Steven G. Rozen

List of Publications by Year
in descending order

125 papers	43,822 citations	18436 62 h-index	16605 123 g-index
139 all docs	139 docs citations	139 times ranked	64257 citing authors

#	Article	IF	Citations
1	Accuracy of mutational signature software on correlated signatures. Scientific Reports, 2022, 12, 390.	1.6	6
2	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, .	3.3	22
3	Genetic characterization of a missense mutation in the X-linked TAF7L gene identified in an oligozoospermic man. Biology of Reproduction, 2022, 107, 157-167.	1.2	4
4	The mutational landscape of earlyâ€•and typicalâ€onset oral tongue squamous cell carcinoma. Cancer, 2021, 127, 544-553.	2.0	27
5	Family history assessment significantly enhances delivery of precision medicine in the genomics era. Genome Medicine, 2021, 13, 3.	3.6	19
6	Mutational processes in cancer preferentially affect binding of particular transcription factors. Scientific Reports, 2021, 11, 3339.	1.6	2
7	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.	1.6	11
8	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.	6.1	36
9	Mutational selection in normal urothelium. Science, 2020, 370, 34-35.	6.0	7
10	Whole exome sequencing identifies clinically relevant mutational signatures in resected hepatocellular carcinoma. Liver Cancer International, 2020, 1, 25-35.	0.2	5
11	Toward clinical understanding of aristolochic acid upper-tract urothelial carcinoma. Theranostics, 2020, 10, 5578-5580.	4.6	9
12	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.	3.3	23
13	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.	2.4	32
14	SRSF1 mediates cytokine-induced impaired imatinib sensitivity in chronic myeloid leukemia. Leukemia, 2020, 34, 1787-1798.	3.3	12
15	The repertoire of mutational signatures in human cancer. Nature, 2020, 578, 94-101.	13.7	2,104
16	Lack of Targetable FGFR2 Fusions in Endemic Fluke-Associated Cholangiocarcinoma. JCO Global Oncology, 2020, 6, 628-638.	0.8	35
17	A functional network of gastric-cancer-associated splicing events controlled by dysregulated splicing factors. NAR Genomics and Bioinformatics, 2020, 2, lqaa013.	1.5	5
18	Genomic and epigenomic EBF1 alterations modulate TERT expression in gastric cancer. Journal of Clinical Investigation, 2020, 130, 3005-3020.	3.9	12

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19	Digital phenotyping by consumer wearables identifies sleep-associated markers of cardiovascular disease risk and biological aging. Communications Biology, 2019, 2, 361.	2.0	34
20	SigProfilerMatrixGenerator: a tool for visualizing and exploring patterns of small mutational events. BMC Genomics, 2019, 20, 685.	1.2	162
21	Experimental Delineation of Mutational Signatures Is an Essential Tool in Cancer Epidemiology and Prevention. Chemical Research in Toxicology, 2019, 32, 2153-2155.	1.7	8
22	Implementation of genomics in medical practice to deliver precision medicine for an Asian population. Npj Genomic Medicine, 2019, 4, 12.	1.7	17
23	Experimental and pan-cancer genome analyses reveal widespread contribution of acrylamide exposure to carcinogenesis in humans. Genome Research, 2019, 29, 521-531.	2.4	57
24	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.	1.3	5
25	In-depth characterization of the cisplatin mutational signature in human cell lines and in esophageal and liver tumors. Genome Research, 2018, 28, 654-665.	2.4	126
26	Genomic and Epigenomic Profiling of High-Risk Intestinal Metaplasia Reveals Molecular Determinants of Progression to Gastric Cancer. Cancer Cell, 2018, 33, 137-150.e5.	7.7	175
27	HoxC5 and miR-615-3p target newly evolved genomic regions to repress hTERT and inhibit tumorigenesis. Nature Communications, 2018, 9, 100.	5.8	38
28	Amenable epigenetic traits of dental pulp stem cells underlie high capability of xeno-free episomal reprogramming. Stem Cell Research and Therapy, 2018, 9, 68.	2.4	9
29	Functional genomics identifies specific vulnerabilities in PTEN-deficient breast cancer. Breast Cancer Research, 2018, 20, 22.	2.2	15
30	Beyond fitness tracking: The use of consumer-grade wearable data from normal volunteers in cardiovascular and lipidomics research. PLoS Biology, 2018, 16, e2004285.	2.6	57
31	Individualised multiplexed circulating tumour DNA assays for monitoring of tumour presence in patients after colorectal cancer surgery. Scientific Reports, 2017, 7, 40737.	1.6	62
32	Multiregion ultraâ€deep sequencing reveals early intermixing and variable levels of intratumoral heterogeneity in colorectal cancer. Molecular Oncology, 2017, 11, 124-139.	2.1	38
33	Molecular Genetics of Renal Cell Carcinoma. , 2017, , 83-103.		1
34	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, .	5.8	165
35	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.	3.2	16
36	Nucleus-Translocated ACSS2 Promotes Gene Transcription for Lysosomal Biogenesis and Autophagy. Molecular Cell, 2017, 66, 684-697.e9.	4.5	227

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37	Epigenomic Promoter Alterations Amplify Gene Isoform and Immunogenic Diversity in Gastric Adenocarcinoma. Cancer Discovery, 2017, 7, 630-651.	7.7	48
38	Wnts synergize to activate Î²-catenin signaling. Journal of Cell Science, 2017, 130, 1532-1544.	1.2	58
39	The draft genome of tropical fruit durian (Durio zibethinus). Nature Genetics, 2017, 49, 1633-1641.	9.4	150
40	Aristolochic acids and their derivatives are widely implicated in liver cancers in Taiwan and throughout Asia. Science Translational Medicine, 2017, 9, .	5.8	272
41	VHL Deficiency Drives Enhancer Activation of Oncogenes in Clear Cell Renal Cell Carcinoma. Cancer Discovery, 2017, 7, 1284-1305.	7.7	111
42	Genome-scale mutational signatures of aflatoxin in cells, mice, and human tumors. Genome Research, 2017, 27, 1475-1486.	2.4	90
43	Whole-Genome and Epigenomic Landscapes of Etiologically Distinct Subtypes of Cholangiocarcinoma. Cancer Discovery, 2017, 7, 1116-1135.	7.7	637
44	Wnt proteins synergize to activate Î²-catenin signaling. Development (Cambridge), 2017, 144, e1.1-e1.1.	1.2	1
45	MiRNA-128 regulates the proliferation and neurogenesis of neural precursors by targeting PCM1 in the developing cortex. ELife, 2016, 5, .	2.8	67
46	Angiopoietin receptor TEK mutations underlie primary congenital glaucoma with variable expressivity. Journal of Clinical Investigation, 2016, 126, 2575-2587.	3.9	175
47	ADAR-Mediated RNA Editing Predicts Progression and Prognosis of Gastric Cancer. Gastroenterology, 2016, 151, 637-650.e10.	0.6	127
48	Distinct Responses of Stem Cells to Telomere Uncappingâ€"A Potential Strategy to Improve the Safety of Cell Therapy. Stem Cells, 2016, 34, 2471-2484.	1.4	22
49	Exome sequencing reveals recurrent REV3L mutations in cisplatin-resistant squamous cell carcinoma of head and neck. Scientific Reports, 2016, 6, 19552.	1.6	26
50	Transcription-associated mutation of lasR in Pseudomonas aeruginosa. DNA Repair, 2016, 46, 9-19.	1.3	11
51	NanoString expression profiling identifies candidate biomarkers of RAD001 response in metastatic gastric cancer. ESMO Open, 2016, 1, e000009.	2.0	16
52	Epigenomic profiling of primary gastric adenocarcinoma reveals super-enhancer heterogeneity. Nature Communications, 2016, 7, 12983.	5.8	123
53	Inherited breast cancer predisposition in Asians: multigene panel testing outcomes from Singapore. Npj Genomic Medicine, 2016, 1, 15003.	1.7	44
54	Global reâ€wiring of p53 transcription regulation by the hepatitis B virus X protein. Molecular Oncology, 2016, 10, 1183-1195.	2.1	23

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55	SETD2histone modifier loss in aggressive GI stromal tumours. Gut, 2016, 65, 1960-1972.	6.1	49
56	Abundant copy-number loss of CYCLOPS and STOP genes in gastric adenocarcinoma. Gastric Cancer, 2016, 19, 453-465.	2.7	9
57	NOTUM is a potential pharmacodynamic biomarker of Wnt pathway inhibition. Oncotarget, 2016, 7, 12386-12392.	0.8	20
58	MSIseq: Software for Assessing Microsatellite Instability from Catalogs of Somatic Mutations. Scientific Reports, 2015, 5, 13321.	1.6	113
59	<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.	3.3	145
60	Mutational landscapes of tongue carcinoma reveal recurrent mutations in genes of therapeutic and prognostic relevance. Genome Medicine, 2015, 7, 98.	3.6	74
61	Exome-wide Sequencing Shows Low Mutation Rates and Identifies Novel Mutated Genes in Seminomas. European Urology, 2015, 68, 77-83.	0.9	56
62	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.	1.8	86
63	Pathogenesis of cholangiocarcinoma: From genetics to signalling pathways. Bailliere's Best Practice and Research in Clinical Gastroenterology, 2015, 29, 233-244.	1.0	34
64	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.	3.8	42
65	Genomic landscapes of breast fibroepithelial tumors. Nature Genetics, 2015, 47, 1341-1345.	9.4	167
66	Fanconi anemia gene variants in therapy-related myeloid neoplasms. Blood Cancer Journal, 2015, 5, e323-e323.	2.8	32
67	Mutation signatures implicate aristolochic acid in bladder cancer development. Genome Medicine, 2015, 7, 38.	3.6	87
68	Integrative Analysis of Head and Neck Cancer Identifies Two Biologically Distinct HPV and Three Non-HPV Subtypes. Clinical Cancer Research, 2015, 21, 870-881.	3.2	303
69	Regulatory crosstalk between lineage-survival oncogenesKLF5, GATA4andGATA6cooperatively promotes gastric cancer development. Gut, 2015, 64, 707-719.	6.1	148
70	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.	1.1	35
71	Regionally-Specified Second Trimester Fetal Neural Stem Cells Reveals Differential Neurogenic Programming. PLoS ONE, 2014, 9, e105985.	1.1	5
72	Lipidomics identifies a requirement for peroxisomal function during influenza virus replication. Journal of Lipid Research, 2014, 55, 1357-1365.	2.0	84

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73	Mammalian Y chromosomes retain widely expressed dosage-sensitive regulators. Nature, 2014, 508, 494-499.	13.7	546
74	Sequencing the Mouse Y Chromosome Reveals Convergent Gene Acquisition and Amplification on Both Sex Chromosomes. Cell, 2014, 159, 800-813.	13.5	291
75	Mutation signatures of carcinogen exposure: genome-wide detection and new opportunities for cancer prevention. Genome Medicine, 2014, 6, 24.	3.6	75
76	Exome sequencing identifies highly recurrent MED12 somatic mutations in breast fibroadenoma. Nature Genetics, 2014, 46, 877-880.	9.4	172
77	Nanoscale chromatin profiling of gastric adenocarcinoma reveals cancer-associated cryptic promoters and somatically acquired regulatory elements. Nature Communications, 2014, 5, 4361.	5.8	72
78	Evaluation and optimisation of indel detection workflows for ion torrent sequencing of the BRCA1 and BRCA2 genes. BMC Genomics, 2014, 15, 516.	1.2	36
79	Exome sequencing identifies distinct mutational patterns in liver flukeâ€“related and non-infection-related bile duct cancers. Nature Genetics, 2013, 45, 1474-1478.	9.4	426
80	Genome-Wide Mutational Signatures of Aristolochic Acid and Its Application as a Screening Tool. Science Translational Medicine, 2013, 5, 197ra101.	5.8	233
81	Identification of Molecular Subtypes of Gastric Cancer With Different Responses to PI3-Kinase Inhibitors and 5-Fluorouracil. Gastroenterology, 2013, 145, 554-565.	0.6	381
82	CYP1B1, MYOC, and LTBP2 Mutations in Primary Congenital Glaucoma Patients in the United States. American Journal of Ophthalmology, 2013, 155, 508-517.e5.	1.7	66
83	Host Cell Transcriptome Profile during Wild-Type and Attenuated Dengue Virus Infection. PLoS Neglected Tropical Diseases, 2013, 7, e2107.	1.3	68
84	Janus Kinase 3â€“Activating Mutations Identified in Natural Killer/T-cell Lymphoma. Cancer Discovery, 2012, 2, 591-597.	7.7	236
85	Primer3â€”new capabilities and interfaces. Nucleic Acids Research, 2012, 40, e115-e115.	6.5	7,501
86	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.	3.2	65
87	Strict evolutionary conservation followed rapid gene loss on human and rhesus Y chromosomes. Nature, 2012, 483, 82-86.	13.7	245
88	Methylation Subtypes and Large-Scale Epigenetic Alterations in Gastric Cancer. Science Translational Medicine, 2012, 4, 156ra140.	5.8	163
89	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.	6.1	562
90	Primer-BLAST: A tool to design target-specific primers for polymerase chain reaction. BMC Bioinformatics, 2012, 13, 134.	1.2	4,446

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91	Genomics and Genetics of Human and Primate Y Chromosomes. Annual Review of Genomics and Human Genetics, 2012, 13, 83-108.	2.5	90
92	Exome sequencing of gastric adenocarcinoma identifies recurrent somatic mutations in cell adhesion and chromatin remodeling genes. Nature Genetics, 2012, 44, 570-574.	9.4	560
93	AZFc Deletions and Spermatogenic Failure: A Population-Based Survey of 20,000 Y Chromosomes. American Journal of Human Genetics, 2012, 91, 890-896.	2.6	113
94	Exome sequencing of liver flukeâ€“associated cholangiocarcinoma. Nature Genetics, 2012, 44, 690-693.	9.4	412
95	Improving Indel Detection Specificity of the Ion Torrent PGM Benchtop Sequencer. PLoS ONE, 2012, 7, e45798.	1.1	48
96	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.	1.4	37
97	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.	13.9	19
98	Metabolomic changes in autopsyâ€confirmed Alzheimer's disease. Alzheimer's and Dementia, 2011, 7, 309-317.	0.4	132
99	Genetic and Structural Variation in the Gastric Cancer Kinome Revealed through Targeted Deep Sequencing. Cancer Research, 2011, 71, 29-39.	0.4	74
100	Defending Male Fertility. Science Translational Medicine, 2011, 3, 92ps31.	5.8	5
101	Assessing Matched Normal and Tumor Pairs in Next-Generation Sequencing Studies. PLoS ONE, 2011, 6, e17810.	1.1	7
102	Metabolomics in Early Alzheimer's Disease: Identification of Altered Plasma Sphingolipidome Using Shotgun Lipidomics. PLoS ONE, 2011, 6, e21643.	1.1	367
103	Genome-Scale Technologies Foster Advances in Neurological and Behavioral Research. Current Psychiatry Reviews, 2010, 6, 74-81.	0.9	0
104	Chimpanzee and human Y chromosomes are remarkably divergent in structure and gene content. Nature, 2010, 463, 536-539.	13.7	381
105	Convergent evolution of chicken Z and human X chromosomes by expansion and gene acquisition. Nature, 2010, 466, 612-616.	13.7	210
106	Opioid use affects antioxidant activity and purine metabolism: preliminary results. Human Psychopharmacology, 2009, 24, 666-675.	0.7	52
107	Alterations in tryptophan and purine metabolism in cocaine addiction: a metabolomic study. Psychopharmacology, 2009, 206, 479-489.	1.5	70
108	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.	2.6	39

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109	Has the chimpanzee Y chromosome been sequenced?. Nature Genetics, 2006, 38, 853-854.	9.4	5
110	High mutation rates have driven extensive structural polymorphism among human Y chromosomes. Nature Genetics, 2006, 38, 463-467.	9.4	237
111	Conservation of Y-linked genes during human evolution revealed by comparative sequencing in chimpanzee. Nature, 2005, 437, 100-103.	13.7	151
112	Metabolomic analysis and signatures in motor neuron disease. Metabolomics, 2005, 1, 101-108.	1.4	152
113	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.	1.3	196
114	Are Sequence Family Variants Useful for Identifying Deletions in the Human Y Chromosome?. American Journal of Human Genetics, 2004, 75, 514-517.	2.6	24
115	The male-specific region of the human Y chromosome is a mosaic of discrete sequence classes. Nature, 2003, 423, 825-837.	13.7	1,887
116	Abundant gene conversion between arms of palindromes in human and ape Y chromosomes. Nature, 2003, 423, 873-876.	13.7	540
117	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.	9.4	399
118	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.	2.6	410
119	The AZFc region of the Y chromosome features massive palindromes and uniform recurrent deletions in infertile men. Nature Genetics, 2001, 29, 279-286.	9.4	617
120	A physical map of the human Y chromosome. Nature, 2001, 409, 943-945.	13.7	239
121	Primer3 on the WWW for General Users and for Biologist Programmers. , 2000, 132, 365-386.		9,865
122	Large-Scale Identification, Mapping, and Genotyping of Single-Nucleotide Polymorphisms in the Human Genome. Science, 1998, 280, 1077-1082.	6.0	1,993
123	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.	9.4	427
124	Diverse spermatogenic defects in humans caused by Y chromosome deletions encompassing a novel RNAâ€“binding protein gene. Nature Genetics, 1995, 10, 383-393.	9.4	1,183
125	Quantitative Chromatographic Estimation of Î±-Amino-Acids. Nature, 1948, 161, 763-763.	13.7	66