Scott J Emrich

List of Publications by Year
in descending order

81 papers	3,964 citations	304743 22 h-index	168389 53 g-index
87 all docs	87 docs citations	87 times ranked	6226 citing authors

#	Article	IF	Citations
1	VectorBase: an updated bioinformatics resource for invertebrate vectors and other organisms related with human diseases. Nucleic Acids Research, 2015, 43, D707-D713.	14.5	556
2	Extensive introgression in a malaria vector species complex revealed by phylogenomics. Science, 2015, 347, 1258524.	12.6	527
3	Highly evolvable malaria vectors: The genomes of 16 *Anopheles* mosquitoes. Science, 2015, 347, 1258522.	12.6	492
4	A molecular mechanism of artemisinin resistance in Plasmodium falciparum malaria. Nature, 2015, 520, 683-687.	27.8	485
5	Genome of *Rhodnius prolixus* , an insect vector of Chagas disease, reveals unique adaptations to hematophagy and parasite infection. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 14936-14941.	7.1	329
6	Evolutionary superscaffolding and chromosome anchoring to improve Anopheles genome assemblies. BMC Biology, 2020, 18, 1.	3.8	177
7	Experimental evidence of genome-wide impact of ecological selection during early stages of speciation-with-gene-flow. Ecology Letters, 2015, 18, 817-825.	6.4	137
8	Genome analysis of a major urban malaria vector mosquito, Anopheles stephensi. Genome Biology, 2014, 15, 459.	8.8	119
9	Widespread position-specific conservation of synonymous rare codons within coding sequences. PLoS Computational Biology, 2017, 13, e1005531.	3.2	98
10	Radical remodeling of the Y chromosome in a recent radiation of malaria mosquitoes. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, E2114-23.	7.1	92
11	The native ORAI channel trio underlies the diversity of Ca2+ signaling events. Nature Communications, 2020, 11, 2444.	12.8	90
12	A calcium/cAMP signaling loop at the ORAI1 mouth drives channel inactivation to shape NFAT induction. Nature Communications, 2019, 10, 1971.	12.8	73
13	Distinct pharmacological profiles of ORAI1, ORAI2, and ORAI3 channels. Cell Calcium, 2020, 91, 102281.	2.4	71
14	Omnitemporal choreographies of all five STIM/Orai and IP3Rs underlie the complexity of mammalian Ca2+ signaling. Cell Reports, 2021, 34, 108760.	6.4	57
15	Physiological Functions of CRAC Channels. Annual Review of Physiology, 2022, 84, 355-379.	13.1	53
16	The Evolution of the *Anopheles* 16 Genomes Project. G3: Genes, Genomes, Genetics, 2013, 3, 1191-1194.	1.8	49
17	%MinMax: A versatile tool for calculating and comparing synonymous codon usage and its impact on protein folding. Protein Science, 2018, 27, 356-362.	7.6	47
18	L-type Ca $^{2+}$ channel blockers promote vascular remodeling through activation of STIM proteins. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 17369-17380.	7.1	37

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19	Cross-talk between N-terminal and C-terminal domains in stromal interaction molecule 2 (STIM2) determines enhanced STIM2 sensitivity. Journal of Biological Chemistry, 2019, 294, 6318-6332.	3.4	36
20	Harnessing parallelism in multicore clusters with the All-Pairs, Wavefront, and Makeflow abstractions. Cluster Computing, 2010, 13, 243-256.	5.0	35
21	High-quality genetic mapping with ddRADseq in the non-model tree Quercus rubra. BMC Genomics, 2017, 18, 417.	2.8	29
22	Examination of the genetic basis for sexual dimorphism in the Aedes aegypti (dengue vector mosquito) pupal brain. Biology of Sex Differences, 2014, 5, 10.	4.1	27
23	Activation of endothelial cells by extracellular vesicles derived from Mycobacterium tuberculosis infected macrophages or mice. PLoS ONE, 2018, 13, e0198337.	2.5	24
24	Genetic Characterization of a Novel Iflavirus Associated with Vomiting Disease in the Chinese Oak Silkmoth Antheraea pernyi. PLoS ONE, 2014, 9, e92107.	2.5	23
25	GRAFENE: Graphlet-based alignment-free network approach integrates 3D structural and sequence (residue order) data to improve protein structural comparison. Scientific Reports, 2017, 7, 14890.	3.3	21
26	Combining Static and Dynamic Storage Management for Data Intensive Scientific Workflows. IEEE Transactions on Parallel and Distributed Systems, 2018, 29, 338-350.	5.6	21
27	The anatomy of native CRAC channel(s). Current Opinion in Physiology, 2020, 17, 89-95.	1.8	21
28	RNA-seq implicates deregulation of the immune system in the pathogenesis of diverticulitis. American Journal of Physiology - Renal Physiology, 2017, 313, G277-G284.	3.4	20
29	MIReAD, a minimum information standard for reporting arthropod abundance data. Scientific Data, 2019, 6, 40.	5.3	20
30	The genome of the stable fly, Stomoxys calcitrans, reveals potential mechanisms underlying reproduction, host interactions, and novel targets for pest control. BMC Biology, 2021, 19, 41.	3.8	19
31	Taming complex bioinformatics workflows with weaver, makeflow, and starch. , 2010, , .		12
32	Scaling up genome annotation using MAKER and work queue. International Journal of Bioinformatics Research and Applications, 2014, 10, 447.	0.2	11
33	RNA-Rocket: an RNA-Seq analysis resource for infectious disease research. Bioinformatics, 2015, 31, 1496-1498.	4.1	11
34	Analysis of computational codon usage models and their association with translationally slow codons. PLoS ONE, 2020, 15, e0232003.	2.5	9
35	A protocol for detecting elemental calcium signals (Ca2+ puffs) in mammalian cells using total internal reflection fluorescence microscopy. STAR Protocols, 2021, 2, 100618.	1.2	8
36	<scp>CHARMING</scp>: Harmonizing synonymous codon usage to replicate a desired codon usage pattern. Protein Science, 2022, 31, 221-231.	7.6	8

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37	Detecting inversions with PCA in the presence of population structure. PLoS ONE, 2020, 15, e0240429.	2.5	8
38	The anatomy of CRAC channel(s). Current Opinion in Physiology, 2020, 17, 89-95.	1.8	8
39	Biocompute 2.0: an improved collaborative workspace for data intensive bioâ€science. Concurrency Computation Practice and Experience, 2011, 23, 2305-2314.	2.2	7
40	Reduced-representation sequencing identifies small effective population sizes of Anopheles gambiae in the north-western Lake Victoria basin, Uganda. Malaria Journal, 2018, 17, 285.	2.3	7
41	A two-stage machine learning approach for pathway analysis. , 2010, , .		6
42	Mapping genomic features to functional traits through microbial whole genome sequences. International Journal of Bioinformatics Research and Applications, 2014, 10, 461.	0.2	6
43	Single molecule sequencing-guided scaffolding and correction of draft assemblies. BMC Genomics, 2017, 18, 879.	2.8	6
44	HECIL: A Hybrid Error Correction Algorithm for Long Reads with Iterative Learning. Scientific Reports, 2018, 8, 9936.	3.3	6
45	Network analysis of synonymous codon usage. Bioinformatics, 2020, 36, 4876-4884.	4.1	6
46	Networks' characteristics are important for systems biology. Network Science, 2014, 2, 139-161.	1.0	5
47	Prediction of fine-tuned promoter activity from DNA sequence. F1000Research, 2016, 5, 158.	1.6	5
48	The airway smooth muscle sodium/calcium exchanger NCLX is critical for airway remodeling and hyperresponsiveness in asthma. Journal of Biological Chemistry, 2022, 298, 102259.	3.4	5
49	Case Studies in Designing Elastic Applications. , 2013, , .		4
50	Accelerating Comparative Genomics Workflows in a Distributed Environment with Optimized Data Partitioning. , 2014, , .		4
51	Scaling Up Bioinformatics Workflows with Dynamic Job Expansion: A Case Study Using Galaxy and Makeflow. , 2015, , .		4
52	Inversion detection using PacBio long reads. , 2017, , .		3
53	Predicting Local Inversions Using Rectangle Clustering and Representative Rectangle Prediction. , 2018, , .		3
54	An unsupervised learning approach to assembly validation. , 2013, , .		2

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55	Balancing Thread-Level and Task-Level Parallelism for Data-Intensive Workloads on Clusters and Clouds. , 2015, , .		2
56	HAPI-Gen. , 2016, , .		2
57	Adjusted likelihood-ratio test for variants with unknown genotypes. Journal of Bioinformatics and Computational Biology, 2018, 16, 1840020.	0.8	2
58	Predicting Local Inversions Using Rectangle Clustering and Representative Rectangle Prediction. IEEE Transactions on Nanobioscience, 2019, 18, 316-323.	3.3	2
59	PeakMatcher facilitates updated Aedes aegypti embryonic cis-regulatory element map. Hereditas, 2021, 158, 7.	1.4	2
60	Multiâ€layer sequential network analysis improves protein <scp>3D</scp> structural classification. Proteins: Structure, Function and Bioinformatics, 2022, 90, 1721-1731.	2.6	2
61	Robust haplotype reconstruction of eukaryotic read data with Hapler. , 2011, , .		1
62	Predicting bacterial functional traits from whole genome sequences using random forest. , 2013, , .		1
63	A computational framework for integrative analysis of large microbial genomics data. , 2015, , .		1
64	Stable feature ranking with logistic regression ensembles. , 2017, , .		1
65	Phlebotomus papatasi sand fly predicted salivary protein diversity and immune response potential based on in silico prediction in Egypt and Jordan populations. PLoS Neglected Tropical Diseases, 2020, 14, e0007489.	3.0	1
66	Rodent Virus Diversity and Differentiation across Post-Katrina New Orleans. Sustainability, 2021, 13, 8034.	3.2	1
67	Workshop: Opportunities and challenges of non-model ecoinformatics. , 2012, , .		0
68	Expanding Tasks of Logical Workflows Into Independent Workflows for Improved Scalability. , 2014, , .		0
69	Global maximum-parsimony based ancestral reconstruction with non-universal genes. , 2015, , .		0
70	Single molecule sequencing-guided scaffolding and correction of draft assemblies. , 2016, , .		0
71	Rheumatoid arthritis: Relief of IKAROS transcriptional repression of Orai3 in T-cells. Cell Calcium, 2021, 97, 102409.	2.4	0
72	Attachment of Suspension Cells for TEM Processing. Microscopy and Microanalysis, 2021, 27, 1396-1397.	0.4	0

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73	CD163L1+CXCL10+ Macrophages are Enriched Within Colonic Lamina Propria of Diverticulitis Patients. Journal of Surgical Research, 2021, 267, 527-535.	1.6	0
74	Title is missing!. , 2019, 15, e1008453.		0
75	Title is missing!. , 2019, 15, e1008453.		0
76	Title is missing!. , 2019, 15, e1008453.		0
77	Analysis of computational codon usage models and their association with translationally slow codons. , 2020, 15, e0232003.		0
78	Analysis of computational codon usage models and their association with translationally slow codons. , 2020, 15, e0232003.		0
79	Analysis of computational codon usage models and their association with translationally slow codons. , 2020, 15, e0232003.		0
80	Analysis of computational codon usage models and their association with translationally slow codons. , 2020, 15, e0232003.		0
81	A New Look at Codon Usage and Protein Expression. , 2019, 60, 104-112.		0