

# Evgeny M Zdobnov

## List of Publications by Year in descending order

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Version: 2024-02-01

117  
papers

46,417  
citations

21215

62  
h-index

20625

120  
g-index

132  
all docs

132  
docs citations

132  
times ranked

53240  
citing authors

#	ARTICLE	IF	CITATIONS
1	Comprehensive mouse microbiota genome catalog reveals major difference to its human counterpart. <i>PLoS Computational Biology</i> , 2022, 18, e1009947.	1.5	36
2	Bacterial, Phytoplankton, and Viral Distributions and Their Biogeochemical Contexts in Meromictic Lake Cadagno Offer Insights into the Proterozoic Ocean Microbial Loop. <i>MBio</i> , 2022, 13, .	1.8	8
3	OrthoDB in 2020: evolutionary and functional annotations of orthologs. <i>Nucleic Acids Research</i> , 2021, 49, D389-D393.	6.5	103
4	The influence of human genetic variation on Epstein-Barr virus sequence diversity. <i>Scientific Reports</i> , 2021, 11, 4586.	1.6	8
5	The genome of the stable fly, <i>Stomoxys calcitrans</i> , reveals potential mechanisms underlying reproduction, host interactions, and novel targets for pest control. <i>BMC Biology</i> , 2021, 19, 41.	1.7	19
6	BUSCO Update: Novel and Streamlined Workflows along with Broader and Deeper Phylogenetic Coverage for Scoring of Eukaryotic, Prokaryotic, and Viral Genomes. <i>Molecular Biology and Evolution</i> , 2021, 38, 4647-4654.	3.5	1,968
7	Enterovirus D: A Small but Versatile Species. <i>Microorganisms</i> , 2021, 9, 1758.	1.6	6
8	BUSCO: Assessing Genomic Data Quality and Beyond. <i>Current Protocols</i> , 2021, 1, e323.	1.3	333
9	The Genome of the Blind Soil-Dwelling and Ancestrally Wingless Dipluran <i>Campodea augens</i> : A Key Reference Hexapod for Studying the Emergence of Insect Innovations. <i>Genome Biology and Evolution</i> , 2020, 12, 3534-3549.	1.1	3
10	A Novel Anphevirus in <i>Aedes albopictus</i> Mosquitoes Is Distributed Worldwide and Interacts with the Host RNA Interference Pathway. <i>Viruses</i> , 2020, 12, 1264.	1.5	10
11	Genome-enabled insights into the biology of thrips as crop pests. <i>BMC Biology</i> , 2020, 18, 142.	1.7	54
12	ATLAS: a Snakemake workflow for assembly, annotation, and genomic binning of metagenome sequence data. <i>BMC Bioinformatics</i> , 2020, 21, 257.	1.2	91
13	Brown marmorated stink bug, <i>Halyomorpha halys</i> (Stål), genome: putative underpinnings of polyphagy, insecticide resistance potential and biology of a top worldwide pest. <i>BMC Genomics</i> , 2020, 21, 227.	1.2	60
14	LEMMI: a continuous benchmarking platform for metagenomics classifiers. <i>Genome Research</i> , 2020, 30, 1208-1216.	2.4	11
15	Gene content evolution in the arthropods. <i>Genome Biology</i> , 2020, 21, 15.	3.8	150
16	Enhanced genome assembly and a new official gene set for <i>Tribolium castaneum</i> . <i>BMC Genomics</i> , 2020, 21, 47.	1.2	84
17	Phigaro: high-throughput prophage sequence annotation. <i>Bioinformatics</i> , 2020, 36, 3882-3884.	1.8	75
18	Sawfly Genomes Reveal Evolutionary Acquisitions That Fostered the Mega-Radiation of Parasitoid and Eusocial Hymenoptera. <i>Genome Biology and Evolution</i> , 2020, 12, 1099-1188.	1.1	17

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19	Comparative genomics groups phages of Negativicutes and classical Firmicutes despite different Gram staining properties. <i>Environmental Microbiology</i> , 2019, 21, 3989-4001.	1.8	8
20	Viral Sequences Detection by High-Throughput Sequencing in Cerebrospinal Fluid of Individuals with and without Central Nervous System Disease. <i>Genes</i> , 2019, 10, 625.	1.0	11
21	BUSCO: Assessing Genome Assembly and Annotation Completeness. <i>Methods in Molecular Biology</i> , 2019, 1962, 227-245.	0.4	1,382
22	Molecular evolutionary trends and feeding ecology diversification in the Hemiptera, anchored by the milkweed bug genome. <i>Genome Biology</i> , 2019, 20, 64.	3.8	114
23	Identification of Viral Signatures Using High-Throughput Sequencing on Blood of Patients With Kawasaki Disease. <i>Frontiers in Pediatrics</i> , 2019, 7, 524.	0.9	20
24	OrthoDB v10: sampling the diversity of animal, plant, fungal, protist, bacterial and viral genomes for evolutionary and functional annotations of orthologs. <i>Nucleic Acids Research</i> , 2019, 47, D807-D811.	6.5	715
25	Using BUSCO to Assess Insect Genomic Resources. <i>Methods in Molecular Biology</i> , 2019, 1858, 59-74.	0.4	27
26	BUSCO Applications from Quality Assessments to Gene Prediction and Phylogenomics. <i>Molecular Biology and Evolution</i> , 2018, 35, 543-548.	3.5	1,844
27	Propagation of respiratory viruses in human airway epithelia reveals persistent virus-specific signatures. <i>Journal of Allergy and Clinical Immunology</i> , 2018, 141, 2074-2084.	1.5	101
28	In silico Analysis Suggests Common Appearance of scaRNAs in Type II Systems and Their Association With Bacterial Virulence. <i>Frontiers in Genetics</i> , 2018, 9, 474.	1.1	8
29	Gearing up to handle the mosaic nature of life in the quest for orthologs. <i>Bioinformatics</i> , 2018, 34, 323-329.	1.8	36
30	ACL <sup>1</sup> beta-lactamase is widespread across human gut microbiomes in Negativicutes due to transposons harboured by tailed prophages. <i>Environmental Microbiology</i> , 2018, 20, 2288-2300.	1.8	20
31	Metagenomics analysis of the virome of 300 concentrates from a Swiss platelet bank. <i>Vox Sanguinis</i> , 2018, 113, 601-604.	0.7	9
32	Understanding key features of bacterial restriction-modification systems through quantitative modeling. <i>BMC Systems Biology</i> , 2017, 11, 1-15.	3.0	16
33	Metagenomics analysis of red blood cell and fresh frozen plasma units. <i>Transfusion</i> , 2017, 57, 1787-1800.	0.8	24
34	Genomic features of the damselfly <i>Calopteryx splendens</i> representing a sister clade to most insect orders. <i>Genome Biology and Evolution</i> , 2017, 9, evx006.	1.1	53
35	Scoring Targets of Transcription in Bacteria Rather than Focusing on Individual Binding Sites. <i>Frontiers in Microbiology</i> , 2017, 8, 2314.	1.5	1
36	OrthoDB v9.1: cataloging evolutionary and functional annotations for animal, fungal, plant, archaeal, bacterial and viral orthologs. <i>Nucleic Acids Research</i> , 2017, 45, D744-D749.	6.5	413

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37	Astrovirus MLB2, a New Gastroenteric Virus Associated with Meningitis and Disseminated Infection. <i>Emerging Infectious Diseases</i> , 2016, 22, 846-853.	2.0	107
38	Astrovirus VA1 identified by next-generation sequencing in a nasopharyngeal specimen of a febrile Tanzanian child with acute respiratory disease of unknown etiology. <i>Emerging Microbes and Infections</i> , 2016, 5, 1-3.	3.0	24
39	Genome Sequencing of the Phytoseiid Predatory Mite <i>Metaseiulus occidentalis</i> Reveals Completely Atomized <i>Hox</i> Genes and Superdynamic Intron Evolution. <i>Genome Biology and Evolution</i> , 2016, 8, 1762-1775.	1.1	102
40	Genome of the Asian longhorned beetle ( <i>Anoplophora glabripennis</i> ), a globally significant invasive species, reveals key functional and evolutionary innovations at the beetle–plant interface. <i>Genome Biology</i> , 2016, 17, 227.	3.8	244
41	CEGA—a catalog of conserved elements from genomic alignments. <i>Nucleic Acids Research</i> , 2016, 44, D96-D100.	6.5	18
42	Unique features of a global human ectoparasite identified through sequencing of the bed bug genome. <i>Nature Communications</i> , 2016, 7, 10165.	5.8	184
43	Genomic insights into the <i>Ixodes scapularis</i> tick vector of Lyme disease. <i>Nature Communications</i> , 2016, 7, 10507.	5.8	450
44	Astrovirus MLB2, a New Gastroenteric Virus Associated with Meningitis and Disseminated Infection. <i>Emerging Infectious Diseases</i> , 2016, 22, 846-853.	2.0	33
45	E119D Neuraminidase Mutation Conferring Pan-Resistance to Neuraminidase Inhibitors in an A(H1N1)pdm09 Isolate From a Stem-Cell Transplant Recipient. <i>Journal of Infectious Diseases</i> , 2015, 212, 1726-1734.	1.9	54
46	A depauperate immune repertoire precedes evolution of sociality in bees. <i>Genome Biology</i> , 2015, 16, 83.	3.8	130
47	A Massive Expansion of Effector Genes Underlies Gall-Formation in the Wheat Pest <i>Mayetiola destructor</i> . <i>Current Biology</i> , 2015, 25, 613-620.	1.8	171
48	BUSCO: assessing genome assembly and annotation completeness with single-copy orthologs. <i>Bioinformatics</i> , 2015, 31, 3210-3212.	1.8	9,712
49	The genomes of two key bumblebee species with primitive eusocial organization. <i>Genome Biology</i> , 2015, 16, 76.	3.8	330
50	Genomic signatures of evolutionary transitions from solitary to group living. <i>Science</i> , 2015, 348, 1139-1143.	6.0	357
51	Clinical features and viral kinetics in a rapidly cured patient with Ebola virus disease: a case report. <i>Lancet Infectious Diseases</i> , The, 2015, 15, 1034-1040.	4.6	46
52	<i>Lucilia cuprina</i> genome unlocks parasitic fly biology to underpin future interventions. <i>Nature Communications</i> , 2015, 6, 7344.	5.8	67
53	OrthoDB v8: update of the hierarchical catalog of orthologs and the underlying free software. <i>Nucleic Acids Research</i> , 2015, 43, D250-D256.	6.5	303
54	Highly evolvable malaria vectors: The genomes of 16 <i>Anopheles</i> mosquitoes. <i>Science</i> , 2015, 347, 1258-1262.	6.0	492

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55	Fifteen years SIB Swiss Institute of Bioinformatics: life science databases, tools and support. <i>Nucleic Acids Research</i> , 2014, 42, W436-W441.	6.5	13
56	Comprehensive metagenomic analysis of glioblastoma reveals absence of known virus despite antiviral-like type I interferon gene response. <i>International Journal of Cancer</i> , 2014, 135, 1381-1389.	2.3	35
57	Gene Age Predicts the Strength of Purifying Selection Acting on Gene Expression Variation in Humans. <i>American Journal of Human Genetics</i> , 2014, 95, 660-674.	2.6	35
58	Finding the missing honey bee genes: lessons learned from a genome upgrade. <i>BMC Genomics</i> , 2014, 15, 86.	1.2	375
59	Repression of Arginase-2 Expression in Dendritic Cells by MicroRNA-155 Is Critical for Promoting T Cell Proliferation. <i>Journal of Immunology</i> , 2014, 193, 1690-1700.	0.4	54
60	Comprehensive Human Virus Screening Using High-Throughput Sequencing with a User-Friendly Representation of Bioinformatics Analysis: a Pilot Study. <i>Journal of Clinical Microbiology</i> , 2014, 52, 3351-3361.	1.8	60
61	Social insect genomes exhibit dramatic evolution in gene composition and regulation while preserving regulatory features linked to sociality. <i>Genome Research</i> , 2013, 23, 1235-1247.	2.4	205
62	miRmap web: comprehensive microRNA target prediction online. <i>Nucleic Acids Research</i> , 2013, 41, W165-W168.	6.5	137
63	OrthoDB: a hierarchical catalog of animal, fungal and bacterial orthologs. <i>Nucleic Acids Research</i> , 2013, 41, D358-D365.	6.5	333
64	Identification of Site-Specific Adaptations Conferring Increased Neural Cell Tropism during Human Enterovirus 71 Infection. <i>PLoS Pathogens</i> , 2012, 8, e1002826.	2.1	91
65	miRmap: Comprehensive prediction of microRNA target repression strength. <i>Nucleic Acids Research</i> , 2012, 40, 11673-11683.	6.5	322
66	Impact of highly active antiretroviral therapy on the molecular epidemiology of newly diagnosed HIV infections. <i>Aids</i> , 2012, 26, 2079-2086.	1.0	47
67	Rhinovirus Genome Variation during Chronic Upper and Lower Respiratory Tract Infections. <i>PLoS ONE</i> , 2011, 6, e21163.	1.1	52
68	Correlating Traits of Gene Retention, Sequence Divergence, Duplicability and Essentiality in Vertebrates, Arthropods, and Fungi. <i>Genome Biology and Evolution</i> , 2011, 3, 75-86.	1.1	81
69	Silencing of c-Fos expression by microRNA-155 is critical for dendritic cell maturation and function. <i>Blood</i> , 2011, 117, 4490-4500.	0.6	131
70	A remarkably stable TipE gene cluster: evolution of insect Para sodium channel auxiliary subunits. <i>BMC Evolutionary Biology</i> , 2011, 11, 337.	3.2	16
71	The Ecoresponsive Genome of <i>Daphnia pulex</i> . <i>Science</i> , 2011, 331, 555-561.	6.0	1,086
72	OrthoDB: the hierarchical catalog of eukaryotic orthologs in 2011. <i>Nucleic Acids Research</i> , 2011, 39, D283-D288.	6.5	128

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73	Loss of Dicer in Sertoli Cells Has a Major Impact on the Testicular Proteome of Mice. <i>Molecular and Cellular Proteomics</i> , 2011, 10, M900587-MCP200.	2.5	80
74	Sequencing of <i>Culex quinquefasciatus</i> Establishes a Platform for Mosquito Comparative Genomics. <i>Science</i> , 2010, 330, 86-88.	6.0	424
75	The Newick utilities: high-throughput phylogenetic tree processing in the Unix shell. <i>Bioinformatics</i> , 2010, 26, 1669-1670.	1.8	573
76	Functional Characterization of Transcription Factor Motifs Using Cross-species Comparison across Large Evolutionary Distances. <i>PLoS Computational Biology</i> , 2010, 6, e1000652.	1.5	28
77	Sociality Is Linked to Rates of Protein Evolution in a Highly Social Insect. <i>Molecular Biology and Evolution</i> , 2010, 27, 497-500.	3.5	50
78	Genome sequences of the human body louse and its primary endosymbiont provide insights into the permanent parasitic lifestyle. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 12168-12173.	3.3	482
79	Pathogenomics of <i>Culex quinquefasciatus</i> and Meta-Analysis of Infection Responses to Diverse Pathogens. <i>Science</i> , 2010, 330, 88-90.	6.0	150
80	Functional and Evolutionary Insights from the Genomes of Three Parasitoid <i>Nasonia</i> Species. <i>Science</i> , 2010, 327, 343-348.	6.0	808
81	A Teratocarcinoma-Like Human Embryonic Stem Cell (hESC) Line and Four hESC Lines Reveal Potentially Oncogenic Genomic Changes. <i>PLoS ONE</i> , 2010, 5, e10263.	1.1	45
82	Rhinovirus Genome Evolution during Experimental Human Infection. <i>PLoS ONE</i> , 2010, 5, e10588.	1.1	48
83	The impact of transmission clusters on primary drug resistance in newly diagnosed HIV-1 infection. <i>Aids</i> , 2009, 23, 1415-1423.	1.0	96
84	New Respiratory Enterovirus and Recombinant Rhinoviruses among Circulating Picornaviruses. <i>Emerging Infectious Diseases</i> , 2009, 15, 719-726.	2.0	130
85	miOrtho: computational survey of microRNA genes. <i>Nucleic Acids Research</i> , 2009, 37, D111-D117.	6.5	65
86	Integration of microRNA miR-122 in hepatic circadian gene expression. <i>Genes and Development</i> , 2009, 23, 1313-1326.	2.7	349
87	Expression profiles of urbilaterian genes uniquely shared between honey bee and vertebrates. <i>BMC Genomics</i> , 2009, 10, 17.	1.2	8
88	The Genome Sequence of Taurine Cattle: A Window to Ruminant Biology and Evolution. <i>Science</i> , 2009, 324, 522-528.	6.0	1,038
89	Sertoli cell Dicer is essential for spermatogenesis in mice. <i>Developmental Biology</i> , 2009, 326, 250-259.	0.9	171
90	The bovine lactation genome: insights into the evolution of mammalian milk. <i>Genome Biology</i> , 2009, 10, R43.	13.9	164

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91	Mapping of Small RNAs in the Human ENCODE Regions. American Journal of Human Genetics, 2008, 82, 971-981.	2.6	25
92	The genome of the model beetle and pest <i>Tribolium castaneum</i> . Nature, 2008, 452, 949-955.	13.7	1,255
93	The <i>cis</i> -acting replication elements define human enterovirus and rhinovirus species. Rna, 2008, 14, 1568-1578.	1.6	51
94	VectorBase: a home for invertebrate vectors of human pathogens. Nucleic Acids Research, 2007, 35, D503-D505.	6.5	107
95	OrthoDB: the hierarchical catalog of eukaryotic orthologs. Nucleic Acids Research, 2007, 36, D271-D275.	6.5	113
96	Quantification of ortholog losses in insects and vertebrates. Genome Biology, 2007, 8, R242.	13.9	66
97	Computational and transcriptional evidence for microRNAs in the honey bee genome. Genome Biology, 2007, 8, R97.	13.9	82
98	Life cycle transcriptome of the malaria mosquito <i>Anopheles gambiae</i> and comparison with the fruitfly <i>Drosophila melanogaster</i> . Proceedings of the National Academy of Sciences of the United States of America, 2007, 104, 11304-11309.	3.3	70
99	Genome Sequence of <i>Aedes aegypti</i> , a Major Arbovirus Vector. Science, 2007, 316, 1718-1723.	6.0	1,025
100	Evolutionary Dynamics of Immune-Related Genes and Pathways in Disease-Vector Mosquitoes. Science, 2007, 316, 1738-1743.	6.0	550
101	Evolution of genes and genomes on the <i>Drosophila</i> phylogeny. Nature, 2007, 450, 203-218.	13.7	1,886
102	New complete genome sequences of human rhinoviruses shed light on their phylogeny and genomic features. BMC Genomics, 2007, 8, 224.	1.2	63
103	Quantification of insect genome divergence. Trends in Genetics, 2007, 23, 16-20.	2.9	134
104	Overgrowth caused by misexpression of a microRNA with dispensable wild-type function. Developmental Biology, 2006, 291, 314-324.	0.9	46
105	AnoEST: Toward <i>A. gambiae</i> functional genomics. Genome Research, 2005, 15, 893-899.	2.4	19
106	Comparative architectures of mammalian and chicken genomes reveal highly variable rates of genomic rearrangements across different lineages. Genome Research, 2005, 15, 98-110.	2.4	150
107	Protein coding potential of retroviruses and other transposable elements in vertebrate genomes. Nucleic Acids Research, 2005, 33, 946-954.	6.5	47
108	Consistency of genome-based methods in measuring Metazoan evolution. FEBS Letters, 2005, 579, 3355-3361.	1.3	26

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109	Genome sequence of the Brown Norway rat yields insights into mammalian evolution. <i>Nature</i> , 2004, 428, 493-521.	13.7	1,943
110	Genome evolution reveals biochemical networks and functional modules. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2003, 100, 15428-15433.	3.3	140
111	A Genome-Wide Survey of Human Pseudogenes. <i>Genome Research</i> , 2003, 13, 2559-2567.	2.4	248
112	Comparative Genome and Proteome Analysis of <i>Anopheles gambiae</i> and <i>Drosophila melanogaster</i> . <i>Science</i> , 2002, 298, 149-159.	6.0	531
113	Comparative genomic analysis in the region of a major Plasmodium-refractoriness locus of <i>Anopheles gambiae</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2002, 99, 8179-8184.	3.3	34
114	The EBI SRS server--new features. <i>Bioinformatics</i> , 2002, 18, 1149-1150.	1.8	94
115	The Genome Sequence of the Malaria Mosquito <i>Anopheles gambiae</i> . <i>Science</i> , 2002, 298, 129-149.	6.0	1,859
116	Immunity-Related Genes and Gene Families in <i>Anopheles gambiae</i> . <i>Science</i> , 2002, 298, 159-165.	6.0	845
117	Initial sequencing and comparative analysis of the mouse genome. <i>Nature</i> , 2002, 420, 520-562.	13.7	6,319