Rong Chen

List of Publications by Year
in descending order

40 papers	2,478 citations	361413 20 h-index	377865 34 g-index
42 all docs	42 docs citations	42 times ranked	5984 citing authors

#	Article	IF	Citations
1	Targeted Next-Generation Sequencing Reveals Exceptionally High Rates of Molecular Driver Mutations in Never-Smokers With Lung Adenocarcinoma. Oncologist, 2022, 27, 476-486.	3.7	15
2	Clinical utility of next-generation sequencing for prostate cancer in the context of a changing treatment landscape.. Journal of Clinical Oncology, 2022, 40, 112-112.	1.6	1
3	Extraction of Treatment Information From Electronic Health Records and Evaluation of Testosterone Recovery in Patients With Prostate Cancer. JCO Clinical Cancer Informatics, 2022, , .	2.1	1
4	USP8 and TP53 Drivers are Associated with CNV in a Corticotroph Adenoma Cohort Enriched for Aggressive Tumors. Journal of Clinical Endocrinology and Metabolism, 2021, 106, 826-842.	3.6	34
5	AKI in Hospitalized Patients with COVID-19. Journal of the American Society of Nephrology: JASN, 2021, 32, 151-160.	6.1	500
6	A Drosophila platform identifies a novel, personalized therapy for a patient with adenoid cystic carcinoma. IScience, 2021, 24, 102212.	4.1	23
7	Phenotyping of clinical trial eligibility text from cancer studies into computable criteria in electronic health records.. Journal of Clinical Oncology, 2021, 39, 6592-6592.	1.6	0
8	Extracting longitudinal anticancer treatments at scale using deep natural language processing and temporal reasoning.. Journal of Clinical Oncology, 2021, 39, e18747-e18747.	1.6	0
9	Analyzing treatment patterns and time to the next treatment in chronic lymphocytic leukemia real-world data using automated temporal phenotyping.. Journal of Clinical Oncology, 2021, 39, e19512-e19512.	1.6	1
10	Human GPR17 missense variants identified in metabolic disease patients have distinct downstream signaling profiles. Journal of Biological Chemistry, 2021, 297, 100881.	3.4	3
11	Medically actionable pathogenic variants in a population of 13,131 healthy elderly individuals. Genetics in Medicine, 2020, 22, 1883-1886.	2.4	20
12	Using real-world data to investigate time-dependent blood count response to PD-1 and PD-L1 inhibitors and its impact on survival in advanced non-small cell lung cancers.. Journal of Clinical Oncology, 2020, 38, e21514-e21514.	1.6	0
13	Representing cancer clinical trial criteria and attributes using ontologies: An NLP-assisted approach.. Journal of Clinical Oncology, 2020, 38, e14079-e14079.	1.6	0
14	Genome-wide analysis indicates association between heterozygote advantage and healthy aging in humans. BMC Genetics, 2019, 20, 52.	2.7	10
15	Integrative analysis of loss-of-function variants in clinical and genomic data reveals novel genes associated with cardiovascular traits. BMC Medical Genomics, 2019, 12, 108.	1.5	8
16	A personalized platform identifies trametinib plus zoledronate for a patient with KRAS-mutant metastatic colorectal cancer. Science Advances, 2019, 5, eaav6528.	10.3	74
17	Leveraging Big Data to Transform Drug Discovery. Methods in Molecular Biology, 2019, 1939, 91-118.	0.9	27
18	Phase 2 Trial of Gemcitabine, Cisplatin, plus Ipilimumab in Patients with Metastatic Urothelial Cancer and Impact of DNA Damage Response Gene Mutations on Outcomes. European Urology, 2018, 73, 751-759.	1.9	99

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19	Melanocortin 4 Receptor Pathway Dysfunction in Obesity: Patient Stratification Aimed at MC4R Agonist Treatment. Journal of Clinical Endocrinology and Metabolism, 2018, 103, 2601-2612.	3.6	50
20	Novel Therapeutics Identification for Fibrosis in Renal Allograft Using Integrative Informatics Approach. Scientific Reports, 2017, 7, 39487.	3.3	28
21	Identification of a novel RASD1 somatic mutation in a USP8-mutated corticotroph adenoma. Journal of Physical Education and Sports Management, 2017, 3, a001602.	1.2	8
22	Pulmonary Sarcomatoid Carcinomas Commonly Harbor Either Potentially Targetable Genomic Alterations or High Tumor Mutational Burden as Observed by Comprehensive Genomic Profiling. Journal of Thoracic Oncology, 2017, 12, 932-942.	1.1	129
23	Institutional profile: translational pharmacogenomics at the Icahn School of Medicine at Mount Sinai. Pharmacogenomics, 2017, 18, 1381-1386.	1.3	20
24	Inhibition of the Nuclear Export Receptor XPO1 as a Therapeutic Target for Platinum-Resistant Ovarian Cancer. Clinical Cancer Research, 2017, 23, 1552-1563.	7.0	65
25	Cancer gene profiling in non-small cell lung cancers reveals activating mutations in JAK2 and JAK3 with therapeutic implications. Genome Medicine, 2017, 9, 89.	8.2	39
26	Genomic profiling reveals mutational landscape in parathyroid carcinomas. JCI Insight, 2017, 2, e92061.	5.0	84
27	DNA damage response (DDR) gene mutations (mut), mut load, and sensitivity to chemotherapy plus immune checkpoint blockade in urothelial cancer (UC).. Journal of Clinical Oncology, 2017, 35, 300-300.	1.6	7
28	DIVAS: a centralized genetic variant repository representing 150â€‰000 individuals from multiple disease cohorts. Bioinformatics, 2016, 32, 151-153.	4.1	8
29	Analysis of 589,306 genomes identifies individuals resilient to severe Mendelian childhood diseases. Nature Biotechnology, 2016, 34, 531-538.	17.5	273
30	Acute Intermittent Porphyria: Predicted Pathogenicity ofHMBSVariants Indicates Extremely Low Penetrance of the Autosomal Dominant Disease. Human Mutation, 2016, 37, 1215-1222.	2.5	129
31	A loss of function variant in CASP7 protects against Alzheimerâ€™s disease in homozygous APOE Îµ4 allele carriers. BMC Genomics, 2016, 17, 445.	2.8	26
32	Development and clinical application of an integrative genomic approach to personalized cancer therapy. Genome Medicine, 2016, 8, 62.	8.2	71
33	Anabolic actions of Notch on mature bone. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, E2152-61.	7.1	46
34	Integrating 400 million variants from 80,000 human samples with extensive annotations: towards a knowledge base to analyze disease cohorts. BMC Bioinformatics, 2016, 17, 24.	2.6	13
35	Airway Epithelial Expression Quantitative Trait Loci Reveal Genes Underlying Asthma and Other Airway Diseases. American Journal of Respiratory Cell and Molecular Biology, 2016, 54, 177-187.	2.9	28
36	Personalized Circulating Tumor DNA Biomarkers Dynamically Predict Treatment Response and Survival In Gynecologic Cancers. PLoS ONE, 2015, 10, e0145754.	2.5	129

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37	Shared genetic etiology underlying Alzheimer's disease and type 2 diabetes. Molecular Aspects of Medicine, 2015, 43-44, 66-76.	6.4	63
38	ClinLabGeneticist: a tool for clinical management of genetic variants from whole exome sequencing in clinical genetic laboratories. Genome Medicine, 2015, 7, 77.	8.2	5
39	Identification of type 2 diabetes subgroups through topological analysis of patient similarity. Science Translational Medicine, 2015, 7, 311ra174.	12.4	426
40	AN INTEGRATIVE PIPELINE FOR MULTI-MODAL DISCOVERY OF DISEASE RELATIONSHIPS. , 2014, , .		15