

Chris K Tuggle

List of Publications by Year in descending order

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121
papers

6,431
citations

81743

39
h-index

76769

74
g-index

131
all docs

131
docs citations

131
times ranked

6240
citing authors

#	ARTICLE	IF	CITATIONS
1	Swine models for translational oncological research: an evolving landscape and regulatory considerations. <i>Mammalian Genome</i> , 2022, 33, 230-240.	1.0	6
2	The Agricultural Genome to Phenome Initiative (AG2PI): creating a shared vision across crop and livestock research communities. <i>Genome Biology</i> , 2022, 23, 3.	3.8	5
3	Differential induction of innate memory in porcine monocytes by β -glucan or bacillus Calmette-Guerin. <i>Innate Immunity</i> , 2021, 27, 448-460.	1.1	13
4	Gene expression in tonsils in swine following infection with porcine reproductive and respiratory syndrome virus. <i>BMC Veterinary Research</i> , 2021, 17, 88.	0.7	12
5	Functional annotations of three domestic animal genomes provide vital resources for comparative and agricultural research. <i>Nature Communications</i> , 2021, 12, 1821.	5.8	105
6	Reference Transcriptomes of Porcine Peripheral Immune Cells Created Through Bulk and Single-Cell RNA Sequencing. <i>Frontiers in Genetics</i> , 2021, 12, 689406.	1.1	36
7	Quantitative analysis of the blood transcriptome of young healthy pigs and its relationship with subsequent disease resilience. <i>BMC Genomics</i> , 2021, 22, 614.	1.2	9
8	Effect of ARTEMIS (DCLRE1C) deficiency and microinjection timing on editing efficiency during somatic cell nuclear transfer and in vitro fertilization using the CRISPR/Cas9 system. <i>Theriogenology</i> , 2021, 170, 107-116.	0.9	2
9	Associations of natural variation in the CD163 and other candidate genes on host response of nursery pigs to porcine reproductive and respiratory syndrome virus infection. <i>Journal of Animal Science</i> , 2021, 99, .	0.2	6
10	Pig genome functional annotation enhances the biological interpretation of complex traits and human disease. <i>Nature Communications</i> , 2021, 12, 5848.	5.8	70
11	A comparative analysis of chromatin accessibility in cattle, pig, and mouse tissues. <i>BMC Genomics</i> , 2020, 21, 698.	1.2	43
12	From FAANG to fork: application of highly annotated genomes to improve farmed animal production. <i>Genome Biology</i> , 2020, 21, 285.	3.8	74
13	Changes in H3K27ac at Gene Regulatory Regions in Porcine Alveolar Macrophages Following LPS or PolyIC Exposure. <i>Frontiers in Genetics</i> , 2020, 11, 817.	1.1	23
14	An improved pig reference genome sequence to enable pig genetics and genomics research. <i>GigaScience</i> , 2020, 9, .	3.3	187
15	Novel Engraftment and T Cell Differentiation of Human Hematopoietic Cells in ART ^{+/+} /IL2RG ^{+/+} /SCID Pigs. <i>Frontiers in Immunology</i> , 2020, 11, 100.	2.2	21
16	CD3 ⁺ Cells in Pigs With Severe Combined Immunodeficiency Due to Defects in ARTEMIS. <i>Frontiers in Immunology</i> , 2020, 11, 510.	2.2	5
17	Acute systemic inflammatory response to lipopolysaccharide stimulation in pigs divergently selected for residual feed intake. <i>BMC Genomics</i> , 2019, 20, 728.	1.2	10
18	Successful development of methodology for detection of hapten-specific contact hypersensitivity (CHS) memory in swine. <i>PLoS ONE</i> , 2019, 14, e0223483.	1.1	0

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19	A Comprehensive Protocol for Laparotomy in Swine to Facilitate Ultrasound-Guided Injection into the Fetal Intraperitoneal Space. <i>Comparative Medicine</i> , 2019, 69, 123-129.	0.4	4
20	Improved annotation of the domestic pig genome through integration of Iso-Seq and RNA-seq data. <i>BMC Genomics</i> , 2019, 20, 344.	1.2	80
21	Infectivity of GII.4 human norovirus does not differ between T-B-NK+ severe combined immunodeficiency (SCID) and non-SCID gnotobiotic pigs, implicating the role of NK cells in mediation of human norovirus infection. <i>Virus Research</i> , 2019, 267, 21-25.	1.1	6
22	Survival of human cadaver skin on severe combined immune deficiency pigs: Proof of concept. <i>Wound Repair and Regeneration</i> , 2019, 27, 426-430.	1.5	4
23	Human Ovarian Cancer Tumor Formation in Severe Combined Immunodeficient (SCID) Pigs. <i>Frontiers in Oncology</i> , 2019, 9, 9.	1.3	32
24	The effects of a globin blocker on the resolution of 3â€™ mRNA sequencing data in porcine blood. <i>BMC Genomics</i> , 2019, 20, 741.	1.2	4
25	Functional Annotation of Animal Genomes (FAANG): Current Achievements and Roadmap. <i>Annual Review of Animal Biosciences</i> , 2019, 7, 65-88.	3.6	172
26	Porcine signal regulatory protein alpha binds to human CD47 to inhibit phagocytosis: Implications for human hematopoietic stem cell transplantation into severe combined immunodeficient pigs. <i>Xenotransplantation</i> , 2019, 26, e12466.	1.6	21
27	Creating effective biocontainment facilities and maintenance protocols for raising specific pathogen-free, severe combined immunodeficient (SCID) pigs. <i>Laboratory Animals</i> , 2018, 52, 402-412.	0.5	21
28	Development of Severe Combined Immunodeficient (SCID) Pig Models for Translational Cancer Modeling: Future Insights on How Humanized SCID Pigs Can Improve Preclinical Cancer Research. <i>Frontiers in Oncology</i> , 2018, 8, 559.	1.3	32
29	Genetic architecture of gene expression underlying variation in host response to porcine reproductive and respiratory syndrome virus infection. <i>Scientific Reports</i> , 2017, 7, 46203.	1.6	32
30	Pigs with Severe Combined Immunodeficiency Are Impaired in Controlling Influenza A Virus Infection. <i>Journal of Innate Immunity</i> , 2017, 9, 193-202.	1.8	12
31	A high-quality annotated transcriptome of swine peripheral blood. <i>BMC Genomics</i> , 2017, 18, 479.	1.2	7
32	T Cell Lymphoma and Leukemia in Severe Combined Immunodeficiency Pigs following Bone Marrow Transplantation: A Case Report. <i>Frontiers in Immunology</i> , 2017, 8, 813.	2.2	18
33	Genomewide association of piglet responses to infection with one of two porcine reproductive and respiratory syndrome virus isolates1. <i>Journal of Animal Science</i> , 2017, 95, 16-38.	0.2	26
34	SCID pigs: An emerging large animal NK model. <i>Journal of Rare Diseases Research & Treatment</i> , 2017, 2, 1-6.	1.1	20
35	SCID pigs: An emerging large animal NK model. , 2017, 2, 1-6.		12
36	Identification of potential serum biomarkers to predict feed efficiency in young pigs1. <i>Journal of Animal Science</i> , 2016, 94, 1482-1492.	0.2	16

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37	Post-weaning blood transcriptomic differences between Yorkshire pigs divergently selected for residual feed intake. <i>BMC Genomics</i> , 2016, 17, 73.	1.2	53
38	NK cells are intrinsically functional in pigs with Severe Combined Immunodeficiency (SCID) caused by spontaneous mutations in the <i>Artemis</i> gene. <i>Veterinary Immunology and Immunopathology</i> , 2016, 175, 1-6.	0.5	29
39	<sc>GO</sc>â€œ<sc>FAANG</sc> meeting: a Gathering On Functional Annotation of <sc>Animal</sc> Genomes. <i>Animal Genetics</i> , 2016, 47, 528-533.	0.6	65
40	Applications of Systems Biology to Improve Pig Health. , 2016, , 33-59.		0
41	Bioinformatic analyses in early host response to Porcine Reproductive and Respiratory Syndrome virus (PRRSV) reveals pathway differences between pigs with alternate genotypes for a major host response QTL. <i>BMC Genomics</i> , 2016, 17, 196.	1.2	24
42	Genome-wide whole blood microRNAome and transcriptome analyses reveal miRNA-mRNA regulated host response to foodborne pathogen <i>Salmonella</i> infection in swine. <i>Scientific Reports</i> , 2015, 5, 12620.	1.6	33
43	Detecting Differentially Expressed Genes with RNA-seq Data Using Backward Selection to Account for the Effects of Relevant Covariates. <i>Journal of Agricultural, Biological, and Environmental Statistics</i> , 2015, 20, 577-597.	0.7	7
44	Assessing peripheral blood cell profile of Yorkshire pigs divergently selected for residual feed intake. <i>Journal of Animal Science</i> , 2015, 93, 892.	0.2	22
45	Livestock Models in Translational Medicine. <i>ILAR Journal</i> , 2015, 56, 1-6.	1.8	48
46	Identification of a putative quantitative trait nucleotide in guanylate binding protein 5 for host response to PRRS virus infection. <i>BMC Genomics</i> , 2015, 16, 412.	1.2	75
47	Activation of the Transcription Factor Nuclear Factor-Kappa B in Uterine Luminal Epithelial Cells by Interleukin 1 Beta 2: A Novel Interleukin 1 Expressed by the Elongating Pig Conceptus1. <i>Biology of Reproduction</i> , 2015, 92, 107.	1.2	40
48	Coordinated international action to accelerate genome-to-phenome with FAANG, the Functional Annotation of Animal Genomes project. <i>Genome Biology</i> , 2015, 16, 57.	3.8	331
49	Tuberculosis-resistant transgenic cattle. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 3854-3855.	3.3	11
50	<i>Salmonella enterica</i> serovar Typhimurium-infected pigs with different shedding levels exhibit distinct clinical, peripheral cytokine and transcriptomic immune response phenotypes. <i>Innate Immunity</i> , 2015, 21, 227-241.	1.1	37
51	Whole blood microarray analysis of pigs showing extreme phenotypes after a porcine reproductive and respiratory syndrome virus infection. <i>BMC Genomics</i> , 2015, 16, 516.	1.2	13
52	Not All SCID Pigs Are Created Equally: Two Independent Mutations in the <i>Artemis</i> Gene Cause SCID in Pigs. <i>Journal of Immunology</i> , 2015, 195, 3171-3179.	0.4	43
53	Current transcriptomics in pig immunity research. <i>Mammalian Genome</i> , 2015, 26, 1-20.	1.0	34
54	Analysis of blood leukocytes in a naturally occurring immunodeficiency of pigs shows the defect is localized to B and T cells. <i>Veterinary Immunology and Immunopathology</i> , 2014, 162, 174-179.	0.5	14

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55	Increasing gene discovery and coverage using RNA-seq of globin RNA reduced porcine blood samples. BMC Genomics, 2014, 15, 954.	1.2	43
56	Organic barn dust extract exposure impairs porcine macrophage function in vitro: Implications for respiratory health. Veterinary Immunology and Immunopathology, 2014, 157, 20-30.	0.5	18
57	Endometrial gene expression profiling in pregnant Meishan and Yorkshire pigs on day 12 of gestation. BMC Genomics, 2014, 15, 156.	1.2	40
58	Gene co-expression network analysis identifies porcine genes associated with variation in Salmonella shedding. BMC Genomics, 2014, 15, 452.	1.2	65
59	MicroRNA Buffering and Altered Variance of Gene Expression in Response to Salmonella Infection. PLoS ONE, 2014, 9, e94352.	1.1	17
60	Structural and functional annotation of the porcine immunome. BMC Genomics, 2013, 14, 332.	1.2	203
61	Pig immune response to general stimulus and to porcine reproductive and respiratory syndrome virus infection: a meta-analysis approach. BMC Genomics, 2013, 14, 220.	1.2	31
62	Profiling the gastrointestinal microbiota in response to Salmonella: Low versus high Salmonella shedding in the natural porcine host. Infection, Genetics and Evolution, 2013, 16, 330-340.	1.0	71
63	The impact of breed and tissue compartment on the response of pig macrophages to lipopolysaccharide. BMC Genomics, 2013, 14, 581.	1.2	83
64	Comparative Analysis of Monocyte Subsets in the Pig. Journal of Immunology, 2013, 190, 6389-6396.	0.4	91
65	Characterizing differential individual response to porcine reproductive and respiratory syndrome virus infection through statistical and functional analysis of gene expression. Frontiers in Genetics, 2013, 3, 321.	1.1	18
66	Analyses of pig genomes provide insight into porcine demography and evolution. Nature, 2012, 491, 393-398.	13.7	1,190
67	A gene expression atlas of the domestic pig. BMC Biology, 2012, 10, 90.	1.7	199
68	Pig Bone Marrow-Derived Macrophages Resemble Human Macrophages in Their Response to Bacterial Lipopolysaccharide. Journal of Immunology, 2012, 188, 3382-3394.	0.4	147
69	Functional Genomics Unique to Week 20 Post Wounding in the Deep Cone/Fat Dome of the Duroc/Yorkshire Porcine Model of Fibroproliferative Scarring. PLoS ONE, 2011, 6, e19024.	1.1	21
70	Distinct Peripheral Blood RNA Responses to Salmonella in Pigs Differing in Salmonella Shedding Levels: Intersection of IFNG, TLR and miRNA Pathways. PLoS ONE, 2011, 6, e28768.	1.1	47
71	Use of bioinformatic SNP predictions in differentially expressed genes to find SNPs associated with Salmonella colonization in swine. Journal of Animal Breeding and Genetics, 2011, 128, 354-365.	0.8	9
72	Integrating comparative expression profiling data and association of SNPs with <i>Salmonella</i> shedding for improved food safety and porcine disease resistance. Animal Genetics, 2011, 42, 521-534.	0.6	14

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73	Gene expression profiling of the short-term adaptive response to acute caloric restriction in liver and adipose tissues of pigs differing in feed efficiency. <i>American Journal of Physiology - Regulatory Integrative and Comparative Physiology</i> , 2010, 298, R494-R507.	0.9	83
74	Methods for transcriptomic analyses of the porcine host immune response: Application to Salmonella infection using microarrays. <i>Veterinary Immunology and Immunopathology</i> , 2010, 138, 280-291.	0.5	10
75	Microarray gene expression profiles of fasting induced changes in liver and adipose tissues of pigs expressing the melanocortin-4 receptor D298N variant. <i>Physiological Genomics</i> , 2009, 38, 98-111.	1.0	44
76	Identification of differential gene expression during porcine conceptus rapid trophoblastic elongation and attachment to uterine luminal epithelium. <i>Physiological Genomics</i> , 2009, 36, 140-148.	1.0	81
77	Correlating blood immune parameters and a CCT7 genetic variant with the shedding of Salmonella enterica serovar Typhimurium in swine. <i>Veterinary Microbiology</i> , 2009, 135, 384-388.	0.8	29
78	ANEXdb: an integrated animal ANnotation and microarray EXpression database. <i>Mammalian Genome</i> , 2009, 20, 768-777.	1.0	28
79	Analysis of Porcine Transcriptional Response to Salmonella enterica serovar Choleraesuis suggests novel targets of NFkappaB are activated in the Mesenteric Lymph Node. <i>BMC Genomics</i> , 2008, 9, 437.	1.2	41
80	Expression of Collagen Genes in the Cones of Skin in the Duroc/Yorkshire Porcine Model of Fibroproliferative Scarring. <i>Journal of Burn Care and Research</i> , 2008, 29, 815-827.	0.2	28
81	Computational Integration of Structural and Functional Genomics Data across Species to Develop Information on the Porcine Inflammatory Gene Regulatory Pathway. <i>Developments in Biologicals</i> , 2008, 132, 105-113.	0.4	2
82	Global transcriptional response of porcine mesenteric lymph nodes to Salmonella enterica serovar Typhimurium. <i>Genomics</i> , 2007, 90, 72-84.	1.3	36
83	Porcine differential gene expression in response to Salmonella enterica serovars Choleraesuis and Typhimurium. <i>Molecular Immunology</i> , 2007, 44, 2900-2914.	1.0	40
84	Advances in Swine Transcriptomics. <i>International Journal of Biological Sciences</i> , 2007, 3, 132-152.	2.6	52
85	Gene expression profiling in Salmonella Choleraesuis-infected porcine lung using a long oligonucleotide microarray. <i>Mammalian Genome</i> , 2006, 17, 777-789.	1.0	41
86	Analysis of porcine differential gene expression following challenge with Salmonella enterica serovar Choleraesuis using suppression subtractive hybridization. <i>Veterinary Microbiology</i> , 2006, 114, 60-71.	0.8	17
87	Transcriptional profiling using a novel cDNA array identifies differential gene expression during porcine embryo elongation. <i>Molecular Reproduction and Development</i> , 2005, 71, 129-139.	1.0	19
88	Physical mapping of genes in the porcine ovarian transcriptome. <i>Animal Genetics</i> , 2005, 36, 322-330.	0.6	5
89	Physical mapping of eight pig genes whose expression level is acutely affected by Salmonella challenge. <i>Animal Genetics</i> , 2005, 36, 359-362.	0.6	1
90	Mapping of 443 porcine EST improves the comparative maps for SSC1 and SSC7 with the human genome. <i>Animal Genetics</i> , 2005, 36, 381-389.	0.6	12

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91	Ectopic HOXA5 expression results in abnormal differentiation, migration and p53-independent cell death of superficial dorsal horn neurons. <i>Developmental Brain Research</i> , 2005, 159, 87-97.	2.1	5
92	Dynamic expression of murine HOXA5 protein in the central nervous system. <i>Gene Expression Patterns</i> , 2005, 5, 792-800.	0.3	16
93	Validation of a first-generation long-oligonucleotide microarray for transcriptional profiling in the pig. <i>Genomics</i> , 2005, 86, 618-625.	1.3	64
94	Transgenic mice ectopically expressing HOXA5 in the dorsal spinal cord show structural defects of the cervical spinal cord along with sensory and motor defects of the forelimb. <i>Developmental Brain Research</i> , 2004, 150, 125-139.	2.1	8
95	High-resolution comparative mapping of pig Chromosome 4, emphasizing the FAT1 region. <i>Mammalian Genome</i> , 2004, 15, 717-731.	1.0	25
96	Linkage mapping and expression analyses of a novel gene, placentally expressed transcript 1 (PLET1) in the pig. <i>Animal Genetics</i> , 2004, 35, 72-74.	0.6	3
97	PLET1 (C11orf34), a highly expressed and processed novel gene in pig and mouse placenta, is transcribed but poorly spliced in human. <i>Genomics</i> , 2004, 84, 114-125.	1.3	20
98	EST-based gene discovery in pig: virtual expression patterns and comparative mapping to human. <i>Mammalian Genome</i> , 2003, 14, 565-579.	1.0	54
99	Complementary DNA macroarray analyses of differential gene expression in porcine fetal and postnatal muscle1. <i>Journal of Animal Science</i> , 2003, 81, 2179-2188.	0.2	44
100	Neonatal Meishan pigs show POU1F1 genotype effects on plasma GH and PRL concentration. <i>Animal Reproduction Science</i> , 2002, 69, 223-237.	0.5	41
101	Precise mapping of breakpoints in conserved synteny between human chromosome 1 and pig chromosomes 4, 6 and 9. <i>Animal Genetics</i> , 2002, 33, 91-96.	0.6	13
102	Linkage mapping of porcine STCH further refines the HSA3/21 breakpoint on pig chromosome 13. <i>Animal Genetics</i> , 2002, 33, 395-397.	0.6	0
103	CLONING OF THE FULL LENGTH PIGPIT1 (POU1F1) CDNA AND A NOVEL ALTERNATIVE PIT1 TRANSCRIPT, AND FUNCTIONAL STUDIES OF THEIR ENCODED PROTEINS. <i>Animal Biotechnology</i> , 2001, 12, 1-19.	0.7	14
104	Rapid communication: genetic linkage and physical mapping of the porcine phospholipid transfer protein (PLTP) gene.. <i>Journal of Animal Science</i> , 2001, 79, 1633.	0.2	3
105	Rapid communication: Genetic linkage and physical mapping of the porcine lipopolysaccharide-binding protein (LBP) gene.. <i>Journal of Animal Science</i> , 2001, 79, 556.	0.2	4
106	Cytogenetic and radiation hybrid mapping reveals conserved synteny and gene order between human Chromosome 21 and pig Chromosome 13. <i>Mammalian Genome</i> , 2001, 12, 397-399.	1.0	28
107	Rapid communication: Mapping of the myeloperoxidase (MPO) gene to pig chromosome 12.. <i>Journal of Animal Science</i> , 2000, 78, 3189.	0.2	2
108	Rapid communication: mapping of the Mannose-Binding Lectin 2 (MBL2) gene to pig chromosome 14.. <i>Journal of Animal Science</i> , 2000, 78, 2992.	0.2	7

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109	Rapid communication: localization of POU1F1 to bovine, ovine, and caprine 1q21-22.. Journal of Animal Science, 2000, 78, 242.	0.2	30
110	Physical assignments of human chromosome 13 genes on pig chromosome 11 demonstrate extensive synteny and gene order conservation between pig and human. Animal Genetics, 1999, 30, 304-308.	0.6	10
111	Mapping genes for fatness and growth on pig chromosome 13: a search in the region close to the pig PIT1 gene. Journal of Animal Breeding and Genetics, 1999, 116, 269-280.	0.8	38
112	New insights into porcine-human synteny conservation. Mammalian Genome, 1999, 10, 488-491.	1.0	19
113	Human chromosome 3 and pig chromosome 13 show complete synteny conservation but extensive gene-order differences. Cytogenetic and Genome Research, 1999, 85, 273-278.	0.6	42
114	Mapping of the melatonin receptor 1a (MTNR1A) gene in pigs, sheep, and cattle. Mammalian Genome, 1997, 8, 368-370.	1.0	84
115	Control of growth hormone synthesis. Domestic Animal Endocrinology, 1996, 13, 1-33.	0.8	85
116	The PiGMaP consortium linkage map of the pig (Sus scrofa). Mammalian Genome, 1995, 6, 157-175.	1.0	475
117	Association of PIT1 polymorphisms with growth and carcass traits in pigs. Journal of Animal Science, 1995, 73, 1282-1288.	0.2	73
118	Expression pattern, genomic cloning and RFLP analyses of the swine PIT1 gene. Animal Genetics, 1994, 25, 229-233.	0.6	12
119	Cloning and restriction fragment length polymorphism analysis of a cDNA for swine PIT1, a gene controlling growth hormone expression*. Animal Genetics, 1993, 24, 17-21.	0.6	25
120	Region-specific enhancers near two mammalian homeo box genes define adjacent rostrocaudal domains in the central nervous system.. Genes and Development, 1990, 4, 180-189.	2.7	73
121	Spatial regulation of homeobox gene fusions in the embryonic central nervous system of transgenic mice. Neuron, 1988, 1, 679-691.	3.8	114