

Sohrab P Shah

List of Publications by Year in descending order

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144
papers

30,054
citations

11651

70
h-index

10158

140
g-index

171
all docs

171
docs citations

171
times ranked

40280
citing authors

#	ARTICLE	IF	CITATIONS
1	Harnessing multimodal data integration to advance precision oncology. <i>Nature Reviews Cancer</i> , 2022, 22, 114-126.	28.4	168
2	Semisupervised Training of a Brain MRI Tumor Detection Model Using Mined Annotations. <i>Radiology</i> , 2022, 303, 80-89.	7.3	7
3	Genomic characterization of metastatic patterns from prospective clinical sequencing of 25,000 patients. <i>Cell</i> , 2022, 185, 563-575.e11.	28.9	223
4	Tumor-associated antigen PRAME exhibits dualistic functions that are targetable in diffuse large B cell lymphoma. <i>Journal of Clinical Investigation</i> , 2022, 132, .	8.2	12
5	Fundamental immune oncogenicity trade-offs define driver mutation fitness. <i>Nature</i> , 2022, 606, 172-179.	27.8	23
6	Tumor-induced double positive T cells display distinct lineage commitment mechanisms and functions. <i>Journal of Experimental Medicine</i> , 2022, 219, .	8.5	8
7	Multimodal data integration using machine learning improves risk stratification of high-grade serous ovarian cancer. <i>Nature Cancer</i> , 2022, 3, 723-733.	13.2	82
8	Dhaka: variational autoencoder for unmasking tumor heterogeneity from single cell genomic data. <i>Bioinformatics</i> , 2021, 37, 1535-1543.	4.1	38
9	Initial Whole-Genome Sequencing of Plasma Cell Neoplasms in First Responders and Recovery Workers Exposed to the World Trade Center Attack of September 11, 2001. <i>Clinical Cancer Research</i> , 2021, 27, 2111-2118.	7.0	5
10	Characterization of DLBCL with a PMBL gene expression signature. <i>Blood</i> , 2021, 138, 136-148.	1.4	19
11	Clonal fitness inferred from time-series modelling of single-cell cancer genomes. <i>Nature</i> , 2021, 595, 585-590.	27.8	71
12	Tim-4+ cavity-resident macrophages impair anti-tumor CD8+ T cell immunity. <i>Cancer Cell</i> , 2021, 39, 973-988.e9.	16.8	93
13	Single-cell profiling reveals the importance of CXCL13/CXCR5 axis biology in lymphocyte-rich classic Hodgkin lymphoma. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	7.1	26
14	Single-Cell Profiling Reveals Clinically Relevant Evolutionary Trajectories and Alternate Biologies in Human Follicular Lymphoma. <i>Blood</i> , 2021, 138, 450-450.	1.4	0
15	Single-Cell Transcriptome Analysis Reveals Disease-Defining T-cell Subsets in the Tumor Microenvironment of Classic Hodgkin Lymphoma. <i>Cancer Discovery</i> , 2020, 10, 406-421.	9.4	155
16	Single cell transcriptomes of normal endometrial derived organoids uncover novel cell type markers and cryptic differentiation of primary tumours. <i>Journal of Pathology</i> , 2020, 252, 201-214.	4.5	31
17	Epiclomal: Probabilistic clustering of sparse single-cell DNA methylation data. <i>PLoS Computational Biology</i> , 2020, 16, e1008270.	3.2	18
18	Chemogenomic profiling of breast cancer patient-derived xenografts reveals targetable vulnerabilities for difficult-to-treat tumors. <i>Communications Biology</i> , 2020, 3, 310.	4.4	28

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19	Eleven grand challenges in single-cell data science. <i>Genome Biology</i> , 2020, 21, 31.	8.8	742
20	TMEM30A loss-of-function mutations drive lymphomagenesis and confer therapeutically exploitable vulnerability in B-cell lymphoma. <i>Nature Medicine</i> , 2020, 26, 577-588.	30.7	46
21	Non-coding somatic mutations converge on the PAX8 pathway in ovarian cancer. <i>Nature Communications</i> , 2020, 11, 2020.	12.8	52
22	Single Cell Profiling Reveals Unique CXCL13 Positive T Cell Subsets in the Tumor Microenvironment of Lymphocyte Rich Classic Hodgkin Lymphoma. <i>Blood</i> , 2020, 136, 32-33.	1.4	0
23	Initial Whole Genome Sequencing of Plasma Cell Neoplasms in First Responders and Recovery Workers Exposed to the World Trade Center Attack of September 11, 2001. <i>Blood</i> , 2020, 136, 50-51.	1.4	0
24	The Tumor Associated Antigen PRAME Exhibits Dualistic Functions That Are Targetable in Diffuse Large B-Cell Lymphoma. <i>Blood</i> , 2020, 136, 34-34.	1.4	1
25	Molecular profiling and molecular classification of endometrioid ovarian carcinomas. <i>Gynecologic Oncology</i> , 2019, 154, 516-523.	1.4	62
26	Regulation of pH by Carbonic Anhydrase 9 Mediates Survival of Pancreatic Cancer Cells With Activated KRAS in Response to Hypoxia. <i>Gastroenterology</i> , 2019, 157, 823-837.	1.3	153
27	Dissociation of solid tumor tissues with cold active protease for single-cell RNA-seq minimizes conserved collagenase-associated stress responses. <i>Genome Biology</i> , 2019, 20, 210.	8.8	171
28	Clonal Decomposition and DNA Replication States Defined by Scaled Single-Cell Genome Sequencing. <i>Cell</i> , 2019, 179, 1207-1221.e22.	28.9	162
29	Probabilistic cell-type assignment of single-cell RNA-seq for tumor microenvironment profiling. <i>Nature Methods</i> , 2019, 16, 1007-1015.	19.0	241
30	Molecular and Genetic Characterization of MHC Deficiency Identifies EZH2 as Therapeutic Target for Enhancing Immune Recognition. <i>Cancer Discovery</i> , 2019, 9, 546-563.	9.4	213
31	Pharmacological systems analysis defines EIF4A3 functions in cell-cycle and RNA stress granule formation. <i>Communications Biology</i> , 2019, 2, 165.	4.4	29
32	Targeting Hypoxia-Induced Carbonic Anhydrase IX Enhances Immune-Checkpoint Blockade Locally and Systemically. <i>Cancer Immunology Research</i> , 2019, 7, 1064-1078.	3.4	104
33	clonealign: statistical integration of independent single-cell RNA and DNA sequencing data from human cancers. <i>Genome Biology</i> , 2019, 20, 54.	8.8	92
34	Double-Hit Gene Expression Signature Defines a Distinct Subgroup of Germinal Center B-Cell-Like Diffuse Large B-Cell Lymphoma. <i>Journal of Clinical Oncology</i> , 2019, 37, 190-201.	1.6	257
35	Integrated structural variation and point mutation signatures in cancer genomes using correlated topic models. <i>PLoS Computational Biology</i> , 2019, 15, e1006799.	3.2	44
36	Somatic mutation detection and classification through probabilistic integration of clonal population information. <i>Communications Biology</i> , 2019, 2, 44.	4.4	7

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37	PRAME Expression Is Correlated with Treatment Outcome and Specific Features of the Tumor Microenvironment in Classical Hodgkin Lymphoma. <i>Blood</i> , 2019, 134, 1509-1509.	1.4	1
38	TERT promoter mutation in adult granulosa cell tumor of the ovary. <i>Modern Pathology</i> , 2018, 31, 1107-1115.	5.5	49
39	Observing Clonal Dynamics across Spatiotemporal Axes: A Prelude to Quantitative Fitness Models for Cancer. <i>Cold Spring Harbor Perspectives in Medicine</i> , 2018, 8, a029603.	6.2	9
40	Genome-wide discovery of somatic regulatory variants in diffuse large B-cell lymphoma. <i>Nature Communications</i> , 2018, 9, 4001.	12.8	102
41	Copy number signatures in ovarian cancer. <i>Nature Genetics</i> , 2018, 50, 1208-1209.	21.4	4
42	Interpretable dimensionality reduction of single cell transcriptome data with deep generative models. <i>Nature Communications</i> , 2018, 9, 2002.	12.8	271
43	Interfaces of Malignant and Immunologic Clonal Dynamics in Ovarian Cancer. <i>Cell</i> , 2018, 173, 1755-1769.e22.	28.9	261
44	Molecular and Genetic Characterization of MHC Deficiency Identifies EZH2 As a Therapeutic Target for Restoring MHC Expression in Diffuse Large B-Cell Lymphoma. <i>Blood</i> , 2018, 132, 1560-1560.	1.4	2
45	Somatic PRAME Deletions Are Associated with Decreased Immunogenicity, Apoptosis Resistance and Poor Outcomes in Diffuse Large B-Cell Lymphoma. <i>Blood</i> , 2018, 132, 667-667.	1.4	1
46	The Double-Hit Gene Expression Signature Defines a Clinically and Biologically Distinct Subgroup within GCB-DLBCL. <i>Blood</i> , 2018, 132, 921-921.	1.4	1
47	Scalable whole-genome single-cell library preparation without preamplification. <i>Nature Methods</i> , 2017, 14, 167-173.	19.0	164
48	CX-5461 is a DNA G-quadruplex stabilizer with selective lethality in BRCA1/2 deficient tumours. <i>Nature Communications</i> , 2017, 8, 14432.	12.8	379
49	ddClone: joint statistical inference of clonal populations from single cell and bulk tumour sequencing data. <i>Genome Biology</i> , 2017, 18, 44.	8.8	52
50	Genomic consequences of aberrant DNA repair mechanisms stratify ovarian cancer histotypes. <i>Nature Genetics</i> , 2017, 49, 856-865.	21.4	220
51	E-scape: interactive visualization of single-cell phylogenetics and cancer evolution. <i>Nature Methods</i> , 2017, 14, 549-550.	19.0	46
52	CDK12 regulates alternative last exon mRNA splicing and promotes breast cancer cell invasion. <i>Nucleic Acids Research</i> , 2017, 45, 6698-6716.	14.5	114
53	Enhancing knowledge discovery from cancer genomics data with Galaxy. <i>GigaScience</i> , 2017, 6, 1-13.	6.4	6
54	Genetic profiling of MYC and BCL2 in diffuse large B-cell lymphoma determines cell-of-origin-specific clinical impact. <i>Blood</i> , 2017, 129, 2760-2770.	1.4	112

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55	CLK-dependent exon recognition and conjoined gene formation revealed with a novel small molecule inhibitor. <i>Nature Communications</i> , 2017, 8, 7.	12.8	108
56	The driver landscape of sporadic chordoma. <i>Nature Communications</i> , 2017, 8, 890.	12.8	115
57	LINE-1 retrotransposon-mediated DNA transductions in endometriosis associated ovarian cancers. <i>Gynecologic Oncology</i> , 2017, 147, 642-647.	1.4	13
58	Engineered in-vitro cell line mixtures and robust evaluation of computational methods for clonal decomposition and longitudinal dynamics in cancer. <i>Scientific Reports</i> , 2017, 7, 13467.	3.3	4
59	Genetic and epigenetic inactivation of <i>SESTRIN1</i> controls mTORC1 and response to EZH2 inhibition in follicular lymphoma. <i>Science Translational Medicine</i> , 2017, 9, .	12.4	52
60	Kronos: a workflow assembler for genome analytics and informatics. <i>GigaScience</i> , 2017, 6, 1-10.	6.4	8
61	ReMixT: clone-specific genomic structure estimation in cancer. <i>Genome Biology</i> , 2017, 18, 140.	8.8	29
62	Prognostic Model to Predict Post-Autologous Stem-Cell Transplantation Outcomes in Classical Hodgkin Lymphoma. <i>Journal of Clinical Oncology</i> , 2017, 35, 3722-3733.	1.6	48
63	Divergent modes of clonal spread and intraperitoneal mixing in high-grade serous ovarian cancer. <i>Nature Genetics</i> , 2016, 48, 758-767.	21.4	287
64	Clonal genotype and population structure inference from single-cell tumor sequencing. <i>Nature Methods</i> , 2016, 13, 573-576.	19.0	108
65	densityCut: an efficient and versatile topological approach for automatic clustering of biological data. <i>Bioinformatics</i> , 2016, 32, 2567-2576.	4.1	40
66	Overexpression screens identify conserved dosage chromosome instability genes in yeast and human cancer. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, 9967-9976.	7.1	67
67	The genomic landscape of epithelioid sarcoma cell lines and tumours. <i>Journal of Pathology</i> , 2016, 238, 63-73.	4.5	43
68	Robust high-performance nanoliter-volume single-cell multiple displacement amplification on planar substrates. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, 8484-8489.	7.1	45
69	The somatic mutation profiles of 2,433 breast cancers refine their genomic and transcriptomic landscapes. <i>Nature Communications</i> , 2016, 7, 11479.	12.8	1,221
70	Identification of the epigenetic reader CBX2 as a potential drug target in advanced prostate cancer. <i>Clinical Epigenetics</i> , 2016, 8, 16.	4.1	55
71	Divergent clonal selection dominates medulloblastoma at recurrence. <i>Nature</i> , 2016, 529, 351-357.	27.8	266
72	A Novel Prognostic Model Based on Tumor Microenvironment Biology in Relapse Biopsies Predicts Post-Autologous Stem Cell Transplantation Outcomes in Classical Hodgkin Lymphoma. <i>Blood</i> , 2016, 128, 1093-1093.	1.4	12

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73	Histological Transformation and Progression in Follicular Lymphoma: A Clonal Evolution Study. PLoS Medicine, 2016, 13, e1002197.	8.4	185
74	Targeted Sequencing Reveals Novel Gene Mutations Associated with Transformation and Early Progression in Follicular Lymphoma. Blood, 2016, 128, 2919-2919.	1.4	5
75	Frequent Genetic Alterations of PI3K-AKT Pathway and Their Clinical Significance in Germinal Center B-Cell-like Diffuse Large B-Cell Lymphoma. Blood, 2016, 128, 607-607.	1.4	1
76	Divergent Modes of Tumor Evolution Underlie Histological Transformation and Early Progression of Follicular Lymphoma. Blood, 2016, 128, 1091-1091.	1.4	0
77	An RCOR1 loss-associated gene expression signature identifies a prognostically significant DLBCL subgroup. Blood, 2015, 125, 959-966.	1.4	24
78	Cell of origin of transformed follicular lymphoma. Blood, 2015, 126, 2118-2127.	1.4	91
79	Cis-regulatory somatic mutations and gene-expression alteration in B-cell lymphomas. Genome Biology, 2015, 16, 84.	8.8	36
80	Spatial genomic heterogeneity within localized, multifocal prostate cancer. Nature Genetics, 2015, 47, 736-745.	21.4	395
81	Multifocal endometriotic lesions associated with cancer are clonal and carry a high mutation burden. Journal of Pathology, 2015, 236, 201-209.	4.5	131
82	Using Somatic Mutations to Guide Treatment Decisions. JAMA Oncology, 2015, 1, 275.	7.1	15
83	Synchronous Endometrial and Ovarian Carcinomas: Evidence of Clonality. Journal of the National Cancer Institute, 2015, 108, djv428.	6.3	128
84	A tumor DNA complex aberration index is an independent predictor of survival in breast and ovarian cancer. Molecular Oncology, 2015, 9, 115-127.	4.6	38
85	Hereditary Diffuse Gastric Cancer Syndrome. JAMA Oncology, 2015, 1, 23.	7.1	540
86	Multifocal clonal evolution characterized using circulating tumour DNA in a case of metastatic breast cancer. Nature Communications, 2015, 6, 8760.	12.8	409
87	Systematic analysis of somatic mutations impacting gene expression in 12 tumour types. Nature Communications, 2015, 6, 8554.	12.8	102
88	Dynamics of genomic clones in breast cancer patient xenografts at single-cell resolution. Nature, 2015, 518, 422-426.	27.8	545
89	TITAN: inference of copy number architectures in clonal cell populations from tumor whole-genome sequence data. Genome Research, 2014, 24, 1881-1893.	5.5	322
90	DNA barcoding reveals diverse growth kinetics of human breast tumour subclones in serially passaged xenografts. Nature Communications, 2014, 5, 5871.	12.8	86

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91	Intratumoral heterogeneity in a minority of ovarian low-grade serous carcinomas. <i>BMC Cancer</i> , 2014, 14, 982.	2.6	27
92	Ovarian and endometrial endometrioid carcinomas have distinct CTNNB1 and PTEN mutation profiles. <i>Modern Pathology</i> , 2014, 27, 128-134.	5.5	218
93	Genomic rearrangements involving programmed death ligands are recurrent in primary mediastinal large B-cell lymphoma. <i>Blood</i> , 2014, 123, 2062-2065.	1.4	259
94	Recurrent somatic mutations of PTPN1 in primary mediastinal B cell lymphoma and Hodgkin lymphoma. <i>Nature Genetics</i> , 2014, 46, 329-335.	21.4	180
95	Small cell carcinoma of the ovary, hypercalcemic type, displays frequent inactivating germline and somatic mutations in SMARCA4. <i>Nature Genetics</i> , 2014, 46, 427-429.	21.4	298
96	PyClone: statistical inference of clonal population structure in cancer. <i>Nature Methods</i> , 2014, 11, 396-398.	19.0	817
97	Mutational Context and Diverse Clonal Development in Early and Late Bladder Cancer. <i>Cell Reports</i> , 2014, 7, 1649-1663.	6.4	128
98	Analysis of Relapse Biopsies in Classical Hodgkin Lymphoma Reveals Correlations with Outcome after Autologous Stem Cell Transplantation. <i>Blood</i> , 2014, 124, 136-136.	1.4	0
99	iReckon: Simultaneous isoform discovery and abundance estimation from RNA-seq data. <i>Genome Research</i> , 2013, 23, 519-529.	5.5	123
100	Distinguishing Somatic and Germline Copy Number Events in Cancer Patient DNA Hybridized to Whole-Genome SNP Genotyping Arrays. <i>Methods in Molecular Biology</i> , 2013, 973, 355-372.	0.9	6
101	Distinct evolutionary trajectories of primary high-grade serous ovarian cancers revealed through spatial mutational profiling. <i>Journal of Pathology</i> , 2013, 231, 21-34.	4.5	357
102	Mutational and structural analysis of diffuse large B-cell lymphoma using whole-genome sequencing. <i>Blood</i> , 2013, 122, 1256-1265.	1.4	349
103	A robust hidden semi-Markov model with application to aCGH data processing. <i>International Journal of Data Mining and Bioinformatics</i> , 2013, 8, 427.	0.1	4
104	Genomic Rearrangements Involving Programmed Death Ligands Are Recurrent In Primary Mediastinal Large B-Cell Lymphoma. <i>Blood</i> , 2013, 122, 635-635.	1.4	3
105	Type-Specific Cell Line Models for Type-Specific Ovarian Cancer Research. <i>PLoS ONE</i> , 2013, 8, e72162.	2.5	200
106	Protein Tyrosine Phosphatase Type-1 (PTPN1) Is Frequently Mutated In Primary Mediastinal B Cell Lymphoma and Hodgkin Lymphoma. <i>Blood</i> , 2013, 122, 242-242.	1.4	1
107	BRCA1 and BRCA2 mutations correlate with TP53 abnormalities and presence of immune cell infiltrates in ovarian high-grade serous carcinoma. <i>Modern Pathology</i> , 2012, 25, 740-750.	5.5	151
108	nFuse: Discovery of complex genomic rearrangements in cancer using high-throughput sequencing. <i>Genome Research</i> , 2012, 22, 2250-2261.	5.5	67

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109	Recurrent Somatic <i>DICER1</i> Mutations in Nonepithelial Ovarian Cancers. <i>New England Journal of Medicine</i> , 2012, 366, 234-242.	27.0	401
110	Integrative analysis of genome-wide loss of heterozygosity and monoallelic expression at nucleotide resolution reveals disrupted pathways in triple-negative breast cancer. <i>Genome Research</i> , 2012, 22, 1995-2007.	5.5	237
111	Feature-based classifiers for somatic mutation detection in tumour-normal paired sequencing data. <i>Bioinformatics</i> , 2012, 28, 167-175.	4.1	130
112	14-3-3 fusion oncogenes in high-grade endometrial stromal sarcoma. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 929-934.	7.1	239
113	JointSNVMix: a probabilistic model for accurate detection of somatic mutations in normal/tumour paired next-generation sequencing data. <i>Bioinformatics</i> , 2012, 28, 907-913.	4.1	159
114	DriverNet: uncovering the impact of somatic driver mutations on transcriptional networks in cancer. <i>Genome Biology</i> , 2012, 13, R124.	9.6	247
115	Mutation Discovery in Regions of Segmental Cancer Genome Amplifications with CoNAN-SNV: A Mixture Model for Next Generation Sequencing of Tumors. <i>PLoS ONE</i> , 2012, 7, e41551.	2.5	4
116	The genomic and transcriptomic architecture of 2,000 breast tumours reveals novel subgroups. <i>Nature</i> , 2012, 486, 346-352.	27.8	4,708
117	Use of mutation profiles to refine the classification of endometrial carcinomas. <i>Journal of Pathology</i> , 2012, 228, 20-30.	4.5	261
118	The clonal and mutational evolution spectrum of primary triple-negative breast cancers. <i>Nature</i> , 2012, 486, 395-399.	27.8	1,778
119	Large-Scale High Resolution Integration of Copy Number and Gene Expression in DLBCL Reveals Focal and Frequent Deletions in Chromatin Modifying Genes with Outcome Correlation. <i>Blood</i> , 2012, 120, 295-295.	1.4	0
120	MHC class II transactivator CIITA is a recurrent gene fusion partner in lymphoid cancers. <i>Nature</i> , 2011, 471, 377-381.	27.8	551
121	Subtype-specific mutation of <i>PPP2R1A</i> in endometrial and ovarian carcinomas. <i>Journal of Pathology</i> , 2011, 223, 567-573.	4.5	114
122	Comrad: detection of expressed rearrangements by integrated analysis of RNA-Seq and low coverage genome sequence data. <i>Bioinformatics</i> , 2011, 27, 1481-1488.	4.1	39
123	deFuse: An Algorithm for Gene Fusion Discovery in Tumor RNA-Seq Data. <i>PLoS Computational Biology</i> , 2011, 7, e1001138.	3.2	477
124	CSF1R Expression of Hodgkin Reed Sternberg Cells Is Associated with the Number of Macrophages in the Tumor Microenvironment and Is Correlated with Treatment Outcome. <i>Blood</i> , 2011, 118, 427-427.	1.4	0
125	High resolution analysis of follicular lymphoma genomes reveals somatic recurrent sites of copy-neutral loss of heterozygosity and copy number alterations that target single genes. <i>Genes Chromosomes and Cancer</i> , 2010, 49, 669-681.	2.8	51
126	Somatic mutations altering EZH2 (Tyr641) in follicular and diffuse large B-cell lymphomas of germinal-center origin. <i>Nature Genetics</i> , 2010, 42, 181-185.	21.4	1,504

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127	Acquired <i>TNFRSF14</i> Mutations in Follicular Lymphoma Are Associated with Worse Prognosis. <i>Cancer Research</i> , 2010, 70, 9166-9174.	0.9	160
128	Robust hidden semi-Markov modeling of array CGH data. , 2010, , .		1
129	SNVMix: predicting single nucleotide variants from next-generation sequencing of tumors. <i>Bioinformatics</i> , 2010, 26, 730-736.	4.1	192
130	Tumor-Associated Macrophages and Survival in Classic Hodgkin's Lymphoma. <i>New England Journal of Medicine</i> , 2010, 362, 875-885.	27.0	1,141
131	<i>ARID1A</i> Mutations in Endometriosis-Associated Ovarian Carcinomas. <i>New England Journal of Medicine</i> , 2010, 363, 1532-1543.	27.0	1,460
132	Model-based clustering of array CGH data. <i>Bioinformatics</i> , 2009, 25, i30-i38.	4.1	17
133	Mutational evolution in a lobular breast tumour profiled at single nucleotide resolution. <i>Nature</i> , 2009, 461, 809-813.	27.8	984
134	Mutation of <i>FOXL2</i> in Granulosa-Cell Tumors of the Ovary. <i>New England Journal of Medicine</i> , 2009, 360, 2719-2729.	27.0	706
135	Genome-wide profiling of follicular lymphoma by array comparative genomic hybridization reveals prognostically significant DNA copy number imbalances. <i>Blood</i> , 2009, 113, 137-148.	1.4	122
136	Tyrosine 641 of the EZH2 Oncogene Is Frequently Mutated in Follicular and Diffuse Large B-Cell Lymphomas of Germinal Center Origin.. <i>Blood</i> , 2009, 114, 139-139.	1.4	3
137	Gene Expression Profiling of Microdissected Hodgkin Reed Sternberg Cells: Molecular Subtypes and Treatment Outcome Correlations.. <i>Blood</i> , 2009, 114, 268-268.	1.4	12
138	<i>TNFRSF14</i> Is Mutated in a Subset of Follicular Lymphoma and Correlated with Inferior Prognosis.. <i>Blood</i> , 2009, 114, 1919-1919.	1.4	1
139	Computational methods for identification of recurrent copy number alteration patterns by array CGH. <i>Cytogenetic and Genome Research</i> , 2008, 123, 343-351.	1.1	20
140	Deletion in Chromosome 17p12 and Gains in Chromosome 9q33.3 by Array Comparative Hybridization Are Associated with R-CHOP Treatment Failure in Patients with Diffuse Large B Cell Lymphoma. <i>Blood</i> , 2008, 112, 477-477.	1.4	2
141	Genetic Alterations Detected by High-Resolution Array Comparative Genomic Hybridization in Microdissected HRS Cells Correlate with Treatment Outcome in Classical Hodgkin Lymphoma. <i>Blood</i> , 2008, 112, 522-522.	1.4	1
142	Genome-Wide Expression Profiling Predicts Treatment Outcome in Classical Hodgkin Lymphoma. <i>Blood</i> , 2008, 112, 520-520.	1.4	0
143	Modeling recurrent DNA copy number alterations in array CGH data. <i>Bioinformatics</i> , 2007, 23, i450-i458.	4.1	58
144	Integrating copy number polymorphisms into array CGH analysis using a robust HMM. <i>Bioinformatics</i> , 2006, 22, e431-e439.	4.1	144