

# 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	The Ecoresponsive Genome of <i>Daphnia pulex</i> . <i>Science</i> , 2011, 331, 555-561.	12.6	1,086
2	A comprehensive evolutionary classification of proteins encoded in complete eukaryotic genomes. <i>Genome Biology</i> , 2004, 5, R7.	9.6	814
3	Selection in the evolution of gene duplications. <i>Genome Biology</i> , 2002, 3, research0008.1.	9.6	625
4	Origin of a substantial fraction of human regulatory sequences from transposable elements. <i>Trends in Genetics</i> , 2003, 19, 68-72.	6.7	511
5	Essential Genes Are More Evolutionarily Conserved Than Are Nonessential Genes in Bacteria. <i>Genome Research</i> , 2002, 12, 962-968.	5.5	491
6	Genome sequence of the cyanobacterium <i>Prochlorococcus marinus</i> SS120, a nearly minimal oxyphototrophic genome. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2003, 100, 10020-10025.	7.1	442
7	Somatic hypermutagenesis in immunoglobulin genes. <i>Biochimica Et Biophysica Acta Gene Regulatory Mechanisms</i> , 1992, 1171, 11-18.	2.4	414
8	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
9	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
10	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
11	Genome trees and the tree of life. <i>Trends in Genetics</i> , 2002, 18, 472-479.	6.7	336
12	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
13	Origin and evolution of spliceosomal introns. <i>Biology Direct</i> , 2012, 7, 11.	4.6	292
14	Diversity and Function of Adaptive Immune Receptors in a Jawless Vertebrate. <i>Science</i> , 2005, 310, 1970-1973.	12.6	291
15	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
16	Somatic mutation hotspots correlate with DNA polymerase $\epsilon$ error spectrum. <i>Nature Immunology</i> , 2001, 2, 530-536.	14.5	282
17	Genome trees constructed using five different approaches suggest new major bacterial clades. <i>BMC Evolutionary Biology</i> , 2001, 1, 8.	3.2	272
18	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

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19	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
20	Analysis of evolution of exon-intron structure of eukaryotic genes. <i>Briefings in Bioinformatics</i> , 2005, 6, 118-134.	6.5	230
21	Coelomata and Not Ecdysozoa: Evidence From Genome-Wide Phylogenetic Analysis. <i>Genome Research</i> , 2003, 14, 29-36.	5.5	221
22	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
23	Error rate and specificity of human and murine DNA polymerase $\beta$ . <i>Journal of Molecular Biology</i> , 2001, 312, 335-346.	4.2	171
24	129-derived Strains of Mice Are Deficient in DNA Polymerase $\beta$ and Have Normal Immunoglobulin Hypermutation. <i>Journal of Experimental Medicine</i> , 2003, 198, 635-643.	8.5	169
25	Connected gene neighborhoods in prokaryotic genomes. <i>Nucleic Acids Research</i> , 2002, 30, 2212-2223.	14.5	167
26	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
27	A Detailed History of Intron-rich Eukaryotic Ancestors Inferred from a Global Survey of 100 Complete Genomes. <i>PLoS Computational Biology</i> , 2011, 7, e1002150.	3.2	160
28	Three distinct modes of intron dynamics in the evolution of eukaryotes. <i>Genome Research</i> , 2007, 17, 1034-1044.	5.5	159
29	Evolution of the deaminase fold and multiple origins of eukaryotic editing and mutagenic nucleic acid deaminases from bacterial toxin systems. <i>Nucleic Acids Research</i> , 2011, 39, 9473-9497.	14.5	154
30	Evolution of protein domain promiscuity in eukaryotes. <i>Genome Research</i> , 2008, 18, 449-461.	5.5	153
31	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
32	Analysis of donor splice sites in different eukaryotic organisms. <i>Journal of Molecular Evolution</i> , 1997, 45, 50-59.	1.8	148
33	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
34	Low-fidelity DNA synthesis by human DNA polymerase theta. <i>Nucleic Acids Research</i> , 2008, 36, 3847-3856.	14.5	126
35	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
36	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

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37	Roles of DNA Polymerases in Replication, Repair, and Recombination in Eukaryotes. <i>International Review of Cytology</i> , 2006, 255, 41-132.	6.2	112
38	Purifying and directional selection in overlapping prokaryotic genes. <i>Trends in Genetics</i> , 2002, 18, 228-232.	6.7	110
39	Unique Error Signature of the Four-subunit Yeast DNA Polymerase $\delta$ . <i>Journal of Biological Chemistry</i> , 2003, 278, 43770-43780.	3.4	109
40	Intron sliding in conserved gene families. <i>Trends in Genetics</i> , 2000, 16, 430-432.	6.7	104
41	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. <i>Biology Direct</i> , 2009, 4, 11.	4.6	102
42	Microevolutionary Genomics of Bacteria. <i>Theoretical Population Biology</i> , 2002, 61, 435-447.	1.1	100
43	Congruent evolution of different classes of non-coding DNA in prokaryotic genomes. <i>Nucleic Acids Research</i> , 2002, 30, 4264-4271.	14.5	99
44	AID/APOBEC cytosine deaminase induces genome-wide kataegis. <i>Biology Direct</i> , 2012, 7, 47; discussion 47.	4.6	92
45	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
46	Conservation versus parallel gains in intron evolution. <i>Nucleic Acids Research</i> , 2005, 33, 1741-1748.	14.5	90
47	Domain mobility in proteins: functional and evolutionary implications. <i>Briefings in Bioinformatics</i> , 2008, 10, 205-216.	6.5	87
48	Widespread Positive Selection in Synonymous Sites of Mammalian Genes. <i>Molecular Biology and Evolution</i> , 2007, 24, 1821-1831.	8.9	86
49	Negative Correlation between Expression Level and Evolutionary Rate of Long Intergenic Noncoding RNAs. <i>Genome Biology and Evolution</i> , 2011, 3, 1390-1404.	2.5	86
50	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
51	Comparative analysis of orthologous eukaryotic mRNAs: potential hidden functional signals. <i>Nucleic Acids Research</i> , 2004, 32, 1774-1782.	14.5	82
52	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
53	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
54	Analysis of Rare Genomic Changes Does Not Support the Unikont–Bikont Phylogeny and Suggests Cyanobacterial Symbiosis as the Point of Primary Radiation of Eukaryotes. <i>Genome Biology and Evolution</i> , 2009, 1, 99-113.	2.5	77

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55	Context of deletions and insertions in human coding sequences. <i>Human Mutation</i> , 2004, 23, 177-185.	2.5	76
56	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
57	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
58	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
59	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
60	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
61	Evolutionarily conserved genes preferentially accumulate introns. <i>Genome Research</i> , 2007, 17, 1045-1050.	5.5	68
62	Analysis of phylogenetically reconstructed mutational spectra in human mitochondrial DNA control region. <i>Human Genetics</i> , 2002, 111, 46-53.	3.8	67
63	Patterns of intron gain and conservation in eukaryotic genes. <i>BMC Evolutionary Biology</i> , 2007, 7, 192.	3.2	67
64	Mismatch Repair-Independent Increase in Spontaneous Mutagenesis in Yeast Lacking Non-Essential Subunits of DNA Polymerase $\delta$ . <i>PLoS Genetics</i> , 2010, 6, e1001209.	3.5	66
65	Exploring background mutational processes to decipher cancer genetic heterogeneity. <i>Nucleic Acids Research</i> , 2017, 45, W514-W522.	14.5	65
66	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
67	A late origin of the extant eukaryotic diversity: divergence time estimates using rare genomic changes. <i>Biology Direct</i> , 2011, 6, 26.	4.6	63
68	Computational approaches for the analysis of gene neighbourhoods in prokaryotic genomes. <i>Briefings in Bioinformatics</i> , 2004, 5, 131-149.	6.5	62
69	Evolution of alternative and constitutive regions of mammalian 5'UTRs. <i>BMC Genomics</i> , 2009, 10, 162.	2.8	62
70	The Vast, Conserved Mammalian lincRNome. <i>PLoS Computational Biology</i> , 2013, 9, e1002917.	3.2	62
71	Transcription of mammalian messenger RNAs by a nuclear RNA polymerase of mitochondrial origin. <i>Nature</i> , 2005, 436, 735-739.	27.8	61
72	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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73	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
74	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
75	Reconstruction of Ancestral Protosplice Sites. <i>Current Biology</i> , 2004, 14, 1505-1508.	3.9	51
76	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
77	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
78	Primate and Rodent Specific Intron Gains and the Origin of Retrogenes with Splice Variants. <i>Molecular Biology and Evolution</i> , 2011, 28, 33-37.	8.9	48
79	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
80	Transposable Element Insertions in Long Intergenic Non-Coding RNA Genes. <i>Frontiers in Bioengineering and Biotechnology</i> , 2015, 3, 71.	4.1	45
81	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
82	Selection on start codons in prokaryotes and potential compensatory nucleotide substitutions. <i>Scientific Reports</i> , 2017, 7, 12422.	3.3	43
83	Evidence of Splice Signal Migration from Exon to Intron during Intron Evolution. <i>Current Biology</i> , 2003, 13, 2170-2174.	3.9	42
84	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
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	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
87	A highly conserved family of inactivated archaeal B family DNA polymerases. <i>Biology Direct</i> , 2008, 3, 32.	4.6	40
88	Differential Action of Natural Selection on the N and C-terminal Domains of 2 <sup>5</sup> A <sup>2</sup> 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
89	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
90	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

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91	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
92	Use of mutation spectra analysis software. <i>Human Mutation</i> , 2001, 17, 83-102.	2.5	35
93	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
94	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
95	Germline viral "fossils" guide in silico reconstruction of a mid-Cenozoic era marsupial adeno-associated virus. <i>Scientific Reports</i> , 2016, 6, 28965.	3.3	34
96	Similarity pattern analysis in mutational distributions. <i>Mutation Research - Fundamental and Molecular Mechanisms of Mutagenesis</i> , 1999, 430, 55-74.	1.0	33
97	Molecular dating: ape bones agree with chicken entrails. <i>Trends in Genetics</i> , 2005, 21, 89-92.	6.7	33
98	Accumulation of GC donor splice signals in mammals. <i>Biology Direct</i> , 2008, 3, 30.	4.6	33
99	Mutational signatures and mutable motifs in cancer genomes. <i>Briefings in Bioinformatics</i> , 2017, 19, 1085-1101.	6.5	32
100	Diverse roles of RAD18 and Y-family DNA polymerases in tumorigenesis. <i>Cell Cycle</i> , 2018, 17, 833-843.	2.6	32
101	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
102	Purifying and positive selection in the evolution of stop codons. <i>Scientific Reports</i> , 2018, 8, 9260.	3.3	31
103	Method of predicting splice sites based on signal interactions. <i>Biology Direct</i> , 2006, 1, 10.	4.6	30
104	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
105	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
106	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
107	In search of lost introns. <i>Bioinformatics</i> , 2007, 23, i87-i96.	4.1	27
108	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

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109	Somatic hypermutagenesis in immunoglobulin genes. I. Correlation between somatic mutations and repeats. Somatic mutation properties and clonal selection. <i>Biochimica Et Biophysica Acta Gene Regulatory Mechanisms</i> , 1991, 1089, 175-182.	2.4	26
110	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
111	Low-fidelity DNA synthesis by the L979F mutator derivative of <i>Saccharomyces cerevisiae</i> DNA polymerase $\beta$ . <i>Nucleic Acids Research</i> , 2009, 37, 3774-3787.	14.5	26
112	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
113	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
114	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
115	Replication Protein A (RPA) Hampers the Processive Action of APOBEC3G Cytosine Deaminase on Single-Stranded DNA. <i>PLoS ONE</i> , 2011, 6, e24848.	2.5	25
116	Complexity of Gene Expression Evolution after Duplication: Protein Dosage Rebalancing. <i>Genetics Research International</i> , 2014, 2014, 1-8.	2.0	25
117	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
118	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
119	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
120	Somatic hypermutagenesis in immunoglobulin genes. III. Somatic mutations in the chicken light chain locus. <i>Biochimica Et Biophysica Acta Gene Regulatory Mechanisms</i> , 1996, 1306, 171-178.	2.4	23
121	Primordial spliceosomal introns were probably U2-type. <i>Trends in Genetics</i> , 2008, 24, 525-528.	6.7	23
122	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
123	A glimpse of a putative pre-intron phase of eukaryotic evolution. <i>Trends in Genetics</i> , 2007, 23, 105-108.	6.7	21
124	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
125	Computational Prediction of Polycomb-Associated Long Non-Coding RNAs. <i>PLoS ONE</i> , 2012, 7, e44878.	2.5	19
126	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



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127	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
128	Dollo parsimony and the reconstruction of genome evolution. , 2006, , 190-200.		18
129	Characterization of several LINE-1 elements in <i>Microtus kirgisorum</i> . <i>Mammalian Genome</i> , 1999, 10, 724-729.	2.2	17
130	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
131	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
132	Computational analysis of mutation spectra. <i>Briefings in Bioinformatics</i> , 2003, 4, 210-227.	6.5	16
133	Identification of murine B cell lines that undergo somatic hypermutation focused to A:T and G:C residues. <i>European Journal of Immunology</i> , 2008, 38, 227-239.	2.9	16
134	Comparative mutational analyses of influenza A viruses. <i>Rna</i> , 2015, 21, 36-47.	3.5	16
135	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
136	Prediction of Human Gene Structure. , 1998, , 215-259.		16
137	LINE-1 element in the vole <i>Microtus subarvalis</i> . <i>Mammalian Genome</i> , 1993, 4, 624-626.	2.2	15
138	Gene structure prediction using information on homologous protein sequence. <i>Bioinformatics</i> , 1996, 12, 161-170.	4.1	15
139	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
140	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
141	Genome-Wide Changes in Protein Translation Efficiency Are Associated with Autism. <i>Genome Biology and Evolution</i> , 2018, 10, 1902-1919.	2.5	15
142	Nucleotide Weight Matrices Reveal Ubiquitous Mutational Footprints of AID/APOBEC Deaminases in Human Cancer Genomes. <i>Cancers</i> , 2019, 11, 211.	3.7	15
143	Computer prediction of sites associated with various elements of the nuclear matrix. <i>Briefings in Bioinformatics</i> , 2000, 1, 33-44.	6.5	14
144	P53 Gain-of-Function: Tumor Biology and Bioinformatics Come Together. <i>Cell Cycle</i> , 2005, 4, 686-688.	2.6	14

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145	The cytidine deaminase AID exhibits similar functional properties in yeast and mammals. <i>Molecular Immunology</i> , 2006, 43, 1481-1484.	2.2	14
146	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
147	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
148	Unravelling roles of error-prone DNA polymerases in shaping cancer genomes. <i>Oncogene</i> , 2021, 40, 6549-6565.	5.9	14
149	Evolution of the Mouse Polyubiquitin-C Gene. <i>Journal of Molecular Evolution</i> , 2002, 55, 202-210.	1.8	13
150	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
151	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
152	On the Etruscan Mitochondrial DNA Contribution to Modern Humans. <i>American Journal of Human Genetics</i> , 2004, 75, 920-923.	6.2	12
153	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
154	Low Variability of the POLG (CAG) n Repeat in North Eurasian Populations. <i>Human Biology</i> , 2005, 77, 355-365.	0.2	11
155	Prediction and phylogenetic analysis of mammalian short interspersed elements (SINEs). <i>Briefings in Bioinformatics</i> , 2000, 1, 260-274.	6.5	10
156	Rapid Evolution of a Cyclin A Inhibitor Gene, <i>roughex</i> , in <i>Drosophila</i> . <i>Molecular Biology and Evolution</i> , 2001, 18, 2110-2118.	8.9	10
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