Sohrab P Shah

List of Publications by Year
in descending order

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	The genomic and transcriptomic architecture of 2,000 breast tumours reveals novel subgroups. Nature, 2012, 486, 346-352.	27.8	4,708
2	The clonal and mutational evolution spectrum of primary triple-negative breast cancers. Nature, 2012, 486, 395-399.	27.8	1,778
3	Somatic mutations altering EZH2 (Tyr641) in follicular and diffuse large B-cell lymphomas of germinal-center origin. Nature Genetics, 2010, 42, 181-185.	21.4	1,504
4	ARID1AMutations in Endometriosis-Associated Ovarian Carcinomas. New England Journal of Medicine, 2010, 363, 1532-1543.	27.0	1,460
5	The somatic mutation profiles of 2,433 breast cancers refine their genomic and transcriptomic landscapes. Nature Communications, 2016, 7, 11479.	12.8	1,221
6	Tumor-Associated Macrophages and Survival in Classic Hodgkin's Lymphoma. New England Journal of Medicine, 2010, 362, 875-885.	27.0	1,141
7	Mutational evolution in a lobular breast tumour profiled at single nucleotide resolution. Nature, 2009, 461, 809-813.	27.8	984
8	PyClone: statistical inference of clonal population structure in cancer. Nature Methods, 2014, 11, 396-398.	19.0	817
9	Eleven grand challenges in single-cell data science. Genome Biology, 2020, 21, 31.	8.8	742
10	Mutation ofFOXL2in Granulosa-Cell Tumors of the Ovary. New England Journal of Medicine, 2009, 360, 2719-2729.	27.0	706
11	MHC class II transactivator CIITA is a recurrent gene fusion partner in lymphoid cancers. Nature, 2011, 471, 377-381.	27.8	551
12	Dynamics of genomic clones in breast cancer patient xenografts at single-cell resolution. Nature, 2015, 518, 422-426.	27.8	545
13	Hereditary Diffuse Gastric Cancer Syndrome. JAMA Oncology, 2015, 1, 23.	7.1	540
14	deFuse: An Algorithm for Gene Fusion Discovery in Tumor RNA-Seq Data. PLoS Computational Biology, 2011, 7, e1001138.	3.2	477
15	Multifocal clonal evolution characterized using circulating tumour DNA in a case of metastatic breast cancer. Nature Communications, 2015, 6, 8760.	12.8	409
16	Recurrent SomaticDICER1Mutations in Nonepithelial Ovarian Cancers. New England Journal of Medicine, 2012, 366, 234-242.	27.0	401
17	Spatial genomic heterogeneity within localized, multifocal prostate cancer. Nature Genetics, 2015, 47, 736-745.	21.4	395
18	CX-5461 is a DNA G-quadruplex stabilizer with selective lethality in BRCA1/2 deficient tumours. Nature Communications, 2017, 8, 14432.	12.8	379

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19	Distinct evolutionary trajectories of primary highâ€grade serous ovarian cancers revealed through spatial mutational profiling. Journal of Pathology, 2013, 231, 21-34.	4.5	357
20	Mutational and structural analysis of diffuse large B-cell lymphoma using whole-genome sequencing. Blood, 2013, 122, 1256-1265.	1.4	349
21	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
22	Small cell carcinoma of the ovary, hypercalcemic type, displays frequent inactivating germline and somatic mutations in SMARCA4. Nature Genetics, 2014, 46, 427-429.	21.4	298
23	Divergent modes of clonal spread and intraperitoneal mixing in high-grade serous ovarian cancer. Nature Genetics, 2016, 48, 758-767.	21.4	287
24	Interpretable dimensionality reduction of single cell transcriptome data with deep generative models. Nature Communications, 2018, 9, 2002.	12.8	271
25	Divergent clonal selection dominates medulloblastoma at recurrence. Nature, 2016, 529, 351-357.	27.8	266
26	Use of mutation profiles to refine the classification of endometrial carcinomas. Journal of Pathology, 2012, 228, 20-30.	4.5	261
27	Interfaces of Malignant and Immunologic Clonal Dynamics in Ovarian Cancer. Cell, 2018, 173, 1755-1769.e22.	28.9	261
28	Genomic rearrangements involving programmed death ligands are recurrent in primary mediastinal large B-cell lymphoma. Blood, 2014, 123, 2062-2065.	1.4	259
29	Double-Hit Gene Expression Signature Defines a Distinct Subgroup of Germinal Center B-Cell-Like Diffuse Large B-Cell Lymphoma. Journal of Clinical Oncology, 2019, 37, 190-201.	1.6	257
30	DriverNet: uncovering the impact of somatic driver mutations on transcriptional networks in cancer. Genome Biology, 2012, 13, R124.	9.6	247
31	Probabilistic cell-type assignment of single-cell RNA-seq for tumor microenvironment profiling. Nature Methods, 2019, 16, 1007-1015.	19.0	241
32	14-3-3 fusion oncogenes in high-grade endometrial stromal sarcoma. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 929-934.	7.1	239
33	Integrative analysis of genome-wide loss of heterozygosity and monoallelic expression at nucleotide resolution reveals disrupted pathways in triple-negative breast cancer. Genome Research, 2012, 22, 1995-2007.	5.5	237
34	Genomic characterization of metastatic patterns from prospective clinical sequencing of 25,000 patients. Cell, 2022, 185, 563-575.e11.	28.9	223
35	Genomic consequences of aberrant DNA repair mechanisms stratify ovarian cancer histotypes. Nature Genetics, 2017, 49, 856-865.	21.4	220
36	Ovarian and endometrial endometrioid carcinomas have distinct CTNNB1 and PTEN mutation profiles. Modern Pathology, 2014, 27, 128-134.	5.5	218

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37	Molecular and Genetic Characterization of MHC Deficiency Identifies EZH2 as Therapeutic Target for Enhancing Immune Recognition. Cancer Discovery, 2019, 9, 546-563.	9.4	213
38	Type-Specific Cell Line Models for Type-Specific Ovarian Cancer Research. PLoS ONE, 2013, 8, e72162.	2.5	200
39	SNVMix: predicting single nucleotide variants from next-generation sequencing of tumors. Bioinformatics, 2010, 26, 730-736.	4.1	192
40	Histological Transformation and Progression in Follicular Lymphoma: A Clonal Evolution Study. PLoS Medicine, 2016, 13, e1002197.	8.4	185
41	Recurrent somatic mutations of PTPN1 in primary mediastinal B cell lymphoma and Hodgkin lymphoma. Nature Genetics, 2014, 46, 329-335.	21.4	180
42	Dissociation of solid tumor tissues with cold active protease for single-cell RNA-seq minimizes conserved collagenase-associated stress responses. Genome Biology, 2019, 20, 210.	8.8	171
43	Harnessing multimodal data integration to advance precision oncology. Nature Reviews Cancer, 2022, 22, 114-126.	28.4	168
44	Scalable whole-genome single-cell library preparation without preamplification. Nature Methods, 2017, 14, 167-173.	19.0	164
45	Clonal Decomposition and DNA Replication States Defined by Scaled Single-Cell Genome Sequencing. Cell, 2019, 179, 1207-1221.e22.	28.9	162
46	Acquired TNFRSF14 Mutations in Follicular Lymphoma Are Associated with Worse Prognosis. Cancer Research, 2010, 70, 9166-9174.	0.9	160
47	JointSNVMix: a probabilistic model for accurate detection of somatic mutations in normal/tumour paired next-generation sequencing data. Bioinformatics, 2012, 28, 907-913.	4.1	159
48	Single-Cell Transcriptome Analysis Reveals Disease-Defining T-cell Subsets in the Tumor Microenvironment of Classic Hodgkin Lymphoma. Cancer Discovery, 2020, 10, 406-421.	9.4	155
49	Regulation of pH by Carbonic Anhydrase 9 Mediates Survival of Pancreatic Cancer Cells With Activated KRAS in Response to Hypoxia. Gastroenterology, 2019, 157, 823-837.	1.3	153
50	BRCA1 and BRCA2 mutations correlate with TP53 abnormalities and presence of immune cell infiltrates in ovarian high-grade serous carcinoma. Modern Pathology, 2012, 25, 740-750.	5.5	151
51	Integrating copy number polymorphisms into array CGH analysis using a robust HMM. Bioinformatics, 2006, 22, e431-e439.	4.1	144
52	Multifocal endometriotic lesions associated with cancer are clonal and carry a high mutation burden. Journal of Pathology, 2015, 236, 201-209.	4.5	131
53	Feature-based classifiers for somatic mutation detection in tumourâ€“normal paired sequencing data. Bioinformatics, 2012, 28, 167-175.	4.1	130
54	Mutational Context and Diverse Clonal Development in Early and Late Bladder Cancer. Cell Reports, 2014, 7, 1649-1663.	6.4	128

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55	Synchronous Endometrial and Ovarian Carcinomas: Evidence of Clonality. Journal of the National Cancer Institute, 2015, 108, djv428.	6.3	128
56	iReckon: Simultaneous isoform discovery and abundance estimation from RNA-seq data. Genome Research, 2013, 23, 519-529.	5.5	123
57	Genome-wide profiling of follicular lymphoma by array comparative genomic hybridization reveals prognostically significant DNA copy number imbalances. Blood, 2009, 113, 137-148.	1.4	122
58	The driver landscape of sporadic chordoma. Nature Communications, 2017, 8, 890.	12.8	115
59	Subtypeâ€specific mutation of PPP2R1A in endometrial and ovarian carcinomas. Journal of Pathology, 2011, 223, 567-573.	4.5	114
60	CDK12 regulates alternative last exon mRNA splicing and promotes breast cancer cell invasion. Nucleic Acids Research, 2017, 45, 6698-6716.	14.5	114
61	Genetic profiling of MYC and BCL2 in diffuse large B-cell lymphoma determines cell-of-originâ€“specific clinical impact. Blood, 2017, 129, 2760-2770.	1.4	112
62	Clonal genotype and population structure inference from single-cell tumor sequencing. Nature Methods, 2016, 13, 573-576.	19.0	108
63	CLK-dependent exon recognition and conjoined gene formation revealed with a novel small molecule inhibitor. Nature Communications, 2017, 8, 7.	12.8	108
64	Targeting Hypoxia-Induced Carbonic Anhydrase IX Enhances Immune-Checkpoint Blockade Locally and Systemically. Cancer Immunology Research, 2019, 7, 1064-1078.	3.4	104
65	Systematic analysis of somatic mutations impacting gene expression in 12 tumour types. Nature Communications, 2015, 6, 8554.	12.8	102
66	Genome-wide discovery of somatic regulatory variants in diffuse large B-cell lymphoma. Nature Communications, 2018, 9, 4001.	12.8	102
67	Tim-4+ cavity-resident macrophages impair anti-tumor CD8+ TÂcell immunity. Cancer Cell, 2021, 39, 973-988.e9.	16.8	93
68	clonealign: statistical integration of independent single-cell RNA and DNA sequencing data from human cancers. Genome Biology, 2019, 20, 54.	8.8	92
69	Cell of origin of transformed follicular lymphoma. Blood, 2015, 126, 2118-2127.	1.4	91
70	DNA barcoding reveals diverse growth kinetics of human breast tumour subclones in serially passaged xenografts. Nature Communications, 2014, 5, 5871.	12.8	86
71	Multimodal data integration using machine learning improves risk stratification of high-grade serous ovarian cancer. Nature Cancer, 2022, 3, 723-733.	13.2	82
72	Clonal fitness inferred from time-series modelling of single-cell cancer genomes. Nature, 2021, 595, 585-590.	27.8	71

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73	nFuse: Discovery of complex genomic rearrangements in cancer using high-throughput sequencing. Genome Research, 2012, 22, 2250-2261.	5.5	67
74	Overexpression screens identify conserved dosage chromosome instability genes in yeast and human cancer. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, 9967-9976.	7.1	67
75	Molecular profiling and molecular classification of endometrioid ovarian carcinomas. Gynecologic Oncology, 2019, 154, 516-523.	1.4	62
76	Modeling recurrent DNA copy number alterations in array CGH data. Bioinformatics, 2007, 23, i450-i458.	4.1	58
77	Identification of the epigenetic reader CBX2 as a potential drug target in advanced prostate cancer. Clinical Epigenetics, 2016, 8, 16.	4.1	55
78	ddClone: joint statistical inference of clonal populations from single cell and bulk tumour sequencing data. Genome Biology, 2017, 18, 44.	8.8	52
79	Genetic and epigenetic inactivation of SESTRIN1 controls mTORC1 and response to EZH2 inhibition in follicular lymphoma. Science Translational Medicine, 2017, 9, .	12.4	52
80	Non-coding somatic mutations converge on the PAX8 pathway in ovarian cancer. Nature Communications, 2020, 11, 2020.	12.8	52
81	High resolution analysis of follicular lymphoma genomes reveals somatic recurrent sites of copyâ€neutral loss of heterozygosity and copy number alterations that target single genes. Genes Chromosomes and Cancer, 2010, 49, 669-681.	2.8	51
82	TERT promoter mutation in adult granulosa cell tumor of the ovary. Modern Pathology, 2018, 31, 1107-1115.	5.5	49
83	Prognostic Model to Predict Post-Autologous Stem-Cell Transplantation Outcomes in Classical Hodgkin Lymphoma. Journal of Clinical Oncology, 2017, 35, 3722-3733.	1.6	48
84	E-scape: interactive visualization of single-cell phylogenetics and cancer evolution. Nature Methods, 2017, 14, 549-550.	19.0	46
85	TMEM30A loss-of-function mutations drive lymphomagenesis and confer therapeutically exploitable vulnerability in B-cell lymphoma. Nature Medicine, 2020, 26, 577-588.	30.7	46
86	Robust high-performance nanoliter-volume single-cell multiple displacement amplification on planar substrates. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, 8484-8489.	7.1	45
87	Integrated structural variation and point mutation signatures in cancer genomes using correlated topic models. PLoS Computational Biology, 2019, 15, e1006799.	3.2	44
88	The genomic landscape of epithelioid sarcoma cell lines and tumours. Journal of Pathology, 2016, 238, 63-73.	4.5	43
89	densityCut: an efficient and versatile topological approach for automatic clustering of biological data. Bioinformatics, 2016, 32, 2567-2576.	4.1	40
90	Comrad: detection of expressed rearrangements by integrated analysis of RNA-Seq and low coverage genome sequence data. Bioinformatics, 2011, 27, 1481-1488.	4.1	39

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91	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
92	Dhaka: variational autoencoder for unmasking tumor heterogeneity from single cell genomic data. Bioinformatics, 2021, 37, 1535-1543.	4.1	38
93	Cis-regulatory somatic mutations and gene-expression alteration in B-cell lymphomas. Genome Biology, 2015, 16, 84.	8.8	36
94	Single cell transcriptomes of normal endometrial derived organoids uncover novel cell type markers and cryptic differentiation of primary tumours. Journal of Pathology, 2020, 252, 201-214.	4.5	31
95	ReMixT: clone-specific genomic structure estimation in cancer. Genome Biology, 2017, 18, 140.	8.8	29
96	Pharmacological systems analysis defines EIF4A3 functions in cell-cycle and RNA stress granule formation. Communications Biology, 2019, 2, 165.	4.4	29
97	Chemogenomic profiling of breast cancer patient-derived xenografts reveals targetable vulnerabilities for difficult-to-treat tumors. Communications Biology, 2020, 3, 310.	4.4	28
98	Intratumoral heterogeneity in a minority of ovarian low-grade serous carcinomas. BMC Cancer, 2014, 14, 982.	2.6	27
99	Single-cell profiling reveals the importance of CXCL13/CXCR5 axis biology in lymphocyte-rich classic Hodgkin lymphoma. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	7.1	26
100	An RCOR1 lossâ€“associated gene expression signature identifies a prognostically significant DLBCL subgroup. Blood, 2015, 125, 959-966.	1.4	24
101	Fundamental immuneâ€“oncogenicity trade-offs define driver mutationÂfitness. Nature, 2022, 606, 172-179.	27.8	23
102	Computational methods for identification of recurrent copy number alteration patterns by array CGH. Cytogenetic and Genome Research, 2008, 123, 343-351.	1.1	20
103	Characterization of DLBCL with a PMBL gene expression signature. Blood, 2021, 138, 136-148.	1.4	19
104	Epiclomal: Probabilistic clustering of sparse single-cell DNA methylation data. PLoS Computational Biology, 2020, 16, e1008270.	3.2	18
105	Model-based clustering of array CGH data. Bioinformatics, 2009, 25, i30-i38.	4.1	17
106	Using Somatic Mutations to Guide Treatment Decisions. JAMA Oncology, 2015, 1, 275.	7.1	15
107	LINE-1 retrotransposon-mediated DNA transductions in endometriosis associated ovarian cancers. Gynecologic Oncology, 2017, 147, 642-647.	1.4	13
108	A Novel Prognostic Model Based on Tumor Microenvironment Biology in Relapse Biopsies Predicts Post-Autologous Stem Cell Transplantation Outcomes in Classical Hodgkin Lymphoma. Blood, 2016, 128, 1093-1093.	1.4	12

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109	Gene Expression Profiling of Microdissected Hodgkin Reed Sternberg Cells: Molecular Subtypes and Treatment Outcome Correlations.. Blood, 2009, 114, 268-268.	1.4	12
110	Tumor-associated antigen PRAME exhibits dualistic functions that are targetable in diffuse large B cell lymphoma. Journal of Clinical Investigation, 2022, 132, .	8.2	12
111	Observing Clonal Dynamics across Spatiotemporal Axes: A Prelude to Quantitative Fitness Models for Cancer. Cold Spring Harbor Perspectives in Medicine, 2018, 8, a029603.	6.2	9
112	Kronos: a workflow assembler for genome analytics and informatics. GigaScience, 2017, 6, 1-10.	6.4	8
113	Tumor-induced double positive T cells display distinct lineage commitment mechanisms and functions. Journal of Experimental Medicine, 2022, 219, .	8.5	8
114	Somatic mutation detection and classification through probabilistic integration of clonal population information. Communications Biology, 2019, 2, 44.	4.4	7
115	Semisupervised Training of a Brain MRI Tumor Detection Model Using Mined Annotations. Radiology, 2022, 303, 80-89.	7.3	7
116	Distinguishing Somatic and Germline Copy Number Events in Cancer Patient DNA Hybridized to Whole-Genome SNP Genotyping Arrays. Methods in Molecular Biology, 2013, 973, 355-372.	0.9	6
117	Enhancing knowledge discovery from cancer genomics data with Galaxy. GigaScience, 2017, 6, 1-13.	6.4	6
118	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. Clinical Cancer Research, 2021, 27, 2111-2118.	7.0	5
119	Targeted Sequencing Reveals Novel Gene Mutations Associated with Transformation and Early Progression in Follicular Lymphoma. Blood, 2016, 128, 2919-2919.	1.4	5
120	Mutation Discovery in Regions of Segmental Cancer Genome Amplifications with CoNAn-SNV: A Mixture Model for Next Generation Sequencing of Tumors. PLoS ONE, 2012, 7, e41551.	2.5	4
121	A robust hidden semi-Markov model with application to aCGH data processing. International Journal of Data Mining and Bioinformatics, 2013, 8, 427.	0.1	4
122	Engineered in-vitro cell line mixtures and robust evaluation of computational methods for clonal decomposition and longitudinal dynamics in cancer. Scientific Reports, 2017, 7, 13467.	3.3	4
123	Copy number signatures in ovarian cancer. Nature Genetics, 2018, 50, 1208-1209.	21.4	4
124	Tyrosine 641 of the EZH2 Oncogene Is Frequently Mutated in Follicular and Diffuse Large B-Cell Lymphomas of Germinal Center Origin.. Blood, 2009, 114, 139-139.	1.4	3
125	Genomic Rearrangements Involving Programmed Death Ligands Are Recurrent In Primary Mediastinal Large B-Cell Lymphoma. Blood, 2013, 122, 635-635.	1.4	3
126	Molecular and Genetic Characterization of MHC Deficiency Identifies EZH2 As a Therapeutic Target for Restoring MHC Expression in Diffuse Large B-Cell Lymphoma. Blood, 2018, 132, 1560-1560.	1.4	2

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127	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. Blood, 2008, 112, 477-477.	1.4	2
128	Robust hidden semi-Markov modeling of array CGH data. , 2010, , .		1
129	Somatic PRAME Deletions Are Associated with Decreased Immunogenicity, Apoptosis Resistance and Poor Outcomes in Diffuse Large B-Cell Lymphoma. Blood, 2018, 132, 667-667.	1.4	1
130	The Double-Hit Gene Expression Signature Defines a Clinically and Biologically Distinct Subgroup within GCB-DLBCL. Blood, 2018, 132, 921-921.	1.4	1
131	Genetic Alterations Detected by High-Resolution Array Comparative Genomic Hybridization in Microdissected HRS Cells Correlate with Treatment Outcome in Classical Hodgkin Lymphoma. Blood, 2008, 112, 522-522.	1.4	1
132	TNFRSF14 Is Mutated in a Subset of Follicular Lymphoma and Correlated with Inferior Prognosis.. Blood, 2009, 114, 1919-1919.	1.4	1
133	Protein Tyrosine Phosphatase Type-1 (PTPN1) Is Frequently Mutated In Primary Mediastinal B Cell Lymphoma and Hodgkin Lymphoma. Blood, 2013, 122, 242-242.	1.4	1
134	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
135	PRAME Expression Is Correlated with Treatment Outcome and Specific Features of the Tumor Microenvironment in Classical Hodgkin Lymphoma. Blood, 2019, 134, 1509-1509.	1.4	1
136	The Tumor Associated Antigen PRAME Exhibits Dualistic Functions That Are Targetable in Diffuse Large B-Cell Lymphoma. Blood, 2020, 136, 34-34.	1.4	1
137	Genome-Wide Expression Profiling Predicts Treatment Outcome in Classical Hodgkin Lymphoma. Blood, 2008, 112, 520-520.	1.4	0
138	CSF1R Expression of Hodgkin Reed Sternberg Cells Is Associated with the Number of Macrophages in the Tumor Microenvironment and Is Correlated with Treatment Outcome. Blood, 2011, 118, 427-427.	1.4	0
139	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. Blood, 2012, 120, 295-295.	1.4	0
140	Analysis of Relapse Biopsies in Classical Hodgkin Lymphoma Reveals Correlations with Outcome after Autologous Stem Cell Transplantation. Blood, 2014, 124, 136-136.	1.4	0
141	Divergent Modes of Tumor Evolution Underlie Histological Transformation and Early Progression of Follicular Lymphoma. Blood, 2016, 128, 1091-1091.	1.4	0
142	Single-Cell Profiling Reveals Clinically Relevant Evolutionary Trajectories and Alternate Biologies in Human Follicular Lymphoma. Blood, 2021, 138, 450-450.	1.4	0
143	Single Cell Profiling Reveals Unique CXCL13 Positive T Cell Subsets in the Tumor Microenvironment of Lymphocyte Rich Classic Hodgkin Lymphoma. Blood, 2020, 136, 32-33.	1.4	0
144	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. Blood, 2020, 136, 50-51.	1.4	0