

# John L Spouge

## List of Publications by Year in descending order

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74  
papers

7,230  
citations

279798

23  
h-index

88630

70  
g-index

80  
all docs

80  
docs citations

80  
times ranked

9949  
citing authors

#	ARTICLE	IF	CITATIONS
1	Nuclear ribosomal internal transcribed spacer (ITS) region as a universal DNA barcode marker for <i>Fungi</i> . Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 6241-6246.	7.1	4,012
2	Hydrophobicity scales and computational techniques for detecting amphipathic structures in proteins. Journal of Molecular Biology, 1987, 195, 659-685.	4.2	627
3	CBOL Protist Working Group: Barcoding Eukaryotic Richness beyond the Animal, Plant, and Fungal Kingdoms. PLoS Biology, 2012, 10, e1001419.	5.6	488
4	Exact solutions for a diffusion-reaction process in one dimension. Physical Review Letters, 1988, 60, 871-874.	7.8	220
5	HIV requires multiple gp120 molecules for CD4-mediated infection. Nature, 1990, 346, 277-279.	27.8	209
6	Finding functional sequence elements by multiple local alignment. Nucleic Acids Research, 2004, 32, 189-200.	14.5	195
7	Protein Antigenic Structures Recognized by T Cells; Potential Applications to Vaccine Design. Immunological Reviews, 1987, 98, 9-52.	6.0	144
8	Discovery of Kaposi's sarcoma herpesvirus-encoded circular RNAs and a human antiviral circular RNA. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, 12805-12810.	7.1	144
9	Lineage-Specific Gene Expansions in Bacterial and Archaeal Genomes. Genome Research, 2001, 11, 555-565.	5.5	110
10	Statistical analysis of over-represented words in human promoter sequences. Nucleic Acids Research, 2004, 32, 949-958.	14.5	108
11	Statistical significance of clusters of motifs represented by position specific scoring matrices in nucleotide sequences. Nucleic Acids Research, 2002, 30, 3214-3224.	14.5	106
12	Candidate Regulatory Sequence Elements for Cell Cycle-Dependent Transcription in <i>Saccharomyces cerevisiae</i> . Genome Research, 1999, 9, 775-792.	5.5	69
13	An existence theorem for the discrete coagulation-fragmentation equations. Mathematical Proceedings of the Cambridge Philosophical Society, 1984, 96, 351-357.	0.4	56
14	Computation of the Gamma, Digamma, and Trigamma Functions. SIAM Journal on Numerical Analysis, 1994, 31, 931-944.	2.3	47
15	HIV-1 infection kinetics in tissue cultures. Mathematical Biosciences, 1996, 138, 1-22.	1.9	46
16	Monte Carlo results for random coagulation. Journal of Colloid and Interface Science, 1985, 107, 38-43.	9.4	42
17	A New Method for Estimating Species Age Supports the Coexistence of Malaria Parasites and Their Mammalian Hosts. Molecular Biology and Evolution, 2015, 32, 1354-1364.	8.9	39
18	Single-particle survival in gated trapping. Physical Review E, 1996, 54, 2248-2255.	2.1	37

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19	Frameshift alignment: statistics and post-genomic applications. <i>Bioinformatics</i> , 2014, 30, 3575-3582.	4.1	35
20	The size distribution for the AgRBfg Model of polymerization. <i>Journal of Statistical Physics</i> , 1983, 31, 363-378.	1.2	27
21	Speeding up Dynamic Programming Algorithms for Finding Optimal Lattice Paths. <i>SIAM Journal on Applied Mathematics</i> , 1989, 49, 1552-1566.	1.8	27
22	Asymmetric bonding of identical units: a general AgRBfg polymer model. <i>Macromolecules</i> , 1983, 16, 831-835.	4.8	26
23	Equilibrium ring formation in polymer solutions. <i>Journal of Statistical Physics</i> , 1986, 43, 143-196.	1.2	25
24	Threshold Average Precision (TAP-k): a measure of retrieval designed for bioinformatics. <i>Bioinformatics</i> , 2010, 26, 1708-1713.	4.1	25
25	Fungi in Thailand: A Case Study of the Efficacy of an ITS Barcode for Automatically Identifying Species within the <i>Annulohyphoxylon</i> and <i>Hypoxylon</i> Genera. <i>PLoS ONE</i> , 2013, 8, e54529.	2.5	25
26	The whole alignment and nothing but the alignment: the problem of spurious alignment flanks. <i>Nucleic Acids Research</i> , 2008, 36, 5863-5871.	14.5	22
27	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.	3.4	22
28	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.	14.5	20
29	Polymers and random graphs: Asymptotic equivalence to branching processes. <i>Journal of Statistical Physics</i> , 1985, 38, 573-587.	1.2	19
30	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.	14.5	19
31	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.	14.5	15
32	New finite-size correction for local alignment score distributions. <i>BMC Research Notes</i> , 2012, 5, 286.	1.4	14
33	The Practical Evaluation of DNA Barcode Efficacy. <i>Methods in Molecular Biology</i> , 2012, 858, 365-377.	0.9	12
34	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.	7.1	12
35	A comprehensive estimation of country-level basic reproduction numbers R0 for COVID-19: Regime regression can automatically estimate the end of the exponential phase in epidemic data. <i>PLoS ONE</i> , 2021, 16, e0254145.	2.5	12
36	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.	2.6	11

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37	Analytic results for finite systems of ringed flory polymers. Canadian Journal of Chemistry, 1984, 62, 1262-1264.	1.1	10
38	The correlation error and finite-size correction in an ungapped sequence alignment. Bioinformatics, 2002, 18, 1236-1242.	4.1	10
39	Empirical Null Estimation Using Zero-inflated Discrete Mixture Distributions and Its Application to Protein Domain Data. Biometrics, 2018, 74, 458-471.	1.4	9
40	Increasing stability with complexity in a system composed of unstable subsystems. Journal of Mathematical Analysis and Applications, 1986, 118, 502-518.	1.0	8
41	A cytopathic infectivity assay of human immunodeficiency virus type 1 in human primary macrophages. Journal of Virological Methods, 1996, 59, 45-55.	2.1	8
42	Single-particle survival in parallel gated trapping. Physical Review E, 1997, 55, 421-425.	2.1	8
43	A branching-process solution of the polydisperse coagulation equation. Advances in Applied Probability, 1984, 16, 56-69.	0.7	7
44	ALP & FALP: C++ libraries for pairwise local alignment <i>E</i> -values. Bioinformatics, 2016, 32, 304-305.	4.1	7
45	Figures of merit and statistics for detecting faulty species identification with DNA barcodes: A case study in Ramaria and related fungal genera. PLoS ONE, 2020, 15, e0237507.	2.5	7
46	Hemolysis Pathways during Storage of Erythrocytes and Inter-Donor Variability in Erythrocyte Morphology. Transfusion Medicine and Hemotherapy, 2021, 48, 39-47.	1.6	7
47	Finite-size corrections to Poisson approximations of rare events in renewal processes. Journal of Applied Probability, 2001, 38, 554-569.	0.7	7
48	Conserved signatures indicate HIV-1 transmission is under strong selection and thus is not a $\hat{\text{a}}\text{c}\text{e}\text{s}\text{t}\text{o}\text{c}\text{h}\text{a}\text{s}\text{t}\text{i}\text{c}$ process. Retrovirology, 2017, 14, 13.	2.0	6
49	Alignment-free genome comparison enables accurate geographic sourcing of white oak DNA. BMC Genomics, 2018, 19, 896.	2.8	6
50	Stochastically Gated Chemical Reactions. Journal of Physical Chemistry B, 1997, 101, 5026-5030.	2.6	5
51	Finite-size corrections to Poisson approximations of rare events in renewal processes. Journal of Applied Probability, 2001, 38, 554-569.	0.7	5
52	Accelerated convergence and robust asymptotic regression of the Gumbel scale parameter for gapped sequence alignment. Journal of Physics A, 2005, 38, 97-108.	1.6	5
53	Within a sample from a population, the distribution of the number of descendants of a subsample's most recent common ancestor. Theoretical Population Biology, 2014, 92, 51-54.	1.1	5
54	Searching for Multiple Words in a Markov Sequence. INFORMS Journal on Computing, 2004, 16, 341-347.	1.7	4

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55	Path reversal, islands, and the gapped alignment of random sequences. <i>Journal of Applied Probability</i> , 2004, 41, 975-983.	0.7	4
56	Objective method for estimating asymptotic parameters, with an application to sequence alignment. <i>Physical Review E</i> , 2011, 84, 031914.	2.1	4
57	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.	7.1	3
58	Markov Additive Processes and Repeats in Sequences. <i>Journal of Applied Probability</i> , 2007, 44, 514-527.	0.7	3
59	Markov Additive Processes and Repeats in Sequences. <i>Journal of Applied Probability</i> , 2007, 44, 514-527.	0.7	3
60	Measurement of a Barcode's Accuracy in Identifying Species. , 2016, , 29-41.		3
61	Increase of Primary HIV-1 Production in Human Peripheral Blood Mononuclear Cells by Intermittent Medium Replenishment. <i>Biotechnology Progress</i> , 1998, 14, 540-542.	2.6	2
62	Finite-size corrections to Poisson approximations in general renewal-success processes. <i>Journal of Mathematical Analysis and Applications</i> , 2005, 301, 401-418.	1.0	2
63	Inequalities on the overshoot beyond a boundary for independent summands with differing distributions. <i>Statistics and Probability Letters</i> , 2007, 77, 1486-1489.	0.7	2
64	The ruzzo-tompa algorithm can find the maximal paths in weighted, directed graphs on a one-dimensional lattice. , 2012, , .		2
65	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.	0.2	2
66	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.	1.1	2
67	Changes in the Plasticity of HIV-1 Nef RNA during the Evolution of the North American Epidemic. <i>PLoS ONE</i> , 2016, 11, e0163688.	2.5	2
68	The combinatorics and extreme value statistics of protein threading. <i>Annals of Combinatorics</i> , 1999, 3, 81-93.	0.6	1
69	Path reversal, islands, and the gapped alignment of random sequences. <i>Journal of Applied Probability</i> , 2004, 41, 975-983.	0.7	1
70	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.	2.6	1
71	Structural prediction of RNA switches using conditional base-pair probabilities. <i>PLoS ONE</i> , 2019, 14, e0217625.	2.5	1
72	MultiDomainBenchmark: a multi-domain query and subject database suite. <i>BMC Bioinformatics</i> , 2019, 20, 77.	2.6	1

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73	Estimating the basic reproduction number of a pathogen in a single host when only a single founder successfully infects. PLoS ONE, 2020, 15, e0227127.	2.5	0
74	A linear-time algorithm that avoids inverses and computes Jackknife (leave-one-out) products like convolutions or other operators in commutative semigroups. Algorithms for Molecular Biology, 2020, 15, 17.	1.2	0