Eugene Berezikov

List of Publications by Year
in descending order

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111	14,863	38742 50	27406 106
papers	citations	h-index	g-index

120	120	120	18891
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	MicroRNA Expression in Zebrafish Embryonic Development. Science, 2005, 309, 310-311.	12.6	1,448
2	Phylogenetic Shadowing and Computational Identification of Human microRNA Genes. Cell, 2005, 120, 21-24.	28.9	1,194
3	Identification of Functional Elements and Regulatory Circuits by Drosophila modENCODE. Science, 2010, 330, 1787-1797.	12.6	1,124
4	A Role for Piwi and piRNAs in Germ Cell Maintenance and Transposon Silencing in Zebrafish. Cell, 2007, 129, 69-82.	28.9	989
5	Mammalian Mirtron Genes. Molecular Cell, 2007, 28, 328-336.	9.7	675
6	Evolution of microRNA diversity and regulation in animals. Nature Reviews Genetics, 2011, 12, 846-860.	16.3	645
7	The ctenophore genome and the evolutionary origins of neural systems. Nature, 2014, 510, 109-114.	27.8	606
8	Diversity of microRNAs in human and chimpanzee brain. Nature Genetics, 2006, 38, 1375-1377.	21.4	457
9	Approaches to microRNA discovery. Nature Genetics, 2006, 38, S2-S7.	21.4	453
10	Piwi and piRNAs Act Upstream of an Endogenous siRNA Pathway to Suppress Tc3 Transposon Mobility in the Caenorhabditis elegans Germline. Molecular Cell, 2008, 31, 79-90.	9.7	392
11	The TRIM-NHL Protein TRIM32 Activates MicroRNAs and Prevents Self-Renewal in Mouse Neural Progenitors. Cell, 2009, 136, 913-925.	28.9	372
12	Zili is required for germ cell differentiation and meiosis in zebrafish. EMBO Journal, 2008, 27, 2702-2711.	7.8	273
13	Differences in vertebrate microRNA expression. Proceedings of the National Academy of Sciences of the United States of America, 2006, 103, 14385-14389.	7.1	251
14	Genome-wide RNA Tomography in the Zebrafish Embryo. Cell, 2014, 159, 662-675.	28.9	248
15	Many novel mammalian microRNA candidates identified by extensive cloning and RAKE analysis. Genome Research, 2006, 16, 1289-1298.	5.5	242
16	Detection of microRNAs in frozen tissue sections by fluorescence in situ hybridization using locked nucleic acid probes and tyramide signal amplification. Nature Protocols, 2007, 2, 2520-2528.	12.0	221
17	Deep annotation of Drosophila melanogaster microRNAs yields insights into their processing, modification, and emergence. Genome Research, 2011, 21, 203-215.	5.5	207
18	Extremely stable Piwi-induced gene silencing inCaenorhabditis elegans. EMBO Journal, 2012, 31, 3422-3430.	7.8	197

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19	Functionally distinct regulatory RNAs generated by bidirectional transcription and processing of microRNA loci. Genes and Development, 2008, 22, 26-36.	5.9	185
20	microRNAs associated with the different human Argonaute proteins. Nucleic Acids Research, 2012, 40, 9850-9862.	14.5	179
21	Spatially Resolved Genome-wide Transcriptional Profiling Identifies BMP Signaling as Essential Regulator of Zebrafish Cardiomyocyte Regeneration. Developmental Cell, 2016, 36, 36-49.	7.0	176
22	Genetic variation in the zebrafish. Genome Research, 2006, 16, 491-497.	5.5	173
23	Cloning and expression of new microRNAs from zebrafish. Nucleic Acids Research, 2006, 34, 2558-2569.	14.5	169
24	Abundant primary piRNAs, endo-siRNAs, and microRNAs in a Drosophila ovary cell line. Genome Research, 2009, 19, 1776-1785.	5.5	164
25	CDE-1 Affects Chromosome Segregation through Uridylation of CSR-1-Bound siRNAs. Cell, 2009, 139, 135-148.	28.9	164
26	miRNA Nomenclature: A View Incorporating Genetic Origins, Biosynthetic Pathways, and Sequence Variants. Trends in Genetics, 2015, 31, 613-626.	6.7	164
27	Signature of circulating <scp>microRNAs</scp> in patients with acute heart failure. European Journal of Heart Failure, 2016, 18, 414-423.	7.1	162
28	Hen1 is required for oocyte development and piRNA stability in zebrafish. EMBO Journal, 2010, 29, 3688-3700.	7.8	145
29	Genome-wide profiling of nucleosome sensitivity and chromatin accessibility inDrosophila melanogaster. Nucleic Acids Research, 2016, 44, 1036-1051.	14.5	111
30	Repertoire and evolution of miRNA genes in four divergent nematode species. Genome Research, 2009, 19, 2064-2074.	5.5	107
31	Evolutionary flux of canonical microRNAs and mirtrons in Drosophila. Nature Genetics, 2010, 42, 6-9.	21.4	105
32	Systemic miRNA-7 delivery inhibits tumor angiogenesis and growth in murine xenograft glioblastoma. Oncotarget, 2014, 5, 6687-6700.	1.8	105
33	Mouse microRNA profiles determined with a new and sensitive cloning method. Nucleic Acids Research, 2006, 34, e115-e115.	14.5	96
34	Differential Impact of the HEN1 Homolog HENN-1 on 21U and 26G RNAs in the Germline of Caenorhabditis elegans. PLoS Genetics, 2012, 8, e1002702.	3.5	96
35	A Deep Sequencing Approach to Uncover the miRNOME in the Human Heart. PLoS ONE, 2013, 8, e57800.	2.5	88
36	Camels and zebrafish, viruses and cancer: a microRNA update. Human Molecular Genetics, 2005, 14, R183-R190.	2.9	86

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37	SEX ALLOCATION ADJUSTMENT TO MATING GROUP SIZE IN A SIMULTANEOUS HERMAPHRODITE. Evolution; International Journal of Organic Evolution, 2013, 67, 3233-3242.	2.3	82
38	miR-378a-3p modulates tamoxifen sensitivity in breast cancer MCF-7 cells through targeting GOLT1A. Scientific Reports, 2015, 5, 13170.	3.3	82
39	CONREAL: Conserved Regulatory Elements Anchored Alignment Algorithm for Identification of Transcription Factor Binding Sites by Phylogenetic Footprinting. Genome Research, 2003, 14, 170-178.	5.5	78
40	Homologous gene targeting in Caenorhabditis elegans by biolistic transformation. Nucleic Acids Research, 2004, 32, 40e-40.	14.5	78
41	CONREAL web server: identification and visualization of conserved transcription factor binding sites. Nucleic Acids Research, 2005, 33, W447-W450.	14.5	78
42	Small RNAs and the control of transposons and viruses in Drosophila. Trends in Microbiology, 2009, 17, 163-171.	7.7	77
43	Potential role of miR-29b in modulation ofDnmt3aandDnmt3bexpression in primordial germ cells of female mouse embryos. Rna, 2009, 15, 1507-1514.	3.5	70
44	Tdrd1 acts as a molecular scaffold for Piwi proteins and piRNA targets in zebrafish. EMBO Journal, 2011, 30, 3298-3308.	7.8	70
45	MicroRNAâ€“Directed siRNA Biogenesis in Caenorhabditis elegans. PLoS Genetics, 2010, 6, e1000903.	3.5	67
46	Low circulating microRNA levels in heart failure patients are associated with atherosclerotic disease and cardiovascular-related rehospitalizations. Clinical Research in Cardiology, 2017, 106, 598-609.	3.3	66
47	Guanine quadruplex structures localize to heterochromatin. Nucleic Acids Research, 2016, 44, 152-163.	14.5	60
48	Efficient transgenesis and annotated genome sequence of the regenerative flatworm model Macrostomum lignano. Nature Communications, 2017, 8, 2120.	12.8	60
49	Expression patterns of intronic microRNAs in Caenorhabditis elegans. Silence: A Journal of RNA Regulation, 2010, 1, 5.	8.1	59
50	Spatial Transcriptomics of C.Âelegans Males and Hermaphrodites Identifies Sex-Specific Differences in Gene Expression Patterns. Developmental Cell, 2018, 47, 801-813.e6.	7.0	55
51	Evidence for post-transcriptional regulation of clustered microRNAs in Drosophila. BMC Genomics, 2011, 12, 371.	2.8	54
52	Use of biomarkers to establish potential role and function of circulating microRNAs in acute heart failure. International Journal of Cardiology, 2016, 224, 231-239.	1.7	53
53	LPIN2 Is Associated With Type 2 Diabetes, Glucose Metabolism, and Body Composition. Diabetes, 2007, 56, 3020-3026.	0.6	52
54	Single Nucleotide Polymorphisms Associated With Rat Expressed Sequences. Genome Research, 2004, 14, 1438-1443.	5.5	50

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55	Modeling Human Cardiac Hypertrophy in Stem Cell-Derived Cardiomyocytes. Stem Cell Reports, 2018, 10, 794-807.	4.8	49
56	Neuronal Activity Regulates Hippocampal miRNA Expression. PLoS ONE, 2011, 6, e25068.	2.5	48
57	Biological adhesion of the flatworm Macrostomum lignano relies on a duo-gland system and is mediated by a cell type-specific intermediate filament protein. Frontiers in Zoology, 2014, 11, 12.	2.0	46
58	Evidence for Karyotype Polymorphism in the Free-Living Flatworm, Macrostomum lignano, a Model Organism for Evolutionary and Developmental Biology. PLoS ONE, 2016, 11, e0164915.	2.5	46
59	MicroRNA mir-34 provides robustness to environmental stress response via the DAF-16 network in C. elegans. Scientific Reports, 2016, 6, 36766.	3.3	44
60	Transcriptional signatures of somatic neoblasts and germline cells in Macrostomum lignano. ELife, 2016, 5, .	6.0	41
61	Boule-like genes regulate male and female gametogenesis in the flatworm Macrostomum lignano. Developmental Biology, 2011, 357, 117-132.	2.0	39
62	A position-dependent organisation of retinoid response elements is conserved in the vertebrate Hox clusters. Trends in Genetics, 2003, 19, 476-479.	6.7	38
63	Profiling of adhesive-related genes in the freshwater cnidarianHydra magnipapillataby transcriptomics and proteomics. Biofouling, 2016, 32, 1115-1129.	2.2	36
64	Accumulation of 5-oxoproline in myocardial dysfunction and the protective effects of OPLAH. Science Translational Medicine, 2017, 9, .	12.4	36
65	Electrical stimulation shifts healing/scarring towards regeneration in a rat limb amputation model. Scientific Reports, 2019, 9, 11433.	3.3	36
66	MicroRNAs relate to early worsening of renal function in patients with acute heart failure. International Journal of Cardiology, 2016, 203, 564-569.	1.7	35
67	A search for reverse transcriptase-coding sequences reveals new non-LTR retrotransposons in the genome of Drosophila melanogaster. Genome Biology, 2000, 1, research0012.1.	9.6	34
68	Positional RNA-Seq identifies candidate genes for phenotypic engineering of sexual traits. Frontiers in Zoology, 2015, 12, 14.	2.0	34
69	Controlling miRNA Regulation in Disease. Methods in Molecular Biology, 2012, 822, 1-18.	0.9	33
70	The free-living flatworm Macrostomum lignano. EvoDevo, 2020, 11, 5.	3.2	33
71	Fine-tuning the brain: MicroRNAs. Frontiers in Neuroendocrinology, 2010, 31, 128-133.	5.2	31
72	Towards the identification of ancestrally shared regenerative mechanisms across the Metazoa: A Transcriptomic case study in the Demosponge Halisarca caerulea. Marine Genomics, 2018, 37, 135-147.	1.1	31

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73	Sex allocation plasticity on a transcriptome scale: Socially sensitive gene expression in a simultaneous hermaphrodite. Molecular Ecology, 2019, 28, 2321-2341.	3.9	30
74	Organ specific gene expression in the regenerating tail of Macrostomum lignano. Developmental Biology, 2018, 433, 448-460.	2.0	28
75	Multispecies RNA tomography reveals regulators of hematopoietic stem cell birth in the embryonic aorta. Blood, 2020, 136, 831-844.	1.4	28
76	Mesodermal Gene Expression in the Acoel Isodiametra pulchra Indicates a Low Number of Mesodermal Cell Types and the Endomesodermal Origin of the Gonads. PLoS ONE, 2013, 8, e55499.	2.5	26
77	Rodent heart failure models do not reflect the human circulating microRNA signature in heart failure. PLoS ONE, 2017, 12, e0177242.	2.5	25
78	A panâ€metazoan concept for adult stem cells: the wobbling <scp>Penrose</scp> landscape. Biological Reviews, 2022, 97, 299-325.	10.4	25
79	A novel flatworm-specific gene implicated in reproduction in Macrostomum lignano. Scientific Reports, 2018, 8, 3192.	3.3	24
80	Resilience to aging in the regenerationâ€capable flatworm Macrostomum lignano. Aging Cell, 2018, 17, e12739.	6.7	22
81	CASCAD: a database of annotated candidate single nucleotide polymorphisms associated with expressed sequences. BMC Genomics, 2005, 6, 10.	2.8	21
82	The Hippo Pathway Regulates Stem Cells During Homeostasis and Regeneration of the FlatwormMacrostomum Lignano. Stem Cells and Development, 2013, 22, 2174-2185.	2.1	21
83	Chromosome Evolution in the Free-Living Flatworms: First Evidence of Intrachromosomal Rearrangements in Karyotype Evolution of Macrostomum lignano (Platyhelminthes, Macrostomida). Genes, 2017, 8, 298.	2.4	21
84	The FlatwormMacrostomum lignanoIs a Powerful Model Organism for Ion Channel and Stem Cell Research. Stem Cells International, 2012, 2012, 1-10.	2.5	20
85	Influence of temperature on development, reproduction and regeneration in the flatworm model organism, Macrostomum lignano. Zoological Letters, 2019, 5, 7.	1.3	20
86	MicroRNA expression profiles of human leukemias. Leukemia, 2008, 22, 1274-1278.	7.2	19
87	GENOTRACE: cDNA-based local GENOme assembly from TRACE archives. Bioinformatics, 2002, 18, 1396-1397.	4.1	17
88	Tracing the evolution of tissue identity with microRNAs. Genome Biology, 2010, 11, 111.	9.6	16
89	Gene silencing pathways found in the green alga Volvox carteri reveal insights into evolution and origins of small RNA systems in plants. BMC Genomics, 2016, 17, 853.	2.8	15
90	The regenerative flatworm Macrostomum lignano, a model organism with high experimental potential. International Journal of Developmental Biology, 2018, 62, 551-558.	0.6	15

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91	Selenoprotein DIO2 Is a Regulator of Mitochondrial Function, Morphology and UPRmt in Human Cardiomyocytes. International Journal of Molecular Sciences, 2021, 22, 11906.	4.1	13
92	Identification of Waldo-A and Waldo-B, Two Closely Related Non-LTR Retrotransposons in Drosophila. Molecular Biology and Evolution, 2001, 18, 196-205.	8.9	12
93	Functional microRNA screening using a comprehensive lentiviral human microRNA expression library. BMC Genomics, 2011, 12, 546.	2.8	12
94	piRNA dynamics in divergent zebrafish strains reveal long-lasting maternal influence on zygotic piRNA profiles. Rna, 2013, 19, 345-356.	3.5	12
95	Novel small RNA expression libraries uncover hsa-miR-30b and hsa-miR-30c as important factors in anoikis resistance. Rna, 2013, 19, 1711-1725.	3.5	12
96	Biolistic Transformation of Caenorhabditis elegans. Methods in Molecular Biology, 2013, 940, 77-86.	0.9	12
97	Exploring Conservation of Transcription Factor Binding Sites with CONREAL. Methods in Molecular Biology, 2007, 395, 437-448.	0.9	9
98	Expression Pattern Analysis of MicroRNAs in Caenorhabditis elegans. Methods in Molecular Biology, 2013, 936, 129-141.	0.9	8
99	The Evolution of SINEs and LINEs in the Genus Chironomus (Diptera). Journal of Molecular Evolution, 2004, 58, 269-279.	1.8	6
100	Identifying polymorphisms in the Rattus norvegicus D3 dopamine receptor gene and regulatory region. Genes, Brain and Behavior, 2004, 3, 138-148.	2.2	5
101	TIM29 is required for enhanced stem cell activity during regeneration in the flatworm Macrostomum lignano. Scientific Reports, 2021, 11, 1166.	3.3	3
102	Structure and polymorphism of the Chironomus thummi gene encoding special lobe-specific silk protein, ssp1601Published in conjunction with A Wisconsin Gathering Honoring Waclaw Szybalski on the occasion of his 75th year and 20 years of Editorship-in-Chief of Gene, 10â€“11 August 1997, University of Wisconsin, Madison, WI, USA.1. Gene, 1998, 223, 347-354.	2.2	2
103	Sample Preparation for Small RNA Massive Parallel Sequencing. Methods in Molecular Biology, 2012, 786, 167-178.	0.9	2
104	Computational analysis of spliced leader trans-splicing in the regenerative flatworm <i>Macrostomum lignano</i> reveals its prevalence in conserved and stem cell related genes. Vavilovskii Zhurnal Genetiki I Selektsii, 2021, 25, 101-107.	1.1	2
105	Proof of principle for piggyBac-mediated transgenesis in the flatworm Macrostomum lignano. Genetics, 2021, 218, .	2.9	2
106	Hen1 is required for oocyte development and piRNA stability in zebrafish. EMBO Journal, 2012, 31, 248-248.	7.8	0
107	Macrostomum lignano as a model to study the genetics and genomics of parasitic flatworms. Vavilovskii Zhurnal Genetiki I Selektsii, 2021, 25, 108-116.	1.1	0
108	Abstract 1112: Identification of microRNA-based therapeutic candidates using a unique lentiviral microRNA overexpression library. , 2012, , .		0

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109	Random Integration Transgenesis in a Free-Living Regenerative Flatworm Macrostomum lignano. Methods in Molecular Biology, 2022, 2450, 493-508.	0.9	0
110	Exploring Conservation of Transcription Factor Binding Sites with CONREAL. , 0, , 437-448.		0
111	MicroRNA Discovery and Expression Profiling using Next-Generation Sequencing. , 0, , 217-228.		0