Kyle Chang

List of Publications by Year
in descending order

Source: https://exaly.com/author-pdf/141489/publications.pdf

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41	15,886	218677	254184
papers	citations	26	43
		h-index	g-index

45	45	45	33020
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Integrating common and rare genetic variation in diverse human populations. Nature, 2010, 467, 52-58.	27.8	2,625
2	An Integrated TCGA Pan-Cancer Clinical Data Resource to Drive High-Quality Survival Outcome Analytics. Cell, 2018, 173, 400-416.e11.	28.9	2,277
3	Pancreatic cancer genomes reveal aberrations in axon guidance pathway genes. Nature, 2012, 491, 399-405.	27.8	1,741
4	Comprehensive Characterization of Cancer Driver Genes and Mutations. Cell, 2018, 173, 371-385.e18.	28.9	1,670
5	Exome Sequencing of Head and Neck Squamous Cell Carcinoma Reveals Inactivating Mutations in NOTCH1. Science, 2011, 333, 1154-1157.	12.6	1,568
6	Genomic and Molecular Landscape of DNA Damage Repair Deficiency across The Cancer Genome Atlas. Cell Reports, 2018, 23, 239-254.e6.	6.4	801
7	Genomic and Functional Approaches to Understanding Cancer Aneuploidy. Cancer Cell, 2018, 33, 676-689.e3.	16.8	750
8	Natural variation in genome architecture among 205 Drosophila melanogaster Genetic Reference Panel lines. Genome Research, 2014, 24, 1193-1208.	5.5	565
9	Integrative Genomic Characterization of Oral Squamous Cell Carcinoma Identifies Frequent Somatic Drivers. Cancer Discovery, 2013, 3, 770-781.	9.4	484
10	Driver Fusions and Their Implications in the Development and Treatment of Human Cancers. Cell Reports, 2018, 23, 227-238.e3.	6.4	407
11	Inherited causes of clonal haematopoiesis in 97,691 whole genomes. Nature, 2020, 586, 763-768.	27.8	376
12	Somatic Mutational Landscape of Splicing Factor Genes and Their Functional Consequences across 33 Cancer Types. Cell Reports, 2018, 23, 282-296.e4.	6.4	333
13	Characterization of HPV and host genome interactions in primary head and neck cancers. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 15544-15549.	7.1	317
14	Colonic organoids derived from human induced pluripotent stem cells for modeling colorectal cancer and drug testing. Nature Medicine, 2017, 23, 878-884.	30.7	285
15	Deep resequencing reveals excess rare recent variants consistent with explosive population growth. Nature Communications, 2010, 1, 131.	12.8	213
16	Novel somatic and germline mutations in intracranial germ cell tumours. Nature, 2014, 511, 241-245.	27.8	181
17	Oncogenic Kras drives invasion and maintains metastases in colorectal cancer. Genes and Development, 2017, 31, 370-382.	5.9	137
18	Immune Cell Production of Interleukin 17 Induces Stem Cell Features of Pancreatic Intraepithelial Neoplasia Cells. Gastroenterology, 2018, 155, 210-223.e3.	1.3	114

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19	Resolving the Spatial and Cellular Architecture of Lung Adenocarcinoma by Multiregion Single-Cell Sequencing. Cancer Discovery, 2021, 11, 2506-2523.	9.4	68
20	MLH1â€silenced and nonâ€silenced subgroups of hypermutated colorectal carcinomas have distinct mutational landscapes. Journal of Pathology, 2013, 229, 99-110.	4.5	67
21	Genomic Landscape of Colorectal Mucosa and Adenomas. Cancer Prevention Research, 2016, 9, 417-427.	1.5	65
22	Immune Profiling of Premalignant Lesions in Patients With Lynch Syndrome. JAMA Oncology, 2018, 4, 1085.	7.1	62
23	Immune Activation in Mismatch Repairâ€“Deficient Carcinogenesis: More Than Just Mutational Rate. Clinical Cancer Research, 2020, 26, 11-17.	7.0	61
24	Naproxen chemoprevention promotes immune activation in Lynch syndrome colorectal mucosa. Gut, 2021, 70, 555-566.	12.1	37
25	Colorectal premalignancy is associated with consensus molecular subtypes 1 and 2. Annals of Oncology, 2018, 29, 2061-2067.	1.2	35
26	Acetylation of CCAR2 Establishes a BET/BRD9 Acetyl Switch in Response to Combined Deacetylase and Bromodomain Inhibition. Cancer Research, 2019, 79, 918-927.	0.9	28
27	Telomere dysfunction instigates inflammation in inflammatory bowel disease. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	7.1	28
28	Large-scale analysis of acquired chromosomal alterations in non-tumor samples from patients with cancer. Nature Biotechnology, 2020, 38, 90-96.	17.5	27
29	Mutational Heterogeneity in APC and KRAS Arises at the Crypt Level and Leads to Polyclonality in Early Colorectal Tumorigenesis. Clinical Cancer Research, 2017, 23, 5936-5947.	7.0	25
30	Cancer In Silico Drug Discovery: A Systems Biology Tool for Identifying Candidate Drugs to Target Specific Molecular Tumor Subtypes. Molecular Cancer Therapeutics, 2014, 13, 3230-3240.	4.1	21
31	Detection of Pathogenic Germline Variants Among Patients With Advanced Colorectal Cancer Undergoing Tumor Genomic Profiling for Precision Medicine. Diseases of the Colon and Rectum, 2019, 62, 429-437.	1.3	21
32	Defining the Comprehensive Genomic Landscapes of Pancreatic Ductal Adenocarcinoma Using Real-World Endoscopic Aspiration Samples. Clinical Cancer Research, 2021, 27, 1082-1093.	7.0	20
33	An S/T-Q cluster domain census unveils new putative targets under Tel1/Mec1 control. BMC Genomics, 2012, 13, 664.	2.8	19
34	Oncogenic targets Mmp7, S100a9, Nppb and Aldh1a3 from transcriptome profiling of FAP and Pirc adenomas are downregulated in response to tumor suppression by Clotam. International Journal of Cancer, 2017, 140, 460-468.	5.1	18
35	In Silico Systems Biology Analysis of Variants of Uncertain Significance in Lynch Syndrome Supports the Prioritization of Functional Molecular Validation. Cancer Prevention Research, 2017, 10, 580-587.	1.5	9
36	Combination of Sulindac and Bexarotene for Prevention of Intestinal Carcinogenesis in Familial Adenomatous Polyposis. Cancer Prevention Research, 2021, 14, 851-862.	1.5	8

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37	Resequencing ofIRS2reveals rare variants for obesity but not fasting glucose homeostasis in Hispanic children. Physiological Genomics, 2011, 43, 1029-1037.	2.3	6
38	Functional characterization of CNOT3 variants identified in familial adenomatous polyposis adenomas. Oncotarget, 2019, 10, 3939-3951.	1.8	5
39	Chromosomal imbalances detected via RNA-sequencing in 28 cancers. Bioinformatics, 2022, 38, 1483-1490.	4.1	3
40	Transcriptomic-Assisted Immune and Neoantigen Profiling in Premalignancy. Methods in Molecular Biology, 2022, 2435, 95-105.	0.9	1
41	A whole-exome case-control association study to characterize the contribution of rare coding variation to pancreatic cancer risk. Human Genetics and Genomics Advances, 2022, 3, 100078.	1.7	0