Chip Stewart

List of Publications by Year
in descending order

Source: https://exaly.com/author-pdf/8256414/publications.pdf

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55 papers	28,070 citations	47006 47 h-index	144013 57 g-index
63 all docs	63 docs citations	63 times ranked	48268 citing authors

#	Article	IF	Citations
1	Mutational heterogeneity in cancer and the search for new cancer-associated genes. Nature, 2013, 499, 214-218.	27.8	4,761
2	The Molecular Taxonomy of Primary Prostate Cancer. Cell, 2015, 163, 1011-1025.	28.9	2,435
3	Integrated Genomic Characterization of Papillary Thyroid Carcinoma. Cell, 2014, 159, 676-690.	28.9	2,318
4	Prospective Derivation of a Living Organoid Biobank of Colorectal Cancer Patients. Cell, 2015, 161, 933-945.	28.9	1,710
5	Integrated Genomic Characterization of Pancreatic Ductal Adenocarcinoma. Cancer Cell, 2017, 32, 185-203.e13.	16.8	1,428
6	Molecular subtypes of diffuse large B cell lymphoma are associated with distinct pathogenic mechanisms and outcomes. Nature Medicine, 2018, 24, 679-690.	30.7	1,224
7	Evolution and Impact of Subclonal Mutations in Chronic Lymphocytic Leukemia. Cell, 2013, 152, 714-726.	28.9	1,202
8	Mapping copy number variation by population-scale genome sequencing. Nature, 2011, 470, 59-65.	27.8	991
9	The genetic landscape of high-risk neuroblastoma. Nature Genetics, 2013, 45, 279-284.	21.4	990
10	Mutations driving CLL and their evolution in progression and relapse. Nature, 2015, 526, 525-530.	27.8	868
11	Landscape of genomic alterations in cervical carcinomas. Nature, 2014, 506, 371-375.	27.8	708
12	Exome and whole-genome sequencing of esophageal adenocarcinoma identifies recurrent driver events and mutational complexity. Nature Genetics, 2013, 45, 478-486.	21.4	671
13	Scalable Open Science Approach for Mutation Calling of Tumor Exomes Using Multiple Genomic Pipelines. Cell Systems, 2018, 6, 271-281.e7.	6.2	605
14	Targetable genetic features of primary testicular and primary central nervous system lymphomas. Blood, 2016, 127, 869-881.	1.4	429
15	Analyses of non-coding somatic drivers in 2,658Âcancer whole genomes. Nature, 2020, 578, 102-111.	27.8	424
16	Integrative Molecular Characterization of Malignant Pleural Mesothelioma. Cancer Discovery, 2018, 8, 1548-1565.	9.4	422
17	The Genomic Landscape of Pediatric Ewing Sarcoma. Cancer Discovery, 2014, 4, 1326-1341.	9.4	415
18	Exome sequencing identifies BRAF mutations in papillary craniopharyngiomas. Nature Genetics, 2014, 46, 161-165.	21.4	408

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19	Discovery and characterization of artifactual mutations in deep coverage targeted capture sequencing data due to oxidative DNA damage during sample preparation. Nucleic Acids Research, 2013, 41, e67-e67.	14.5	407
20	RNA sequence analysis reveals macroscopic somatic clonal expansion across normal tissues. Science, 2019, 364, .	12.6	369
21	A remarkably simple genome underlies highly malignant pediatric rhabdoid cancers. Journal of Clinical Investigation, 2012, 122, 2983-2988.	8.2	347
22	Paired exome analysis of Barrett's esophagus and adenocarcinoma. Nature Genetics, 2015, 47, 1047-1055.	21.4	310
23	Integrated Molecular Characterization of Uterine Carcinosarcoma. Cancer Cell, 2017, 31, 411-423.	16.8	309
24	SvABA: genome-wide detection of structural variants and indels by local assembly. Genome Research, 2018, 28, 581-591.	5.5	288
25	Clonal evolution in patients with chronic lymphocytic leukaemia developing resistance to BTK inhibition. Nature Communications, 2016, 7, 11589.	12.8	285
26	Identification of heart rateâ€“associated loci and their effects on cardiac conduction and rhythm disorders. Nature Genetics, 2013, 45, 621-631.	21.4	282
27	A Comprehensive Map of Mobile Element Insertion Polymorphisms in Humans. PLoS Genetics, 2011, 7, e1002236.	3.5	278
28	Recurrent and functional regulatory mutations in breast cancer. Nature, 2017, 547, 55-60.	27.8	269
29	MOSAIK: A Hash-Based Algorithm for Accurate Next-Generation Sequencing Short-Read Mapping. PLoS ONE, 2014, 9, e90581.	2.5	249
30	Genetic and Clonal Dissection of Murine Small Cell Lung Carcinoma Progression by Genome Sequencing. Cell, 2014, 156, 1298-1311.	28.9	241
31	The genomic landscape of juvenile myelomonocytic leukemia. Nature Genetics, 2015, 47, 1326-1333.	21.4	233
32	Somatic retrotransposition in human cancer revealed by whole-genome and exome sequencing. Genome Research, 2014, 24, 1053-1063.	5.5	191
33	Widespread Chromosomal Losses and Mitochondrial DNA Alterations as Genetic Drivers in HÃ¼rthle Cell Carcinoma. Cancer Cell, 2018, 34, 242-255.e5.	16.8	185
34	The functional spectrum of low-frequency coding variation. Genome Biology, 2011, 12, R84.	9.6	173
35	Somatic rearrangements across cancer reveal classes of samples with distinct patterns of DNA breakage and rearrangement-induced hypermutability. Genome Research, 2013, 23, 228-235.	5.5	124
36	Genomic Profiling of Smoldering Multiple Myeloma Identifies Patients at a High Risk of Disease Progression. Journal of Clinical Oncology, 2020, 38, 2380-2389.	1.6	110

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37	Genomic analyses of flow-sorted Hodgkin Reed-Sternberg cells reveal complementary mechanisms of immune evasion. Blood Advances, 2019, 3, 4065-4080.	5.2	99
38	Exome sequencing of lymphomas from three dog breeds reveals somatic mutation patterns reflecting genetic background. Genome Research, 2015, 25, 1634-1645.	5.5	96
39	Growth dynamics in naturally progressing chronic lymphocytic leukaemia. Nature, 2019, 570, 474-479.	27.8	86
40	Radiation-related genomic profile of papillary thyroid carcinoma after the Chernobyl accident. Science, 2021, 372, .	12.6	85
41	Genomic analyses of PMBL reveal new drivers and mechanisms of sensitivity to PD-1 blockade. Blood, 2019, 134, 2369-2382.	1.4	72
42	DeTiN: overcoming tumor-in-normal contamination. Nature Methods, 2018, 15, 531-534.	19.0	71
43	Sequence Analysis and Characterization of Active HumanAlusubfamilies Based on the 1000 Genomes Pilot Project. Genome Biology and Evolution, 2015, 7, evv167.	2.5	60
44	Lack of transgenerational effects of ionizing radiation exposure from the Chernobyl accident. Science, 2021, 372, 725-729.	12.6	60
45	Optimizing event selection with the random grid search. Computer Physics Communications, 2018, 228, 245-257.	7.5	52
46	ZBTB33 Is Mutated in Clonal Hematopoiesis and Myelodysplastic Syndromes and Impacts RNA Splicing. Blood Cancer Discovery, 2021, 2, 500-517.	5.0	17
47	Genomic Evolutionary Patterns of Leiomyosarcoma and Liposarcoma. Clinical Cancer Research, 2019, 25, 5135-5142.	7.0	14
48	A (fire)cloud-based DNA methylation data preprocessing and quality control platform. BMC Bioinformatics, 2019, 20, 160.	2.6	7
49	Subclonal Driver Mutations Predict Shorter Progression Free Survival in Chronic Lymphocytic Leukemia Following First-Line Chemo(immuno)Therapy: Results from the CLL8 Trial. Blood, 2014, 124, 1938-1938.	1.4	4
50	Novel Putative Driver Gene Mutations in Chronic Lymphocytic Leukemia (CLL): Results from a Combined Analysis of Whole-Exome Sequencing of 262 Primary CLL Samples. Blood, 2014, 124, 1952-1952.	1.4	4
51	Quantitative Clonal Dynamics Define Mechanisms of CLL Evolution in Response to Combination Chemotherapy. Blood, 2015, 126, 362-362.	1.4	4
52	Validation of the Genetically-Defined DLBCL Subtypes and Generation of a Parsimonious Probabilistic Classifier. Blood, 2019, 134, 920-920.	1.4	3
53	Genomic Correlates of Outcome in Tumor-Infiltrating Lymphocyte Therapy for Metastatic Melanoma. Clinical Cancer Research, 2022, 28, 1911-1924.	7.0	3
54	Comment on â€œDNA damage is a pervasive cause of sequencing errors, directly confounding variant identificationâ€• Science, 2018, 361, .	12.6	2

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55	Actionable Genetic Features of Primary Testicular and Primary Central Nervous System Lymphomas. Blood, 2014, 124, 74-74.	1.4	2