Janine E Deakin

List of Publications by Year
in descending order

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97	4,965	109137	102304
papers	citations	35 h-index	66 g-index

100	100	100	5200
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Sex-specific splicing of Z- and W-bornenr5a1alleles suggests sex determination is controlled by chromosome conformation. Proceedings of the National Academy of Sciences of the United States of America, 2022, 119, .	3.3	11
2	Limited Introgression between Rock-Wallabies with Extensive Chromosomal Rearrangements. Molecular Biology and Evolution, 2022, 39, .	3.5	17
3	High elevation increases the risk of Y chromosome loss in Alpine skink populations with sex reversal. Heredity, 2021, 126, 805-816.	1.2	16
4	Evolution of Marsupial Genomes. Annual Review of Animal Biosciences, 2020, 8, 25-45.	3.6	19
5	Identification of Y chromosome markers in the eastern three-lined skink (Bassiana duperreyi) using in silico whole genome subtraction. BMC Genomics, 2020, 21, 667.	1.2	18
6	Comparative Cytogenetic Mapping and Telomere Analysis Provide Evolutionary Predictions for Devil Facial Tumour 2. Genes, 2020, 11, 480.	1.0	2
7	The Oz Mammals Genomics (OMG) initiative: developing genomic resources for mammal conservation at a continental scale. Australian Zoologist, 2020, 40, 505-509.	0.6	15
8	Chromosomics: Bridging the Gap between Genomes and Chromosomes. Genes, 2019, 10, 627.	1.0	79
9	Sexual conflict in action: An antagonistic relationship between maternal and paternal sex allocation in the tammar wallaby, Notamacropus eugenii. Ecology and Evolution, 2019, 9, 4340-4348.	0.8	5
10	Marsupial chromosomics: bridging the gap between genomes and chromosomes. Reproduction, Fertility and Development, 2019, 31, 1189.	0.1	5
11	Understanding the Evolution of Reptile Chromosomes through Applications of Combined Cytogenetics and Genomics Approaches. Cytogenetic and Genome Research, 2019, 157, 7-20.	0.6	56
12	The methylation and telomere landscape in two families of marsupials with different rates of chromosome evolution. Chromosome Research, 2018, 26, 317-332.	1.0	9
13	Adaptation and conservation insights from the koala genome. Nature Genetics, 2018, 50, 1102-1111.	9.4	163
14	Cytogenetics: an important inclusion in the conservation genetics toolbox. Pacific Conservation Biology, 2018, 24, 280.	0.5	8
15	Chromosome Evolution in Marsupials. Genes, 2018, 9, 72.	1.0	30
16	Implications of monotreme and marsupial chromosome evolution on sex determination and differentiation. General and Comparative Endocrinology, 2017, 244, 130-138.	0.8	4
17	Identification of candidate genes for devil facial tumour disease tumourigenesis. Scientific Reports, 2017, 7, 8761.	1.6	20
18	Chromosomal Speciation in the Genomics Era: Disentangling Phylogenetic Evolution of Rock-wallabies. Frontiers in Genetics, 2017, 8, 10.	1.1	78

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19	Anchoring genome sequence to chromosomes of the central bearded dragon (Pogona vitticeps) enables reconstruction of ancestral squamate macrochromosomes and identifies sequence content of the Z chromosome. BMC Genomics, 2016, 17, 447.	1.2	47
20	Evolution and comparative analysis of the bat MHC-I region. Scientific Reports, 2016, 6, 21256.	1.6	56
21	Marsupials as models for understanding the role of chromosome rearrangements in evolution and disease. Chromosoma, 2016, 125, 633-644.	1.0	8
22	Identification of interleukin genes in Pogona vitticeps using a de novo transcriptome assembly from RNA-seq data. Immunogenetics, 2016, 68, 719-731.	1.2	3
23	Telomeres, species differences, and unusual telomeres in vertebrates: presenting challenges and opportunities to understanding telomere dynamics. AIMS Genetics, 2016, 03, 001-024.	1.9	25
24	High-coverage sequencing and annotated assembly of the genome of the Australian dragon lizard Pogona vitticeps. GigaScience, 2015, 4, 45.	3.3	97
25	Immunofluorescent staining reveals hypermethylation of microchromosomes in the central bearded dragon, Pogona vitticeps. Molecular Cytogenetics, 2015, 8, 104.	0.4	4
26	Global DNA Methylation patterns on marsupial and devil facial tumour chromosomes. Molecular Cytogenetics, 2015, 8, 74.	0.4	24
27	Marsupials and monotremes possess a novel family of MHC class I genes that is lost from the eutherian lineage. BMC Genomics, 2015, 16, 535.	1.2	22
28	A peculiar lamin in a peculiar mammal: Expression of lamin LIII in platypus (Ornithorhynchus anatinus). European Journal of Cell Biology, 2015, 94, 522-530.	1.6	1
29	Comparative Genome Analyses Reveal Distinct Structure in the Saltwater Crocodile MHC. PLoS ONE, 2014, 9, e114631.	1.1	22
30	Repetitive Sequence and Sex Chromosome Evolution in Vertebrates. Advances in Evolutionary Biology, 2014, 2014, 1-9.	1.0	41
31	Tracing the evolution of amniote chromosomes. Chromosoma, 2014, 123, 201-216.	1.0	26
32	Pathogenesis and Molecular Biology of a Transmissible Tumor in the Tasmanian Devil. Annual Review of Animal Biosciences, 2014, 2, 165-187.	3.6	21
33	Comparative epigenomics: an emerging field with breakthrough potential to understand evolution of epigenetic regulation. AIMS Genetics, 2014, 01, 034-054.	1.9	7
34	Smchd1 regulates a subset of autosomal genes subject to monoallelic expression in addition to being critical for X inactivation. Epigenetics and Chromatin, 2013, 6, 19.	1.8	88
35	Sequence and gene content of a large fragment of a lizard sex chromosome and evaluation of candidate sex differentiating gene R-spondin 1. BMC Genomics, 2013, 14, 899.	1.2	41
36	Reconstruction of the ancestral marsupial karyotype from comparative gene maps. BMC Evolutionary Biology, 2013, 13, 258.	3.2	30

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37	Exceptionally high conservation of the MHC class I-related gene, MR1, among mammals. Immunogenetics, 2013, 65, 115-124.	1.2	75
38	The marsupial pouch: implications for reproductive success and mammalian evolution. Australian Journal of Zoology, 2013, 61, 41.	0.6	12
39	Independent Evolution of Transcriptional Inactivation on Sex Chromosomes in Birds and Mammals. PLoS Genetics, 2013, 9, e1003635.	1.5	26
40	Towards an understanding of the genetic basis behind 1080 (sodium fluoroacetate) tolerance and an investigation of the candidate gene ACO2. Australian Journal of Zoology, 2013, 61, 69.	0.6	5
41	Marsupial X chromosome inactivation: past, present and future. Australian Journal of Zoology, 2013, 61, 13.	0.6	12
42	In Vivo Function and Evolution of the Eutherian-Specific Pluripotency Marker UTF1. PLoS ONE, 2013, 8, e68119.	1.1	17
43	Genomic Restructuring in the Tasmanian Devil Facial Tumour: Chromosome Painting and Gene Mapping Provide Clues to Evolution of a Transmissible Tumour. PLoS Genetics, 2012, 8, e1002483.	1.5	92
44	Marsupial Genome Sequences: Providing Insight into Evolution and Disease. Scientifica, 2012, 2012, 1-22.	0.6	16
45	Antigen-presenting genes and genomic copy number variations in the Tasmanian devil MHC. BMC Genomics, 2012, 13, 87.	1.2	54
46	A Comparative Genomics Approach to Understanding Transmissible Cancer in Tasmanian Devils. Annual Review of Genomics and Human Genetics, 2012, 13, 207-222.	2.5	19
47	The Evolution of Marsupial and Monotreme Chromosomes. Cytogenetic and Genome Research, 2012, 137, 113-129.	0.6	34
48	A review of complementary mechanisms which protect the developing marsupial pouch young. Developmental and Comparative Immunology, 2012, 37, 213-220.	1.0	31
49	A cross-species comparison of escape from X inactivation in Eutheria: implications for evolution of X chromosome inactivation. Chromosoma, 2012, 121, 71-78.	1.0	30
50	Extreme Telomere Length Dimorphism in the Tasmanian Devil and Related Marsupials Suggests Parental Control of Telomere Length. PLoS ONE, 2012, 7, e46195.	1.1	27
51	Solving the Mystery of the Evolution of X Chromosome Inactivation. International Journal of Evolution, 2012, 01, .	0.5	0
52	Genome sequence of an Australian kangaroo, Macropus eugenii, provides insight into the evolution of mammalian reproduction and development. Genome Biology, 2011, 12, 414.	13.9	22
53	Genome sequence of an Australian kangaroo, Macropus eugenii, provides insight into the evolution of mammalian reproduction and development. Genome Biology, 2011, 12, R81.	13.9	167
54	A second-generation anchored genetic linkage map of the tammar wallaby (Macropus eugenii). BMC Genetics, 2011, 12, 72.	2.7	15

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55	The tammar wallaby major histocompatibility complex shows evidence of past genomic instability. BMC Genomics, 2011, 12, 421.	1.2	55
56	A first-generation integrated tammar wallaby map and its use in creating a tammar wallaby first-generation virtual genome map. BMC Genomics, 2011, 12, 422.	1.2	19
57	Physical Mapping of Innate Immune Genes, Mucins and Lysozymes, and Other Non-Mucin Proteins in the Tammar Wallaby <i>(Macropus eugenii)</i>. Cytogenetic and Genome Research, 2011, 135, 118-125.	0.6	4
58	Globin gene structure in a reptile supports the transpositional model for amniote Î±- and Î²-globin gene evolution. Chromosome Research, 2010, 18, 897-907.	1.0	12
59	Marsupial Genetics and Genomics. , 2010, , .		5
60	Activity map of the tammar X chromosome shows that marsupial X inactivation is incomplete and escape is stochastic. Genome Biology, 2010, 11, R122.	13.9	45
61	The Evolutionary History of Globin Genes: Insights from Marsupials and Monotremes. , 2010, , 415-433.		0
62	Marsupial Genetics Reveals Insights into Evolution of Mammalian X Chromosome Inactivation. , 2010, , 259-280.		0
63	Physical and Comparative Gene Maps in Marsupials. , 2010, , 101-115.		3
64	Replication asynchrony and differential condensation of X chromosomes in female platypus (Ornithorhynchus anatinus). Reproduction, Fertility and Development, 2009, 21, 952.	0.1	10
65	Physical Mapping of Immune Genes in the Tammar Wallaby <i>(Macropus eugenii)</i>. Cytogenetic and Genome Research, 2009, 127, 21-25.	0.6	5
66	MHC-linked and un-linked class I genes in the wallaby. BMC Genomics, 2009, 10, 310.	1.2	48
67	Unravelling the evolutionary origins of X chromosome inactivation in mammals: insights from marsupials and monotremes. Chromosome Research, 2009, 17, 671-685.	1.0	56
68	Identification of natural killer cell receptor clusters in the platypus genome reveals an expansion of C-type lectin genes. Immunogenetics, 2009, 61, 565-579.	1.2	24
69	Physical map of two tammar wallaby chromosomes: A strategy for mapping in non-model mammals. Chromosome Research, 2008, 16, 1159-1175.	1.0	63
70	Platypus globin genes and flanking loci suggest a new insertional model for beta-globin evolution in birds and mammals. BMC Biology, 2008, 6, 34.	1.7	44
71	Genome analysis of the platypus reveals unique signatures of evolution. Nature, 2008, 453, 175-183.	13.7	657
72	Origin and evolution of candidate mental retardation genes on the human X chromosome (MRX). BMC Genomics, 2008, 9, 65.	1.2	13

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73	Bird-like sex chromosomes of platypus imply recent origin of mammal sex chromosomes. Genome Research, 2008, 18, 965-973.	2.4	268
74	Defensins and the convergent evolution of platypus and reptile venom genes. Genome Research, 2008, 18, 986-994.	2.4	137
75	The Status of Dosage Compensation in the Multiple X Chromosomes of the Platypus. PLoS Genetics, 2008, 4, e1000140.	1.5	102
76	The Evolution of Epigenetic Regulators CTCF and BORIS/CTCFL in Amniotes. PLoS Genetics, 2008, 4, e1000169.	1.5	72
77	A unique T cell receptor discovered in marsupials. Proceedings of the National Academy of Sciences of the United States of America, 2007, 104, 9776-9781.	3.3	119
78	Class I genes have split from the MHC in the tammar wallaby. Cytogenetic and Genome Research, 2007, 116, 205-211.	0.6	37
79	DMRT gene cluster analysis in the platypus: New insights into genomic organization and regulatory regions. Genomics, 2007, 89, 10-21.	1.3	52
80	Characterization of the opossum immune genome provides insights into the evolution of the mammalian immune system. Genome Research, 2007, 17, 982-991.	2.4	100
81	Genome of the marsupial Monodelphis domestica reveals innovation in non-coding sequences. Nature, 2007, 447, 167-177.	13.7	661
82	Isolation of major histocompatibility complex Class I genes from the tammar wallaby (Macropus) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 3	1.2	14
83	Evolution and comparative analysis of the MHC Class III inflammatory region. BMC Genomics, 2006, 7, 281.	1.2	54
84	Reconstructing an Ancestral Mammalian Immune Supercomplex from a Marsupial Major Histocompatibility Complex. PLoS Biology, 2006, 4, e46.	2.6	150
85	Recent Assembly of an Imprinted Domain from Non-Imprinted Components. PLoS Genetics, 2006, 2, e182.	1.5	84
86	Linkage mapping and physical localization of the major histocompatibility complex region of the marsupial Monodelphis domestica. Cytogenetic and Genome Research, 2006, 112, 277-285.	0.6	17
87	Physical mapping¹ of immunoglobulin loci IGH@, IGK@, and IGL@ in the opossum (Monodelphis domestica). Cytogenetic and Genome Research, 2006, 114, 94H-94H.	0.6	10
88	Physical mapping of T cell receptor loci (TRA@, TRB@, TRD@ and TRG@) in the opossum (Monodelphis domestica). Cytogenetic and Genome Research, 2006, 112, 342K-342K.	0.6	10
89	High levels of variability in immune response using antigens from two reproductive proteins in brushtail possums. Wildlife Research, 2005, 32, 1.	0.7	15
90	Autosomal location of genes from the conserved mammalian X in the platypus (Ornithorhynchus) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 401-410.	1.0	48

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91	Characterizing the chromosomes of the Australian model marsupial Macropus eugenii (tammar) Tj ETQq1 1 0.784314 rgBT /Overlock 10	1.0	54
92	Analysis of the genomic region containing the tammar wallaby (Macropus eugenii) orthologues of MHC class III genes. Cytogenetic and Genome Research, 2005, 111, 110-117.	0.6	10
93	Assignment of the DMRT1 gene to tammar wallaby chromosome 3p by fluorescence in situ hybridization. Cytogenetic and Genome Research, 2005, 108, 362E-362E.	0.6	6
94	Characterisation of and immunity to the aerobic bacteria found in the pouch of the brushtail possum Trichosurus vulpecula. Comparative Immunology, Microbiology and Infectious Diseases, 2004, 27, 33-46.	0.7	21
95	The monotreme genome: a patchwork of reptile, mammal and unique features?. Comparative Biochemistry and Physiology Part A, Molecular & Integrative Physiology, 2003, 136, 867-881.	0.8	39
96	cDNA Cloning of Growth Hormone from the Brushtail Possum (Trichosurus vulpecula). General and Comparative Endocrinology, 1998, 111, 68-75.	0.8	8
97	Developmental Expression of the Androgen Receptor during Virilization of the Urogenital System of a Marsupial1. Biology of Reproduction, 1998, 59, 725-732.	1.2	23