

Fuad A Iraqi

List of Publications by Citations

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

53
papers

2,907
citations

25
h-index

53
g-index

58
ext. papers

3,440
ext. citations

5.8
avg. IF

4.49
L-index

#	Paper	IF	Citations
53	The Collaborative Cross, a community resource for the genetic analysis of complex traits. <i>Nature Genetics</i> , 2004 , 36, 1133-7	36.3	822
52	Genetic analysis of complex traits in the emerging Collaborative Cross. <i>Genome Research</i> , 2011 , 21, 1213-22	9.7	263
51	Intestinal microbiota and diet in IBS: causes, consequences, or epiphenomena?. <i>American Journal of Gastroenterology</i> , 2015 , 110, 278-87	0.7	225
50	Genotype is a stronger determinant than sex of the mouse gut microbiota. <i>Microbial Ecology</i> , 2011 , 61, 423-8	4.4	160
49	Fine mapping of trypanosomiasis resistance loci in murine advanced intercross lines. <i>Mammalian Genome</i> , 2000 , 11, 645-8	3.2	121
48	Collaborative Cross mice and their power to map host susceptibility to <i>Aspergillus fumigatus</i> infection. <i>Genome Research</i> , 2011 , 21, 1239-48	9.7	116
47	Localization of genes controlling resistance to trypanosomiasis in mice. <i>Nature Genetics</i> , 1997 , 16, 194-6	36.3	106
46	Status and access to the Collaborative Cross population. <i>Mammalian Genome</i> , 2012 , 23, 706-12	3.2	103
45	The Collaborative Cross, developing a resource for mammalian systems genetics: a status report of the Wellcome Trust cohort. <i>Mammalian Genome</i> , 2008 , 19, 379-81	3.2	89
44	Reproducibility and replicability of rodent phenotyping in preclinical studies. <i>Neuroscience and Biobehavioral Reviews</i> , 2018 , 87, 218-232	9	83
43	Mapping ecologically relevant social behaviours by gene knockout in wild mice. <i>Nature Communications</i> , 2014 , 5, 4569	17.4	58
42	Susceptibility to <i>Klebsiella pneumoniae</i> infection in collaborative cross mice is a complex trait controlled by at least three loci acting at different time points. <i>BMC Genomics</i> , 2014 , 15, 865	4.5	46
41	Cell composition analysis of bulk genomics using single-cell data. <i>Nature Methods</i> , 2019 , 16, 327-332	21.6	45
40	Confirmation and dissection of QTL controlling resistance to malaria in mice. <i>Mammalian Genome</i> , 2004 , 15, 390-8	3.2	43
39	Genotype is an important determinant factor of host susceptibility to periodontitis in the Collaborative Cross and inbred mouse populations. <i>BMC Genetics</i> , 2013 , 14, 68	2.6	39
38	Mapping of a new quantitative trait locus for resistance to malaria in mice by a comparative mapping approach with human Chromosome 5q31-q33. <i>Immunogenetics</i> , 2004 , 56, 115-7	3.2	38
37	High-fat-diet induced development of increased fasting glucose levels and impaired response to intraperitoneal glucose challenge in the collaborative cross mouse genetic reference population. <i>BMC Genetics</i> , 2016 , 17, 10	2.6	37

36	Chromosomal regions controlling resistance to gastro-intestinal nematode infections in mice. <i>Mammalian Genome</i> , 2003 , 14, 184-91	3.2	35
35	Host genetic diversity influences the severity of <i>Pseudomonas aeruginosa</i> pneumonia in the Collaborative Cross mice. <i>BMC Genetics</i> , 2015 , 16, 106	2.6	34
34	Fine mapping and identification of candidate pulmonary adenoma susceptibility 1 genes using advanced intercross lines. <i>Cancer Research</i> , 2003 , 63, 3317-24	10.1	34
33	Heritability and coefficient of genetic variation analyses of phenotypic traits provide strong basis for high-resolution QTL mapping in the Collaborative Cross mouse genetic reference population. <i>Mammalian Genome</i> , 2014 , 25, 109-19	3.2	32
32	Collaborative cross mice in a genetic association study reveal new candidate genes for bone microarchitecture. <i>BMC Genomics</i> , 2015 , 16, 1013	4.5	29
31	Mapping of chromosomal regions influencing immunological responses to gastrointestinal nematode infections in mice. <i>Parasite Immunology</i> , 2003 , 25, 341-9	2.2	29
30	Host genetic background influences the response to the opportunistic <i>Pseudomonas aeruginosa</i> infection altering cell-mediated immunity and bacterial replication. <i>PLoS ONE</i> , 2014 , 9, e106873	3.7	29
29	Glucose tolerance female-specific QTL mapped in collaborative cross mice. <i>Mammalian Genome</i> , 2017 , 28, 20-30	3.2	23
28	Marker-assisted introgression of trypanotolerance QTL in mice. <i>Mammalian Genome</i> , 2005 , 16, 112-9	3.2	19
27	High resolution mapping of chromosomal regions controlling resistance to gastrointestinal nematode infections in an advanced intercross line of mice. <i>Mammalian Genome</i> , 2006 , 17, 584-97	3.2	18
26	Mapping liver fat female-dependent quantitative trait loci in collaborative cross mice. <i>Mammalian Genome</i> , 2016 , 27, 565-573	3.2	16
25	Fine mapping of quantitative trait loci using advanced intercross lines of mice and positional cloning of the corresponding genes. <i>Experimental Lung Research</i> , 2000 , 26, 641-9	2.3	15
24	Genetic analysis of intestinal polyp development in Collaborative Cross mice carrying the <i>Apc</i> (Min/+) mutation. <i>BMC Genetics</i> , 2016 , 17, 46	2.6	13
23	The Collaborative Cross mouse model for dissecting genetic susceptibility to infectious diseases. <i>Mammalian Genome</i> , 2018 , 29, 471-487	3.2	12
22	Modeling the quantitative nature of neurodevelopmental disorders using Collaborative Cross mice. <i>Molecular Autism</i> , 2018 , 9, 63	6.5	12
21	Dissecting the Effect of Genetic Variation on the Hepatic Expression of Drug Disposition Genes across the Collaborative Cross Mouse Strains. <i>Frontiers in Genetics</i> , 2016 , 7, 172	4.5	11
20	Hepatic gene expression variations in response to high-fat diet-induced impaired glucose tolerance using RNAseq analysis in collaborative cross mouse population. <i>Mammalian Genome</i> , 2019 , 30, 260-275	3.2	8
19	Collaborative Cross Mouse Population for Studying Alveolar Bone Changes and Impaired Glucose Tolerance Comorbidity After High-Fat Diet Consumption. <i>Journal of Periodontology</i> , 2017 , 88, e150-e158	4.6	7

18	Translation of mouse model to human gives insights into periodontitis etiology. <i>Scientific Reports</i> , 2020 , 10, 4892	4.9	7
17	Mapping genetic determinants of host susceptibility to <i>Pseudomonas aeruginosa</i> lung infection in mice. <i>BMC Genomics</i> , 2016 , 17, 351	4.5	7
16	High resolution mapping of trypanosomosis resistance loci Tir2 and Tir3 using F12 advanced intercross lines with major locus Tir1 fixed for the susceptible allele. <i>BMC Genomics</i> , 2010 , 11, 394	4.5	7
15	Impact of host genetics on gut microbiome: Take-home lessons from human and mouse studies. <i>Animal Models and Experimental Medicine</i> , 2020 , 3, 229-236	4.2	6
14	Collaborative Cross Mice Yield Genetic Modifiers for <i>Pseudomonas aeruginosa</i> Infection in Human Lung Disease. <i>MBio</i> , 2020 , 11,	7.8	6
13	A genome-wide association study in mice reveals a role for <i>Rhbdf2</i> in skeletal homeostasis. <i>Scientific Reports</i> , 2020 , 10, 3286	4.9	5
12	Dissection of Host Susceptibility to Bacterial Infections and Its Toxins. <i>Methods in Molecular Biology</i> , 2017 , 1488, 551-578	1.4	4
11	Designing a QTL Mapping Study for Implementation in the Realized Collaborative Cross Genetic Reference Population. <i>Current Protocols in Mouse Biology</i> , 2019 , 9, e66	1.1	4
10	Mapping novel genetic loci associated with female liver weight variations using Collaborative Cross mice. <i>Animal Models and Experimental Medicine</i> , 2018 , 1, 212-220	4.2	4
9	Container-aided integrative QTL and RNA-seq analysis of Collaborative Cross mice supports distinct sex-oriented molecular modes of response in obesity. <i>BMC Genomics</i> , 2020 , 21, 761	4.5	3
8	Assessing the host genetic background effects on type 2 diabetes and obesity development in response to mixed-oral bacteria and high-fat diet using the collaborative cross mouse model. <i>Animal Models and Experimental Medicine</i> , 2020 , 3, 152-159	4.2	3
7	Systems genetics analysis of oral squamous cell carcinoma susceptibility using the mouse model: current position and new perspective. <i>Mammalian Genome</i> , 2021 , 32, 323-331	3.2	2
6	Studying the pharmacogenomic effect of cranberry extract on reducing body weight using collaborative cross mice. <i>Food and Function</i> , 2021 , 12, 4972-4982	6.1	1
5	Efficient protocols and methods for high-throughput utilization of the Collaborative Cross mouse model for dissecting the genetic basis of complex traits. <i>Animal Models and Experimental Medicine</i> , 2019 , 2, 137-149	4.2	0
4	Genetics of murine type 2 diabetes and comorbidities.. <i>Mammalian Genome</i> , 2022 , 1	3.2	0
3	Studying host genetic background effects on multimorbidity of intestinal cancer development, type 2 diabetes and obesity in response to oral bacterial infection and high-fat diet using the collaborative cross (CC) lines. <i>Animal Models and Experimental Medicine</i> , 2021 , 4, 27-39	4.2	0
2	Collaborative Cross as the Next-Generation Mouse Genetic Reference Population Designed for Dissecting Complex Traits 2018 , 191-224		0
1	Genetic mapping of novel modifiers for <i>Apc</i> induced intestinal polyps development using the genetic architecture power of the collaborative cross mice. <i>BMC Genomics</i> , 2021 , 22, 566	4.5	0

