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	Genomic Correlates of Outcome in Tumor-Infiltrating Lymphocyte Therapy for Metastatic Melanoma. Clinical Cancer Research, 2022, 28, 1911-1924.	7.0	3
2	Lack of transgenerational effects of ionizing radiation exposure from the Chernobyl accident. Science, 2021, 372, 725-729.	12.6	60
3	Radiation-related genomic profile of papillary thyroid carcinoma after the Chernobyl accident. Science, 2021, 372, .	12.6	85
4	ZBTB33 Is Mutated in Clonal Hematopoiesis and Myelodysplastic Syndromes and Impacts RNA Splicing. Blood Cancer Discovery, 2021, 2, 500-517.	5.0	17
5	Analyses of non-coding somatic drivers in 2,658Âcancer whole genomes. Nature, 2020, 578, 102-111.	27.8	424
6	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
7	RNA sequence analysis reveals macroscopic somatic clonal expansion across normal tissues. Science, 2019, 364, .	12.6	369
8	Growth dynamics in naturally progressing chronic lymphocytic leukaemia. Nature, 2019, 570, 474-479.	27.8	86
9	Genomic Evolutionary Patterns of Leiomyosarcoma and Liposarcoma. Clinical Cancer Research, 2019, 25, 5135-5142.	7.0	14
10	A (fire)cloud-based DNA methylation data preprocessing and quality control platform. BMC Bioinformatics, 2019, 20, 160.	2.6	7
11	Genomic analyses of PMBL reveal new drivers and mechanisms of sensitivity to PD-1 blockade. Blood, 2019, 134, 2369-2382.	1.4	72
12	Genomic analyses of flow-sorted Hodgkin Reed-Sternberg cells reveal complementary mechanisms of immune evasion. Blood Advances, 2019, 3, 4065-4080.	5.2	99
13	Validation of the Genetically-Defined DLBCL Subtypes and Generation of a Parsimonious Probabilistic Classifier. Blood, 2019, 134, 920-920.	1.4	3
14	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
15	Scalable Open Science Approach for Mutation Calling of Tumor Exomes Using Multiple Genomic Pipelines. Cell Systems, 2018, 6, 271-281.e7.	6.2	605
16	SvABA: genome-wide detection of structural variants and indels by local assembly. Genome Research, 2018, 28, 581-591.	5.5	288
17	Comment on â€œDNA damage is a pervasive cause of sequencing errors, directly confounding variant identificationâ€. Science, 2018, 361, .	12.6	2
18	Integrative Molecular Characterization of Malignant Pleural Mesothelioma. Cancer Discovery, 2018, 8, 1548-1565.	9.4	422

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19	DeTiN: overcoming tumor-in-normal contamination. Nature Methods, 2018, 15, 531-534.	19.0	71
20	Widespread Chromosomal Losses and Mitochondrial DNA Alterations as Genetic Drivers in HÃ¼rthle Cell Carcinoma. Cancer Cell, 2018, 34, 242-255.e5.	16.8	185
21	Optimizing event selection with the random grid search. Computer Physics Communications, 2018, 228, 245-257.	7.5	52
22	Integrated Molecular Characterization of Uterine Carcinosarcoma. Cancer Cell, 2017, 31, 411-423.	16.8	309
23	Integrated Genomic Characterization of Pancreatic Ductal Adenocarcinoma. Cancer Cell, 2017, 32, 185-203.e13.	16.8	1,428
24	Recurrent and functional regulatory mutations in breast cancer. Nature, 2017, 547, 55-60.	27.8	269
25	Targetable genetic features of primary testicular and primary central nervous system lymphomas. Blood, 2016, 127, 869-881.	1.4	429
26	Clonal evolution in patients with chronic lymphocytic leukaemia developing resistance to BTK inhibition. Nature Communications, 2016, 7, 11589.	12.8	285
27	Sequence Analysis and Characterization of Active HumanAlusubfamilies Based on the 1000 Genomes Pilot Project. Genome Biology and Evolution, 2015, 7, evv167.	2.5	60
28	Paired exome analysis of Barrett's esophagus and adenocarcinoma. Nature Genetics, 2015, 47, 1047-1055.	21.4	310
29	Prospective Derivation of a Living Organoid Biobank of Colorectal Cancer Patients. Cell, 2015, 161, 933-945.	28.9	1,710
30	The Molecular Taxonomy of Primary Prostate Cancer. Cell, 2015, 163, 1011-1025.	28.9	2,435
31	Exome sequencing of lymphomas from three dog breeds reveals somatic mutation patterns reflecting genetic background. Genome Research, 2015, 25, 1634-1645.	5.5	96
32	Mutations driving CLL and their evolution in progression and relapse. Nature, 2015, 526, 525-530.	27.8	868
33	The genomic landscape of juvenile myelomonocytic leukemia. Nature Genetics, 2015, 47, 1326-1333.	21.4	233
34	Quantitative Clonal Dynamics Define Mechanisms of CLL Evolution in Response to Combination Chemotherapy. Blood, 2015, 126, 362-362.	1.4	4
35	MOSAIK: A Hash-Based Algorithm for Accurate Next-Generation Sequencing Short-Read Mapping. PLoS ONE, 2014, 9, e90581.	2.5	249
36	Integrated Genomic Characterization of Papillary Thyroid Carcinoma. Cell, 2014, 159, 676-690.	28.9	2,318

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37	The Genomic Landscape of Pediatric Ewing Sarcoma. Cancer Discovery, 2014, 4, 1326-1341.	9.4	415
38	Genetic and Clonal Dissection of Murine Small Cell Lung Carcinoma Progression by Genome Sequencing. Cell, 2014, 156, 1298-1311.	28.9	241
39	Somatic retrotransposition in human cancer revealed by whole-genome and exome sequencing. Genome Research, 2014, 24, 1053-1063.	5.5	191
40	Exome sequencing identifies BRAF mutations in papillary craniopharyngiomas. Nature Genetics, 2014, 46, 161-165.	21.4	408
41	Landscape of genomic alterations in cervical carcinomas. Nature, 2014, 506, 371-375.	27.8	708
42	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
43	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
44	Actionable Genetic Features of Primary Testicular and Primary Central Nervous System Lymphomas. Blood, 2014, 124, 74-74.	1.4	2
45	Evolution and Impact of Subclonal Mutations in Chronic Lymphocytic Leukemia. Cell, 2013, 152, 714-726.	28.9	1,202
46	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
47	Exome and whole-genome sequencing of esophageal adenocarcinoma identifies recurrent driver events and mutational complexity. Nature Genetics, 2013, 45, 478-486.	21.4	671
48	Identification of heart rateâ€“associated loci and their effects on cardiac conduction and rhythm disorders. Nature Genetics, 2013, 45, 621-631.	21.4	282
49	Mutational heterogeneity in cancer and the search for new cancer-associated genes. Nature, 2013, 499, 214-218.	27.8	4,761
50	The genetic landscape of high-risk neuroblastoma. Nature Genetics, 2013, 45, 279-284.	21.4	990
51	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
52	A remarkably simple genome underlies highly malignant pediatric rhabdoid cancers. Journal of Clinical Investigation, 2012, 122, 2983-2988.	8.2	347
53	The functional spectrum of low-frequency coding variation. Genome Biology, 2011, 12, R84.	9.6	173
54	Mapping copy number variation by population-scale genome sequencing. Nature, 2011, 470, 59-65.	27.8	991

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55	A Comprehensive Map of Mobile Element Insertion Polymorphisms in Humans. PLoS Genetics, 2011, 7, e1002236.	3.5	278