

Robert Sebra

List of Publications by Year in descending order

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Version: 2024-02-01

129
papers

10,033
citations

66343

42
h-index

46799

89
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133
all docs

133
docs citations

133
times ranked

20688
citing authors

#	ARTICLE	IF	CITATIONS
1	Unannotated small RNA clusters associated with circulating extracellular vesicles detect early stage liver cancer. <i>Gut</i> , 2022, 71, 2069-2080.	12.1	24
2	Association of mutations in DNA polymerase epsilon with increased CD8+ cell infiltration and prolonged progression-free survival in patients with meningiomas. <i>Neurosurgical Focus</i> , 2022, 52, E7.	2.3	4
3	Critical assessment of DNA adenine methylation in eukaryotes using quantitative deconvolution. <i>Science</i> , 2022, 375, 515-522.	12.6	64
4	PPARdelta activation induces metabolic and contractile maturation of human pluripotent stem cell-derived cardiomyocytes. <i>Cell Stem Cell</i> , 2022, 29, 559-576.e7.	11.1	34
5	Robust clinical detection of SARS-CoV-2 variants by RT-PCR/MALDI-TOF multitarget approach. <i>Journal of Medical Virology</i> , 2022, 94, 1606-1616.	5.0	9
6	RT-PCR and Matrix-Assisted Laser Desorption-Ionization Time-of-Flight Mass Spectrometry Diagnostic Target Performance Reflects Circulating Severe Acute Respiratory Syndrome Coronavirus 2 Variant Diversity in New York City. <i>Journal of Molecular Diagnostics</i> , 2022, , .	2.8	3
7	Dissecting mechanisms of chamber-specific cardiac differentiation and its perturbation following retinoic acid exposure. <i>Development (Cambridge)</i> , 2022, 149, .	2.5	5
8	Real-Time Investigation of a Large Nosocomial Influenza A Outbreak Informed by Genomic Epidemiology. <i>Clinical Infectious Diseases</i> , 2021, 73, e4375-e4383.	5.8	13
9	Peritumoral edema correlates with mutational burden in meningiomas. <i>Neuroradiology</i> , 2021, 63, 73-80.	2.2	13
10	NF2 mutation status and tumor mutational burden correlate with immune cell infiltration in meningiomas. <i>Cancer Immunology, Immunotherapy</i> , 2021, 70, 169-176.	4.2	12
11	<i>USP8</i> and <i>TP53</i> Drivers are Associated with CNV in a Corticotroph Adenoma Cohort Enriched for Aggressive Tumors. <i>Journal of Clinical Endocrinology and Metabolism</i> , 2021, 106, 826-842.	3.6	34
12	The Human ApoE4 Variant Reduces Functional Recovery and Neuronal Sprouting After Incomplete Spinal Cord Injury in Male Mice. <i>Frontiers in Cellular Neuroscience</i> , 2021, 15, 626192.	3.7	7
13	A <i>Drosophila</i> platform identifies a novel, personalized therapy for a patient with adenoid cystic carcinoma. <i>IScience</i> , 2021, 24, 102212.	4.1	23
14	SWI/SNF chromatin remodeling complex alterations in meningioma. <i>Journal of Cancer Research and Clinical Oncology</i> , 2021, 147, 3431-3440.	2.5	15
15	Long read, isoform aware sequencing of mouse nucleus accumbens after chronic cocaine treatment. <i>Scientific Reports</i> , 2021, 11, 6729.	3.3	3
16	Rare Germline Pathogenic Variants Identified by Multigene Panel Testing and the Risk of Aggressive Prostate Cancer. <i>Cancers</i> , 2021, 13, 1495.	3.7	12
17	Evaluating the analytical validity of circulating tumor DNA sequencing assays for precision oncology. <i>Nature Biotechnology</i> , 2021, 39, 1115-1128.	17.5	126
18	Pathophysiology of SARS-CoV-2: the Mount Sinai COVID-19 autopsy experience. <i>Modern Pathology</i> , 2021, 34, 1456-1467.	5.5	184

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19	Niche and local geography shape the pangenome of wastewater- and livestock-associated Enterobacteriaceae. <i>Science Advances</i> , 2021, 7, .	10.3	47
20	TOP1 inhibition therapy protects against SARS-CoV-2-induced lethal inflammation. <i>Cell</i> , 2021, 184, 2618-2632.e17.	28.9	80
21	Effect of APOE and a polygenic risk score on incident dementia and cognitive decline in a healthy older population. <i>Aging Cell</i> , 2021, 20, e13384.	6.7	16
22	Molecular evidence of SARS-CoV-2 in New York before the first pandemic wave. <i>Nature Communications</i> , 2021, 12, 3463.	12.8	18
23	Genetic variants associated with inherited cardiovascular disorders among 13,131 asymptomatic older adults of European descent. <i>Npj Genomic Medicine</i> , 2021, 6, 51.	3.8	11
24	Genomic Risk Prediction for Breast Cancer in Older Women. <i>Cancers</i> , 2021, 13, 3533.	3.7	6
25	Protective lipid-lowering variants in healthy older individuals without coronary heart disease. <i>Open Heart</i> , 2021, 8, e001710.	2.3	1
26	Downregulation of exhausted cytotoxic T cells in gene expression networks of multisystem inflammatory syndrome in children. <i>Nature Communications</i> , 2021, 12, 4854.	12.8	42
27	Tissue-based SARS-CoV-2 detection in fatal COVID-19 infections: Sustained direct viral-induced damage is not necessary to drive disease progression. <i>Human Pathology</i> , 2021, 114, 110-119.	2.0	32
28	Single-cell RNA sequencing atlas of bovine caudal intervertebral discs: Discovery of heterogeneous cell populations with distinct roles in homeostasis. <i>FASEB Journal</i> , 2021, 35, e21919.	0.5	28
29	Molecular Profiling of Coronavirus Disease 2019 (COVID-19) Autopsies Uncovers Novel Disease Mechanisms. <i>American Journal of Pathology</i> , 2021, 191, 2064-2071.	3.8	14
30	A library of induced pluripotent stem cells from clinically well-characterized, diverse healthy human individuals. <i>Stem Cell Reports</i> , 2021, 16, 3036-3049.	4.8	14
31	621...NKG2A and HLA-E define a novel mechanism of resistance to immunotherapy with M. bovis BCG in non-muscle-invasive bladder cancer patients. , 2021, 9, A651-A651.		0
32	Extracellular histones, a new class of inhibitory molecules of CNS axonal regeneration. <i>Brain Communications</i> , 2021, 3, fcab271.	3.3	8
33	EPCO-11. SINGLE-NUCLEI TRANSCRIPTOMICS RELATES GLIOBLASTOMA INFILTRATION TO DISTINCT GLIAL PROGENITOR STATES. <i>Neuro-Oncology</i> , 2021, 23, vi3-vi4.	1.2	0
34	314...NKG2A and HLA-E define a novel alternative immune checkpoint axis in bladder cancer. , 2021, 9, A338-A338.		1
35	Single-Cell Profiling Reveals Contribution of Tumor Extrinsic and Intrinsic Factors to BCMA-Targeted CAR-T Cell Efficacy in Multiple Myeloma. <i>Blood</i> , 2021, 138, 326-326.	1.4	5
36	Population-based estimates of breast cancer risk for carriers of pathogenic variants identified by gene-panel testing. <i>Npj Breast Cancer</i> , 2021, 7, 153.	5.2	10

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37	Tumoral and immune heterogeneity in an anti-PD-1-responsive glioblastoma: a case study. <i>Journal of Physical Education and Sports Management</i> , 2020, 6, a004762.	1.2	8
38	Epigenomic characterization of <i>Clostridioides difficile</i> finds a conserved DNA methyltransferase that mediates sporulation and pathogenesis. <i>Nature Microbiology</i> , 2020, 5, 166-180.	13.3	75
39	Negative feedback control of neuronal activity by microglia. <i>Nature</i> , 2020, 586, 417-423.	27.8	520
40	COVID-19: Staging of a New Disease. <i>Cancer Cell</i> , 2020, 38, 594-597.	16.8	48
41	A Novel Framework for Characterizing Genomic Haplotype Diversity in the Human Immunoglobulin Heavy Chain Locus. <i>Frontiers in Immunology</i> , 2020, 11, 2136.	4.8	54
42	Application of Single-Cell Sequencing to Immunotherapy. <i>Urologic Clinics of North America</i> , 2020, 47, 475-485.	1.8	5
43	Integrated Transcriptome and Network Analysis Reveals Spatiotemporal Dynamics of Calvarial Suturogenesis. <i>Cell Reports</i> , 2020, 32, 107871.	6.4	42
44	PathoSPOT genomic epidemiology reveals under-the-radar nosocomial outbreaks. <i>Genome Medicine</i> , 2020, 12, 96.	8.2	13
45	Sampling the host response to SARS-CoV-2 in hospitals under siege. <i>Nature Medicine</i> , 2020, 26, 1157-1158.	30.7	27
46	Genomic Epidemiology of Complex, Multispecies, Plasmid-Borne <i>bla</i> KPC in <i>Enterobacteriales</i> in the United Kingdom from 2009 to 2014. <i>Antimicrobial Agents and Chemotherapy</i> , 2020, 64, .	3.2	26
47	ORF Capture-Seq as a versatile method for targeted identification of full-length isoforms. <i>Nature Communications</i> , 2020, 11, 2326.	12.8	19
48	Introductions and early spread of SARS-CoV-2 in the New York City area. <i>Science</i> , 2020, 369, 297-301.	12.6	356
49	Familial Hypercholesterolemia in a Healthy Elderly Population. <i>Circulation Genomic and Precision Medicine</i> , 2020, 13, e002938.	3.6	8
50	Epigenetic preconditioning with decitabine sensitizes glioblastoma to temozolomide via induction of MLH1. <i>Journal of Neuro-Oncology</i> , 2020, 147, 557-566.	2.9	12
51	Medically actionable pathogenic variants in a population of 13,131 healthy elderly individuals. <i>Genetics in Medicine</i> , 2020, 22, 1883-1886.	2.4	20
52	Genetic associations with clozapine-induced myocarditis in patients with schizophrenia. <i>Translational Psychiatry</i> , 2020, 10, 37.	4.8	24
53	Intratumoral heterogeneity and clonal evolution in liver cancer. <i>Nature Communications</i> , 2020, 11, 291.	12.8	230
54	Cell-to-Cell Variation in Defective Virus Expression and Effects on Host Responses during Influenza Virus Infection. <i>MBio</i> , 2020, 11, .	4.1	38

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55	Prevalence and disease predisposition of p.A91V perforin in an aged population of European ancestry. <i>Blood</i> , 2020, 135, 582-584.	1.4	6
56	STK11 mutation status is associated with decreased survival in meningiomas. <i>Neurological Sciences</i> , 2020, 41, 2585-2589.	1.9	9
57	Limited Mitochondrial Activity Coupled With Strong Expression of CD34, CD90 and EPCR Determines the Functional Fitness of ex vivo Expanded Human Hematopoietic Stem Cells. <i>Frontiers in Cell and Developmental Biology</i> , 2020, 8, 592348.	3.7	8
58	EPCO-20. RELATING GLIOBLASTOMA HETEROGENEITY TO HUMAN FETAL GLIAL DEVELOPMENT THROUGH HIGH RESOLUTION SINGLE NUCLEI TRANSCRIPTOMICS. <i>Neuro-Oncology</i> , 2020, 22, ii73-ii73.	1.2	0
59	PATH-01. BRAIN METASTASES FROM ENDOMETRIAL CARCINOMA: TUMOR GENETIC ALTERATIONS IN A CASE SERIES AND META-ANALYSIS. <i>Neuro-Oncology</i> , 2020, 22, ii163-ii164.	1.2	0
60	Double <i>PIK3CA</i> mutations in cis increase oncogenicity and sensitivity to PI3K \pm inhibitors. <i>Science</i> , 2019, 366, 714-723.	12.6	185
61	Blurred Molecular Epidemiological Lines Between the Two Dominant Methicillin-Resistant <i>Staphylococcus aureus</i> Clones. <i>Open Forum Infectious Diseases</i> , 2019, 6, ofz302.	0.9	11
62	Genetic resilience to Alzheimer's disease in <i>APOE</i> ϵ 4 homozygotes: A systematic review. <i>Alzheimer's and Dementia</i> , 2019, 15, 1612-1623.	0.8	21
63	High-coverage, long-read sequencing of Han Chinese trio reference samples. <i>Scientific Data</i> , 2019, 6, 91.	5.3	13
64	A personalized platform identifies trametinib plus zoledronate for a patient with KRAS-mutant metastatic colorectal cancer. <i>Science Advances</i> , 2019, 5, eaav6528.	10.3	74
65	Mce3R Stress-Resistance Pathway Is Vulnerable to Small-Molecule Targeting That Improves Tuberculosis Drug Activities. <i>ACS Infectious Diseases</i> , 2019, 5, 1239-1251.	3.8	12
66	<i>Klebsiella quasipneumoniae</i> Provides a Window into Carbapenemase Gene Transfer, Plasmid Rearrangements, and Patient Interactions with the Hospital Environment. <i>Antimicrobial Agents and Chemotherapy</i> , 2019, 63, .	3.2	44
67	Single-Molecule Real-Time (SMRT) Full-Length RNA-Sequencing Reveals Novel and Distinct mRNA Isoforms in Human Bone Marrow Cell Subpopulations. <i>Genes</i> , 2019, 10, 253.	2.4	16
68	Don't overlook the little guy: An evaluation of the frequency of small plasmids co-conjugating with larger carbapenemase gene containing plasmids. <i>Plasmid</i> , 2019, 103, 1-8.	1.4	36
69	The genome of a subterrestrial nematode reveals adaptations to heat. <i>Nature Communications</i> , 2019, 10, 5268.	12.8	22
70	Neuronal impact of patient-specific aberrant NRXN1 \pm splicing. <i>Nature Genetics</i> , 2019, 51, 1679-1690.	21.4	91
71	A Complete Genome Screening Program of Clinical Methicillin-Resistant <i>Staphylococcus aureus</i> Isolates Identifies the Origin and Progression of a Neonatal Intensive Care Unit Outbreak. <i>Journal of Clinical Microbiology</i> , 2019, 57, .	3.9	16
72	A physical and genetic map of <i>Cannabis sativa</i> identifies extensive rearrangements at the <i>THC/CBD</i> acid synthase loci. <i>Genome Research</i> , 2019, 29, 146-156.	5.5	160

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73	Sequential evolution of virulence and resistance during clonal spread of community-acquired methicillin-resistant <i>Staphylococcus aureus</i> . Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 1745-1754.	7.1	59
74	Comparative genomic analysis of driver mutations in matched primary and recurrent meningiomas. Oncotarget, 2019, 10, 3506-3517.	1.8	15
75	Single-cell profiling of peanut-responsive T cells in patients with peanut allergy reveals heterogeneous effector TH2 subsets. Journal of Allergy and Clinical Immunology, 2018, 141, 2107-2120.	2.9	88
76	Genetic Basis of Emerging Vancomycin, Linezolid, and Daptomycin Heteroresistance in a Case of Persistent Enterococcus faecium Bacteremia. Antimicrobial Agents and Chemotherapy, 2018, 62, .	3.2	21
77	Cytogenomic identification and long-read single molecule real-time (SMRT) sequencing of a Bardet-Biedl Syndrome 9 (BBS9) deletion. Npj Genomic Medicine, 2018, 3, 3.	3.8	97
78	Analysis of the Aedes albopictus C6/36 genome provides insight into cell line utility for viral propagation. GigaScience, 2018, 7, 1-13.	6.4	51
79	HIV-1 Infection of Primary CD4 ⁺ T Cells Regulates the Expression of Specific Human Endogenous Retrovirus HERV-K (HML-2) Elements. Journal of Virology, 2018, 92, .	3.4	34
80	Metagenomic binning and association of plasmids with bacterial host genomes using DNA methylation. Nature Biotechnology, 2018, 36, 61-69.	17.5	116
81	IMMU-60. MAPPING TUMORAL AND IMMUNE HETEROGENEITY IN PD-1 RESPONSIVE GLIOBLASTOMA. Neuro-Oncology, 2018, 20, vi135-vi135.	1.2	0
82	Detection of endometrial precancer by a targeted gynecologic cancer liquid biopsy. Journal of Physical Education and Sports Management, 2018, 4, a003269.	1.2	11
83	Treatment-associated TP53 DNA-binding domain missense mutations in the pathogenesis of secondary gliosarcoma. Oncotarget, 2018, 9, 2603-2621.	1.8	20
84	Influenza virus infection causes global RNAPII termination defects. Nature Structural and Molecular Biology, 2018, 25, 885-893.	8.2	48
85	Ex vivo human HSC expansion requires coordination of cellular reprogramming with mitochondrial remodeling and p53 activation. Blood Advances, 2018, 2, 2766-2779.	5.2	48
86	Mapping and characterizing N6-methyladenine in eukaryotic genomes using single-molecule real-time sequencing. Genome Research, 2018, 28, 1067-1078.	5.5	80
87	Genome Plasticity of agr ⁻ -Defective Staphylococcus aureus during Clinical Infection. Infection and Immunity, 2018, 86, .	2.2	50
88	Emergence and Evolution of Multidrug-Resistant Klebsiella pneumoniae with both bla _{KPC} and bla _{CTX-M} Integrated in the Chromosome. Antimicrobial Agents and Chemotherapy, 2017, 61, .	3.2	66
89	Prospective Isolation and Comparison of Human Germinal Matrix and Glioblastoma EGFR ⁺ Populations with Stem Cell Properties. Stem Cell Reports, 2017, 8, 1421-1429.	4.8	16
90	Identification of a novel RASD1 somatic mutation in a USP8-mutated corticotroph adenoma. Journal of Physical Education and Sports Management, 2017, 3, a001602.	1.2	8

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91	Chromosomal Integration of the <i>Klebsiella pneumoniae</i> Carbapenemase Gene, <i>bla</i> _{KPC} , in <i>Klebsiella</i> Species Is Elusive but Not Rare. <i>Antimicrobial Agents and Chemotherapy</i> , 2017, 61, .	3.2	46
92	DNA sequencing at ultra-high fidelity. <i>Nature Biotechnology</i> , 2017, 35, 1143-1144.	17.5	0
93	Evolution and Transmission of Carbapenem-Resistant <i>Klebsiella pneumoniae</i> Expressing the <i>bla</i> OXA-232 Gene During an Institutional Outbreak Associated With Endoscopic Retrograde Cholangiopancreatography. <i>Clinical Infectious Diseases</i> , 2017, 64, 894-901.	5.8	39
94	Gaining comprehensive biological insight into the transcriptome by performing a broad-spectrum RNA-seq analysis. <i>Nature Communications</i> , 2017, 8, 59.	12.8	225
95	Genome-Wide Biases in the Rate and Molecular Spectrum of Spontaneous Mutations in <i>Vibrio cholerae</i> and <i>Vibrio fischeri</i> . <i>Molecular Biology and Evolution</i> , 2017, 34, 93-109.	8.9	81
96	Inhibition of the Nuclear Export Receptor XPO1 as a Therapeutic Target for Platinum-Resistant Ovarian Cancer. <i>Clinical Cancer Research</i> , 2017, 23, 1552-1563.	7.0	65
97	A next generation sequencing based approach to identify extracellular vesicle mediated mRNA transfers between cells. <i>BMC Genomics</i> , 2017, 18, 987.	2.8	19
98	Genomic confirmation of vancomycin-resistant <i>Enterococcus</i> transmission from deceased donor to liver transplant recipient. <i>PLoS ONE</i> , 2017, 12, e0170449.	2.5	16
99	Using single-cell multiple omics approaches to resolve tumor heterogeneity. <i>Clinical and Translational Medicine</i> , 2017, 6, 46.	4.0	73
100	Resistance to Ceftazidime-Avibactam Is Due to Transposition of KPC in a Porin-Deficient Strain of <i>Klebsiella pneumoniae</i> with Increased Efflux Activity. <i>Antimicrobial Agents and Chemotherapy</i> , 2017, 61, .	3.2	121
101	Genomic profiling reveals mutational landscape in parathyroid carcinomas. <i>JCI Insight</i> , 2017, 2, e92061.	5.0	84
102	Longitudinal Whole-Genome Analysis Identifies Variants Associated with Vancomycin and Linezolid Resistance Changes in <i>Enterococcus faecium</i> in Response to Treatment. <i>Open Forum Infectious Diseases</i> , 2016, 3, .	0.9	2
103	Epigenetic Switch Driven by DNA Inversions Dictates Phase Variation in <i>Streptococcus pneumoniae</i> . <i>PLoS Pathogens</i> , 2016, 12, e1005762.	4.7	149
104	Continuous Surveillance by Whole-Genome Sequencing to Identify and Manage Methicillin-Resistant <i>Staphylococcus aureus</i> Outbreaks. <i>Open Forum Infectious Diseases</i> , 2016, 3, .	0.9	2
105	Genetic Variation and Altered Virulence Associated With Loss of Agr Quorum-Sensing Functionality in Patients With <i>Staphylococcus aureus</i> Bacteremia. <i>Open Forum Infectious Diseases</i> , 2016, 3, .	0.9	0
106	Epigenomic Landscape of <i>Clostridium difficile</i> : Largely Neglected Complexity and Opportunity Learned from 45 Hospital Isolates. <i>Open Forum Infectious Diseases</i> , 2016, 3, .	0.9	0
107	Comparative Genomics and Assessment of Strain Diversity, Pathogenicity and Transmission of <i>Clostridium difficile</i> Isolates From a Hospital Setting. <i>Open Forum Infectious Diseases</i> , 2016, 3, .	0.9	0
108	Long-Read Single Molecule Real-Time Full Gene Sequencing of Cytochrome P450-2D6. <i>Human Mutation</i> , 2016, 37, 315-323.	2.5	86

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109	Use of Multiple Sequencing Technologies To Produce a High-Quality Genome of the Fungus <i>Pseudogymnoascus destructans</i> , the Causative Agent of Bat White-Nose Syndrome. <i>Genome Announcements</i> , 2016, 4, .	0.8	24
110	Complete Sequencing of Plasmids Containing <i>bla</i> _{OXA-163} and <i>bla</i> _{OXA-48} in <i>Escherichia coli</i> Sequence Type 131. <i>Antimicrobial Agents and Chemotherapy</i> , 2016, 60, 6948-6951.	3.2	19
111	Extensive sequencing of seven human genomes to characterize benchmark reference materials. <i>Scientific Data</i> , 2016, 3, 160025.	5.3	575
112	Nested Russian Doll-Like Genetic Mobility Drives Rapid Dissemination of the Carbapenem Resistance Gene <i>bla</i> _{KPC} . <i>Antimicrobial Agents and Chemotherapy</i> , 2016, 60, 3767-3778.	3.2	255
113	Development and clinical application of an integrative genomic approach to personalized cancer therapy. <i>Genome Medicine</i> , 2016, 8, 62.	8.2	71
114	Evolutionary History of the Global Emergence of the <i>Escherichia coli</i> Epidemic Clone ST131. <i>MBio</i> , 2016, 7, e02162.	4.1	289
115	Complete Genome Sequence of KPC-Producing <i>Klebsiella pneumoniae</i> Strain CAV1193. <i>Genome Announcements</i> , 2016, 4, .	0.8	20
116	Quantifying influenza virus diversity and transmission in humans. <i>Nature Genetics</i> , 2016, 48, 195-200.	21.4	182
117	Genomic Analysis of Uterine Lavage Fluid Detects Early Endometrial Cancers and Reveals a Prevalent Landscape of Driver Mutations in Women without Histopathologic Evidence of Cancer: A Prospective Cross-Sectional Study. <i>PLoS Medicine</i> , 2016, 13, e1002206.	8.4	83
118	The Complete Genome Sequence of the Emerging Pathogen <i>Mycobacterium haemophilum</i> Explains Its Unique Culture Requirements. <i>MBio</i> , 2015, 6, e01313-15.	4.1	30
119	Personalized Circulating Tumor DNA Biomarkers Dynamically Predict Treatment Response and Survival In Gynecologic Cancers. <i>PLoS ONE</i> , 2015, 10, e0145754.	2.5	129
120	Characterizing and Overriding the Structural Mechanism of the Quizartinib-Resistant FLT3 "Gatekeeper" F691L Mutation with PLX3397. <i>Cancer Discovery</i> , 2015, 5, 668-679.	9.4	145
121	Intrahost Dynamics of Antiviral Resistance in Influenza A Virus Reflect Complex Patterns of Segment Linkage, Reassortment, and Natural Selection. <i>MBio</i> , 2015, 6, .	4.1	58
122	<i>Klebsiella pneumoniae</i> Carbapenemase (KPC)-Producing <i>K. pneumoniae</i> at a Single Institution: Insights into Endemicity from Whole-Genome Sequencing. <i>Antimicrobial Agents and Chemotherapy</i> , 2015, 59, 1656-1663.	3.2	140
123	Single molecule-level detection and long read-based phasing of epigenetic variations in bacterial methylomes. <i>Nature Communications</i> , 2015, 6, 7438.	12.8	82
124	Assembly and diploid architecture of an individual human genome via single-molecule technologies. <i>Nature Methods</i> , 2015, 12, 780-786.	19.0	465
125	Quantitative and multiplexed DNA methylation analysis using long-read single-molecule real-time bisulfite sequencing (SMRT-BS). <i>BMC Genomics</i> , 2015, 16, 350.	2.8	68
126	An integrated map of structural variation in 2,504 human genomes. <i>Nature</i> , 2015, 526, 75-81.	27.8	1,994

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127	Whole-Genome Sequencing Identifies Emergence of a Quinolone Resistance Mutation in a Case of <i>Stenotrophomonas maltophilia</i> Bacteremia. <i>Antimicrobial Agents and Chemotherapy</i> , 2015, 59, 7117-7120.	3.2	24
128	The PsychENCODE project. <i>Nature Neuroscience</i> , 2015, 18, 1707-1712.	14.8	371
129	Reâ€replication Origins in <i>Sciara</i> DNA Puffs Revealed by New and Old Genomic Technologies including Nanopore Sequencing. <i>FASEB Journal</i> , 2015, 29, 561.9.	0.5	0