

Kenny Ye

List of Publications by Year in descending order

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Version: 2024-02-01

110
papers

45,398
citations

136740

32
h-index

40881

93
g-index

115
all docs

115
docs citations

115
times ranked

67188
citing authors

#	ARTICLE	IF	CITATIONS
1	Experience with a Perfusion-Only Screening Protocol for Evaluation of Pulmonary Embolism During the COVID-19 Pandemic Surge. <i>Journal of Nuclear Medicine</i> , 2022, 63, 598-601.	2.8	5
2	Epidemiology, Risk Factors and Outcomes of Pneumomediastinum in Patients with Coronavirus Disease 2019: A Case-Control Study. <i>Journal of Intensive Care Medicine</i> , 2022, 37, 12-20.	1.3	7
3	Genome-wide analysis of mitochondrial DNA copy number reveals loci implicated in nucleotide metabolism, platelet activation, and megakaryocyte proliferation. <i>Human Genetics</i> , 2022, 141, 127-146.	1.8	30
4	Single-cell analysis of somatic mutations in human bronchial epithelial cells in relation to aging and smoking. <i>Nature Genetics</i> , 2022, 54, 492-498.	9.4	47
5	An Atypical Form of Diabetes Among Individuals With Low BMI. <i>Diabetes Care</i> , 2022, 45, 1428-1437.	4.3	18
6	Genome Maintenance in Aging and Lung Carcinogenesis. , 2022, , .		0
7	Bronchial Field Progenitor Basal Cells Show Methylome-Wide Characteristics Reflective of Lung Cancer Case-Control, Age, and Smoking Status. , 2022, , .		0
8	Non-operative Management for Acute Appendicitis During the COVID-19 Pandemic Does Not Increase the Rate of Complications. <i>Journal of Gastrointestinal Surgery</i> , 2021, 25, 1327-1329.	0.9	15
9	Framing potential for adverse effects of repetitive subconcussive impacts in soccer in the context of athlete and non-athlete controls. <i>Brain Imaging and Behavior</i> , 2021, 15, 882-895.	1.1	12
10	Computational identification of variables in neonatal vocalizations predictive for postpubertal social behaviors in a mouse model of 16p11.2 deletion. <i>Molecular Psychiatry</i> , 2021, 26, 6578-6588.	4.1	7
11	Cellular viability and death biomarkers enables the evaluation of ocular irritation using the bovine corneal opacity and permeability assay. <i>Toxicology Letters</i> , 2021, 340, 52-57.	0.4	2
12	Diagnostic significance of the CT rim sign in cases of gangrenous cholecystitis. <i>Clinical Imaging</i> , 2021, 73, 53-56.	0.8	3
13	Safety and efficacy of image-guided retrocalcaneal bursa corticosteroid injection for the treatment of retrocalcaneal bursitis. <i>Skeletal Radiology</i> , 2021, 50, 2471-2482.	1.2	4
14	The Hypothalamic-Pituitary-Testicular Axis in Exceptionally Old Men. <i>Journal of the Endocrine Society</i> , 2021, 5, A727-A727.	0.1	0
15	Bronchial Field Progenitor Basal Cells Show Methylome-Wide Characteristics Reflective of Lung Cancer Case-Control, Age, and Smoking Status of the Donor. , 2021, , .		0
16	Extracellular Vesicle Capture by Antibody of Choice and Enzymatic Release (EVâ€CATCHER): A customizable purification assay designed for smallâ€RNA biomarker identification and evaluation of circulating smallâ€EVs. <i>Journal of Extracellular Vesicles</i> , 2021, 10, e12110.	5.5	26
17	The antagonistic pleiotropy of insulinâ€like growth factor 1. <i>Aging Cell</i> , 2021, 20, e13443.	3.0	28
18	Rare genetic coding variants associated with human longevity and protection against age-related diseases. <i>Nature Aging</i> , 2021, 1, 783-794.	5.3	22

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19	The Utility of 18FDG PET/CT Versus Bone Scan for Identification of Bone Metastases in a Pediatric Sarcoma Population and a Review of the Literature. <i>Journal of Pediatric Hematology/Oncology</i> , 2021, 43, 52-58.	0.3	14
20	Emerging Adaptive Strategies Under Temperature Fluctuations in a Laboratory Evolution Experiment of <i>Escherichia Coli</i> . <i>Frontiers in Microbiology</i> , 2021, 12, 724982.	1.5	4
21	Behavioral and Genetic Factors Associated with Successful Long-Term Cessation in Persons with HIV Who Smoke Cigarettes. <i>Journal of Smoking Cessation</i> , 2021, 2021, 1894160.	0.3	0
22	Survival Disparities in Black Patients With EGFR-mutated Non-small-cell Lung Cancer. <i>Clinical Lung Cancer</i> , 2020, 21, 177-185.	1.1	10
23	Lower-extremity Arterial Thrombosis Associated with COVID-19 Is Characterized by Greater Thrombus Burden and Increased Rate of Amputation and Death. <i>Radiology</i> , 2020, 297, E263-E269.	3.6	66
24	Structural Refinement of the Tubulin Ligand (+)-Discodermolide to Attenuate Chemotherapy-Mediated Senescence. <i>Molecular Pharmacology</i> , 2020, 98, 156-167.	1.0	4
25	Effects of Diet Choice on Stem Cell Function Necessitate Clarity in Selection and Reporting. <i>Cell Stem Cell</i> , 2020, 27, 11-12.	5.2	6
26	Impact of Patient-Centered Care on the Patient Experience in Nuclear Medicine. <i>Current Problems in Diagnostic Radiology</i> , 2020, 49, 326-332.	0.6	2
27	Prognostic Factors for North American Adult T Cell Leukemia Lymphoma: Defining Risk Groups Using a Four-Point Score Prognostic System. <i>Blood</i> , 2020, 136, 38-39.	0.6	0
28	A meta-analysis of genome-wide association studies identifies multiple longevity genes. <i>Nature Communications</i> , 2019, 10, 3669.	5.8	214
29	Diffusion Tensor Imaging of the Evolving Response to Mild Traumatic Brain Injury in Rats. <i>Journal of Experimental Neuroscience</i> , 2019, 13, 117906951985862.	2.3	21
30	Multi-modal neuroimaging of dual-task walking: Structural MRI and fNIRS analysis reveals prefrontal grey matter volume moderation of brain activation in older adults. <i>NeuroImage</i> , 2019, 189, 745-754.	2.1	52
31	Genetic Variants Associated with FDNY WTC-Related Sarcoidosis. <i>International Journal of Environmental Research and Public Health</i> , 2019, 16, 1830.	1.2	19
32	The nutritional environment determines which and how intestinal stem cells contribute to homeostasis and tumorigenesis. <i>Carcinogenesis</i> , 2019, 40, 937-946.	1.3	26
33	Exhaled Small, Polar, Energetics-Related Metabolites by GC-MS for Lung Cancer Risk Assessment. , 2019, , .		0
34	Ultra-High-Frequency Reprogramming of Individual Long-Term Hematopoietic Stem Cells Yields Low Somatic Variant Induced Pluripotent Stem Cells. <i>Cell Reports</i> , 2019, 26, 2580-2592.e7.	2.9	14
35	The effect of fear of falling on prefrontal cortex activation and efficiency during walking in older adults. <i>GeroScience</i> , 2019, 41, 89-100.	2.1	34
36	P1.11-11 Initial Discovery of Exhaled Small Polar Energetics-Related Metabolites by GC-MS for Lung Cancer Risk Assessment. <i>Journal of Thoracic Oncology</i> , 2019, 14, S519.	0.5	3

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37	SMALL SIZE LUNG NODULES WITH IRREGULAR BORDER ARE BETTER CAUGHT IN PERIPHERAL AIRWAY BRONCHOSCOPY. <i>Chest</i> , 2019, 156, A1757.	0.4	0
38	Ventricular Arterial Coupling: A Novel Echocardiographic Risk Factor for Disease Progression in Pediatric Dilated Cardiomyopathy. <i>Pediatric Cardiology</i> , 2019, 40, 330-338.	0.6	5
39	Diagnostic yield of head CT in pediatric emergency department patients with acute psychosis or hallucinations. <i>Pediatric Radiology</i> , 2019, 49, 240-244.	1.1	3
40	Improved Dose-Response Relationship of (+)-Discodermolide-Taxol Hybrid Congeners. <i>Journal of Natural Products</i> , 2018, 81, 607-615.	1.5	4
41	Copy number elevation of 22q11.2 genes arrests the developmental maturation of working memory capacity and adult hippocampal neurogenesis. <i>Molecular Psychiatry</i> , 2018, 23, 985-992.	4.1	22
42	Evaluation of Hair Density in Different Ethnicities in a Healthy American Population Using Quantitative Trichoscopic Analysis. <i>Skin Appendage Disorders</i> , 2018, 4, 304-307.	0.5	20
43	Adjustment for covariates using summary statistics of genome-wide association studies. <i>Genetic Epidemiology</i> , 2018, 42, 812-825.	0.6	5
44	Near-Term Decrease in Brain Volume following Mild Traumatic Injury Is Detectible in the Context of Preinjury Volumetric Stability: Neurobiologic Insights from Analysis of Historical Imaging Examinations. <i>American Journal of Neuroradiology</i> , 2018, 39, 1821-1826.	1.2	2
45	Detecting, quantifying, and discriminating the mechanism of mosaic chromosomal aneuploidies using MAD-seq. <i>Genome Research</i> , 2018, 28, 1039-1052.	2.4	3
46	Computational Analysis of Neonatal Mouse Ultrasonic Vocalization. <i>Current Protocols in Mouse Biology</i> , 2018, 8, e46.	1.2	7
47	MicroRNA expression in benign breast tissue and risk of subsequent invasive breast cancer. <i>PLoS ONE</i> , 2018, 13, e0191814.	1.1	9
48	32. Copy Number Variation of 22q11.2 Genes Arrests the Developmental Maturation of Working Memory Capacity and Adult Hippocampal Neurogenesis. <i>Biological Psychiatry</i> , 2017, 81, S14.	0.7	0
49	Association between lifestyle, menstrual/reproductive history, and histological factors and risk of breast cancer in women biopsied for benign breast disease. <i>Breast Cancer Research and Treatment</i> , 2017, 165, 623-631.	1.1	26
50	Measuring shared variants in cohorts of discordant siblings with applications to autism. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, 7073-7076.	3.3	9
51	Evaluation and Adaptation of a Laboratory-Based cDNA Library Preparation Protocol for Retrospective Sequencing of Archived MicroRNAs from up to 35-Year-Old Clinical FFPE Specimens. <i>International Journal of Molecular Sciences</i> , 2017, 18, 627.	1.8	15
52	Molecular Histochemistry Identifies Peptidomic Organization and Reorganization Along Striatal Projection Units. <i>Biological Psychiatry</i> , 2016, 79, 415-420.	0.7	5
53	Structure and function of neonatal social communication in a genetic mouse model of autism. <i>Molecular Psychiatry</i> , 2016, 21, 1208-1214.	4.1	74
54	Detecting dispersed duplications in high-throughput sequencing data using a database-free approach. <i>Bioinformatics</i> , 2016, 32, 505-510.	1.8	14

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55	Abstract LB-066: Proteomic-based senescent biomarker identification and characterization in non-small cell lung cancer. , 2016, , .		0
56	Bayesian detection of embryonic gene expression onset in <i>C. elegans</i> . <i>Annals of Applied Statistics</i> , 2015, 9, .	0.5	5
57	A global reference for human genetic variation. <i>Nature</i> , 2015, 526, 68-74.	13.7	13,998
58	Low load for disruptive mutations in autism genes and their biased transmission. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, E5600-7.	3.3	129
59	The contribution of de novo coding mutations to autism spectrum disorder. <i>Nature</i> , 2014, 515, 216-221.	13.7	2,188
60	Common genetic variants regulating <i>ADD3</i> gene expression alter biliary atresia risk. <i>Journal of Hepatology</i> , 2013, 59, 1285-1291.	1.8	84
61	Design and Statistical Analysis of Pooled Next Generation Sequencing for Rare Variants. <i>Journal of Probability and Statistics</i> , 2012, 2012, 1-19.	0.3	4
62	Genotype Copy Number Variations using Gaussian Mixture Models: Theory and Algorithms. <i>Statistical Applications in Genetics and Molecular Biology</i> , 2012, 11, 5.	0.2	7
63	Reducing system noise in copy number data using principal components of self-self hybridizations. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, E103-E110.	3.3	8
64	Distinguishing Between Longevity and Buffered-Deleterious Genotypes for Exceptional Human Longevity: The Case of the <i>MTP</i> Gene. <i>Journals of Gerontology - Series A Biological Sciences and Medical Sciences</i> , 2012, 67, 1153-1160.	1.7	27
65	De Novo Gene Disruptions in Children on the Autistic Spectrum. <i>Neuron</i> , 2012, 74, 285-299.	3.8	1,311
66	An integrated map of genetic variation from 1,092 human genomes. <i>Nature</i> , 2012, 491, 56-65.	13.7	7,199
67	Effective DNA/RNA Co-Extraction for Analysis of MicroRNAs, mRNAs, and Genomic DNA from Formalin-Fixed Paraffin-Embedded Specimens. <i>PLoS ONE</i> , 2012, 7, e34683.	1.1	55
68	Gene Size Matters. <i>PLoS ONE</i> , 2012, 7, e49093.	1.1	21
69	A Systematic Survey of Loss-of-Function Variants in Human Protein-Coding Genes. <i>Science</i> , 2012, 335, 823-828.	6.0	1,095
70	Rare De Novo and Transmitted Copy-Number Variation in Autistic Spectrum Disorders. <i>Neuron</i> , 2011, 70, 886-897.	3.8	639
71	Estimating Allele Frequency from Next-Generation Sequencing of Pooled Mitochondrial DNA Samples. <i>Frontiers in Genetics</i> , 2011, 2, 51.	1.1	9
72	Mapping copy number variation by population-scale genome sequencing. <i>Nature</i> , 2011, 470, 59-65.	13.7	991

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73	Identification of genes and variants associated with quantitative traits using Bayesian factor screening. BMC Proceedings, 2011, 5, S4.	1.8	1
74	Detecting multiple causal rare variants in exome sequence data. Genetic Epidemiology, 2011, 35, S18-21.	0.6	4
75	Resequencing of pooled DNA for detecting disease associations with rare variants. Genetic Epidemiology, 2010, 34, 492-501.	0.6	23
76	A map of human genome variation from population-scale sequencing. Nature, 2010, 467, 1061-1073.	13.7	7,209
77	Genome-wide analysis of DNA binding and transcriptional regulation by the mammalian Doublesex homolog DMRT1 in the juvenile testis. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 13360-13365.	3.3	92
78	High definition profiling of mammalian DNA methylation by array capture and single molecule bisulfite sequencing. Genome Research, 2009, 19, 1593-1605.	2.4	198
79	Pindel: a pattern growth approach to detect break points of large deletions and medium sized insertions from paired-end short reads. Bioinformatics, 2009, 25, 2865-2871.	1.8	1,811
80	Sensitive and accurate detection of copy number variants using read depth of coverage. Genome Research, 2009, 19, 1586-1592.	2.4	518
81	A partial least-square approach for modeling gene-gene and gene-environment interactions when multiple markers are genotyped. Genetic Epidemiology, 2009, 33, 6-15.	0.6	40
82	Model-robust supersaturated and partially supersaturated designs. Journal of Statistical Planning and Inference, 2009, 139, 45-53.	0.4	20
83	The BCL6 transcriptional program features repression of multiple oncogenes in primary B cells and is deregulated in DLBCL. Blood, 2009, 113, 5536-5548.	0.6	205
84	Meta-Analysis of Microarray Studies Reveals a Novel Hematopoietic Progenitor Cell Signature and Demonstrates Feasibility of Inter-Platform Data Integration. PLoS ONE, 2008, 3, e2965.	1.1	20
85	Computing Power and Sample Size for Case-Control Association Studies with Copy Number Polymorphism: Application of Mixture-Based Likelihood Ratio Test. PLoS ONE, 2008, 3, e3475.	1.1	15
86	An Integrative Genomic and Epigenomic Approach for the Study of Transcriptional Regulation. PLoS ONE, 2008, 3, e1882.	1.1	77
87	Transcriptional signature with differential expression of BCL6 target genes accurately identifies BCL6-dependent diffuse large B cell lymphomas. Proceedings of the National Academy of Sciences of the United States of America, 2007, 104, 3207-3212.	3.3	130
88	Buffering Mechanisms in Aging: A Systems Approach Toward Uncovering the Genetic Component of Aging. PLoS Computational Biology, 2007, 3, e170.	1.5	106
89	A unified genetic theory for sporadic and inherited autism. Proceedings of the National Academy of Sciences of the United States of America, 2007, 104, 12831-12836.	3.3	284
90	Strong Association of De Novo Copy Number Mutations with Autism. Science, 2007, 316, 445-449.	6.0	2,497

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91	Positive association of schizophrenia toJARID2 gene. American Journal of Medical Genetics Part B: Neuropsychiatric Genetics, 2007, 144B, 45-51.	1.1	32
92	Model discriminationâ€”another perspective on model-robust designs. Journal of Statistical Planning and Inference, 2007, 137, 1576-1583.	0.4	20
93	Optimal Orthogonal Three-Level Factorial Designs for Factor Screening and Response Surface Exploration. , 2007, , 221-228.		6
94	Global DNA Methylation Profiling Demonstrates That Idiopathic Myelofibrosis Is Characterized by a Distinct Epigenetic Signature with Aberrant Methylation Changes in Genes Involved in Inflammation and Hematopoiesis. Blood, 2007, 110, 1536-1536.	0.6	2
95	Data Mining of Hematopoietic Stem Cell Microarray Studies Reveals a Novel Stem Cell Gene Expression Signature and Demonstrates Feasibility of Integrating Data from Different Labs and Different Microarray Platforms.. Blood, 2007, 110, 4073-4073.	0.6	3
96	Integrated Epigenomic Profiling Reveals Aberrant DNA Hypomethylation in LGL and Demonstrates That a Combination of Genetic and Epigenetic Events Results in Leukemic Evolution in Model of Large Granular Lymphocytic Leukemia.. Blood, 2007, 110, 2129-2129.	0.6	0
97	Global Epigenomic Profiling Demonstrates That Myelodysplasia Is Characterized by a Distinct Epigenetic Signature with Aberrant DNA Methylation Changes Involving Various Malignant and Hematopoietic Pathways.. Blood, 2007, 110, 2436-2436.	0.6	0
98	Comparative isoschizomer profiling of cytosine methylation: The HELP assay. Genome Research, 2006, 16, 1046-1055.	2.4	355
99	Novel patterns of genome rearrangement and their association with survival in breast cancer. Genome Research, 2006, 16, 1465-1479.	2.4	291
100	A High Resolution Epigenomic Map of Myelofibrosis Reveals Multiple Chromosomal Deletions and Amplifications Accompanied by a High Level of Functionally Important Methylation.. Blood, 2006, 108, 2684-2684.	0.6	2
101	High Resolution Epigenomic Mapping of Myelodysplastic Syndrome Reveals a High Level of Functionally Important Methylation.. Blood, 2006, 108, 2637-2637.	0.6	0
102	Meta-Transcriptome of Bone Marrow Stem Cells Demonstrates Platform and Lab Dependant Variability in Gene Expression and Reveals a Novel Set of Enriched Genes.. Blood, 2006, 108, 4189-4189.	0.6	0
103	Epigenetic Signatures Accurately Distinguish Leukemia Subtypes and Provide a More Comprehensive Representation of Differentially Regulated Genes Than Gene Expression Profiling.. Blood, 2006, 108, 735-735.	0.6	0
104	A Comprehensive Genomic Approach Using Gain of Function and Loss of Function Cell Models and ChIP-on-Chip Technology Identifies Novel Promyelocytic Zinc Finger Protein Target Genes.. Blood, 2006, 108, 1407-1407.	0.6	0
105	A BCL6 Target Gene Signature Predicts the Biological Behavior and Classification of Diffuse Large B-Cell Lymphoma.. Blood, 2006, 108, 616-616.	0.6	0
106	Buffering Mechanisms in Aging: A systems approach towards uncovering the genetic component of aging. PLoS Computational Biology, 2005, preprint, e170.	1.5	2
107	Sources of uncertainty and error in the simulation of flow in porous media. Computational and Applied Mathematics, 2004, 23, .	1.3	8
108	Large-Scale Copy Number Polymorphism in the Human Genome. Science, 2004, 305, 525-528.	6.0	2,293

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109	Representational Oligonucleotide Microarray Analysis: A High-Resolution Method to Detect Genome Copy Number Variation. <i>Genome Research</i> , 2003, 13, 2291-2305.	2.4	376
110	Uncertainty Quantification for Multiscale Simulations1. <i>Journal of Fluids Engineering, Transactions of the ASME</i> , 2002, 124, 29-41.	0.8	44