

# Chris K Tuggle

## List of Publications by Citations

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123  
papers

4,436  
citations

33  
h-index

63  
g-index

131  
ext. papers

5,686  
ext. citations

4.6  
avg, IF

4.97  
L-index

#	Paper	IF	Citations
123	Analyses of pig genomes provide insight into porcine demography and evolution. <i>Nature</i> , <b>2012</b> , 491, 393-8	50.4	928
122	The PiGMaP consortium linkage map of the pig ( <i>Sus scrofa</i> ). <i>Mammalian Genome</i> , <b>1995</b> , 6, 157-75	3.2	402
121	Coordinated international action to accelerate genome-to-phenome with FAANG, the Functional Annotation of Animal Genomes project. <i>Genome Biology</i> , <b>2015</b> , 16, 57	18.3	196
120	Structural and functional annotation of the porcine immunome. <i>BMC Genomics</i> , <b>2013</b> , 14, 332	4.5	128
119	A gene expression atlas of the domestic pig. <i>BMC Biology</i> , <b>2012</b> , 10, 90	7.3	116
118	Spatial regulation of homeobox gene fusions in the embryonic central nervous system of transgenic mice. <i>Neuron</i> , <b>1988</b> , 1, 679-91	13.9	101
117	Pig bone marrow-derived macrophages resemble human macrophages in their response to bacterial lipopolysaccharide. <i>Journal of Immunology</i> , <b>2012</b> , 188, 3382-94	5.3	98
116	Control of growth hormone synthesis. <i>Domestic Animal Endocrinology</i> , <b>1996</b> , 13, 1-33	2.3	74
115	Comparative analysis of monocyte subsets in the pig. <i>Journal of Immunology</i> , <b>2013</b> , 190, 6389-96	5.3	71
114	Mapping of the melatonin receptor 1a (MTNR1A) gene in pigs, sheep, and cattle. <i>Mammalian Genome</i> , <b>1997</b> , 8, 368-70	3.2	70
113	Functional Annotation of Animal Genomes (FAANG): Current Achievements and Roadmap. <i>Annual Review of Animal Biosciences</i> , <b>2019</b> , 7, 65-88	13.7	70
112	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> , <b>2010</b> , 298, R494-507	3.2	67
111	Association of PIT1 polymorphisms with growth and carcass traits in pigs. <i>Journal of Animal Science</i> , <b>1995</b> , 73, 1282-8	0.7	64
110	Identification of a putative quantitative trait nucleotide in guanylate binding protein 5 for host response to PRRS virus infection. <i>BMC Genomics</i> , <b>2015</b> , 16, 412	4.5	63
109	Identification of differential gene expression during porcine conceptus rapid trophoblastic elongation and attachment to uterine luminal epithelium. <i>Physiological Genomics</i> , <b>2009</b> , 36, 140-8	3.6	61
108	An improved pig reference genome sequence to enable pig genetics and genomics research. <i>GigaScience</i> , <b>2020</b> , 9,	7.6	60
107	Region-specific enhancers near two mammalian homeo box genes define adjacent rostrocaudal domains in the central nervous system. <i>Genes and Development</i> , <b>1990</b> , 4, 180-9	12.6	60

106	Profiling the gastrointestinal microbiota in response to Salmonella: low versus high Salmonella shedding in the natural porcine host. <i>Infection, Genetics and Evolution</i> , <b>2013</b> , 16, 330-40	4.5	59
105	Validation of a first-generation long-oligonucleotide microarray for transcriptional profiling in the pig. <i>Genomics</i> , <b>2005</b> , 86, 618-25	4.3	57
104	EST-based gene discovery in pig: virtual expression patterns and comparative mapping to human. <i>Mammalian Genome</i> , <b>2003</b> , 14, 565-79	3.2	50
103	Advances in swine transcriptomics. <i>International Journal of Biological Sciences</i> , <b>2007</b> , 3, 132-52	11.2	46
102	Gene co-expression network analysis identifies porcine genes associated with variation in Salmonella shedding. <i>BMC Genomics</i> , <b>2014</b> , 15, 452	4.5	43
101	Distinct peripheral blood RNA responses to Salmonella in pigs differing in Salmonella shedding levels: intersection of IFNG, TLR and miRNA pathways. <i>PLoS ONE</i> , <b>2011</b> , 6, e28768	3.7	38
100	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> , <b>2008</b> , 9, 437	4.5	38
99	Complementary DNA macroarray analyses of differential gene expression in porcine fetal and postnatal muscle. <i>Journal of Animal Science</i> , <b>2003</b> , 81, 2179-88	0.7	38
98	GO-FAANG meeting: a Gathering On Functional Annotation of Animal Genomes. <i>Animal Genetics</i> , <b>2016</b> , 47, 528-33	2.5	37
97	Gene expression profiling in Salmonella Choleraesuis-infected porcine lung using a long oligonucleotide microarray. <i>Mammalian Genome</i> , <b>2006</b> , 17, 777-89	3.2	37
96	The impact of breed and tissue compartment on the response of pig macrophages to lipopolysaccharide. <i>BMC Genomics</i> , <b>2013</b> , 14, 581	4.5	36
95	Porcine differential gene expression in response to Salmonella enterica serovars Choleraesuis and Typhimurium. <i>Molecular Immunology</i> , <b>2007</b> , 44, 2900-14	4.3	35
94	Neonatal Meishan pigs show POU1F1 genotype effects on plasma GH and PRL concentration. <i>Animal Reproduction Science</i> , <b>2002</b> , 69, 223-37	2.1	35
93	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> , <b>2009</b> , 38, 98-111	3.6	34
92	Livestock models in translational medicine. <i>ILAR Journal</i> , <b>2015</b> , 56, 1-6	1.7	33
91	Not All SCID Pigs Are Created Equally: Two Independent Mutations in the Artemis Gene Cause SCID in Pigs. <i>Journal of Immunology</i> , <b>2015</b> , 195, 3171-9	5.3	32
90	Human chromosome 3 and pig chromosome 13 show complete synteny conservation but extensive gene-order differences. <i>Cytogenetic and Genome Research</i> , <b>1999</b> , 85, 273-8	1.9	32
89	Improved annotation of the domestic pig genome through integration of Iso-Seq and RNA-seq data. <i>BMC Genomics</i> , <b>2019</b> , 20, 344	4.5	31

88	Global transcriptional response of porcine mesenteric lymph nodes to Salmonella enterica serovar Typhimurium. <i>Genomics</i> , <b>2007</b> , 90, 72-84	4.3	31
87	Current transcriptomics in pig immunity research. <i>Mammalian Genome</i> , <b>2015</b> , 26, 1-20	3.2	30
86	Increasing gene discovery and coverage using RNA-seq of globin RNA reduced porcine blood samples. <i>BMC Genomics</i> , <b>2014</b> , 15, 954	4.5	30
85	Mapping genes for fatness and growth on pig chromosome 13: a search in the region close to the pig PIT1 gene. <i>Journal of Animal Breeding and Genetics</i> , <b>1999</b> , 116, 269-280	2.9	30
84	Cytogenetic and radiation hybrid mapping reveals conserved synteny and gene order between human chromosome 21 and pig chromosome 13. <i>Mammalian Genome</i> , <b>2001</b> , 12, 397-9	3.2	28
83	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 conceptus. <i>Biology of Reproduction</i> , <b>2015</b> , 92, 107	3.9	27
82	Salmonella enterica serovar Typhimurium-infected pigs with different shedding levels exhibit distinct clinical, peripheral cytokine and transcriptomic immune response phenotypes. <i>Innate Immunity</i> , <b>2015</b> , 21, 227-41	2.7	27
81	Pig immune response to general stimulus and to porcine reproductive and respiratory syndrome virus infection: a meta-analysis approach. <i>BMC Genomics</i> , <b>2013</b> , 14, 220	4.5	27
80	Genome-wide whole blood microRNAome and transcriptome analyses reveal miRNA-mRNA regulated host response to foodborne pathogen Salmonella infection in swine. <i>Scientific Reports</i> , <b>2015</b> , 5, 12620	4.9	26
79	Correlating blood immune parameters and a CCT7 genetic variant with the shedding of Salmonella enterica serovar Typhimurium in swine. <i>Veterinary Microbiology</i> , <b>2009</b> , 135, 384-8	3.3	25
78	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> , <b>2008</b> , 29, 815-27	0.8	25
77	High-resolution comparative mapping of pig Chromosome 4, emphasizing the FAT1 region. <i>Mammalian Genome</i> , <b>2004</b> , 15, 717-31	3.2	24
76	ANEXdb: an integrated animal ANnotation and microarray EXpression database. <i>Mammalian Genome</i> , <b>2009</b> , 20, 768-77	3.2	23
75	Endometrial gene expression profiling in pregnant Meishan and Yorkshire pigs on day 12 of gestation. <i>BMC Genomics</i> , <b>2014</b> , 15, 156	4.5	22
74	Rapid communication: localization of POU1F1 to bovine, ovine, and caprine 1q21-22. <i>Journal of Animal Science</i> , <b>2000</b> , 78, 242-3	0.7	22
73	From FAANG to fork: application of highly annotated genomes to improve farmed animal production. <i>Genome Biology</i> , <b>2020</b> , 21, 285	18.3	21
72	Genomewide association of piglet responses to infection with one of two porcine reproductive and respiratory syndrome virus isolates. <i>Journal of Animal Science</i> , <b>2017</b> , 95, 16-38	0.7	20
71	Cloning and restriction fragment length polymorphism analysis of a cDNA for swine PIT-1, a gene controlling growth hormone expression. <i>Animal Genetics</i> , <b>1993</b> , 24, 17-21	2.5	20

70	Genetic architecture of gene expression underlying variation in host response to porcine reproductive and respiratory syndrome virus infection. <i>Scientific Reports</i> , <b>2017</b> , 7, 46203	4.9	19
69	Human Ovarian Cancer Tumor Formation in Severe Combined Immunodeficient (SCID) Pigs. <i>Frontiers in Oncology</i> , <b>2019</b> , 9, 9	5.3	19
68	Functional genomics unique to week 20 post wounding in the deep cone/fat dome of the Duroc/Yorkshire porcine model of fibroproliferative scarring. <i>PLoS ONE</i> , <b>2011</b> , 6, e19024	3.7	19
67	PLET1 (C11orf34), a highly expressed and processed novel gene in pig and mouse placenta, is transcribed but poorly spliced in human. <i>Genomics</i> , <b>2004</b> , 84, 114-25	4.3	19
66	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> , <b>2016</b> , 17, 196	4.5	18
65	New insights into porcine-human synteny conservation. <i>Mammalian Genome</i> , <b>1999</b> , 10, 488-91	3.2	18
64	Post-weaning blood transcriptomic differences between Yorkshire pigs divergently selected for residual feed intake. <i>BMC Genomics</i> , <b>2016</b> , 17, 73	4.5	18
63	NK cells are intrinsically functional in pigs with Severe Combined Immunodeficiency (SCID) caused by spontaneous mutations in the Artemis gene. <i>Veterinary Immunology and Immunopathology</i> , <b>2016</b> , 175, 1-6	2	17
62	Assessing peripheral blood cell profile of Yorkshire pigs divergently selected for residual feed intake. <i>Journal of Animal Science</i> , <b>2015</b> , 93, 892-9	0.7	16
61	Organic barn dust extract exposure impairs porcine macrophage function in vitro: implications for respiratory health. <i>Veterinary Immunology and Immunopathology</i> , <b>2014</b> , 157, 20-30	2	16
60	Characterizing differential individual response to porcine reproductive and respiratory syndrome virus infection through statistical and functional analysis of gene expression. <i>Frontiers in Genetics</i> , <b>2012</b> , 3, 321	4.5	16
59	Transcriptional profiling using a novel cDNA array identifies differential gene expression during porcine embryo elongation. <i>Molecular Reproduction and Development</i> , <b>2005</b> , 71, 129-39	2.6	16
58	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> , <b>2018</b> , 8, 559	5.3	16
57	Creating effective biocontainment facilities and maintenance protocols for raising specific pathogen-free, severe combined immunodeficient (SCID) pigs. <i>Laboratory Animals</i> , <b>2018</b> , 52, 402-412	2.6	15
56	Analysis of porcine differential gene expression following challenge with <i>Salmonella enterica</i> serovar Choleraesuis using suppression subtractive hybridization. <i>Veterinary Microbiology</i> , <b>2006</b> , 114, 60-71	3.3	15
55	Dynamic expression of murine HOXA5 protein in the central nervous system. <i>Gene Expression Patterns</i> , <b>2005</b> , 5, 792-800	1.5	15
54	An improved pig reference genome sequence to enable pig genetics and genomics research		15
53	MicroRNA buffering and altered variance of gene expression in response to <i>Salmonella</i> infection. <i>PLoS ONE</i> , <b>2014</b> , 9, e94352	3.7	13

52	T Cell Lymphoma and Leukemia in Severe Combined Immunodeficiency Pigs following Bone Marrow Transplantation: A Case Report. <i>Frontiers in Immunology</i> , <b>2017</b> , 8, 813	8.4	12
51	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> , <b>2014</b> , 162, 174-9	2	12
50	Integrating comparative expression profiling data and association of SNPs with Salmonella shedding for improved food safety and porcine disease resistance. <i>Animal Genetics</i> , <b>2011</b> , 42, 521-34	2.5	12
49	SCID pigs: An emerging large animal NK model <b>2017</b> , 2, 1-6		12
48	SCID pigs: An emerging large animal NK model. <i>Journal of Rare Diseases Research &amp; Treatment</i> , <b>2017</b> , 2, 1-6	1.1	12
47	Functional annotations of three domestic animal genomes provide vital resources for comparative and agricultural research. <i>Nature Communications</i> , <b>2021</b> , 12, 1821	17.4	12
46	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> , <b>2019</b> , 26, e12466	2.8	12
45	Whole blood microarray analysis of pigs showing extreme phenotypes after a porcine reproductive and respiratory syndrome virus infection. <i>BMC Genomics</i> , <b>2015</b> , 16, 516	4.5	11
44	Mapping of 443 porcine EST improves the comparative maps for SSC1 and SSC7 with the human genome. <i>Animal Genetics</i> , <b>2005</b> , 36, 381-9	2.5	11
43	A comparative analysis of chromatin accessibility in cattle, pig, and mouse tissues. <i>BMC Genomics</i> , <b>2020</b> , 21, 698	4.5	11
42	Precise mapping of breakpoints in conserved synteny between human chromosome 1 and pig chromosomes 4, 6 and 9. <i>Animal Genetics</i> , <b>2002</b> , 33, 91-6	2.5	10
41	Cloning of the full length pig PIT1 (POU1F1) CDNA and a novel alternative PIT1 transcript, and functional studies of their encoded proteins. <i>Animal Biotechnology</i> , <b>2001</b> , 12, 1-19	1.4	10
40	Identification of potential serum biomarkers to predict feed efficiency in young pigs. <i>Journal of Animal Science</i> , <b>2016</b> , 94, 1482-92	0.7	10
39	Tuberculosis-resistant transgenic cattle. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2015</b> , 112, 3854-5	11.5	9
38	Methods for transcriptomic analyses of the porcine host immune response: application to Salmonella infection using microarrays. <i>Veterinary Immunology and Immunopathology</i> , <b>2010</b> , 138, 280-91 <sup>2</sup>		9
37	Expression pattern, genomic cloning and RFLP analyses of the swine PIT-1 gene. <i>Animal Genetics</i> , <b>1994</b> , 25, 229-33	2.5	9
36	Pigs with Severe Combined Immunodeficiency Are Impaired in Controlling Influenza A Virus Infection. <i>Journal of Innate Immunity</i> , <b>2017</b> , 9, 193-202	6.9	8
35	Novel Engraftment and T Cell Differentiation of Human Hematopoietic Cells in SCID Pigs. <i>Frontiers in Immunology</i> , <b>2020</b> , 11, 100	8.4	8

34	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> , <b>2004</b> , 150, 125-39		8
33	Changes in H3K27ac at Gene Regulatory Regions in Porcine Alveolar Macrophages Following LPS or PolyIC Exposure. <i>Frontiers in Genetics</i> , <b>2020</b> , 11, 817	4.5	8
32	Physical assignments of human chromosome 13 genes on pig chromosome 11 demonstrate extensive synteny and gene order conservation between pig and human. <i>Animal Genetics</i> , <b>1999</b> , 30, 304-8	3.5	7
31	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> , <b>2015</b> , 20, 577-597	1.9	6
30	Use of bioinformatic SNP predictions in differentially expressed genes to find SNPs associated with Salmonella colonization in swine. <i>Journal of Animal Breeding and Genetics</i> , <b>2011</b> , 128, 354-65	2.9	6
29	Rapid communication: mapping of the Mannose-Binding Lectin 2 (MBL2) gene to pig chromosome 14. <i>Journal of Animal Science</i> , <b>2000</b> , 78, 2992-3	0.7	6
28	Acute systemic inflammatory response to lipopolysaccharide stimulation in pigs divergently selected for residual feed intake. <i>BMC Genomics</i> , <b>2019</b> , 20, 728	4.5	5
27	Introduction to Systems Biology for Animal Scientists <b>2011</b> , 1-30		5
26	Physical mapping of genes in the porcine ovarian transcriptome. <i>Animal Genetics</i> , <b>2005</b> , 36, 322-30	2.5	5
25	Ectopic HOXA5 expression results in abnormal differentiation, migration and p53-independent cell death of superficial dorsal horn neurons. <i>Developmental Brain Research</i> , <b>2005</b> , 159, 87-97		5
24	A high-quality annotated transcriptome of swine peripheral blood. <i>BMC Genomics</i> , <b>2017</b> , 18, 479	4.5	4
23	Rapid communication: Genetic linkage and physical mapping of the porcine lipopolysaccharide-binding protein (LBP) gene. <i>Journal of Animal Science</i> , <b>2001</b> , 79, 556-7	0.7	4
22	Pig genome functional annotation enhances the biological interpretation of complex traits and human disease. <i>Nature Communications</i> , <b>2021</b> , 12, 5848	17.4	4
21	Survival of human cadaver skin on severe combined immune deficiency pigs: Proof of concept. <i>Wound Repair and Regeneration</i> , <b>2019</b> , 27, 426-430	3.6	3
20	Linkage mapping and expression analyses of a novel gene, placentally expressed transcript 1 (PLET1) in the pig. <i>Animal Genetics</i> , <b>2004</b> , 35, 72-4	2.5	3
19	Reference Transcriptomes of Porcine Peripheral Immune Cells Created Through Bulk and Single-Cell RNA Sequencing. <i>Frontiers in Genetics</i> , <b>2021</b> , 12, 689406	4.5	3
18	A Comprehensive Protocol for Laparotomy in Swine to Facilitate Ultrasound-Guided Injection into the Fetal Intraperitoneal Space. <i>Comparative Medicine</i> , <b>2019</b> , 69, 123-129	1.6	2
17	CD3 <sup>+</sup> Cells in Pigs With Severe Combined Immunodeficiency Due to Defects in. <i>Frontiers in Immunology</i> , <b>2020</b> , 11, 510	8.4	2

16	Rapid communication: genetic linkage and physical mapping of the porcine phospholipid transfer protein (PLTP) gene. <i>Journal of Animal Science</i> , <b>2001</b> , 79, 1633-4	0.7	2
15	Analysis of Gene Expression in a Region Associated with Host Response to Porcine Reproductive and Respiratory Syndrome Virus Challenge		2
14	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> , <b>2008</b> , 132, 105-113		2
13	Differential induction of innate memory in porcine monocytes by $\beta$ -glucan or bacillus Calmette-Guerin. <i>Innate Immunity</i> , <b>2021</b> , 27, 448-460	2.7	2
12	The effects of a globin blocker on the resolution of 3 <sup>rd</sup> RNA sequencing data in porcine blood. <i>BMC Genomics</i> , <b>2019</b> , 20, 741	4.5	2
11	Gene expression in tonsils in swine following infection with porcine reproductive and respiratory syndrome virus. <i>BMC Veterinary Research</i> , <b>2021</b> , 17, 88	2.7	2
10	Physical mapping of eight pig genes whose expression level is acutely affected by Salmonella challenge. <i>Animal Genetics</i> , <b>2005</b> , 36, 359-62	2.5	1
9	Rapid communication: Mapping of the myeloperoxidase (MPO) gene to pig chromosome 12. <i>Journal of Animal Science</i> , <b>2000</b> , 78, 3189-90	0.7	1
8	Novel engraftment and T cell differentiation of human hematopoietic cells in Art <sup>-/-</sup> IL2RG <sup>-/-</sup> SCID pigs		1
7	Quantitative analysis of the blood transcriptome of young healthy pigs and its relationship with subsequent disease resilience. <i>BMC Genomics</i> , <b>2021</b> , 22, 614	4.5	1
6	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> , <b>2019</b> , 267, 21-25	6.4	0
5	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> , <b>2021</b> , 170, 107-116	2.8	0
4	Swine models for translational oncological research: an evolving landscape and regulatory considerations. <i>Mammalian Genome</i> , <b>2021</b> , 1	3.2	0
3	Applications of Systems Biology to Improve Pig Health <b>2016</b> , 33-59		
2	Successful development of methodology for detection of hapten-specific contact hypersensitivity (CHS) memory in swine. <i>PLoS ONE</i> , <b>2019</b> , 14, e0223483	3.7	
1	Linkage mapping of porcine STCH further refines the HSA3/21 breakpoint on pig chromosome 13. <i>Animal Genetics</i> , <b>2002</b> , 33, 395-7	2.5	