Wentao Yang

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/11542244/publications.pdf

Version: 2024-02-01

38	1,181	17 h-index	30
papers	citations		g-index
39	39	39	1526
all docs	docs citations	times ranked	citing authors

#	Article	IF	CITATIONS
1	Association of Genetic Ancestry With the Molecular Subtypes and Prognosis of Childhood Acute Lymphoblastic Leukemia. JAMA Oncology, 2022, 8, 354.	7.1	35
2	Noncoding genetic variation in GATA3 increases acute lymphoblastic leukemia risk through local and global changes in chromatin conformation. Nature Genetics, 2022, 54, 170-179.	21.4	29
3	Genome-wide CRISPR/Cas9 screening identifies determinant of panobinostat sensitivity in acute lymphoblastic leukemia. Blood Advances, 2022, 6, 2496-2509.	5. 2	7
4	A developmentally prometastatic niche to hepatoblastoma in neonatal liver mediated by the Cxcl1/Cxcr2 axis. Hepatology, 2022, 76, 1275-1290.	7.3	6
5	Inhibition of mitochondrial complex I reverses NOTCH1-driven metabolic reprogramming in T-cell acute lymphoblastic leukemia. Nature Communications, 2022, 13, 2801.	12.8	25
6	Genome-Wide Association Study of Susceptibility Loci for <i>TCF3-PBX1</i> Acute Lymphoblastic Leukemia in Children. Journal of the National Cancer Institute, 2021, 113, 933-937.	6.3	9
7	Effects of <i>NT5C2</i> Germline Variants on 6â€Mecaptopurine Metabolism in Children With Acute Lymphoblastic Leukemia. Clinical Pharmacology and Therapeutics, 2021, 109, 1538-1545.	4.7	5
8	Network-based systems pharmacology reveals heterogeneity in LCK and BCL2 signaling and therapeutic sensitivity of T-cell acute lymphoblastic leukemia. Nature Cancer, 2021, 2, 284-299.	13.2	70
9	Effector and regulator: Diverse functions of C. elegans C-type lectin-like domain proteins. PLoS Pathogens, 2021, 17, e1009454.	4.7	22
10	Germline RUNX1 variation and predisposition to childhood acute lymphoblastic leukemia. Journal of Clinical Investigation, 2021, 131, .	8.2	20
11	The effects of nested miRNAs and their host genes on immune defense against Bacillus thuringiensis infection in Caenorhabditis elegans. Developmental and Comparative Immunology, 2021, 123, 104144.	2.3	3
12	<i>NUDT15</i> variants confer high incidence of second malignancies in children with acute lymphoblastic leukemia. Blood Advances, 2021, 5, 5420-5428.	5 . 2	4
13	The Impact of T Cell Immunity on Chemotherapy Response in Childhood Acute Lymphoblastic Leukemia. Blood, 2021, 138, 703-703.	1.4	O
14	The functional repertoire contained within the native microbiota of the model nematode <i>Caenorhabditis elegans</i> . ISME Journal, 2020, 14, 26-38.	9.8	68
15	<i>ARID5B</i> Influences Antimetabolite Drug Sensitivity and Prognosis of Acute Lymphoblastic Leukemia. Clinical Cancer Research, 2020, 26, 256-264.	7.0	25
16	The C. elegans GATA transcription factor elt-2 mediates distinct transcriptional responses and opposite infection outcomes towards different Bacillus thuringiensis strains. PLoS Pathogens, 2020, 16, e1008826.	4.7	22
17	Identifying IGH disease clones for MRD monitoring in childhood B-cell acute lymphoblastic leukemia using RNA-Seq. Leukemia, 2020, 34, 2418-2429.	7.2	19
18	Massively parallel variant characterization identifies <i>NUDT15</i> alleles associated with thiopurine toxicity. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 5394-5401.	7.1	95

#	Article	IF	CITATIONS
19	Overcoming NOTCH1-Driven Chemoresistance in T-Cell Acute Lymphoblastic Leukemia Via Metabolic Intervention with Oxphos Inhibitor. Blood, 2020, 136, 18-20.	1.4	2
20	Title is missing!. , 2020, 16, e1008826.		0
21	Title is missing!. , 2020, 16, e1008826.		0
22	Title is missing!. , 2020, 16, e1008826.		0
23	Title is missing!. , 2020, 16, e1008826.		0
24	The Inducible Response of the Nematode Caenorhabditis elegans to Members of Its Natural Microbiota Across Development and Adult Life. Frontiers in Microbiology, 2019, 10, 1793.	3.5	26
25	Mechanisms of <i>NT5C2</i> -Mediated Thiopurine Resistance in Acute Lymphoblastic Leukemia. Molecular Cancer Therapeutics, 2019, 18, 1887-1895.	4.1	17
26	Identification of four novel associations for B-cell acute lymphoblastic leukaemia risk. Nature Communications, 2019, 10, 5348.	12.8	58
27	The genomic basis of Red Queen dynamics during rapid reciprocal host–pathogen coevolution. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 923-928.	7.1	102
28	Germline RUNX1 Variation and Predisposition to T-Cell Acute Lymphoblastic Leukemia in Children. Blood, 2019, 134, 653-653.	1.4	1
29	RNA-Seq Can Help Identify IGH Disease Clones for MRD Monitoring in Childhood B-Lymphoblastic Leukemia. Blood, 2019, 134, 1471-1471.	1.4	1
30	Highly potent host external immunity acts as a strong selective force enhancing rapid parasite virulence evolution. Environmental Microbiology, 2017, 19, 2090-2100.	3.8	11
31	ABSSeq: a new RNA-Seq analysis method based on modelling absolute expression differences. BMC Genomics, 2016, 17, 541.	2.8	31
32	GATA transcription factor as a likely key regulator of the Caenorhabditis elegans innate immune response against gut pathogens. Zoology, 2016, 119, 244-253.	1.2	34
33	Contrasting invertebrate immune defense behaviors caused by a single gene, the Caenorhabditis elegans neuropeptide receptor gene npr-1. BMC Genomics, 2016, 17, 280.	2.8	52
34	Antimicrobial effectors in the nematode <i>Caenorhabditis elegans</i> : an outgroup to the Arthropoda. Philosophical Transactions of the Royal Society B: Biological Sciences, 2016, 371, 20150299.	4.0	81
35	High Innate Immune Specificity through Diversified C-Type Lectin-Like Domain Proteins in Invertebrates. Journal of Innate Immunity, 2016, 8, 129-142.	3.8	126
36	WormExp: a web-based application for a <i>Caenorhabditis elegans</i> enrichment analysis. Bioinformatics, 2016, 32, 943-945.	4.1	93

#	Article	IF	CITATIONS
37	Overlapping and unique signatures in the proteomic and transcriptomic responses of the nematode Caenorhabditis elegans toward pathogenic Bacillus thuringiensis. Developmental and Comparative Immunology, 2015, 51, 1-9.	2.3	49
38	AMD, an Automated Motif Discovery Tool Using Stepwise Refinement of Gapped Consensuses. PLoS ONE, 2011, 6, e24576.	2.5	33