

Nikolay A Kolchanov

List of Publications by Year in descending order

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138
papers

3,948
citations

201575

27
h-index

133188

59
g-index

140
all docs

140
docs citations

140
times ranked

4538
citing authors

#	ARTICLE	IF	CITATIONS
1	Computer analysis of the relation between hydrogen bond stability in SOD1 mutants and the survival time of amyotrophic lateral sclerosis patients. <i>Journal of Molecular Graphics and Modelling</i> , 2022, 110, 108026.	1.3	4
2	Stress Reactivity, Susceptibility to Hypertension, and Differential Expression of Genes in Hypertensive Compared to Normotensive Patients. <i>International Journal of Molecular Sciences</i> , 2022, 23, 2835.	1.8	9
3	A Bioinformatics Model of Human Diseases on the Basis of Differentially Expressed Genes (of Domestic) Tj ETQq1 1 0.784314 rgBT /O Changes. <i>International Journal of Molecular Sciences</i> , 2021, 22, 2346.	1.8	7
4	Disruptive Selection of Human Immunostimulatory and Immunosuppressive Genes Both Provokes and Prevents Rheumatoid Arthritis, Respectively, as a Self-Domestication Syndrome. <i>Frontiers in Genetics</i> , 2021, 12, 610774.	1.1	5
5	Domestication Explains Two-Thirds of Differential-Gene-Expression Variance between Domestic and Wild Animals; The Remaining One-Third Reflects Intraspecific and Interspecific Variation. <i>Animals</i> , 2021, 11, 2667.	1.0	9
6	Leave or Stay: Simulating Motility and Fitness of Microorganisms in Dynamic Aquatic Ecosystems. <i>Biology</i> , 2021, 10, 1019.	1.3	2
7	Characterization of biological peculiarities of the radioprotective activity of double-stranded RNA isolated from <i>Saccharomyces Nerevisiae</i> . <i>International Journal of Radiation Biology</i> , 2020, 96, 1173-1191.	1.0	4
8	GPU Based Composite Elements Discovery In Large DNADatasets. , 2020, , .		0
9	Unannotated single nucleotide polymorphisms in the TATA box of erythropoiesis genes show in vitro positive involvements in cognitive and mental disorders. <i>BMC Medical Genetics</i> , 2020, 21, 165.	2.1	4
10	The Phylogeny of Class B Flavoprotein Monooxygenases and the Origin of the YUCCA Protein Family. <i>Plants</i> , 2020, 9, 1092.	1.6	5
11	Meta-Analysis of Transcriptome Data Detected New Potential Players in Response to Dioxin Exposure in Humans. <i>International Journal of Molecular Sciences</i> , 2020, 21, 7858.	1.8	4
12	Candidate SNP Markers of Atherogenesis Significantly Shifting the Affinity of TATA-Binding Protein for Human Gene Promoters Show Stabilizing Natural Selection as a Sum of Neutral Drift Accelerating Atherogenesis and Directional Natural Selection Slowing It. <i>International Journal of Molecular Sciences</i> , 2020, 21, 1045.	1.8	7
13	Web-Based Computational Tools for the Prediction and Analysis of Posttranslational Modifications of Proteins. <i>Methods in Molecular Biology</i> , 2019, 1934, 1-20.	0.4	5
14	Genomics research at Bioinformatics of Genome Regulation and Structure Systems Biology (BGRSSB) conferences in Novosibirsk. <i>BMC Genomics</i> , 2019, 20, 322.	1.2	5
15	Natural Selection Equally Supports the Human Tendencies in Subordination and Domination: A Genome-Wide Study With in silico Confirmation and in vivo Validation in Mice. <i>Frontiers in Genetics</i> , 2019, 10, 73.	1.1	14
16	Spatial heterogeneity promotes antagonistic evolutionary scenarios in microbial community explained by ecological stratification: a simulation study. <i>Ecological Modelling</i> , 2019, 399, 66-76.	1.2	1
17	Genome analysis identifies the mutant genes for common industrial Silverblue and Hedlund white coat colours in American mink. <i>Scientific Reports</i> , 2019, 9, 4581.	1.6	19
18	Introduction to the 9th Young Scientists School on Systems Biology and Bioinformatics (SBBâ€™2017). <i>Journal of Bioinformatics and Computational Biology</i> , 2018, 16, 1802001.	0.3	6

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19	Argo_CUDA: Exhaustive GPU based approach for motif discovery in large DNA datasets. Journal of Bioinformatics and Computational Biology, 2018, 16, 1740012.	0.3	5
20	Candidate SNP markers of reproductive potential are predicted by a significant change in the affinity of TATA-binding protein for human gene promoters. BMC Genomics, 2018, 19, 0.	1.2	22
21	High temperature and pressure influence the interdomain orientation of Nip7 proteins from <i>P. abyssi</i> and <i>P. furiosus</i> : MD simulations. Journal of Biomolecular Structure and Dynamics, 2018, 36, 68-82.	2.0	2
22	Cancer Stem Cells: Emergent Nature of Tumor Emergency. Frontiers in Genetics, 2018, 9, 544.	1.1	11
23	Initiation Factors $\hat{\tau}$, 2018, , .		0
24	Genomics at Belyaev conference "2017. BMC Genomics, 2018, 19, 79.	1.2	7
25	Pluripotency gene network dynamics: System views from parametric analysis. PLoS ONE, 2018, 13, e0194464.	1.1	14
26	Efficacy of a new cancer treatment strategy based on eradication of tumor-initiating stem cells in a mouse model of Krebs-2 solid adenocarcinoma. Oncotarget, 2018, 9, 28486-28499.	0.8	12
27	Dynamic properties of SOD1 mutants can predict survival time of patients carrying familial amyotrophic lateral sclerosis. Journal of Biomolecular Structure and Dynamics, 2017, 35, 645-656.	2.0	9
28	A quantitative method for determination of $\langle \text{PPDK} \rangle$ concentration in miscanthus leaves. GCB Bioenergy, 2017, 9, 262-269.	2.5	1
29	Editorial "Bioinformatics development at the BGRSSB conference series: 10th anniversary. Journal of Bioinformatics and Computational Biology, 2017, 15, 1702001.	0.3	11
30	Identification of residues of the archaeal RNA-binding Nip7 proteins specific to environmental conditions. Journal of Bioinformatics and Computational Biology, 2017, 15, 1650036.	0.3	3
31	SNP TATA Comparator genomewide landmarks for preventive personalized medicine. Frontiers in Bioscience - Scholar, 2017, 9, 276-306.	0.8	19
32	Candidate SNP Markers of Familial and Sporadic Alzheimer's Diseases Are Predicted by a Significant Change in the Affinity of TATA-Binding Protein for Human Gene Promoters. Frontiers in Aging Neuroscience, 2017, 9, 231.	1.7	23
33	Gene expression profiling of tumor-initiating stem cells from mouse Krebs-2 carcinoma using a novel marker of poorly differentiated cells. Oncotarget, 2017, 8, 9425-9441.	0.8	17
34	Candidate SNP Markers of Chronopathologies Are Predicted by a Significant Change in the Affinity of TATA-Binding Protein for Human Gene Promoters. BioMed Research International, 2016, 2016, 1-21.	0.9	21
35	Candidate SNP Markers of Gender-Biased Autoimmune Complications of Monogenic Diseases Are Predicted by a Significant Change in the Affinity of TATA-Binding Protein for Human Gene Promoters. Frontiers in Immunology, 2016, 7, 130.	2.2	17
36	Properties of internalization factors contributing to the uptake of extracellular DNA into tumor-initiating stem cells of mouse Krebs-2 cell line. Stem Cell Research and Therapy, 2016, 7, 76.	2.4	16

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37	Mechanical Behavior of Cells within a Cell-Based Model of Wheat Leaf Growth. <i>Frontiers in Plant Science</i> , 2016, 7, 1878.	1.7	6
38	A compendium of human genes regulating feeding behavior and body weight, its functional characterization and identification of GWAS genes involved in brain-specific PPI network. <i>BMC Genetics</i> , 2016, 17, 158.	2.7	15
39	Impact of Terahertz Radiation on Stress-Sensitive Genes of E.Coli Cell. <i>IEEE Transactions on Terahertz Science and Technology</i> , 2016, 6, 435-441.	2.0	28
40	Computational genomics at BGRSSB-2016: introductory note. <i>BMC Genomics</i> , 2016, 17, 996.	1.2	33
41	Candidate SNP markers of aggressiveness-related complications and comorbidities of genetic diseases are predicted by a significant change in the affinity of TATA-binding protein for human gene promoters. <i>BMC Genomics</i> , 2016, 17, 995.	1.2	20
42	Application of reproductive technologies to improve dairy cattle genomic selection. <i>Russian Journal of Genetics: Applied Research</i> , 2016, 6, 321-329.	0.4	5
43	A strategy to eradicate well-developed Krebs-2 ascites in mice. <i>Oncotarget</i> , 2016, 7, 11580-11594.	0.8	23
44	Modeling evolution of spatially distributed bacterial communities: a simulation with the haploid evolutionary constructor. <i>BMC Evolutionary Biology</i> , 2015, 15, S3.	3.2	9
45	Obesity-related known and candidate SNP markers can significantly change affinity of TATA-binding protein for human gene promoters. <i>BMC Genomics</i> , 2015, 16, S5.	1.2	24
46	Prediction of tissue-specific effects of gene knockout on apoptosis in different anatomical structures of human brain. <i>BMC Genomics</i> , 2015, 16, S3.	1.2	8
47	The evolution of <i>Homo sapiens denisova</i> and <i>Homo sapiens neanderthalensis</i> miRNA targeting genes in the prenatal and postnatal brain. <i>BMC Genomics</i> , 2015, 16, S4.	1.2	3
48	Effect of flanking sequences on the accuracy of the recognition of transcription factor binding sites. <i>Russian Journal of Genetics: Applied Research</i> , 2015, 5, 322-329.	0.4	1
49	Mechanisms of the formation and propagation of sociobiological interactions: a computer simulation study. <i>Russian Journal of Genetics: Applied Research</i> , 2015, 5, 672-678.	0.4	0
50	Influence of serotonin transporter allele polymorphism on individual characteristics of cerebral hemodynamics in humans under the "Signal" experimental paradigm. <i>Russian Journal of Genetics: Applied Research</i> , 2015, 5, 666-671.	0.4	0
51	Identification of the relationship between the variability of the expression of signaling pathway genes in the human brain and the affinity of TATA-binding protein to their promoters. <i>Russian Journal of Genetics: Applied Research</i> , 2015, 5, 626-634.	0.4	6
52	Association of anxiety level with polymorphic variants of serotonin transporter gene in Russians and Tuvians. <i>Russian Journal of Genetics: Applied Research</i> , 2015, 5, 656-665.	0.4	4
53	ANDSystem: an Associative Network Discovery System for automated literature mining in the field of biology. <i>BMC Systems Biology</i> , 2015, 9, S2.	3.0	58
54	Molecular association of pathogenetic contributors to pre-eclampsia (pre-eclampsia associome). <i>BMC Systems Biology</i> , 2015, 9, S4.	3.0	25

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55	Neurometabolic Effect of Altaian Fungus <i>Ganoderma lucidum</i> (Reishi Mushroom) in Rats Under Moderate Alcohol Consumption. <i>Alcoholism: Clinical and Experimental Research</i> , 2015, 39, 1128-1136.	1.4	5
56	How to Use SNP_TATA_Comparator to Find a Significant Change in Gene Expression Caused by the Regulatory SNP of This Gene's Promoter via a Change in Affinity of the TATA-Binding Protein for This Promoter. <i>BioMed Research International</i> , 2015, 2015, 1-17.	0.9	34
57	Human Genes Encoding Transcription Factors and Chromatin-Modifying Proteins Have Low Levels of Promoter Polymorphism: A Study of 1000 Genomes Project Data. <i>International Journal of Genomics</i> , 2015, 2015, 1-15.	0.8	13
58	Permanent proteins in the urine of healthy humans during the Mars-500 experiment. <i>Journal of Bioinformatics and Computational Biology</i> , 2015, 13, 1540001.	0.3	17
59	Introductory note for BGRSSB-2014 special issue. <i>Journal of Bioinformatics and Computational Biology</i> , 2015, 13, 1502001.	0.3	20
60	Isolation of prospective microalgal strains with high saturated fatty acid content for biofuel production. <i>Algal Research</i> , 2015, 12, 368-376.	2.4	47
61	A New Stochastic Model for Subgenomic Hepatitis C Virus Replication Considers Drug Resistant Mutants. <i>PLoS ONE</i> , 2014, 9, e91502.	1.1	12
62	Genetic basis of olfactory cognition: extremely high level of DNA sequence polymorphism in promoter regions of the human olfactory receptor genes revealed using the 1000 Genomes Project dataset. <i>Frontiers in Psychology</i> , 2014, 5, 247.	1.1	28
63	Molecular dynamics simulations of the Nip7 proteins from the marine deep- and shallow-water <i>Pyrococcus</i> species. <i>BMC Structural Biology</i> , 2014, 14, 23.	2.3	6
64	The Mechanism by which TATA-Box Polymorphisms Associated with Human Hereditary Diseases Influence Interactions with the TATA-Binding Protein. <i>Human Mutation</i> , 2014, 35, 601-608.	1.1	41
65	Insights into pathophysiology of dystropy through the analysis of gene networks: an example of bronchial asthma and tuberculosis. <i>Immunogenetics</i> , 2014, 66, 457-465.	1.2	21
66	Program complex SNP-MED for analysis of single-nucleotide polymorphism (SNP) effects on the function of genes associated with socially significant diseases. <i>Russian Journal of Genetics: Applied Research</i> , 2014, 4, 159-167.	0.4	8
67	Molecular analysis of the benthos microbial community in Zavarzin thermal spring (Uzon Caldera, Tj ETQq1 1 0.784314 rgBT/Overlo	1.2	39
68	Chromatin Interaction Analysis with Paired-End Tag (ChIA-PET) sequencing technology and application. <i>BMC Genomics</i> , 2014, 15, S11.	1.2	75
69	Time-course human urine proteomics in space-flight simulation experiments. <i>BMC Genomics</i> , 2014, 15, S2.	1.2	35
70	Studying the non-thermal effects of terahertz radiation on <i>E. coli</i> /pKatG-GFP biosensor cells. <i>Bioelectromagnetics</i> , 2013, 34, 15-21.	0.9	26
71	Computerized analysis of the relationship between allergenicity of microorganisms and their habitats. <i>Russian Journal of Genetics: Applied Research</i> , 2013, 3, 171-175.	0.4	1
72	Modeling of plant embryo morphodynamics at early developmental stages. <i>Russian Journal of Genetics: Applied Research</i> , 2013, 3, 176-183.	0.4	0

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73	Modification of cellulose as a promising direction in the design of new materials. <i>Polymer Science - Series B</i> , 2013, 55, 409-429.	0.3	31
74	Research on the biodiversity of Western Siberia microalgae for third-generation biofuel production processes. <i>Russian Journal of Genetics: Applied Research</i> , 2013, 3, 487-492.	0.4	3
75	HOW MULTIPLE AUXIN RESPONSIVE ELEMENTS MAY INTERACT IN PLANT PROMOTERS: A REVERSE PROBLEM SOLUTION. <i>Journal of Bioinformatics and Computational Biology</i> , 2013, 11, 1340011.	0.3	11
76	SUBCELLULAR LOCALIZATION CHARTS: A NEW VISUAL METHODOLOGY FOR THE SEMI-AUTOMATIC LOCALIZATION OF PROTEIN-RELATED DATA SETS. <i>Journal of Bioinformatics and Computational Biology</i> , 2013, 11, 1340005.	0.3	13
77	INTRODUCTORY NOTE FOR BGRS-2012 SPECIAL ISSUE. <i>Journal of Bioinformatics and Computational Biology</i> , 2013, 11, 1302001.	0.3	17
78	An Experimental Verification of the Predicted Effects of Promoter TATA-Box Polymorphisms Associated with Human Diseases on Interactions between the TATA Boxes and TATA-Binding Protein. <i>PLoS ONE</i> , 2013, 8, e54626.	1.1	55
79	Abundances of microRNAs in human cells can be estimated as a function of the abundances of YRHB and RHHK tetranucleotides in these microRNAs as an ill-posed inverse problem solution. <i>Frontiers in Genetics</i> , 2013, 4, 122.	1.1	3
80	Combined in silico/in vivo analysis of mechanisms providing for root apical meristem self-organization and maintenance. <i>Annals of Botany</i> , 2012, 110, 349-360.	1.4	55
81	SitEx: a computer system for analysis of projections of protein functional sites on eukaryotic genes. <i>Nucleic Acids Research</i> , 2012, 40, D278-D283.	6.5	5
82	Contextual DNA features significant for the DNA damage by the 193-nm ultraviolet laser beam. <i>Doklady Biochemistry and Biophysics</i> , 2012, 447, 267-272.	0.3	2
83	Potential of microalgae as a source of bioenergy. <i>Catalysis in Industry</i> , 2012, 4, 202-208.	0.3	15
84	Extraction of quantitative characteristics describing wheat leaf pubescence with a novel image-processing technique. <i>Planta</i> , 2012, 236, 1943-1954.	1.6	20
85	The Importance of Changes to Microrna in the Evolution of Homo Neanderthalensis and Homo Denisova. <i>Archaeology, Ethnology and Anthropology of Eurasia</i> , 2012, 40, 22-30.	0.1	3
86	Computer analysis of metagenomic data – Prediction of quantitative value of specific activity of proteins. <i>Doklady Biochemistry and Biophysics</i> , 2012, 443, 76-80.	0.3	4
87	Computer modeling of genome complexity variation trends in prokaryotic communities under varying habitat conditions. <i>Ecological Modelling</i> , 2012, 224, 124-129.	1.2	5
88	Change of TATA-binding protein affinity to oligonucleotides corresponding to TATA boxes in human gene promoters bearing polymorphisms associated with hereditary diseases. <i>Russian Journal of Genetics: Applied Research</i> , 2012, 2, 1-6.	0.4	1
89	From Published Expression and Phenotype Data to Structured Knowledge: The Arabidopsis Gene Net Supplementary Database and Its Applications. <i>Lecture Notes in Computer Science</i> , 2011, , 101-120.	1.0	0
90	Study of a one-dimensional model, accounting for cell division, of regulation of the renewing zone size in a biological tissue. <i>Journal of Applied and Industrial Mathematics</i> , 2011, 5, 601-611.	0.1	4

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91	Acute immune response to the intranasal application of nanoparticles of SiO ₂ (Tarkosil 25) in mice of two strains. <i>Nanotechnologies in Russia</i> , 2011, 6, 763-772.	0.7	1
92	Development of computational methods to search for FoxA transcription factor binding sites, their experimental verification and application to the analysis of ChIP-seq data. <i>Doklady Biochemistry and Biophysics</i> , 2011, 436, 12-15.	0.3	2
93	Important role of hydrophobic interactions in high-pressure adaptation of proteins. <i>Doklady Biochemistry and Biophysics</i> , 2011, 438, 113-116.	0.3	2
94	A new variety of Chinese silver grass (<i>Miscanthus sinensis</i> Anders.) : A promising source of cellulose-containing raw material. <i>Russian Journal of Genetics: Applied Research</i> , 2011, 1, 29-32.	0.4	4
95	Effect of TATA Box polymorphisms in human \hat{I}^2 -globin gene promoter associated with \hat{I}^2 -thalassemia on interaction with TATA-binding protein. <i>Russian Journal of Genetics: Applied Research</i> , 2011, 1, 183-188.	0.4	2
96	Molecular evolution of cyclin proteins in animals and fungi. <i>BMC Evolutionary Biology</i> , 2011, 11, 224.	3.2	30
97	Visualization and Analysis of a Cardio Vascular Disease and MUPP1-related Biological Network combining Text Mining and Data Warehouse Approaches. <i>Journal of Integrative Bioinformatics</i> , 2010, 7, .	1.0	10
98	Possibility spaces and evolution. <i>Paleontological Journal</i> , 2010, 44, 1491-1499.	0.2	0
99	Specific/nonspecific binding of TBP to promoter DNA of the auxin response factor genes in plants correlated with ARFs function on gene transcription (activator/repressor). <i>Doklady Biochemistry and Biophysics</i> , 2010, 433, 191-196.	0.3	10
100	SNPS IN THE HIV-1 TATA BOX AND THE AIDS PANDEMIC. <i>Journal of Bioinformatics and Computational Biology</i> , 2010, 08, 607-625.	0.3	19
101	A new form of <i>Miscanthus</i> (Chinese silver grass, <i>Miscanthus sinensis</i> Andersson) as a promising source of cellulosic biomass. <i>Advances in Bioscience and Biotechnology (Print)</i> , 2010, 01, 167-170.	0.3	14
102	Visualization and analysis of a cardio vascular disease- and MUPP1-related biological network combining text mining and data warehouse approaches. <i>Journal of Integrative Bioinformatics</i> , 2010, 7, 148.	1.0	11
103	Molecular evolution of the hyperthermophilic archaea of the <i>Pyrococcus</i> genus: analysis of adaptation to different environmental conditions. <i>BMC Genomics</i> , 2009, 10, 639.	1.2	28
104	TATA box polymorphisms in human gene promoters and associated hereditary pathologies. <i>Biochemistry (Moscow)</i> , 2009, 74, 117-129.	0.7	54
105	Adaptive evolution of genes of archaea belonging to the genus <i>Pyrococcus</i> associated with adaptation to life under high-pressure conditions. <i>Doklady Biochemistry and Biophysics</i> , 2009, 425, 91-93.	0.3	1
106	The evolution of key cell cycle proteins correlates with an increase in the complexity of eukaryotic organisms. <i>Doklady Biochemistry and Biophysics</i> , 2009, 426, 147-151.	0.3	0
107	A step-by-step model of TBP/TATA box binding allows predicting human hereditary diseases by single nucleotide polymorphism. <i>Doklady Biochemistry and Biophysics</i> , 2008, 419, 88-92.	0.3	42
108	The abundance of microRNA in <i>Arabidopsis thaliana</i> correlates with the presence of tetranucleotides WRHW and DRYD in their sequences. <i>Doklady Biochemistry and Biophysics</i> , 2008, 420, 150-154.	0.3	2

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109	uORFs, reinitiation and alternative translation start sites in human mRNAs. FEBS Letters, 2008, 582, 1293-1297.	1.3	57
110	Genetic algorithm and optimized weight matrix application for peroxisome proliferator response elements recognition: Prerequisites of accuracy growth for wide genome research. Intelligent Data Analysis, 2008, 12, 513-526.	0.4	2
111	Combined experimental and computational approaches to study the regulatory elements in eukaryotic genes. Briefings in Bioinformatics, 2007, 8, 266-274.	3.2	28
112	Bioinformatical and experimental approaches to investigation of transcription factor binding sites in vertebrate genes. Biochemistry (Moscow), 2007, 72, 1187-1193.	0.7	8
113	AUG_hairpin: prediction of a downstream secondary structure influencing the recognition of a translation start site. BMC Bioinformatics, 2007, 8, 318.	1.2	46
114	Effective transcription factor binding site prediction using a combination of optimization, a genetic algorithm and discriminant analysis to capture distant interactions. BMC Bioinformatics, 2007, 8, 481.	1.2	35
115	Recognition of interferon-inducible sites, promoters, and enhancers. BMC Bioinformatics, 2007, 8, 56.	1.2	13
116	Mathematical model of auxin distribution in the plant root. Russian Journal of Developmental Biology, 2007, 38, 374-382.	0.1	8
117	Search for new binding sites for the transcriptional factor SF-1 by the SITECON method: Experimental verification and analysis of regulatory regions of orthologous genes. Doklady Biochemistry and Biophysics, 2007, 415, 165-169.	0.3	2
118	INTERACTION OF RECOMBINANT TATA-BINDING PROTEIN WITH MAMMALS GENES PROMOTER TATA. Ecological Genetics, 2007, 5, 44-49.	0.1	9
119	Simulation of coevolution in community by using the "Evolutionary Constructor" program. In Silico Biology, 2007, 7, 261-75.	0.4	6
120	Novel genes identified by manual annotation and microarray expression analysis in the pancreas. Genomics, 2006, 88, 752-761.	1.3	6
121	The role of alternative translation start sites in the generation of human protein diversity. Molecular Genetics and Genomics, 2005, 273, 491-496.	1.0	61
122	ARGO: a web system for the detection of degenerate motifs and large-scale recognition of eukaryotic promoters. Nucleic Acids Research, 2005, 33, W417-W422.	6.5	14
123	CRASP: a program for analysis of coordinated substitutions in multiple alignments of protein sequences. Nucleic Acids Research, 2004, 32, W64-W68.	6.5	37
124	NPRD: Nucleosome Positioning Region Database. Nucleic Acids Research, 2004, 33, D67-D70.	6.5	17
125	Apoptosis Gene Network: Description in the GeneNet and TRRD Databases. Annals of the New York Academy of Sciences, 2003, 1010, 16-18.	1.8	7
126	NotI flanking sequences: a tool for gene discovery and verification of the human genome. Nucleic Acids Research, 2002, 30, 3163-3170.	6.5	20

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127	A fast genetic algorithm for RNA secondary structure analysis. Russian Chemical Bulletin, 2002, 51, 1135-1144.	0.4	21
128	GeneNet database: description and modeling of gene networks. In Silico Biology, 2002, 2, 97-110.	0.4	5
129	Transcription Regulatory Regions Database (TRRD): its status in 1999. Nucleic Acids Research, 1999, 27, 303-306.	6.5	27
130	Point mutations within 663-666 bp of intron 6 of the human TDO2 gene, associated with a number of psychiatric disorders, damage the YY-1 transcription factor binding site. FEBS Letters, 1999, 462, 85-88.	1.3	32
131	Eukaryotic mRNAs encoding abundant and scarce proteins are statistically dissimilar in many structural features. FEBS Letters, 1998, 440, 351-355.	1.3	97
132	Databases on transcriptional regulation: TRANSFAC, TRRD and COMPEL. Nucleic Acids Research, 1998, 26, 362-367.	6.5	1,345
133	Generating Programs for Predicting the Activity of Functional Sites. Journal of Computational Biology, 1997, 4, 83-90.	0.8	10
134	TRANSFAC, TRRD and COMPEL: towards a federated database system on transcriptional regulation. Nucleic Acids Research, 1997, 25, 265-268.	6.5	141
135	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
136	A compilation of composite regulatory elements affecting gene transcription in vertebrates. Nucleic Acids Research, 1995, 23, 4097-4103.	6.5	96
137	Can three-dimensional contacts in protein structures be predicted by analysis of correlated mutations?. Protein Engineering, Design and Selection, 1994, 7, 349-358.	1.0	262
138	Single amino acid substitutions producing instability of globular proteins. Calculation of their frequencies in the entire mutational spectra of the α_1 - and β_2 -subunits of human hemoglobin. Journal of Molecular Evolution, 1988, 27, 154-162.	0.8	1