

Charles R Farber

List of Publications by Year in descending order

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Version: 2024-02-01

95
papers

6,355
citations

109264

35
h-index

74108

75
g-index

106
all docs

106
docs citations

106
times ranked

10210
citing authors

#	ARTICLE	IF	CITATIONS
1	Fentanyl-induced acute and conditioned behaviors in two inbred mouse lines: Potential role for Glyoxalase. <i>Physiology and Behavior</i> , 2022, 243, 113630.	1.0	1
2	MicroRNA-30b Is Both Necessary and Sufficient for Interleukin-21 Receptor-Mediated Angiogenesis in Experimental Peripheral Arterial Disease. <i>International Journal of Molecular Sciences</i> , 2022, 23, 271.	1.8	9
3	Genome-Wide mRNA Expression Analysis of Acute Psychological Stress Responses. <i>MEDICC Review</i> , 2022, 24, 35.	0.5	1
4	Exercise during pregnancy mitigates negative effects of parental obesity on metabolic function in adult mouse offspring. <i>Journal of Applied Physiology</i> , 2021, 130, 605-616.	1.2	11
5	Genomic variants within chromosome 14q32.32 regulate bone mass through MARK3 signaling in osteoblasts. <i>Journal of Clinical Investigation</i> , 2021, 131, .	3.9	4
6	Using “omics” Data to Inform Genome-wide Association Studies (GWASs) in the Osteoporosis Field. <i>Current Osteoporosis Reports</i> , 2021, 19, 369-380.	1.5	4
7	Systems genetics in diversity outbred mice inform BMD GWAS and identify determinants of bone strength. <i>Nature Communications</i> , 2021, 12, 3408.	5.8	31
8	Current evidence on potential of adipose derived stem cells to enhance bone regeneration and future projection. <i>World Journal of Stem Cells</i> , 2021, 13, 1248-1277.	1.3	9
9	A computational approach for identification of core modules from a co-expression network and GWAS data. <i>STAR Protocols</i> , 2021, 2, 100768.	0.5	0
10	Genetic variability affects the skeletal response to immobilization in founder strains of the diversity outbred mouse population. <i>Bone Reports</i> , 2021, 15, 101140.	0.2	5
11	Genetic variability affects the response of skeletal muscle to disuse. <i>Journal of Musculoskeletal Neuronal Interactions</i> , 2021, 21, 387-396.	0.1	0
12	Dynamic changes in immune gene co-expression networks predict development of type 1 diabetes. <i>Scientific Reports</i> , 2021, 11, 22651.	1.6	3
13	Genetic determinants of bone mass and osteoporotic fracture. , 2020, , 1615-1630.		1
14	Identification of a Core Module for Bone Mineral Density through the Integration of a Co-expression Network and GWAS Data. <i>Cell Reports</i> , 2020, 32, 108145.	2.9	21
15	Sexually Dimorphic Crosstalk at the Maternal-Fetal Interface. <i>Journal of Clinical Endocrinology and Metabolism</i> , 2020, 105, e4831-e4847.	1.8	48
16	RNA-sequencing analysis of differential gene expression associated with arterial stiffness. <i>Vascular</i> , 2020, 28, 655-663.	0.4	3
17	Genetic analysis of osteoblast activity identifies Zbtb40 as a regulator of osteoblast activity and bone mass. <i>PLoS Genetics</i> , 2020, 16, e1008805.	1.5	15
18	Acute psychological stress, autonomic function, and arterial stiffness among women. <i>International Journal of Psychophysiology</i> , 2020, 155, 219-226.	0.5	9

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19	Old Mice Have Less Transcriptional Activation But Similar Periosteal Cell Proliferation Compared to Young Adult Mice in Response to in vivo Mechanical Loading. <i>Journal of Bone and Mineral Research</i> , 2020, 35, 1751-1764.	3.1	26
20	A novel voluntary weightlifting model in mice promotes muscle adaptation and insulin sensitivity with simultaneous enhancement of autophagy and mTOR pathway. <i>FASEB Journal</i> , 2020, 34, 7330-7344.	0.2	42
21	Osteoblasts Generate Testosterone From DHEA and Activate Androgen Signaling in Prostate Cancer Cells. <i>Journal of Bone and Mineral Research</i> , 2020, 36, 1566-1579.	3.1	3
22	Identification of Known and Novel Long Noncoding RNAs Potentially Responsible for the Effects of Bone Mineral Density (BMD) Genomewide Association Study (GWAS) Loci. <i>Journal of Bone and Mineral Research</i> , 2020, 37, 1500-1510.	3.1	2
23	The RNA demethylase FTO is required for maintenance of bone mass and functions to protect osteoblasts from genotoxic damage. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 17980-17989.	3.3	65
24	Mouse genome-wide association and systems genetics identifies Lhfp as a regulator of bone mass. <i>PLoS Genetics</i> , 2019, 15, e1008123.	1.5	22
25	Differences in First-Trimester Maternal Metabolomic Profiles in Pregnancies Conceived From Fertility Treatments. <i>Journal of Clinical Endocrinology and Metabolism</i> , 2019, 104, 1005-1019.	1.8	15
26	Genetic Dissection of Femoral and Tibial Microarchitecture. <i>JBMR Plus</i> , 2019, 3, e10241.	1.3	6
27	Antiangiogenic VEGF ¹⁶⁵ Regulates Macrophage Polarization via S100A8/S100A9 in Peripheral Artery Disease. <i>Circulation</i> , 2019, 139, 226-242.	1.6	75
28	Dissecting the Genetics of Osteoporosis using Systems Approaches. <i>Trends in Genetics</i> , 2019, 35, 55-67.	2.9	43
29	Differential gene expression during placentation in pregnancies conceived with different fertility treatments compared with spontaneous pregnancies. <i>Fertility and Sterility</i> , 2019, 111, 535-546.	0.5	12
30	Single limb immobilization model for bone loss from unloading. <i>Journal of Biomechanics</i> , 2019, 83, 181-189.	0.9	19
31	Genetics of Bone Fat and Energy Regulation. , 2018, , 301-315.		0
32	Sex differences in the late first trimester human placenta transcriptome. <i>Biology of Sex Differences</i> , 2018, 9, 4.	1.8	109
33	Integrating GWAS and Co-expression Network Data Identifies Bone Mineral Density Genes SPTBN1 and MARK3 and an Osteoblast Functional Module. <i>Cell Systems</i> , 2017, 4, 46-59.e4.	2.9	124
34	Genetic Dissection of a QTL Affecting Bone Geometry. <i>G3: Genes, Genomes, Genetics</i> , 2017, 7, 865-870.	0.8	4
35	The State of Systems Genetics in 2017. <i>Cell Systems</i> , 2017, 4, 7-15.	2.9	29
36	A MicroRNA93a Interferon Regulatory Factor-9 Immunoresponse Gene-1 Itaconic Acid Pathway Modulates M2-Like Macrophage Polarization to Revascularize Ischemic Muscle. <i>Circulation</i> , 2017, 135, 2403-2425.	1.6	102

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37	Using GWAS to identify novel therapeutic targets for osteoporosis. <i>Translational Research</i> , 2017, 181, 15-26.	2.2	45
38	A Systems-Level Understanding of Cardiovascular Disease through Networks. , 2016, , 59-81.		3
39	Genomic Modifiers of Natural Killer Cells, Immune Responsiveness and Lymphoid Tissue Remodeling Together Increase Host Resistance to Viral Infection. <i>PLoS Pathogens</i> , 2016, 12, e1005419.	2.1	8
40	The Hybrid Mouse Diversity Panel: a resource for systems genetics analyses of metabolic and cardiovascular traits. <i>Journal of Lipid Research</i> , 2016, 57, 925-942.	2.0	143
41	Optimization of techniques for multiple platform testing in small, precious samples such as human chorionic villus sampling. <i>Prenatal Diagnosis</i> , 2016, 36, 1061-1070.	1.1	18
42	Network Analysis Implicates Alpha-Synuclein (Snca) in the Regulation of Ovariectomy-Induced Bone Loss. <i>Scientific Reports</i> , 2016, 6, 29475.	1.6	17
43	RhoA determines lineage fate of mesenchymal stem cells by modulating CTGF-VEGF complex in extracellular matrix. <i>Nature Communications</i> , 2016, 7, 11455.	5.8	61
44	Epigenome-Wide Association of Liver Methylation Patterns and Complex Metabolic Traits in Mice. <i>Cell Metabolism</i> , 2015, 21, 905-917.	7.2	98
45	Wnt-Lrp5 Signaling Regulates Fatty Acid Metabolism in the Osteoblast. <i>Molecular and Cellular Biology</i> , 2015, 35, 1979-1991.	1.1	115
46	Overlapping mouse subcongenic strains successfully separate two linked body fat QTL on distal MMU 2. <i>BMC Genomics</i> , 2015, 16, 16.	1.2	16
47	ADAM12: a genetic modifier of preclinical peripheral arterial disease. <i>American Journal of Physiology - Heart and Circulatory Physiology</i> , 2015, 309, H790-H803.	1.5	34
48	Whole-genome sequencing identifies EN1 as a determinant of bone density and fracture. <i>Nature</i> , 2015, 526, 112-117.	13.7	483
49	Bioenergetics During Calvarial Osteoblast Differentiation Reflect Strain Differences in Bone Mass. <i>Endocrinology</i> , 2014, 155, 1589-1595.	1.4	131
50	A Novel <i>IFITM5</i> Mutation in Severe Atypical Osteogenesis Imperfecta Type VI Impairs Osteoblast Production of Pigment Epithelium-Derived Factor. <i>Journal of Bone and Mineral Research</i> , 2014, 29, 1402-1411.	3.1	63
51	Glucagon Regulates Hepatic Kisspeptin to Impair Insulin Secretion. <i>Cell Metabolism</i> , 2014, 19, 667-681.	7.2	168
52	<i>Bicc1</i> is a genetic determinant of osteoblastogenesis and bone mineral density. <i>Journal of Clinical Investigation</i> , 2014, 124, 2736-2749.	3.9	51
53	<i>Trps1</i> Differentially Modulates the Bone Mineral Density between Male and Female Mice and Its Polymorphism Associates with BMD Differently between Women and Men. <i>PLoS ONE</i> , 2014, 9, e84485.	1.1	16
54	Quantitative trait loci for bone mineral density and femoral morphology in an advanced intercross population of mice. <i>Bone</i> , 2013, 55, 222-229.	1.4	7

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55	MicroRNA-93 Controls Perfusion Recovery After Hindlimb Ischemia by Modulating Expression of Multiple Genes in the Cell Cycle Pathway. <i>Circulation</i> , 2013, 127, 1818-1828.	1.6	86
56	Systems-Level Analysis of Genome-Wide Association Data. <i>G3: Genes, Genomes, Genetics</i> , 2013, 3, 119-129.	0.8	55
57	Contemporary Approaches for Identifying Rare Bone Disease Causing Genes. <i>Bone Research</i> , 2013, 1, 301-310.	5.4	1
58	Systems Genetic Analysis of Osteoblast-Lineage Cells. <i>PLoS Genetics</i> , 2012, 8, e1003150.	1.5	48
59	Hybrid mouse diversity panel: a panel of inbred mouse strains suitable for analysis of complex genetic traits. <i>Mammalian Genome</i> , 2012, 23, 680-692.	1.0	134
60	Unraveling Inflammatory Responses using Systems Genetics and Gene-Environment Interactions in Macrophages. <i>Cell</i> , 2012, 151, 658-670.	13.5	134
61	Genome Scans for Transmission Ratio Distortion Regions in Mice. <i>Genetics</i> , 2012, 191, 247-259.	1.2	31
62	Systems Genetics: A Novel Approach to Dissect the Genetic Basis of Osteoporosis. <i>Current Osteoporosis Reports</i> , 2012, 10, 228-235.	1.5	12
63	Increasing Association Mapping Power and Resolution in Mouse Genetic Studies Through the Use of Meta-Analysis for Structured Populations. <i>Genetics</i> , 2012, 191, 959-967.	1.2	14
64	Gene networks associated with conditional fear in mice identified using a systems genetics approach. <i>BMC Systems Biology</i> , 2011, 5, 43.	3.0	71
65	Systems genetics analysis of mouse chondrocyte differentiation. <i>Journal of Bone and Mineral Research</i> , 2011, 26, 747-760.	3.1	14
66	Identification of quantitative trait loci influencing skeletal architecture in mice: Emergence of <i>Cdh11</i> as a primary candidate gene regulating femoral morphology. <i>Journal of Bone and Mineral Research</i> , 2011, 26, 2174-2183.	3.1	26
67	Comparative Analysis of Proteome and Transcriptome Variation in Mouse. <i>PLoS Genetics</i> , 2011, 7, e1001393.	1.5	548
68	Mouse Genome-Wide Association and Systems Genetics Identify <i>Asxl2</i> As a Regulator of Bone Mineral Density and Osteoclastogenesis. <i>PLoS Genetics</i> , 2011, 7, e1002038.	1.5	108
69	Genetic analyses involving microsatellite ETH10 genotypes on bovine chromosome 5 and performance trait measures in Angus- and Brahman-influenced cattle. <i>Journal of Animal Science</i> , 2011, 89, 2031-2041.	0.2	9
70	Hippocampal Gene Expression Analysis Highlights <i>Ly6a/Sca-1</i> as Candidate Gene for Previously Mapped Novelty Induced Behaviors in Mice. <i>PLoS ONE</i> , 2011, 6, e20716.	1.1	4
71	Identification of a gene module associated with BMD through the integration of network analysis and genome-wide association data. <i>Journal of Bone and Mineral Research</i> , 2010, 25, 2359-2367.	3.1	78
72	Serious limitations of the QTL/Microarray approach for QTL gene discovery. <i>BMC Biology</i> , 2010, 8, 96.	1.7	29

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73	A high-resolution association mapping panel for the dissection of complex traits in mice. <i>Genome Research</i> , 2010, 20, 281-290.	2.4	299
74	Segregation Analysis of a Sex Ratio Distortion Locus in Congenic Mice. <i>Journal of Heredity</i> , 2010, 101, 351-359.	1.0	3
75	An Integration of Genome-Wide Association Study and Gene Expression Profiling to Prioritize the Discovery of Novel Susceptibility Loci for Osteoporosis-Related Traits. <i>PLoS Genetics</i> , 2010, 6, e1000977.	1.5	191
76	Using global gene expression to dissect the genetics of osteoporosis. <i>IBMS BoneKEy</i> , 2010, 7, 353-363.	0.1	1
77	Genetics of Osteoporosis. <i>Translational Endocrinology & Metabolism</i> , 2010, , 87-116.	0.2	1
78	Genetic dissection of a major mouse obesity QTL (<i>Carfhg2</i>): integration of gene expression and causality modeling. <i>Physiological Genomics</i> , 2009, 37, 294-302.	1.0	23
79	Evidence of maternal QTL affecting growth and obesity in adult mice. <i>Mammalian Genome</i> , 2009, 20, 269-280.	1.0	23
80	Polymorphisms in the <i>STAT6</i> gene and their association with carcass traits in feedlot cattle. <i>Animal Genetics</i> , 2009, 40, 878-882.	0.6	47
81	Validation of candidate causal genes for obesity that affect shared metabolic pathways and networks. <i>Nature Genetics</i> , 2009, 41, 415-423.	9.4	257
82	An Integrative Genetics Approach to Identify Candidate Genes Regulating BMD: Combining Linkage, Gene Expression, and Association. <i>Journal of Bone and Mineral Research</i> , 2009, 24, 105-116.	3.1	52
83	Future of Osteoporosis Genetics: Enhancing Genome-Wide Association Studies. <i>Journal of Bone and Mineral Research</i> , 2009, 24, 1937-1942.	3.1	25
84	Overexpression of <i>Scg5</i> increases enzymatic activity of PCSK2 and is inversely correlated with body weight in congenic mice. <i>BMC Genetics</i> , 2008, 9, 34.	2.7	14
85	High-Resolution Mapping of Gene Expression Using Association in an Outbred Mouse Stock. <i>PLoS Genetics</i> , 2008, 4, e1000149.	1.5	53
86	Integrating Global Gene Expression Analysis and Genetics. <i>Advances in Genetics</i> , 2008, 60, 571-601.	0.8	48
87	Fine Mapping Reveals Sex Bias in Quantitative Trait Loci Affecting Growth, Skeletal Size and Obesity-Related Traits on Mouse Chromosomes 2 and 11. <i>Genetics</i> , 2007, 175, 349-360.	1.2	38
88	Dissection of a genetically complex cluster of growth and obesity QTLs on mouse chromosome 2 using subcongenic intercrosses. <i>Mammalian Genome</i> , 2007, 18, 635-645.	1.0	19
89	Genome-wide isolation of growth and obesity QTL using mouse speed congenic strains. <i>BMC Genomics</i> , 2006, 7, 102.	1.2	27
90	Identification of putative homology between horse microsatellite flanking sequences and cross-species ESTs, mRNAs and genomic sequences. <i>Animal Genetics</i> , 2004, 35, 28-33.	0.6	17

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91	The Collaborative Cross, a community resource for the genetic analysis of complex traits. <i>Nature Genetics</i> , 2004, 36, 1133-1137.	9.4	1,034
92	Putative in silico mapping of DNA sequences to livestock genome maps using SSLP flanking sequences. <i>Animal Genetics</i> , 2003, 34, 11-18.	0.6	16
93	The nature and identification of quantitative trait loci: a community's view. <i>Nature Reviews Genetics</i> , 2003, 4, 911-916.	7.7	390
94	Comparative mapping of genes flanking the human chromosome 12 evolutionary breakpoint in the pig. <i>Cytogenetic and Genome Research</i> , 2003, 102, 139-144.	0.6	9
95	Mapping of Porcine Genetic Markers Generated by Representational Difference Analysis. <i>Animal Biotechnology</i> , 2003, 14, 87-102.	0.7	1