7.0	122
105	Patient Derived Xenograft (PDX) Models Faithfully Recapitulate The Genetic Composition Of Primary AML. Blood, 2013, 122, 1328-1328.	1.4	2
106	Integrated Genetic Profiling Of JAK2 Wildtype Chronic-Phase Myeloproliferative Neoplasms. Blood, 2013, 122, 1588-1588.	1.4	1
107	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.	1.4	3
108	Identification Of Actionable Genomic Alterations In Hematologic Malignancies By a Clinical Next Generation Sequencing-Based Assay. Blood, 2013, 122, 230-230.	1.4	2

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109	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.	1.4	2
110	Pilot Study To Evaluate The Prevalence Of Actionable Oncogenic Mutations In Patients With Relapsed Refractory Multiple Myeloma. Blood, 2013, 122, 755-755.	1.4	1
111	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.	1.6	1
112	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.	1.6	4
113	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.	1.6	4
114	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.	1.6	2
115	Frequent LOH of CYP2D6 in ER+ breast cancer determined by next-generation sequencing (NGS).. Journal of Clinical Oncology, 2013, 31, 534-534.	1.6	0
116	Next-generation sequencing (NGS) in patients with advanced metastatic breast cancer: Identification of molecular alterations and analysis of associations with treatment on phase I studies at MD Anderson Cancer Center.. Journal of Clinical Oncology, 2013, 31, 1051-1051.	1.6	0
117	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.	1.6	8
118	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.	1.6	1
119	Overview Of The Genomic Landscape Of High Risk Diffuse Large B-Cell Lymphoma Using Targeted DNA and RNA Sequencing. Blood, 2013, 122, 501-501.	1.4	0
120	Mutational Profiling Of Myeloid Malignancies For Prediction Of Disease Relapse Following Allogeneic Stem Cell Transplantation. Blood, 2013, 122, 2096-2096.	1.4	0
121	Comprehensive Mutational Profiling In Myelodysplastic Syndromes Treated With Decitabine and Tretinoin. Blood, 2013, 122, 2791-2791.	1.4	0
122	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.	1.4	0
123	Targeted genomic sequencing of pediatric Burkitt lymphoma identifies recurrent alterations in antiapoptotic and chromatin-remodeling genes. Blood, 2012, 120, 5181-5184.	1.4	96
124	Identification of new ALK and RET gene fusions from colorectal and lung cancer biopsies. Nature Medicine, 2012, 18, 382-384.	30.7	782
125	Cancer gene profile of metastatic breast cancer.. Journal of Clinical Oncology, 2012, 30, 1015-1015.	1.6	3
126	Next-generation sequencing of FFPE solid tumor specimens for clinical use.. Journal of Clinical Oncology, 2012, 30, 10524-10524.	1.6	3

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127	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.	1.6	3
128	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.	1.6	7
129	Discovery of recurrent KIF5B-RET fusions and other targetable alterations from clinical NSCLC specimens.. Journal of Clinical Oncology, 2012, 30, 7510-7510.	1.6	4
130	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.	1.6	0
131	Frequency of actionable genomic alterations in early-stage lung adenocarcinoma (LA) detected by next-generation sequencing (NGS).. Journal of Clinical Oncology, 2012, 30, e17541-e17541.	1.6	1
132	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.	1.6	0
133	Targeted next-generation sequencing (NGS) of advanced prostate cancer (PCA) using formalin-fixed tissue.. Journal of Clinical Oncology, 2012, 30, 4649-4649.	1.6	0
134	Concordance of driver mutations in primary and matched metastasis from patients with non-small cell lung cancer (NSCLC) using next-generation sequencing (NGS).. Journal of Clinical Oncology, 2012, 30, 7529-7529.	1.6	0
135	Novel Genomic Alterations in MCL1 and ARID1A Identified in Pediatric Burkitt Lymphoma Using Targeted High-Throughput Sequencing. Blood, 2012, 120, 899-899.	1.4	0
136	Estimation of the multiple testing burden for genomewide association studies of nearly all common variants. Genetic Epidemiology, 2008, 32, 381-385.	1.3	699
137	Estimation of the Multiple Testing Burden for Genomewide Association Studies of Common Variants. Nature Precedings, 2007, , .	0.1	2
138	Evaluating and improving power in whole-genome association studies using fixed marker sets. Nature Genetics, 2006, 38, 663-667.	21.4	274
139	Transferability of tag SNPs in genetic association studies in multiple populations. Nature Genetics, 2006, 38, 1298-1303.	21.4	224
140	Efficiency and power in genetic association studies. Nature Genetics, 2005, 37, 1217-1223.	21.4	1,597