Rong Chen

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/632574/publications.pdf

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40 papers

2,478 citations

361413 20 h-index 377865 34 g-index

42 all docs 42 docs citations

times ranked

42

5984 citing authors

#	Article	IF	CITATIONS
1	AKI in Hospitalized Patients with COVID-19. Journal of the American Society of Nephrology: JASN, 2021, 32, 151-160.	6.1	500
2	Identification of type 2 diabetes subgroups through topological analysis of patient similarity. Science Translational Medicine, 2015, 7, 311ra174.	12.4	426
3	Analysis of 589,306 genomes identifies individuals resilient to severe Mendelian childhood diseases. Nature Biotechnology, 2016, 34, 531-538.	17.5	273
4	Personalized Circulating Tumor DNA Biomarkers Dynamically Predict Treatment Response and Survival In Gynecologic Cancers. PLoS ONE, 2015, 10, e0145754.	2.5	129
5	Acute Intermittent Porphyria: Predicted Pathogenicity of <i>HMBS </i> Variants Indicates Extremely Low Penetrance of the Autosomal Dominant Disease. Human Mutation, 2016, 37, 1215-1222.	2.5	129
6	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
7	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
8	Genomic profiling reveals mutational landscape in parathyroid carcinomas. JCI Insight, 2017, 2, e92061.	5.0	84
9	A personalized platform identifies trametinib plus zoledronate for a patient with KRAS-mutant metastatic colorectal cancer. Science Advances, 2019, 5, eaav6528.	10.3	74
10	Development and clinical application of an integrative genomic approach to personalized cancer therapy. Genome Medicine, 2016, 8, 62.	8.2	71
11	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
12	Shared genetic etiology underlying Alzheimer's disease and type 2 diabetes. Molecular Aspects of Medicine, 2015, 43-44, 66-76.	6.4	63
13	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
14	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
15	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
16	<i>USP8</i> and <i>TP53</i> 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
17	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
18	Novel Therapeutics Identification for Fibrosis in Renal Allograft Using Integrative Informatics Approach. Scientific Reports, 2017, 7, 39487.	3.3	28

#	Article	IF	Citations
19	Leveraging Big Data to Transform Drug Discovery. Methods in Molecular Biology, 2019, 1939, 91-118.	0.9	27
20	A loss of function variant in CASP7 protects against Alzheimer's disease in homozygous APOE Îμ4 allele carriers. BMC Genomics, 2016, 17, 445.	2.8	26
21	A Drosophila platform identifies a novel, personalized therapy for a patient with adenoid cystic carcinoma. IScience, 2021, 24, 102212.	4.1	23
22	Institutional profile: translational pharmacogenomics at the Icahn School of Medicine at Mount Sinai. Pharmacogenomics, 2017, 18, 1381-1386.	1.3	20
23	Medically actionable pathogenic variants in a population of 13,131 healthy elderly individuals. Genetics in Medicine, 2020, 22, 1883-1886.	2.4	20
24	AN INTEGRATIVE PIPELINE FOR MULTI-MODAL DISCOVERY OF DISEASE RELATIONSHIPS. , 2014, , .		15
25	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
26	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
27	Genome-wide analysis indicates association between heterozygote advantage and healthy aging in humans. BMC Genetics, 2019, 20, 52.	2.7	10
28	DIVAS: a centralized genetic variant repository representing 150 000 individuals from multiple disease cohorts. Bioinformatics, 2016, 32, 151-153.	4.1	8
29	Identification of a novel <i>RASD1</i> somatic mutation in a <i>USP8</i> mutated corticotroph adenoma. Journal of Physical Education and Sports Management, 2017, 3, a001602.	1.2	8
30	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
31	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
32	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
33	Human GPR17 missense variants identified in metabolic disease patients have distinct downstream signaling profiles. Journal of Biological Chemistry, 2021, 297, 100881.	3.4	3
34	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
35	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
36	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

#	Article	IF	CITATIONS
37	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
38	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
39	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
40	Representing cancer clinical trial criteria and attributes using ontologies: An NLP-assisted approach Journal of Clinical Oncology, 2020, 38, e14079-e14079.	1.6	0