

Don L Armstrong

List of Publications by Year in descending order

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Version: 2024-02-01

30
papers

3,080
citations

394421

19
h-index

477307

29
g-index

35
all docs

35
docs citations

35
times ranked

5523
citing authors

#	ARTICLE	IF	CITATIONS
1	Transcriptomic profiling of fetal membranes of mice deficient in biglycan and decorin as a model of preterm birth. <i>Biology of Reproduction</i> , 2021, 104, 611-623.	2.7	3
2	Maternal weight affects placental DNA methylation of genes involved in metabolic pathways in the common marmoset monkey (<i>Callithrix jacchus</i>). <i>American Journal of Primatology</i> , 2020, 82, e23101.	1.7	10
3	Methylomic profiles reveal sex-specific differences in leukocyte composition associated with post-traumatic stress disorder. <i>Brain, Behavior, and Immunity</i> , 2019, 81, 280-291.	4.1	14
4	Early Experiences of Threat, but Not Deprivation, Are Associated With Accelerated Biological Aging in Children and Adolescents. <i>Biological Psychiatry</i> , 2019, 85, 268-278.	1.3	211
5	Traumatic stress and accelerated DNA methylation age: A meta-analysis. <i>Psychoneuroendocrinology</i> , 2018, 92, 123-134.	2.7	190
6	Replication of Simulated Prebiotic Amphiphilic Vesicles in a Finite Environment Exhibits Complex Behavior That Includes High Progeny Variability and Competition. <i>Astrobiology</i> , 2018, 18, 419-430.	3.0	8
7	Epigenetic profiles associated with major depression in the human brain. <i>Psychiatry Research</i> , 2018, 260, 439-442.	3.3	15
8	Epigenetic meta-analysis across three civilian cohorts identifies <i>NRG1</i> and <i>HGS</i> as blood-based biomarkers for post-traumatic stress disorder. <i>Epigenomics</i> , 2018, 10, 1585-1601.	2.1	39
9	Developing reproducible bioinformatics analysis workflows for heterogeneous computing environments to support African genomics. <i>BMC Bioinformatics</i> , 2018, 19, 457.	2.6	33
10	Extracellular Vesicles and the Promise of Continuous Liquid Biopsies. <i>Journal of Pathology and Translational Medicine</i> , 2018, 52, 1-8.	1.1	68
11	Organizing and running bioinformatics hackathons within Africa: The H3ABioNet cloud computing experience. <i>AAS Open Research</i> , 2018, 1, 9.	1.5	11
12	The core transcriptome of mammalian placentas and the divergence of expression with placental shape. <i>Placenta</i> , 2017, 57, 71-78.	1.5	62
13	333. Sex Differences in Leukocyte Composition and Transcriptional Profiles Associated with Lifetime Post-Traumatic Stress Disorder (PTSD). <i>Biological Psychiatry</i> , 2017, 81, S136-S137.	1.3	0
14	Development of Bioinformatics Infrastructure for Genomics Research. <i>Global Heart</i> , 2017, 12, 91.	2.3	47
15	A novel drug conjugate, NEO212, targeting proneural and mesenchymal subtypes of patient-derived glioma cancer stem cells. <i>Cancer Letters</i> , 2016, 371, 240-250.	7.2	24
16	Systemic Lupus Erythematosus-associated Neutrophil Cytosolic Factor 2 Mutation Affects the Structure of NADPH Oxidase Complex. <i>Journal of Biological Chemistry</i> , 2015, 290, 12595-12602.	3.4	28
17	CWAS identifies novel SLE susceptibility genes and explains the association of the HLA region. <i>Genes and Immunity</i> , 2014, 15, 347-354.	4.1	109
18	Lupus-associated causal mutation in neutrophil cytosolic factor 2 (NCF2) brings unique insights to the structure and function of NADPH oxidase. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, E59-67.	7.1	151

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19	Thrombospondin-1 Modulates the Angiogenic Phenotype of Human Cerebral Arteriovenous Malformation Endothelial Cells. <i>Neurosurgery</i> , 2011, 68, 1342-1353.	1.1	23
20	Replication of simulated prebiotic amphiphile vesicles controlled by experimental lipid physicochemical properties. <i>Physical Biology</i> , 2011, 8, 066001.	1.8	9
21	Identification of <i>IRAK1</i> as a risk gene with critical role in the pathogenesis of systemic lupus erythematosus. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 6256-6261.	7.1	218
22	High-density genotyping of STAT4 reveals multiple haplotypic associations with systemic lupus erythematosus in different racial groups. <i>Arthritis and Rheumatism</i> , 2009, 60, 1085-1095.	6.7	82
23	Identification of new SLE-associated genes with a two-step Bayesian study design. <i>Genes and Immunity</i> , 2009, 10, 446-456.	4.1	41
24	Function2Gene: A gene selection tool to increase the power of genetic association studies by utilizing public databases and expert knowledge. <i>BMC Bioinformatics</i> , 2008, 9, 311.	2.6	6
25	Amplification of Diacylglycerol Activation of Protein Kinase C by Cholesterol. <i>Biophysical Journal</i> , 2008, 94, 4700-4710.	0.5	15
26	Identification of novel susceptibility genes in childhood-onset systemic lupus erythematosus using a uniquely designed candidate gene pathway platform. <i>Arthritis and Rheumatism</i> , 2007, 56, 4164-4173.	6.7	71
27	Role of the MEOX2 homeobox gene in neurovascular dysfunction in Alzheimer disease. <i>Nature Medicine</i> , 2005, 11, 959-965.	30.7	274
28	RAGE mediates amyloid- β peptide transport across the blood-brain barrier and accumulation in brain. <i>Nature Medicine</i> , 2003, 9, 907-913.	30.7	1,277
29	Synergistic perturbation of phosphatidylcholine/sphingomyelin bilayers by diacylglycerol and cholesterol. <i>Biochemical and Biophysical Research Communications</i> , 2002, 296, 806-812.	2.1	13
30	Transmembrane domains in the functions of Fc receptors. <i>Biophysical Chemistry</i> , 2002, 100, 555-575.	2.8	26