

# Marc Robinson-Rechavi

## List of Publications by Year in descending order

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146  
papers

12,693  
citations

50244

46  
h-index

27389

106  
g-index

185  
all docs

185  
docs citations

185  
times ranked

15507  
citing authors

#	ARTICLE	IF	CITATIONS
1	Genome duplication in the teleost fish <i>Tetraodon nigroviridis</i> reveals the early vertebrate proto-karyotype. <i>Nature</i> , 2004, 431, 946-957.	13.7	1,801
2	The amphioxus genome and the evolution of the chordate karyotype. <i>Nature</i> , 2008, 453, 1064-1071.	13.7	1,496
3	Genome sequence of the metazoan plant-parasitic nematode <i>Meloidogyne incognita</i> . <i>Nature Biotechnology</i> , 2008, 26, 909-915.	9.4	1,012
4	The amphioxus genome illuminates vertebrate origins and cephalochordate biology. <i>Genome Research</i> , 2008, 18, 1100-1111.	2.4	456
5	The nuclear receptor superfamily. <i>Journal of Cell Science</i> , 2003, 116, 585-586.	1.2	424
6	Gene Loss and Evolutionary Rates Following Whole-Genome Duplication in Teleost Fishes. <i>Molecular Biology and Evolution</i> , 2006, 23, 1808-1816.	3.5	352
7	Evolutionary Genomics of Nuclear Receptors: From Twenty-Five Ancestral Genes to Derived Endocrine Systems. <i>Molecular Biology and Evolution</i> , 2004, 21, 1923-1937.	3.5	319
8	RRTree: Relative-Rate Tests between groups of sequences on a phylogenetic tree. <i>Bioinformatics</i> , 2000, 16, 296-297.	1.8	317
9	A benchmark of gene expression tissue-specificity metrics. <i>Briefings in Bioinformatics</i> , 2017, 18, bbw008.	3.2	302
10	Evidence for two distinct functional glucocorticoid receptors in teleost fish. <i>Journal of Molecular Endocrinology</i> , 2003, 31, 141-156.	1.1	220
11	Resolving the Ortholog Conjecture: Orthologs Tend to Be Weakly, but Significantly, More Similar in Function than Paralogs. <i>PLoS Computational Biology</i> , 2012, 8, e1002514.	1.5	217
12	How many nuclear hormone receptors are there in the human genome?. <i>Trends in Genetics</i> , 2001, 17, 554-556.	2.9	209
13	Euteleost Fish Genomes are Characterized by Expansion of Gene Families. <i>Genome Research</i> , 2001, 11, 781-788.	2.4	201
14	Evidence for Polygenic Adaptation to Pathogens in the Human Genome. <i>Molecular Biology and Evolution</i> , 2013, 30, 1544-1558.	3.5	181
15	Sensitivity of the relative-rate test to taxonomic sampling. <i>Molecular Biology and Evolution</i> , 1998, 15, 1091-1098.	3.5	180
16	How confident can we be that orthologs are similar, but paralogs differ?. <i>Trends in Genetics</i> , 2009, 25, 210-216.	2.9	156
17	One Billion Years of bZIP Transcription Factor Evolution: Conservation and Change in Dimerization and DNA-Binding Site Specificity. <i>Molecular Biology and Evolution</i> , 2006, 24, 827-835.	3.5	155
18	Patterns of Positive Selection in Seven Ant Genomes. <i>Molecular Biology and Evolution</i> , 2014, 31, 1661-1685.	3.5	138

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19	Bgee: Integrating and Comparing Heterogeneous Transcriptome Data Among Species. <i>Lecture Notes in Computer Science</i> , 2008, , 124-131.	1.0	137
20	Contribution of Electrostatic Interactions, Compactness and Quaternary Structure to Protein Thermostability: Lessons from Structural Genomics of <i>Thermotoga maritima</i> . <i>Journal of Molecular Biology</i> , 2006, 356, 547-557.	2.0	132
21	Characterization of oestrogen receptors in zebrafish ( <i>Danio rerio</i> ). <i>Journal of Molecular Endocrinology</i> , 2002, 28, 153-163.	1.1	124
22	Community-wide plasmid gene mobilization and selection. <i>ISME Journal</i> , 2013, 7, 1173-1186.	4.4	124
23	The Branch-Site Test of Positive Selection Is Surprisingly Robust but Lacks Power under Synonymous Substitution Saturation and Variation in GC. <i>Molecular Biology and Evolution</i> , 2013, 30, 1675-1686.	3.5	122
24	Unification of multi-species vertebrate anatomy ontologies for comparative biology in Uberon. <i>Journal of Biomedical Semantics</i> , 2014, 5, 21.	0.9	121
25	Low number of fixed somatic mutations in a long-lived oak tree. <i>Nature Plants</i> , 2017, 3, 926-929.	4.7	120
26	An ancestral whole-genome duplication may not have been responsible for the abundance of duplicated fish genes. <i>Current Biology</i> , 2001, 11, R458-R459.	1.8	112
27	The Bgee suite: integrated curated expression atlas and comparative transcriptomics in animals. <i>Nucleic Acids Research</i> , 2021, 49, D831-D847.	6.5	112
28	Big data and other challenges in the quest for orthologs. <i>Bioinformatics</i> , 2014, 30, 2993-2998.	1.8	109
29	Neofunctionalization in Vertebrates: The Example of Retinoic Acid Receptors. <i>PLoS Genetics</i> , 2006, 2, e102.	1.5	108
30	Explosive Lineage-Specific Expansion of the Orphan Nuclear Receptor HNF4 in Nematodes. <i>Journal of Molecular Evolution</i> , 2005, 60, 577-586.	0.8	100
31	Developmental Constraints on Vertebrate Genome Evolution. <i>PLoS Genetics</i> , 2008, 4, e1000311.	1.5	99
32	Molecular Phylogeny of Rodents, with Special Emphasis on Murids: Evidence from Nuclear Gene LCAT. <i>Molecular Phylogenetics and Evolution</i> , 1997, 8, 423-434.	1.2	88
33	A conserved retinoid X receptor (RXR) from the mollusk <i>Biomphalaria glabrata</i> transactivates transcription in the presence of retinoids. <i>Journal of Molecular Endocrinology</i> , 2005, 34, 567-582.	1.1	82
34	Evolutionary Rates of Duplicate Genes in Fish and Mammals. <i>Molecular Biology and Evolution</i> , 2001, 18, 681-683.	3.5	80
35	Rapid Divergence of the Ecdysone Receptor in Diptera and Lepidoptera Suggests Coevolution Between ECR and USP-RXR. <i>Molecular Biology and Evolution</i> , 2003, 20, 541-553.	3.5	73
36	Pervasive positive selection on duplicated and nonduplicated vertebrate protein coding genes. <i>Genome Research</i> , 2008, 18, 1393-1402.	2.4	73

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37	The Hourglass and the Early Conservation Modelsâ€™ Co-Existing Patterns of Developmental Constraints in Vertebrates. <i>PLoS Genetics</i> , 2013, 9, e1003476.	1.5	73
38	Phylogenetic Dating and Characterization of Gene Duplications in Vertebrates: The Cartilaginous Fish Reference. <i>Molecular Biology and Evolution</i> , 2004, 21, 580-586.	3.5	70
39	Tissue-Specificity of Gene Expression Diverges Slowly between Orthologs, and Rapidly between Paralogs. <i>PLoS Computational Biology</i> , 2016, 12, e1005274.	1.5	66
40	Selectome update: quality control and computational improvements to a database of positive selection. <i>Nucleic Acids Research</i> , 2014, 42, D917-D921.	6.5	65
41	The SIB Swiss Institute of Bioinformaticsâ€™™ resources: focus on curated databases. <i>Nucleic Acids Research</i> , 2016, 44, D27-D37.	6.5	64
42	Bayesian association scan reveals loci associated with human lifespan and linked biomarkers. <i>Nature Communications</i> , 2017, 8, 15842.	5.8	64
43	When orthologs diverge between human and mouse. <i>Briefings in Bioinformatics</i> , 2011, 12, 436-441.	3.2	63
44	What to compare and how: Comparative transcriptomics for Evoâ€™Devo. <i>Journal of Experimental Zoology Part B: Molecular and Developmental Evolution</i> , 2015, 324, 372-382.	0.6	63
45	Structural Genomics of <i>Thermotoga maritima</i> Proteins Shows that Contact Order Is a Major Determinant of Protein Thermostability. <i>Structure</i> , 2005, 13, 857-860.	1.6	58
46	Genomic Features of Parthenogenetic Animals. <i>Journal of Heredity</i> , 2021, 112, 19-33.	1.0	55
47	Molecular Evidence for a Functional Ecdysone Signaling System in <i>Brugia malayi</i> . <i>PLoS Neglected Tropical Diseases</i> , 2010, 4, e625.	1.3	52
48	Comparative genome analysis of <i>Pseudomonas knackmussii</i> â€™... <i>B</i> 13, the first bacterium known to degrade chloroaromatic compounds. <i>Environmental Microbiology</i> , 2015, 17, 91-104.	1.8	52
49	Interactome Mapping of the Phosphatidylinositol 3-Kinase-Mammalian Target of Rapamycin Pathway Identifies Deformed Epidermal Autoregulatory Factor-1 as a New Glycogen Synthase Kinase-3 Interactor. <i>Molecular and Cellular Proteomics</i> , 2010, 9, 1578-1593.	2.5	51
50	Age-dependent gain of alternative splice forms and biased duplication explain the relation between splicing and duplication. <i>Genome Research</i> , 2011, 21, 357-363.	2.4	50
51	Comparative analysis of human and mouse expression data illuminates tissue-specific evolutionary patterns of miRNAs. <i>Nucleic Acids Research</i> , 2012, 40, 5890-5900.	6.5	48
52	Detection of Pathways Affected by Positive Selection in Primate Lineages Ancestral to Humans. <i>Molecular Biology and Evolution</i> , 2017, 34, 1391-1402.	3.5	47
53	Structural and Evolutionary Innovation of the Heterodimerization Interface between USP and the Ecdysone Receptor ECR in Insects. <i>Molecular Biology and Evolution</i> , 2009, 26, 753-768.	3.5	45
54	How much does the amphioxus genome represent the ancestor of chordates?. <i>Briefings in Functional Genomics</i> , 2012, 11, 89-95.	1.3	45

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55	Genomic changes underlying host specialization in the bee gut symbiont <i>Lactobacillus Firm5</i> . <i>Molecular Ecology</i> , 2019, 28, 2224-2237.	2.0	45
56	Selective Constraints on Coding Sequences of Nervous System Genes Are a Major Determinant of Duplicate Gene Retention in Vertebrates. <i>Molecular Biology and Evolution</i> , 2017, 34, 2773-2791.	3.5	43
57	Tissue-Specific Evolution of Protein Coding Genes in Human and Mouse. <i>PLoS ONE</i> , 2015, 10, e0131673.	1.1	40
58	NUREBASE: database of nuclear hormone receptors. <i>Nucleic Acids Research</i> , 2002, 30, 364-368.	6.5	39
59	Evolution of the epithelial sodium channel and the sodium pump as limiting factors of aldosterone action on sodium transport. <i>Physiological Genomics</i> , 2011, 43, 844-854.	1.0	39
60	A protein interaction atlas for the nuclear receptors: properties and quality of a hub-based dimerisation network. <i>BMC Systems Biology</i> , 2007, 1, 34.	3.0	38
61	Selectome: a database of positive selection. <i>Nucleic Acids Research</i> , 2009, 37, D404-D407.	6.5	38
62	The Confidence Information Ontology: a step towards a standard for asserting confidence in annotations. <i>Database: the Journal of Biological Databases and Curation</i> , 2015, 2015, bav043-bav043.	1.4	37
63	Gearing up to handle the mosaic nature of life in the quest for orthologs. <i>Bioinformatics</i> , 2018, 34, 323-329.	1.8	36
64	Identifying gene function and module connections by the integration of multispecies expression compendia. <i>Genome Research</i> , 2019, 29, 2034-2045.	2.4	36
65	Molecular signaling in zebrafish development and the vertebrate phylotypic period. <i>Evolution &amp; Development</i> , 2010, 12, 144-156.	1.1	33
66	Conceptual framework and pilot study to benchmark phylogenomic databases based on reference gene trees. <i>Briefings in Bioinformatics</i> , 2011, 12, 423-435.	3.2	33
67	Fast Evolution of Interleukin-2 in Mammals and Positive Selection in Ruminants. <i>Journal of Molecular Evolution</i> , 2000, 51, 234-244.	0.8	32
68	Nuclear receptors are markers of animal genome evolution. <i>Journal of Structural and Functional Genomics</i> , 2003, 3, 177-184.	1.2	32
69	Sequencing and characterizing the genome of <i>Estrella lausannensis</i> as an undergraduate project: training students and biological insights. <i>Frontiers in Microbiology</i> , 2015, 6, 101.	1.5	32
70	Evolution of isochores in rodents. <i>Molecular Biology and Evolution</i> , 1997, 14, 823-828.	3.5	31
71	OncoMX: A Knowledgebase for Exploring Cancer Biomarkers in the Context of Related Cancer and Healthy Data. <i>JCO Clinical Cancer Informatics</i> , 2020, 4, 210-220.	1.0	30
72	Large-Scale Comparative Analysis of Codon Models Accounting for Protein and Nucleotide Selection. <i>Molecular Biology and Evolution</i> , 2019, 36, 1316-1332.	3.5	28

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73	Methods detecting rhythmic gene expression are biologically relevant only for strong signal. <i>PLoS Computational Biology</i> , 2020, 16, e1007666.	1.5	28
74	Inventing a Sex-Specific Gene: A Conserved Role of DMRT1 in Teleost Fishes Plus a Recent Duplication in the Medaka <i>Oryzias latipes</i> Resulted in DMY. <i>Journal of Molecular Evolution</i> , 2003, 57, S148-S153.	0.8	27
75	Genomic signatures accompanying the dietary shift to phytophagy in polyphagan beetles. <i>Genome Biology</i> , 2019, 20, 98.	3.8	27
76	BgeeDB, an R package for retrieval of curated expression datasets and for gene list expression localization enrichment tests. <i>F1000Research</i> , 2016, 5, 2748.	0.8	27
77	Convergent consequences of parthenogenesis on stick insect genomes. <i>Science Advances</i> , 2022, 8, eabg3842.	4.7	27
78	Meta-analysis of estrogen response in MCF-7 distinguishes early target genes involved in signaling and cell proliferation from later target genes involved in cell cycle and DNA repair. <i>BMC Systems Biology</i> , 2011, 5, 138.	3.0	26
79	Repeated Evolution of Asexuality Involves Convergent Gene Expression Changes. <i>Molecular Biology and Evolution</i> , 2019, 36, 350-364.	3.5	26
80	Optimization strategies for fast detection of positive selection on phylogenetic trees. <i>Bioinformatics</i> , 2014, 30, 1129-1137.	1.8	24
81	The Genome of the Toluene-Degrading <i>Pseudomonas veronii</i> Strain 1YdBTEX2 and Its Differential Gene Expression in Contaminated Sand. <i>PLoS ONE</i> , 2016, 11, e0165850.	1.1	24
82	Update of NUREBASE: nuclear hormone receptor functional genomics. <i>Nucleic Acids Research</i> , 2004, 32, 165D-167.	6.5	23
83	Developmental Constraints on Genome Evolution in Four Bilaterian Model Species. <i>Genome Biology and Evolution</i> , 2018, 10, 2266-2277.	1.1	23
84	Enabling semantic queries across federated bioinformatics databases. <i>Database: the Journal of Biological Databases and Curation</i> , 2019, 2019, .	1.4	23
85	Inter-embryo gene expression variability recapitulates the hourglass pattern of evo-devo. <i>BMC Biology</i> , 2020, 18, 129.	1.7	23
86	Haplotype divergence supports long-term asexuality in the oribatid mite <i>Oppiella nova</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	3.3	23
87	BgeeDB, an R package for retrieval of curated expression datasets and for gene list expression localization enrichment tests. <i>F1000Research</i> , 2016, 5, 2748.	0.8	23
88	Sex-biased gene expression is repeatedly masculinized in asexual females. <i>Nature Communications</i> , 2019, 10, 4638.	5.8	21
89	JaDis: computing distances between nucleic acid sequences. <i>Bioinformatics</i> , 1999, 15, 424-425.	1.8	20
90	Homolonto: generating homology relationships by pairwise alignment of ontologies and application to vertebrate anatomy. <i>Bioinformatics</i> , 2010, 26, 1766-1771.	1.8	20

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91	Detecting patterns of species diversification in the presence of both rate shifts and mass extinctions. <i>BMC Evolutionary Biology</i> , 2015, 15, 157.	3.2	20
92	Robust inference of positive selection on regulatory sequences in the human brain. <i>Science Advances</i> , 2020, 6, .	4.7	20
93	vHOG, a multispecies vertebrate ontology of homologous organs groups. <i>Bioinformatics</i> , 2012, 28, 1017-1020.	1.8	19
94	Correcting for the bias due to expression specificity improves the estimation of constrained evolution of expression between mouse and human. <i>Bioinformatics</i> , 2012, 28, 1865-1872.	1.8	19
95	Large-Scale Analysis of Orthologs and Paralogs under Covarion-Like and Constant-but-Different Models of Amino Acid Evolution. <i>Molecular Biology and Evolution</i> , 2010, 27, 2618-2627.	3.5	17
96	Evidence for an episodic model of protein sequence evolution. <i>Biochemical Society Transactions</i> , 2009, 37, 783-786.	1.6	16
97	Nuclear receptors are markers of animal genome evolution. <i>Journal of Structural and Functional Genomics</i> , 2003, 3, 177-84.	1.2	16
98	An ontology to clarify homology-related concepts. <i>Trends in Genetics</i> , 2010, 26, 99-102.	2.9	15
99	IQRray, a new method for Affymetrix microarray quality control, and the homologous organ conservation score, a new benchmark method for quality control metrics. <i>Bioinformatics</i> , 2014, 30, 1392-1399.	1.8	15
100	Sex differentiation in grayling ( <i>Salmonidae</i> ) goes through an all-male stage and is delayed in genetic males who instead grow faster. <i>Scientific Reports</i> , 2017, 7, 15024.	1.6	15
101	Adaptive Evolution of Animal Proteins over Development: Support for the Darwin Selection Opportunity Hypothesis of Evo-Devo. <i>Molecular Biology and Evolution</i> , 2018, 35, 2862-2872.	3.5	15
102	Convergent evolution of venom gland transcriptomes across Metazoa. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022, 119, .	3.3	15
103	Orthologues of the <i>Drosophila melanogaster</i> E75 molting control gene in the filarial parasites <i>Brugia malayi</i> and <i>Dirofilaria immitis</i> . <i>Molecular and Biochemical Parasitology</i> , 2008, 157, 92-97.	0.5	14
104	The challenge of modeling nuclear receptor regulatory networks in mammalian cells. <i>Molecular and Cellular Endocrinology</i> , 2011, 334, 91-97.	1.6	14
105	Uncovering hidden duplicated content in public transcriptomics data. <i>Database: the Journal of Biological Databases and Curation</i> , 2013, 2013, bat010.	1.4	14
106	Quality Matters: Biocuration Experts on the Impact of Duplication and Other Data Quality Issues in Biological Databases. <i>Genomics, Proteomics and Bioinformatics</i> , 2020, 18, 91-103.	3.0	14
107	Dynamics of sex-biased gene expression during development in the stick insect <i>Timema californicum</i> . <i>Heredity</i> , 2022, 129, 113-122.	1.2	14
108	Inference of Evolutionary Forces Acting on Human Biological Pathways. <i>Genome Biology and Evolution</i> , 2015, 7, 1546-1558.	1.1	13

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109	An ancient truncated duplication of the anti-allergic hormone receptor type 2 gene is a potential conserved master sex determinant in the Pangasiidae catfish family. <i>Molecular Ecology Resources</i> , 2022, 22, 2411-2428.	2.2	13
110	Nuclear Gene LCAT Supports Rodent Monophyly. <i>Molecular Biology and Evolution</i> , 2000, 17, 1410-1412.	3.5	12
111	SlimCodeML: An Optimized Version of CodeML for the Branch-Site Model. , 2012, , .		12
112	Sex-specific changes in gene expression in response to estrogen pollution around the onset of sex differentiation in grayling ( <i>Salmonidae</i> ). <i>BMC Genomics</i> , 2019, 20, 583.	1.2	11
113	Cross-species functional modules link proteostasis to human normal aging. <i>PLoS Computational Biology</i> , 2019, 15, e1007162.	1.5	11
114	No evidence for the radiation time lag model after whole genome duplications in Teleostei. <i>PLoS ONE</i> , 2017, 12, e0176384.	1.1	11
115	Impact of changes in GC content on the silent molecular clock in murids. <i>Gene</i> , 1997, 205, 317-322.	1.0	9
116	Bioinformatics of Nuclear Receptors. <i>Methods in Enzymology</i> , 2003, 364, 93-118.	0.4	9
117	Comparative modular analysis of gene expression in vertebrate organs. <i>BMC Genomics</i> , 2012, 13, 124.	1.2	9
118	Single-cell transcriptomics allows novel insights into aging and circadian processes. <i>Briefings in Functional Genomics</i> , 2020, 19, 343-349.	1.3	9
119	First annotated draft genomes of nonmarine ostracods ( <i>Ostracoda</i> , <i>Crustacea</i> ) with different reproductive modes. <i>G3: Genes, Genomes, Genetics</i> , 2021, 11, .	0.8	9
120	The hourglass model of evolutionary conservation during embryogenesis extends to developmental enhancers with signatures of positive selection. <i>Genome Research</i> , 2021, 31, 1573-1581.	2.4	9
121	Special Care Is Needed in Applying Phylogenetic Comparative Methods to Gene Trees with Speciation and Duplication Nodes. <i>Molecular Biology and Evolution</i> , 2021, 38, 1614-1626.	3.5	8
122	Re: Revisiting recent challenges to the ancient fish-specific genome duplication hypothesis. <i>Current Biology</i> , 2001, 11, R1007-R1008.	1.8	7
123	State aggregation for fast likelihood computations in molecular evolution. <i>Bioinformatics</i> , 2017, 33, 354-362.	1.8	7
124	The expansion of amino-acid repeats is not associated to adaptive evolution in mammalian genes. <i>BMC Genomics</i> , 2009, 10, 619.	1.2	6
125	OMAmer: tree-driven and alignment-free protein assignment to subfamilies outperforms closest sequence approaches. <i>Bioinformatics</i> , 2021, 37, 2866-2873.	1.8	5
126	gcodeml: a Grid-enabled tool for detecting positive selection in biological evolution. <i>Studies in Health Technology and Informatics</i> , 2012, 175, 59-68.	0.2	5



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127	USAGE OPTIMIZATION OF UNEVENLY SAMPLED DATA THROUGH THE COMBINATION OF QUARTET TREES: A EUTHERIAN DRAFT PHYLOGENY BASED ON 640 NUCLEAR AND MITOCHONDRIAL PROTEINS. Israel Journal of Zoology, 2001, 47, 259-270.	0.2	4
128	Molecular evolution of angrogen receptors in fish. Fish Physiology and Biochemistry, 2003, 28, 207-208.	0.9	4
129	Bio-SODA: Enabling Natural Language Question Answering over Knowledge Graphs without Training Data. , 2021, , .		4
130	Performance of a phylogenetic independent contrast method and an improved pairwise comparison under different scenarios of trait evolution after speciation and duplication. Methods in Ecology and Evolution, 2021, 12, 1875-1887.	2.2	4
131	Large-Scale Analyses of Positive Selection Using Codon Models. , 2009, , 217-235.		3
132	Determinants of protein evolutionary rates in light of ENCODE functional genomics. BMC Bioinformatics, 2014, 15, .	1.2	2
133	Nuclear receptors are markers of animal genome evolution. , 2003, , 177-184.		2
134	Perspective: From molecular endocrinology of mouse to genomic endocrinology of animals. Molecular and Cellular Endocrinology, 2008, 293, 2-4.	1.6	1
135	DATABASE, The Journal of Biological Databases and Curation, is now the official journal of the International Society for Biocuration. Database: the Journal of Biological Databases and Curation, 2013, 2013, bat077-bat077.	1.4	1
136	Phylogenetic code in the cloud - can it meet the expectations?. Studies in Health Technology and Informatics, 2010, 159, 55-63.	0.2	1
137	Bio-SODA UX: enabling natural language question answering over knowledge graphs with user disambiguation. Distributed and Parallel Databases, 0, , .	1.0	1
138	Bioinformatics for Evolutionary Developmental Biology. , 2009, , 355-378.		0
139	Genomics is changing Evo&#x2013;Devo. Journal of Experimental Zoology Part B: Molecular and Developmental Evolution, 2015, 324, 315-315.	0.6	0
140	Combining molecular information on chromatin organisation with eQTLs and evolutionary conservation provides strong candidates for the evolution of gene regulation in mammalian brains. Peer Community in Evolutionary Biology, 2018, , 100035.	0.0	0
141	Methods detecting rhythmic gene expression are biologically relevant only for strong signal. , 2020, 16, e1007666.		0
142	Methods detecting rhythmic gene expression are biologically relevant only for strong signal. , 2020, 16, e1007666.		0
143	Methods detecting rhythmic gene expression are biologically relevant only for strong signal. , 2020, 16, e1007666.		0
144	Methods detecting rhythmic gene expression are biologically relevant only for strong signal. , 2020, 16, e1007666.		0

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145	Methods detecting rhythmic gene expression are biologically relevant only for strong signal. , 2020, 16, e1007666.		0
146	Methods detecting rhythmic gene expression are biologically relevant only for strong signal. , 2020, 16, e1007666.		0