Fuad A Iraqi

List of Publications by Year
in descending order

54 papers	3,679 citations	236612 25 h-index	161609 54 g-index
58 all docs	58 docs citations	58 times ranked	4276 citing authors

#	Article	IF	Citations
1	The Collaborative Cross, a community resource for the genetic analysis of complex traits. Nature Genetics, 2004, 36, 1133-1137.	9.4	1,034
2	Genetic analysis of complex traits in the emerging Collaborative Cross. Genome Research, 2011, 21, 1213-1222.	2.4	327
3	Intestinal Microbiota And Diet in IBS: Causes, Consequences, or Epiphenomena?. American Journal of Gastroenterology, 2015, 110, 278-287.	0.2	283
4	Genotype Is a Stronger Determinant than Sex of the Mouse Gut Microbiota. Microbial Ecology, 2011, 61, 423-428.	1.4	201
5	Reproducibility and replicability of rodent phenotyping in preclinical studies. Neuroscience and Biobehavioral Reviews, 2018, 87, 218-232.	2.9	153
6	Collaborative Cross mice and their power to map host susceptibility to *Aspergillus fumigatus* infection. Genome Research, 2011, 21, 1239-1248.	2.4	138
7	Status and access to the Collaborative Cross population. Mammalian Genome, 2012, 23, 706-712.	1.0	134
8	Fine mapping of trypanosomiasis resistance loci in murine advanced intercross lines. Mammalian Genome, 2000, 11, 645-648.	1.0	128
9	Localization of genes controlling resistance to trypanosomiasis in mice. Nature Genetics, 1997, 16, 194-196.	9.4	115
10	The Collaborative Cross, developing a resource for mammalian systems genetics: A status report of the Wellcome Trust cohort. Mammalian Genome, 2008, 19, 379-381.	1.0	111
11	Cell composition analysis of bulk genomics using single-cell data. Nature Methods, 2019, 16, 327-332.	9.0	94
12	Mapping ecologically relevant social behaviours by gene knockout in wild mice. Nature Communications, 2014, 5, 4569.	5.8	88
13	Susceptibility to klebsiella pneumonaie infection in collaborative cross mice is a complex trait controlled by at least three loci acting at different time points. BMC Genomics, 2014, 15, 865.	1.2	55
14	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. BMC Genetics, 2016, 17, 10.	2.7	51
15	Confirmation and dissection of QTL controlling resistanceto malaria in mice. Mammalian Genome, 2004, 15, 390-398.	1.0	48
16	Host genetic diversity influences the severity of Pseudomonas aeruginosa pneumonia in the Collaborative Cross mice. BMC Genetics, 2015, 16, 106.	2.7	44
17	Mapping of a new quantitative trait locus for resistance to malaria in mice by a comparative mapping approach with human Chromosome 5q31-q33. Immunogenetics, 2004, 56, 115-117.	1.2	42
18	Genotype is an important determinant factor of host susceptibility to periodontitis in the Collaborative Cross and inbred mouse populations. BMC Genetics, 2013, 14, 68.	2.7	42

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19	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. Mammalian Genome, 2014, 25, 109-119.	1.0	40
20	Collaborative cross mice in a genetic association study reveal new candidate genes for bone microarchitecture. BMC Genomics, 2015, 16, 1013.	1.2	39
21	Fine mapping and identification of candidate pulmonary adenoma susceptibility 1 genes using advanced intercross lines. Cancer Research, 2003, 63, 3317-24.	0.4	39
22	Chromosomal regions controlling resistance to gastro-intestinal nematode infections in mice. Mammalian Genome, 2003, 14, 184-191.	1.0	37
23	Host Genetic Background Influences the Response to the Opportunistic Pseudomonas aeruginosa Infection Altering Cell-Mediated Immunity and Bacterial Replication. PLoS ONE, 2014, 9, e106873.	1.1	36
24	Mapping of chromosomal regions influencing immunological responses to gastrointestinal nematode infections in mice. Parasite Immunology, 2003, 25, 341-349.	0.7	33
25	Glucose tolerance female-specific QTL mapped in collaborative cross mice. Mammalian Genome, 2017, 28, 20-30.	1.0	31
26	The Collaborative Cross mouse model for dissecting genetic susceptibility to infectious diseases. Mammalian Genome, 2018, 29, 471-487.	1.0	27
27	Impact of host genetics on gut microbiome: Take‐home lessons from human and mouse studies. Animal Models and Experimental Medicine, 2020, 3, 229-236.	1.3	27
28	Modeling the quantitative nature of neurodevelopmental disorders using Collaborative Cross mice. Molecular Autism, 2018, 9, 63.	2.6	22
29	High resolution mapping of chromosomal regions controlling resistance to gastrointestinal nematode infections in an advanced intercross line of mice. Mammalian Genome, 2006, 17, 584-597.	1.0	21
30	Mapping liver fat female-dependent quantitative trait loci in collaborative cross mice. Mammalian Genome, 2016, 27, 565-573.	1.0	20
31	Marker-assisted introgression of Trypanotolerance QTL in mice. Mammalian Genome, 2005, 16, 112-119.	1.0	19
32	FINE MAPPING OF QUANTITATIVE TRAIT LOCI USING ADVANCED INTERCROSS LINES OF MICE AND POSITIONAL CLONING OF THE CORRESPONDING GENES. Experimental Lung Research, 2000, 26, 641-649.	0.5	18
33	Genetic analysis of intestinal polyp development in Collaborative Cross mice carrying the Apc Min/+ mutation. BMC Genetics, 2016, 17, 46.	2.7	18
34	Collaborative Cross Mice Yield Genetic Modifiers for Pseudomonas aeruginosa Infection in Human Lung Disease. MBio, 2020, 11, .	1.8	17
35	Genetics of murine type 2 diabetes and comorbidities. Mammalian Genome, 2022, 33, 421-436.	1.0	16
36	Hepatic gene expression variations in response to high-fat diet-induced impaired glucose tolerance using RNAseq analysis in collaborative cross mouse population. Mammalian Genome, 2019, 30, 260-275.	1.0	13

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37	Dissecting the Effect of Genetic Variation on the Hepatic Expression of Drug Disposition Genes across the Collaborative Cross Mouse Strains. Frontiers in Genetics, 2016, 7, 172.	1.1	12
38	Translation of mouse model to human gives insights into periodontitis etiology. Scientific Reports, 2020, 10, 4892.	1.6	12
39	Mapping genetic determinants of host susceptibility to Pseudomonas aeruginosa lung infection in mice. BMC Genomics, 2016, 17, 351.	1.2	10
40	Collaborative Cross Mouse Population for Studying Alveolar Bone Changes and Impaired Glucose Tolerance Comorbidity After High-Fat Diet Consumption. Journal of Periodontology, 2017, 88, e150-e158.	1.7	10
41	A genome-wide association study in mice reveals a role for Rhbdf2 in skeletal homeostasis. Scientific Reports, 2020, 10, 3286.	1.6	10
42	High resolution mapping of trypanosomosis resistance loci Tir 2 and Tir 3 using F12 advanced intercross lines with major locus Tir 1 fixed for the susceptible allele. BMC Genomics, 2010, 11, 394.	1.2	8
43	Genetic mapping of novel modifiers for ApcMin induced intestinal polyps' development using the genetic architecture power of the collaborative cross mice. BMC Genomics, 2021, 22, 566.	1.2	8
44	Container-aided integrative QTL and RNA-seq analysis of Collaborative Cross mice supports distinct sex-oriented molecular modes of response in obesity. BMC Genomics, 2020, 21, 761.	1.2	7
45	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. Animal Models and Experimental Medicine, 2020, 3, 152-159.	1.3	7
46	Mapping novel genetic loci associated with female liver weight variations using Collaborative Cross mice. Animal Models and Experimental Medicine, 2018, 1, 212-220.	1.3	6
47	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. Animal Models and Experimental Medicine, 2021, 4, 27-39.	1.3	6
48	Designing a QTL Mapping Study for Implementation in the Realized Collaborative Cross Genetic Reference Population. Current Protocols in Mouse Biology, 2019, 9, e66.	1.2	5
49	Dissection of Host Susceptibility to Bacterial Infections and Its Toxins. Methods in Molecular Biology, 2017, 1488, 551-578.	0.4	4
50	Efficient protocols and methods for high-throughput utilization of the Collaborative Cross mouse model for dissecting the genetic basis of complex traits. Animal Models and Experimental Medicine, 2019, 2, 137-149.	1.3	3
51	Systems genetics analysis of oral squamous cell carcinoma susceptibility using the mouse model: current position and new perspective. Mammalian Genome, 2021, 32, 323-331.	1.0	3
52	Collaborative Cross as the Next-Generation Mouse Genetic Reference Population Designed for Dissecting Complex Traits. , 2018, , 191-224.		2
53	Studying the pharmacogenomic effect of cranberry extract on reducing body weight using collaborative cross mice. Food and Function, 2021, 12, 4972-4982.	2.1	2
54	Leveraging the cell lineage to predict cell-type specificity of regulatory variation from bulk genomics. Genetics, 2021, 217, .	1.2	1