David M Irwin

List of Publications by Year
in descending order

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235 papers	9,199 citations	61857 43 h-index	53109 85 g-index
242 all docs	242 docs citations	242 times ranked	11163 citing authors

#	Article	IF	Citations
1	A new canine distemper virus lineage identified from red pandas in China. Transboundary and Emerging Diseases, 2022, 69, .	1.3	14
2	Hen raising helps chicks establish gut microbiota in their early life and improve microbiota stability after H9N2 challenge. Microbiome, 2022, 10, 14.	4.9	17
3	Circular RNA Profiling Identifies Novel circPPARA that Promotes Intramuscular Fat Deposition in Pigs. Journal of Agricultural and Food Chemistry, 2022, 70, 4123-4137.	2.4	22
4	Adaptive Evolution of the Fox Coronavirus Based on Genome-Wide Sequence Analysis. BioMed Research International, 2022, 2022, 1-8.	0.9	0
5	Adaptation of gut microbiome and host metabolic systems to lignocellulosic degradation in bamboo rats. ISME Journal, 2022, 16, 1980-1992.	4.4	14
6	Genome-wide identification of functional enhancers and their potential roles in pig breeding. Journal of Animal Science and Biotechnology, 2022, 13, .	2.1	3
7	Evolution of the mammalian insulin (Ins) gene; Changes in proteolytic processing. Peptides, 2021, 135, 170435.	1.2	6
8	Integrating Genomic and Transcriptomic Data to Reveal Genetic Mechanisms Underlying Piao Chicken Rumpless Trait. Genomics, Proteomics and Bioinformatics, 2021, 19, 787-799.	3.0	7
9	Differences in the gut microbiomes of dogs and wolves: roles of antibiotics and starch. BMC Veterinary Research, 2021, 17, 112.	0.7	9
10	Evolution of the Insulin Gene: Changes in Gene Number, Sequence, and Processing. Frontiers in Endocrinology, 2021, 12, 649255.	1.5	12
11	Base Composition and Host Adaptation of the SARS-CoV-2: Insight From the Codon Usage Perspective. Frontiers in Microbiology, 2021, 12, 548275.	1.5	26
12	Pathogenicity and transmissibility of a novel respirovirus isolated from a Malayan pangolin. Journal of General Virology, 2021, 102, .	1.3	7
13	Diverse phylogenomic datasets uncover a concordant scenario of laurasiatherian interordinal relationships. Molecular Phylogenetics and Evolution, 2021, 157, 107065.	1.2	4
14	Covariation of the Fecal Microbiome with Diet in Nonpasserine Birds. MSphere, 2021, 6, .	1.3	22
15	Pooled Sequencing Analysis of Geese (Anser cygnoides) Reveals Genomic Variations Associated With Feather Color. Frontiers in Genetics, 2021, 12, 650013.	1.1	6
16	Host Adaptive Evolution of Avian-Origin H3N2 Canine Influenza Virus. Frontiers in Microbiology, 2021, 12, 655228.	1.5	6
17	Whole Genome Sequencing Reveals Signatures for Artificial Selection for Different Sizes in Japanese Primitive Dog Breeds. Frontiers in Genetics, 2021, 12, 671686.	1.1	3
18	Variation in the Evolution and Sequences of Proglucagon and the Receptors for Proglucagon-Derived Peptides in Mammals. Frontiers in Endocrinology, 2021, 12, 700066.	1.5	6

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19	Comparative study of gut microbiota from captive and confiscated-rescued wild pangolins. Journal of Genetics and Genomics, 2021, 48, 825-835.	1.7	20
20	Parallel Independent Losses of G-Type Lysozyme Genes in Hairless Aquatic Mammals. Genome Biology and Evolution, 2021, 13, .	1.1	2
21	Mucosal Microbiota and Metabolome in the Ileum of Hu Sheep Offered a Low-Grain, Pelleted or Non-pelleted High-Grain Diet. Frontiers in Microbiology, 2021, 12, 718884.	1.5	4
22	Evolutionary perspectives and adaptation dynamics of human seasonal influenza viruses from 2009 to 2019: An insight from codon usage. Infection, Genetics and Evolution, 2021, 96, 105067.	1.0	2
23	A New World Monkey Resembles Human in Bitter Taste Receptor Evolution and Function via a Single Parallel Amino Acid Substitution. Molecular Biology and Evolution, 2021, 38, 5472-5479.	3.5	3
24	Decoding the RNA viromes in rodent lungs provides new insight into the origin and evolutionary patterns of rodent-borne pathogens in Mainland Southeast Asia. Microbiome, 2021, 9, 18.	4.9	43
25	Single-cell RNA Sequencing Reveals Thoracolumbar Vertebra Heterogeneity and Rib-genesis in Pigs. Genomics, Proteomics and Bioinformatics, 2021, 19, 423-436.	3.0	6
26	Molecular evolution of GIP and Exendin and their receptors. Peptides, 2020, 125, 170158.	1.2	3
27	The recombination hot spots and genetic diversity of the genomes of African swine fever viruses. Journal of Infection, 2020, 80, 121-142.	1.7	19
28	The fit of codon usage of human-isolated avian influenza A viruses to human. Infection, Genetics and Evolution, 2020, 81, 104181.	1.0	6
29	Variation in the rates of evolution of the insulin and glucagon hormone and receptor genes in rodents. Gene, 2020, 728, 144296.	1.0	7
30	Convergent genomic signatures of high-altitude adaptation among domestic mammals. National Science Review, 2020, 7, 952-963.	4.6	52
31	Two newly identified genotypes for African swine fever virus are incorrect. Journal of Infection, 2020, 80, 469-496.	1.7	1
32	Rare homologous recombination in H3N2 avian influenza A viruses. Journal of Infection, 2020, 80, 350-371.	1.7	3
33	Ambient Temperature is A Strong Selective Factor Influencing Human Development and Immunity. Genomics, Proteomics and Bioinformatics, 2020, 18, 489-500.	3.0	5
34	Host Adaptation and Evolutionary Analysis of Zaire ebolavirus: Insights From Codon Usage Based Investigations. Frontiers in Microbiology, 2020, 11, 570131.	1.5	12
35	Origin and Evolution of H1N1/pdm2009: A Codon Usage Perspective. Frontiers in Microbiology, 2020, 11, 1615.	1.5	8
36	Adaptive Evolution of Feline Coronavirus Genes Based on Selection Analysis. BioMed Research International, 2020, 2020, 1-7.	0.9	6

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37	Unveiling the Biogeography and Potential Functions of the Intestinal Digesta- and Mucosa-Associated Microbiome of Donkeys. Frontiers in Microbiology, 2020, 11, 596882.	1.5	11
38	Identification of Candidate Circular RNAs Underlying Intramuscular Fat Content in the Donkey. Frontiers in Genetics, 2020, 11, 587559.	1.1	16
39	Genome and single-cell RNA-sequencing of the earthworm Eisenia andrei identifies cellular mechanisms underlying regeneration. Nature Communications, 2020, 11, 2656.	5.8	43
40	Emergence of SARS-like coronavirus poses new challenge in China. Journal of Infection, 2020, 80, 350-371.	1.7	56
41	Evolution and transition of expression trajectory during human brain development. BMC Evolutionary Biology, 2020, 20, 72.	3.2	10
42	Accelerated Evolution of Limb-Related Gene Hoxd11 in the Common Ancestor of Cetaceans and Ruminants (Cetruminantia). G3: Genes, Genomes, Genetics, 2020, 10, 515-524.	0.8	4
43	A missense mutation in ASIP is associated with light point variation in donkeys. Animal Genetics, 2020, 51, 629-629.	0.6	2
44	Overexpression of DUSP6 enhances chemotherapy-resistance of ovarian epithelial cancer by regulating the ERK signaling pathway. Journal of Cancer, 2020, 11, 3151-3164.	1.2	18
45	Genetic Diversity, Inbreeding Level, and Genetic Load in Endangered Snub-Nosed Monkeys (Rhinopithecus). Frontiers in Genetics, 2020, 11, 615926.	1.1	14
46	Population Genomics Analysis Revealed Origin and High-altitude Adaptation of Tibetan Pigs. Scientific Reports, 2019, 9, 11463.	1.6	44
47	Exosomes from Macrophages Exposed to Apoptotic Breast Cancer Cells Promote Breast Cancer Proliferation and Metastasis. Journal of Cancer, 2019, 10, 2892-2906.	1.2	36
48	Adaptive Evolution of Human-Isolated H5Nx Avian Influenza A Viruses. Frontiers in Microbiology, 2019, 10, 1328.	1.5	12
49	Stromal vascular fraction promotes migration of fibroblasts and angiogenesis through regulation of extracellular matrix in the skin wound healing process. Stem Cell Research and Therapy, 2019, 10, 302.	2.4	83
50	Viral Hormones: Do They Impact Human Endocrinology?. Endocrinology, 2019, 160, 2326-2327.	1.4	3
51	Adaptive Evolution of C-Type Lysozyme in Vampire Bats. Journal of Molecular Evolution, 2019, 87, 309-316.	0.8	6
52	Vaccine against Middle East respiratory syndrome coronavirus. Lancet Infectious Diseases, The, 2019, 19, 1053-1054.	4.6	4
53	Application of a TLR overexpression cell model in pyrogen detection. Biotechnology and Bioengineering, 2019, 116, 1269-1279.	1.7	2
54	Construction of a sensitive pyrogenâ€testing cell model by siteâ€specific knockâ€in of multiple genes. Biotechnology and Bioengineering, 2019, 116, 2652-2661.	1.7	1

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55	Better fit of codon usage of the polymerase and nucleoprotein genes to the chicken host for H7N9 than H9N2 AIVs. Journal of Infection, 2019, 79, 174-187.	1.7	17
56	Phylogeographic patterns of the African swine fever virus. Journal of Infection, 2019, 79, 174-187.	1.7	14
57	Whole genomes and transcriptomes reveal adaptation and domestication of pistachio. Genome Biology, 2019, 20, 79.	3.8	81
58	Avian influenza A viruses H5Nx (N1, N2, N6 and N8) show different adaptations of their codon usage patterns to their hosts. Journal of Infection, 2019, 79, 174-187.	1.7	5
59	No gene communication of HA gene between the human H3N2 and H1N1 pandemic 2009 influenza A viruses. Journal of Infection, 2019, 79, 174-187.	1.7	0
60	Human-isolated H7N9 obtained internal genes from duck and human influenza viruses. Journal of Infection, 2019, 78, 491-503.	1.7	1
61	Comparison of whole embryonic development in the duck (Anas platyrhynchos) and goose (Anser) Tj ETQq1 1 0.784314 rgBT /Overlock	1.5	25
62	Synergy betweenMC1RandASIPfor coat color in horses (Equus caballus)1. Journal of Animal Science, 2019, 97, 1578-1585.	0.2	9
63	Apoptotic SKOV3 cells stimulate M0 macrophages to differentiate into M2 macrophages and promote the¿½proliferation and migration of ovarian cancer¿½cells by activating the ERK signaling pathway. International Journal of Molecular Medicine, 2019, 45, 10-22.	1.8	20
64	547 transcriptomes from 44 brain areas reveal features of the aging brain in non-human primates. Genome Biology, 2019, 20, 258.	3.8	26
65	Rapid evolving H7N9 avian influenza A viruses pose new challenge. Journal of Infection, 2019, 78, 249-259.	1.7	22
66	Duplication and diversification of insulin genes in ray-finned fish. Zoological Research, 2019, 40, 185-197.	0.9	8
67	Diversification of the functions of proglucagon and glucagon receptor genes in fish. General and Comparative Endocrinology, 2018, 261, 148-165.	0.8	21
68	The genetic and phylogenetic analysis of a highly pathogenic influenza A H5N6 virus from a heron, southern China, 2013. Infection, Genetics and Evolution, 2018, 59, 72-74.	1.0	6
69	Convergent Evolution of Human-Isolated H7N9 Avian Influenza A Viruses. Journal of Infectious Diseases, 2018, 217, 1699-1707.	1.9	49
70	Out of Southern East Asia of the Brown Rat Revealed by Large-Scale Genome Sequencing. Molecular Biology and Evolution, 2018, 35, 149-158.	3.5	36
71	The H7N9 viruses have lost most of their previous lineages in the fifth wave. Journal of Infection, 2018, 76, 417-418.	1.7	1
72	Viral Insulin/IGF-1â€"Like Peptides: Novel Regulators of Physiology and Pathophysiology?. Endocrinology, 2018, 159, 3659-3660.	1.4	1

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73	Evolutionary dynamics of avian influenza A H7N9 virus across five waves in mainland China, 2013â€“2017. Journal of Infection, 2018, 77, 205-211.	1.7	12
74	Increasing the potential ability of human infections in H5N6 avian influenza A viruses. Journal of Infection, 2018, 77, 349-356.	1.7	12
75	Genome wide analyses uncover allele-specific RNA editing in human and mouse. Nucleic Acids Research, 2018, 46, 8888-8897.	6.5	47
76	Molecular signatures and functional analysis of beige adipocytes induced from in vivo intra-abdominal adipocytes. Science Advances, 2018, 4, eaar5319.	4.7	18
77	Retention and losses of ultraviolet-sensitive visual pigments in bats. Scientific Reports, 2018, 8, 11933.	1.6	10
78	The evolutionary dynamics of H1N1/pdm2009 in India. Infection, Genetics and Evolution, 2018, 65, 276-282.	1.0	13
79	Analysis of Circulating Tumor Cells in Ovarian Cancer and Their Clinical Value as a Biomarker. Cellular Physiology and Biochemistry, 2018, 48, 1983-1994.	1.1	63
80	Evolution of Trichocyte Keratin Associated Proteins. Advances in Experimental Medicine and Biology, 2018, 1054, 47-56.	0.8	10
81	The origin of chow chows in the light of the East Asian breeds. BMC Genomics, 2017, 18, 174.	1.2	8
82	Highly pathogenic H5N6 influenza A viruses recovered from wild birds in Guangdong, southern China, 2014â€“2015. Scientific Reports, 2017, 7, 44410.	1.6	18
83	PigVar: a database of pig variations and positive selection signatures. Database: the Journal of Biological Databases and Curation, 2017, 2017, .	1.4	11
84	Evolution of the vertebrate insulin receptor substrate (Irs) gene family. BMC Evolutionary Biology, 2017, 17, 148.	3.2	22
85	Excessive Autophagy Activation and Increased Apoptosis Are Associated with Palmitic Acid-Induced Cardiomyocyte Insulin Resistance. Journal of Diabetes Research, 2017, 2017, 1-11.	1.0	35
86	Comparison of glyburide and insulin in the management of gestational diabetes: A meta-analysis. PLoS ONE, 2017, 12, e0182488.	1.1	39
87	Tumacrophage: macrophages transformed into tumor stem-like cells by virulent genetic material from tumor cells. Oncotarget, 2017, 8, 82326-82343.	0.8	28
88	Identification of HNF4A Mutation p.T130I and HNF1A Mutations p.I27L and p.S487N in a Han Chinese Family with Early-Onset Maternally Inherited Type 2 Diabetes. Journal of Diabetes Research, 2016, 2016, 1-8.	1.0	12
89	Molecular Evolution of the Nuclear Factor (Erythroid-Derived 2)-Like 2 Gene Nrf2 in Old World Fruit Bats (Chiroptera: Pteropodidae). PLoS ONE, 2016, 11, e0146274.	1.1	10
90	Genomic analysis of snub-nosed monkeys (Rhinopithecus) identifies genes and processes related to high-altitude adaptation. Nature Genetics, 2016, 48, 947-952.	9.4	109

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91	Bats: Body mass index, forearm mass index, blood glucose levels and SLC2A2 genes for diabetes. Scientific Reports, 2016, 6, 29960.	1.6	21
92	Positive selection rather than relaxation of functional constraint drives the evolution of vision during chicken domestication. Cell Research, 2016, 26, 556-573.	5.7	69
93	Host genetics is associated with the gut microbial community membership rather than the structure. Molecular BioSystems, 2016, 12, 1676-1686.	2.9	11
94	Prolonged treatment with 3-isobutyl-1-methylxanthine improves the efficiency of differentiating 3T3-L1 cells into adipocytes. Analytical Biochemistry, 2016, 507, 18-20.	1.1	8
95	Xinmailong mitigated epirubicin-induced cardiotoxicity via inhibiting autophagy. Journal of Ethnopharmacology, 2016, 192, 459-470.	2.0	15
96	Genetic variations associated with six-white-point coat pigmentation in Diannan small-ear pigs. Scientific Reports, 2016, 6, 27534.	1.6	22
97	Comparative population genomics reveals genetic basis underlying body size of domestic chickens. Journal of Molecular Cell Biology, 2016, 8, 542-552.	1.5	41
98	Multiple specialised goose-type lysozymes potentially compensate for an exceptional lack of chicken-type lysozymes in Atlantic cod. Scientific Reports, 2016, 6, 28318.	1.6	12
99	Diversification of Sisorid catfishes (Teleostei: Siluriformes) in relation to the orogeny of the Himalayan Plateau. Science Bulletin, 2016, 61, 991-1002.	4.3	5
100	Repetitive transpositions of mitochondrial DNA sequences to the nucleus during the radiation of horseshoe bats (Rhinolophus, Chiroptera). Gene, 2016, 581, 161-169.	1.0	8
101	Out of southern East Asia: the natural history of domestic dogs across the world. Cell Research, 2016, 26, 21-33.	5.7	271
102	Population Variation Reveals Independent Selection toward Small Body Size in Chinese Debao Pony. Genome Biology and Evolution, 2016, 8, 42-50.	1.1	57
103	Contrasting Patterns in the Evolution of Vertebrate MLX Interacting Protein (MLXIP) and MLX Interacting Protein-Like (MLXIPL) Genes. PLoS ONE, 2016, 11, e0149682.	1.1	6
104	DNA methylation signatures of long intergenic noncoding RNAs in porcine adipose and muscle tissues. Scientific Reports, 2015, 5, 15435.	1.6	29
105	Genetic adaptations of the plateau zokor in high-elevation burrows. Scientific Reports, 2015, 5, 17262.	1.6	48
106	Staurosporine Induced Apoptosis May Activate Cancer Stem-Like Cells (CD44⁺/CD24⁻) in MCF-7 by Upregulating Mucin1 and EpCAM. Journal of Cancer, 2015, 6, 1049-1057.	1.2	11
107	Exposure of Tumor-Associated Macrophages to Apoptotic MCF-7 Cells Promotes Breast Cancer Growth and Metastasis. International Journal of Molecular Sciences, 2015, 16, 11966-11982.	1.8	36
108	Nocturnal to Diurnal Transition in the Common Ancestor of Haplorrhines: Evidence from Genomic-Scan for Positively Selected Genes. Journal of Genetics and Genomics, 2015, 42, 33-37.	1.7	4

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109	DoGSD: the dog and wolf genome SNP database. Nucleic Acids Research, 2015, 43, D777-D783.	6.5	76
110	Evolutionary and Functional Novelty of Pancreatic Ribonuclease: a Study of Musteloidea (order) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 70	1.6	28
111	Whole-genome sequence of the Tibetan frog Nanorana parkeri and the comparative evolution of tetrapod genomes. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, E1257-62.	3.3	159
112	Integrative analyses of RNA editing, alternative splicing, and expression of young genes in human brain transcriptome by deep RNA sequencing. Journal of Molecular Cell Biology, 2015, 7, 314-325.	1.5	12
113	Role of Glucokinase in the Subcellular Localization of Glucokinase Regulatory Protein. International Journal of Molecular Sciences, 2015, 16, 7377-7393.	1.8	13
114	Genomic Analyses Reveal Potential Independent Adaptation to High Altitude in Tibetan Chickens. Molecular Biology and Evolution, 2015, 32, 1880-1889.	3.5	193
115	Complete mitochondrial genome of the Indian peafowl (Pavo cristatus), with phylogenetic analysis in phasianidae. Mitochondrial DNA, 2015, 26, 912-913.	0.6	8
116	Genome-wide identification and characterization of teleost-specific microRNAs within zebrafish. Gene, 2015, 561, 181-189.	1.0	8
117	Phosphoenolpyruvate Carboxykinase 1 Gene (Pck1) Displays Parallel Evolution between Old World and New World Fruit Bats. PLoS ONE, 2015, 10, e0118666.	1.1	7
118	Evolution of the Vertebrate Resistin Gene Family. PLoS ONE, 2015, 10, e0130188.	1.1	10
119	Genomic organization and evolution of ruminant lysozyme c genes. Zoological Research, 2015, 36, 1-17.	0.6	11
120	Relaxed Evolution in the Tyrosine Aminotransferase Gene Tat in Old World Fruit Bats (Chiroptera:) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50	1.1	6
121	Differential Expression of Meis2, Mab21l2 and Tbx3 during Limb Development Associated with Diversification of Limb Morphology in Mammals. PLoS ONE, 2014, 9, e106100.	1.1	17
122	The Great Roundleaf Bat (Hipposideros armiger) as a Good Model for Cold-Induced Browning of Intra-Abdominal White Adipose Tissue. PLoS ONE, 2014, 9, e112495.	1.1	7
123	Introgression of mitochondrial DNA promoted by natural selection in the Japanese pipistrelle bat (Pipistrellus abramus). Genetica, 2014, 142, 483-494.	0.5	4
124	Domestication of the Dog from the Wolf Was Promoted by Enhanced Excitatory Synaptic Plasticity: A Hypothesis. Genome Biology and Evolution, 2014, 6, 3115-3121.	1.1	38
125	Complete mtDNA genomes reveal similar penetrances of maternally inherited type 2 diabetes in two Chinese families. Mitochondrial DNA, 2014, 27, 1-10.	0.6	1
126	Integrative analysis of young genes, positively selected genes and lncRNAs in the development of Drosophila melanogaster. BMC Evolutionary Biology, 2014, 14, 241.	3.2	11

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127	â€œOut of Pollenâ€•Hypothesis for Origin of New Genes in Flowering Plants: Study from Arabidopsis thaliana. Genome Biology and Evolution, 2014, 6, 2822-2829.	1.1	28
128	Genome-Wide Identification of Long Intergenic Noncoding RNA Genes and Their Potential Association with Domestication in Pigs. Genome Biology and Evolution, 2014, 6, 1387-1392.	1.1	121
129	GdX/UBL4A Specifically Stabilizes the TC45/STAT3 Association and Promotes Dephosphorylation of STAT3 to Repress Tumorigenesis. Molecular Cell, 2014, 53, 752-765.	4.5	54
130	Long term liver specific glucokinase gene defect induced diabetic cardiomyopathy by up regulating NADPH oxidase and down regulating insulin receptor and p-AMPK. Cardiovascular Diabetology, 2014, 13, 24.	2.7	10
131	Evolution of glucose utilization: Glucokinase and glucokinase regulator protein. Molecular Phylogenetics and Evolution, 2014, 70, 195-203.	1.2	40
132	Population Variation Revealed High-Altitude Adaptation of Tibetan Mastiffs. Molecular Biology and Evolution, 2014, 31, 1200-1205.	3.5	130
133	Domestication Genomics: Evidence from Animals. Annual Review of Animal Biosciences, 2014, 2, 65-84.	3.6	98
134	Parallel Evolution of the Glycogen Synthase 1 (Muscle) Gene Gys1 Between Old World and New World Fruit Bats (Order: Chiroptera). Biochemical Genetics, 2014, 52, 443-458.	0.8	6
135	Mitogenomic analyses propose positive selection in mitochondrial genes for high-altitude adaptation in galliform birds. Mitochondrion, 2014, 18, 70-75.	1.6	70
136	Evolution of the vertebrate goose-type lysozyme gene family. BMC Evolutionary Biology, 2014, 14, 188.	3.2	22
137	Evolution of receptors for peptides similar to glucagon. General and Comparative Endocrinology, 2014, 209, 50-60.	0.8	18
138	Balancing Selection on CDH2 May Be Related to the Behavioral Features of the Belgian Malinois. PLoS ONE, 2014, 9, e110075.	1.1	13
139	Resistin disrupts glycogen synthesis under high insulin and high glucose levels by down-regulating the hepatic levels of GSK3Î². Gene, 2013, 529, 50-56.	1.0	17
140	QcReads: An Adapter and Quality Trimming Tool for Next-Generation Sequencing Reads. Journal of Genetics and Genomics, 2013, 40, 639-642.	1.7	5
141	Rapid Evolution of the Mammalian HILS1 Gene and the Nuclear Condensation Process during Mammalian Spermiogenesis. Journal of Genetics and Genomics, 2013, 40, 55-59.	1.7	5
142	Differential expression of genes and changes in glucose metabolism in the liver of liver-specific glucokinase gene knockout mice. Gene, 2013, 516, 248-254.	1.0	12
143	The genomics of selection in dogs and the parallel evolution between dogs and humans. Nature Communications, 2013, 4, 1860.	5.8	275
144	Differential Expression of Genes Associated with the Progression of Renal Disease in the Kidneys of Liver-Specific Glucokinase Gene Knockout Mice. International Journal of Molecular Sciences, 2013, 14, 6467-6486.	1.8	8

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145	The Wnt Signaling Pathway Effector TCF7L2 Controls Gut and Brain Proglucagon Gene Expression and Glucose Homeostasis. Diabetes, 2013, 62, 789-800.	0.3	98
146	Genome-Wide Scans for Candidate Genes Involved in the Aquatic Adaptation of Dolphins. Genome Biology and Evolution, 2013, 5, 130-139.	1.1	49
147	Draft genome sequence of the Tibetan antelope. Nature Communications, 2013, 4, 1858.	5.8	229
148	Evolution of Hepatic Glucose Metabolism: Liver-Specific Glucokinase Deficiency Explained by Parallel Loss of the Gene for Glucokinase Regulatory Protein (GCKR). PLoS ONE, 2013, 8, e60896.	1.1	11
149	Adaptive Evolution of the Hox Gene Family for Development in Bats and Dolphins. PLoS ONE, 2013, 8, e65944.	1.1	15
150	An Over Expression APP Model for Anti-Alzheimer Disease Drug Screening Created by Zinc Finger Nuclease Technology. PLoS ONE, 2013, 8, e75493.	1.1	6
151	Signature of Balancing Selection at the MC1R Gene in Kunming Dog Populations. PLoS ONE, 2013, 8, e55469.	1.1	19
152	Direct Regulation of the Proglucagon Gene by Insulin, Leptin, and cAMP in Embryonic versus Adult Hypothalamic Neurons. Molecular Endocrinology, 2012, 26, 1339-1355.	3.7	12
153	Differences in Selection Drive Olfactory Receptor Genes in Different Directions in Dogs and Wolf. Molecular Biology and Evolution, 2012, 29, 3475-3484.	3.5	30
154	Positive Selection on the Gene RNASEL: Correlation between Patterns of Evolution and Function. Molecular Biology and Evolution, 2012, 29, 3161-3168.	3.5	12
155	Genetic Adaptation of the Hypoxia-Inducible Factor Pathway to Oxygen Pressure among Eurasian Human Populations. Molecular Biology and Evolution, 2012, 29, 3359-3370.	3.5	29
156	Characterization of the gene expression profile of heterozygous liver-specific glucokinase knockout mice at a young age. Biomedicine and Pharmacotherapy, 2012, 66, 587-596.	2.5	6
157	The Motilin Gene Evolved a New Function in Kangaroo Rats and Kangaroo Mice (Dipodomyinae). Journal of Molecular Evolution, 2012, 75, 112-118.	0.8	3
158	Expression of the Human Glucokinase Gene: Important Roles of the 5â€² Flanking and Intron 1 Sequences. PLoS ONE, 2012, 7, e45824.	1.1	9
159	CREPT Accelerates Tumorigenesis by Regulating the Transcription of Cell-Cycle-Related Genes. Cancer Cell, 2012, 21, 92-104.	7.7	71
160	Origin and convergent evolution of exendin genes. General and Comparative Endocrinology, 2012, 175, 27-33.	0.8	17
161	Multiple Episodes of Convergence in Genes of the Dim Light Vision Pathway in Bats. PLoS ONE, 2012, 7, e34564.	1.1	10
162	Genome-Wide Scan for Bats and Dolphin to Detect Their Genetic Basis for New Locomotive Styles. PLoS ONE, 2012, 7, e46455.	1.1	6

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163	Long-term renal changes in the liver-specific glucokinase knockout mouse: implications for renal disease in maturity-onset diabetes of the young 2. Translational Research, 2011, 157, 111-116.	2.2	10
164	Incretin hormones and the expanding families of glucagonâ€like sequences and their receptors. Diabetes, Obesity and Metabolism, 2011, 13, 69-81.	2.2	25
165	Evolution of the mammalian lysozyme gene family. BMC Evolutionary Biology, 2011, 11, 166.	3.2	52
166	Correlated Evolution among Six Gene Families in Drosophila Revealed by Parallel Change of Gene Numbers. Genome Biology and Evolution, 2011, 3, 396-400.	1.1	8
167	Evaluating the Roles of Energetic Functional Constraints on Teleost Mitochondrial-Encoded Protein Evolution. Molecular Biology and Evolution, 2011, 28, 39-44.	3.5	84
168	De Novo Origin of Human Protein-Coding Genes. PLoS Genetics, 2011, 7, e1002379.	1.5	153
169	Stepwise loss of motilin and its specific receptor genes in rodents. Journal of Molecular Endocrinology, 2010, 44, 37-44.	1.1	86
170	Parallel and Convergent Evolution of the Dim-Light Vision Gene RH1 in Bats (Order: Chiroptera). PLoS ONE, 2010, 5, e8838.	1.1	32
171	Mixed S-Nitrosylated Polymerized Bovine Hemoglobin Species Moderate Hemodynamic Effects in Acutely Hypoxic Rats. American Journal of Respiratory Cell and Molecular Biology, 2010, 42, 200-209.	1.4	9
172	Adaptive evolution of energy metabolism genes and the origin of flight in bats. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 8666-8671.	3.3	239
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