

Yong Kong

List of Publications by Year in descending order

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Version: 2024-02-01

102
papers

8,708
citations

94433

37
h-index

46799

89
g-index

111
all docs

111
docs citations

111
times ranked

17192
citing authors

#	ARTICLE	IF	CITATIONS
1	Distributions of successions of arbitrary multisets. Communications in Statistics - Theory and Methods, 2022, 51, 1693-1705.	1.0	2
2	Multiple consecutive runs of multi-state trials: Distributions of $\langle \text{mml:math xmlns:mml="http://www.w3.org/1998/Math/MathML" display="inline" id="d1e22"} \rangle$		

#	ARTICLE	IF	CITATIONS
19	Ketogenic diet activates protective $\hat{I}^3\hat{I}$ T cell responses against influenza virus infection. <i>Science Immunology</i> , 2019, 4, .	11.9	98
20	The Lupus Susceptibility Locus Sgp3 Encodes the Suppressor of Endogenous Retrovirus Expression SNERV. <i>Immunity</i> , 2019, 50, 334-347.e9.	14.3	61
21	Generating Function Methods for Run and Scan Statistics. , 2019, , 1-19.		2
22	Desynchronization of the molecular clock contributes to the heterogeneity of the inflammatory response. <i>Science Signaling</i> , 2019, 12, .	3.6	30
23	Reply to IÃ±iguez et al.: ERVmap is a validated approach to mapping proviral endogenous retroviruses in the human genome. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 21352-21353.	7.1	2
24	Exosomal MicroRNAs Associate With Neuropsychological Performance in Individuals With HIV Infection on Antiretroviral Therapy. <i>Journal of Acquired Immune Deficiency Syndromes (1999)</i> , 2019, 82, 514-522.	2.1	15
25	Decoupling Combinatorial Complexity: a Two-Step Approach to Distributions of Runs. <i>Methodology and Computing in Applied Probability</i> , 2019, 21, 789-803.	1.2	5
26	Gastrointestinal Microbiota Disruption and Risk of Colonization With Carbapenem-resistant <i>Pseudomonas aeruginosa</i> in Intensive Care Unit Patients. <i>Clinical Infectious Diseases</i> , 2019, 69, 604-613.	5.8	43
27	Type I interferons instigate fetal demise after Zika virus infection. <i>Science Immunology</i> , 2018, 3, .	11.9	212
28	<i>Haemophilus influenzae</i> genome evolution during persistence in the human airways in chronic obstructive pulmonary disease. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, E3256-E3265.	7.1	57
29	ERVmap analysis reveals genome-wide transcription of human endogenous retroviruses. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, 12565-12572.	7.1	134
30	Regional Differences in Airway Epithelial Cells Reveal Tradeoff between Defense against Oxidative Stress and Defense against Rhinovirus. <i>Cell Reports</i> , 2018, 24, 3000-3007.e3.	6.4	46
31	Changes in IgA Protease Expression Are Conferred by Changes in Genomes during Persistent Infection by Nontypeable <i>Haemophilus influenzae</i> in Chronic Obstructive Pulmonary Disease. <i>Infection and Immunity</i> , 2018, 86, .	2.2	15
32	Number of appearances of events in random sequences: a new generating function approach to Type II and Type III runs. <i>Annals of the Institute of Statistical Mathematics</i> , 2017, 69, 489-495.	0.8	7
33	The mth longest runs of multivariate random sequences. <i>Annals of the Institute of Statistical Mathematics</i> , 2017, 69, 497-512.	0.8	5
34	IFT56 regulates vertebrate developmental patterning by maintaining IFTB integrity and ciliary microtubule architecture. <i>Development (Cambridge)</i> , 2017, 144, 1544-1553.	2.5	25
35	Macrophage function in tissue repair and remodeling requires IL-4 or IL-13 with apoptotic cells. <i>Science</i> , 2017, 356, 1072-1076.	12.6	408
36	Aging impairs both primary and secondary RIG-I signaling for interferon induction in human monocytes. <i>Science Signaling</i> , 2017, 10, .	3.6	113

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37	Antimicrobial activity of antisense peptide-peptide nucleic acid conjugates against non-typeable <i>Haemophilus influenzae</i> in planktonic and biofilm forms. <i>Journal of Antimicrobial Chemotherapy</i> , 2017, 72, 137-144.	3.0	33
38	IFT56 regulates vertebrate developmental patterning by maintaining IFTB complex integrity and ciliary microtubule architecture. <i>Journal of Cell Science</i> , 2017, 130, e1.2-e1.2.	2.0	1
39	A uniform survey of allele-specific binding and expression over 1000-Genomes-Project individuals. <i>Nature Communications</i> , 2016, 7, 11101.	12.8	78
40	Effect of Fluoroquinolones and Macrolides on Eradication and Resistance of <i>Haemophilus influenzae</i> in Chronic Obstructive Pulmonary Disease. <i>Antimicrobial Agents and Chemotherapy</i> , 2016, 60, 4151-4158.	3.2	26
41	The Adventitious Angles Problem: The Lonely Fractional Derived Angle. <i>American Mathematical Monthly</i> , 2016, 123, 814.	0.3	0
42	Association of sputum microbiota profiles with severity of community-acquired pneumonia in children. <i>BMC Infectious Diseases</i> , 2016, 16, 317.	2.9	44
43	The regulatory element READ1 epistatically influences reading and language, with both deleterious and protective alleles. <i>Journal of Medical Genetics</i> , 2016, 53, 163-171.	3.2	29
44	Viral Spread to Enteric Neurons Links Genital HSV-1 Infection to Toxic Megacolon and Lethality. <i>Cell Host and Microbe</i> , 2016, 19, 788-799.	11.0	58
45	Number of appearances of events in random sequences: A new approach to non-overlapping runs. <i>Communications in Statistics - Theory and Methods</i> , 2016, 45, 6765-6772.	1.0	6
46	Expression of IgA Proteases by <i>Haemophilus influenzae</i> in the Respiratory Tract of Adults With Chronic Obstructive Pulmonary Disease. <i>Journal of Infectious Diseases</i> , 2015, 212, 1798-1805.	4.0	29
47	Distributions of Runs Revisited. <i>Communications in Statistics - Theory and Methods</i> , 2015, 44, 4663-4678.	1.0	7
48	Analysis of gene-environment interactions in postnatal development of the mammalian intestine. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 1929-1936.	7.1	77
49	Exome sequencing identifies recurrent mutations in NF1 and RASopathy genes in sun-exposed melanomas. <i>Nature Genetics</i> , 2015, 47, 996-1002.	21.4	348
50	Nanoparticles that deliver triplex-forming peptide nucleic acid molecules correct F508del CFTR in airway epithelium. <i>Nature Communications</i> , 2015, 6, 6952.	12.8	114
51	An international effort towards developing standards for best practices in analysis, interpretation and reporting of clinical genome sequencing results in the CLARITY Challenge. <i>Genome Biology</i> , 2014, 15, R53.	9.6	101
52	Rare SF3B1 R625 mutations in cutaneous melanoma. <i>Melanoma Research</i> , 2014, 24, 332-334.	1.2	64
53	Forward genetics defines Xylt1 as a key, conserved regulator of early chondrocyte maturation and skeletal length. <i>Developmental Biology</i> , 2014, 385, 67-82.	2.0	44
54	Distributions of positive signals in pyrosequencing. <i>Journal of Mathematical Biology</i> , 2014, 69, 39-54.	1.9	0

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55	Dynamic Changes in the <i>Streptococcus pneumoniae</i> Transcriptome during Transition from Biofilm Formation to Invasive Disease upon Influenza A Virus Infection. <i>Infection and Immunity</i> , 2014, 82, 4607-4619.	2.2	121
56	Alleles of a Polymorphic ETV6 Binding Site in DCDC2 Confer Risk of Reading and Language Impairment. <i>American Journal of Human Genetics</i> , 2014, 94, 798.	6.2	1
57	Computational Analysis in Cancer Exome Sequencing. <i>Methods in Molecular Biology</i> , 2014, 1176, 219-227.	0.9	1
58	Length distribution of sequencing by synthesis: fixed flow cycle model. <i>Journal of Mathematical Biology</i> , 2013, 67, 389-410.	1.9	1
59	Integrative Annotation of Variants from 1092 Humans: Application to Cancer Genomics. <i>Science</i> , 2013, 342, 1235-1237.	12.6	341
60	Forward genetics identifies Klf1/1810019J16Rik as an essential regulator of the proliferation-differentiation decision in epidermal progenitor cells. <i>Developmental Biology</i> , 2013, 383, 201-213.	2.0	31
61	Negligible impact of rare autoimmune-locus coding-region variants on missing heritability. <i>Nature</i> , 2013, 498, 232-235.	27.8	184
62	Alleles of a Polymorphic ETV6 Binding Site in DCDC2 Confer Risk of Reading and Language Impairment. <i>American Journal of Human Genetics</i> , 2013, 93, 19-28.	6.2	60
63	Adjusting for Background Mutation Frequency Biases Improves the Identification of Cancer Driver Genes. <i>IEEE Transactions on Nanobioscience</i> , 2013, 12, 150-157.	3.3	10
64	Upper Respiratory Tract Microbial Communities, Acute Otitis Media Pathogens, and Antibiotic Use in Healthy and Sick Children. <i>Applied and Environmental Microbiology</i> , 2012, 78, 6262-6270.	3.1	172
65	Exome sequencing identifies recurrent somatic RAC1 mutations in melanoma. <i>Nature Genetics</i> , 2012, 44, 1006-1014.	21.4	1,052
66	Exon capture and bulk segregant analysis: rapid discovery of causative mutations using high-throughput sequencing. <i>BMC Genomics</i> , 2012, 13, 649.	2.8	16
67	Forward genetics uncovers Transmembrane protein 107 as a novel factor required for ciliogenesis and Sonic hedgehog signaling. <i>Developmental Biology</i> , 2012, 368, 382-392.	2.0	40
68	AlleleSeq: analysis of allele-specific expression and binding in a network framework. <i>Molecular Systems Biology</i> , 2011, 7, 522.	7.2	284
69	The Expectation of Sample Central Moments. <i>American Statistician</i> , 2011, 65, 198-199.	1.6	2
70	Btrim: A fast, lightweight adapter and quality trimming program for next-generation sequencing technologies. <i>Genomics</i> , 2011, 98, 152-153.	2.9	531
71	Microbial Communities of the Upper Respiratory Tract and Otitis Media in Children. <i>MBio</i> , 2011, 2, e00245-10.	4.1	193
72	MU2A-reconciling the genome and transcriptome to determine the effects of base substitutions. <i>Bioinformatics</i> , 2011, 27, 416-418.	4.1	7

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73	Analysis of genomic variation in non-coding elements using population-scale sequencing data from the 1000 Genomes Project. <i>Nucleic Acids Research</i> , 2011, 39, 7058-7076.	14.5	81
74	<i>Streptococcus pneumoniae</i> Serotype 6C: an Intra- and Interclonal Complex Comparison. <i>Journal of Bacteriology</i> , 2011, 193, 3409-3410.	2.2	4
75	Note: Solution of one-dimensional self-assembly problem in multiple-component systems with correction of overcounting of non-symmetrical complexes. <i>Journal of Chemical Physics</i> , 2011, 135, 156101.	3.0	5
76	Construction and maintenance of randomized retroviral expression libraries for transmembrane protein engineering. <i>Protein Engineering, Design and Selection</i> , 2011, 24, 311-320.	2.1	6
77	<i>Streptococcus pneumoniae</i> Clonal Complex 199: Genetic Diversity and Tissue-Specific Virulence. <i>PLoS ONE</i> , 2011, 6, e18649.	2.5	16
78	Heterologous quaternary structure of CXCL12 and its relationship to the CC chemokine family. <i>Proteins: Structure, Function and Bioinformatics</i> , 2010, 78, 1331-1337.	2.6	40
79	Statistical Distributions of Pyrosequencing. <i>Journal of Computational Biology</i> , 2009, 16, 31-42.	1.6	4
80	Integrating Sequencing Technologies in Personal Genomics: Optimal Low Cost Reconstruction of Structural Variants. <i>PLoS Computational Biology</i> , 2009, 5, e1000432.	3.2	14
81	Calculating complexity of large randomized libraries. <i>Journal of Theoretical Biology</i> , 2009, 259, 641-645.	1.7	6
82	Statistical Distributions of Sequencing by Synthesis with Probabilistic Nucleotide Incorporation. <i>Journal of Computational Biology</i> , 2009, 16, 817-827.	1.6	4
83	Substrate Discrimination among Mitogen-activated Protein Kinases through Distinct Docking Sequence Motifs. <i>Journal of Biological Chemistry</i> , 2008, 283, 19511-19520.	3.4	130
84	Generalized Correlation Functions and Their Applications in Selection of Optimal Multiple Spaced Seeds for Homology Search. <i>Journal of Computational Biology</i> , 2007, 14, 238-254.	1.6	10
85	Asymptotics of the monomer-dimer model on two-dimensional semi-infinite lattices. <i>Physical Review E</i> , 2007, 75, 051123.	2.1	5
86	Keck Foundation Biotechnology Resource Laboratory, Yale University. <i>Yale Journal of Biology and Medicine</i> , 2007, 80, 195-211.	0.2	3
87	Monomer-dimer model in two-dimensional rectangular lattices with fixed dimer density. <i>Physical Review E</i> , 2006, 74, 061102.	2.1	20
88	Packing dimers on $(2p+1)\tilde{A}-(2q+1)\tilde{B}$ lattices. <i>Physical Review E</i> , 2006, 73, 016106.	2.1	26
89	Distribution of Runs and Longest Runs. <i>Journal of the American Statistical Association</i> , 2006, 101, 1253-1263.	3.1	23
90	Logarithmic corrections in the free energy of monomer-dimer model on plane lattices with free boundaries. <i>Physical Review E</i> , 2006, 74, 011102.	2.1	22

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91	MicroRNA: Biological and Computational Perspective. <i>Genomics, Proteomics and Bioinformatics</i> , 2005, 3, 62-72.	6.9	39
92	Extension of Goulden's Jackson cluster method on pattern occurrences in random sequences and comparison with Rognier's Szpankowski method. <i>Journal of Difference Equations and Applications</i> , 2005, 11, 1265-1271.	1.1	7
93	Fluorescence Anisotropy Studies on the Ku-DNA Interaction. <i>Journal of Biological Chemistry</i> , 2004, 279, 42826-42835.	3.4	35
94	A Protein Interaction Map of <i>Drosophila melanogaster</i> . <i>Science</i> , 2003, 302, 1727-1736.	12.6	2,151
95	A note on the quantitative properties of McGhee-von Hippel model. <i>Biophysical Chemistry</i> , 2002, 95, 1-6.	2.8	3
96	A Simple Method for Evaluating Partition Functions of Linear Polymers. <i>Journal of Physical Chemistry B</i> , 2001, 105, 10111-10114.	2.6	16
97	A Summation Identity: 10575. <i>American Mathematical Monthly</i> , 1999, 106, 266.	0.3	0
98	Ligand binding on ladder lattices. <i>Biophysical Chemistry</i> , 1999, 81, 7-21.	2.8	4
99	General recurrence theory of ligand binding on a three-dimensional lattice. <i>Journal of Chemical Physics</i> , 1999, 111, 4790-4799.	3.0	9
100	Crystal structures of the Klenow fragment of <i>Thermus aquaticus</i> DNA polymerase I complexed with deoxyribonucleoside triphosphates. <i>Protein Science</i> , 1998, 7, 1116-1123.	7.6	102
101	Calculation of the reaction field due to off-center point multipoles. <i>Journal of Chemical Physics</i> , 1997, 107, 481-492.	3.0	55
102	Theory of multivalent binding in one and two-dimensional lattices. <i>Biophysical Chemistry</i> , 1996, 61, 107-124.	2.8	36