

John L Spouge

List of Publications by Year in descending order

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74
papers

7,230
citations

318942

23
h-index

100535

70
g-index

80
all docs

80
docs citations

80
times ranked

11047
citing authors

#	ARTICLE	IF	CITATIONS
1	Hemolysis Pathways during Storage of Erythrocytes and Inter-Donor Variability in Erythrocyte Morphology. <i>Transfusion Medicine and Hemotherapy</i> , 2021, 48, 39-47.	0.7	7
2	A comprehensive estimation of country-level basic reproduction numbers R_0 for COVID-19: Regime regression can automatically estimate the end of the exponential phase in epidemic data. <i>PLoS ONE</i> , 2021, 16, e0254145.	1.1	12
3	Estimating the basic reproduction number of a pathogen in a single host when only a single founder successfully infects. <i>PLoS ONE</i> , 2020, 15, e0227127.	1.1	0
4	A linear-time algorithm that avoids inverses and computes Jackknife (leave-one-out) products like convolutions or other operators in commutative semigroups. <i>Algorithms for Molecular Biology</i> , 2020, 15, 17.	0.3	0
5	Figures of merit and statistics for detecting faulty species identification with DNA barcodes: A case study in <i>Ramaria</i> and related fungal genera. <i>PLoS ONE</i> , 2020, 15, e0237507.	1.1	7
6	Structural prediction of RNA switches using conditional base-pair probabilities. <i>PLoS ONE</i> , 2019, 14, e0217625.	1.1	1
7	An accurate approximation for the expected site frequency spectrum in a Galton-Watson process under an infinite sites mutation model. <i>Theoretical Population Biology</i> , 2019, 127, 7-15.	0.5	2
8	MultiDomainBenchmark: a multi-domain query and subject database suite. <i>BMC Bioinformatics</i> , 2019, 20, 77.	1.2	1
9	Empirical Null Estimation Using Zero-inflated Discrete Mixture Distributions and Its Application to Protein Domain Data. <i>Biometrics</i> , 2018, 74, 458-471.	0.8	9
10	Alignment-free genome comparison enables accurate geographic sourcing of white oak DNA. <i>BMC Genomics</i> , 2018, 19, 896.	1.2	6
11	Discovery of Kaposi's sarcoma herpesvirus-encoded circular RNAs and a human antiviral circular RNA. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, 12805-12810.	3.3	144
12	Conserved signatures indicate HIV-1 transmission is under strong selection and thus is not a stochastic process. <i>Retrovirology</i> , 2017, 14, 13.	0.9	6
13	Patterns of conserved gp120 epitope presentation on attached HIV-1 virions. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, E9893-E9902.	3.3	12
14	ALP & FALP: C++ libraries for pairwise local alignment E -values. <i>Bioinformatics</i> , 2016, 32, 304-305.	1.8	7
15	Measurement of a Barcode's Accuracy in Identifying Species. , 2016, , 29-41.		3
16	Most of the tight positional conservation of transcription factor binding sites near the transcription start site reflects their co-localization within regulatory modules. <i>BMC Bioinformatics</i> , 2016, 17, 479.	1.2	1
17	Changes in the Plasticity of HIV-1 Nef RNA during the Evolution of the North American Epidemic. <i>PLoS ONE</i> , 2016, 11, e0163688.	1.1	2
18	A New Method for Estimating Species Age Supports the Coexistence of Malaria Parasites and Their Mammalian Hosts. <i>Molecular Biology and Evolution</i> , 2015, 32, 1354-1364.	3.5	39

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19	Conserved Molecular Signatures in gp120 Are Associated with the Genetic Bottleneck during Simian Immunodeficiency Virus (SIV), SIV-Human Immunodeficiency Virus (SHIV), and HIV Type 1 (HIV-1) Transmission. <i>Journal of Virology</i> , 2015, 89, 3619-3629.	1.5	22
20	Frameshift alignment: statistics and post-genomic applications. <i>Bioinformatics</i> , 2014, 30, 3575-3582.	1.8	35
21	Within a sample from a population, the distribution of the number of descendants of a subsample's most recent common ancestor. <i>Theoretical Population Biology</i> , 2014, 92, 51-54.	0.5	5
22	Searching for repeats, as an example of using the generalised Ruzzo-Tompa algorithm to find optimal subsequences with gaps. <i>International Journal of Bioinformatics Research and Applications</i> , 2014, 10, 384.	0.1	2
23	Fungi in Thailand: A Case Study of the Efficacy of an ITS Barcode for Automatically Identifying Species within the Annulohyphoxylon and Hyphoxylon Genera. <i>PLoS ONE</i> , 2013, 8, e54529.	1.1	25
24	CBOL Protist Working Group: Barcoding Eukaryotic Richness beyond the Animal, Plant, and Fungal Kingdoms. <i>PLoS Biology</i> , 2012, 10, e1001419.	2.6	488
25	The Practical Evaluation of DNA Barcode Efficacy. <i>Methods in Molecular Biology</i> , 2012, 858, 365-377.	0.4	12
26	The ruzzo-tompa algorithm can find the maximal paths in weighted, directed graphs on a one-dimensional lattice. , 2012, . .		2
27	Nuclear ribosomal internal transcribed spacer (ITS) region as a universal DNA barcode marker for <i>Fungi</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 6241-6246.	3.3	4,012
28	New finite-size correction for local alignment score distributions. <i>BMC Research Notes</i> , 2012, 5, 286.	0.6	14
29	Objective method for estimating asymptotic parameters, with an application to sequence alignment. <i>Physical Review E</i> , 2011, 84, 031914.	0.8	4
30	Threshold Average Precision (TAP-k): a measure of retrieval designed for bioinformatics. <i>Bioinformatics</i> , 2010, 26, 1708-1713.	1.8	25
31	Estimating the Gumbel scale parameter for local alignment of random sequences by importance sampling with stopping times. <i>Annals of Statistics</i> , 2009, 37, 3697.	1.4	11
32	The whole alignment and nothing but the alignment: the problem of spurious alignment flanks. <i>Nucleic Acids Research</i> , 2008, 36, 5863-5871.	6.5	22
33	The biological function of some human transcription factor binding motifs varies with position relative to the transcription start site. <i>Nucleic Acids Research</i> , 2008, 36, 2777-2786.	6.5	19
34	The identification of complete domains within protein sequences using accurate E-values for semi-global alignment. <i>Nucleic Acids Research</i> , 2007, 35, 4678-4685.	6.5	15
35	Markov Additive Processes and Repeats in Sequences. <i>Journal of Applied Probability</i> , 2007, 44, 514-527.	0.4	3
36	Markov Additive Processes and Repeats in Sequences. <i>Journal of Applied Probability</i> , 2007, 44, 514-527.	0.4	3

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37	Inequalities on the overshoot beyond a boundary for independent summands with differing distributions. <i>Statistics and Probability Letters</i> , 2007, 77, 1486-1489.	0.4	2
38	Finite-size corrections to Poisson approximations in general renewal-success processes. <i>Journal of Mathematical Analysis and Applications</i> , 2005, 301, 401-418.	0.5	2
39	Accelerated convergence and robust asymptotic regression of the Gumbel scale parameter for gapped sequence alignment. <i>Journal of Physics A</i> , 2005, 38, 97-108.	1.6	5
40	The Gumbel pre-factor k for gapped local alignment can be estimated from simulations of global alignment. <i>Nucleic Acids Research</i> , 2005, 33, 4987-4994.	6.5	20
41	Path reversal, islands, and the gapped alignment of random sequences. <i>Journal of Applied Probability</i> , 2004, 41, 975-983.	0.4	1
42	Finding functional sequence elements by multiple local alignment. <i>Nucleic Acids Research</i> , 2004, 32, 189-200.	6.5	195
43	Statistical analysis of over-represented words in human promoter sequences. <i>Nucleic Acids Research</i> , 2004, 32, 949-958.	6.5	108
44	Searching for Multiple Words in a Markov Sequence. <i>INFORMS Journal on Computing</i> , 2004, 16, 341-347.	1.0	4
45	Path reversal, islands, and the gapped alignment of random sequences. <i>Journal of Applied Probability</i> , 2004, 41, 975-983.	0.4	4
46	The correlation error and finite-size correction in an ungapped sequence alignment. <i>Bioinformatics</i> , 2002, 18, 1236-1242.	1.8	10
47	Statistical significance of clusters of motifs represented by position specific scoring matrices in nucleotide sequences. <i>Nucleic Acids Research</i> , 2002, 30, 3214-3224.	6.5	106
48	Finite-size corrections to Poisson approximations of rare events in renewal processes. <i>Journal of Applied Probability</i> , 2001, 38, 554-569.	0.4	5
49	Lineage-Specific Gene Expansions in Bacterial and Archaeal Genomes. <i>Genome Research</i> , 2001, 11, 555-565.	2.4	110
50	Finite-size corrections to Poisson approximations of rare events in renewal processes. <i>Journal of Applied Probability</i> , 2001, 38, 554-569.	0.4	7
51	A practical method for simultaneously determining the effective burst sizes and cycle times of viruses. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1999, 96, 7017-7022.	3.3	3
52	The combinatorics and extreme value statistics of protein threading. <i>Annals of Combinatorics</i> , 1999, 3, 81-93.	0.3	1
53	Candidate Regulatory Sequence Elements for Cell Cycle-Dependent Transcription in <i>Saccharomyces cerevisiae</i> . <i>Genome Research</i> , 1999, 9, 775-792.	2.4	69
54	Increase of Primary HIV-1 Production in Human Peripheral Blood Mononuclear Cells by Intermittent Medium Replenishment. <i>Biotechnology Progress</i> , 1998, 14, 540-542.	1.3	2

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55	Single-particle survival in parallel gated trapping. <i>Physical Review E</i> , 1997, 55, 421-425.	0.8	8
56	Stochastically Gated Chemical Reactions. <i>Journal of Physical Chemistry B</i> , 1997, 101, 5026-5030.	1.2	5
57	HIV-1 infection kinetics in tissue cultures. <i>Mathematical Biosciences</i> , 1996, 138, 1-22.	0.9	46
58	A cytopathic infectivity assay of human immunodeficiency virus type 1 in human primary macrophages. <i>Journal of Virological Methods</i> , 1996, 59, 45-55.	1.0	8
59	Single-particle survival in gated trapping. <i>Physical Review E</i> , 1996, 54, 2248-2255.	0.8	37
60	Computation of the Gamma, Digamma, and Trigamma Functions. <i>SIAM Journal on Numerical Analysis</i> , 1994, 31, 931-944.	1.1	47
61	HIV requires multiple gp120 molecules for CD4-mediated infection. <i>Nature</i> , 1990, 346, 277-279.	13.7	209
62	Speeding up Dynamic Programming Algorithms for Finding Optimal Lattice Paths. <i>SIAM Journal on Applied Mathematics</i> , 1989, 49, 1552-1566.	0.8	27
63	Exact solutions for a diffusion-reaction process in one dimension. <i>Physical Review Letters</i> , 1988, 60, 871-874.	2.9	220
64	Hydrophobicity scales and computational techniques for detecting amphipathic structures in proteins. <i>Journal of Molecular Biology</i> , 1987, 195, 659-685.	2.0	627
65	Protein Antigenic Structures Recognized by T Cells; Potential Applications to Vaccine Design. <i>Immunological Reviews</i> , 1987, 98, 9-52.	2.8	144
66	Increasing stability with complexity in a system composed of unstable subsystems. <i>Journal of Mathematical Analysis and Applications</i> , 1986, 118, 502-518.	0.5	8
67	Equilibrium ring formation in polymer solutions. <i>Journal of Statistical Physics</i> , 1986, 43, 143-196.	0.5	25
68	Polymers and random graphs: Asymptotic equivalence to branching processes. <i>Journal of Statistical Physics</i> , 1985, 38, 573-587.	0.5	19
69	Monte Carlo results for random coagulation. <i>Journal of Colloid and Interface Science</i> , 1985, 107, 38-43.	5.0	42
70	An existence theorem for the discrete coagulation-fragmentation equations. <i>Mathematical Proceedings of the Cambridge Philosophical Society</i> , 1984, 96, 351-357.	0.3	56
71	Analytic results for finite systems of ringed flory polymers. <i>Canadian Journal of Chemistry</i> , 1984, 62, 1262-1264.	0.6	10
72	A branching-process solution of the polydisperse coagulation equation. <i>Advances in Applied Probability</i> , 1984, 16, 56-69.	0.4	7

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73	The size distribution for the $A_g B_f$ Model of polymerization. Journal of Statistical Physics, 1983, 31, 363-378.	0.5	27
74	Asymmetric bonding of identical units: a general $A_g B_f$ -g polymer model. Macromolecules, 1983, 16, 831-835.	2.2	26