Mikhail Gelfand

List of Publications by Year
in descending order

270 papers	15,146 citations

16451
64 h-index

23533
111 g-index

288 all docs	288 docs citations	288 times ranked	15885 citing authors

#	Article	IF	Citations
1	Experimental Determination and System Level Analysis of Essential Genes in Escherichia coli MG1655. Journal of Bacteriology, 2003, 185, 5673-5684.	2.2	678
2	Frequent Alternative Splicing of Human Genes. Genome Research, 1999, 9, 1288-1293.	5.5	462
3	Comparative Genomics of the Vitamin B12 Metabolism and Regulation in Prokaryotes. Journal of Biological Chemistry, 2003, 278, 41148-41159.	3.4	417
4	Comparative Genomics of Thiamin Biosynthesis in Procaryotes. Journal of Biological Chemistry, 2002, 277, 48949-48959.	3.4	326
5	Active chromatin and transcription play a key role in chromosome partitioning into topologically associating domains. Genome Research, 2016, 26, 70-84.	5.5	311
6	Regulation of riboflavin biosynthesis and transport genes in bacteria by transcriptional and translational attenuation. Nucleic Acids Research, 2002, 30, 3141-3151.	14.5	308
7	Gene recognition via spliced sequence alignment.. Proceedings of the National Academy of Sciences of the United States of America, 1996, 93, 9061-9066.	7.1	284
8	A Novel Class of Modular Transporters for Vitamins in Prokaryotes. Journal of Bacteriology, 2009, 191, 42-51.	2.2	280
9	Riboswitches: the oldest mechanism for the regulation of gene expression?. Trends in Genetics, 2004, 20, 44-50.	6.7	274
10	Comparative and Functional Genomic Analysis of Prokaryotic Nickel and Cobalt Uptake Transporters: Evidence for a Novel Group of ATP-Binding Cassette Transporters. Journal of Bacteriology, 2006, 188, 317-327.	2.2	269
11	Dissimilatory Metabolism of Nitrogen Oxides in Bacteria: Comparative Reconstruction of Transcriptional Networks. PLoS Computational Biology, 2005, 1, e55.	3.2	260
12	Comparative genomic analyses of nickel, cobalt and vitamin B12 utilization. BMC Genomics, 2009, 10, 78.	2.8	260
13	Comparative genomics of bacterial zinc regulons: Enhanced ion transport, pathogenesis, and rearrangement of ribosomal proteins. Proceedings of the National Academy of Sciences of the United States of America, 2003, 100, 9912-9917.	7.1	256
14	Deinococcus geothermalis: The Pool of Extreme Radiation Resistance Genes Shrinks. PLoS ONE, 2007, 2, e955.	2.5	212
15	Increase of functional diversity by alternative splicing. Trends in Genetics, 2003, 19, 124-128.	6.7	208
16	Conservation of the Biotin Regulon and the BirA Regulatory Signal in Eubacteria and Archaea. Genome Research, 2002, 12, 1507-1516.	5.5	196
17	A conserved RNA structure element involved in the regulation of bacterial riboflavin synthesis genes. Trends in Genetics, 1999, 15, 439-442.	6.7	191
18	Widespread splicing changes in human brain development and aging. Molecular Systems Biology, 2013, 9, 633.	7.2	183

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19	RegPrecise: a database of curated genomic inferences of transcriptional regulatory interactions in prokaryotes. Nucleic Acids Research, 2010, 38, D111-D118.	14.5	172
20	Combining diverse evidence for gene recognition in completely sequenced bacterial genomes. Nucleic Acids Research, 1998, 26, 2941-2947.	14.5	171
21	Regulation of the vitamin B12 metabolism and transport in bacteria by a conserved RNA structural element. Rna, 2003, 9, 1084-1097.	3.5	170
22	Regulation of lysine biosynthesis and transport genes in bacteria: yet another RNA riboswitch?. Nucleic Acids Research, 2003, 31, 6748-6757.	14.5	170
23	Genome-Wide Analysis of Cell Type-Specific Gene Transcription during Spore Formation in Clostridium difficile. PLoS Genetics, 2013, 9, e1003756.	3.5	167
24	Prediction of transcription regulatory sites in Archaea by a comparative genomic approach. Nucleic Acids Research, 2000, 28, 695-705.	14.5	166
25	How gene order is influenced by the biophysics of transcription regulation. Proceedings of the National Academy of Sciences of the United States of America, 2007, 104, 13948-13953.	7.1	165
26	Reconstruction of regulatory and metabolic pathways in metal-reducing delta-proteobacteria. Genome Biology, 2004, 5, R90.	9.6	162
27	Comparative genomics of the methionine metabolism in Gram-positive bacteria: a variety of regulatory systems. Nucleic Acids Research, 2004, 32, 3340-3353.	14.5	159
28	Pro-Frame: similarity-based gene recognition in eukaryotic DNA sequences with errors. Bioinformatics, 2001, 17, 13-15.	4.1	144
29	Computational Reconstruction of Iron- and Manganese-Responsive Transcriptional Networks in Î±-Proteobacteria. PLoS Computational Biology, 2006, 2, e163.	3.2	138
30	Evaluation and Comparison of Current Fetal Ultrasound Image Segmentation Methods for Biometric Measurements: A Grand Challenge. IEEE Transactions on Medical Imaging, 2014, 33, 797-813.	8.9	137
31	Lowâ€molecularâ€weight postâ€translationally modified microcins. Molecular Microbiology, 2007, 65, 1380-1394.	2.5	132
32	De novo sequencing and characterization of floral transcriptome in two species of buckwheat (Fagopyrum). BMC Genomics, 2011, 12, 30.	2.8	132
33	RegPredict: an integrated system for regulon inference in prokaryotes by comparative genomics approach. Nucleic Acids Research, 2010, 38, W299-W307.	14.5	130
34	Low conservation of alternative splicing patterns in the human and mouse genomes. Human Molecular Genetics, 2003, 12, 1313-1320.	2.9	128
35	Using Orthologous and Paralogous Proteins to Identify Specificity-determining Residues in Bacterial Transcription Factors. Journal of Molecular Biology, 2002, 321, 7-20.	4.2	127
36	Prediction of Function in DNA Sequence Analysis. Journal of Computational Biology, 1995, 2, 87-115.	1.6	125

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37	Avoidance of palindromic words in bacterial and archaeal genomes: a close connection with restriction enzymes. Nucleic Acids Research, 1997, 25, 2430-2439.	14.5	124
38	Software for analysis of bacterial genomes. Molecular Biology, 2000, 34, 222-231.	1.3	123
39	Computer analysis of transcription regulatory patterns in completely sequenced bacterial genomes. Nucleic Acids Research, 1999, 27, 2981-2989.	14.5	120
40	Comparative Genomics and Experimental Characterization of N-Acetylglucosamine Utilization Pathway of Shewanella oneidensis. Journal of Biological Chemistry, 2006, 281, 29872-29885.	3.4	120
41	Comparative genomic analysis of T-box regulatory systems in bacteria. Rna, 2008, 14, 717-735.	3.5	120
42	Comparative Genomics of Regulation of Fatty Acid and Branched-Chain Amino Acid Utilization in Proteobacteria. Journal of Bacteriology, 2009, 191, 52-64.	2.2	115
43	Evolution of Pan-Genomes of Escherichia coli, Shigella spp., and Salmonella enterica. Journal of Bacteriology, 2013, 195, 2786-2792.	2.2	115
44	Automated selection of positions determining functional specificity of proteins by comparative analysis of orthologous groups in protein families. Protein Science, 2004, 13, 443-456.	7.6	110
45	Comparative genomics of the KdgR regulon in Erwinia chrysanthemi 3937 and other gamma-proteobacteria. Microbiology (United Kingdom), 2004, 150, 3571-3590.	1.8	108
46	Systematic prediction of control proteins and their DNA binding sites. Nucleic Acids Research, 2009, 37, 441-451.	14.5	102
47	GntR Family of Bacterial Transcription Factors and Their DNA Binding Motifs: Structure, Positioning and Co-Evolution. PLoS ONE, 2015, 10, e0132618.	2.5	102
48	Comparative analysis of FUR regulons in gamma-proteobacteria. Nucleic Acids Research, 2001, 29, 5195-5206.	14.5	100
49	Computational analysis of candidate intron regulatory elements for tissue-specific alternative pre-mRNA splicing. Nucleic Acids Research, 2001, 29, 2338-2348.	14.5	99
50	A Gibbs sampler for identification of symmetrically structured, spaced DNA motifs with improved estimation of the signal length. Bioinformatics, 2005, 21, 2240-2245.	4.1	95
51	RegTransBase--a database of regulatory sequences and interactions in a wide range of prokaryotic genomes. Nucleic Acids Research, 2007, 35, D407-D412.	14.5	95
52	Genome-Wide Molecular Clock and Horizontal Gene Transfer in Bacterial Evolution. Journal of Bacteriology, 2004, 186, 6575-6585.	2.2	93
53	Living without Fur: the subtlety and complexity of iron-responsive gene regulation in the symbiotic bacterium Rhizobium and other Î±-proteobacteria. BioMetals, 2007, 20, 501-511.	4.1	92
54	SDPpred: a tool for prediction of amino acid residues that determine differences in functional specificity of homologous proteins. Nucleic Acids Research, 2004, 32, W424-W428.	14.5	89

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55	Bioinformatics classification and functional analysis of PhoH homologs. In Silico Biology, 2003, 3, 3-15.	0.9	84
56	Nuclear lamina integrity is required for proper spatial organization of chromatin in Drosophila. Nature Communications, 2019, 10, 1176.	12.8	83
57	Crosslinking-immunoprecipitation (iCLIP) analysis reveals global regulatory roles of hnRNP L. RNA Biology, 2014, 11, 146-155.	3.1	82
58	A metabolic network in the evolutionary context: Multiscale structure and modularity. Proceedings of the National Academy of Sciences of the United States of America, 2006, 103, 8774-8779.	7.1	77
59	Transcriptional regulation of pentose utilisation systems in the Bacillus/Clostridium group of bacteria. FEMS Microbiology Letters, 2001, 205, 305-314.	1.8	76
60	Comparative genomics and evolution of regulons of the LacI-family transcription factors. Frontiers in Microbiology, 2014, 5, 294.	3.5	76
61	Modulation of alternative splicing by long-range RNA structures in Drosophila. Nucleic Acids Research, 2009, 37, 4533-4544.	14.5	71
62	Neanderthal ancestry drives evolution of lipid catabolism in contemporary Europeans. Nature Communications, 2014, 5, 3584.	12.8	70
63	Genome-wide transcription start site mapping of Bradyrhizobium japonicum grown free-living or in symbiosis â€" a rich resource to identify new transcripts, proteins and to study gene regulation. BMC Genomics, 2016, 17, 302.	2.8	70
64	RegTransBase â€" a database of regulatory sequences and interactions based on literature: a resource for investigating transcriptional regulation in prokaryotes. BMC Genomics, 2013, 14, 213.	2.8	69
65	Identification of a bacterial regulatory system for ribonucleotide reductases by phylogenetic profiling. Trends in Genetics, 2005, 21, 385-389.	6.7	68
66	Attenuation regulation of amino acid biosynthetic operons in proteobacteria: comparative genomics analysis. FEMS Microbiology Letters, 2004, 234, 357-370.	1.8	67
67	Transcriptional regulation of NAD metabolism in bacteria: genomic reconstruction of NiaR (YrxA) regulon. Nucleic Acids Research, 2008, 36, 2032-2046.	14.5	67
68	Comparative genomics of regulation of heavy metal resistance in Eubacteria. BMC Microbiology, 2006, 6, 49.	3.3	66
69	Nitrogen Fixation and Molecular Oxygen: Comparative Genomic Reconstruction of Transcription Regulation in Alphaproteobacteria. Frontiers in Microbiology, 2016, 7, 1343.	3.5	66
70	Genomic Analysis of Caldithrix abyssi, the Thermophilic Anaerobic Bacterium of the Novel Bacterial Phylum Calditrichaeota. Frontiers in Microbiology, 2017, 8, 195.	3.5	66
71	A Polar Mechanism Coordinates Different Regions of Alternative Splicing within a Single Gene. Molecular Cell, 2005, 19, 393-404.	9.7	63
72	Comparative analysis of regulatory patterns in bacterial genomes. Briefings in Bioinformatics, 2000, 1, 357-371.	6.5	62

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73	Evolution of transcriptional regulatory networks in microbial genomes. Current Opinion in Structural Biology, 2006, 16, 420-429.	5.7	61
74	Prediction of the exon-intron structure by a dynamic programming approach. BioSystems, 1993, 30, 173-182.	2.0	60
75	Complete Genome and Proteome of Acholeplasma laidlawii. Journal of Bacteriology, 2011, 193, 4943-4953.	2.2	60
76	Structural analysis of conserved base pairs in protein-DNA complexes. Nucleic Acids Research, 2002, 30, 1704-1711.	14.5	59
77	Comparative genomic reconstruction of transcriptional networks controlling central metabolism in the Shewanella genus. BMC Genomics, 2011, 12, S3.	2.8	59
78	Evidence for widespread association of mammalian splicing and conserved long-range RNA structures. Rna, 2012, 18, 1-15.	3.5	58
79	Transcriptional regulation of transport and utilization systems for hexuronides, hexuronates and hexonates in gamma purple bacteria. Molecular Microbiology, 2000, 38, 673-683.	2.5	56
80	Conservation of the binding site for the arginine repressor in all bacterial lineages. Genome Biology, 2001, 2, research0013.1.	9.6	55
81	A transporter of Escherichia coli specific for l- and d-methionine is the prototype for a new family within the ABC superfamily. Archives of Microbiology, 2003, 180, 88-100.	2.2	55
82	Abundance and functional diversity of riboswitches in microbial communities. BMC Genomics, 2007, 8, 347.	2.8	54
83	An automated stochastic approach to the identification of the protein specificity determinants and functional subfamilies. Algorithms for Molecular Biology, 2010, 5, 29.	1.2	53
84	ANA HEp-2 cells image classification using number, size, shape and localization of targeted cell regions. Pattern Recognition, 2014, 47, 2360-2366.	8.1	53
85	Genomics of Sponge-Associated Streptomyces spp. Closely Related to Streptomyces albus J1074: Insights into Marine Adaptation and Secondary Metabolite Biosynthesis Potential. PLoS ONE, 2014, 9, e96719.	2.5	51
86	Identification of replication origins in prokaryotic genomes. Briefings in Bioinformatics, 2008, 9, 376-391.	6.5	50
87	Evolutionary Dynamics of Clustered Irregularly Interspaced Short Palindromic Repeat Systems in the Ocean Metagenome. Applied and Environmental Microbiology, 2010, 76, 2136-2144.	3.1	49
88	Order and stochasticity in the folding of individual Drosophila genomes. Nature Communications, 2021, 12, 41.	12.8	49
89	Comparative genomic analysis of regulation of anaerobic respiration in ten genomes from three families of gamma-proteobacteria (Enterobacteriaceae, Pasteurellaceae, Vibrionaceae). BMC Genomics, 2007, 8, 54.	2.8	48
90	Comparative Genomics of the Dormancy Regulons in Mycobacteria. Journal of Bacteriology, 2011, 193, 3446-3452.	2.2	48

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91	Genomic study of the Ket: a Paleo-Eskimo-related ethnic group with significant ancient North Eurasian ancestry. Scientific Reports, 2016, 6, 20768.	3.3	48
92	Comparative Genomics and Evolution of Alternative Splicing:â€‰ The Pessimists' Science. Chemical Reviews, 2007, 107, 3407-3430.	47.7	47
93	Computer prediction of the exon-intron structure of mammalian pre-mRNAs. Nucleic Acids Research, 1990, 18, 5865-5869.	14.5	46
94	Functional diversification of ROK-family transcriptional regulators of sugar catabolism in the Thermotogae phylum. Nucleic Acids Research, 2013, 41, 790-803.	14.5	44
95	Regulation of biosynthesis and transport of aromatic amino acids in low-GC Gram-positive bacteria. FEMS Microbiology Letters, 2003, 222, 211-220.	1.8	43
96	Evolution of exon-intron structure and alternative splicing in fruit flies and malarial mosquito genomes. Genome Research, 2006, 16, 505-509.	5.5	43
97	Statistical analysis of mammalian pre-mRNA splicing sites. Nucleic Acids Research, 1989, 17, 6369-6382.	14.5	42
98	Damage-repair error-prone polymerases of eubacteria: association with mobile genome elements. Gene, 2002, 293, 133-140.	2.2	42
99	Regulation and Evolution of Malonate and Propionate Catabolism in Proteobacteria. Journal of Bacteriology, 2012, 194, 3234-3240.	2.2	42
100	Genome-Wide Transcription Start Site Mapping and Promoter Assignments to a Sigma Factor in the Human Enteropathogen Clostridioides difficile. Frontiers in Microbiology, 2020, 11, 1939.	3.5	42
101	ASDB: database of alternatively spliced genes. Nucleic Acids Research, 1999, 27, 301-302.	14.5	41
102	Alternative splicing and protein function. BMC Bioinformatics, 2005, 6, 266.	2.6	41
103	Comparative analysis of RNA regulatory elements of amino acid metabolism genes in Actinobacteria. BMC Microbiology, 2005, 5, 54.	3.3	41
104	Structure and Function of an ADP-Ribose-Dependent Transcriptional Regulator of NAD Metabolism. Structure, 2009, 17, 939-951.	3.3	41
105	ASDB: database of alternatively spliced genes. Nucleic Acids Research, 2000, 28, 296-297.	14.5	40
106	Gene cloning, expression and characterization of novel phytase from Obesumbacterium proteus. FEMS Microbiology Letters, 2004, 236, 283-290.	1.8	40
107	Application of sorting and next generation sequencing to study 5Î,-UTR influence on translation efficiency in Escherichia coli. Nucleic Acids Research, 2017, 45, 3487-3502.	14.5	40
108	Global Transcriptional Response of Nitrosomonas europaea to Chloroform and Chloromethane. Applied and Environmental Microbiology, 2007, 73, 3440-3445.	3.1	39

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109	Engineering transcription factors with novel DNA-binding specificity using comparative genomics. Nucleic Acids Research, 2009, 37, 2493-2503.	14.5	39
110	Recognition of regulatory sites by genomic comparison. Research in Microbiology, 1999, 150, 755-771.	2.1	38
111	Gene recognition in eukaryotic DNA by comparison of genomic sequences. Bioinformatics, 2001, 17, 1011-1018.	4.1	38
112	Combining specificity determining and conserved residues improves functional site prediction. BMC Bioinformatics, 2009, 10, 174.	2.6	37
113	Genome analysis of E. coli isolated from Crohnâ€™s disease patients. BMC Genomics, 2017, 18, 544.	2.8	37
114	Attenuation regulation of amino acid biosynthetic operons in proteobacteria: comparative genomics analysis. FEMS Microbiology Letters, 2004, 234, 357-370.	1.8	37
115	Starts of bacterial genes: estimating the reliability of computer predictions. Gene, 1999, 234, 257-265.	2.2	36
116	Fast rate of evolution in alternatively spliced coding regions of mammalian genes. BMC Genomics, 2006, 7, 84.	2.8	36
117	Glutamine versus Ammonia Utilization in the NAD Synthetase Family. PLoS ONE, 2012, 7, e39115.	2.5	36
118	Pangenomic Definition of Prokaryotic Species and the Phylogenetic Structure of Prochlorococcus spp.. Frontiers in Microbiology, 2018, 9, 428.	3.5	36
119	Determination of mutual orientation of identical particles from their projections by the moments method. Ultramicroscopy, 1988, 25, 317-327.	1.9	35
120	Performance-Guarantee Gene Predictions via Spliced Alignment. Genomics, 1998, 51, 332-339.	2.9	34
121	Comparative Genomic Analysis of the Hexuronate Metabolism Genes and Their Regulation in Gammaproteobacteria. Journal of Bacteriology, 2011, 193, 3956-3963.	2.2	34
122	Statistical Analysis of the Exon-Intron Structure of Higher and Lower Eukaryote Genes. Journal of Biomolecular Structure and Dynamics, 1999, 17, 281-288.	3.5	32
123	Mining sequence annotation databanks for association patterns. Bioinformatics, 2005, 21, iii49-iii57.	4.1	32
124	Temporal Regulation of Viral Transcription during Development of Thermus thermophilus Bacteriophage Ï•YS40. Journal of Molecular Biology, 2007, 366, 420-435.	4.2	32
125	Computational analysis of splicing errors and mutations in human transcripts. BMC Genomics, 2008, 9, 13.	2.8	32
126	Computational analysis of the transcriptional regulation of pentose utilization systems in the gamma subdivision of Proteobacteria. FEMS Microbiology Letters, 2001, 205, 315-322.	1.8	31

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127	Restriction–modification systems and bacteriophage invasion: Who wins?. Journal of Theoretical Biology, 2010, 266, 550-559.	1.7	30
128	Genome rearrangements and selection in multi-chromosome bacteria Burkholderia spp.. BMC Genomics, 2018, 19, 965.	2.8	30
129	Comparative Genomic Analysis of Holospora spp., Intranuclear Symbionts of Paramecia. Frontiers in Microbiology, 2018, 9, 738.	3.5	29
130	Regulation of aromatic amino acid biosynthesis in gamma-proteobacteria. Journal of Molecular Microbiology and Biotechnology, 2001, 3, 529-43.	1.0	28
131	Segmentation of yeast DNA using hidden Markov models. Bioinformatics, 1999, 15, 980-986.	4.1	27
132	Computational identification of BioR, a transcriptional regulator of biotin metabolism inAlphaproteobacteria, and of its binding signal. FEMS Microbiology Letters, 2006, 255, 102-107.	1.8	27
133	Transcriptional regulation of the methionine and cysteine transport and metabolism in streptococci. FEMS Microbiology Letters, 2007, 276, 207-215.	1.8	27
134	Purifying selection in mitochondria, free-living and obligate intracellular proteobacteria. BMC Evolutionary Biology, 2007, 7, 17.	3.2	27
135	Asymmetric and non-uniform evolution of recently duplicated human genes. Biology Direct, 2010, 5, 54.	4.6	27
136	Conserved and species-specific alternative splicing in mammalian genomes. BMC Evolutionary Biology, 2007, 7, 249.	3.2	26
137	Translation at first sight: the influence of leading codons. Nucleic Acids Research, 2020, 48, 6931-6942.	14.5	26
138	Single-cell Hi-C data analysis: safety in numbers. Briefings in Bioinformatics, 2021, 22, .	6.5	26
139	Using orthologous and paralogous proteins to identify specificity determining residues. Genome Biology, 2002, 3, preprint0002.1.	9.6	25
140	Comparative genomics and functional annotation of bacterial transporters. Physics of Life Reviews, 2008, 5, 22-49.	2.8	25
141	A Novel Intra-U1 snRNP Cross-Regulation Mechanism: Alternative Splicing Switch Links U1C and U1-70K Expression. PLoS Genetics, 2013, 9, e1003856.	3.5	25
142	Comparative analysis of CRISPR cassettes from the human gut metagenomic contigs. BMC Genomics, 2014, 15, 202.	2.8	25
143	Evolution of the Exon-Intron Structure in Ciliate Genomes. PLoS ONE, 2016, 11, e0161476.	2.5	25
144	Cooption of heat shock regulatory system for anhydrobiosis in the sleeping chironomid <i>Polypedilum vanderplanki</i>. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, E2477-E2486.	7.1	25

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145	Towards practical applications in quantum computational biology. Nature Computational Science, 2021, 1, 114-119.	8.0	24
146	SELEX_DB: a database on in vitro selected oligomers adapted for recognizing natural sites and for analyzing both SNPs and site-directed mutagenesis data. Nucleic Acids Research, 2002, 30, 195-199.	14.5	23
147	EVOLUTION OF THE NADR REGULON IN ENTEROBACTERIACEAE. Journal of Bioinformatics and Computational Biology, 2005, 03, 1007-1019.	0.8	22
148	Regulation of nitrogen metabolism in gram-positive bacteria. Molecular Biology, 2006, 40, 829-836.	1.3	22
149	Positive Selection in Alternatively Spliced Exons of Human Genes. American Journal of Human Genetics, 2008, 83, 94-98.	6.2	22
150	Comparative approach to analysis of regulation in complete genomes: multidrug resistance systems in gamma-proteobacteria. Journal of Molecular Microbiology and Biotechnology, 2001, 3, 319-24.	1.0	22
151	Evolution of the Exonâ€"Intron Structure and Alternative Splicing of the MAGE-A Family of Cancer/Testis Antigens. Journal of Molecular Evolution, 2004, 59, 620-631.	1.8	21
152	Temporal Regulation of Gene Expression of the Escherichia coli Bacteriophage phiEco32. Journal of Molecular Biology, 2012, 416, 389-399.	4.2	21
153	Comparative Genomic Analysis of the Regulation of Aromatic Metabolism in Betaproteobacteria. Frontiers in Microbiology, 2019, 10, 642.	3.5	21
154	Influence of the spacer region between the Shineâ€"Dalgarno box and the start codon for fineâ€‘tuning of the translation efficiency in <i>Escherichia coli</i>. Microbial Biotechnology, 2020, 13, 1254-1261.	4.2	21
155	Comparative Genomics of Transcriptional Regulation of Methionine Metabolism in Proteobacteria. PLoS ONE, 2014, 9, e113714.	2.5	20
156	Sequenceâ€‘derived structural features driving proteolytic processing. Proteomics, 2014, 14, 42-50.	2.2	20
157	Chlamydia pan-genomic analysis reveals balance between host adaptation and selective pressure to genome reduction. BMC Genomics, 2019, 20, 710.	2.8	20
158	Functional implications of splicing polymorphisms in the human genome. Human Molecular Genetics, 2013, 22, 3449-3459.	2.9	19
159	Activation of the alpha-globin gene expression correlates with dramatic upregulation of nearby non-globin genes and changes in local and large-scale chromatin spatial structure. Epigenetics and Chromatin, 2017, 10, 35.	3.9	19
160	New Intranuclear Symbiotic Bacteria from Macronucleus of Paramecium putrinumâ€"â€œCandidatus Gortzia Yakuticaâ€. Diversity, 2020, 12, 198.	1.7	19
161	Simplification of Ribosomes in Bacteria with Tiny Genomes. Molecular Biology and Evolution, 2021, 38, 58-66.	8.9	19
162	Statistical analysis and prediction of the exonic structure of human genes. Journal of Molecular Evolution, 1992, 35, 239-52.	1.8	18

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163	Evolution of transcription factor DNA binding sites. Gene, 2005, 347, 255-263.	2.2	18
164	Comparative Genomics of CytR, an Unusual Member of the LacI Family of Transcription Factors. PLoS ONE, 2012, 7, e44194.	2.5	16
165	Gene cloning, expression and characterization of novel phytase from Obesumbacterium proteus. FEMS Microbiology Letters, 2004, 236, 283-290.	1.8	16
166	Spatial Proximity and Similarity of the Epigenetic State of Genome Domains. PLoS ONE, 2012, 7, e33947.	2.5	15
167	Horizontal gene transfer and genome evolution in Methanosarcina. BMC Evolutionary Biology, 2015, 15, 102.	3.2	15
168	Algorithms and software for support of gene identification experiments. Bioinformatics, 1998, 14, 14-19.	4.1	14
169	Common and specific amino acid residues in the prokaryotic polypeptide release factors RF1 and RF2: possible functional implications. Nucleic Acids Research, 2005, 33, 5226-5234.	14.5	14
170	Weak Negative and Positive Selection and the Drift Load at Splice Sites. Genome Biology and Evolution, 2014, 6, 1437-1447.	2.5	14
171	Conservation, evolution, and regulation of splicing during prefrontal cortex development in humans, chimpanzees, and macaques. Rna, 2018, 24, 585-596.	3.5	14
172	Combinatorial approaches to gene recognition. Computers & Chemistry, 1997, 21, 229-235.	1.2	13
173	Heat Shock (σ^{32} and HrcA/CIRCE) Regulons in β-, γ- and μ-Proteobacteria. Journal of Molecular Microbiology and Biotechnology, 2003, 6, 174-181.	1.0	13
174	Microbiomes of gall-inducing copepod crustaceans from the corals Stylophora pistillata (Scleractinia) and Gorgonia ventalina (Alcyonacea). Scientific Reports, 2018, 8, 11563.	3.3	13
175	High Rates of Genome Rearrangements and Pathogenicity of Shigella spp.. Frontiers in Microbiology, 2021, 12, 628622.	3.5	13
176	Adaptive evolution at mRNA editing sites in soft-bodied cephalopods. PeerJ, 2020, 8, e10456.	2.0	13
177	Recognition of Genes in Human DNA Sequences. Journal of Computational Biology, 1996, 3, 223-234.	1.6	12
178	Comparative genomic analysis of fungal TPP-riboswitches. Fungal Genetics and Biology, 2018, 114, 34-41.	2.1	12
179	Micro-evolution of three Streptococcus species: selection, antigenic variation, and horizontal gene inflow. BMC Evolutionary Biology, 2019, 19, 83.	3.2	12
180	Bacteriocin Production by Gram-Positive Bacteria and the Mechanisms of Transcriptional Regulation. Russian Journal of Genetics, 2002, 38, 628-641.	0.6	11

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181	Evolutionary patterns of phosphorylated serines. Biology Direct, 2011, 6, 8.	4.6	11
182	Analysis of gene expression and mutation data points on contribution of transcription to the mutagenesis by APOBEC enzymes. NAR Cancer, 2021, 3, zcab025.	3.1	11
183	A machine learning framework for the prediction of chromatin folding in *Drosophila* using epigenetic features. PeerJ Computer Science, 2020, 6, e307.	4.5	11
184	Genome rearrangements and phylogeny reconstruction in *Yersinia pestis*. PeerJ, 2018, 6, e4545.	2.0	11
185	BATMAS30: Amino acid substitution matrix for alignment of bacterial transporters. Proteins: Structure, Function and Bioinformatics, 2003, 51, 85-95.	2.6	10
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