

Georgii A Bazykin

List of Publications by Year in descending order

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Version: 2024-02-01

72
papers

2,361
citations

304368

22
h-index

264894

42
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108
all docs

108
docs citations

108
times ranked

4181
citing authors

#	ARTICLE	IF	CITATIONS
1	Genomic evidence for ameiotic evolution in the bdelloid rotifer <i>Adineta vaga</i> . <i>Nature</i> , 2013, 500, 453-457.	13.7	352
2	Prevalence of Epistasis in the Evolution of Influenza A Surface Proteins. <i>PLoS Genetics</i> , 2011, 7, e1001301.	1.5	182
3	APOBEC-induced mutations in human cancers are strongly enriched on the lagging DNA strand during replication. <i>Genome Research</i> , 2016, 26, 174-182.	2.4	156
4	Alternative translation start sites are conserved in eukaryotic genomes. <i>Nucleic Acids Research</i> , 2011, 39, 567-577.	6.5	133
5	Fast Evolution from Precast Bricks: Genomics of Young Freshwater Populations of Threespine Stickleback <i>Gasterosteus aculeatus</i> . <i>PLoS Genetics</i> , 2014, 10, e1004696.	1.5	119
6	Negative selection in humans and fruit flies involves synergistic epistasis. <i>Science</i> , 2017, 356, 539-542.	6.0	103
7	Positive selection at sites of multiple amino acid replacements since rat-mouse divergence. <i>Nature</i> , 2004, 429, 558-562.	13.7	70
8	Young proteins experience more variable selection pressures than old proteins. <i>Genome Research</i> , 2010, 20, 1574-1581.	2.4	69
9	Genomic epidemiology of the early stages of the SARS-CoV-2 outbreak in Russia. <i>Nature Communications</i> , 2021, 12, 649.	5.8	63
10	Coordinated Evolution of Influenza A Surface Proteins. <i>PLoS Genetics</i> , 2015, 11, e1005404.	1.5	58
11	Transcriptome-based phylogeny of endemic Lake Baikal amphipod species flock: fast speciation accompanied by frequent episodes of positive selection. <i>Molecular Ecology</i> , 2017, 26, 536-553.	2.0	55
12	Intrasubtype Reassortments Cause Adaptive Amino Acid Replacements in H3N2 Influenza Genes. <i>PLoS Genetics</i> , 2014, 10, e1004037.	1.5	43
13	Extraordinary Genetic Diversity in a Wood Decay Mushroom. <i>Molecular Biology and Evolution</i> , 2015, 32, 2775-2783.	3.5	42
14	Human mismatch repair system balances mutation rates between strands by removing more mismatches from the lagging strand. <i>Genome Research</i> , 2017, 27, 1336-1343.	2.4	37
15	Heterogeneity of the Transition/Transversion Ratio in <i>Drosophila</i> and Hominidae Genomes. <i>Molecular Biology and Evolution</i> , 2012, 29, 1943-1955.	3.5	36
16	Slightly deleterious genomic variants and transcriptome perturbations in Down syndrome embryonic selection. <i>Genome Research</i> , 2018, 28, 1-10.	2.4	36
17	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
18	Changing preferences: deformation of single position amino acid fitness landscapes and evolution of proteins. <i>Biology Letters</i> , 2015, 11, .	1.0	33

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19	Extensive parallelism in protein evolution. <i>Biology Direct</i> , 2007, 2, 20.	1.9	32
20	Genomic signatures of recombination in a natural population of the bdelloid rotifer <i>Adineta vaga</i> . <i>Nature Communications</i> , 2020, 11, 6421.	5.8	31
21	Evolution of Prokaryotic Genes by Shift of Stop Codons. <i>Journal of Molecular Evolution</i> , 2011, 72, 138-146.	0.8	29
22	Bursts of nonsynonymous substitutions in HIV-1 evolution reveal instances of positive selection at conservative protein sites. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006, 103, 19396-19401.	3.3	28
23	Prevalence of Multinucleotide Replacements in Evolution of Primates and <i>Drosophila</i> . <i>Molecular Biology and Evolution</i> , 2013, 30, 1315-1325.	3.5	28
24	Error-prone bypass of DNA lesions during lagging-strand replication is a common source of germline and cancer mutations. <i>Nature Genetics</i> , 2019, 51, 36-41.	9.4	28
25	Fitness conferred by replaced amino acids declines with time. <i>Biology Letters</i> , 2012, 8, 825-828.	1.0	27
26	Evolution of local mutation rate and its determinants. <i>Molecular Biology and Evolution</i> , 2017, 34, msx060.	3.5	27
27	Strong Mutational Bias Toward Deletions in the <i>Drosophila melanogaster</i> Genome Is Compensated by Selection. <i>Genome Biology and Evolution</i> , 2013, 5, 514-524.	1.1	26
28	Natural Selection for Nucleotide Usage at Synonymous and Nonsynonymous Sites in Influenza A Virus Genes. <i>Journal of Virology</i> , 2008, 82, 4938-4945.	1.5	25
29	APOBEC3A/B-induced mutagenesis is responsible for 20% of heritable mutations in the TpCpW context. <i>Genome Research</i> , 2017, 27, 175-184.	2.4	24
30	The rise and spread of the SARS-CoV-2 AY.122 lineage in Russia. <i>Virus Evolution</i> , 2022, 8, veac017.	2.2	24
31	Parallel Evolution of Metazoan Mitochondrial Proteins. <i>Genome Biology and Evolution</i> , 2017, 9, 1341-1350.	1.1	23
32	Architecture of Parallel Adaptation in Ten Lacustrine Threespine Stickleback Populations from the White Sea Area. <i>Genome Biology and Evolution</i> , 2019, 11, 2605-2618.	1.1	23
33	Directionality in the evolution of influenza A haemagglutinin. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2008, 275, 2455-2464.	1.2	21
34	Insertions and deletions trigger adaptive walks in <i>Drosophila</i> proteins. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2012, 279, 3075-3082.	1.2	20
35	Major role of positive selection in the evolution of conservative segments of <i>Drosophila</i> proteins. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2012, 279, 3409-3417.	1.2	19
36	Functional implications of splicing polymorphisms in the human genome. <i>Human Molecular Genetics</i> , 2013, 22, 3449-3459.	1.4	19

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37	Polymerase $\hat{\eta}$ Activity Is Linked to Replication Timing in Humans: Evidence from Mutational Signatures. <i>Molecular Biology and Evolution</i> , 2015, 32, msv184.	3.5	19
38	Matching population diversity of rhizobial <i>nodA</i> and legume <i>NFR5</i> genes in plant-microbe symbiosis. <i>Ecology and Evolution</i> , 2019, 9, 10377-10386.	0.8	15
39	SHORT INDELS ARE SUBJECT TO INSERTION-BIASED GENE CONVERSION. <i>Evolution; International Journal of Organic Evolution</i> , 2013, 67, 2604-2613.	1.1	14
40	Weak Negative and Positive Selection and the Drift Load at Splice Sites. <i>Genome Biology and Evolution</i> , 2014, 6, 1437-1447.	1.1	14
41	A new species of <i>Cyanea</i> jellyfish sympatric to <i>C. capillata</i> in the White Sea. <i>Polar Biology</i> , 2015, 38, 1439-1451.	0.5	14
42	Adaptive evolution at mRNA editing sites in soft-bodied cephalopods. <i>PeerJ</i> , 2020, 8, e10456.	0.9	13
43	Detecting Past Positive Selection through Ongoing Negative Selection. <i>Genome Biology and Evolution</i> , 2011, 3, 1006-1013.	1.1	12
44	Fitness Consequences of Advanced Ancestral Age over Three Generations in Humans. <i>PLoS ONE</i> , 2015, 10, e0128197.	1.1	11
45	Allele-specific nonstationarity in evolution of influenza A virus surface proteins. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 21104-21112.	3.3	10
46	Rapid Accumulation of Mutations in Growing Mycelia of a Hypervariable Fungus <i>Schizophyllum commune</i> . <i>Molecular Biology and Evolution</i> , 2020, 37, 2279-2286.	3.5	10
47	COMPARATIVE GENOMICS OF TRANSCRIPTIONAL REGULATION IN YEASTS AND ITS APPLICATION TO IDENTIFICATION OF A CANDIDATE ALPHA-ISOPROPYLMALATE TRANSPORTER. <i>Journal of Bioinformatics and Computational Biology</i> , 2006, 04, 981-998.	0.3	8
48	Genome-Level Analysis of Selective Constraint without Apparent Sequence Conservation. <i>Genome Biology and Evolution</i> , 2013, 5, 532-541.	1.1	8
49	Correlated Evolution of Nucleotide Positions within Splice Sites in Mammals. <i>PLoS ONE</i> , 2015, 10, e0144388.	1.1	8
50	Females Delay Dispersal and Breeding in a Solitary Gerbil, <i>Meriones tamariscinus</i> . <i>Journal of Mammalogy</i> , 2004, 85, 105-112.	0.6	7
51	Rate of promoter class turn-over in yeast evolution. <i>BMC Evolutionary Biology</i> , 2006, 6, 14.	3.2	7
52	Substitutions into amino acids that are pathogenic in human mitochondrial proteins are more frequent in lineages closely related to human than in distant lineages. <i>PeerJ</i> , 2017, 5, e4143.	0.9	7
53	Pairs of Mutually Compensatory Frameshifting Mutations Contribute to Protein Evolution. <i>Molecular Biology and Evolution</i> , 2022, 39, .	3.5	7
54	Polymorphism Due to Multiple Amino Acid Substitutions at a Codon Site Within <i>Ciona savignyi</i> . <i>Genetics</i> , 2009, 181, 685-690.	1.2	6

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55	Complex Selection on Human Polyadenylation Signals Revealed by Polymorphism and Divergence Data. <i>Genome Biology and Evolution</i> , 2016, 8, 1971-1979.	1.1	6
56	Episodic evolution of coadapted sets of amino acid sites in mitochondrial proteins. <i>PLoS Genetics</i> , 2021, 17, e1008711.	1.5	6
57	A broad comparative genomics approach to understanding the pathogenicity of Complex I mutations. <i>Scientific Reports</i> , 2021, 11, 19578.	1.6	5
58	Complex fitness landscape shapes variation in a hyperpolymorphic species. <i>ELife</i> , 2022, 11, .	2.8	5
59	Senescence and entrenchment in evolution of amino acid sites. <i>Nature Communications</i> , 2020, 11, 4603.	5.8	4
60	Convergent Adaptation in Mitochondria of Phylogenetically Distant Birds: Does it Exist?. <i>Genome Biology and Evolution</i> , 2021, 13, .	1.1	4
61	Sergey Ivanovitch Ognev and the formation of theriology in Russia. <i>Mammalia</i> , 2012, 76, .	0.3	3
62	Are Nonsense Alleles of <i>Drosophila melanogaster</i> Genes under Any Selection?. <i>Genome Biology and Evolution</i> , 2018, 10, 1012-1018.	1.1	3
63	SELVa: Simulator of evolution with landscape variation. <i>PLoS ONE</i> , 2020, 15, e0242225.	1.1	3
64	Accurate fetal variant calling in the presence of maternal cell contamination. <i>European Journal of Human Genetics</i> , 2020, 28, 1615-1623.	1.4	2
65	Molecular Epidemiology of HIV-1 in Oryol Oblast, Russia. <i>Virus Evolution</i> , 0, , .	2.2	2
66	Compensatory Evolution of Intrinsic Transcription Terminators in <i>Bacillus Cereus</i> . <i>Genome Biology and Evolution</i> , 2017, 9, 340-349.	1.1	1
67	Genetics of Adaptation of the Ascomycetous Fungus <i>Podospora anserina</i> to Submerged Cultivation. <i>Genome Biology and Evolution</i> , 2019, 11, 2807-2817.	1.1	1
68	Bursts of amino acid replacements in protein evolution. <i>Royal Society Open Science</i> , 2019, 6, 181095.	1.1	1
69	Excessive Parallelism in Protein Evolution of Lake Baikal Amphipod Species Flock. <i>Genome Biology and Evolution</i> , 2020, 12, 1493-1503.	1.1	1
70	Prevalence of loss-of-function alleles does not correlate with lifetime fecundity and other life-history traits in metazoans. <i>Biology Direct</i> , 2018, 13, 4.	1.9	0
71	The limits of normal approximation for adult height. <i>European Journal of Human Genetics</i> , 2021, 29, 1082-1091.	1.4	0
72	Phylogenetic inference of changes in amino acid propensities with single-position resolution. <i>PLoS Computational Biology</i> , 2022, 18, e1009878.	1.5	0