

Richard Emes

List of Publications by Year in descending order

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Version: 2024-02-01

132
papers

13,928
citations

87888

38
h-index

21540

114
g-index

162
all docs

162
docs citations

162
times ranked

19826
citing authors

#	ARTICLE	IF	CITATIONS
1	Initial sequencing and comparative analysis of the mouse genome. <i>Nature</i> , 2002, 420, 520-562.	27.8	6,319
2	Genome sequence of the Brown Norway rat yields insights into mammalian evolution. <i>Nature</i> , 2004, 428, 493-521.	27.8	1,943
3	Mutations in Radial Spoke Head Protein Genes RSPH9 and RSPH4A Cause Primary Ciliary Dyskinesia with Central-Microtubular-Pair Abnormalities. <i>American Journal of Human Genetics</i> , 2009, 84, 197-209.	6.2	303
4	Synaptic scaffold evolution generated components of vertebrate cognitive complexity. <i>Nature Neuroscience</i> , 2013, 16, 16-24.	14.8	229
5	Comparison of the genomes of human and mouse lays the foundation of genome zoology. <i>Human Molecular Genetics</i> , 2003, 12, 701-709.	2.9	191
6	TP53 copy number expansion is associated with the evolution of increased body size and an enhanced DNA damage response in elephants. <i>ELife</i> , 2016, 5, .	6.0	191
7	Paternal diet programs offspring health through sperm- and seminal plasma-specific pathways in mice. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, 10064-10069.	7.1	185
8	Splice-Site Mutations in the Axonemal Outer Dynein Arm Docking Complex Gene CCDC114 Cause Primary Ciliary Dyskinesia. <i>American Journal of Human Genetics</i> , 2013, 92, 88-98.	6.2	176
9	Mutations in <i>CCDC39</i> and <i>CCDC40</i> are the Major Cause of Primary Ciliary Dyskinesia with Axonemal Disorganization and Absent Inner Dynein Arms. <i>Human Mutation</i> , 2013, 34, 462-472.	2.5	176
10	Evolutionary expansion and anatomical specialization of synapse proteome complexity. <i>Nature Neuroscience</i> , 2008, 11, 799-806.	14.8	171
11	Mutations in ZMYND10, a Gene Essential for Proper Axonemal Assembly of Inner and Outer Dynein Arms in Humans and Flies, Cause Primary Ciliary Dyskinesia. <i>American Journal of Human Genetics</i> , 2013, 93, 346-356.	6.2	167
12	A new sequence motif linking lissencephaly, Treacher Collins and oral-facial-digital type 1 syndromes, microtubule dynamics and cell migration. <i>Human Molecular Genetics</i> , 2001, 10, 2813-2820.	2.9	163
13	N6-methyladenosine regulates the stability of RNA:DNA hybrids in human cells. <i>Nature Genetics</i> , 2020, 52, 48-55.	21.4	147
14	X-linked primary ciliary dyskinesia due to mutations in the cytoplasmic axonemal dynein assembly factor PIH1D3. <i>Nature Communications</i> , 2017, 8, 14279.	12.8	133
15	Evolution of Synapse Complexity and Diversity. <i>Annual Review of Neuroscience</i> , 2012, 35, 111-131.	10.7	131
16	Exome sequencing identifies <i>DYNC2H1</i> mutations as a common cause of asphyxiating thoracic dystrophy (Jeune syndrome) without major polydactyly, renal or retinal involvement. <i>Journal of Medical Genetics</i> , 2013, 50, 309-323.	3.2	127
17	Quantitative, high-resolution epigenetic profiling of CpG loci identifies associations with cord blood plasma homocysteine and birth weight in humans. <i>Epigenetics</i> , 2011, 6, 86-94.	2.7	123
18	Evolution of complexity in the zebrafish synapse proteome. <i>Nature Communications</i> , 2017, 8, 14613.	12.8	112

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19	Sexual Selection and the Adaptive Evolution of Mammalian Ejaculate Proteins. <i>Molecular Biology and Evolution</i> , 2007, 25, 207-219.	8.9	109
20	Mutations in the Gene Encoding IFT Dynein Complex Component WDR34 Cause Jeune Asphyxiating Thoracic Dystrophy. <i>American Journal of Human Genetics</i> , 2013, 93, 932-944.	6.2	108
21	Evolution and Comparative Genomics of Odorant- and Pheromone-Associated Genes in Rodents. <i>Genome Research</i> , 2004, 14, 591-602.	5.5	97
22	LINE-1 DNA methylation is inversely correlated with cord plasma homocysteine in man: A preliminary study. <i>Epigenetics</i> , 2009, 4, 394-398.	2.7	97
23	Evolution of NMDA receptor cytoplasmic interaction domains: implications for organisation of synaptic signalling complexes. <i>BMC Neuroscience</i> , 2008, 9, 6.	1.9	90
24	Genome-wide DNA methylation profiling in rheumatoid arthritis identifies disease-associated methylation changes that are distinct to individual T- and B-lymphocyte populations. <i>Epigenetics</i> , 2014, 9, 1228-1237.	2.7	90
25	Control of gene expression in <i>Plasmodium falciparum</i> – Ten years on. <i>Molecular and Biochemical Parasitology</i> , 2009, 164, 9-25.	1.1	88
26	Combined exome and whole-genome sequencing identifies mutations in <i>ARMC4</i> as a cause of primary ciliary dyskinesia with defects in the outer dynein arm. <i>Journal of Medical Genetics</i> , 2014, 51, 61-67.	3.2	88
27	Targeted NGS gene panel identifies mutations in <i>RSPH1</i> causing primary ciliary dyskinesia and a common mechanism for ciliary central pair agenesis due to radial spoke defects. <i>Human Molecular Genetics</i> , 2014, 23, 3362-3374.	2.9	82
28	Comparative Evolutionary Genomics of Androgen-Binding Protein Genes. <i>Genome Research</i> , 2004, 14, 1516-1529.	5.5	79
29	The role of positive selection in determining the molecular cause of species differences in disease. <i>BMC Evolutionary Biology</i> , 2008, 8, 273.	3.2	74
30	Quantitative, genome-wide analysis of the DNA methylome in sporadic pituitary adenomas. <i>Endocrine-Related Cancer</i> , 2012, 19, 805-816.	3.1	66
31	Assembly, Assessment, and Availability of De novo Generated Eukaryotic Transcriptomes. <i>Frontiers in Genetics</i> , 2015, 6, 361.	2.3	57
32	Genome-wide profiling in treatment-naïve early rheumatoid arthritis reveals DNA methylome changes in T and B lymphocytes. <i>Epigenomics</i> , 2016, 8, 209-224.	2.1	55
33	A Trematode Parasite Derived Growth Factor Binds and Exerts Influences on Host Immune Functions via Host Cytokine Receptor Complexes. <i>PLoS Pathogens</i> , 2016, 12, e1005991.	4.7	55
34	Opsonic Phagocytosis in Chronic Obstructive Pulmonary Disease Is Enhanced by Nrf2 Agonists. <i>American Journal of Respiratory and Critical Care Medicine</i> , 2018, 198, 739-750.	5.6	53
35	Maternal genome-wide DNA methylation profiling in gestational diabetes shows distinctive disease-associated changes relative to matched healthy pregnancies. <i>Epigenetics</i> , 2018, 13, 122-128.	2.7	52
36	Molecular Epidemiology of <i>Streptococcus uberis</i> Clinical Mastitis in Dairy Herds: Strain Heterogeneity and Transmission. <i>Journal of Clinical Microbiology</i> , 2016, 54, 68-74.	3.9	50

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37	Epigenome-wide profiling identifies significant differences in DNA methylation between matched-pairs of T- and B-lymphocytes from healthy individuals. <i>Epigenetics</i> , 2013, 8, 1188-1197.	2.7	42
38	Methylation of HOXA9 and ISL1 Predicts Patient Outcome in High-Grade Non-Invasive Bladder Cancer. <i>PLoS ONE</i> , 2015, 10, e0137003.	2.5	40
39	Identification of DNA methylation biomarkers from Infinium arrays. <i>Frontiers in Genetics</i> , 2012, 3, 161.	2.3	39
40	Unbiased Analysis of the Impact of Micropatterned Biomaterials on Macrophage Behavior Provides Insights beyond Predefined Polarization States. <i>ACS Biomaterials Science and Engineering</i> , 2017, 3, 969-978.	5.2	39
41	Adaptive evolution of Toll-like receptor 5 in domesticated mammals. <i>BMC Evolutionary Biology</i> , 2012, 12, 122.	3.2	38
42	Insights into the evolution of Darwin's finches from comparative analysis of the <i>Geospiza magnirostris</i> genome sequence. <i>BMC Genomics</i> , 2013, 14, 95.	2.8	38
43	Quantitative genome-wide methylation analysis of high-grade non-muscle invasive bladder cancer. <i>Epigenetics</i> , 2016, 11, 237-246.	2.7	36
44	A distinct bacterial dysbiosis associated skin inflammation in ovine footrot. <i>Scientific Reports</i> , 2017, 7, 45220.	3.3	36
45	Detection and analysis of RNA methylation. <i>F1000Research</i> , 2019, 8, 559.	1.6	36
46	DNA methylation at diagnosis is associated with response to disease-modifying drugs in early rheumatoid arthritis. <i>Epigenomics</i> , 2017, 9, 419-428.	2.1	35
47	A consensus approach to vertebrate de novo transcriptome assembly from RNA-seq data: assembly of the duck (<i>Anas platyrhynchos</i>) transcriptome. <i>Frontiers in Genetics</i> , 2014, 5, 190.	2.3	33
48	Virulence related sequences; insights provided by comparative genomics of <i>Streptococcus uberis</i> of differing virulence. <i>BMC Genomics</i> , 2015, 16, 334.	2.8	32
49	Comparison of Clustering Methods for Investigation of Genome-Wide Methylation Array Data. <i>Frontiers in Genetics</i> , 2011, 2, 88.	2.3	30
50	Acute <i>Toxoplasma Gondii</i> Infection in Cats Induced Tissue-Specific Transcriptional Response Dominated by Immune Signatures. <i>Frontiers in Immunology</i> , 2018, 9, 2403.	4.8	30
51	Duplicated Paralogous Genes Subject to Positive Selection in the Genome of <i>Trypanosoma brucei</i> . <i>PLoS ONE</i> , 2008, 3, e2295.	2.5	29
52	Mitochondrial phosphoenolpyruvate carboxykinase (PEPCK-M) and serine biosynthetic pathway genes are co-ordinately increased during anabolic agent-induced skeletal muscle growth. <i>Scientific Reports</i> , 2016, 6, 28693.	3.3	29
53	Diverse spatial, temporal, and sexual expression of recently duplicated androgen-binding protein genes in <i>Mus musculus</i> . <i>BMC Evolutionary Biology</i> , 2005, 5, 40.	3.2	27
54	Methylation of the <i>FGFR2</i> gene is associated with high birth weight centile in humans. <i>Epigenomics</i> , 2014, 6, 477-491.	2.1	27

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55	Identification of stable reference genes for quantitative PCR in koalas. <i>Scientific Reports</i> , 2018, 8, 3364.	3.3	26
56	A novel member of the let-7 microRNA family is associated with developmental transitions in filarial nematode parasites. <i>BMC Genomics</i> , 2015, 16, 331.	2.8	25
57	Discrimination of contagious and environmental strains of <i>Streptococcus uberis</i> in dairy herds by means of mass spectrometry and machine-learning. <i>Scientific Reports</i> , 2018, 8, 17517.	3.3	25
58	Hsp-90 and the biology of nematodes. <i>BMC Evolutionary Biology</i> , 2009, 9, 254.	3.2	24
59	Knockdown of embryonic myosin heavy chain reveals an essential role in the morphology and function of the developing heart. <i>Development (Cambridge)</i> , 2011, 138, 3955-3966.	2.5	23
60	TGF- β 2 superfamily members from the helminth <i>Fasciola hepatica</i> show intrinsic effects on viability and development. <i>Veterinary Research</i> , 2015, 46, 29.	3.0	23
61	Identifying genes for neuron survival and axon outgrowth in <i>Hirudo medicinalis</i> . <i>Journal of Anatomy</i> , 2004, 204, 13-24.	1.5	22
62	Area 51: How do <i>Acanthamoeba</i> invade the central nervous system?. <i>Trends in Parasitology</i> , 2011, 27, 185-189.	3.3	22
63	Identifying the Cellular Targets of Drug Action in the Central Nervous System Following Corticosteroid Therapy. <i>ACS Chemical Neuroscience</i> , 2014, 5, 51-63.	3.5	22
64	Analysis of Mitochondrial haemoglobin in Parkinson's disease brain. <i>Mitochondrion</i> , 2016, 29, 45-52.	3.4	22
65	Metagenomics reveals impact of geography and acute diarrheal disease on the Central Indian human gut microbiome. <i>Gut Microbes</i> , 2020, 12, 1752605.	9.8	22
66	Koala retrovirus viral load and disease burden in distinct northern and southern koala populations. <i>Scientific Reports</i> , 2020, 10, 263.	3.3	22
67	Characterisation of a group of endogenous gammaretroviruses in the canine genome. <i>Veterinary Journal</i> , 2013, 196, 28-33.	1.7	21
68	The effect of maternal undernutrition on the rat placental transcriptome: protein restriction up-regulates cholesterol transport. <i>Genes and Nutrition</i> , 2016, 11, 27.	2.5	20
69	Genetic diversity of Koala retrovirus env gene subtypes: insights into northern and southern koala populations. <i>Journal of General Virology</i> , 2019, 100, 1328-1339.	2.9	20
70	The Human Postsynaptic Density Shares Conserved Elements with Proteomes of Unicellular Eukaryotes and Prokaryotes. <i>Frontiers in Neuroscience</i> , 2011, 5, 44.	2.8	19
71	Adaptation to the chicken intestine in <i>Salmonella Enteritidis</i> PT4 studied by transcriptional analysis. <i>Veterinary Microbiology</i> , 2011, 153, 198-204.	1.9	19
72	Make way for the "next generation": application and prospects for genome-wide, epigenome-specific technologies in endocrine research. <i>Journal of Molecular Endocrinology</i> , 2012, 49, R19-R27.	2.5	19

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73	Analysis of the spatial and temporal arrangement of transcripts over intergenic regions in the human malarial parasite <i>Plasmodium falciparum</i> . <i>BMC Genomics</i> , 2013, 14, 267.	2.8	19
74	The Cross-Talk between miR-511-3p and C-Type Lectin Receptors on Dendritic Cells Affects Dendritic Cell Function. <i>Journal of Immunology</i> , 2019, 203, 148-157.	0.8	19
75	Phenotypic Microarrays Suggest <i>Escherichia coli</i> ST131 Is Not a Metabolically Distinct Lineage of Extra-Intestinal Pathogenic <i>E. coli</i> . <i>PLoS ONE</i> , 2014, 9, e88374.	2.5	18
76	Thapsigargin at Non-Cytotoxic Levels Induces a Potent Host Antiviral Response that Blocks Influenza A Virus Replication. <i>Viruses</i> , 2020, 12, 1093.	3.3	18
77	Pathological Findings in Koala Retrovirus-positive Koalas (<i>Phascolarctos cinereus</i>) from Northern and Southern Australia. <i>Journal of Comparative Pathology</i> , 2020, 176, 50-66.	0.4	18
78	A predictive model for canine dilated cardiomyopathy—a meta-analysis of Doberman Pinscher data. <i>PeerJ</i> , 2015, 3, e842.	2.0	17
79	DNA methylation profiling of synovial fluid FLS in rheumatoid arthritis reveals changes common with tissue-derived FLS. <i>Epigenomics</i> , 2015, 7, 539-551.	2.1	16
80	Epidrug mediated re-expression of miRNA targeting the HMGA transcripts in pituitary cells. <i>Pituitary</i> , 2015, 18, 674-684.	2.9	16
81	<i>Hirudo medicinalis</i> : A Platform for Investigating Genes in Neural Repair. <i>Cellular and Molecular Neurobiology</i> , 2005, 25, 427-440.	3.3	15
82	Multiple Groups of Endogenous Epsilon-Like Retroviruses Conserved across Primates. <i>Journal of Virology</i> , 2014, 88, 12464-12471.	3.4	15
83	HmCRIP, a cysteine-rich intestinal protein, is expressed by an identified regenerating nerve cell. <i>FEBS Letters</i> , 2003, 533, 124-128.	2.8	14
84	Characterisation of retroviruses in the horse genome and their transcriptional activity via transcriptome sequencing. <i>Virology</i> , 2012, 433, 55-63.	2.4	14
85	Combined influence of gene-specific cord blood methylation and maternal smoking habit on birth weight. <i>Epigenomics</i> , 2013, 5, 37-49.	2.1	14
86	Interspecific Variation in One-Carbon Metabolism within the Ovarian Follicle, Oocyte, and Preimplantation Embryo: Consequences for Epigenetic Programming of DNA Methylation. <i>International Journal of Molecular Sciences</i> , 2021, 22, 1838.	4.1	13
87	The Beta-adrenergic agonist, Ractopamine, increases skeletal muscle expression of Asparagine Synthetase as part of an integrated stress response gene program. <i>Scientific Reports</i> , 2018, 8, 15915.	3.3	12
88	Molecular Characterisation of Canine Osteosarcoma in High Risk Breeds. <i>Cancers</i> , 2020, 12, 2405.	3.7	12
89	The Multiple Sclerosis Severity Score: associations with MC1R single nucleotide polymorphisms and host response to ultraviolet radiation. <i>Multiple Sclerosis Journal</i> , 2010, 16, 1109-1116.	3.0	11
90	The <i>EFEMP1</i> Gene: A Frequent Target for Epigenetic Silencing in Multiple Human Pituitary Adenoma Subtypes. <i>Neuroendocrinology</i> , 2013, 98, 200-211.	2.5	11

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91	A Comparative Approach to Understanding Tissue-Specific Expression of Uncoupling Protein 1 Expression in Adipose Tissue. <i>Frontiers in Genetics</i> , 2012, 3, 304.	2.3	11
92	Mapping polyclonal antibody responses to bacterial infection using next generation phage display. <i>Scientific Reports</i> , 2016, 6, 24232.	3.3	11
93	HumanMethylation450K Array Identified Biomarkers Predict Tumour Recurrence/Progression at Initial Diagnosis of High-risk Non-muscle Invasive Bladder Cancer. <i>Biomarkers in Cancer</i> , 2018, 10, 1179299X1775192.	3.6	11
94	A Paradox in Bacterial Pathogenesis: Activation of the Local Macrophage Inflammasome Is Required for Virulence of <i>Streptococcus uberis</i> . <i>Pathogens</i> , 2020, 9, 997.	2.8	11
95	Cancer reversion with oocyte extracts is mediated by cell cycle arrest and induction of tumour dormancy. <i>Oncotarget</i> , 2018, 9, 16008-16027.	1.8	11
96	Bioinformatic perspectives in the neuronal ceroid lipofuscinoses. <i>Biochimica Et Biophysica Acta - Molecular Basis of Disease</i> , 2013, 1832, 1831-1841.	3.8	10
97	Antiepileptic drugs and the fetal epigenome. <i>Epilepsia</i> , 2013, 54, e16-9.	5.1	10
98	Homopolymer tract organization in the human malarial parasite <i>Plasmodium falciparum</i> and related Apicomplexan parasites. <i>BMC Genomics</i> , 2014, 15, 848.	2.8	10
99	The Applied Development of a Tiered Multilocus Sequence Typing (MLST) Scheme for <i>Dichelobacter nodosus</i> . <i>Frontiers in Microbiology</i> , 2018, 9, 551.	3.5	10
100	Evolution of gene expression levels in the male reproductive organs of <i>Anopheles</i> mosquitoes. <i>Life Science Alliance</i> , 2019, 2, e201800191.	2.8	10
101	Inferring Function from Homology. <i>Methods in Molecular Biology</i> , 2008, 453, 149-168.	0.9	9
102	Triaging informative cis-regulatory elements for the combinatorial control of temporal gene expression during <i>Plasmodium falciparum</i> intraerythrocytic development. <i>Parasites and Vectors</i> , 2015, 8, 81.	2.5	9
103	A proteomic investigation into mechanisms underpinning corticosteroid effects on neural stem cells. <i>Molecular and Cellular Neurosciences</i> , 2018, 86, 30-40.	2.2	8
104	LINE-1 transcription in round spermatids is associated with accretion of 5-carboxylcytosine in their open reading frames. <i>Communications Biology</i> , 2021, 4, 691.	4.4	8
105	A Data-Centric Strategy for Modern Biobanking. <i>Advances in Experimental Medicine and Biology</i> , 2015, 864, 165-169.	1.6	8
106	RNA expression of TLR10 in normal equine tissues. <i>BMC Research Notes</i> , 2016, 9, 353.	1.4	7
107	Safe nanoengineering and incorporation of transplant populations in a neurosurgical grade biomaterial, DuraGen Plus™, for protected cell therapy applications. <i>Journal of Controlled Release</i> , 2020, 321, 553-563.	9.9	7
108	Novel ovine polymorphisms and adaptive evolution in mammalian TLR2 suggest existence of multiple pathogen binding regions. <i>Gene</i> , 2014, 540, 217-225.	2.2	6

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109	Complete Genome Sequences of <i>Vibrio cholerae</i> -Specific Bacteriophages 24 and X29. <i>Genome Announcements</i> , 2017, 5, .	0.8	6
110	Whole-Genome Sequence of a Plant Growth-Promoting Strain, <i>Serratia marcescens</i> BTL07, Isolated from the Rhizosphere of <i>Capsicum annuum</i> L. <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.6	6
111	Transcriptomic and genomic variants between koala populations reveals underlying genetic components to disorders in a bottlenecked population. <i>Conservation Genetics</i> , 2021, 22, 329-340.	1.5	6
112	Pneumolysin Is Responsible for Differential Gene Expression and Modifications in the Epigenetic Landscape of Primary Monocyte Derived Macrophages. <i>Frontiers in Immunology</i> , 2021, 12, 573266.	4.8	6
113	Characterisation of the horse transcriptome from immunologically active tissues. <i>PeerJ</i> , 2014, 2, e382.	2.0	6
114	Cloning and characterisation of <i>mmc-1</i> , a microfilarial-specific gene, from <i>Brugia pahangi</i> . <i>International Journal for Parasitology</i> , 2002, 32, 415-424.	3.1	5
115	The A2 gene of alcelaphine herpesvirus-1 is a transcriptional regulator affecting cytotoxicity in virus-infected T cells but is not required for malignant catarrhal fever induction in rabbits. <i>Virus Research</i> , 2014, 188, 68-80.	2.2	5
116	Inferring Function from Homology. <i>Methods in Molecular Biology</i> , 2017, 1526, 23-40.	0.9	5
117	Novel insights into viral infection and oncogenesis from koala retrovirus (KoRV) infection of HEK293T cells. <i>Gene</i> , 2020, 733, 144366.	2.2	5
118	PIMMS (Pragmatic Insertional Mutation Mapping System) Laboratory Methodology a Readily Accessible Tool for Identification of Essential Genes in <i>Streptococcus</i> . <i>Frontiers in Microbiology</i> , 2016, 7, 1645.	3.5	4
119	Mapping B-cell responses to <i>Salmonella enterica</i> serovars Typhimurium and Enteritidis in chickens for the discrimination of infected from vaccinated animals. <i>Scientific Reports</i> , 2016, 6, 31186.	3.3	4
120	Differential and defective transcription of koala retrovirus indicates the complexity of host and virus evolution. <i>Journal of General Virology</i> , 2022, 103, .	2.9	4
121	Transposon insertion mapping with PIMMS – Pragmatic Insertional Mutation Mapping System. <i>Frontiers in Genetics</i> , 2015, 06, 139.	2.3	3
122	Method for RNA extraction and transcriptomic analysis of single fungal spores. <i>MethodsX</i> , 2020, 7, 100760.	1.6	3
123	Molecular Characterization of Adipose Tissue in the African Elephant (<i>Loxodonta africana</i>). <i>PLoS ONE</i> , 2014, 9, e91717.	2.5	3
124	Epigenetic regulation of 5 α -reductase-1 underlies adaptive plasticity of reproductive function and pubertal timing. <i>BMC Biology</i> , 2022, 20, 11.	3.8	3
125	Complete Genome Sequences of Seven <i>Vibrio cholerae</i> Phages Isolated in China. <i>Genome Announcements</i> , 2017, 5, .	0.8	1
126	A new sequence motif linking lissencephaly, Treacher Collins and oral “facial” digital type 1 syndromes, microtubule dynamics and cell migration. , 0, .		1

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127	Gene Expression Profile Induced by Two Different Variants of Street Rabies Virus in Mice. <i>Viruses</i> , 2022, 14, 692.	3.3	1
128	Genome-Wide DNA Methylation Profiling Identifies Distinct Changes in T- and B-Cell Populations from Patients with Rheumatoid Arthritis. <i>Rheumatology</i> , 2014, 53, i157-i158.	1.9	0
129	Skeletal muscle hypertrophy in pigs is associated with an increased expression of serine biosynthetic pathway genes along with genes associated with an endoplasmic reticulum stress response. <i>Proceedings of the Nutrition Society</i> , 2015, 74, .	1.0	0
130	Clinical research: developing an appropriate career structure. <i>Veterinary Record</i> , 2015, 177, 544-547.	0.3	0
131	SNP based transmission study of badgers infected with <i>Mycobacterium bovis</i> in the edge risk area of England. <i>Access Microbiology</i> , 2019, 1, .	0.5	0
132	Is it a wonderful life? How well do we assess quality of life in cats?. , 0, , 557-557.		0