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	Chromosomal imbalances detected via RNA-sequencing in 28 cancers. Bioinformatics, 2022, 38, 1483-1490.	4.1	3
2	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
3	Transcriptomic-Assisted Immune and Neoantigen Profiling in Premalignancy. Methods in Molecular Biology, 2022, 2435, 95-105.	0.9	1
4	Naproxen chemoprevention promotes immune activation in Lynch syndrome colorectal mucosa. Gut, 2021, 70, 555-566.	12.1	37
5	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
6	Resolving the Spatial and Cellular Architecture of Lung Adenocarcinoma by Multiregion Single-Cell Sequencing. Cancer Discovery, 2021, 11, 2506-2523.	9.4	68
7	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
8	Combination of Sulindac and Bexarotene for Prevention of Intestinal Carcinogenesis in Familial Adenomatous Polyposis. Cancer Prevention Research, 2021, 14, 851-862.	1.5	8
9	Immune Activation in Mismatch Repairâ€“Deficient Carcinogenesis: More Than Just Mutational Rate. Clinical Cancer Research, 2020, 26, 11-17.	7.0	61
10	Large-scale analysis of acquired chromosomal alterations in non-tumor samples from patients with cancer. Nature Biotechnology, 2020, 38, 90-96.	17.5	27
11	Inherited causes of clonal haematopoiesis in 97,691 whole genomes. Nature, 2020, 586, 763-768.	27.8	376
12	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
13	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
14	Functional characterization of CNOT3 variants identified in familial adenomatous polyposis adenomas. Oncotarget, 2019, 10, 3939-3951.	1.8	5
15	Immune Profiling of Premalignant Lesions in Patients With Lynch Syndrome. JAMA Oncology, 2018, 4, 1085.	7.1	62
16	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
17	Comprehensive Characterization of Cancer Driver Genes and Mutations. Cell, 2018, 173, 371-385.e18.	28.9	1,670
18	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

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19	Driver Fusions and Their Implications in the Development and Treatment of Human Cancers. Cell Reports, 2018, 23, 227-238.e3.	6.4	407
20	Genomic and Molecular Landscape of DNA Damage Repair Deficiency across The Cancer Genome Atlas. Cell Reports, 2018, 23, 239-254.e6.	6.4	801
21	Immune Cell Production of Interleukin 17 Induces Stem Cell Features of Pancreatic Intraepithelial Neoplasia Cells. Gastroenterology, 2018, 155, 210-223.e3.	1.3	114
22	Genomic and Functional Approaches to Understanding Cancer Aneuploidy. Cancer Cell, 2018, 33, 676-689.e3.	16.8	750
23	Colorectal premalignancy is associated with consensus molecular subtypes 1 and 2. Annals of Oncology, 2018, 29, 2061-2067.	1.2	35
24	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
25	Oncogenic Kras drives invasion and maintains metastases in colorectal cancer. Genes and Development, 2017, 31, 370-382.	5.9	137
26	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
27	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
28	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
29	Genomic Landscape of Colorectal Mucosa and Adenomas. Cancer Prevention Research, 2016, 9, 417-427.	1.5	65
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	Natural variation in genome architecture among 205 Drosophila melanogaster Genetic Reference Panel lines. Genome Research, 2014, 24, 1193-1208.	5.5	565
32	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
33	Novel somatic and germline mutations in intracranial germ cell tumours. Nature, 2014, 511, 241-245.	27.8	181
34	MLH1â€silenced and nonâ€silenced subgroups of hypermutated colorectal carcinomas have distinct mutational landscapes. Journal of Pathology, 2013, 229, 99-110.	4.5	67
35	Integrative Genomic Characterization of Oral Squamous Cell Carcinoma Identifies Frequent Somatic Drivers. Cancer Discovery, 2013, 3, 770-781.	9.4	484
36	Pancreatic cancer genomes reveal aberrations in axon guidance pathway genes. Nature, 2012, 491, 399-405.	27.8	1,741

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37	An S/T-Q cluster domain census unveils new putative targets under Tel1/Mec1 control. BMC Genomics, 2012, 13, 664.	2.8	19
38	Resequencing ofIRS2reveals rare variants for obesity but not fasting glucose homeostasis in Hispanic children. Physiological Genomics, 2011, 43, 1029-1037.	2.3	6
39	Exome Sequencing of Head and Neck Squamous Cell Carcinoma Reveals Inactivating Mutations in NOTCH1. Science, 2011, 333, 1154-1157.	12.6	1,568
40	Integrating common and rare genetic variation in diverse human populations. Nature, 2010, 467, 52-58.	27.8	2,625
41	Deep resequencing reveals excess rare recent variants consistent with explosive population growth. Nature Communications, 2010, 1, 131.	12.8	213