

Mark L Blaxter

List of Publications by Year in descending order

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Version: 2024-02-01

293
papers

31,719
citations

5896

81
h-index

6300

158
g-index

329
all docs

329
docs citations

329
times ranked

29829
citing authors

#	ARTICLE	IF	CITATIONS
1	The Earth BioGenome Project 2020: Starting the clock. Proceedings of the National Academy of Sciences of the United States of America, 2022, 119, .	7.1	124
2	Standards recommendations for the Earth BioGenome Project. Proceedings of the National Academy of Sciences of the United States of America, 2022, 119, .	7.1	33
3	Why sequence all eukaryotes?. Proceedings of the National Academy of Sciences of the United States of America, 2022, 119, .	7.1	51
4	Sequence locally, think globally: The Darwin Tree of Life Project. Proceedings of the National Academy of Sciences of the United States of America, 2022, 119, .	7.1	120
5	Africa: sequence 100,000 species to safeguard biodiversity. Nature, 2022, 603, 388-392.	27.8	19
6	Genome-enabled discovery of candidate virulence loci in <i>Striga hermonthica</i> , a devastating parasite of African cereal crops. New Phytologist, 2022, 236, 622-638.	7.3	12
7	Rapid parallel adaptation despite gene flow in silent crickets. Nature Communications, 2021, 12, 50.	12.8	26
8	MolluscDB: a genome and transcriptome database for molluscs. Philosophical Transactions of the Royal Society B: Biological Sciences, 2021, 376, 20200157.	4.0	17
9	The genome sequence of the Norway rat, <i>Rattus norvegicus</i> Berkenhout 1769. Wellcome Open Research, 2021, 6, 118.	1.8	16
10	Launching the Tree of Life Gateway. Wellcome Open Research, 2021, 6, 125.	1.8	13
11	The genome sequence of the brown trout, <i>Salmo trutta</i> Linnaeus 1758. Wellcome Open Research, 2021, 6, 108.	1.8	15
12	A Bivalve Biomineralization Toolbox. Molecular Biology and Evolution, 2021, 38, 4043-4055.	8.9	27
13	The genome sequence of the European golden eagle, <i>Aquila chrysaetos chrysaetos</i> Linnaeus 1758. Wellcome Open Research, 2021, 6, 112.	1.8	3
14	A dense linkage map for a large repetitive genome: discovery of the sex-determining region in hybridizing fire-bellied toads (<i>Bombina bombina</i> and <i>Bombina variegata</i>). G3: Genes, Genomes, Genetics, 2021, 11, .	1.8	2
15	A telomere-to-telomere assembly of <i>Oscheius tipulae</i> and the evolution of rhabditid nematode chromosomes. G3: Genes, Genomes, Genetics, 2021, 11, .	1.8	45
16	The genome sequence of the bootlace worm, <i>Lineus longissimus</i> (Gunnerus, 1770). Wellcome Open Research, 2021, 6, 272.	1.8	8
17	Building genomic infrastructure: Sequencing platinum-standard reference-quality genomes of all cetacean species. Marine Mammal Science, 2020, 36, 1356-1366.	1.8	10
18	BlobToolKit – Interactive Quality Assessment of Genome Assemblies. G3: Genes, Genomes, Genetics, 2020, 10, 1361-1374.	1.8	883

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19	The Genome of <i>Caenorhabditis bovis</i> . <i>Current Biology</i> , 2020, 30, 1023-1031.e4.	3.9	35
20	Formin, an opinion. <i>Development (Cambridge)</i> , 2020, 147, .	2.5	5
21	Field cricket genome reveals the footprint of recent, abrupt adaptation in the wild. <i>Evolution Letters</i> , 2020, 4, 19-33.	3.3	32
22	The genome sequence of the Eurasian red squirrel, <i>Sciurus vulgaris</i> Linnaeus 1758. <i>Wellcome Open Research</i> , 2020, 5, 18.	1.8	3
23	The genome sequence of the eastern grey squirrel, <i>Sciurus carolinensis</i> Gmelin, 1788. <i>Wellcome Open Research</i> , 2020, 5, 27.	1.8	4
24	Genome sequence of the root-knot nematode <i>Meloidogyne luci</i> . <i>Journal of Nematology</i> , 2020, 52, 1-5.	0.9	37
25	The genome sequence of the Eurasian river otter, <i>Lutra lutra</i> Linnaeus 1758. <i>Wellcome Open Research</i> , 2020, 5, 33.	1.8	6
26	Horizontal Gene Transfer in Metazoa: Examples and Methods. , 2019, , 203-226.		5
27	Genomic architecture and introgression shape a butterfly radiation. <i>Science</i> , 2019, 366, 594-599.	12.6	365
28	Genomic dissection of an extended phenotype: Oak galling by a cynipid gall wasp. <i>PLoS Genetics</i> , 2019, 15, e1008398.	3.5	44
29	A chromosome-level genome assembly of <i>Cydia pomonella</i> provides insights into chemical ecology and insecticide resistance. <i>Nature Communications</i> , 2019, 10, 4237.	12.8	102
30	Comparative Epigenomics Reveals that RNA Polymerase II Pausing and Chromatin Domain Organization Control Nematode piRNA Biogenesis. <i>Developmental Cell</i> , 2019, 48, 793-810.e6.	7.0	37
31	Secretion of an Argonaute protein by a parasitic nematode and the evolution of its siRNA guides. <i>Nucleic Acids Research</i> , 2019, 47, 3594-3606.	14.5	75
32	Genome-wide methylation is modified by caloric restriction in <i>Daphnia magna</i> . <i>BMC Genomics</i> , 2019, 20, 197.	2.8	21
33	Chromosome-Wide Evolution and Sex Determination in the Three-Sexed Nematode <i>Auanema rhodensis</i> . <i>G3: Genes, Genomes, Genetics</i> , 2019, 9, 1211-1230.	1.8	39
34	Males as somatic investment in a parthenogenetic nematode. <i>Science</i> , 2019, 363, 1210-1213.	12.6	24
35	Comparative genomics of 10 new <i>Caenorhabditis</i> species. <i>Evolution Letters</i> , 2019, 3, 217-236.	3.3	106
36	Signatures of the Evolution of Parthenogenesis and Cryptobiosis in the Genomes of Panagrolaimid Nematodes. <i>IScience</i> , 2019, 21, 587-602.	4.1	27

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37	Dissection of Ramularia Leaf Spot Disease by Integrated Analysis of Barley and Ramularia collo-cygni Transcriptome Responses. <i>Molecular Plant-Microbe Interactions</i> , 2019, 32, 176-193.	2.6	21
38	High genetic diversity in the <i>Dirofilaria repens</i> species complex revealed by mitochondrial genomes of feline microfilaria samples from Narathiwat, Thailand. <i>Transboundary and Emerging Diseases</i> , 2019, 66, 389-399.	3.0	22
39	Genomic dissection of an extended phenotype: Oak galling by a cynipid gall wasp. , 2019, 15, e1008398.		0
40	Genomic dissection of an extended phenotype: Oak galling by a cynipid gall wasp. , 2019, 15, e1008398.		0
41	Genomic dissection of an extended phenotype: Oak galling by a cynipid gall wasp. , 2019, 15, e1008398.		0
42	The ash dieback invasion of Europe was founded by two genetically divergent individuals. <i>Nature Ecology and Evolution</i> , 2018, 2, 1000-1008.	7.8	82
43	<i>Daphnia magna</i> microRNA's respond to nutritional stress and ageing but are not transgenerational. <i>Molecular Ecology</i> , 2018, 27, 1402-1412.	3.9	21
44	Sex- and Gamete-Specific Patterns of X Chromosome Segregation in a Trioecious Nematode. <i>Current Biology</i> , 2018, 28, 93-99.e3.	3.9	22
45	Improving the annotation of the <i>Heterorhabditis bacteriophora</i> genome. <i>GigaScience</i> , 2018, 7, .	6.4	18
46	Characterisation of the British honey bee metagenome. <i>Nature Communications</i> , 2018, 9, 4995.	12.8	51
47	Molecular palaeontology illuminates the evolution of ecdysozoan vision. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2018, 285, .	2.6	25
48	A high-coverage draft genome of the mycalesine butterfly <i>Bicyclus anynana</i> . <i>GigaScience</i> , 2017, 6, 1-7.	6.4	55
49	Comparative Genomics of Apomictic Root-Knot Nematodes: Hybridization, Ploidy, and Dynamic Genome Change. <i>Genome Biology and Evolution</i> , 2017, 9, 2844-2861.	2.5	98
50	KinFin: Software for Taxon-Aware Analysis of Clustered Protein Sequences. <i>G3: Genes, Genomes, Genetics</i> , 2017, 7, 3349-3357.	1.8	72
51	GenomeHubs: simple containerized setup of a custom Ensembl database and web server for any species. <i>Database: the Journal of Biological Databases and Curation</i> , 2017, 2017, .	3.0	13
52	Toward Universal Forward Genetics: Using a Draft Genome Sequence of the Nematode <i>Oscheius tipulae</i> To Identify Mutations Affecting Vulva Development. <i>Genetics</i> , 2017, 206, 1747-1761.	2.9	18
53	<i>Caenorhabditis monodelphis</i> sp. n.: defining the stem morphology and genomics of the genus <i>Caenorhabditis</i> . <i>BMC Zoology</i> , 2017, 2, .	1.0	33
54	Genome comparisons indicate recent transfer of <i>Wolbachia</i> between sister species <i>Drosophila suzukii</i> and <i>D. Åsubpulchrella</i> . <i>Ecology and Evolution</i> , 2017, 7, 9391-9404.	1.9	49

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55	Comparative genomics of the tardigrades <i>Hypsibius dujardini</i> and <i>Ramazzottius varieornatus</i> . <i>PLoS Biology</i> , 2017, 15, e2002266.	5.6	170
56	Annotated mitochondrial genome with Nanopore R9 signal for <i>Nippostrongylus brasiliensis</i> . <i>F1000Research</i> , 2017, 6, 56.	1.6	14
57	The genome of the emerging barley pathogen <i>Ramularia collo-cygni</i> . <i>BMC Genomics</i> , 2016, 17, 584.	2.8	36
58	Para-allopatry in hybridizing fire-bellied toads (<i>Bombina bombina</i> and <i>B. variegata</i>): Inference from transcriptome-wide coalescence analyses. <i>Evolution; International Journal of Organic Evolution</i> , 2016, 70, 1803-1818.	2.3	25
59	Genetic Drift, Not Life History or RNAi, Determine Long-Term Evolution of Transposable Elements. <i>Genome Biology and Evolution</i> , 2016, 8, 2964-2978.	2.5	58
60	How many biological replicates are needed in an RNA-seq experiment and which differential expression tool should you use?. <i>Rna</i> , 2016, 22, 839-851.	3.5	622
61	Stage-specific Proteomes from <i>Onchocerca ochengi</i> , Sister Species of the Human River Blindness Parasite, Uncover Adaptations to a Nodular Lifestyle. <i>Molecular and Cellular Proteomics</i> , 2016, 15, 2554-2575.	3.8	23
62	Formin Is Associated with Left-Right Asymmetry in the Pond Snail and the Frog. <i>Current Biology</i> , 2016, 26, 654-660.	3.9	135
63	Reminder to deposit DNA sequences. <i>Science</i> , 2016, 352, 780-780.	12.6	24
64	Characterization of the mantle transcriptome in bivalves: <i>Pecten maximus</i> , <i>Mytilus edulis</i> and <i>Crassostrea gigas</i> . <i>Marine Genomics</i> , 2016, 27, 9-15.	1.1	46
65	Imagining Sisyphus happy: DNA barcoding and the unnamed majority. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2016, 371, 20150329.	4.0	30
66	A molecular palaeobiological exploration of arthropod terrestrialization. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2016, 371, 20150133.	4.0	131
67	The genome of the yellow potato cyst nematode, <i>Globodera rostochiensis</i> , reveals insights into the basis of parasitism and virulence. <i>Genome Biology</i> , 2016, 17, 124.	8.8	156
68	No evidence for extensive horizontal gene transfer in the genome of the tardigrade <i>Hypsibius dujardini</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, 5053-5058.	7.1	214
69	A supergene determines highly divergent male reproductive morphs in the ruff. <i>Nature Genetics</i> , 2016, 48, 79-83.	21.4	411
70	A metagenetic approach to determine the diversity and distribution of cyst nematodes at the level of the country, the field and the individual. <i>Molecular Ecology</i> , 2015, 24, 5842-5851.	3.9	22
71	Supergroup C <i>Wolbachia</i> , mutualist symbionts of filarial nematodes, have a distinct genome structure. <i>Open Biology</i> , 2015, 5, 150099.	3.6	38
72	Oviposition but Not Sex Allocation Is Associated with Transcriptomic Changes in Females of the Parasitoid Wasp <i>Nasonia vitripennis</i> . <i>G3: Genes, Genomes, Genetics</i> , 2015, 5, 2885-2892.	1.8	11

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73	The evolution of parasitism in Nematoda. <i>Parasitology</i> , 2015, 142, S26-S39.	1.5	199
74	A single chromosome assembly of <i>Bacteroides fragilis</i> strain BE1 from Illumina and MinION nanopore sequencing data. <i>GigaScience</i> , 2015, 4, 60.	6.4	64
75	poRe: an R package for the visualization and analysis of nanopore sequencing data. <i>Bioinformatics</i> , 2015, 31, 114-115.	4.1	85
76	Ancient and Novel Small RNA Pathways Compensate for the Loss of piRNAs in Multiple Independent Nematode Lineages. <i>PLoS Biology</i> , 2015, 13, e1002061.	5.6	118
77	Statistical models for RNA-seq data derived from a two-condition 48-replicate experiment. <i>Bioinformatics</i> , 2015, 31, 3625-3630.	4.1	76
78	The genomes of two key bumblebee species with primitive eusocial organization. <i>Genome Biology</i> , 2015, 16, 76.	8.8	330
79	Extracellular <i>Onchocerca</i> -derived small RNAs in host nodules and blood. <i>Parasites and Vectors</i> , 2015, 8, 58.	2.5	98
80	ReproPhylo: An Environment for Reproducible Phylogenomics. <i>PLoS Computational Biology</i> , 2015, 11, e1004447.	3.2	16
81	Palaeosymbiosis Revealed by Genomic Fossils of <i>Wolbachia</i> in a Strongyloidean Nematode. <i>PLoS Genetics</i> , 2014, 10, e1004397.	3.5	49
82	Quality control of next-generation sequencing data without a reference. <i>Frontiers in Genetics</i> , 2014, 5, 111.	2.3	75
83	Exosomes secreted by nematode parasites transfer small RNAs to mammalian cells and modulate innate immunity. <i>Nature Communications</i> , 2014, 5, 5488.	12.8	640
84	Development: The Maternalâ€Zygotic Transition Revisited. <i>Current Biology</i> , 2014, 24, R72-R75.	3.9	3
85	Comparative Analysis of the Secretome from a Model Filarial Nematode (<i>Litomosoides sigmodontis</i>) Reveals Maximal Diversity in Gravid Female Parasites. <i>Molecular and Cellular Proteomics</i> , 2014, 13, 2527-2544.	3.8	32
86	The Evolution of Tyrosine-Recombinase Elements in Nematoda. <i>PLoS ONE</i> , 2014, 9, e106630.	2.5	6
87	A conserved set of maternal genes? Insights from a molluscan transcriptome. <i>International Journal of Developmental Biology</i> , 2014, 58, 501-511.	0.6	28
88	The complex hybrid origins of the root knot nematodes revealed through comparative genomics. <i>PeerJ</i> , 2014, 2, e356.	2.0	99
89	Transcriptome analyses of <i>Anguillicola crassus</i> from native and novel hosts. <i>PeerJ</i> , 2014, 2, e684.	2.0	7
90	<i>Drosophila suzukii</i> . <i>Current Biology</i> , 2013, 23, R8-R9.	3.9	137

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91	Genome-wide evidence for speciation with gene flow in <i>Heliconius</i> butterflies. <i>Genome Research</i> , 2013, 23, 1817-1828.	5.5	609
92	afterParty: turning raw transcriptomes into permanent resources. <i>BMC Bioinformatics</i> , 2013, 14, 301.	2.6	8
93	The genome of <i>Romanomermis culicivorax</i> : revealing fundamental changes in the core developmental genetic toolkit in Nematoda. <i>BMC Genomics</i> , 2013, 14, 923.	2.8	43
94	Genome-wide patterns of divergence and gene flow across a butterfly radiation. <i>Molecular Ecology</i> , 2013, 22, 814-826.	3.9	160
95	Phylogenomics: A Primer. By Rob DeSalle and Jeffrey A. Rosenfeld. New York: Garland Science (Taylor & Francis Group), 2013, 88, 352-352.	0.1	0
96	Special features of RAD Sequencing data: implications for genotyping. <i>Molecular Ecology</i> , 2013, 22, 3151-3164.	3.9	318
97	Functional diversification of <i>Argonautes</i> in nematodes: an expanding universe. <i>Biochemical Society Transactions</i> , 2013, 41, 881-886.	3.4	47
98	Badger: an accessible genome exploration environment. <i>Bioinformatics</i> , 2013, 29, 2788-2789.	4.1	8
99	Phylogenomics and Analysis of Shared Genes Suggest a Single Transition to Mutualism in <i>Wolbachia</i> of Nematodes. <i>Genome Biology and Evolution</i> , 2013, 5, 1668-1674.	2.5	49
100	RAD-Seq derived markers flank the shell colour and banding loci of the <i>Cepaea nemoralis</i> supergene. <i>Molecular Ecology</i> , 2013, 22, 3077-3089.	3.9	72
101	Linking Genomics and Ecology to Investigate the Complex Evolution of an Invasive <i>Drosophila</i> Pest. <i>Genome Biology and Evolution</i> , 2013, 5, 745-757.	2.5	138
102	The CCAP KnowledgeBase: linking protistan and cyanobacterial biological resources with taxonomic and molecular data. <i>Systematics and Biodiversity</i> , 2013, 11, 407-413.	1.2	20
103	The transcriptome of the invasive eel swimbladder nematode parasite <i>Anguillicola crassus</i> . <i>BMC Genomics</i> , 2013, 14, 87.	2.8	8
104	Fine Mapping of the Pond Snail Left-Right Asymmetry (Chirality) Locus Using RAD-Seq and Fibre-FISH. <i>PLoS ONE</i> , 2013, 8, e71067.	2.5	26
105	Blobology: exploring raw genome data for contaminants, symbionts and parasites using taxon-annotated GC-coverage plots. <i>Frontiers in Genetics</i> , 2013, 4, 237.	2.3	258
106	The Transcriptomic Basis of Oviposition Behaviour in the Parasitoid Wasp <i>Nasonia vitripennis</i> . <i>PLoS ONE</i> , 2013, 8, e68608.	2.5	21
107	Toward 959 nematode genomes. <i>Worm</i> , 2012, 1, 42-50.	1.0	51
108	A Transcriptomic Analysis of <i>Echinococcus granulosus</i> Larval Stages: Implications for Parasite Biology and Host Adaptation. <i>PLoS Neglected Tropical Diseases</i> , 2012, 6, e1897.	3.0	72

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109	The genome of the heartworm, <i>Dirofilaria immitis</i> , reveals drug and vaccine targets. FASEB Journal, 2012, 26, 4650-4661.	0.5	124
110	The biology of nematode- and IL4R1-dependent murine macrophage polarization in vivo as defined by RNA-Seq and targeted lipidomics. Blood, 2012, 120, e93-e104.	1.4	52
111	Silencing of Germline-Expressed Genes by DNA Elimination in Somatic Cells. Developmental Cell, 2012, 23, 1072-1080.	7.0	101
112	A molecular analysis of desiccation tolerance mechanisms in the anhydrobiotic nematode Panagrolaimus superbus using expressed sequenced tags. BMC Research Notes, 2012, 5, 68.	1.4	41
113	959 Nematode Genomes: a semantic wiki for coordinating sequencing projects. Nucleic Acids Research, 2012, 40, D1295-D1300.	14.5	44
114	Analysis of gene expression from the <i>Wolbachia</i> genome of a filarial nematode supports both metabolic and defensive roles within the symbiosis. Genome Research, 2012, 22, 2467-2477.	5.5	155
115	The phylogenetics of Anguillicolidae (Nematoda: Anguilliculoidea), swimbladder parasites of eels. BMC Evolutionary Biology, 2012, 12, 60.	3.2	56
116	Quantitative genome re-sequencing defines multiple mutations conferring chloroquine resistance in rodent malaria. BMC Genomics, 2012, 13, 106.	2.8	40
117	Characterisation of QTL-linked and genome-wide restriction site-associated DNA (RAD) markers in farmed Atlantic salmon. BMC Genomics, 2012, 13, 244.	2.8	120
118	The worm in the world and the world in the worm. BMC Biology, 2012, 10, 57.	3.8	14
119	Genomic islands of divergence in hybridizing <i>Heliconius</i> butterflies identified by large-scale targeted sequencing. Philosophical Transactions of the Royal Society B: Biological Sciences, 2012, 367, 343-353.	4.0	294
120	Butterfly genome reveals promiscuous exchange of mimicry adaptations among species. Nature, 2012, 487, 94-98.	27.8	1,086
121	Genomics and transcriptomics across the diversity of the Nematoda. Parasite Immunology, 2012, 34, 108-120.	1.5	22
122	Developing EPIC markers for chalcidoid Hymenoptera from EST and genomic data. Molecular Ecology Resources, 2011, 11, 521-529.	4.8	17
123	Genome-wide genetic marker discovery and genotyping using next-generation sequencing. Nature Reviews Genetics, 2011, 12, 499-510.	16.3	2,198
124	Polyphenism in social insects: insights from a transcriptome-wide analysis of gene expression in the life stages of the key pollinator, <i>Bombus terrestris</i> . BMC Genomics, 2011, 12, 623.	2.8	63
125	NEMBASE4: The nematode transcriptome resource. International Journal for Parasitology, 2011, 41, 881-894.	3.1	60
126	Velvet worms. Current Biology, 2011, 21, R238-R240.	3.9	8

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127	Simultaneous genome sequencing of symbionts and their hosts. <i>Symbiosis</i> , 2011, 55, 119-126.	2.3	37
128	iPhy: an integrated phylogenetic workbench for supermatrix analyses. <i>BMC Bioinformatics</i> , 2011, 12, 30.	2.6	10
129	Proteomic analysis of secretory products from the model gastrointestinal nematode <i>Heligmosomoides polygyrus</i> reveals dominance of Venom Allergen-Like (VAL) proteins. <i>Journal of Proteomics</i> , 2011, 74, 1573-1594.	2.4	136
130	Deep resequencing of serial sputum isolates of <i>Mycobacterium tuberculosis</i> during therapeutic failure due to poor compliance reveals stepwise mutation of key resistance genes on an otherwise stable genetic background. <i>Journal of Infection</i> , 2011, 62, 212-217.	3.3	52
131	RADSeq: next-generation population genetics. <i>Briefings in Functional Genomics</i> , 2011, 10, 108-108.	2.7	12
132	Linkage Mapping and Comparative Genomics Using Next-Generation RAD Sequencing of a Non-Model Organism. <i>PLoS ONE</i> , 2011, 6, e19315.	2.5	270
133	Nematodes: The Worm and Its Relatives. <i>PLoS Biology</i> , 2011, 9, e1001050.	5.6	110
134	jMOTU and Taxonator: Turning DNA Barcode Sequences into Annotated Operational Taxonomic Units. <i>PLoS ONE</i> , 2011, 6, e19259.	2.5	180
135	Ecdysozoan Mitogenomics: Evidence for a Common Origin of the Legged Invertebrates, the Panarthropoda. <i>Genome Biology and Evolution</i> , 2010, 2, 425-440.	2.5	154
136	Experimental evolution, genetic analysis and genome re-sequencing reveal the mutation conferring artemisinin resistance in an isogenic lineage of malaria parasites. <i>BMC Genomics</i> , 2010, 11, 499.	2.8	74
137	Comparing de novo assemblers for 454 transcriptome data. <i>BMC Genomics</i> , 2010, 11, 571.	2.8	217
138	Linking toxicant physiological mode of action with induced gene expression changes in <i>Caenorhabditis elegans</i> . <i>BMC Systems Biology</i> , 2010, 4, 32.	3.0	46
139	Phylogeny and DNA barcoding of inquiline oak gallwasps (Hymenoptera: Cynipidae) of the Western Palaearctic. <i>Molecular Phylogenetics and Evolution</i> , 2010, 55, 210-225.	2.7	92
140	Revealing the Dark Matter of the Genome. <i>Science</i> , 2010, 330, 1758-1759.	12.6	52
141	The Nematode Story: Hox Gene Loss and Rapid Evolution. <i>Advances in Experimental Medicine and Biology</i> , 2010, 689, 101-110.	1.6	14
142	Transcriptional host-virus interaction of <i>Emiliania huxleyi</i> (Haptophyceae) and EhV-86 deduced from combined analysis of expressed sequence tags and microarrays. <i>European Journal of Phycology</i> , 2010, 45, 1-12.	2.0	22
143	RADSeq: next-generation population genetics. <i>Briefings in Functional Genomics</i> , 2010, 9, 416-423.	2.7	600
144	Second-generation environmental sequencing unmask marine metazoan biodiversity. <i>Nature Communications</i> , 2010, 1, 98.	12.8	321

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145	Comparative Genome Analysis Provides Insights into the Evolution and Adaptation of <i>Pseudomonas syringae</i> pv. <i>aesculi</i> on <i>Aesculus hippocastanum</i> . PLoS ONE, 2010, 5, e10224.	2.5	104
146	A Cryptoendolithic Community in Volcanic Glass. Astrobiology, 2009, 9, 369-381.	3.0	55
147	A P2X receptor from the tardigrade species <i>Hypsibius dujardini</i> with fast kinetics and sensitivity to zinc and copper. BMC Evolutionary Biology, 2009, 9, 17.	3.2	44
148	The components of the <i>Daphnia pulex</i> immune system as revealed by complete genome sequencing. BMC Genomics, 2009, 10, 175.	2.8	93
149	Analysis of the genome sequences of three <i>Drosophila melanogaster</i> spontaneous mutation accumulation lines. Genome Research, 2009, 19, 1195-1201.	5.5	343
150	Expressed Sequence Tags: An Overview. Methods in Molecular Biology, 2009, 533, 1-12.	0.9	86
151	Obtaining Accurate Translations from Expressed Sequence Tags. Methods in Molecular Biology, 2009, 533, 221-239.	0.9	5
152	EST Processing: From Trace to Sequence. Methods in Molecular Biology, 2009, 533, 189-220.	0.9	3
153	Genome sequence of the metazoan plant-parasitic nematode <i>Meloidogyne incognita</i> . Nature Biotechnology, 2008, 26, 909-915.	17.5	1,012
154	annot8: GO, EC and KEGG annotation of EST datasets. BMC Bioinformatics, 2008, 9, 180.	2.6	87
155	Transcriptome profiling of developmental and xenobiotic responses in a keystone soil animal, the oligochaete annelid <i>Lumbricus rubellus</i> . BMC Genomics, 2008, 9, 266.	2.8	93
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157	Bacterial Colonization and Weathering of Terrestrial Obsidian in Iceland. Geomicrobiology Journal, 2008, 25, 25-37.	2.0	49
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