Don L Armstrong

List of Publications by Year
in descending order

30 papers	3,080 citations	394286 19 h-index	477173 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 birthâ€. Biology of Reproduction, 2021, 104, 611-623.	1.2	3
2	Maternal weight affects placental DNA methylation of genes involved in metabolic pathways in the common marmoset monkey (*Callithrix jacchus*). American Journal of Primatology, 2020, 82, e23101.	0.8	10
3	Methylomic profiles reveal sex-specific differences in leukocyte composition associated with post-traumatic stress disorder. Brain, Behavior, and Immunity, 2019, 81, 280-291.	2.0	14
4	Early Experiences of Threat, but Not Deprivation, Are Associated With Accelerated Biological Aging in Children and Adolescents. Biological Psychiatry, 2019, 85, 268-278.	0.7	211
5	Traumatic stress and accelerated DNA methylation age: A meta-analysis. Psychoneuroendocrinology, 2018, 92, 123-134.	1.3	190
6	Replication of Simulated Prebiotic Amphiphilic Vesicles in a Finite Environment Exhibits Complex Behavior That Includes High Progeny Variability and Competition. Astrobiology, 2018, 18, 419-430.	1.5	8
7	Epigenetic profiles associated with major depression in the human brain. Psychiatry Research, 2018, 260, 439-442.	1.7	15
8	Epigenetic meta-analysis across three civilian cohorts identifies *NRG1* and *HGS* as blood-based biomarkers for post-traumatic stress disorder. Epigenomics, 2018, 10, 1585-1601.	1.0	39
9	Developing reproducible bioinformatics analysis workflows for heterogeneous computing environments to support African genomics. BMC Bioinformatics, 2018, 19, 457.	1.2	33
10	Extracellular Vesicles and the Promise of Continuous Liquid Biopsies. Journal of Pathology and Translational Medicine, 2018, 52, 1-8.	0.4	68
11	Organizing and running bioinformatics hackathons within Africa: The H3ABioNet cloud computing experience. AAS Open Research, 2018, 1, 9.	1.5	11
12	The core transcriptome of mammalian placentas and the divergence of expression with placental shape. Placenta, 2017, 57, 71-78.	0.7	62
13	333. Sex Differences in Leukocyte Composition and Transcriptional Profiles Associated with Lifetime Post-Traumatic Stress Disorder (PTSD). Biological Psychiatry, 2017, 81, S136-S137.	0.7	0
14	Development of Bioinformatics Infrastructure for Genomics Research. Global Heart, 2017, 12, 91.	0.9	47
15	A novel drug conjugate, NEO212, targeting proneural and mesenchymal subtypes of patient-derived glioma cancer stem cells. Cancer Letters, 2016, 371, 240-250.	3.2	24
16	Systemic Lupus Erythematosus-associated Neutrophil Cytosolic Factor 2 Mutation Affects the Structure of NADPH Oxidase Complex. Journal of Biological Chemistry, 2015, 290, 12595-12602.	1.6	28
17	GWAS identifies novel SLE susceptibility genes and explains the association of the HLA region. Genes and Immunity, 2014, 15, 347-354.	2.2	109
18	Lupus-associated causal mutation in neutrophil cytosolic factor 2 (NCF2) brings unique insights to the structure and function of NADPH oxidase. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, E59-67.	3.3	151

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19	Thrombospondin-1 Modulates the Angiogenic Phenotype of Human Cerebral Arteriovenous Malformation Endothelial Cells. Neurosurgery, 2011, 68, 1342-1353.	0.6	23
20	Replication of simulated prebiotic amphiphile vesicles controlled by experimental lipid physicochemical properties. Physical Biology, 2011, 8, 066001.	0.8	9
21	Identification of <i>IRAK1</i> as a risk gene with critical role in the pathogenesis of systemic lupus erythematosus. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 6256-6261.	3.3	218
22	High‐density genotyping of STAT4 reveals multiple haplotypic associations with systemic lupus erythematosus in different racial groups. Arthritis and Rheumatism, 2009, 60, 1085-1095.	6.7	82
23	Identification of new SLE-associated genes with a two-step Bayesian study design. Genes and Immunity, 2009, 10, 446-456.	2.2	41
24	Function2Gene: A gene selection tool to increase the power of genetic association studies by utilizing public databases and expert knowledge. BMC Bioinformatics, 2008, 9, 311.	1.2	6
25	Amplification of Diacylglycerol Activation of Protein Kinase C by Cholesterol. Biophysical Journal, 2008, 94, 4700-4710.	0.2	15
26	Identification of novel susceptibility genes in childhood‐onset systemic lupus erythematosus using a uniquely designed candidate gene pathway platform. Arthritis and Rheumatism, 2007, 56, 4164-4173.	6.7	71
27	Role of the MEOX2 homeobox gene in neurovascular dysfunction in Alzheimer disease. Nature Medicine, 2005, 11, 959-965.	15.2	274
28	RAGE mediates amyloid-β peptide transport across the blood-brain barrier and accumulation in brain. Nature Medicine, 2003, 9, 907-913.	15.2	1,277
29	Synergistic perturbation of phosphatidylcholine/sphingomyelin bilayers by diacylglycerol and cholesterol. Biochemical and Biophysical Research Communications, 2002, 296, 806-812.	1.0	13
30	Transmembrane domains in the functions of Fc receptors. Biophysical Chemistry, 2002, 100, 555-575.	1.5	26