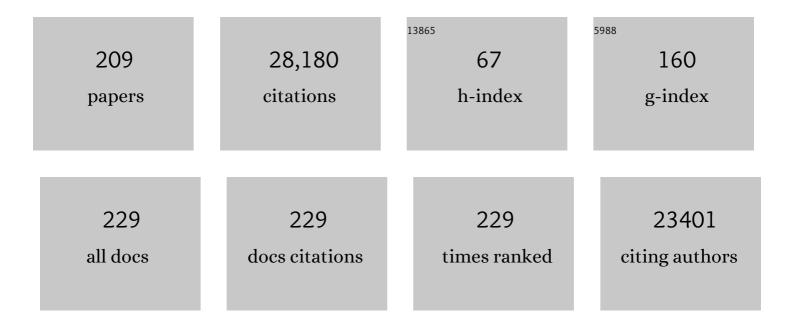
## **Diethard Tautz**

List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	A non-radioactive in situ hybridization method for the localization of specific RNAs in Drosophila embryos reveals translational control of the segmentation gene hunchback. Chromosoma, 1989, 98, 81-85.	2.2	2,665
2	Animals in a bacterial world, a new imperative for the life sciences. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 3229-3236.	7.1	2,181
3	Hypervariability of simple sequences as a general source for polymorphic DNA markers. Nucleic Acids Research, 1989, 17, 6463-6471.	14.5	1,990
4	The genome of the model beetle and pest Tribolium castaneum. Nature, 2008, 452, 949-955.	27.8	1,255
5	Simple sequences are ubiquitous repetitive components of eukaryotic genomes. Nucleic Acids Research, 1984, 12, 4127-4138.	14.5	1,180
6	Slippage synthesis of simple sequence DNA. Nucleic Acids Research, 1992, 20, 211-215.	14.5	1,000
7	A plea for DNA taxonomy. Trends in Ecology and Evolution, 2003, 18, 70-74.	8.7	781
8	The evolutionary origin of orphan genes. Nature Reviews Genetics, 2011, 12, 692-702.	16.3	663
9	Cryptic simplicity in DNA is a major source of genetic variation. Nature, 1986, 322, 652-656.	27.8	621
10	An optimized freeze-squeeze method for the recovery of DNA fragments from agarose gels. Analytical Biochemistry, 1983, 132, 14-19.	2.4	568
11	A morphogenetic gradient of hunchback protein organizes the expression of the gap genes Krüppel and knirps in the early Drosophila embryo. Nature, 1990, 346, 577-580.	27.8	479
12	Finger protein of novel structure encoded by hunchback, a second member of the gap class of Drosophila segmentation genes. Nature, 1987, 327, 383-389.	27.8	426
13	Sympatric speciation suggested by monophyly of crater lake cichlids. Nature, 1994, 368, 629-632.	27.8	419
14	A phylogenetically based transcriptome age index mirrors ontogenetic divergence patterns. Nature, 2010, 468, 815-818.	27.8	374
15	A phylostratigraphy approach to uncover the genomic history of major adaptations in metazoan lineages. Trends in Genetics, 2007, 23, 533-539.	6.7	364
16	Ribosomal DNA phylogeny of the major extant arthropod classes and the evolution of myriapods. Nature, 1995, 376, 165-167.	27.8	360
17	Regulation of the Drosophila segmentation gene hunchback by two maternal morphogenetic centres. Nature, 1988, 332, 281-284.	27.8	350
18	Conservation of polymorphic simple sequence loci in cetacean species. Nature, 1991, 354, 63-65.	27.8	336

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19	Social structure of pilot whales revealed by analytical DNA profiling. Science, 1993, 260, 670-672.	12.6	334
20	Isolation of simple-sequence loci for use in polymerase chain reaction-based DNA fingerprinting. Electrophoresis, 1991, 12, 113-118.	2.4	327
21	An evaluation of LSU rDNA D1-D2 sequences for their use in species identification. Frontiers in Zoology, 2007, 4, 6.	2.0	306
22	Simple sequences. Current Opinion in Genetics and Development, 1994, 4, 832-837.	3.3	282
23	Mitochondrial protein phylogeny joins myriapods with chelicerates. Nature, 2001, 413, 154-157.	27.8	272
24	Chromosomal homogeneity of Drosophila ribosomal DNA arrays suggests intrachromosomal exchanges drive concerted evolution. Current Biology, 1994, 4, 777-783.	3.9	252
25	Phylostratigraphic tracking of cancer genes suggests a link to the emergence of multicellularity in metazoa. BMC Biology, 2010, 8, 66.	3.8	235
26	Intracommunity relationships, dispersal pattern and paternity success in a wild living community of Bonobos (Pan paniscus) determined from DNA analysis of faecal samples. Proceedings of the Royal Society B: Biological Sciences, 1999, 266, 1189-1195.	2.6	233
27	Phylogenomic analysis reveals bees and wasps (Hymenoptera) at the base of the radiation of Holometabolous insects. Genome Research, 2006, 16, 1334-1338.	5.5	233
28	An Evolutionary Analysis of Orphan Genes in Drosophila. Genome Research, 2003, 13, 2213-2219.	5.5	223
29	Phylogenetic patterns of emergence of new genes support a model of frequent de novo evolution. BMC Genomics, 2013, 14, 117.	2.8	218
30	Minimal homology requirements for PCR primers. Nucleic Acids Research, 1989, 17, 6749-6749.	14.5	203
31	Understanding the onset of hybrid speciation. Trends in Genetics, 2010, 26, 54-58.	6.7	200
32	Chapter 30 In Situ Hybridization to RNA. Methods in Cell Biology, 1994, 44, 575-598.	1.1	198
33	Genetic and ecological divergence of a monophyletic cichlid species pair under fully sympatric conditions in Lake Ejagham, Cameroon. Molecular Ecology, 2001, 10, 1471-1488.	3.9	197
34	Problems and paradigms: Redundancies, development and the flow of information. BioEssays, 1992, 14, 263-266.	2.5	196
35	Posterior segmentation of the Drosophila embryo in the absence of a maternal posterior organizer gene. Nature, 1989, 338, 629-632.	27.8	191
36	Mitochondrial sequence analysis of Salamandra taxa suggests old splits of major lineages and postglacial recolonizations of Central Europe from distinct source populations of Salamandra salamandra. Molecular Ecology, 2000, 9, 397-410.	3.9	189

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37	An invasive lineage of sculpins, <i>Cottus</i> sp. (Pisces, Teleostei) in the Rhine with new habitat adaptations has originated from hybridization between old phylogeographic groups. Proceedings of the Royal Society B: Biological Sciences, 2005, 272, 2379-2387.	2.6	180
38	Emergence of a New Gene from an Intergenic Region. Current Biology, 2009, 19, 1527-1531.	3.9	177
39	Cross-regulatory interactions among the gap genes of Drosophila. Nature, 1986, 324, 668-670.	27.8	169
40	DNA points the way ahead in taxonomy. Nature, 2002, 418, 479-479.	27.8	162
41	An Ancient Evolutionary Origin of Genes Associated with Human Genetic Diseases. Molecular Biology and Evolution, 2008, 25, 2699-2707.	8.9	161
42	Involvement of an orthologue of the Drosophila pair-rule gene hairy in segment formation of the short germ-band embryo of Tribolium (Coleoptera). Nature, 1993, 361, 448-450.	27.8	159
43	Evolution of transcriptional regulation. Current Opinion in Genetics and Development, 2000, 10, 575-579.	3.3	158
44	Reverse taxonomy: an approach towards determining the diversity of meiobenthic organisms based on ribosomal RNA signature sequences. Philosophical Transactions of the Royal Society B: Biological Sciences, 2005, 360, 1917-1924.	4.0	149
45	A Segmentation Gene in Tribolium Produces a Polycistronic mRNA that Codes for Multiple Conserved Peptides. Cell, 2006, 126, 559-569.	28.9	149
46	Molecular technologies for biodiversity evaluation: Opportunities and challenges. Nature Biotechnology, 1997, 15, 625-628.	17.5	147
47	Notes on the definition and nomenclature of tandemly repetitive DNA sequences. , 1993, 67, 21-28.		139
48	Evolutionary divergence of promoters and spacers in the rDNA family of four Drosophila species. Journal of Molecular Biology, 1987, 195, 525-542.	4.2	135
49	Genome Patterns of Selection and Introgression of Haplotypes in Natural Populations of the House Mouse (Mus musculus). PLoS Genetics, 2012, 8, e1002891.	3.5	128
50	Segmentation. Developmental Cell, 2004, 7, 301-312.	7.0	125
51	Nucleotide divergence vs. gene expression differentiation: comparative transcriptome sequencing in natural isolates from the carrion crow and its hybrid zone with the hooded crow. Molecular Ecology, 2010, 19, 162-175.	3.9	125
52	Genomic resources for wild populations of the house mouse, Mus musculus and its close relative Mus spretus. Scientific Data, 2016, 3, 160075.	5.3	125
53	Northern range expansion of <scp>E</scp> uropean populations of the wasp spider <i><scp>A</scp>rgiope bruennichi</i> is associated with global warming–correlated genetic admixture and populationâ€specific temperature adaptations. Molecular Ecology, 2013, 22, 2232-2248.	3.9	117
54	Fast turnover of genome transcription across evolutionary time exposes entire non-coding DNA to de novo gene emergence. ELife, 2016, 5, e09977.	6.0	113

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55	Polymorphism and Locus-Specific Effects on Polymorphism at Microsatellite Loci in Natural <i>Drosophila melanogaster</i> Populations. Genetics, 1997, 146, 309-320.	2.9	112
56	Next Generation Molecular Ecology. Molecular Ecology, 2010, 19, 1-3.	3.9	109
57	Tests of rRNA hybridization to microarrays suggest that hybridization characteristics of oligonucleotide probes for species discrimination cannot be predicted. Nucleic Acids Research, 2006, 34, e66-e66.	14.5	101
58	Evolution and Phylogeny of the Diptera: A Molecular Phylogenetic Analysis Using 28S rDNA Sequences. Systematic Biology, 1997, 46, 674-698.	5.6	100
59	The root of the East African cichlid radiations. BMC Evolutionary Biology, 2009, 9, 186.	3.2	97
60	An Analysis of Signatures of Selective Sweeps in Natural Populations of the House Mouse. Molecular Biology and Evolution, 2006, 23, 790-797.	8.9	95
61	The expression of the proximodistal axis patterning genes Distal-less and dachshund in the appendages of Glomeris marginata (Myriapoda: Diplopoda) suggests a special role of these genes in patterning the head appendages. Developmental Biology, 2003, 260, 97-112.	2.0	93
62	Neurogenesis in the spider <i>Cupiennius salei</i> . Development (Cambridge), 2001, 128, 2673-2688.	2.5	89
63	Anterior and posterior waves of cyclic her1 gene expression are differentially regulated in the presomitic mesoderm of zebrafish. Development (Cambridge), 2003, 130, 4269-4278.	2.5	88
64	Tracing the first step to speciation: ecological and genetic differentiation of a salamander population in a small forest. Molecular Ecology, 2007, 16, 4550-4561.	3.9	88
65	Divergence patterns of genic copy number variation in natural populations of the house mouse (Mus) Tj ETQq1 I Genome Research, 2015, 25, 1114-1124.	0.784314 5.5	4 rgBT /Overl 88
66	Genomic Networks of Hybrid Sterility. PLoS Genetics, 2014, 10, e1004162.	3.5	84
67	A Hox class 3 orthologue from the spider Cupiennius salei is expressed in a Hox-gene-like fashion. Development Genes and Evolution, 1998, 208, 586-590.	0.9	82
68	Parallel Selection Mapping Using Artificially Selected Mice Reveals Body Weight Control Loci. Current Biology, 2012, 22, 794-800.	3.9	82
69	Random sequences are an abundant source of bioactive RNAs or peptides. Nature Ecology and Evolution, 2017, 1, 0217.	7.8	76
70	The genetic population structure of the gray mouse lemur ( Microcebus murinus), a basal primate from Madagascar. Behavioral Ecology and Sociobiology, 2002, 52, 166-175.	1.4	75
71	Transcription of the tandem array of ribosomal DNA in <i>Drosophila melanogaster</i> does not terminate at any fixed point. EMBO Journal, 1986, 5, 1267-1273.	7.8	74
72	House mouse colonization patterns on the sub-Antarctic Kerguelen Archipelago suggest singular primary invasions and resilience against re-invasion. BMC Evolutionary Biology, 2010, 10, 325.	3.2	74

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73	No evidence for phylostratigraphic bias impacting inferences on patterns of gene emergence and evolution. Molecular Biology and Evolution, 2017, 34, msw284.	8.9	74
74	Tracing early stages of species differentiation: Ecological, morphological and genetic divergence of Galápagos sea lion populations. BMC Evolutionary Biology, 2008, 8, 150.	3.2	73
75	Tracing the dynamics of gene transcripts after organismal death. Open Biology, 2017, 7, 160267.	3.6	72
76	Contrasting evolution of expression differences in the testis between species and subspecies of the house mouse. Genome Research, 2007, 17, 42-49.	5.5	67
77	Mapping of Craniofacial Traits in Outbred Mice Identifies Major Developmental Genes Involved in Shape Determination. PLoS Genetics, 2015, 11, e1005607.	3.5	67
78	Segmentation gene expression in the mothmidge Clogmia albipunctata (Diptera, Psychodidae) and other primitive dipterans. Development Genes and Evolution, 1999, 209, 145-154.	0.9	66
79	Adaptive divergence vs. environmental plasticity: tracing local genetic adaptation of metamorphosis traits in salamanders. Molecular Ecology, 2004, 13, 1665-1677.	3.9	66
80	The hidden matrilineal structure of a solitary lemur: implications for primate social evolution. Proceedings of the Royal Society B: Biological Sciences, 2002, 269, 1755-1763.	2.6	65
81	Zebrafish zic1 expression in brain and somites is affected by BMP and Hedgehog signalling. Mechanisms of Development, 1999, 85, 147-159.	1.7	60
82	Two orthodenticle -related genes in the short-germ beetle Tribolium castaneum. Development Genes and Evolution, 1996, 206, 35-45.	0.9	59
83	A genetic uncertainty problem. Trends in Genetics, 2000, 16, 475-477.	6.7	59
84	Eurasian house mouse (Mus musculus L.) differentiation at microsatellite loci identifies the Iranian plateau as a phylogeographic hotspot. BMC Evolutionary Biology, 2015, 15, 26.	3.2	59
85	A Role for Ultrasonic Vocalisation in Social Communication and Divergence of Natural Populations of the House Mouse (Mus musculus domesticus). PLoS ONE, 2014, 9, e97244.	2.5	59
86	Oligonucleotide microarrays: widely applied poorly understood. Briefings in Functional Genomics & Proteomics, 2007, 6, 141-148.	3.8	58
87	Use of a natural hybrid zone for genomewide association mapping of craniofacial traits in the house mouse. Molecular Ecology, 2014, 23, 5756-5770.	3.9	58
88	Rapid formation of distinct hybrid lineages after secondary contact of two fish species ( <i>Cottus</i> ) Tj ETQq0	0	Overlock 10 T

89	Sperm usage in honey bees. Behavioral Ecology and Sociobiology, 1998, 42, 247-255.	1.4	56
90	Delimiting the conserved features of <i>hunchback</i> function for the trunk organization of insects. Development (Cambridge), 2008, 135, 881-888.	2.5	56

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91	The role of the segmentation gene hairy in Tribolium. Development Genes and Evolution, 2008, 218, 465-477.	0.9	55
92	Simple DNA sequences of Drosophila virilis isolated by screening with RNA. Journal of Molecular Biology, 1984, 172, 229-235.	4.2	54
93	Molecular Phylogenetics at the Felsenstein Zone: Approaching the Strepsiptera Problem Using 5.8S and 28S rDNA Sequences. Molecular Phylogenetics and Evolution, 1998, 9, 470-480.	2.7	54
94	Evolution: Dynamics of De Novo Gene Emergence. Current Biology, 2014, 24, R238-R240.	3.9	54
95	Ecoâ€genomic analysis of the poleward range expansion of the wasp spider <i><scp>A</scp>rgiope bruennichi</i> shows rapid adaptation and genomic admixture. Global Change Biology, 2015, 21, 4320-4332.	9.5	54
96	Evolution of segmentation genes in insects. Trends in Genetics, 1995, 11, 23-27.	6.7	53
97	Homologues of c-hairy1 ( her9 ) and lunatic fringe in zebrafish are expressed in the developing central nervous system, but not in the presomitic mesoderm. Development Genes and Evolution, 2001, 211, 493-500.	0.9	53
98	Galápagos and Californian sea lions are separate species: Genetic analysis of the genus Zalophus and its implications for conservation management. Frontiers in Zoology, 2007, 4, 20.	2.0	53
99	Regulatory and coding regions of the segmentation gene hunchback are functionally conserved between Drosophila virilis and Drosophila melanogaster. Mechanisms of Development, 1994, 45, 105-115.	1.7	52
100	The role of Suppressor of Hairless in Notch mediated signalling during zebrafish somitogenesis. Mechanisms of Development, 2003, 120, 1083-1094.	1.7	52
101	Identification of Selective Sweeps in Closely Related Populations of the House Mouse Based on Microsatellite Scans. Genetics, 2008, 180, 1537-1545.	2.9	52
102	WHAT WE HAVE ALSO LEARNED: ADAPTIVE SPECTIATION IS THEORETICALLY PLAUSIBLE. Evolution; International Journal of Organic Evolution, 2005, 59, 691-695.	2.3	51
103	Physico-chemical foundations underpinning microarray and next-generation sequencing experiments. Nucleic Acids Research, 2013, 41, 2779-2796.	14.5	49
104	What we have also learned: adaptive speciation is theoretically plausible. Evolution; International Journal of Organic Evolution, 2005, 59, 691-5; discussion 696-9.	2.3	48
105	Correlated Evolution of Synonymous and Nonsynonymous Sites in Drosophila. Journal of Molecular Evolution, 2004, 59, 771-779.	1.8	47
106	Genome-wide acceleration of protein evolution in flies (Diptera). BMC Evolutionary Biology, 2006, 6, 7.	3.2	47
107	Expression patterns oftwist andsnail inTribolium (Coleoptera) suggest a homologous formation of mesoderm in long and short germ band insects. Genesis, 1994, 15, 32-37.	2.1	45
108	Abdominal-B expressionin a spider suggests a general role forAbdominal-B specifying the genital structure. , 1999, 285, 85-91.		44

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109	The Discovery of De Novo Gene Evolution. Perspectives in Biology and Medicine, 2014, 57, 149-161.	0.5	44
110	Insect embryogenesis - what is ancestral and what is derived?. Development (Cambridge), 1994, 1994, 1994, 193-199.	2.5	43
111	Separable stripe enhancer elements for the pairâ€rule gene hairy in the beetle Tribolium. EMBO Reports, 2004, 5, 638-642.	4.5	42
112	Isolation and characterization of polymorphic tetranucleotide microsatellite loci in the Fire salamander Salamandra salamandra (Amphibia: Caudata). Molecular Ecology Notes, 2004, 4, 626-628.	1.7	41
113	Direct cloning of microsatellite loci from Cottus gobio through a simplified enrichment procedure. Molecular Ecology Notes, 2005, 5, 628-636.	1.7	41
114	her11 is involved in the somitogenesis clock in zebrafish. Development Genes and Evolution, 2004, 214, 393-406.	0.9	40
115	Large Number of Replacement Polymorphisms in Rapidly Evolving Genes of Drosophila: Implications for Genome-Wide Surveys of DNA Polymorphism. Genetics, 1999, 153, 1717-1729.	2.9	40
116	The impact of stocking on the genetic integrity of Arctic charr (Salvelinus) populations from the Alpine region. Molecular Ecology, 2002, 11, 1017-1027.	3.9	39
117	Insect calcium channels. FEBS Letters, 1994, 339, 189-194.	2.8	38
118	Elimination of EVE protein by CALI in the short germ band insect Tribolium suggests a conserved pair-rule function for even skipped. Mechanisms of Development, 1999, 80, 191-195.	1.7	37
119	A de novo evolved gene in the house mouse regulates female pregnancy cycles. ELife, 2019, 8, .	6.0	37
120	Debatable homologies. Nature, 1998, 395, 17-19.	27.8	35
121	Neurogenesis in the spider: new insights from comparative analysis of morphological processes and gene expression patterns. Arthropod Structure and Development, 2003, 32, 5-16.	1.4	35
122	An Evaluation of the Use of the LSU rRNA D1-D5 Domain for DNA-based Taxonomy of Eukaryotic Protists. Protist, 2010, 161, 342-352.	1.5	35
123	Exploring the effects of gene dosage on mandible shape in mice as a model for studying the genetic basis of natural variation. Development Genes and Evolution, 2013, 223, 279-287.	0.9	34
124	Evolution of dorsal-ventral axis formation in arthropod appendages: H15 and optomotor-blind/bifid-type T-box genes in the millipede Glomeris marginata (Myriapoda: Diplopoda). Evolution & Development, 2005, 7, 51-57.	2.0	32
125	Copy Number Changes of CNV Regions in Intersubspecific Crosses of the House Mouse. Molecular Biology and Evolution, 2010, 27, 1845-1856.	8.9	32
126	Molecular phylogeny of the salamandrid genus Neurergus: evidence for an intrageneric switch of reproductive biology. Amphibia - Reptilia, 2002, 23, 419-431.	0.5	31

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127	Paternal imprinting of mating preferences between natural populations of house mice ( <i><scp>M</scp>us musculus domesticus</i> ). Molecular Ecology, 2013, 22, 2549-2562.	3.9	30
128	From genes to individuals: developmental genes and the generation of the phenotype. Philosophical Transactions of the Royal Society B: Biological Sciences, 1998, 353, 231-240.	4.0	29
129	Prospero and Snail expression during spider neurogenesis. Development Genes and Evolution, 2003, 213, 554-566.	0.9	28
130	her1 and her13.2 are jointly required for somitic border specification along the entire axis of the fish embryo. Developmental Biology, 2006, 293, 242-251.	2.0	28
131	Semi-automatic landmark point annotation for geometric morphometrics. Frontiers in Zoology, 2014, 11, .	2.0	27
132	An algorithm and program for finding sequence specific oligonucleotide probes for species identification. BMC Bioinformatics, 2002, 3, 9.	2.6	26
133	Polycistronic peptide coding genes in eukaryoteshow widespread are they?. Briefings in Functional Genomics & Proteomics, 2008, 8, 68-74.	3.8	26
134	Micro-evolutionary divergence patterns of mandible shapes in wild house mouse (Mus musculus) populations. BMC Evolutionary Biology, 2011, 11, 306.	3.2	26
135	TINA manual landmarking tool: software for the precise digitization of 3D landmarks. Frontiers in Zoology, 2012, 9, 6.	2.0	26
136	Low-level mitochondrial heteroplasmy modulates DNA replication, glucose metabolism and lifespan in mice. Scientific Reports, 2018, 8, 5872.	3.3	26
137	Craniofacial shape transition across the house mouse hybrid zone: implications for the genetic architecture and evolution of between-species differences. Development Genes and Evolution, 2016, 226, 173-186.	0.9	24
138	Selection on cis-Regulatory Variation at B4galnt2 and Its Influence on von Willebrand Factor in House Mice. Molecular Biology and Evolution, 2008, 26, 567-578.	8.9	23
139	Chromophore-assisted laser inactivation of even skipped in Drosophila precisely phenocopies genetic loss of function. Development Genes and Evolution, 1996, 206, 86-88.	0.9	21
140	Development of new microsatellite loci and evaluation of loci from other pinniped species for the Galápagos sea lion (Zalophus californianus wollebaeki). Conservation Genetics, 2006, 7, 461-465.	1.5	21
141	A comparative assessment of mandible shape in a consomic strain panel of the house mouse (Mus) Tj ETQq1 1 0. Biology, 2011, 11, 309.	784314 r 3.2	gBT /Overloc 21
142	Molecular and phenotypic distinction of the very recently evolved insular subspecies Mus musculus helgolandicus ZIMMERMANN, 1953. BMC Evolutionary Biology, 2015, 15, 160.	3.2	20
143	Inbred lab mice are not isogenic: genetic variation within inbred strains used to infer the mutation rate per nucleotide site. Heredity, 2021, 126, 107-116.	2.6	20
144	What's new: Genomic finger printing goes simple. BioEssays, 1990, 12, 44-46.	2.5	18

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145	Comparative molecular embryology of arthropods: the expression of Hox genes in the spider <i>Cupiennius salei</i> . Invertebrate Reproduction and Development, 1999, 36, 203-209.	0.8	17
146	A TEST OF THE NEUTRAL MODEL OF EXPRESSION CHANGE IN NATURAL POPULATIONS OF HOUSE MOUSE SUBSPECIES. Evolution; International Journal of Organic Evolution, 2010, 64, 549-560.	2.3	17
147	Genetic Differentiation of Hypothalamus Parentally Biased Transcripts in Populations of the House Mouse Implicate the Prader–Willi Syndrome Imprinted Region as a Possible Source of Behavioral Divergence. Molecular Biology and Evolution, 2014, 31, 3240-3249.	8.9	17
148	Characterization of spotted hyena,Crocuta crocutamicrosatellite loci. Molecular Ecology Notes, 2003, 3, 360-362.	1.7	16
149	Not just another genome. BMC Biology, 2011, 9, 8.	3.8	16
150	Human core duplicon gene families: game changers or game players?. Briefings in Functional Genomics, 2019, 18, 402-411.	2.7	16
151	WHAT WE HAVE ALSO LEARNED: ADAPTIVE SPECIATION IS THEORETICALLY PLAUSIBLE. Evolution; International Journal of Organic Evolution, 2005, 59, 691.	2.3	15
152	A Revised Design for Microarray Experiments to Account for Experimental Noise and Uncertainty of Probe Response. PLoS ONE, 2014, 9, e91295.	2.5	15
153	Testing Implications of the Omnigenic Model for the Genetic Analysis of Loci Identified through Genome-wide Association. Current Biology, 2021, 31, 1092-1098.e6.	3.9	15
154	TECHNICAL ARTICLE: A pooling approach to detect signatures of selective sweeps in genome scans using microsatellites. Molecular Ecology Notes, 2007, 7, 400-403.	1.7	14
155	Increased mitochondrial mutation frequency after an island colonization: positive selection or accumulation of slightly deleterious mutations?. Biology Letters, 2013, 9, 20121123.	2.3	14
156	A Comparison of Homologous Developmental Genes from Drosophila and Tribolium Reveals Major Differences in Length and Trinucleotide Repeat Content. Journal of Molecular Evolution, 1999, 49, 558-566.	1.8	13
157	The imprinted lncRNA <i>Peg13</i> regulates sexual preference and the sex-specific brain transcriptome in mice. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	7.1	13
158	Asynchronous mitotic domains during blastoderm formation inMusca domestica L. (Diptera). Roux's Archives of Developmental Biology, 1991, 199, 373-376.	1.2	12
159	Effects of a male meiotic driver on male and female transcriptomes in the house mouse. Proceedings of the Royal Society B: Biological Sciences, 2019, 286, 20191927.	2.6	12
160	Evolution and Phylogeny of the Diptera: A Molecular Phylogenetic Analysis Using 28S rDNA Sequences. Systematic Biology, 1997, 46, 674.	5.6	12
161	Meta-populational demes constitute a reservoir for large MHC allele diversity in wild house mice (Mus musculus). Frontiers in Zoology, 2018, 15, 15.	2.0	11
162	The Effects of Sequence Length and Composition of Random Sequence Peptides on the Growth of E. coli Cells. Genes, 2021, 12, 1913.	2.4	11

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163	Splitting in space. Nature, 2003, 421, 225-226.	27.8	10

Copy number variants and selective sweeps in natural populations of the house mouse (Mus musculus) Tj ETQq0 0.0 gBT /Overlock 10 2.3 gBT /Overlock 10

165	Dealing with the adaptive immune system during de novo evolution of genes from intergenic sequences. BMC Evolutionary Biology, 2018, 18, 121.	3.2	10
166	Conservation of major nuclease S1-sensitive sites in the non-conserved spacer region of ribosomal DNA in Drosophila species. Journal of Molecular Biology, 1985, 183, 519-527.	4.2	9
167	Simultaneous quantification of multiple nucleic acid targets in complex rRNA mixtures using high density microarrays and nonspecific hybridization as a source of information. Journal of Microbiological Methods, 2008, 75, 92-102.	1.6	9
168	Selective sweeps versus introgression - population genetic dynamics of the murine leukemia virus receptor Xpr1 in wild populations of the house mouse (Mus musculus). BMC Evolutionary Biology, 2015, 15, 248.	3.2	9
169	Effects of the Expression of Random Sequence Clones on Growth and Transcriptome Regulation in Escherichia coli. Genes, 2022, 13, 53.	2.4	9
170	Chordate Evolution in a New Light. Cell, 2003, 113, 812-813.	28.9	8
171	Segmental duplications and evolutionary acquisition of UV damage response in the SPATA31 gene family of primates and humans. BMC Genomics, 2017, 18, 222.	2.8	8
172	Using the <i>Mus musculus</i> hybrid zone to assess covariation and genetic architecture of limb bone lengths. Molecular Ecology Resources, 2018, 18, 908-921.	4.8	8
173	The mutational load in natural populations is significantly affected by high primary rates of retroposition. Proceedings of the National Academy of Sciences of the United States of America, 2021,	7.1	8
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174	118, . Automated Phenotyping Indicates Pupal Size in <i>Drosophila</i> Is a Highly Heritable Trait with an Apparent Polygenic Basis. G3: Genes, Genomes, Genetics, 2017, 7, 1277-1286.	1.8	7
174 175	118, . Automated Phenotyping Indicates Pupal Size in <i>Drosophila</i> Is a Highly Heritable Trait with an		
	118, . Automated Phenotyping Indicates Pupal Size in <i>Drosophila</i> Is a Highly Heritable Trait with an Apparent Polygenic Basis. G3: Genes, Genomes, Genetics, 2017, 7, 1277-1286.	1.8	7
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175 176	<ul> <li>118, .</li> <li>Automated Phenotyping Indicates Pupal Size in <i>Drosophila</i> Is a Highly Heritable Trait with an Apparent Polygenic Basis. G3: Genes, Genomes, Genetics, 2017, 7, 1277-1286.</li> <li>Involvement of SPATA31 copy number variable genes in human lifespan. Aging, 2018, 10, 674-688.</li> <li>Of statistics and genomes. Trends in Genetics, 2004, 20, 344-346.</li> <li>Microsatellite variability in wild populations of the house mouse is not influenced by differences in</li> </ul>	1.8 3.1 6.7	7 7 6
175 176 177	<ul> <li>118, .</li> <li>Automated Phenotyping Indicates Pupal Size in <i>Drosophila</i> Is a Highly Heritable Trait with an Apparent Polygenic Basis. G3: Genes, Genomes, Genetics, 2017, 7, 1277-1286.</li> <li>Involvement of SPATA31 copy number variable genes in human lifespan. Aging, 2018, 10, 674-688.</li> <li>Of statistics and genomes. Trends in Genetics, 2004, 20, 344-346.</li> <li>Microsatellite variability in wild populations of the house mouse is not influenced by differences in chromosomal recombination rates. Biological Journal of the Linnean Society, 2005, 84, 629-635.</li> <li>An algorithm for the determination and quantification of components of nucleic acid mixtures based</li> </ul>	1.8 3.1 6.7 1.6	7 7 6 6

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