

# Eugene Berezikov

## List of Publications by Year in descending order

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111  
papers

14,863  
citations

38742

50  
h-index

27406

106  
g-index

120  
all docs

120  
docs citations

120  
times ranked

18891  
citing authors

#	ARTICLE	IF	CITATIONS
1	A pan-€metazoan concept for adult stem cells: the wobbling <sc>Penrose</sc> landscape. Biological Reviews, 2022, 97, 299-325.	10.4	25
2	Random Integration Transgenesis in a Free-Living Regenerative Flatworm <i>Macrostomum lignano</i> . Methods in Molecular Biology, 2022, 2450, 493-508.	0.9	0
3	<i>Macrostomum lignano</i> as a model to study the genetics and genomics of parasitic flatworms. Vavilovskii Zhurnal Genetiki I Seleksii, 2021, 25, 108-116.	1.1	0
4	Computational analysis of spliced leader trans-splicing in the regenerative flatworm &lt;i>Macrostomum lignano</i> reveals its prevalence in conserved and stem cell related genes. Vavilovskii Zhurnal Genetiki I Seleksii, 2021, 25, 101-107.	1.1	2
5	Proof of principle for piggyBac-mediated transgenesis in the flatworm <i>Macrostomum lignano</i> . Genetics, 2021, 218, .	2.9	2
6	TIM29 is required for enhanced stem cell activity during regeneration in the flatworm <i>Macrostomum lignano</i> . Scientific Reports, 2021, 11, 1166.	3.3	3
7	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
8	Multispecies RNA tomography reveals regulators of hematopoietic stem cell birth in the embryonic aorta. Blood, 2020, 136, 831-844.	1.4	28
9	The free-living flatworm <i>Macrostomum lignano</i> . EvoDevo, 2020, 11, 5.	3.2	33
10	Electrical stimulation shifts healing/scarring towards regeneration in a rat limb amputation model. Scientific Reports, 2019, 9, 11433.	3.3	36
11	Sex allocation plasticity on a transcriptome scale: Socially sensitive gene expression in a simultaneous hermaphrodite. Molecular Ecology, 2019, 28, 2321-2341.	3.9	30
12	Influence of temperature on development, reproduction and regeneration in the flatworm model organism, <i>Macrostomum lignano</i> . Zoological Letters, 2019, 5, 7.	1.3	20
13	Modeling Human Cardiac Hypertrophy in Stem Cell-Derived Cardiomyocytes. Stem Cell Reports, 2018, 10, 794-807.	4.8	49
14	Resilience to aging in the regeneration-€capable flatworm <i>Macrostomum lignano</i>. Aging Cell, 2018, 17, e12739.	6.7	22
15	A novel flatworm-specific gene implicated in reproduction in <i>Macrostomum lignano</i> . Scientific Reports, 2018, 8, 3192.	3.3	24
16	Organ specific gene expression in the regenerating tail of <i>Macrostomum lignano</i> . Developmental Biology, 2018, 433, 448-460.	2.0	28
17	Spatial Transcriptomics of <i>C.Ælegans</i> Males and Hermaphrodites Identifies Sex-Specific Differences in Gene Expression Patterns. Developmental Cell, 2018, 47, 801-813.e6.	7.0	55
18	The regenerative flatworm <i>Macrostomum lignano</i> , a model organism with high experimental potential. International Journal of Developmental Biology, 2018, 62, 551-558.	0.6	15

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19	Towards the identification of ancestrally shared regenerative mechanisms across the Metazoa: A Transcriptomic case study in the Demosponge <i>Halisarca caerulea</i> . <i>Marine Genomics</i> , 2018, 37, 135-147.	1.1	31
20	Low circulating microRNA levels in heart failure patients are associated with atherosclerotic disease and cardiovascular-related rehospitalizations. <i>Clinical Research in Cardiology</i> , 2017, 106, 598-609.	3.3	66
21	Efficient transgenesis and annotated genome sequence of the regenerative flatworm model <i>Macrostomum lignano</i> . <i>Nature Communications</i> , 2017, 8, 2120.	12.8	60
22	Accumulation of 5-oxoproline in myocardial dysfunction and the protective effects of OPLAH. <i>Science Translational Medicine</i> , 2017, 9, .	12.4	36
23	Chromosome Evolution in the Free-Living Flatworms: First Evidence of Intrachromosomal Rearrangements in Karyotype Evolution of <i>Macrostomum lignano</i> (Platyhelminthes, Macrostomida). <i>Genes</i> , 2017, 8, 298.	2.4	21
24	Rodent heart failure models do not reflect the human circulating microRNA signature in heart failure. <i>PLoS ONE</i> , 2017, 12, e0177242.	2.5	25
25	Evidence for Karyotype Polymorphism in the Free-Living Flatworm, <i>Macrostomum lignano</i> , a Model Organism for Evolutionary and Developmental Biology. <i>PLoS ONE</i> , 2016, 11, e0164915.	2.5	46
26	Gene silencing pathways found in the green alga <i>Volvox carteri</i> reveal insights into evolution and origins of small RNA systems in plants. <i>BMC Genomics</i> , 2016, 17, 853.	2.8	15
27	Signature of circulating <sc>microRNAs</sc> in patients with acute heart failure. <i>European Journal of Heart Failure</i> , 2016, 18, 414-423.	7.1	162
28	MicroRNA mir-34 provides robustness to environmental stress response via the DAF-16 network in <i>C. elegans</i> . <i>Scientific Reports</i> , 2016, 6, 36766.	3.3	44
29	Use of biomarkers to establish potential role and function of circulating microRNAs in acute heart failure. <i>International Journal of Cardiology</i> , 2016, 224, 231-239.	1.7	53
30	Profiling of adhesive-related genes in the freshwater cnidarian <i>Hydra magnipapillata</i> by transcriptomics and proteomics. <i>Biofouling</i> , 2016, 32, 1115-1129.	2.2	36
31	Spatially Resolved Genome-wide Transcriptional Profiling Identifies BMP Signaling as Essential Regulator of Zebrafish Cardiomyocyte Regeneration. <i>Developmental Cell</i> , 2016, 36, 36-49.	7.0	176
32	MicroRNAs relate to early worsening of renal function in patients with acute heart failure. <i>International Journal of Cardiology</i> , 2016, 203, 564-569.	1.7	35
33	Guanine quadruplex structures localize to heterochromatin. <i>Nucleic Acids Research</i> , 2016, 44, 152-163.	14.5	60
34	Genome-wide profiling of nucleosome sensitivity and chromatin accessibility in <i>Drosophila melanogaster</i> . <i>Nucleic Acids Research</i> , 2016, 44, 1036-1051.	14.5	111
35	Transcriptional signatures of somatic neoblasts and germline cells in <i>Macrostomum lignano</i> . <i>ELife</i> , 2016, 5, .	6.0	41
36	miR-378a-3p modulates tamoxifen sensitivity in breast cancer MCF-7 cells through targeting GOLT1A. <i>Scientific Reports</i> , 2015, 5, 13170.	3.3	82

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37	Positional RNA-Seq identifies candidate genes for phenotypic engineering of sexual traits. <i>Frontiers in Zoology</i> , 2015, 12, 14.	2.0	34
38	miRNA Nomenclature: A View Incorporating Genetic Origins, Biosynthetic Pathways, and Sequence Variants. <i>Trends in Genetics</i> , 2015, 31, 613-626.	6.7	164
39	Biological adhesion of the flatworm <i>Macrostomum lignano</i> relies on a duo-gland system and is mediated by a cell type-specific intermediate filament protein. <i>Frontiers in Zoology</i> , 2014, 11, 12.	2.0	46
40	The ctenophore genome and the evolutionary origins of neural systems. <i>Nature</i> , 2014, 510, 109-114.	27.8	606
41	Genome-wide RNA Tomography in the Zebrafish Embryo. <i>Cell</i> , 2014, 159, 662-675.	28.9	248
42	Systemic miRNA-7 delivery inhibits tumor angiogenesis and growth in murine xenograft glioblastoma. <i>Oncotarget</i> , 2014, 5, 6687-6700.	1.8	105
43	piRNA dynamics in divergent zebrafish strains reveal long-lasting maternal influence on zygotic piRNA profiles. <i>Rna</i> , 2013, 19, 345-356.	3.5	12
44	Expression Pattern Analysis of MicroRNAs in <i>Caenorhabditis elegans</i> . <i>Methods in Molecular Biology</i> , 2013, 936, 129-141.	0.9	8
45	Mesodermal Gene Expression in the Acoel <i>Isodiametra pulchra</i> Indicates a Low Number of Mesodermal Cell Types and the Endomesodermal Origin of the Gonads. <i>PLoS ONE</i> , 2013, 8, e55499.	2.5	26
46	The Hippo Pathway Regulates Stem Cells During Homeostasis and Regeneration of the Flatworm <i>Macrostomum Lignano</i> . <i>Stem Cells and Development</i> , 2013, 22, 2174-2185.	2.1	21
47	Novel small RNA expression libraries uncover hsa-miR-30b and hsa-miR-30c as important factors in anoikis resistance. <i>Rna</i> , 2013, 19, 1711-1725.	3.5	12
48	A Deep Sequencing Approach to Uncover the miRNOME in the Human Heart. <i>PLoS ONE</i> , 2013, 8, e57800.	2.5	88
49	SEX ALLOCATION ADJUSTMENT TO MATING GROUP SIZE IN A SIMULTANEOUS HERMAPHRODITE. <i>Evolution; International Journal of Organic Evolution</i> , 2013, 67, 3233-3242.	2.3	82
50	Biolistic Transformation of <i>Caenorhabditis elegans</i> . <i>Methods in Molecular Biology</i> , 2013, 940, 77-86.	0.9	12
51	Extremely stable Piwi-induced gene silencing in <i>Caenorhabditis elegans</i> . <i>EMBO Journal</i> , 2012, 31, 3422-3430.	7.8	197
52	Hen1 is required for oocyte development and piRNA stability in zebrafish. <i>EMBO Journal</i> , 2012, 31, 248-248.	7.8	0
53	The Flatworm <i>Macrostomum lignano</i> a Powerful Model Organism for Ion Channel and Stem Cell Research. <i>Stem Cells International</i> , 2012, 2012, 1-10.	2.5	20
54	Differential Impact of the HEN1 Homolog HENN-1 on 21U and 26G RNAs in the Germline of <i>Caenorhabditis elegans</i> . <i>PLoS Genetics</i> , 2012, 8, e1002702.	3.5	96

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55	microRNAs associated with the different human Argonaute proteins. <i>Nucleic Acids Research</i> , 2012, 40, 9850-9862.	14.5	179
56	Sample Preparation for Small RNA Massive Parallel Sequencing. <i>Methods in Molecular Biology</i> , 2012, 786, 167-178.	0.9	2
57	Controlling miRNA Regulation in Disease. <i>Methods in Molecular Biology</i> , 2012, 822, 1-18.	0.9	33
58	Abstract 1112: Identification of microRNA-based therapeutic candidates using a unique lentiviral microRNA overexpression library. , 2012, , .		0
59	Tdrd1 acts as a molecular scaffold for Piwi proteins and piRNA targets in zebrafish. <i>EMBO Journal</i> , 2011, 30, 3298-3308.	7.8	70
60	Evolution of microRNA diversity and regulation in animals. <i>Nature Reviews Genetics</i> , 2011, 12, 846-860.	16.3	645
61	Boule-like genes regulate male and female gametogenesis in the flatworm <i>Macrostomum lignano</i> . <i>Developmental Biology</i> , 2011, 357, 117-132.	2.0	39
62	Evidence for post-transcriptional regulation of clustered microRNAs in <i>Drosophila</i> . <i>BMC Genomics</i> , 2011, 12, 371.	2.8	54
63	Functional microRNA screening using a comprehensive lentiviral human microRNA expression library. <i>BMC Genomics</i> , 2011, 12, 546.	2.8	12
64	Deep annotation of <i>Drosophila melanogaster</i> microRNAs yields insights into their processing, modification, and emergence. <i>Genome Research</i> , 2011, 21, 203-215.	5.5	207
65	Neuronal Activity Regulates Hippocampal miRNA Expression. <i>PLoS ONE</i> , 2011, 6, e25068.	2.5	48
66	Fine-tuning the brain: MicroRNAs. <i>Frontiers in Neuroendocrinology</i> , 2010, 31, 128-133.	5.2	31
67	Expression patterns of intronic microRNAs in <i>Caenorhabditis elegans</i> . <i>Silence: A Journal of RNA Regulation</i> , 2010, 1, 5.	8.1	59
68	Hen1 is required for oocyte development and piRNA stability in zebrafish. <i>EMBO Journal</i> , 2010, 29, 3688-3700.	7.8	145
69	Evolutionary flux of canonical microRNAs and mirtrons in <i>Drosophila</i> . <i>Nature Genetics</i> , 2010, 42, 6-9.	21.4	105
70	MicroRNA-directed siRNA Biogenesis in <i>Caenorhabditis elegans</i> . <i>PLoS Genetics</i> , 2010, 6, e1000903.	3.5	67
71	Identification of Functional Elements and Regulatory Circuits by <i>Drosophila</i> modENCODE. <i>Science</i> , 2010, 330, 1787-1797.	12.6	1,124
72	Tracing the evolution of tissue identity with microRNAs. <i>Genome Biology</i> , 2010, 11, 111.	9.6	16

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73	Potential role of miR-29b in modulation of <i>Dnmt3a</i> and <i>Dnmt3b</i> expression in primordial germ cells of female mouse embryos. <i>Rna</i> , 2009, 15, 1507-1514.	3.5	70
74	Abundant primary piRNAs, endo-siRNAs, and microRNAs in a <i>Drosophila</i> ovary cell line. <i>Genome Research</i> , 2009, 19, 1776-1785.	5.5	164
75	Repertoire and evolution of miRNA genes in four divergent nematode species. <i>Genome Research</i> , 2009, 19, 2064-2074.	5.5	107
76	The TRIM-NHL Protein TRIM32 Activates MicroRNAs and Prevents Self-Renewal in Mouse Neural Progenitors. <i>Cell</i> , 2009, 136, 913-925.	28.9	372
77	CDE-1 Affects Chromosome Segregation through Uridylation of CSR-1-Bound siRNAs. <i>Cell</i> , 2009, 139, 135-148.	28.9	164
78	Small RNAs and the control of transposons and viruses in <i>Drosophila</i> . <i>Trends in Microbiology</i> , 2009, 17, 163-171.	7.7	77
79	Zili is required for germ cell differentiation and meiosis in zebrafish. <i>EMBO Journal</i> , 2008, 27, 2702-2711.	7.8	273
80	MicroRNA expression profiles of human leukemias. <i>Leukemia</i> , 2008, 22, 1274-1278.	7.2	19
81	Piwi and piRNAs Act Upstream of an Endogenous siRNA Pathway to Suppress Tc3 Transposon Mobility in the <i>Caenorhabditis elegans</i> Germline. <i>Molecular Cell</i> , 2008, 31, 79-90.	9.7	392
82	Functionally distinct regulatory RNAs generated by bidirectional transcription and processing of microRNA loci. <i>Genes and Development</i> , 2008, 22, 26-36.	5.9	185
83	<i>LPIN2</i> Is Associated With Type 2 Diabetes, Glucose Metabolism, and Body Composition. <i>Diabetes</i> , 2007, 56, 3020-3026.	0.6	52
84	A Role for Piwi and piRNAs in Germ Cell Maintenance and Transposon Silencing in Zebrafish. <i>Cell</i> , 2007, 129, 69-82.	28.9	989
85	Mammalian Mirtron Genes. <i>Molecular Cell</i> , 2007, 28, 328-336.	9.7	675
86	Detection of microRNAs in frozen tissue sections by fluorescence in situ hybridization using locked nucleic acid probes and tyramide signal amplification. <i>Nature Protocols</i> , 2007, 2, 2520-2528.	12.0	221
87	Exploring Conservation of Transcription Factor Binding Sites with CONREAL. <i>Methods in Molecular Biology</i> , 2007, 395, 437-448.	0.9	9
88	Cloning and expression of new microRNAs from zebrafish. <i>Nucleic Acids Research</i> , 2006, 34, 2558-2569.	14.5	169
89	Approaches to microRNA discovery. <i>Nature Genetics</i> , 2006, 38, S2-S7.	21.4	453
90	Diversity of microRNAs in human and chimpanzee brain. <i>Nature Genetics</i> , 2006, 38, 1375-1377.	21.4	457

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91	Mouse microRNA profiles determined with a new and sensitive cloning method. <i>Nucleic Acids Research</i> , 2006, 34, e115-e115.	14.5	96
92	Differences in vertebrate microRNA expression. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006, 103, 14385-14389.	7.1	251
93	Genetic variation in the zebrafish. <i>Genome Research</i> , 2006, 16, 491-497.	5.5	173
94	Many novel mammalian microRNA candidates identified by extensive cloning and RAKE analysis. <i>Genome Research</i> , 2006, 16, 1289-1298.	5.5	242
95	CASCAD: a database of annotated candidate single nucleotide polymorphisms associated with expressed sequences. <i>BMC Genomics</i> , 2005, 6, 10.	2.8	21
96	Camels and zebrafish, viruses and cancer: a microRNA update. <i>Human Molecular Genetics</i> , 2005, 14, R183-R190.	2.9	86
97	CONREAL web server: identification and visualization of conserved transcription factor binding sites. <i>Nucleic Acids Research</i> , 2005, 33, W447-W450.	14.5	78
98	Phylogenetic Shadowing and Computational Identification of Human microRNA Genes. <i>Cell</i> , 2005, 120, 21-24.	28.9	1,194
99	MicroRNA Expression in Zebrafish Embryonic Development. <i>Science</i> , 2005, 309, 310-311.	12.6	1,448
100	Homologous gene targeting in <i>Caenorhabditis elegans</i> by biolistic transformation. <i>Nucleic Acids Research</i> , 2004, 32, 40e-40.	14.5	78
101	Single Nucleotide Polymorphisms Associated With Rat Expressed Sequences. <i>Genome Research</i> , 2004, 14, 1438-1443.	5.5	50
102	Identifying polymorphisms in the <i>Rattus norvegicus</i> D3 dopamine receptor gene and regulatory region. <i>Genes, Brain and Behavior</i> , 2004, 3, 138-148.	2.2	5
103	The Evolution of SINEs and LINEs in the Genus <i>Chironomus</i> (Diptera). <i>Journal of Molecular Evolution</i> , 2004, 58, 269-279.	1.8	6
104	A position-dependent organisation of retinoid response elements is conserved in the vertebrate Hox clusters. <i>Trends in Genetics</i> , 2003, 19, 476-479.	6.7	38
105	CONREAL: Conserved Regulatory Elements Anchored Alignment Algorithm for Identification of Transcription Factor Binding Sites by Phylogenetic Footprinting. <i>Genome Research</i> , 2003, 14, 170-178.	5.5	78
106	GENOTRACE: cDNA-based local GENOME assembly from TRACE archives. <i>Bioinformatics</i> , 2002, 18, 1396-1397.	4.1	17
107	Identification of Waldo-A and Waldo-B, Two Closely Related Non-LTR Retrotransposons in <i>Drosophila</i> . <i>Molecular Biology and Evolution</i> , 2001, 18, 196-205.	8.9	12
108	A search for reverse transcriptase-coding sequences reveals new non-LTR retrotransposons in the genome of <i>Drosophila melanogaster</i> . <i>Genome Biology</i> , 2000, 1, research0012.1.	9.6	34

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109	Structure and polymorphism of the <i>Chironomus thummi</i> 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
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