

Scott J Emrich

List of Publications by Year in descending order

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Version: 2024-02-01

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	Physiological Functions of CRAC Channels. <i>Annual Review of Physiology</i> , 2022, 84, 355-379.	13.1	53
2	<scp>CHARMING</scp>: Harmonizing synonymous codon usage to replicate a desired codon usage pattern. <i>Protein Science</i> , 2022, 31, 221-231.	7.6	8
3	Multi-layer sequential network analysis improves protein <scp>3D</scp> structural classification. <i>Proteins: Structure, Function and Bioinformatics</i> , 2022, 90, 1721-1731.	2.6	2
4	The airway smooth muscle sodium/calcium exchanger NCLX is critical for airway remodeling and hyperresponsiveness in asthma. <i>Journal of Biological Chemistry</i> , 2022, 298, 102259.	3.4	5
5	PeakMatcher facilitates updated <i>Aedes aegypti</i> embryonic cis-regulatory element map. <i>Hereditas</i> , 2021, 158, 7.	1.4	2
6	Omnitemporal choreographies of all five STIM/Orai and IP3Rs underlie the complexity of mammalian Ca ²⁺ signaling. <i>Cell Reports</i> , 2021, 34, 108760.	6.4	57
7	The genome of the stable fly, <i>Stomoxys calcitrans</i> , reveals potential mechanisms underlying reproduction, host interactions, and novel targets for pest control. <i>BMC Biology</i> , 2021, 19, 41.	3.8	19
8	Rodent Virus Diversity and Differentiation across Post-Katrina New Orleans. <i>Sustainability</i> , 2021, 13, 8034.	3.2	1
9	Rheumatoid arthritis: Relief of IKAROS transcriptional repression of Orai3 in T-cells. <i>Cell Calcium</i> , 2021, 97, 102409.	2.4	0
10	Attachment of Suspension Cells for TEM Processing. <i>Microscopy and Microanalysis</i> , 2021, 27, 1396-1397.	0.4	0
11	A protocol for detecting elemental calcium signals (Ca ²⁺ puffs) in mammalian cells using total internal reflection fluorescence microscopy. <i>STAR Protocols</i> , 2021, 2, 100618.	1.2	8
12	CD163L1+CXCL10+ Macrophages are Enriched Within Colonic Lamina Propria of Diverticulitis Patients. <i>Journal of Surgical Research</i> , 2021, 267, 527-535.	1.6	0
13	Evolutionary superscaffolding and chromosome anchoring to improve <i>Anopheles</i> genome assemblies. <i>BMC Biology</i> , 2020, 18, 1.	3.8	177
14	The anatomy of native CRAC channel(s). <i>Current Opinion in Physiology</i> , 2020, 17, 89-95.	1.8	21
15	Distinct pharmacological profiles of ORAI1, ORAI2, and ORAI3 channels. <i>Cell Calcium</i> , 2020, 91, 102281.	2.4	71
16	<i>Phlebotomus papatasi</i> sand fly predicted salivary protein diversity and immune response potential based on in silico prediction in Egypt and Jordan populations. <i>PLoS Neglected Tropical Diseases</i> , 2020, 14, e0007489.	3.0	1
17	The native ORAI channel trio underlies the diversity of Ca ²⁺ signaling events. <i>Nature Communications</i> , 2020, 11, 2444.	12.8	90
18	Analysis of computational codon usage models and their association with translationally slow codons. <i>PLoS ONE</i> , 2020, 15, e0232003.	2.5	9

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19	Network analysis of synonymous codon usage. <i>Bioinformatics</i> , 2020, 36, 4876-4884.	4.1	6
20	L-type Ca ²⁺ channel blockers promote vascular remodeling through activation of STIM proteins. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 17369-17380.	7.1	37
21	Detecting inversions with PCA in the presence of population structure. <i>PLoS ONE</i> , 2020, 15, e0240429.	2.5	8
22	The anatomy of CRAC channel(s). <i>Current Opinion in Physiology</i> , 2020, 17, 89-95.	1.8	8
23	Analysis of computational codon usage models and their association with translationally slow codons. , 2020, 15, e0232003.		0
24	Analysis of computational codon usage models and their association with translationally slow codons. , 2020, 15, e0232003.		0
25	Analysis of computational codon usage models and their association with translationally slow codons. , 2020, 15, e0232003.		0
26	Analysis of computational codon usage models and their association with translationally slow codons. , 2020, 15, e0232003.		0
27	Predicting Local Inversions Using Rectangle Clustering and Representative Rectangle Prediction. <i>IEEE Transactions on Nanobioscience</i> , 2019, 18, 316-323.	3.3	2
28	A calcium/cAMP signaling loop at the ORAI1 mouth drives channel inactivation to shape NFAT induction. <i>Nature Communications</i> , 2019, 10, 1971.	12.8	73
29	MIReAD, a minimum information standard for reporting arthropod abundance data. <i>Scientific Data</i> , 2019, 6, 40.	5.3	20
30	Cross-talk between N-terminal and C-terminal domains in stromal interaction molecule 2 (STIM2) determines enhanced STIM2 sensitivity. <i>Journal of Biological Chemistry</i> , 2019, 294, 6318-6332.	3.4	36
31	Title is missing!. , 2019, 15, e1008453.		0
32	Title is missing!. , 2019, 15, e1008453.		0
33	Title is missing!. , 2019, 15, e1008453.		0
34	A New Look at Codon Usage and Protein Expression. , 2019, 60, 104-112.		0
35	Combining Static and Dynamic Storage Management for Data Intensive Scientific Workflows. <i>IEEE Transactions on Parallel and Distributed Systems</i> , 2018, 29, 338-350.	5.6	21
36	%MinMax: A versatile tool for calculating and comparing synonymous codon usage and its impact on protein folding. <i>Protein Science</i> , 2018, 27, 356-362.	7.6	47

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37	Predicting Local Inversions Using Rectangle Clustering and Representative Rectangle Prediction. , 2018, , .		3
38	Adjusted likelihood-ratio test for variants with unknown genotypes. Journal of Bioinformatics and Computational Biology, 2018, 16, 1840020.	0.8	2
39	HECIL: A Hybrid Error Correction Algorithm for Long Reads with Iterative Learning. Scientific Reports, 2018, 8, 9936.	3.3	6
40	Activation of endothelial cells by extracellular vesicles derived from Mycobacterium tuberculosis infected macrophages or mice. PLoS ONE, 2018, 13, e0198337.	2.5	24
41	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
42	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
43	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
44	High-quality genetic mapping with ddRADseq in the non-model tree Quercus rubra. BMC Genomics, 2017, 18, 417.	2.8	29
45	Stable feature ranking with logistic regression ensembles. , 2017, , .		1
46	Inversion detection using PacBio long reads. , 2017, , .		3
47	Single molecule sequencing-guided scaffolding and correction of draft assemblies. BMC Genomics, 2017, 18, 879.	2.8	6
48	Widespread position-specific conservation of synonymous rare codons within coding sequences. PLoS Computational Biology, 2017, 13, e1005531.	3.2	98
49	HAPI-Gen. , 2016, , .		2
50	Single molecule sequencing-guided scaffolding and correction of draft assemblies. , 2016, , .		0
51	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
52	Prediction of fine-tuned promoter activity from DNA sequence. F1000Research, 2016, 5, 158.	1.6	5
53	Global maximum-parsimony based ancestral reconstruction with non-universal genes. , 2015, , .		0
54	Balancing Thread-Level and Task-Level Parallelism for Data-Intensive Workloads on Clusters and Clouds. , 2015, , .		2

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55	Experimental evidence of genome-wide impact of ecological selection during early stages of speciation with gene flow. <i>Ecology Letters</i> , 2015, 18, 817-825.	6.4	137
56	Scaling Up Bioinformatics Workflows with Dynamic Job Expansion: A Case Study Using Galaxy and Makeflow. , 2015, , .		4
57	Genome of <i>Rhodnius prolixus</i> , an insect vector of Chagas disease, reveals unique adaptations to hematophagy and parasite infection. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 14936-14941.	7.1	329
58	A computational framework for integrative analysis of large microbial genomics data. , 2015, , .		1
59	RNA-Rocket: an RNA-Seq analysis resource for infectious disease research. <i>Bioinformatics</i> , 2015, 31, 1496-1498.	4.1	11
60	A molecular mechanism of artemisinin resistance in <i>Plasmodium falciparum</i> malaria. <i>Nature</i> , 2015, 520, 683-687.	27.8	485
61	VectorBase: an updated bioinformatics resource for invertebrate vectors and other organisms related with human diseases. <i>Nucleic Acids Research</i> , 2015, 43, D707-D713.	14.5	556
62	Extensive introgression in a malaria vector species complex revealed by phylogenomics. <i>Science</i> , 2015, 347, 1258524.	12.6	527
63	Highly evolvable malaria vectors: The genomes of 16 <i>Anopheles</i> mosquitoes. <i>Science</i> , 2015, 347, 1258522.	12.6	492
64	Examination of the genetic basis for sexual dimorphism in the <i>Aedes aegypti</i> (dengue vector mosquito) pupal brain. <i>Biology of Sex Differences</i> , 2014, 5, 10.	4.1	27
65	Genome analysis of a major urban malaria vector mosquito, <i>Anopheles stephensi</i> . <i>Genome Biology</i> , 2014, 15, 459.	8.8	119
66	Accelerating Comparative Genomics Workflows in a Distributed Environment with Optimized Data Partitioning. , 2014, , .		4
67	Networks' characteristics are important for systems biology. <i>Network Science</i> , 2014, 2, 139-161.	1.0	5
68	Expanding Tasks of Logical Workflows Into Independent Workflows for Improved Scalability. , 2014, , .		0
69	Scaling up genome annotation using MAKER and work queue. <i>International Journal of Bioinformatics Research and Applications</i> , 2014, 10, 447.	0.2	11
70	Mapping genomic features to functional traits through microbial whole genome sequences. <i>International Journal of Bioinformatics Research and Applications</i> , 2014, 10, 461.	0.2	6
71	Genetic Characterization of a Novel Iflavirus Associated with Vomiting Disease in the Chinese Oak Silkworm <i>Antheraea pernyi</i> . <i>PLoS ONE</i> , 2014, 9, e92107.	2.5	23
72	The Evolution of the <i>Anopheles</i> 16 Genomes Project. <i>G3: Genes, Genomes, Genetics</i> , 2013, 3, 1191-1194.	1.8	49

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73	Predicting bacterial functional traits from whole genome sequences using random forest. , 2013, , .		1
74	Case Studies in Designing Elastic Applications. , 2013, , .		4
75	An unsupervised learning approach to assembly validation. , 2013, , .		2
76	Workshop: Opportunities and challenges of non-model ecoinformatics. , 2012, , .		0
77	Robust haplotype reconstruction of eukaryotic read data with Hapler. , 2011, , .		1
78	Biocompute 2.0: an improved collaborative workspace for data intensive bioinformatics. Concurrency Computation Practice and Experience, 2011, 23, 2305-2314.	2.2	7
79	Harnessing parallelism in multicore clusters with the All-Pairs, Wavefront, and Makeflow abstractions. Cluster Computing, 2010, 13, 243-256.	5.0	35
80	A two-stage machine learning approach for pathway analysis. , 2010, , .		6
81	Taming complex bioinformatics workflows with weaver, makeflow, and starch. , 2010, , .		12