

Marek Kimmel

List of Publications by Year in descending order

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114
papers

6,024
citations

94433

37
h-index

76900

74
g-index

132
all docs

132
docs citations

132
times ranked

6836
citing authors

#	ARTICLE	IF	CITATIONS
1	Alveolar soft-part sarcoma. A clinico-pathologic study of half a century. <i>Cancer</i> , 1989, 63, 1-13.	4.1	438
2	The Effect of Surgical Treatment on Survival from Early Lung Cancer. <i>Chest</i> , 1992, 101, 1013-1018.	0.8	344
3	simuPOP: a forward-time population genetics simulation environment. <i>Bioinformatics</i> , 2005, 21, 3686-3687.	4.1	287
4	Mathematical model of NF- κ B regulatory module. <i>Journal of Theoretical Biology</i> , 2004, 228, 195-215.	1.7	264
5	Mammary angiosarcoma: The prognostic significance of tumor differentiation. <i>Cancer</i> , 1988, 62, 2145-2151.	4.1	235
6	Lymphomas in dogs a morphologic, immunologic, and clinical study. <i>Cancer</i> , 1990, 66, 480-490.	4.1	232
7	Signatures of Population Expansion in Microsatellite Repeat Data. <i>Genetics</i> , 1998, 148, 1921-1930.	2.9	221
8	The sensitivity of bladder wash flow cytometry, bladder wash cytology, and voided cytology in the detection of bladder carcinoma. <i>Cancer</i> , 1987, 60, 1423-1427.	4.1	211
9	Chronic Infection Depletes Hematopoietic Stem Cells through Stress-Induced Terminal Differentiation. <i>Cell Reports</i> , 2016, 17, 2584-2595.	6.4	196
10	Prediction of missense mutation functionality depends on both the algorithm and sequence alignment employed. <i>Human Mutation</i> , 2011, 32, 661-668.	2.5	195
11	An Accurate, Sensitive, and Scalable Method to Identify Functional Sites in Protein Structures. <i>Journal of Molecular Biology</i> , 2003, 326, 255-261.	4.2	174
12	Chronic infection drives Dnmt3a-loss-of-function clonal hematopoiesis via IFN γ signaling. <i>Cell Stem Cell</i> , 2021, 28, 1428-1442.e6.	11.1	164
13	Impact of Reduced Tobacco Smoking on Lung Cancer Mortality in the United States During 1975-2000. <i>Journal of the National Cancer Institute</i> , 2012, 104, 541-548.	6.3	145
14	Evolutionary Action Score of TP53 Identifies High-Risk Mutations Associated with Decreased Survival and Increased Distant Metastases in Head and Neck Cancer. <i>Cancer Research</i> , 2015, 75, 1527-1536.	0.9	139
15	Transcriptional stochasticity in gene expression. <i>Journal of Theoretical Biology</i> , 2006, 238, 348-367.	1.7	120
16	Screening for lung cancer: The Mayo lung project revisited. <i>Cancer</i> , 1993, 72, 1573-1580.	4.1	104
17	NF- κ B and IRF pathways: cross-regulation on target genes promoter level. <i>BMC Genomics</i> , 2015, 16, 307.	2.8	104
18	Branching Processes in Biology. <i>Interdisciplinary Applied Mathematics</i> , 2015, , .	0.3	104

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19	A Study of 53 Patients. <i>Annals of Surgery</i> , 1987, 205, 144-150.	4.2	103
20	Mathematical modeling as a tool for planning anticancer therapy. <i>European Journal of Pharmacology</i> , 2009, 625, 108-121.	3.5	97
21	Wee-1 Kinase Inhibition Overcomes Cisplatin Resistance Associated with High-Risk TP53 Mutations in Head and Neck Cancer through Mitotic Arrest Followed by Senescence. <i>Molecular Cancer Therapeutics</i> , 2015, 14, 608-619.	4.1	97
22	Microarray experiments and factors which affect their reliability. <i>Biology Direct</i> , 2015, 10, 46.	4.6	91
23	Measures of Variation at DNA Repeat Loci under a General Stepwise Mutation Model. <i>Theoretical Population Biology</i> , 1996, 50, 345-367.	1.1	87
24	Assessment of Luminal and Basal Phenotypes in Bladder Cancer. <i>Scientific Reports</i> , 2020, 10, 9743.	3.3	83
25	Cell fate in antiviral response arises in the crosstalk of IRF, NF- κ B and JAK/STAT pathways. <i>Nature Communications</i> , 2018, 9, 493.	12.8	81
26	Evolutionary Action Score of TP53 Coding Variants Is Predictive of Platinum Response in Head and Neck Cancer Patients. <i>Cancer Research</i> , 2015, 75, 1205-1215.	0.9	78
27	Dynamics of Repeat Polymorphisms Under a Forward-Backward Mutation Model: Within- and Between-Population Variability at Microsatellite Loci. <i>Genetics</i> , 1996, 143, 549-555.	2.9	74
28	Analysis of a cell cycle model based on unequal division of metabolic constituents to daughter cells during cytokinesis. <i>Journal of Theoretical Biology</i> , 1984, 110, 637-664.	1.7	66
29	A Power Analysis of Microsatellite-Based Statistics for Inferring Past Population Growth. <i>Molecular Biology and Evolution</i> , 2000, 17, 1859-1868.	8.9	62
30	Evolutionary action and structural basis of the allosteric switch controlling β 2AR functional selectivity. <i>Nature Communications</i> , 2017, 8, 2169.	12.8	61
31	Hematopoiesis and its disorders: a systems biology approach. <i>Blood</i> , 2010, 115, 2339-2347.	1.4	60
32	Stability analysis of models of cell production systems. <i>Mathematical Modelling</i> , 1986, 7, 1269-1300.	0.2	51
33	Asymptotic Analysis of a Cell Cycle Model Based on Unequal Division. <i>SIAM Journal on Applied Mathematics</i> , 1987, 47, 128-145.	1.8	51
34	Mathematical modeling of the loss of telomere sequences. <i>Journal of Theoretical Biology</i> , 1995, 177, 45-57.	1.7	51
35	Simulations Provide Support for the Common Disease-Common Variant Hypothesis. <i>Genetics</i> , 2007, 175, 763-776.	2.9	47
36	Comparison of Approaches to Modeling of Cell Population Dynamics. <i>SIAM Journal on Applied Mathematics</i> , 1993, 53, 1480-1504.	1.8	43

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37	Role of stem-cell divisions in cancer risk. <i>Nature</i> , 2017, 548, E13-E14.	27.8	42
38	Factors Influencing Ascertainment Bias of Microsatellite Allele Sizes: Impact on Estimates of Mutation Rates. <i>Genetics</i> , 2013, 195, 563-572.	2.9	40
39	Stochastic models of telomere shortening. <i>Mathematical Biosciences</i> , 1999, 158, 75-92.	1.9	35
40	Using SVD and SVM methods for selection, classification, clustering and modeling of DNA microarray data. <i>Engineering Applications of Artificial Intelligence</i> , 2004, 17, 417-427.	8.1	34
41	Dynamic Cross Talk Model of the Epithelial Innate Immune Response to Double-Stranded RNA Stimulation: Coordinated Dynamics Emerging from Cell-Level Noise. <i>PLoS ONE</i> , 2014, 9, e93396.	2.5	33
42	Minimal residual disease in acute myelogenous leukaemia and myelodysplastic syndromes: a follow-up of patients in clinical remission. <i>British Journal of Haematology</i> , 1997, 99, 64-75.	2.5	30
43	Interferon Gamma Mediates Hematopoietic Stem Cell Activation and Niche Relocalization through BST2. <i>Cell Reports</i> , 2020, 33, 108530.	6.4	29
44	Reaction-Difusion Model of Early Carcinogenesis: The Effects of Influx of Mutated Cells. <i>Mathematical Modelling of Natural Phenomena</i> , 2008, 3, 90-114.	2.4	27
45	Replication Stress Leading to Apoptosis within the S-phase Contributes to Synergism between Vorinostat and AZD1775 in HNSCC Harboring High-Risk <i>TP53</i> Mutation. <i>Clinical Cancer Research</i> , 2017, 23, 6541-6554.	7.0	27
46	Modeling of long-term screening for lung carcinoma. <i>Cancer</i> , 2001, 92, 1531-1540.	4.1	26
47	Stochastic Hypothesis of Transition from Inborn Neutropenia to AML: Interactions of Cell Population Dynamics and Population Genetics. <i>Frontiers in Oncology</i> , 2013, 3, 89.	2.8	19
48	System Engineering Approach to Planning Anticancer Therapies. , 2016, , .		19
49	Urothelial-to-Neural Plasticity Drives Progression to Small Cell Bladder Cancer. <i>IScience</i> , 2020, 23, 101201.	4.1	18
50	Cell cycle kinetics with supramitotic control, two cell types, and unequal division: a model of transformed embryonic cells. <i>Mathematical Biosciences</i> , 1991, 105, 47-79.	1.9	17
51	Dynamics of Growth and Signaling along Linear and Surface Structures in Very Early Tumors. <i>Computational and Mathematical Methods in Medicine</i> , 2006, 7, 189-213.	1.3	17
52	Quantitative analysis reveals crosstalk mechanisms of heat shock-induced attenuation of NF- κ B signaling at the single cell level. <i>PLoS Computational Biology</i> , 2018, 14, e1006130.	3.2	17
53	DNA Dinucleotide Evolution in Humans: Fitting Theory to Facts. <i>Genetics</i> , 2001, 159, 737-747.	2.9	17
54	The dependence of expression of NF- κ B-dependent genes: statistics and evolutionary conservation of control sequences in the promoter and in the 3' UTR. <i>BMC Genomics</i> , 2012, 13, 182.	2.8	16

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55	Cross talk between cytokine and hyperthermia-induced pathways: identification of different subsets of NF- κ B-dependent genes regulated by TNF α and heat shock. <i>Molecular Genetics and Genomics</i> , 2015, 290, 1979-1990.	2.1	16
56	Mathematical modelling reveals unexpected inheritance and variability patterns of cell cycle parameters in mammalian cells. <i>PLoS Computational Biology</i> , 2019, 15, e1007054.	3.2	16
57	Non-homogeneous infinite sites model under demographic change: mathematical description and asymptotic behavior of pairwise distributions. <i>Mathematical Biosciences</i> , 2002, 175, 83-115.	1.9	15
58	Multitype Bellman-Harris branching model provides biological predictors of early stages of adult hippocampal neurogenesis. <i>BMC Systems Biology</i> , 2017, 11, 90.	3.0	15
59	Gene characteristics predicting missense, nonsense and frameshift mutations in tumor samples. <i>BMC Bioinformatics</i> , 2018, 19, 430.	2.6	14
60	How the Number of Alleles Influences Gene Expression. <i>Journal of Statistical Physics</i> , 2007, 128, 511-533.	1.2	13
61	Alternatives to the Wright-Fisher model: The robustness of mitochondrial Eve dating. <i>Theoretical Population Biology</i> , 2010, 78, 165-172.	1.1	13
62	A note on estimation of dynamics of multiple gene expression based on singular value decomposition. <i>Mathematical Biosciences</i> , 2003, 182, 183-199.	1.9	12
63	Modeling neutral evolution of Alu elements using a branching process. <i>BMC Genomics</i> , 2010, 11, S11.	2.8	12
64	Irradiation with UV-C inhibits TNF α -dependent activation of the NF- κ B pathway in a mechanism potentially mediated by reactive oxygen species. <i>Genes To Cells</i> , 2017, 22, 45-58.	1.2	12
65	Mathematical model predicts response to chemotherapy in advanced non-resectable non-small cell lung cancer patients treated with platinum-based doublet. <i>PLoS Computational Biology</i> , 2020, 16, e1008234.	3.2	12
66	CAVITY-AWARE MOTIFS REDUCE FALSE POSITIVES IN PROTEIN FUNCTION PREDICTION. , 2006, , .		12
67	Heat shock factor 1 (HSF1) cooperates with estrogen receptor α (ER α) in the regulation of estrogen action in breast cancer cells. <i>ELife</i> , 2021, 10, .	6.0	12
68	Asymptotic behavior of joint distributions of characteristics of a pair of randomly chosen individuals in discrete-time Fisher-Wright models with mutations and drift. <i>Theoretical Population Biology</i> , 2004, 66, 355-367.	1.1	11
69	Different rates of DNA replication at early versus late S-phase sections: Multiscale modeling of stochastic events related to DNA content/EdU (5-ethynyl- ² -deoxyuridine) incorporation distributions. <i>Cytometry Part A: the Journal of the International Society for Analytical Cytology</i> , 2014, 85, 785-797.	1.5	11
70	Stochasticity and Determinism in Models of Hematopoiesis. <i>Advances in Experimental Medicine and Biology</i> , 2014, 844, 119-152.	1.6	11
71	Bone Marrow Stromal Antigen 2 Is Critical for IFN γ -Dependent Hematopoietic Stem Cell Activation. <i>Blood</i> , 2020, 136, 2-3.	1.4	11
72	A semigroup representation and asymptotic behavior of certain statistics of the fisher-wright-moran coalescent. <i>Handbook of Statistics</i> , 2001, 19, 215-247.	0.6	10

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73	Heat shock response regulates stimulus-specificity and sensitivity of the pro-inflammatory NF- κ B signalling. <i>Cell Communication and Signaling</i> , 2020, 18, 77.	6.5	10
74	A random evolution related to a Fisher-Wright-Moran model with mutation, recombination and drift. <i>Mathematical Methods in the Applied Sciences</i> , 2003, 26, 1587-1599.	2.3	9
75	A statistical model to correct systematic bias introduced by algorithmic thresholds in protein structural comparison algorithms. , 2008, , .		9
76	ERROR DETECTION IN GENETIC LINKAGE DATA FOR HUMAN PEDIGREES USING LIKELIHOOD RATIO METHODS. <i>Journal of Biological Systems</i> , 1995, 03, 13-25.	1.4	8
77	Asymptotic behavior of a Moran model with mutations, drift and recombination among multiple loci. <i>Journal of Mathematical Biology</i> , 2010, 61, 455-473.	1.9	8
78	Stability of bacterial toggle switches is enhanced by cell-cycle lengthening by several orders of magnitude. <i>Physical Review E</i> , 2014, 89, 022710.	2.1	8
79	Coalescence computations for large samples drawn from populations of time-varying sizes. <i>PLoS ONE</i> , 2017, 12, e0170701.	2.5	8
80	Modeling epigenetic regulation of PRC1 protein accumulation in the cell cycle. <i>Biology Direct</i> , 2015, 10, 62.	4.6	7
81	Mutation, drift and selection in single-driver hematologic malignancy: Example of secondary myelodysplastic syndrome following treatment of inherited neutropenia. <i>PLoS Computational Biology</i> , 2019, 15, e1006664.	3.2	7
82	Application of the Moran Model in Estimating Selection Coefficient of Mutated CSF3R Clones in the Evolution of Severe Congenital Neutropenia to Myeloid Neoplasia. <i>Frontiers in Physiology</i> , 2020, 11, 806.	2.8	7
83	ASYMPTOTIC BEHAVIOUR OF AN OPERATOR EXPONENTIAL RELATED TO BRANCHING RANDOM WALK MODELS OF DNA REPEATS. <i>Journal of Biological Systems</i> , 1999, 07, 33-43.	1.4	6
84	Predicting time to relapse in acute myeloid leukemia through stochastic modeling of minimal residual disease based on clonality data. <i>Computational and Systems Oncology</i> , 2021, 1, e1026.	1.5	6
85	A mathematical model as a tool to identify microRNAs with highest impact on transcriptome changes. <i>BMC Genomics</i> , 2019, 20, 114.	2.8	5
86	COMPOSITE MOTIFS INTEGRATING MULTIPLE PROTEIN STRUCTURES INCREASE SENSITIVITY FOR FUNCTION PREDICTION. , 2007, , .		5
87	Modeling Lung Cancer Screening. <i>Wiley Series in Probability and Statistics</i> , 2006, , 161-175.	0.0	4
88	Statistical Analysis of Missense Mutation Classifiers. <i>Human Mutation</i> , 2013, 34, 405-406.	2.5	4
89	Analysis of two mechanisms of telomere maintenance based on the theory of g-Networks and stochastic automata networks. <i>BMC Genomics</i> , 2020, 21, 587.	2.8	4
90	Interactions of Neanderthals and Modern Humans: What Can Be Inferred from Mitochondrial DNA?. <i>Mathematical Biosciences and Engineering</i> , 2005, 2, 487-498.	1.9	4

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91	Predicting Minimal Residual Disease in Acute Myeloid Leukemia through Stochastic Modeling of Clonality. <i>Blood</i> , 2019, 134, 1448-1448.	1.4	3
92	Effect of the unfolded protein response and oxidative stress on mutagenesis in <i>CSF3R</i> : a model for evolution of severe congenital neutropenia to myelodysplastic syndrome/acute myeloid leukemia. <i>Mutagenesis</i> , 2020, 35, 381-389.	2.6	3
93	Population dynamics coded in DNA: genetic traces of the expansion of modern humans. <i>Physica A: Statistical Mechanics and Its Applications</i> , 1999, 273, 158-168.	2.6	2
94	Analysis of differences in amino acid substitution patterns, using multilevel G-tests. <i>Comptes Rendus - Biologies</i> , 2005, 328, 632-641.	0.2	2
95	Ovide Arino, a personal memory. <i>Journal of Theoretical Biology</i> , 2007, 244, 365-366.	1.7	2
96	Non-homogeneous infinitely many sites discrete-time model with exact coalescent. <i>Mathematical Methods in the Applied Sciences</i> , 2010, 33, 713-732.	2.3	2
97	Modeling Neutral Evolution Using an Infinite-Allele Markov Branching Process. <i>International Journal of Stochastic Analysis</i> , 2013, 2013, 1-10.	0.3	2
98	Modeling the Natural History and Detection of Lung Cancer Based on Smoking Behavior. <i>PLoS ONE</i> , 2014, 9, e93430.	2.5	2
99	Time to the MRCA of a sample in a Wright-Fisher model with variable population size. <i>Theoretical Population Biology</i> , 2011, 80, 265-271.	1.1	1
100	Spatial and Stochastic Effects in a Model of Viral Infection. <i>Fundamenta Informaticae</i> , 2012, 118, 327-343.	0.4	1
101	Genomic trajectory in leukemogenesis of myeloproliferative neoplasms: a case report. <i>BMC Medical Genomics</i> , 2021, 14, 137.	1.5	1
102	Griffiths' Pakes branching process as a model for evolution of Alu elements. <i>Lecture Notes in Statistics</i> , 2010, , 179-189.	0.2	1
103	Chronic Infection Depletes Hematopoietic Stem Cells through Stress-Induced Terminal Differentiation. <i>Blood</i> , 2016, 128, 732-732.	1.4	1
104	Infection Is a Driver of Dnmt3a-Mutant Clonal Hematopoiesis. <i>Blood</i> , 2019, 134, 817-817.	1.4	1
105	WHY MATHEMATICS IS NEEDED TO UNDERSTAND COMPLEX GENETICS DISEASES. <i>Journal of Biological Systems</i> , 2002, 10, 359-380.	1.4	0
106	Bernoulli mixture models in application to the evaluation of algorithms estimating functionality of missense mutations. <i>BMC Proceedings</i> , 2012, 6, .	1.6	0
107	Application of the stochastic Moran Model of population genetics to understanding the timing of a driver mutation in Myelodysplastic Syndrome (MDS). <i>IFAC Postprint Volumes IPPV / International Federation of Automatic Control</i> , 2014, 47, 11542-11546.	0.4	0
108	Genetic demographic networks: Mathematical model and applications. <i>Theoretical Population Biology</i> , 2016, 111, 75-86.	1.1	0

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109	Model Identification and Parameter Estimation. , 2016, , 171-198.		0
110	Stationary Distribution of Telomere Lengths in Cells with Telomere Length Maintenance and its Parametric Inference. Bulletin of Mathematical Biology, 2020, 82, 150.	1.9	0
111	A Novel Role for Bst2 and E-Selectin in IFN γ -Stimulated HSC Niche Relocalization. Blood, 2018, 132, 874-874.	1.4	0
112	Effect of the Unfolded Protein Response and Oxidative Stress on Mutagenesis of CSF3R a Model of Evolution of Severe Congenital Neutropenia to Myelodysplastic Syndrome/Acute Myeloid Leukemia. Blood, 2019, 134, 3752-3752.	1.4	0
113	IFN γ Stimulation Induces Hematopoietic Stem Cell Homing and Niche Relocalization. Blood, 2019, 134, 3726-3726.	1.4	0
114	Stochastic models of stem cells and their descendants under different criticality assumptions. Stochastic Models, 2023, 39, 249-264.	0.5	0