

# Igor B Rogozin

## List of Publications by Year in descending order

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191  
papers

16,208  
citations

17440

63  
h-index

18130

120  
g-index

198  
all docs

198  
docs citations

198  
times ranked

18328  
citing authors

#	ARTICLE	IF	CITATIONS
1	Analysis of Stop Codons within Prokaryotic Protein-Coding Genes Suggests Frequent Readthrough Events. <i>International Journal of Molecular Sciences</i> , 2021, 22, 1876.	4.1	6
2	Compensation for the absence of the catalytically active half of DNA polymerase $\mu$ in yeast by positively selected mutations in <i>CDC28</i> . <i>Genetics</i> , 2021, 218, .	2.9	7
3	DNA Methylation, Deamination, and Translesion Synthesis Combine to Generate Footprint Mutations in Cancer Driver Genes in B-Cell Derived Lymphomas and Other Cancers. <i>Frontiers in Genetics</i> , 2021, 12, 671866.	2.3	4
4	The Functional Consequences of the Novel Ribosomal Pausing Site in SARS-CoV-2 Spike Glycoprotein RNA. <i>International Journal of Molecular Sciences</i> , 2021, 22, 6490.	4.1	12
5	AID and APOBECs as Multifaceted Intrinsic Virus-Restricting Factors: Emerging Concepts in the Light of COVID-19. <i>Frontiers in Immunology</i> , 2021, 12, 690416.	4.8	8
6	Unravelling roles of error-prone DNA polymerases in shaping cancer genomes. <i>Oncogene</i> , 2021, 40, 6549-6565.	5.9	14
7	Template switching and duplications in SARS-CoV-2 genomes give rise to insertion variants that merit monitoring. <i>Communications Biology</i> , 2021, 4, 1343.	4.4	27
8	Frequent Recombination Events in <i>Leishmania donovani</i> : Mining Population Data. <i>Pathogens</i> , 2020, 9, 572.	2.8	4
9	Evolutionary aspects and enzymology of metazoan carotenoid cleavage oxygenases. <i>Biochimica Et Biophysica Acta - Molecular and Cell Biology of Lipids</i> , 2020, 1865, 158665.	2.4	16
10	Palmitoylation of Metazoan Carotenoid Oxygenases. <i>Molecules</i> , 2020, 25, 1942.	3.8	4
11	Stable Intronic Sequences and Exon Skipping Events in the Human RPE65 Gene: Analysis of Expression in Retinal Pigment Epithelium Cells and Cell Culture Models. <i>Frontiers in Genetics</i> , 2019, 10, 634.	2.3	3
12	Comment on "A commensal strain of <i>Staphylococcus epidermidis</i> protects against skin neoplasia" by Nakatsuji <i>et al</i> .. <i>Science Advances</i> , 2019, 5, eaaw3915.	10.3	5
13	Volatile Evolution of Long Non-Coding RNA Repertoire in Retinal Pigment Epithelium: Insights from Comparison of Bovine and Human RNA Expression Profiles. <i>Genes</i> , 2019, 10, 205.	2.4	10
14	Nucleotide Weight Matrices Reveal Ubiquitous Mutational Footprints of AID/APOBEC Deaminases in Human Cancer Genomes. <i>Cancers</i> , 2019, 11, 211.	3.7	15
15	Crossing fitness valleys via double substitutions within codons. <i>BMC Biology</i> , 2019, 17, 105.	3.8	7
16	Aberrant RNA splicing is the major pathogenic effect in a knock-in mouse model of the dominantly inherited c.1430A>G human <i>RPE65</i> mutation. <i>Human Mutation</i> , 2019, 40, 426-443.	2.5	22
17	Diverse roles of RAD18 and Y-family DNA polymerases in tumorigenesis. <i>Cell Cycle</i> , 2018, 17, 833-843.	2.6	32
18	Viral discovery and diversity in trypanosomatid protozoa with a focus on relatives of the human parasite <i>Leishmania</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, E506-E515.	7.1	75

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19	DNA polymerase $\beta$ mutational signatures are found in a variety of different types of cancer. <i>Cell Cycle</i> , 2018, 17, 348-355.	2.6	32
20	The Presence of Genotoxic and/or Pro-inflammatory Bacterial Genes in Gut Metagenomic Databases and Their Possible Link With Inflammatory Bowel Diseases. <i>Frontiers in Genetics</i> , 2018, 9, 116.	2.3	14
21	Genome-Wide Changes in Protein Translation Efficiency Are Associated with Autism. <i>Genome Biology and Evolution</i> , 2018, 10, 1902-1919.	2.5	15
22	Purifying and positive selection in the evolution of stop codons. <i>Scientific Reports</i> , 2018, 8, 9260.	3.3	31
23	Mutational signatures and mutable motifs in cancer genomes. <i>Briefings in Bioinformatics</i> , 2017, 19, 1085-1101.	6.5	32
24	Exploring background mutational processes to decipher cancer genetic heterogeneity. <i>Nucleic Acids Research</i> , 2017, 45, W514-W522.	14.5	65
25	Selection on start codons in prokaryotes and potential compensatory nucleotide substitutions. <i>Scientific Reports</i> , 2017, 7, 12422.	3.3	43
26	Phylogenetic analysis of the metazoan carotenoid oxygenase superfamily: a new ancestral gene assemblage of BCO-like (BCOL) proteins. <i>Scientific Reports</i> , 2017, 7, 13192.	3.3	20
27	Recombination Is Responsible for the Increased Recovery of Drug-Resistant Mutants with Hypermutated Genomes in Resting Yeast Diploids Expressing APOBEC Deaminases. <i>Frontiers in Genetics</i> , 2017, 8, 202.	2.3	5
28	Involvement of DNA mismatch repair in the maintenance of heterochromatic DNA stability in <i>Saccharomyces cerevisiae</i> . <i>PLoS Genetics</i> , 2017, 13, e1007074.	3.5	5
29	Conservation of the Exon-Intron Structure of Long Intergenic Non-Coding RNA Genes in Eutherian Mammals. <i>Life</i> , 2016, 6, 27.	2.4	18
30	Activation induced deaminase mutational signature overlaps with CpG methylation sites in follicular lymphoma and other cancers. <i>Scientific Reports</i> , 2016, 6, 38133.	3.3	26
31	Germline viral $\beta$ -guide in silico reconstruction of a mid-Cenozoic era marsupial adeno-associated virus. <i>Scientific Reports</i> , 2016, 6, 28965.	3.3	34
32	Evolutionary switches between two serine codon sets are driven by selection. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, 13109-13113.	7.1	25
33	Transposable Element Insertions in Long Intergenic Non-Coding RNA Genes. <i>Frontiers in Bioengineering and Biotechnology</i> , 2015, 3, 71.	4.1	45
34	Genetics in Genomic Era. <i>Genetics Research International</i> , 2015, 2015, 1-2.	2.0	10
35	Disruption of Transcriptional Coactivator Sub1 Leads to Genome-Wide Re-distribution of Clustered Mutations Induced by APOBEC in Active Yeast Genes. <i>PLoS Genetics</i> , 2015, 11, e1005217.	3.5	49
36	Emergence and subsequent functional specialization of kindlins during evolution of cell adhesiveness. <i>Molecular Biology of the Cell</i> , 2015, 26, 786-796.	2.1	17

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37	Retention of duplicated ITAM-containing transmembrane signaling subunits in the tetraploid amphibian species <i>Xenopus laevis</i> . <i>Developmental and Comparative Immunology</i> , 2015, 53, 158-168.	2.3	0
38	Comparative mutational analyses of influenza A viruses. <i>Rna</i> , 2015, 21, 36-47.	3.5	16
39	MitoCOGs: clusters of orthologous genes from mitochondria and implications for the evolution of eukaryotes. <i>BMC Evolutionary Biology</i> , 2014, 14, 237.	3.2	34
40	Gene Family Level Comparative Analysis of Gene Expression in Mammals Validates the Ortholog Conjecture. <i>Genome Biology and Evolution</i> , 2014, 6, 754-762.	2.5	51
41	Complexity of Gene Expression Evolution after Duplication: Protein Dosage Rebalancing. <i>Genetics Research International</i> , 2014, 2014, 1-8.	2.0	25
42	Generalized Portrait of Cancer Metabolic Pathways Inferred from a List of Genes Overexpressed in Cancer. <i>Genetics Research International</i> , 2014, 2014, 1-8.	2.0	14
43	Genetic characterization of feline calicivirus strains associated with varying disease manifestations during an outbreak season in Missouri (1995–1996). <i>Virus Genes</i> , 2014, 48, 96-110.	1.6	25
44	Impairment of translation in neurons as a putative causative factor for autism. <i>Biology Direct</i> , 2014, 9, 16.	4.6	9
45	Whence genes in pieces: reconstruction of the exon–intron gene structures of the last eukaryotic common ancestor and other ancestral eukaryotes. <i>Wiley Interdisciplinary Reviews RNA</i> , 2013, 4, 93-105.	6.4	47
46	The Vast, Conserved Mammalian lincRNome. <i>PLoS Computational Biology</i> , 2013, 9, e1002917.	3.2	62
47	Genome-Wide Mutation Avalanches Induced in Diploid Yeast Cells by a Base Analog or an APOBEC Deaminase. <i>PLoS Genetics</i> , 2013, 9, e1003736.	3.5	54
48	Modulation of mutagenesis in eukaryotes by DNA replication fork dynamics and quality of nucleotide pools. <i>Environmental and Molecular Mutagenesis</i> , 2012, 53, 699-724.	2.2	28
49	Origin and evolution of spliceosomal introns. <i>Biology Direct</i> , 2012, 7, 11.	4.6	292
50	AID/APOBEC cytosine deaminase induces genome-wide kataegis. <i>Biology Direct</i> , 2012, 7, 47; discussion 47.	4.6	92
51	Oncogenic potential is related to activating effect of cancer single and double somatic mutations in receptor tyrosine kinases. <i>Human Mutation</i> , 2012, 33, 1566-1575.	2.5	26
52	Computational Prediction of Polycomb-Associated Long Non-Coding RNAs. <i>PLoS ONE</i> , 2012, 7, e44878.	2.5	19
53	Origin and Evolution of Retinoid Isomerization Machinery in Vertebrate Visual Cycle: Hint from Jawless Vertebrates. <i>PLoS ONE</i> , 2012, 7, e49975.	2.5	37
54	Tandem termination signal in plant mRNAs. <i>Gene</i> , 2011, 481, 1-6.	2.2	4

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55	Replication Protein A (RPA) Hampers the Processive Action of APOBEC3G Cytosine Deaminase on Single-Stranded DNA. PLoS ONE, 2011, 6, e24848.	2.5	25
56	The Ecoresponsive Genome of <i>Daphnia pulex</i> . Science, 2011, 331, 555-561.	12.6	1,086
57	A late origin of the extant eukaryotic diversity: divergence time estimates using rare genomic changes. Biology Direct, 2011, 6, 26.	4.6	63
58	Negative Correlation between Expression Level and Evolutionary Rate of Long Intergenic Noncoding RNAs. Genome Biology and Evolution, 2011, 3, 1390-1404.	2.5	86
59	Primate and Rodent Specific Intron Gains and the Origin of Retrogenes with Splice Variants. Molecular Biology and Evolution, 2011, 28, 33-37.	8.9	48
60	A Detailed History of Intron-rich Eukaryotic Ancestors Inferred from a Global Survey of 100 Complete Genomes. PLoS Computational Biology, 2011, 7, e1002150.	3.2	160
61	Evolution of the deaminase fold and multiple origins of eukaryotic editing and mutagenic nucleic acid deaminases from bacterial toxin systems. Nucleic Acids Research, 2011, 39, 9473-9497.	14.5	154
62	High frequency of somatic mutations in rat liver mitochondrial DNA. Mutation Research - Fundamental and Molecular Mechanisms of Mutagenesis, 2010, 685, 97-102.	1.0	8
63	Genome Evolution. Advances in Bioinformatics, 2010, 2010, 1-2.	5.7	3
64	EREM: Parameter Estimation and Ancestral Reconstruction by Expectation-Maximization Algorithm for a Probabilistic Model of Genomic Binary Characters Evolution. Advances in Bioinformatics, 2010, 2010, 1-4.	5.7	8
65	Mismatch Repair-Independent Increase in Spontaneous Mutagenesis in Yeast Lacking Non-Essential Subunits of DNA Polymerase $\delta$ . PLoS Genetics, 2010, 6, e1001209.	3.5	66
66	Low-fidelity DNA synthesis by the L979F mutator derivative of <i>Saccharomyces cerevisiae</i> DNA polymerase $\delta$ . Nucleic Acids Research, 2009, 37, 3774-3787.	14.5	26
67	Analysis of Rare Genomic Changes Does Not Support the Unikont-Bikont Phylogeny and Suggests Cyanobacterial Symbiosis as the Point of Primary Radiation of Eukaryotes. Genome Biology and Evolution, 2009, 1, 99-113.	2.5	77
68	Evolution of alternative and constitutive regions of mammalian 5'UTRs. BMC Genomics, 2009, 10, 162.	2.8	62
69	Evolution of DNA polymerases: an inactivated polymerase-exonuclease module in Pol $\delta$ and a chimeric origin of eukaryotic polymerases from two classes of archaeal ancestors. Biology Direct, 2009, 4, 11.	4.6	102
70	A Maximum Likelihood Method for Reconstruction of the Evolution of Eukaryotic Gene Structure. Methods in Molecular Biology, 2009, 541, 357-371.	0.9	6
71	Identification of murine B cell lines that undergo somatic hypermutation focused to A:T and G:C residues. European Journal of Immunology, 2008, 38, 227-239.	2.9	16
72	Primordial spliceosomal introns were probably U2-type. Trends in Genetics, 2008, 24, 525-528.	6.7	23

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73	U12 intron positions are more strongly conserved between animals and plants than U2 intron positions. <i>Biology Direct</i> , 2008, 3, 19.	4.6	40
74	Accumulation of GC donor splice signals in mammals. <i>Biology Direct</i> , 2008, 3, 30.	4.6	33
75	A highly conserved family of inactivated archaeal B family DNA polymerases. <i>Biology Direct</i> , 2008, 3, 32.	4.6	40
76	Homoplasy in genome-wide analysis of rare amino acid replacements: the molecular-evolutionary basis for Vavilov's law of homologous series. <i>Biology Direct</i> , 2008, 3, 7.	4.6	43
77	A Dual Origin of the Xist Gene from a Protein-Coding Gene and a Set of Transposable Elements. <i>PLoS ONE</i> , 2008, 3, e2521.	2.5	162
78	X-ray structure of the complex of regulatory subunits of human DNA polymerase delta. <i>Cell Cycle</i> , 2008, 7, 3026-3036.	2.6	81
79	Low-fidelity DNA synthesis by human DNA polymerase theta. <i>Nucleic Acids Research</i> , 2008, 36, 3847-3856.	14.5	126
80	Domain mobility in proteins: functional and evolutionary implications. <i>Briefings in Bioinformatics</i> , 2008, 10, 205-216.	6.5	87
81	Extremely Intron-Rich Genes in the Alveolate Ancestors Inferred with a Flexible Maximum-Likelihood Approach. <i>Molecular Biology and Evolution</i> , 2008, 25, 903-911.	8.9	55
82	Evolution of protein domain promiscuity in eukaryotes. <i>Genome Research</i> , 2008, 18, 449-461.	5.5	153
83	Widespread Positive Selection in Synonymous Sites of Mammalian Genes. <i>Molecular Biology and Evolution</i> , 2007, 24, 1821-1831.	8.9	86
84	Support for the Coelomata Clade of Animals from a Rigorous Analysis of the Pattern of Intron Conservation. <i>Molecular Biology and Evolution</i> , 2007, 24, 2583-2592.	8.9	68
85	Analysis of Rare Amino Acid Replacements Supports the Coelomata Clade. <i>Molecular Biology and Evolution</i> , 2007, 24, 2594-2597.	8.9	41
86	Evolutionary Dynamics of Introns in Plastid-Derived Genes in Plants: Saturation Nearly Reached but Slow Intron Gain Continues. <i>Molecular Biology and Evolution</i> , 2007, 25, 111-119.	8.9	27
87	Three distinct modes of intron dynamics in the evolution of eukaryotes. <i>Genome Research</i> , 2007, 17, 1034-1044.	5.5	159
88	Completion of the mapping of transcription start sites for the five-gene block subgenomic RNAs of Beet yellows Closterovirus and identification of putative subgenomic promoters. <i>Virus Research</i> , 2007, 128, 153-158.	2.2	8
89	Known components of the immunoglobulin A:T mutational machinery are intact in Burkitt lymphoma cell lines with G:C bias. <i>Molecular Immunology</i> , 2007, 44, 2659-2666.	2.2	25
90	Evolutionarily conserved genes preferentially accumulate introns. <i>Genome Research</i> , 2007, 17, 1045-1050.	5.5	68

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91	Ecdysozoan Clade Rejected by Genome-Wide Analysis of Rare Amino Acid Replacements. <i>Molecular Biology and Evolution</i> , 2007, 24, 1080-1090.	8.9	63
92	In search of lost introns. <i>Bioinformatics</i> , 2007, 23, i87-i96.	4.1	27
93	Evolution and diversification of lamprey antigen receptors: evidence for involvement of an AID-APOBEC family cytosine deaminase. <i>Nature Immunology</i> , 2007, 8, 647-656.	14.5	263
94	Patterns of intron gain and conservation in eukaryotic genes. <i>BMC Evolutionary Biology</i> , 2007, 7, 192.	3.2	67
95	A glimpse of a putative pre-intron phase of eukaryotic evolution. <i>Trends in Genetics</i> , 2007, 23, 105-108.	6.7	21
96	A Rigorous Analysis of the Pattern of Intron Conservation Supports the Coelomata Clade of Animals. <i>Lecture Notes in Computer Science</i> , 2007, , 177-191.	1.3	0
97	Roles of DNA Polymerases in Replication, Repair, and Recombination in Eukaryotes. <i>International Review of Cytology</i> , 2006, 255, 41-132.	6.2	112
98	Method of predicting splice sites based on signal interactions. <i>Biology Direct</i> , 2006, 1, 10.	4.6	30
99	Mutational hotspots in the TP53 gene and, possibly, other tumor suppressors evolve by positive selection. <i>Biology Direct</i> , 2006, 1, 4.	4.6	10
100	The cytidine deaminase AID exhibits similar functional properties in yeast and mammals. <i>Molecular Immunology</i> , 2006, 43, 1481-1484.	2.2	14
101	Signs of positive selection of somatic mutations in human cancers detected by EST sequence analysis. <i>BMC Cancer</i> , 2006, 6, 36.	2.6	13
102	Compensatory relationship between splice sites and exonic splicing signals depending on the length of vertebrate introns. <i>BMC Genomics</i> , 2006, 7, 311.	2.8	73
103	Dollo parsimony and the reconstruction of genome evolution. , 2006, , 190-200.		18
104	Evolutionary conservation suggests a regulatory function of AUG triplets in 5'-UTRs of eukaryotic genes. <i>Nucleic Acids Research</i> , 2005, 33, 5512-5520.	14.5	91
105	Transcription of mammalian messenger RNAs by a nuclear RNA polymerase of mitochondrial origin. <i>Nature</i> , 2005, 436, 735-739.	27.8	61
106	Molecular dating: ape bones agree with chicken entrails. <i>Trends in Genetics</i> , 2005, 21, 89-92.	6.7	33
107	Expression of human AID in yeast induces mutations in context similar to the context of somatic hypermutation at G-C pairs in immunoglobulin genes. <i>BMC Immunology</i> , 2005, 6, 10.	2.2	34
108	The role of alternative translation start sites in the generation of human protein diversity. <i>Molecular Genetics and Genomics</i> , 2005, 273, 491-496.	2.1	61

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109	Diversity and Function of Adaptive Immune Receptors in a Jawless Vertebrate. <i>Science</i> , 2005, 310, 1970-1973.	12.6	291
110	P53 Gain-of-Function: Tumor Biology and Bioinformatics Come Together. <i>Cell Cycle</i> , 2005, 4, 686-688.	2.6	14
111	DNA Polymerase $\delta$ Contributes to Strand Bias of Mutations of A versus T in Immunoglobulin Genes. <i>Journal of Immunology</i> , 2005, 174, 7781-7786.	0.8	74
112	Conservation versus parallel gains in intron evolution. <i>Nucleic Acids Research</i> , 2005, 33, 1741-1748.	14.5	90
113	Analysis of evolution of exon-intron structure of eukaryotic genes. <i>Briefings in Bioinformatics</i> , 2005, 6, 118-134.	6.5	230
114	APOBEC4, a New Member of the AID/APOBEC Family of Polynucleotide (Deoxy)Cytidine Deaminases Predicted by Computational Analysis. <i>Cell Cycle</i> , 2005, 4, 1281-1285.	2.6	118
115	Low Variability of the POLG (CAG) n Repeat in North Eurasian Populations. <i>Human Biology</i> , 2005, 77, 355-365.	0.2	11
116	From context-dependence of mutations to molecular mechanisms of mutagenesis. <i>Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing</i> , 2005, , 409-20.	0.7	10
117	Computational approaches for the analysis of gene neighbourhoods in prokaryotic genomes. <i>Briefings in Bioinformatics</i> , 2004, 5, 131-149.	6.5	62
118	Prevalence of intron gain over intron loss in the evolution of paralogous gene families. <i>Nucleic Acids Research</i> , 2004, 32, 3724-3733.	14.5	141
119	The SPANX gene family of cancer/testis-specific antigens: Rapid evolution and amplification in African great apes and hominids. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2004, 101, 3077-3082.	7.1	77
120	Cutting Edge: DGYW/WRCH Is a Better Predictor of Mutability at G:C Bases in Ig Hypermutation Than the Widely Accepted RGYW/WRCY Motif and Probably Reflects a Two-Step Activation-Induced Cytidine Deaminase-Triggered Process. <i>Journal of Immunology</i> , 2004, 172, 3382-3384.	0.8	184
121	Reconstruction of Ancestral Protosplice Sites. <i>Current Biology</i> , 2004, 14, 1505-1508.	3.9	51
122	Mutation hotspots in the p53 gene in tumors of different origin: correlation with evolutionary conservation and signs of positive selection. <i>Biochimica Et Biophysica Acta Gene Regulatory Mechanisms</i> , 2004, 1679, 95-106.	2.4	24
123	Context of deletions and insertions in human coding sequences. <i>Human Mutation</i> , 2004, 23, 177-185.	2.5	76
124	A comprehensive evolutionary classification of proteins encoded in complete eukaryotic genomes. <i>Genome Biology</i> , 2004, 5, R7.	9.6	814
125	Preferential loss and gain of introns in 3' portions of genes suggests a reverse-transcription mechanism of intron insertion. <i>Gene</i> , 2004, 338, 85-91.	2.2	70
126	On the Etruscan Mitochondrial DNA Contribution to Modern Humans. <i>American Journal of Human Genetics</i> , 2004, 75, 920-923.	6.2	12



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127	Comparative analysis of orthologous eukaryotic mRNAs: potential hidden functional signals. <i>Nucleic Acids Research</i> , 2004, 32, 1774-1782.	14.5	82
128	FROM CONTEXT-DEPENDENCE OF MUTATIONS TO MOLECULAR MECHANISMS OF MUTAGENESIS. , 2004, , .		10
129	Concerted Changes in the Nucleotide Sequences of the Intragenic Promoter Regions of Eukaryotic Genes for tRNAs of All Specificities. <i>Journal of Molecular Evolution</i> , 2003, 57, 520-532.	1.8	5
130	Remarkable Interkingdom Conservation of Intron Positions and Massive, Lineage-Specific Intron Loss and Gain in Eukaryotic Evolution. <i>Current Biology</i> , 2003, 13, 1512-1517.	3.9	413
131	Evidence of Splice Signal Migration from Exon to Intron during Intron Evolution. <i>Current Biology</i> , 2003, 13, 2170-2174.	3.9	42
132	Origin of a substantial fraction of human regulatory sequences from transposable elements. <i>Trends in Genetics</i> , 2003, 19, 68-72.	6.7	511
133	A significant fraction of conserved noncoding DNA in human and mouse consists of predicted matrix attachment regions. <i>Trends in Genetics</i> , 2003, 19, 119-124.	6.7	83
134	Coelomata and Not Ecdysozoa: Evidence From Genome-Wide Phylogenetic Analysis. <i>Genome Research</i> , 2003, 14, 29-36.	5.5	221
135	Differential Action of Natural Selection on the N and C-terminal Domains of 2â€²-5â€² Oligoadenylate Synthetases and the Potential Nuclease Function of the C-terminal Domain. <i>Journal of Molecular Biology</i> , 2003, 326, 1449-1461.	4.2	38
136	Theoretical analysis of mutation hotspots and their DNA sequence context specificity. <i>Mutation Research - Reviews in Mutation Research</i> , 2003, 544, 65-85.	5.5	149
137	Genome sequence of the cyanobacterium <i>Prochlorococcus marinus</i> SS120, a nearly minimal oxypototrophic genome. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2003, 100, 10020-10025.	7.1	442
138	Computational analysis of mutation spectra. <i>Briefings in Bioinformatics</i> , 2003, 4, 210-227.	6.5	16
139	Gene Loss, Protein Sequence Divergence, Gene Dispensability, Expression Level, and Interactivity Are Correlated in Eukaryotic Evolution. <i>Genome Research</i> , 2003, 13, 2229-2235.	5.5	367
140	129-derived Strains of Mice Are Deficient in DNA Polymerase Î² and Have Normal Immunoglobulin Hypermutation. <i>Journal of Experimental Medicine</i> , 2003, 198, 635-643.	8.5	169
141	ESTMAP: a system for expressed sequence tags mapping on genomic sequences. <i>IEEE Transactions on Nanobioscience</i> , 2003, 2, 75-78.	3.3	4
142	Unique Error Signature of the Four-subunit Yeast DNA Polymerase Î¼. <i>Journal of Biological Chemistry</i> , 2003, 278, 43770-43780.	3.4	109
143	Transcriptome dynamics of <i>Deinococcus radiodurans</i> recovering from ionizing radiation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2003, 100, 4191-4196.	7.1	345
144	Yeast POL5 Is an Evolutionarily Conserved Regulator of rDNA Transcription Unrelated to Any Known DNA Polymerases. <i>Cell Cycle</i> , 2003, 2, 120-122.	2.6	15

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145	A DNA repair system specific for thermophilic Archaea and bacteria predicted by genomic context analysis. <i>Nucleic Acids Research</i> , 2002, 30, 482-496.	14.5	331
146	Cross-Species Conservation of SEL1L, a Human Pancreas-Specific Expressing Gene. <i>OMICS A Journal of Integrative Biology</i> , 2002, 6, 187-198.	2.0	15
147	The complete genome of hyperthermophile <i>Methanopyrus kandleri</i> AV19 and monophyly of archaeal methanogens. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2002, 99, 4644-4649.	7.1	283
148	Correlation of somatic hypermutation specificity and A-T base pair substitution errors by DNA polymerase $\delta$ during copying of a mouse immunoglobulin $\lambda$ light chain transgene. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2002, 99, 9954-9959.	7.1	121
149	Essential Genes Are More Evolutionarily Conserved Than Are Nonessential Genes in Bacteria. <i>Genome Research</i> , 2002, 12, 962-968.	5.5	491
150	Congruent evolution of different classes of non-coding DNA in prokaryotic genomes. <i>Nucleic Acids Research</i> , 2002, 30, 4264-4271.	14.5	99
151	Microevolutionary Genomics of Bacteria. <i>Theoretical Population Biology</i> , 2002, 61, 435-447.	1.1	100
152	Selection in the evolution of gene duplications. <i>Genome Biology</i> , 2002, 3, research0008.1.	9.6	625
153	Double-strand breaks in DNA during somatic hypermutation of Ig genes: cause or consequence?. <i>Trends in Immunology</i> , 2002, 23, 12-13.	6.8	3
154	Purifying and directional selection in overlapping prokaryotic genes. <i>Trends in Genetics</i> , 2002, 18, 228-232.	6.7	110
155	Genome trees and the tree of life. <i>Trends in Genetics</i> , 2002, 18, 472-479.	6.7	336
156	Evolution of the Mouse Polyubiquitin-C Gene. <i>Journal of Molecular Evolution</i> , 2002, 55, 202-210.	1.8	13
157	Analysis of phylogenetically reconstructed mutational spectra in human mitochondrial DNA control region. <i>Human Genetics</i> , 2002, 111, 46-53.	3.8	67
158	Connected gene neighborhoods in prokaryotic genomes. <i>Nucleic Acids Research</i> , 2002, 30, 2212-2223.	14.5	167
159	Constant relative rate of protein evolution and detection of functional diversification among bacterial, archaeal and eukaryotic proteins. <i>Genome Biology</i> , 2001, 2, research0053.1.	9.6	36
160	Error rate and specificity of human and murine DNA polymerase $\delta$ . <i>Journal of Molecular Biology</i> , 2001, 312, 335-346.	4.2	171
161	Genome Alignment, Evolution of Prokaryotic Genome Organization, and Prediction of Gene Function Using Genomic Context. <i>Genome Research</i> , 2001, 11, 356-372.	5.5	270
162	Rapid Evolution of a Cyclin A Inhibitor Gene, roughex, in <i>Drosophila</i> . <i>Molecular Biology and Evolution</i> , 2001, 18, 2110-2118.	8.9	10

#	ARTICLE	IF	CITATIONS
163	Use of mutation spectra analysis software. <i>Human Mutation</i> , 2001, 17, 83-102.	2.5	35
164	Somatic mutation hotspots correlate with DNA polymerase $\beta$ error spectrum. <i>Nature Immunology</i> , 2001, 2, 530-536.	14.5	282
165	Response 1 to 'Smaller role for pol $\beta$ ?'. <i>Nature Immunology</i> , 2001, 2, 983-984.	14.5	10
166	Comparative study and prediction of DNA fragments associated with various elements of the nuclear matrix. <i>Biochimica Et Biophysica Acta Gene Regulatory Mechanisms</i> , 2001, 1517, 351-364.	2.4	28
167	Mutagenic specificity of the base analog 6-N-hydroxylaminopurine in the LYS2 gene of yeast <i>Saccharomyces cerevisiae</i> . <i>Mutation Research - Fundamental and Molecular Mechanisms of Mutagenesis</i> , 2001, 473, 151-161.	1.0	12
168	Genome trees constructed using five different approaches suggest new major bacterial clades. <i>BMC Evolutionary Biology</i> , 2001, 1, 8.	3.2	272
169	Cloning and Functional Analysis of SEL1L Promoter Region, a Pancreas-Specific Gene. <i>DNA and Cell Biology</i> , 2001, 20, 1-9.	1.9	17
170	Intron sliding in conserved gene families. <i>Trends in Genetics</i> , 2000, 16, 430-432.	6.7	104
171	B2 elements present in the human genome. <i>Mammalian Genome</i> , 2000, 11, 177-179.	2.2	6
172	Prediction and phylogenetic analysis of mammalian short interspersed elements (SINEs). <i>Briefings in Bioinformatics</i> , 2000, 1, 260-274.	6.5	10
173	Computer prediction of sites associated with various elements of the nuclear matrix. <i>Briefings in Bioinformatics</i> , 2000, 1, 33-44.	6.5	14
174	Characterization of several LINE-1 elements in <i>Microtus kirgisorum</i> . <i>Mammalian Genome</i> , 1999, 10, 724-729.	2.2	17
175	Similarity pattern analysis in mutational distributions. <i>Mutation Research - Fundamental and Molecular Mechanisms of Mutagenesis</i> , 1999, 430, 55-74.	1.0	33
176	Protein-coding regions prediction combining similarity searches and conservative evolutionary properties of protein-coding sequences. <i>Gene</i> , 1999, 226, 129-137.	2.2	18
177	Repetitive DNA sequences in the common vole: cloning, characterization and chromosome localization of two novel complex repeats MS3 and MS4 from the genome of the East European vole <i>Microtus rossiaemeridionalis</i> . <i>Chromosome Research</i> , 1998, 6, 351-360.	2.2	26
178	A novel subfamily of LINE-derived elements in mice. <i>Mammalian Genome</i> , 1998, 9, 881-885.	2.2	2
179	Multiple antimutagenesis mechanisms affect mutagenic activity and specificity of the base analog 6-N-hydroxylaminopurine in bacteria and yeast. <i>Mutation Research - Fundamental and Molecular Mechanisms of Mutagenesis</i> , 1998, 402, 41-50.	1.0	41
180	The Subclass Approach for Mutational Spectrum Analysis: Application of the SEM Algorithm. <i>Journal of Theoretical Biology</i> , 1998, 192, 475-487.	1.7	37

#	ARTICLE	IF	CITATIONS
181	Prediction of Human Gene Structure. , 1998, , 215-259.		16
182	Sequence and Gene Content in 35 kb Genomic Clone Mapping in the Human Xq27.1 Region. DNA Sequence, 1997, 8, 1-15.	0.7	7
183	Identification of a U7snRNA homologue mapping to the human Xq27.1 region, between the DXS1232 and DXS119 loci. Gene, 1997, 187, 221-224.	2.2	2
184	Analysis of donor splice sites in different eukaryotic organisms. Journal of Molecular Evolution, 1997, 45, 50-59.	1.8	148
185	Somatic hypermutagenesis in immunoglobulin genes. III. Somatic mutations in the chicken light chain locus. Biochimica Et Biophysica Acta Gene Regulatory Mechanisms, 1996, 1306, 171-178.	2.4	23
186	Gene structure prediction using information on homologous protein sequence. Bioinformatics, 1996, 12, 161-170.	4.1	15
187	LINE-1 element in the vole <i>Microtus subarvalis</i> . Mammalian Genome, 1993, 4, 624-626.	2.2	15
188	Molecular organization and evolution of the D17Leh80-like loci in the mouse t complex. Mammalian Genome, 1992, 3, 11-16.	2.2	3
189	Somatic hypermutagenesis in immunoglobulin genes. Biochimica Et Biophysica Acta Gene Regulatory Mechanisms, 1992, 1171, 11-18.	2.4	414
190	Somatic hypermutagenesis in immunoglobulin genes. I. Correlation between somatic mutations and repeats. Somatic mutation properties and clonal selection. Biochimica Et Biophysica Acta Gene Regulatory Mechanisms, 1991, 1089, 175-182.	2.4	26
191	B2-like repetitive sequence from the X Chromosome of the American mink ( <i>Mustela vison</i> ). Mammalian Genome, 1991, 1, 165-170.	2.2	8