

Marc Robinson-Rechavi

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144
papers

9,946
citations

42
h-index

98
g-index

185
ext. papers

11,582
ext. citations

7.9
avg, IF

5.98
L-index

#	Paper	IF	Citations
144	Genome duplication in the teleost fish <i>Tetraodon nigroviridis</i> reveals the early vertebrate proto-karyotype. <i>Nature</i> , 2004 , 431, 946-57	50.4	1543
143	The amphioxus genome and the evolution of the chordate karyotype. <i>Nature</i> , 2008 , 453, 1064-71	50.4	1266
142	Genome sequence of the metazoan plant-parasitic nematode <i>Meloidogyne incognita</i> . <i>Nature Biotechnology</i> , 2008 , 26, 909-15	44.5	790
141	The amphioxus genome illuminates vertebrate origins and cephalochordate biology. <i>Genome Research</i> , 2008 , 18, 1100-11	9.7	387
140	The nuclear receptor superfamily. <i>Journal of Cell Science</i> , 2003 , 116, 585-6	5.3	344
139	RRTree: relative-rate tests between groups of sequences on a phylogenetic tree. <i>Bioinformatics</i> , 2000 , 16, 296-7	7.2	305
138	Gene loss and evolutionary rates following whole-genome duplication in teleost fishes. <i>Molecular Biology and Evolution</i> , 2006 , 23, 1808-16	8.3	302
137	Evolutionary genomics of nuclear receptors: from twenty-five ancestral genes to derived endocrine systems. <i>Molecular Biology and Evolution</i> , 2004 , 21, 1923-37	8.3	266
136	Evidence for two distinct functional glucocorticoid receptors in teleost fish. <i>Journal of Molecular Endocrinology</i> , 2003 , 31, 141-56	4.5	193
135	How many nuclear hormone receptors are there in the human genome?. <i>Trends in Genetics</i> , 2001 , 17, 554-6	8.5	179
134	Euteleost fish genomes are characterized by expansion of gene families. <i>Genome Research</i> , 2001 , 11, 781-8	9.7	172
133	Sensitivity of the relative-rate test to taxonomic sampling. <i>Molecular Biology and Evolution</i> , 1998 , 15, 1091-8	8.3	170
132	A benchmark of gene expression tissue-specificity metrics. <i>Briefings in Bioinformatics</i> , 2017 , 18, 205-214	13.4	153
131	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	5	136
130	Evidence for polygenic adaptation to pathogens in the human genome. <i>Molecular Biology and Evolution</i> , 2013 , 30, 1544-58	8.3	132
129	How confident can we be that orthologs are similar, but paralogs differ?. <i>Trends in Genetics</i> , 2009 , 25, 210-6	8.5	124
128	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, 547-57	6.5	117

127	Characterization of oestrogen receptors in zebrafish (<i>Danio rerio</i>). <i>Journal of Molecular Endocrinology</i> , 2002 , 28, 153-63	4.5	116
126	One billion years of bZIP transcription factor evolution: conservation and change in dimerization and DNA-binding site specificity. <i>Molecular Biology and Evolution</i> , 2007 , 24, 827-35	8.3	111
125	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, 1675-86	8.3	103
124	Bgee: Integrating and Comparing Heterogeneous Transcriptome Data Among Species. <i>Lecture Notes in Computer Science</i> , 2008 , 124-131	0.9	103
123	Patterns of positive selection in seven ant genomes. <i>Molecular Biology and Evolution</i> , 2014 , 31, 1661-85	8.3	101
122	Community-wide plasmid gene mobilization and selection. <i>ISME Journal</i> , 2013 , 7, 1173-86	11.9	96
121	An ancestral whole-genome duplication may not have been responsible for the abundance of duplicated fish genes. <i>Current Biology</i> , 2001 , 11, R458-9	6.3	93
120	Neofunctionalization in vertebrates: the example of retinoic acid receptors. <i>PLoS Genetics</i> , 2006 , 2, e1026		90
119	Explosive lineage-specific expansion of the orphan nuclear receptor HNF4 in nematodes. <i>Journal of Molecular Evolution</i> , 2005 , 60, 577-86	3.1	90
118	Developmental constraints on vertebrate genome evolution. <i>PLoS Genetics</i> , 2008 , 4, e1000311	6	84
117	Unification of multi-species vertebrate anatomy ontologies for comparative biology in Uberon. <i>Journal of Biomedical Semantics</i> , 2014 , 5, 21	2.2	80
116	Molecular phylogeny of rodents, with special emphasis on murids: evidence from nuclear gene LCAT. <i>Molecular Phylogenetics and Evolution</i> , 1997 , 8, 423-34	4.1	78
115	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, 567-82	4.5	76
114	Low number of fixed somatic mutations in a long-lived oak tree. <i>Nature Plants</i> , 2017 , 3, 926-929	11.5	74
113	Evolutionary rates of duplicate genes in fish and mammals. <i>Molecular Biology and Evolution</i> , 2001 , 18, 681-3	8.3	73
112	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, 541-53	8.3	69
111	Pervasive positive selection on duplicated and nonduplicated vertebrate protein coding genes. <i>Genome Research</i> , 2008 , 18, 1393-402	9.7	64
110	Phylogenetic dating and characterization of gene duplications in vertebrates: the cartilaginous fish reference. <i>Molecular Biology and Evolution</i> , 2004 , 21, 580-6	8.3	58

109	The hourglass and the early conservation models--co-existing patterns of developmental constraints in vertebrates. <i>PLoS Genetics</i> , 2013 , 9, e1003476	6	51
108	When orthologs diverge between human and mouse. <i>Briefings in Bioinformatics</i> , 2011 , 12, 436-41	13.4	50
107	Structural genomics of thermotoga maritima proteins shows that contact order is a major determinant of protein thermostability. <i>Structure</i> , 2005 , 13, 857-60	5.2	49
106	Selectome update: quality control and computational improvements to a database of positive selection. <i>Nucleic Acids Research</i> , 2014 , 42, D917-21	20.1	45
105	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, 1578-93	7.6	43
104	What to compare and how: Comparative transcriptomics for Evo-Devo. <i>Journal of Experimental Zoology Part B: Molecular and Developmental Evolution</i> , 2015 , 324, 372-82	1.8	42
103	Molecular evidence for a functional ecdysone signaling system in <i>Brugia malayi</i> . <i>PLoS Neglected Tropical Diseases</i> , 2010 , 4, e625	4.8	42
102	Age-dependent gain of alternative splice forms and biased duplication explain the relation between splicing and duplication. <i>Genome Research</i> , 2011 , 21, 357-63	9.7	42
101	Comparative analysis of human and mouse expression data illuminates tissue-specific evolutionary patterns of miRNAs. <i>Nucleic Acids Research</i> , 2012 , 40, 5890-900	20.1	42
100	The SIB Swiss Institute of Bioinformatics Resources: focus on curated databases. <i>Nucleic Acids Research</i> , 2016 , 44, D27-37	20.1	41
99	How much does the amphioxus genome represent the ancestor of chordates?. <i>Briefings in Functional Genomics</i> , 2012 , 11, 89-95	4.9	40
98	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, 753-68	8.3	40
97	Bayesian association scan reveals loci associated with human lifespan and linked biomarkers. <i>Nature Communications</i> , 2017 , 8, 15842	17.4	39
96	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, 844-54	3.6	35
95	Tissue-Specificity of Gene Expression Diverges Slowly between Orthologs, and Rapidly between Paralogs. <i>PLoS Computational Biology</i> , 2016 , 12, e1005274	5	35
94	Detection of Pathways Affected by Positive Selection in Primate Lineages Ancestral to Humans. <i>Molecular Biology and Evolution</i> , 2017 , 34, 1391-1402	8.3	33
93	Selectome: a database of positive selection. <i>Nucleic Acids Research</i> , 2009 , 37, D404-7	20.1	32
92	Comparative genome analysis of <i>Pseudomonas knackmussii</i> B13, the first bacterium known to degrade chloroaromatic compounds. <i>Environmental Microbiology</i> , 2015 , 17, 91-104	5.2	30

91	NUREBASE: database of nuclear hormone receptors. <i>Nucleic Acids Research</i> , 2002 , 30, 364-8	20.1	30
90	Nuclear receptors are markers of animal genome evolution. <i>Journal of Structural and Functional Genomics</i> , 2003 , 3, 177-184		28
89	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	5	27
88	Conceptual framework and pilot study to benchmark phylogenomic databases based on reference gene trees. <i>Briefings in Bioinformatics</i> , 2011 , 12, 423-35	13.4	27
87	Evolution of isochores in rodents. <i>Molecular Biology and Evolution</i> , 1997 , 14, 823-8	8.3	27
86	Fast evolution of interleukin-2 in mammals and positive selection in ruminants. <i>Journal of Molecular Evolution</i> , 2000 , 51, 234-44	3.1	26
85	Tissue-Specific Evolution of Protein Coding Genes in Human and Mouse. <i>PLoS ONE</i> , 2015 , 10, e0131673	3.7	26
84	The Bgee suite: integrated curated expression atlas and comparative transcriptomics in animals. <i>Nucleic Acids Research</i> , 2021 , 49, D831-D847	20.1	26
83	Molecular signaling in zebrafish development and the vertebrate phylotypic period. <i>Evolution & Development</i> , 2010 , 12, 144-56	2.6	25
82	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	3.5	25
81	Gearing up to handle the mosaic nature of life in the quest for orthologs. <i>Bioinformatics</i> , 2018 , 34, 323-329		25
80	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	8.3	24
79	Update of NUREBASE: nuclear hormone receptor functional genomics. <i>Nucleic Acids Research</i> , 2004 , 32, D165-7	20.1	23
78	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 Suppl 1, S148-53 ^{3.1}		23
77	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	5.7	21
76	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	3.5	21
75	JaDis: computing distances between nucleic acid sequences. <i>Bioinformatics</i> , 1999 , 15, 424-5	7.2	20
74	BgeeDB, an R package for retrieval of curated expression datasets and for gene list expression localization enrichment tests. <i>F1000Research</i> , 2016 , 5, 2748	3.6	20

73	Genomic signatures accompanying the dietary shift to phytophagy in polyphagan beetles. <i>Genome Biology</i> , 2019 , 20, 98	18.3	18
72	Genomic changes underlying host specialization in the bee gut symbiont <i>Lactobacillus Firm5</i> . <i>Molecular Ecology</i> , 2019 , 28, 2224-2237	5.7	18
71	Optimization strategies for fast detection of positive selection on phylogenetic trees. <i>Bioinformatics</i> , 2014 , 30, 1129-1137	7.2	18
70	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, 2618-27	8.3	17
69	BgeeDB, an R package for retrieval of curated expression datasets and for gene list expression localization enrichment tests. <i>F1000Research</i> , 2016 , 5, 2748	3.6	17
68	Genomic Features of Parthenogenetic Animals. <i>Journal of Heredity</i> , 2021 , 112, 19-33	2.4	17
67	Homolonto: generating homology relationships by pairwise alignment of ontologies and application to vertebrate anatomy. <i>Bioinformatics</i> , 2010 , 26, 1766-71	7.2	16
66	vHOG, a multispecies vertebrate ontology of homologous organs groups. <i>Bioinformatics</i> , 2012 , 28, 1017-20	7.2	16
65	Large-Scale Comparative Analysis of Codon Models Accounting for Protein and Nucleotide Selection. <i>Molecular Biology and Evolution</i> , 2019 , 36, 1316-1332	8.3	15
64	Uncovering hidden duplicated content in public transcriptomics data. <i>Database: the Journal of Biological Databases and Curation</i> , 2013 , 2013, bat010	5	14
63	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, 1865-72	7.2	14
62	Evidence for an episodic model of protein sequence evolution. <i>Biochemical Society Transactions</i> , 2009 , 37, 783-6	5.1	14
61	Nuclear receptors are markers of animal genome evolution. <i>Journal of Structural and Functional Genomics</i> , 2003 , 3, 177-84		14
60	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	5.2	13
59	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	3.7	13
58	Inference of Evolutionary Forces Acting on Human Biological Pathways. <i>Genome Biology and Evolution</i> , 2015 , 7, 1546-58	3.9	12
57	Detecting patterns of species diversification in the presence of both rate shifts and mass extinctions. <i>BMC Evolutionary Biology</i> , 2015 , 15, 157	3	12
56	An ontology to clarify homology-related concepts. <i>Trends in Genetics</i> , 2010 , 26, 99-102	8.5	12

55	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, 92-7	1.9	12
54	Nuclear gene LCAT supports rodent monophyly. <i>Molecular Biology and Evolution</i> , 2000 , 17, 1410-2	8.3	12
53	Enabling semantic queries across federated bioinformatics databases. <i>Database: the Journal of Biological Databases and Curation</i> , 2019 , 2019,	5	12
52	Repeated Evolution of Asexuality Involves Convergent Gene Expression Changes. <i>Molecular Biology and Evolution</i> , 2019 , 36, 350-364	8.3	11
51	Developmental Constraints on Genome Evolution in Four Bilaterian Model Species. <i>Genome Biology and Evolution</i> , 2018 , 10, 2266-2277	3.9	11
50	The challenge of modeling nuclear receptor regulatory networks in mammalian cells. <i>Molecular and Cellular Endocrinology</i> , 2011 , 334, 91-7	4.4	11
49	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	8.3	11
48	Sex differentiation in grayling (Salmonidae) goes through an all-male stage and is delayed in genetic males who instead grow faster. <i>Scientific Reports</i> , 2017 , 7, 15024	4.9	10
47	Identifying gene function and module connections by the integration of multispecies expression compendia. <i>Genome Research</i> , 2019 , 29, 2034-2045	9.7	10
46	Cross-species functional modules link proteostasis to human normal aging. <i>PLoS Computational Biology</i> , 2019 , 15, e1007162	5	9
45	No evidence for the radiation time lag model after whole genome duplications in Teleostei. <i>PLoS ONE</i> , 2017 , 12, e0176384	3.7	9
44	Methods detecting rhythmic gene expression are biologically relevant only for strong signal. <i>PLoS Computational Biology</i> , 2020 , 16, e1007666	5	8
43	Sex-biased gene expression is repeatedly masculinized in asexual females. <i>Nature Communications</i> , 2019 , 10, 4638	17.4	8
42	IQRay, 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, 1392-1392	7.2	7
41	SlimCodeML: An Optimized Version of CodeML for the Branch-Site Model 2012 ,		7
40	Impact of changes in GC content on the silent molecular clock in murids. <i>Gene</i> , 1997 , 205, 317-22	3.8	7
39	Re: Revisiting recent challenges to the ancient fish-specific genome duplication hypothesis. <i>Current Biology</i> , 2001 , 11, R1007-R1008	6.3	7
38	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	6.5	7

37	Robust inference of positive selection on regulatory sequences in the human brain. <i>Science Advances</i> , 2020 , 6,	14.3	7
36	Inter-embryo gene expression variability recapitulates the hourglass pattern of evo-devo. <i>BMC Biology</i> , 2020 , 18, 129	7.3	7
35	Comparative modular analysis of gene expression in vertebrate organs. <i>BMC Genomics</i> , 2012 , 13, 124	4.5	6
34	Single-cell transcriptomics allows novel insights into aging and circadian processes. <i>Briefings in Functional Genomics</i> , 2020 , 19, 343-349	4.9	5
33	The expansion of amino-acid repeats is not associated to adaptive evolution in mammalian genes. <i>BMC Genomics</i> , 2009 , 10, 619	4.5	5
32	gcodeml: a Grid-enabled tool for detecting positive selection in biological evolution. <i>Studies in Health Technology and Informatics</i> , 2012 , 175, 59-68	0.5	5
31	Sex-specific changes in gene expression in response to estrogen pollution around the onset of sex differentiation in grayling (Salmonidae). <i>BMC Genomics</i> , 2019 , 20, 583	4.5	4
30	Molecular evolution of angrogen receptors in fish. <i>Fish Physiology and Biochemistry</i> , 2003 , 28, 207-208	2.7	4
29	Bioinformatics of Nuclear Receptors. <i>Methods in Enzymology</i> , 2003 , 364, 93-118	1.7	4
28	The Bgee suite: integrated curated expression atlas and comparative transcriptomics in animals		4
27	USAGE OPTIMIZATION OF UNEVENLY SAMPLED DATA THROUGH THE COMBINATION OF QUARTET TREES: A EUTHERIAN DRAFT PHYLOGENY BASED ON 640 NUCLEAR AND MITOCHONDRIAL PROTEINS. <i>Israel Journal of Zoology</i> , 2001 , 47, 259-270		3
26	Large-Scale Analyses of Positive Selection Using Codon Models 2009 , 217-235		3
25	State aggregation for fast likelihood computations in molecular evolution. <i>Bioinformatics</i> , 2017 , 33, 354-362	7.62	3
24	First annotated draft genomes of nonmarine ostracods (Ostracoda, Crustacea) with different reproductive modes. <i>G3: Genes, Genomes, Genetics</i> , 2021 , 11,	3.2	3
23	Convergent consequences of parthenogenesis on stick insect genomes.. <i>Science Advances</i> , 2022 , 8, eabg1142	14.3	3
22	Determinants of protein evolutionary rates in light of ENCODE functional genomics. <i>BMC Bioinformatics</i> , 2014 , 15,	3.6	2
21	Sex-specific changes in gene expression and delayed sex differentiation in response to estrogen pollution in grayling (Salmonidae)		2
20	Convergent consequences of parthenogenesis on stick insect genomes		2

19	Quality Matters: Biocuration Experts on the Impact of Duplication and Other Data Quality Issues in Biological Databases		2
18	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	9.7	2
17	Haplotype divergence supports long-term asexuality in the oribatid mite. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021 , 118,	11.5	2
16	An ancient truncated duplication of the anti-Mullerian hormone receptor type 2 gene is a potential conserved master sex determinant in the Pangasiidae catfish family.. <i>Molecular Ecology Resources</i> , 2022 ,	8.4	2
15	Perspective: from molecular endocrinology of mouse to genomic endocrinology of animals. <i>Molecular and Cellular Endocrinology</i> , 2008 , 293, 2-4	4.4	1
14	Robust inference of positive selection on regulatory sequences in human brain		1
13	Genomic features of parthenogenetic animals		1
12	Identifying gene function and module connections by the integration of multi-species expression compendia		1
11	Enabling Semantic Queries Across Federated Bioinformatics Databases		1
10	Selection against expression noise explains the origin of the hourglass pattern of Evo-Devo		1
9	Tissue-specificity of gene expression diverges slowly between orthologs, and rapidly between paralogs		1
8	Selective constraints on coding sequences of nervous system genes are a major determinant of duplicate gene retention in vertebrates		1
7	The hourglass model of evolutionary conservation during embryogenesis extends to developmental enhancers with signatures of positive selection		1
6	Sex-biased gene expression is masculinized in asexual females		1
5	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	8.3	1
4	Phylogenetic code in the cloud - can it meet the expectations?. <i>Studies in Health Technology and Informatics</i> , 2010 , 159, 55-63	0.5	1
3	Nuclear receptors are markers of animal genome evolution 2003 , 177-184		0
2	Performance of a phylogenetic independent contrast method and an improved pairwise comparison under different scenarios of trait evolution after speciation and duplication. <i>Methods in Ecology and Evolution</i> , 2021 , 12, 1875	7.7	0

1 Bioinformatics for Evolutionary Developmental Biology **2009**, 355-378