

# Mikhail Gelfand

## List of Publications by Year in descending order

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270  
papers

15,146  
citations

18887

64  
h-index

26792

111  
g-index

288  
all docs

288  
docs citations

288  
times ranked

17848  
citing authors

#	ARTICLE	IF	CITATIONS
1	OUP accepted manuscript. Nucleic Acids Research, 2022, , .	6.5	6
2	Simplification of Ribosomes in Bacteria with Tiny Genomes. Molecular Biology and Evolution, 2021, 38, 58-66.	3.5	19
3	Towards practical applications in quantum computational biology. Nature Computational Science, 2021, 1, 114-119.	3.8	24
4	High Rates of Genome Rearrangements and Pathogenicity of Shigella spp.. Frontiers in Microbiology, 2021, 12, 628622.	1.5	13
5	Comparative Analysis of the IclR-Family of Bacterial Transcription Factors and Their DNA-Binding Motifs: Structure, Positioning, Co-Evolution, Regulon Content. Frontiers in Microbiology, 2021, 12, 675815.	1.5	6
6	Analysis of gene expression and mutation data points on contribution of transcription to the mutagenesis by APOBEC enzymes. NAR Cancer, 2021, 3, zcab025.	1.6	11
7	Single-cell Hi-C data analysis: safety in numbers. Briefings in Bioinformatics, 2021, 22, .	3.2	26
8	Structural and biochemical characterization of a novel ZntB (CmaX) transporter protein from Pseudomonas aeruginosa. International Journal of Biological Macromolecules, 2021, 184, 760-767.	3.6	8
9	Order and stochasticity in the folding of individual Drosophila genomes. Nature Communications, 2021, 12, 41.	5.8	49
10	Perspectives for the reconstruction of 3D chromatin conformation using single cell Hi-C data. PLoS Computational Biology, 2021, 17, e1009546.	1.5	5
11	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.	1.5	42
12	Translation at first sight: the influence of leading codons. Nucleic Acids Research, 2020, 48, 6931-6942.	6.5	26
13	New Intranuclear Symbiotic Bacteria from Macronucleus of Paramecium putrinumâ€”â€œCandidatus Gortzia Yakuticaâ€”. Diversity, 2020, 12, 198.	0.7	19
14	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.	2.0	21
15	A machine learning framework for the prediction of chromatin folding in <i>Drosophila</i> using epigenetic features. PeerJ Computer Science, 2020, 6, e307.	2.7	11
16	Phospho-islands and the evolution of phosphorylated amino acids in mammals. PeerJ, 2020, 8, e10436.	0.9	5
17	Adaptive evolution at mRNA editing sites in soft-bodied cephalopods. PeerJ, 2020, 8, e10456.	0.9	13
18	Cumulative contact frequency of a chromatin region is an intrinsic property linked to its function. PeerJ, 2020, 8, e9566.	0.9	2

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19	HiChew: a Tool for TAD Clustering in Embryogenesis. Lecture Notes in Computer Science, 2020, , 381-388.	1.0	1
20	Predictive models of protease specificity based on quantitative protease-activity profiling data. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2019, 1867, 140253.	1.1	1
21	Chlamydia pan-genomic analysis reveals balance between host adaptation and selective pressure to genome reduction. BMC Genomics, 2019, 20, 710.	1.2	20
22	Comparative Genomic Analysis of the Regulation of Aromatic Metabolism in Betaproteobacteria. Frontiers in Microbiology, 2019, 10, 642.	1.5	21
23	Micro-evolution of three Streptococcus species: selection, antigenic variation, and horizontal gene inflow. BMC Evolutionary Biology, 2019, 19, 83.	3.2	12
24	Nuclear lamina integrity is required for proper spatial organization of chromatin in Drosophila. Nature Communications, 2019, 10, 1176.	5.8	83
25	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.	3.3	25
26	The genes of the sulphoquinovose catabolism in Escherichia coli are also associated with a previously unknown pathway of lactose degradation. Scientific Reports, 2018, 8, 3177.	1.6	8
27	Conservation, evolution, and regulation of splicing during prefrontal cortex development in humans, chimpanzees, and macaques. Rna, 2018, 24, 585-596.	1.6	14
28	Comparative genomic analysis of fungal TPP-riboswitches. Fungal Genetics and Biology, 2018, 114, 34-41.	0.9	12
29	Prediction of 3D Chromatin Structure Using Recurrent Neural Networks. , 2018, , .		0
30	Reconstruction of the chromatin 3D conformation from single cell Hi-C data. , 2018, , .		0
31	Genome rearrangements and selection in multi-chromosome bacteria Burkholderia spp.. BMC Genomics, 2018, 19, 965.	1.2	30
32	Pangenomic Definition of Prokaryotic Species and the Phylogenetic Structure of Prochlorococcus spp.. Frontiers in Microbiology, 2018, 9, 428.	1.5	36
33	Comparative Genomic Analysis of Holospora spp., Intranuclear Symbionts of Paramecia. Frontiers in Microbiology, 2018, 9, 738.	1.5	29
34	Neanderthal and Denisovan ancestry in Papuans: A functional study. Journal of Bioinformatics and Computational Biology, 2018, 16, 1840011.	0.3	4
35	Microbiomes of gall-inducing copepod crustaceans from the corals Stylophora pistillata (Scleractinia) and Gorgonia ventalina (Alcyonacea). Scientific Reports, 2018, 8, 11563.	1.6	13
36	Genome rearrangements and phylogeny reconstruction in <i>Yersinia pestis</i> . PeerJ, 2018, 6, e4545.	0.9	11

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37	Genome analysis of <i>E. coli</i> isolated from Crohn's disease patients. <i>BMC Genomics</i> , 2017, 18, 544.	1.2	37
38	Genomic Analysis of <i>Caldithrix abyssi</i> , the Thermophilic Anaerobic Bacterium of the Novel Bacterial Phylum Calditrichaeota. <i>Frontiers in Microbiology</i> , 2017, 8, 195.	1.5	66
39	Application of sorting and next generation sequencing to study 5',-UTR influence on translation efficiency in <i>Escherichia coli</i> . <i>Nucleic Acids Research</i> , 2017, 45, 3487-3502.	6.5	40
40	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. <i>Epigenetics and Chromatin</i> , 2017, 10, 35.	1.8	19
41	Sugar Lego: gene composition of bacterial carbohydrate metabolism genomic loci. <i>Biology Direct</i> , 2017, 12, 28.	1.9	4
42	Nitrogen Fixation and Molecular Oxygen: Comparative Genomic Reconstruction of Transcription Regulation in Alphaproteobacteria. <i>Frontiers in Microbiology</i> , 2016, 7, 1343.	1.5	66
43	Evolution of the Exon-Intron Structure in Ciliate Genomes. <i>PLoS ONE</i> , 2016, 11, e0161476.	1.1	25
44	Identification of Position-Specific Correlations between DNA-Binding Domains and Their Binding Sites. Application to the MerR Family of Transcription Factors. <i>PLoS ONE</i> , 2016, 11, e0162681.	1.1	7
45	Small Open Reading Frames, Non-Coding RNAs and Repetitive Elements in <i>Bradyrhizobium japonicum</i> USDA 110. <i>PLoS ONE</i> , 2016, 11, e0165429.	1.1	9
46	Recombination Processes and Nonlinear Markov Chains. <i>Journal of Computational Biology</i> , 2016, 23, 711-717.	0.8	2
47	Introduction to selected papers from MCCMB 2015. <i>Journal of Bioinformatics and Computational Biology</i> , 2016, 14, 1602003.	0.3	0
48	Detection of homologous recombination in closely related strains. <i>Journal of Bioinformatics and Computational Biology</i> , 2016, 14, 1641001.	0.3	1
49	History of chromosome rearrangements reflects the spatial organization of yeast chromosomes. <i>Journal of Bioinformatics and Computational Biology</i> , 2016, 14, 1641002.	0.3	5
50	Changes in snoRNA and snRNA abundance in the human, chimpanzee, macaque and mouse brain. <i>Genome Biology and Evolution</i> , 2016, 8, evw038.	1.1	10
51	Genome-wide transcription start site mapping of <i>Bradyrhizobium japonicum</i> grown free-living or in symbiosis – a rich resource to identify new transcripts, proteins and to study gene regulation. <i>BMC Genomics</i> , 2016, 17, 302.	1.2	70
52	Genomic study of the Ket: a Paleo-Eskimo-related ethnic group with significant ancient North Eurasian ancestry. <i>Scientific Reports</i> , 2016, 6, 20768.	1.6	48
53	Active chromatin and transcription play a key role in chromosome partitioning into topologically associating domains. <i>Genome Research</i> , 2016, 26, 70-84.	2.4	311
54	Changes in segmentation and setation along the anterior/posterior axis of the homonomous trunk limbs of a remipede (Crustacea, Arthropoda). <i>PeerJ</i> , 2016, 4, e2305.	0.9	2

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55	Selectoscope: A Modern Web-App for Positive Selection Analysis of Genomic Data. Lecture Notes in Computer Science, 2016, , 253-257.	1.0	0
56	GntR Family of Bacterial Transcription Factors and Their DNA Binding Motifs: Structure, Positioning and Co-Evolution. PLoS ONE, 2015, 10, e0132618.	1.1	102
57	Correlated Evolution of Nucleotide Positions within Splice Sites in Mammals. PLoS ONE, 2015, 10, e0144388.	1.1	8
58	Horizontal gene transfer and genome evolution in Methanosarcina. BMC Evolutionary Biology, 2015, 15, 102.	3.2	15
59	Russian science loses to politics. Nature, 2015, 522, 419-419.	13.7	1
60	Natural variation of gene models in Drosophila melanogaster. BMC Genomics, 2015, 16, 198.	1.2	6
61	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.	1.1	51
62	Comparative Genomics of Transcriptional Regulation of Methionine Metabolism in Proteobacteria. PLoS ONE, 2014, 9, e113714.	1.1	20
63	Comparative genomics and evolution of regulons of the LacI-family transcription factors. Frontiers in Microbiology, 2014, 5, 294.	1.5	76
64	Comparative analysis of CRISPR cassettes from the human gut metagenomic contigs. BMC Genomics, 2014, 15, 202.	1.2	25
65	Sequence-derived structural features driving proteolytic processing. Proteomics, 2014, 14, 42-50.	1.3	20
66	Weak Negative and Positive Selection and the Drift Load at Splice Sites. Genome Biology and Evolution, 2014, 6, 1437-1447.	1.1	14
67	Crosslinking-immunoprecipitation (iCLIP) analysis reveals global regulatory roles of hnRNP L. RNA Biology, 2014, 11, 146-155.	1.5	82
68	RNA editing: Classical cases and outlook of new technologies. Molecular Biology, 2014, 48, 11-15.	0.4	2
69	Neanderthal ancestry drives evolution of lipid catabolism in contemporary Europeans. Nature Communications, 2014, 5, 3584.	5.8	70
70	ANA HEp-2 cells image classification using number, size, shape and localization of targeted cell regions. Pattern Recognition, 2014, 47, 2360-2366.	5.1	53
71	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.	5.4	137
72	RegTransBase – a database of regulatory sequences and interactions based on literature: a resource for investigating transcriptional regulation in prokaryotes. BMC Genomics, 2013, 14, 213.	1.2	69

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73	Functional implications of splicing polymorphisms in the human genome. <i>Human Molecular Genetics</i> , 2013, 22, 3449-3459.	1.4	19
74	Genome-Wide Analysis of Cell Type-Specific Gene Transcription during Spore Formation in <i>Clostridium difficile</i> . <i>PLoS Genetics</i> , 2013, 9, e1003756.	1.5	167
75	A Novel Intra-U1 snRNP Cross-Regulation Mechanism: Alternative Splicing Switch Links U1C and U1-70K Expression. <i>PLoS Genetics</i> , 2013, 9, e1003856.	1.5	25
76	Functional diversification of ROK-family transcriptional regulators of sugar catabolism in the Thermotogae phylum. <i>Nucleic Acids Research</i> , 2013, 41, 790-803.	6.5	44
77	Evolution of Pan-Genomes of <i>Escherichia coli</i> , <i>Shigella</i> spp., and <i>Salmonella enterica</i> . <i>Journal of Bacteriology</i> , 2013, 195, 2786-2792.	1.0	115
78	Widespread splicing changes in human brain development and aging. <i>Molecular Systems Biology</i> , 2013, 9, 633.	3.2	183
79	What is to be done about Russian science?. <i>Nature</i> , 2013, 500, 379-379.	13.7	2
80	Evidence for widespread association of mammalian splicing and conserved long-range RNA structures. <i>Rna</i> , 2012, 18, 1-15.	1.6	58
81	Temporal Regulation of Gene Expression of the <i>Escherichia coli</i> Bacteriophage phiEco32. <i>Journal of Molecular Biology</i> , 2012, 416, 389-399.	2.0	21
82	Evolution of transcriptional regulation in closely related bacteria. <i>BMC Evolutionary Biology</i> , 2012, 12, 200.	3.2	10
83	Spatial Proximity and Similarity of the Epigenetic State of Genome Domains. <i>PLoS ONE</i> , 2012, 7, e33947.	1.1	15
84	Comparative Genomics of CytR, an Unusual Member of the LacI Family of Transcription Factors. <i>PLoS ONE</i> , 2012, 7, e44194.	1.1	16
85	Glutamine versus Ammonia Utilization in the NAD Synthetase Family. <i>PLoS ONE</i> , 2012, 7, e39115.	1.1	36
86	Regulation and Evolution of Malonate and Propionate Catabolism in Proteobacteria. <i>Journal of Bacteriology</i> , 2012, 194, 3234-3240.	1.0	42
87	Biases in read coverage demonstrated by interlaboratory and interplatform comparison of 117 mRNA and genome sequencing experiments. <i>BMC Bioinformatics</i> , 2012, 13, S4.	1.2	6
88	Complete Genome and Proteome of <i>Acholeplasma laidlawii</i> . <i>Journal of Bacteriology</i> , 2011, 193, 4943-4953.	1.0	60
89	Comparative genomic reconstruction of transcriptional networks controlling central metabolism in the <i>Shewanella</i> genus. <i>BMC Genomics</i> , 2011, 12, S3.	1.2	59
90	Comparative Genomics of the Dormancy Regulons in Mycobacteria. <i>Journal of Bacteriology</i> , 2011, 193, 3446-3452.	1.0	48

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91	Regulation of multidrug resistance genes by transcription factors of the BltR subfamily. <i>Molecular Biology</i> , 2011, 45, 658-666.	0.4	2
92	Machine learning study of DNA binding by transcription factors from the LacI family. <i>Molecular Biology</i> , 2011, 45, 667-679.	0.4	2
93	Rid Russian science of corruption. <i>Nature</i> , 2011, 478, 324-324.	13.7	1
94	Evolutionary patterns of phosphorylated serines. <i>Biology Direct</i> , 2011, 6, 8.	1.9	11
95	De novo sequencing and characterization of floral transcriptome in two species of buckwheat ( <i>Fagopyrum</i> ). <i>BMC Genomics</i> , 2011, 12, 30.	1.2	132
96	Comparative Genomic Analysis of the Hexuronate Metabolism Genes and Their Regulation in Gammaproteobacteria. <i>Journal of Bacteriology</i> , 2011, 193, 3956-3963.	1.0	34
97	Evolution of Regulatory Motifs of Bacterial Transcription Factors. <i>In Silico Biology</i> , 2010, 10, 163-183.	0.4	5
98	Restriction modification systems and bacteriophage invasion: Who wins?. <i>Journal of Theoretical Biology</i> , 2010, 266, 550-559.	0.8	30
99	Asymmetric and non-uniform evolution of recently duplicated human genes. <i>Biology Direct</i> , 2010, 5, 54.	1.9	27
100	An automated stochastic approach to the identification of the protein specificity determinants and functional subfamilies. <i>Algorithms for Molecular Biology</i> , 2010, 5, 29.	0.3	53
101	Evolutionary Dynamics of Clustered Irregularly Interspaced Short Palindromic Repeat Systems in the Ocean Metagenome. <i>Applied and Environmental Microbiology</i> , 2010, 76, 2136-2144.	1.4	49
102	RegPrecise: a database of curated genomic inferences of transcriptional regulatory interactions in prokaryotes. <i>Nucleic Acids Research</i> , 2010, 38, D111-D118.	6.5	172
103	RegPredict: an integrated system for regulon inference in prokaryotes by comparative genomics approach. <i>Nucleic Acids Research</i> , 2010, 38, W299-W307.	6.5	130
104	INTRODUCTION. <i>Journal of Bioinformatics and Computational Biology</i> , 2010, 08, v-vii.	0.3	0
105	Large-Scale Identification and Analysis of C-Proteins. <i>Methods in Molecular Biology</i> , 2010, 674, 269-282.	0.4	7
106	Machine Learning Study of DNA Binding by Transcription Factors from the LacI Family. <i>Lecture Notes in Computer Science</i> , 2010, , 15-26.	1.0	0
107	Systematic prediction of control proteins and their DNA binding sites. <i>Nucleic Acids Research</i> , 2009, 37, 441-451.	6.5	102
108	Engineering transcription factors with novel DNA-binding specificity using comparative genomics. <i>Nucleic Acids Research</i> , 2009, 37, 2493-2503.	6.5	39

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109	Modulation of alternative splicing by long-range RNA structures in <i>Drosophila</i> . <i>Nucleic Acids Research</i> , 2009, 37, 4533-4544.	6.5	71
110	Structure and Function of an ADP-Ribose-Dependent Transcriptional Regulator of NAD Metabolism. <i>Structure</i> , 2009, 17, 939-951.	1.6	41
111	Combining specificity determining and conserved residues improves functional site prediction. <i>BMC Bioinformatics</i> , 2009, 10, 174.	1.2	37
112	Rodent-specific alternative exons are more frequent in rapidly evolving genes and in paralogs. <i>BMC Evolutionary Biology</i> , 2009, 9, 142.	3.2	7
113	Comparative genomic analyses of nickel, cobalt and vitamin B12 utilization. <i>BMC Genomics</i> , 2009, 10, 78.	1.2	260
114	Alternative splicing tends to involve protein phosphorylation sites. <i>Molecular Biology</i> , 2009, 43, 528-530.	0.4	0
115	Cometabolic activity of aphid <i>Acyrtosiphon pisum</i> and symbiotic bacterium <i>Buchnera aphidicola</i> APS. <i>Molecular Biology</i> , 2009, 43, 1019-1020.	0.4	0
116	A Novel Class of Modular Transporters for Vitamins in Prokaryotes. <i>Journal of Bacteriology</i> , 2009, 191, 42-51.	1.0	280
117	Comparative Genomics of Regulation of Fatty Acid and Branched-Chain Amino Acid Utilization in Proteobacteria. <i>Journal of Bacteriology</i> , 2009, 191, 52-64.	1.0	115
118	Evolution of Regulatory Systems in Bacteria (Invited Keynote Talk). <i>Lecture Notes in Computer Science</i> , 2009, , 1-4.	1.0	0
119	Comparative genomics and functional annotation of bacterial transporters. <i>Physics of Life Reviews</i> , 2008, 5, 22-49.	1.5	25
120	Positive Selection in Alternatively Spliced Exons of Human Genes. <i>American Journal of Human Genetics</i> , 2008, 83, 94-98.	2.6	22
121	Some alphabets easily beat Russian letter count. <i>Nature</i> , 2008, 454, 691-691.	13.7	0
122	Benchmarking of programs that predict the position of transmembrane segments in beta-barrel proteins. <i>Biophysics (Russian Federation)</i> , 2008, 53, 134-139.	0.2	0
123	Computational analysis of splicing errors and mutations in human transcripts. <i>BMC Genomics</i> , 2008, 9, 13.	1.2	32
124	Identification of replication origins in prokaryotic genomes. <i>Briefings in Bioinformatics</i> , 2008, 9, 376-391.	3.2	50
125	Transcriptional regulation of NAD metabolism in bacteria: genomic reconstruction of NiaR (YrxA) regulon. <i>Nucleic Acids Research</i> , 2008, 36, 2032-2046.	6.5	67
126	Comparative genomic analysis of T-box regulatory systems in bacteria. <i>Rna</i> , 2008, 14, 717-735.	1.6	120



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127	OVERLAPPING ALTERNATIVE DONOR SPLICE SITES IN THE HUMAN GENOME. <i>Journal of Bioinformatics and Computational Biology</i> , 2007, 05, 991-1004.	0.3	8
128	RegTransBase—a database of regulatory sequences and interactions in a wide range of prokaryotic genomes. <i>Nucleic Acids Research</i> , 2007, 35, D407-D412.	6.5	95
129	Global Transcriptional Response of <i>Nitrosomonas europaea</i> to Chloroform and Chloromethane. <i>Applied and Environmental Microbiology</i> , 2007, 73, 3440-3445.	1.4	39
130	Temporal Regulation of Viral Transcription during Development of <i>Thermus thermophilus</i> Bacteriophage $\Psi$ S40. <i>Journal of Molecular Biology</i> , 2007, 366, 420-435.	2.0	32
131	How gene order is influenced by the biophysics of transcription regulation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007, 104, 13948-13953.	3.3	165
132	Comparative Genomics and Evolution of Alternative Splicing: The Pessimists' Science. <i>Chemical Reviews</i> , 2007, 107, 3407-3430.	23.0	47
133	Regulation of methionine/cysteine biosynthesis in <i>Corynebacterium glutamicum</i> and related organisms. <i>Molecular Biology</i> , 2007, 41, 126-136.	0.4	6
134	Computational method for predicting protein functional sites with the use of specificity determinants. <i>Molecular Biology</i> , 2007, 41, 137-147.	0.4	6
135	Regulation of bacterial respiration: Comparison of microarray and comparative genomics data. <i>Molecular Biology</i> , 2007, 41, 497-512.	0.4	0
136	Taxon-specific regulation of the SOS response in $\beta$ -proteobacteria. <i>Molecular Biology</i> , 2007, 41, 827-835.	0.4	2
137	Low-molecular-weight post-translationally modified microcins. <i>Molecular Microbiology</i> , 2007, 65, 1380-1394.	1.2	132
138	Low-molecular-weight post-translationally modified microcins. <i>Molecular Microbiology</i> , 2007, 66, 277-277.	1.2	1
139	Transcriptional regulation of the methionine and cysteine transport and metabolism in streptococci. <i>FEMS Microbiology Letters</i> , 2007, 276, 207-215.	0.7	27
140	A model of evolution with constant selective pressure for regulatory DNA sites. <i>BMC Evolutionary Biology</i> , 2007, 7, 125.	3.2	0
141	Purifying selection in mitochondria, free-living and obligate intracellular proteobacteria. <i>BMC Evolutionary Biology</i> , 2007, 7, 17.	3.2	27
142	Conserved and species-specific alternative splicing in mammalian genomes. <i>BMC Evolutionary Biology</i> , 2007, 7, 249.	3.2	26
143	Abundance and functional diversity of riboswitches in microbial communities. <i>BMC Genomics</i> , 2007, 8, 347.	1.2	54
144	Comparative genomic analysis of regulation of anaerobic respiration in ten genomes from three families of gamma-proteobacteria ( <i>Enterobacteriaceae</i> , <i>Pasteurellaceae</i> , <i>Vibrionaceae</i> ). <i>BMC Genomics</i> , 2007, 8, 54.	1.2	48

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145	Living without Fur: the subtlety and complexity of iron-responsive gene regulation in the symbiotic bacterium <i>Rhizobium</i> and other $\hat{\pm}$ -proteobacteria. <i>BioMetals</i> , 2007, 20, 501-511.	1.8	92
146	<i>Deinococcus geothermalis</i> : The Pool of Extreme Radiation Resistance Genes Shrinks. <i>PLoS ONE</i> , 2007, 2, e955.	1.1	212
147	Amino acid residues that determine functional specificity of NADP- and NAD-dependent isocitrate and isopropylmalate dehydrogenases. <i>Proteins: Structure, Function and Bioinformatics</i> , 2006, 64, 1001-1009.	1.5	8
148	Computational identification of BioR, a transcriptional regulator of biotin metabolism in $\hat{\pm}$ -proteobacteria, and of its binding signal. <i>FEMS Microbiology Letters</i> , 2006, 255, 102-107.	0.7	27
149	Use of the flux model of amino acid metabolism of <i>Escherichia coli</i> . <i>Biochemistry (Moscow)</i> , 2006, 71, 1256-1260.	0.7	3
150	Evolutionary differences between alternative and constitutive protein-coding regions of alternatively spliced genes of <i>Drosophila</i> . <i>Biophysics (Russian Federation)</i> , 2006, 51, 515-522.	0.2	2
151	EDASâ€™A database of alternatively spliced human genes. <i>Biophysics (Russian Federation)</i> , 2006, 51, 523-526.	0.2	8
152	Second Moscow Conference on Computational Molecular Biology MCCMBâ€™05. <i>Biophysics (Russian)</i> Tj ETQq0 0.0,rgBT /Oerlock 10	0.2	0
153	Bacterial cis-regulatory RNA structures. <i>Molecular Biology</i> , 2006, 40, 541-550.	0.4	7
154	Regulation of nitrogen metabolism in gram-positive bacteria. <i>Molecular Biology</i> , 2006, 40, 829-836.	0.4	22
155	Evolution of transcriptional regulatory networks in microbial genomes. <i>Current Opinion in Structural Biology</i> , 2006, 16, 420-429.	2.6	61
156	Fast rate of evolution in alternatively spliced coding regions of mammalian genes. <i>BMC Genomics</i> , 2006, 7, 84.	1.2	36
157	Comparative genomics of regulation of heavy metal resistance in Eubacteria. <i>BMC Microbiology</i> , 2006, 6, 49.	1.3	66
158	A metabolic network in the evolutionary context: Multiscale structure and modularity. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006, 103, 8774-8779.	3.3	77
159	Computational Reconstruction of Iron- and Manganese-Responsive Transcriptional Networks in $\hat{\pm}$ -Proteobacteria. <i>PLoS Computational Biology</i> , 2006, 2, e163.	1.5	138
160	Evolution of exon-intron structure and alternative splicing in fruit flies and malarial mosquito genomes. <i>Genome Research</i> , 2006, 16, 505-509.	2.4	43
161	Comparative Genomics and Experimental Characterization of N-Acetylglucosamine Utilization Pathway of <i>Shewanella oneidensis</i> . <i>Journal of Biological Chemistry</i> , 2006, 281, 29872-29885.	1.6	120
162	Comparative and Functional Genomic Analysis of Prokaryotic Nickel and Cobalt Uptake Transporters: Evidence for a Novel Group of ATP-Binding Cassette Transporters. <i>Journal of Bacteriology</i> , 2006, 188, 317-327.	1.0	269

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163	RECOGNITION OF TRANSMEMBRANE SEGMENTS IN PROTEINS: REVIEW AND CONSISTENCY-BASED BENCHMARKING OF INTERNET SERVERS. <i>Journal of Bioinformatics and Computational Biology</i> , 2006, 04, 1033-1056.	0.3	10
164	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
165	Common and specific amino acid residues in the prokaryotic polypeptide release factors RF1 and RF2: possible functional implications. <i>Nucleic Acids Research</i> , 2005, 33, 5226-5234.	6.5	14
166	Identification of a bacterial regulatory system for ribonucleotide reductases by phylogenetic profiling. <i>Trends in Genetics</i> , 2005, 21, 385-389.	2.9	68
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