Steven G. Rozen

List of Publications by Year
in descending order

125 papers	43,822 citations	18482 62 h-index	16650 123 g-index
139 all docs	139 docs citations	139 times ranked	64257 citing authors

#	Article	IF	Citations
1	Primer3 on the WWW for General Users and for Biologist Programmers. , 2000, 132, 365-386.		9,865
2	Primer3â€"new capabilities and interfaces. Nucleic Acids Research, 2012, 40, e115-e115.	14.5	7,501
3	Primer-BLAST: A tool to design target-specific primers for polymerase chain reaction. BMC Bioinformatics, 2012, 13, 134.	2.6	4,446
4	The repertoire of mutational signatures in human cancer. Nature, 2020, 578, 94-101.	27.8	2,104
5	Large-Scale Identification, Mapping, and Genotyping of Single-Nucleotide Polymorphisms in the Human Genome. Science, 1998, 280, 1077-1082.	12.6	1,993
6	The male-specific region of the human Y chromosome is a mosaic of discrete sequence classes. Nature, 2003, 423, 825-837.	27.8	1,887
7	Diverse spermatogenic defects in humans caused by Y chromosome deletions encompassing a novel RNAâ€"binding protein gene. Nature Genetics, 1995, 10, 383-393.	21.4	1,183
8	Whole-Genome and Epigenomic Landscapes of Etiologically Distinct Subtypes of Cholangiocarcinoma. Cancer Discovery, 2017, 7, 1116-1135.	9.4	637
9	The AZFc region of the Y chromosome features massive palindromes and uniform recurrent deletions in infertile men. Nature Genetics, 2001, 29, 279-286.	21.4	617
10	A comprehensive survey of genomic alterations in gastric cancer reveals systematic patterns of molecular exclusivity and co-occurrence among distinct therapeutic targets. Gut, 2012, 61, 673-684.	12.1	562
11	Exome sequencing of gastric adenocarcinoma identifies recurrent somatic mutations in cell adhesion and chromatin remodeling genes. Nature Genetics, 2012, 44, 570-574.	21.4	560
12	Mammalian Y chromosomes retain widely expressed dosage-sensitive regulators. Nature, 2014, 508, 494-499.	27.8	546
13	Abundant gene conversion between arms of palindromes in human and ape Y chromosomes. Nature, 2003, 423, 873-876.	27.8	540
14	The DAZ gene cluster on the human Y chromosome arose from an autosomal gene that was transposed, repeatedly amplified and pruned. Nature Genetics, 1996, 14, 292-299.	21.4	427
15	Exome sequencing identifies distinct mutational patterns in liver flukeâ€"related and non-infection-related bile duct cancers. Nature Genetics, 2013, 45, 1474-1478.	21.4	426
16	Exome sequencing of liver flukeâ€"associated cholangiocarcinoma. Nature Genetics, 2012, 44, 690-693.	21.4	412
17	Recombination between Palindromes P5 and P1 on the Human Y Chromosome Causes Massive Deletions and Spermatogenic Failure. American Journal of Human Genetics, 2002, 71, 906-922.	6.2	410
18	Polymorphism for a 1.6-Mb deletion of the human Y chromosome persists through balance between recurrent mutation and haploid selection. Nature Genetics, 2003, 35, 247-251.	21.4	399

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19	Chimpanzee and human Y chromosomes are remarkably divergent in structure and gene content. Nature, 2010, 463, 536-539.	27.8	381
20	Identification of Molecular Subtypes of Gastric Cancer With Different Responses to PI3-Kinase Inhibitors and 5-Fluorouracil. Gastroenterology, 2013, 145, 554-565.	1.3	381
21	Metabolomics in Early Alzheimer's Disease: Identification of Altered Plasma Sphingolipidome Using Shotgun Lipidomics. PLoS ONE, 2011, 6, e21643.	2.5	367
22	Integrative Analysis of Head and Neck Cancer Identifies Two Biologically Distinct HPV and Three Non-HPV Subtypes. Clinical Cancer Research, 2015, 21, 870-881.	7.0	303
23	Sequencing the Mouse Y Chromosome Reveals Convergent Gene Acquisition and Amplification on Both Sex Chromosomes. Cell, 2014, 159, 800-813.	28.9	291
24	Aristolochic acids and their derivatives are widely implicated in liver cancers in Taiwan and throughout Asia. Science Translational Medicine, 2017, 9, .	12.4	272
25	Strict evolutionary conservation followed rapid gene loss on human and rhesus Y chromosomes. Nature, 2012, 483, 82-86.	27.8	245
26	A physical map of the human Y chromosome. Nature, 2001, 409, 943-945.	27.8	239
27	High mutation rates have driven extensive structural polymorphism among human Y chromosomes. Nature Genetics, 2006, 38, 463-467.	21.4	237
28	Janus Kinase 3â€“Activating Mutations Identified in Natural Killer/T-cell Lymphoma. Cancer Discovery, 2012, 2, 591-597.	9.4	236
29	Genome-Wide Mutational Signatures of Aristolochic Acid and Its Application as a Screening Tool. Science Translational Medicine, 2013, 5, 197ra101.	12.4	233
30	Nucleus-Translocated ACSS2 Promotes Gene Transcription for Lysosomal Biogenesis and Autophagy. Molecular Cell, 2017, 66, 684-697.e9.	9.7	227
31	Convergent evolution of chicken Z and human X chromosomes by expansion and gene acquisition. Nature, 2010, 466, 612-616.	27.8	210
32	A family of human Y chromosomes has dispersed throughout northern Eurasia despite a 1.8-Mb deletion in the azoospermia factor c region. Genomics, 2004, 83, 1046-1052.	2.9	196
33	Angiopoietin receptor TEK mutations underlie primary congenital glaucoma with variable expressivity. Journal of Clinical Investigation, 2016, 126, 2575-2587.	8.2	175
34	Genomic and Epigenomic Profiling of High-Risk Intestinal Metaplasia Reveals Molecular Determinants of Progression to Gastric Cancer. Cancer Cell, 2018, 33, 137-150.e5.	16.8	175
35	Exome sequencing identifies highly recurrent MED12 somatic mutations in breast fibroadenoma. Nature Genetics, 2014, 46, 877-880.	21.4	172
36	Genomic landscapes of breast fibroepithelial tumors. Nature Genetics, 2015, 47, 1341-1345.	21.4	167

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37	Loss of tumor suppressor KDM6A amplifies PRC2-regulated transcriptional repression in bladder cancer and can be targeted through inhibition of EZH2. Science Translational Medicine, 2017, 9, .	12.4	165
38	Methylation Subtypes and Large-Scale Epigenetic Alterations in Gastric Cancer. Science Translational Medicine, 2012, 4, 156ra140.	12.4	163
39	SigProfilerMatrixGenerator: a tool for visualizing and exploring patterns of small mutational events. BMC Genomics, 2019, 20, 685.	2.8	162
40	Metabolomic analysis and signatures in motor neuron disease. Metabolomics, 2005, 1, 101-108.	3.0	152
41	Conservation of Y-linked genes during human evolution revealed by comparative sequencing in chimpanzee. Nature, 2005, 437, 100-103.	27.8	151
42	The draft genome of tropical fruit durian (Durio zibethinus). Nature Genetics, 2017, 49, 1633-1641.	21.4	150
43	Regulatory crosstalk between lineage-survival oncogenesKLF5, GATA4andGATA6cooperatively promotes gastric cancer development. Gut, 2015, 64, 707-719.	12.1	148
44	<scp>TEX</scp> 11 is mutated in infertile men with azoospermia and regulates genomeâ€wide recombination rates in mouse. EMBO Molecular Medicine, 2015, 7, 1198-1210.	6.9	145
45	Metabolomic changes in autopsyâ€confirmed Alzheimer's disease. Alzheimer's and Dementia, 2011, 7, 309-317.	0.8	132
46	ADAR-Mediated RNA Editing Predicts Progression and Prognosis of Gastric Cancer. Gastroenterology, 2016, 151, 637-650.e10.	1.3	127
47	In-depth characterization of the cisplatin mutational signature in human cell lines and in esophageal and liver tumors. Genome Research, 2018, 28, 654-665.	5.5	126
48	Epigenomic profiling of primary gastric adenocarcinoma reveals super-enhancer heterogeneity. Nature Communications, 2016, 7, 12983.	12.8	123
49	AZFc Deletions and Spermatogenic Failure: A Population-Based Survey of 20,000 Y Chromosomes. American Journal of Human Genetics, 2012, 91, 890-896.	6.2	113
50	MSIseq: Software for Assessing Microsatellite Instability from Catalogs of Somatic Mutations. Scientific Reports, 2015, 5, 13321.	3.3	113
51	VHL Deficiency Drives Enhancer Activation of Oncogenes in Clear Cell Renal Cell Carcinoma. Cancer Discovery, 2017, 7, 1284-1305.	9.4	111
52	Genomics and Genetics of Human and Primate Y Chromosomes. Annual Review of Genomics and Human Genetics, 2012, 13, 83-108.	6.2	90
53	Genome-scale mutational signatures of aflatoxin in cells, mice, and human tumors. Genome Research, 2017, 27, 1475-1486.	5.5	90
54	Mutation signatures implicate aristolochic acid in bladder cancer development. Genome Medicine, 2015, 7, 38.	8.2	87

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55	Whole-Exome Sequencing Studies of Parathyroid Carcinomas Reveal NovelPRUNE2Mutations, Distinctive Mutational Spectra Related to APOBEC-Catalyzed DNA Mutagenesis and Mutational Enrichment in Kinases Associated With Cell Migration and Invasion. Journal of Clinical Endocrinology and Metabolism, 2015, 100, E360-E364.	3.6	86
56	Lipidomics identifies a requirement for peroxisomal function during influenza virus replication. Journal of Lipid Research, 2014, 55, 1357-1365.	4.2	84
57	Mutation signatures of carcinogen exposure: genome-wide detection and new opportunities for cancer prevention. Genome Medicine, 2014, 6, 24.	8.2	75
58	Genetic and Structural Variation in the Gastric Cancer Kinome Revealed through Targeted Deep Sequencing. Cancer Research, 2011, 71, 29-39.	0.9	74
59	Mutational landscapes of tongue carcinoma reveal recurrent mutations in genes of therapeutic and prognostic relevance. Genome Medicine, 2015, 7, 98.	8.2	74
60	Nanoscale chromatin profiling of gastric adenocarcinoma reveals cancer-associated cryptic promoters and somatically acquired regulatory elements. Nature Communications, 2014, 5, 4361.	12.8	72
61	Alterations in tryptophan and purine metabolism in cocaine addiction: a metabolomic study. Psychopharmacology, 2009, 206, 479-489.	3.1	70
62	Host Cell Transcriptome Profile during Wild-Type and Attenuated Dengue Virus Infection. PLoS Neglected Tropical Diseases, 2013, 7, e2107.	3.0	68
63	MiRNA-128 regulates the proliferation and neurogenesis of neural precursors by targeting PCM1 in the developing cortex. ELife, 2016, 5, .	6.0	67
64	Quantitative Chromatographic Estimation of Î±-Amino-Acids. Nature, 1948, 161, 763-763.	27.8	66
65	CYP1B1, MYOC, and LTBP2 Mutations in Primary Congenital Glaucoma Patients in the United States. American Journal of Ophthalmology, 2013, 155, 508-517.e5.	3.3	66
66	TP53 Genomic Status Regulates Sensitivity of Gastric Cancer Cells to the Histone Methylation Inhibitor 3-Deazaneplanocin A (DZNep). Clinical Cancer Research, 2012, 18, 4201-4212.	7.0	65
67	Individualised multiplexed circulating tumour DNA assays for monitoring of tumour presence in patients after colorectal cancer surgery. Scientific Reports, 2017, 7, 40737.	3.3	62
68	Wnts synergize to activate Î²-catenin signaling. Journal of Cell Science, 2017, 130, 1532-1544.	2.0	58
69	Experimental and pan-cancer genome analyses reveal widespread contribution of acrylamide exposure to carcinogenesis in humans. Genome Research, 2019, 29, 521-531.	5.5	57
70	Beyond fitness tracking: The use of consumer-grade wearable data from normal volunteers in cardiovascular and lipidomics research. PLoS Biology, 2018, 16, e2004285.	5.6	57
71	Exome-wide Sequencing Shows Low Mutation Rates and Identifies Novel Mutated Genes in Seminomas. European Urology, 2015, 68, 77-83.	1.9	56
72	Opioid use affects antioxidant activity and purine metabolism: preliminary results. Human Psychopharmacology, 2009, 24, 666-675.	1.5	52

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73	SETD2histone modifier loss in aggressive GI stromal tumours. Gut, 2016, 65, 1960-1972.	12.1	49
74	Improving Indel Detection Specificity of the Ion Torrent PGM Benchtop Sequencer. PLoS ONE, 2012, 7, e45798.	2.5	48
75	Epigenomic Promoter Alterations Amplify Gene Isoform and Immunogenic Diversity in Gastric Adenocarcinoma. Cancer Discovery, 2017, 7, 630-651.	9.4	48
76	Inherited breast cancer predisposition in Asians: multigene panel testing outcomes from Singapore. Npj Genomic Medicine, 2016, 1, 15003.	3.8	44
77	High-depth sequencing of over 750 genes supports linear progression of primary tumors and metastases in most patients with liver-limited metastatic colorectal cancer. Genome Biology, 2015, 16, 32.	8.8	42
78	Remarkably Little Variation in Proteins Encoded by the Y Chromosome's Single-Copy Genes, Implying Effective Purifying Selection. American Journal of Human Genetics, 2009, 85, 923-928.	6.2	39
79	Multiregion ultraâ€deep sequencing reveals early intermixing and variable levels of intratumoral heterogeneity in colorectal cancer. Molecular Oncology, 2017, 11, 124-139.	4.6	38
80	HoxC5 and miR-615-3p target newly evolved genomic regions to repress hTERT and inhibit tumorigenesis. Nature Communications, 2018, 9, 100.	12.8	38
81	Differential pulmonary transcriptomic profiles in murine lungs infected with low and highly virulent influenza H3N2 viruses reveal dysregulation of TREM1 signaling, cytokines, and chemokines. Functional and Integrative Genomics, 2012, 12, 105-117.	3.5	37
82	Evaluation and optimisation of indel detection workflows for ion torrent sequencing of the BRCA1 and BRCA2 genes. BMC Genomics, 2014, 15, 516.	2.8	36
83	Integrated paired-end enhancer profiling and whole-genome sequencing reveals recurrent CCNE1 and IGF2 enhancer hijacking in primary gastric adenocarcinoma. Gut, 2020, 69, 1039-1052.	12.1	36
84	Massively Parallel Sequencing of Patients with Intellectual Disability, Congenital Anomalies and/or Autism Spectrum Disorders with a Targeted Gene Panel. PLoS ONE, 2014, 9, e93409.	2.5	35
85	Lack of Targetable FGFR2 Fusions in Endemic Fluke-Associated Cholangiocarcinoma. JCO Global Oncology, 2020, 6, 628-638.	1.8	35
86	Pathogenesis of cholangiocarcinoma: From genetics to signalling pathways. Bailliere's Best Practice and Research in Clinical Gastroenterology, 2015, 29, 233-244.	2.4	34
87	Digital phenotyping by consumer wearables identifies sleep-associated markers of cardiovascular disease risk and biological aging. Communications Biology, 2019, 2, 361.	4.4	34
88	Fanconi anemia gene variants in therapy-related myeloid neoplasms. Blood Cancer Journal, 2015, 5, e323-e323.	6.2	32
89	Characterization of colibactin-associated mutational signature in an Asian oral squamous cell carcinoma and in other mucosal tumor types. Genome Research, 2020, 30, 803-813.	5.5	32
90	The mutational landscape of earlyâ€and typicalâ€onset oral tongue squamous cell carcinoma. Cancer, 2021, 127, 544-553.	4.1	27

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91	Exome sequencing reveals recurrent REV3L mutations in cisplatin-resistant squamous cell carcinoma of head and neck. Scientific Reports, 2016, 6, 19552.	3.3	26
92	Are Sequence Family Variants Useful for Identifying Deletions in the Human Y Chromosome?. American Journal of Human Genetics, 2004, 75, 514-517.	6.2	24
93	Global reâ€wiring of p53 transcription regulation by the hepatitis B virus X protein. Molecular Oncology, 2016, 10, 1183-1195.	4.6	23
94	A tumor-associated splice-isoform of MAP2K7 drives dedifferentiation in MBNL1-low cancers via JNK activation. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 16391-16400.	7.1	23
95	Distinct Responses of Stem Cells to Telomere Uncappingâ€"A Potential Strategy to Improve the Safety of Cell Therapy. Stem Cells, 2016, 34, 2471-2484.	3.2	22
96	Recurrent mutations in topoisomerase IIÎ± cause a previously undescribed mutator phenotype in human cancers. Proceedings of the National Academy of Sciences of the United States of America, 2022, 119, .	7.1	22
97	NOTUM is a potential pharmacodynamic biomarker of Wnt pathway inhibition. Oncotarget, 2016, 7, 12386-12392.	1.8	20
98	First somatic mutation of E2F1 in a critical DNA binding residue discovered in well-differentiated papillary mesothelioma of the peritoneum. Genome Biology, 2011, 12, R96.	9.6	19
99	Family history assessment significantly enhances delivery of precision medicine in the genomics era. Genome Medicine, 2021, 13, 3.	8.2	19
100	Implementation of genomics in medical practice to deliver precision medicine for an Asian population. Npj Genomic Medicine, 2019, 4, 12.	3.8	17
101	NanoString expression profiling identifies candidate biomarkers of RAD001 response in metastatic gastric cancer. ESMO Open, 2016, 1, e000009.	4.5	16
102	A formalin-fixed paraffin-embedded (FFPE)-based prognostic signature to predict metastasis in clinically low risk stage I/II microsatellite stable colorectal cancer. Cancer Letters, 2017, 403, 13-20.	7.2	16
103	Functional genomics identifies specific vulnerabilities in PTEN-deficient breast cancer. Breast Cancer Research, 2018, 20, 22.	5.0	15
104	SRSF1 mediates cytokine-induced impaired imatinib sensitivity in chronic myeloid leukemia. Leukemia, 2020, 34, 1787-1798.	7.2	12
105	Genomic and epigenomic EBF1 alterations modulate TERT expression in gastric cancer. Journal of Clinical Investigation, 2020, 130, 3005-3020.	8.2	12
106	Transcription-associated mutation of lasR in Pseudomonas aeruginosa. DNA Repair, 2016, 46, 9-19.	2.8	11
107	Enhancer-derived long non-coding RNAs CCAT1 and CCAT2 at rs6983267 has limited predictability for early stage colorectal carcinoma metastasis. Scientific Reports, 2021, 11, 404.	3.3	11
108	Abundant copy-number loss of CYCLOPS and STOP genes in gastric adenocarcinoma. Gastric Cancer, 2016, 19, 453-465.	5.3	9

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109	Amenable epigenetic traits of dental pulp stem cells underlie high capability of xeno-free episomal reprogramming. Stem Cell Research and Therapy, 2018, 9, 68.	5.5	9
110	Toward clinical understanding of aristolochic acid upper-tract urothelial carcinoma. Theranostics, 2020, 10, 5578-5580.	10.0	9
111	Experimental Delineation of Mutational Signatures Is an Essential Tool in Cancer Epidemiology and Prevention. Chemical Research in Toxicology, 2019, 32, 2153-2155.	3.3	8
112	Mutational selection in normal urothelium. Science, 2020, 370, 34-35.	12.6	7
113	Assessing Matched Normal and Tumor Pairs in Next-Generation Sequencing Studies. PLoS ONE, 2011, 6, e17810.	2.5	7
114	Accuracy of mutational signature software on correlated signatures. Scientific Reports, 2022, 12, 390.	3.3	6
115	Has the chimpanzee Y chromosome been sequenced?. Nature Genetics, 2006, 38, 853-854.	21.4	5
116	Defending Male Fertility. Science Translational Medicine, 2011, 3, 92ps31.	12.4	5
117	Regionally-Specified Second Trimester Fetal Neural Stem Cells Reveals Differential Neurogenic Programming. PLoS ONE, 2014, 9, e105985.	2.5	5
118	DNA epigenetic signature predictive of benefit from neoadjuvant chemotherapy in oesophageal adenocarcinoma: results from the MRC OE02 trial. European Journal of Cancer, 2019, 123, 48-57.	2.8	5
119	Whole exome sequencing identifies clinically relevant mutational signatures in resected hepatocellular carcinoma. Liver Cancer International, 2020, 1, 25-35.	1.3	5
120	A functional network of gastric-cancer-associated splicing events controlled by dysregulated splicing factors. NAR Genomics and Bioinformatics, 2020, 2, lqaa013.	3.2	5
121	Genetic characterization of a missense mutation in the X-linked TAF7L gene identified in an oligozoospermic man. Biology of Reproduction, 2022, 107, 157-167.	2.7	4
122	Mutational processes in cancer preferentially affect binding of particular transcription factors. Scientific Reports, 2021, 11, 3339.	3.3	2
123	Molecular Genetics of Renal Cell Carcinoma. , 2017, , 83-103.		1
124	Wnt proteins synergize to activate Î²-catenin signaling. Development (Cambridge), 2017, 144, e1.1-e1.1.	2.5	1
125	Genome-Scale Technologies Foster Advances in Neurological and Behavioral Research. Current Psychiatry Reviews, 2010, 6, 74-81.	0.9	0