

# Denis Milan

## List of Publications by Year in descending order

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58  
papers

5,701  
citations

218662

26  
h-index

138468

58  
g-index

58  
all docs

58  
docs citations

58  
times ranked

5286  
citing authors

#	ARTICLE	IF	CITATIONS
1	A genome-wide association study of production traits in a commercial population of Large White pigs: evidence of haplotypes affecting meat quality. <i>Genetics Selection Evolution</i> , 2014, 46, 12.	3.0	71
2	Fine mapping of fatness QTL on porcine chromosome X and analyses of three positional candidate genes. <i>BMC Genetics</i> , 2013, 14, 46.	2.7	11
3	A Genome-Wide Association Study Points out the Causal Implication of SOX9 in the Sex-Reversal Phenotype in XX Pigs. <i>PLoS ONE</i> , 2013, 8, e79882.	2.5	17
4	Analyses of pig genomes provide insight into porcine demography and evolution. <i>Nature</i> , 2012, 491, 393-398.	27.8	1,190
5	High-resolution autosomal radiation hybrid maps of the pig genome and their contribution to the genome sequence assembly. <i>BMC Genomics</i> , 2012, 13, 585.	2.8	16
6	A high density recombination map of the pig reveals a correlation between sex-specific recombination and GC content. <i>BMC Genomics</i> , 2012, 13, 586.	2.8	150
7	Joint analysis of quantitative trait loci and major-effect causative mutations affecting meat quality and carcass composition traits in pigs. <i>BMC Genetics</i> , 2011, 12, 76.	2.7	20
8	A locally congenic backcross design in pig: a new regional fine QTL mapping approach miming congenic strains used in mouse.. <i>BMC Genetics</i> , 2011, 12, 6.	2.7	8
9	Genetic and functional evaluation of MITF as a candidate gene for cutaneous melanoma predisposition in pigs. <i>Mammalian Genome</i> , 2011, 22, 602-612.	2.2	7
10	Progeny-testing of full-sibs IBD in a SSC2 QTL region highlights epistatic interactions for fatness traits in pigs. <i>BMC Genetics</i> , 2011, 12, 92.	2.7	4
11	Pig genome sequence - analysis and publication strategy. <i>BMC Genomics</i> , 2010, 11, 438.	2.8	132
12	Recombinational landscape of porcine X chromosome and individual variation in female meiotic recombination associated with haplotypes of Chinese pigs. <i>BMC Genomics</i> , 2010, 11, 159.	2.8	27
13	Design of a High Density SNP Genotyping Assay in the Pig Using SNPs Identified and Characterized by Next Generation Sequencing Technology. <i>PLoS ONE</i> , 2009, 4, e6524.	2.5	568
14	The carnitine acetyltransferase gene (CRAT): A characterization of porcine transcripts with insights into the 5' end variants of mammalian transcripts and their possible sub-cellular localization. <i>Cellular and Molecular Biology Letters</i> , 2009, 14, 90-9.	7.0	2
15	Chromosomal assignment of the porcine NALP5 gene, a candidate gene for female reproductive traits. <i>Animal Reproduction Science</i> , 2009, 112, 397-401.	1.5	7
16	Detection of quantitative trait loci for reproduction and production traits in Large White and French Landrace pig populations (Open Access publication). <i>Genetics Selection Evolution</i> , 2008, 40, 61-78.	3.0	25
17	Linked and pleiotropic QTLs influencing carcass composition traits detected on porcine chromosome 7. <i>Genetical Research</i> , 2007, 89, 65-72.	0.9	16
18	Metabolic and histochemical characteristics of fat and muscle tissues in homozygous or heterozygous pigs for the body composition QTL located on chromosome 7. <i>Physiological Genomics</i> , 2007, 30, 232-241.	2.3	13

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19	A high utility integrated map of the pig genome. <i>Genome Biology</i> , 2007, 8, R139.	9.6	130
20	Detection of novel quantitative trait loci for cutaneous melanoma by genome-wide scan in the MeLiM swine model. <i>International Journal of Cancer</i> , 2007, 120, 303-320.	5.1	38
21	Evolutionary breakpoints through a high-resolution comparative map between porcine chromosomes 2 and 16 and human chromosomes. <i>Genomics</i> , 2006, 88, 504-512.	2.9	13
22	Radiation hybrid map of the porcine genome comprising 2035 EST loci. <i>Mammalian Genome</i> , 2006, 17, 878-885.	2.2	24
23	Cloning, sequencing, and chromosomal localization of pig peripheral benzodiazepine receptor: three different forms produced by alternative splicing. <i>Mammalian Genome</i> , 2006, 17, 1050-1062.	2.2	8
24	High resolution physical map of porcine chromosome 7 QTL region and comparative mapping of this region among vertebrate genomes. <i>BMC Genomics</i> , 2006, 7, 13.	2.8	21
25	A gene-based radiation hybrid map of chicken microchromosome 14: Comparison to human and alignment to the assembled chicken sequence. <i>Genetics Selection Evolution</i> , 2005, 37, 229-51.	3.0	13
26	Swine Genome Sequencing Consortium (SGSC): A Strategic Roadmap for Sequencing The Pig Genome. <i>Comparative and Functional Genomics</i> , 2005, 6, 251-255.	2.0	93
27	An assessment of European pig diversity using molecular markers: Partitioning of diversity among breeds. <i>Conservation Genetics</i> , 2005, 6, 729-741.	1.5	40
28	CARHTA GENE: multipopulation integrated genetic and radiation hybrid mapping. <i>Bioinformatics</i> , 2005, 21, 1703-1704.	4.1	403
29	Piggy-BACing the human genome. <i>Genomics</i> , 2005, 86, 739-752.	2.9	103
30	A high-resolution comparative map between pig chromosome 17 and human chromosomes 4, 8, and 20: Identification of synteny breakpoints. <i>Genomics</i> , 2005, 86, 405-413.	2.9	14
31	A 12,000-rad porcine radiation hybrid (IMNpRH2) panel refines the conserved synteny between SSC12 and HSA17. <i>Genomics</i> , 2005, 86, 731-738.	2.9	16
32	Dynamics of Mammalian Chromosome Evolution Inferred from Multispecies Comparative Maps. <i>Science</i> , 2005, 309, 613-617.	12.6	542
33	A high-resolution radiation hybrid map of chicken chromosome 5 and comparison with human chromosomes. <i>BMC Genomics</i> , 2004, 5, 66.	2.8	21
34	High-resolution comparative mapping of pig Chromosome 4, emphasizing the FAT1 region. <i>Mammalian Genome</i> , 2004, 15, 717-731.	2.2	25
35	Development of a gene-based radiation hybrid map of chicken Chromosome 7 and comparison to human and mouse. <i>Mammalian Genome</i> , 2004, 15, 732-739.	2.2	11
36	A physical map of large segments of pig Chromosome 7q11â€“q14: comparative analysis with human Chromosome 6p21. <i>Mammalian Genome</i> , 2004, 15, 982-995.	2.2	22

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37	Identification of five chromosomal regions involved in predisposition to melanoma by genome-wide scan in the MeLiM swine model. <i>International Journal of Cancer</i> , 2004, 110, 39-50.	5.1	31
38	Contribution to high-resolution mapping in pigs with 101 type I markers and progress in comparative map between humans and pigs. <i>Mammalian Genome</i> , 2003, 14, 275-288.	2.2	35
39	Rearranged gene order between pig and human in a QTL region on SSC 7. <i>Mammalian Genome</i> , 2003, 14, 71-80.	2.2	31
40	A high resolution physical and RH map of pig chromosome 6q1.2 and comparative analysis with human chromosome 19q13.1. <i>BMC Genomics</i> , 2003, 4, 20.	2.8	14
41	The GENETPIG database: a tool for comparative mapping in pig ( <i>Sus scrofa</i> ). <i>Nucleic Acids Research</i> , 2003, 31, 138-141.	14.5	7
42	A further look at quantitative trait loci affecting growth and fatness in a cross between Meishan and Large White pig populations. <i>Genetics Selection Evolution</i> , 2002, 34, 193-210.	3.0	47
43	Detection of quantitative trait loci for carcass composition traits in pigs. <i>Genetics Selection Evolution</i> , 2002, 34, 705-28.	3.0	108
44	A first-generation EST RH comparative map of the porcine and human genome. <i>Mammalian Genome</i> , 2002, 13, 578-587.	2.2	81
45	Comparative Analysis of a BAC Contig of the Porcine RN Region and the Human Transcript Map: Implications for the Cloning of Trait Loci. <i>Genomics</i> , 2001, 72, 297-303.	2.9	20
46	Construction of a high-resolution RH map of the human 2q35 region on TNG panel and comparison with a physical map of the porcine homologous region 15q25. <i>Mammalian Genome</i> , 2001, 12, 380-386.	2.2	7
47	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.	2.2	28
48	In the QTL region surrounding porcine MHC, gene order is conserved with human genome. <i>Mammalian Genome</i> , 2001, 12, 246-249.	2.2	23
49	Detection of quantitative trait loci for growth and fatness in pigs. <i>Genetics Selection Evolution</i> , 2001, 33, 289-309.	3.0	194
50	Boosting EM for Radiation Hybrid and Genetic Mapping. <i>Lecture Notes in Computer Science</i> , 2001, , 41-51.	1.3	21
51	Genetic diversity of eleven European pig breeds. <i>Genetics Selection Evolution</i> , 2000, 32, 187-203.	3.0	182
52	A high-density linkage map of the RN region in pigs. <i>Genetics Selection Evolution</i> , 2000, 32, 321-9.	3.0	6
53	Combined Analyses of Data From Quantitative Trait Loci Mapping Studies: Chromosome 4 Effects on Porcine Growth and Fatness. <i>Genetics</i> , 2000, 155, 1369-1378.	2.9	128
54	A radiation hybrid map of the RN region in pigs demonstrates conserved gene order compared with the human and mouse genomes. <i>Mammalian Genome</i> , 1999, 10, 565-568.	2.2	11

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55	A successful strategy for comparative mapping with human ESTs: 65 new regional assignments in the pig. <i>Mammalian Genome</i> , 1999, 10, 145-153.	2.2	44
56	A first-generation porcine whole-genome radiation hybrid map. <i>Mammalian Genome</i> , 1999, 10, 824-830.	2.2	305
57	The cytogenetic map of the domestic pig ( <i>Sus scrofa domestica</i> ). <i>Mammalian Genome</i> , 1997, 8, 592-607.	2.2	39
58	Human and Porcine Correspondence of Chromosome Segments Using Bidirectional Chromosome Painting. <i>Genomics</i> , 1996, 36, 252-262.	2.9	518