

Mikhail P Ponomarenko

List of Publications by Year in descending order

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69
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1,133
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331670

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71
docs citations

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times ranked

621
citing authors

#	ARTICLE	IF	CITATIONS
1	Conformational and physicochemical DNA features specific for transcription factor binding sites. <i>Bioinformatics</i> , 1999, 15, 654-668.	4.1	67
2	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.	2.5	55
3	TATA box polymorphisms in human gene promoters and associated hereditary pathologies. <i>Biochemistry (Moscow)</i> , 2009, 74, 117-129.	1.5	54
4	rSNP_Guide: An integrated database-tools system for studying SNPs and site-directed mutations in transcription factor binding sites. <i>Human Mutation</i> , 2002, 20, 239-248.	2.5	49
5	Identification of sequence-dependent DNA features correlating to activity of DNA sites interacting with proteins. <i>Bioinformatics</i> , 1999, 15, 687-703.	4.1	46
6	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.	0.9	42
7	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.	2.5	41
8	Oligonucleotide frequency matrices addressed to recognizing functional DNA sites. <i>Bioinformatics</i> , 1999, 15, 631-643.	4.1	39
9	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.	1.9	34
10	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. <i>FEBS Letters</i> , 1999, 462, 85-88.	2.8	32
11	ASPD (Artificially Selected Proteins/Peptides Database): a database of proteins and peptides evolved in vitro. <i>Nucleic Acids Research</i> , 2002, 30, 200-202.	14.5	29
12	rSNP_Guide, a database system for analysis of transcription factor binding to target sequences: application to SNPs and site-directed mutations. <i>Nucleic Acids Research</i> , 2001, 29, 312-316.	14.5	28
13	rSNP_Guide, a database system for analysis of transcription factor binding to DNA with variations: application to genome annotation. <i>Nucleic Acids Research</i> , 2003, 31, 118-121.	14.5	27
14	ACTIVITY: a database on DNA/RNA sites activity adapted to apply sequence-activity relationships from one system to another. <i>Nucleic Acids Research</i> , 2001, 29, 284-287.	14.5	25
15	Prediction of the affinity of the TATA-binding protein to TATA boxes with single nucleotide polymorphisms. <i>Molecular Biology</i> , 2009, 43, 472-479.	1.3	25
16	Nucleosomal DNA property database. <i>Bioinformatics</i> , 1999, 15, 582-592.	4.1	24
17	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.	2.8	24
18	Prediction of eukaryotic mRNA translational properties. <i>Bioinformatics</i> , 1999, 15, 704-712.	4.1	23

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19	SELEX_DB: a database on in vitro selected oligomers adapted for recognizing natural sites and for analyzing both SNPs and site-directed mutagenesis data. <i>Nucleic Acids Research</i> , 2002, 30, 195-199.	14.5	23
20	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. <i>Frontiers in Aging Neuroscience</i> , 2017, 9, 231.	3.4	23
21	Candidate SNP markers of reproductive potential are predicted by a significant change in the affinity of TATA-binding protein for human gene promoters. <i>BMC Genomics</i> , 2018, 19, 0.	2.8	22
22	Integrated databases and computer systems for studying eukaryotic gene expression. <i>Bioinformatics</i> , 1999, 15, 669-686.	4.1	21
23	SELEX_DB: an activated database on selected randomized DNA/RNA sequences addressed to genomic sequence annotation. <i>Nucleic Acids Research</i> , 2000, 28, 205-208.	14.5	21
24	Candidate SNP Markers of Chronopathologies Are Predicted by a Significant Change in the Affinity of TATA-Binding Protein for Human Gene Promoters. <i>BioMed Research International</i> , 2016, 2016, 1-21.	1.9	21
25	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.	2.8	20
26	TATA box polymorphisms in genes of commercial and laboratory animals and plants associated with selectively valuable traits. <i>Russian Journal of Genetics</i> , 2010, 46, 394-403.	0.6	19
27	A precise equation of equilibrium of four steps of TBP binding with the TATA box for prognosis of phenotypic manifestation of mutations. <i>Biophysics (Russian Federation)</i> , 2010, 55, 358-369.	0.7	19
28	SNPS IN THE HIV-1 TATA BOX AND THE AIDS PANDEMIC. <i>Journal of Bioinformatics and Computational Biology</i> , 2010, 08, 607-625.	0.8	19
29	SNP TATA Comparator genomewide landmarks for preventive personalized medicine. <i>Frontiers in Bioscience - Scholar</i> , 2017, 9, 276-306.	2.1	19
30	Thermodynamic and kinetic basis for recognition and repair of 8-oxoguanine in DNA by human 8-oxoguanine-DNA glycosylase. <i>Nucleic Acids Research</i> , 2011, 39, 4836-4850.	14.5	18
31	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. <i>Frontiers in Immunology</i> , 2016, 7, 130.	4.8	17
32	Sequence-based prediction of transcription upregulation by auxin in plants. <i>Journal of Bioinformatics and Computational Biology</i> , 2015, 13, 1540009.	0.8	14
33	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.	2.3	14
34	Candidate SNP markers of social dominance, which may affect the affinity of the TATA-binding protein for human gene promoters. <i>Russian Journal of Genetics: Applied Research</i> , 2017, 7, 523-537.	0.4	12
35	Evolution of Brain Active Gene Promoters in Human Lineage Towards the Increased Plasticity of Gene Regulation. <i>Molecular Neurobiology</i> , 2018, 55, 1871-1904.	4.0	12
36	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.	0.8	11

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37	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). Doklady Biochemistry and Biophysics, 2010, 433, 191-196.	0.9	10
38	Mining DNA sequences to predict sites which mutations cause genetic diseases. Knowledge-Based Systems, 2002, 15, 225-233.	7.1	9
39	A Rat Model of Human Behavior Provides Evidence of Natural Selection Against Underexpression of Aggressiveness-Related Genes in Humans. Frontiers in Genetics, 2019, 10, 1267.	2.3	9
40	Domestication Explains Two-Thirds of Differential-Gene-Expression Variance between Domestic and Wild Animals; The Remaining One-Third Reflects Intraspecific and Interspecific Variation. Animals, 2021, 11, 2667.	2.3	9
41	Stress Reactivity, Susceptibility to Hypertension, and Differential Expression of Genes in Hypertensive Compared to Normotensive Patients. International Journal of Molecular Sciences, 2022, 23, 2835.	4.1	9
42	Program complex SNP-MED for analysis of single-nucleotide polymorphism (SNP) effects on the function of genes associated with socially significant diseases. Russian Journal of Genetics: Applied Research, 2014, 4, 159-167.	0.4	8
43	Hypothetical SNP markers that significantly affect the affinity of the TATA-binding protein to VEGFA, ERBB2, IGF1R, FLT1, KDR, and MET oncogene promoters as chemotherapy targets. Molecular Biology, 2016, 50, 141-152.	1.3	8
44	Disruptive natural selection by male reproductive potential prevents underexpression of protein-coding genes on the human Y chromosome as a self-domestication syndrome. BMC Genetics, 2020, 21, 89.	2.7	8
45	rSNP_Guide-based evaluation of SNPs in promoters of the human APC and MLH1 genes associated with colon cancer. Russian Journal of Genetics: Applied Research, 2014, 4, 245-253.	0.4	7
46	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. International Journal of Molecular Sciences, 2020, 21, 1045.	4.1	7
47	A Bioinformatics Model of Human Diseases on the Basis of Differentially Expressed Genes (of Domestic) Tj ETQq1 1 0.784314 rgBT /Ove Changes. International Journal of Molecular Sciences, 2021, 22, 2346.	4.1	7
48	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. Russian Journal of Genetics: Applied Research, 2015, 5, 626-634.	0.4	6
49	Disruptive Selection of Human Immunostimulatory and Immunosuppressive Genes Both Provokes and Prevents Rheumatoid Arthritis, Respectively, as a Self-Domestication Syndrome. Frontiers in Genetics, 2021, 12, 610774.	2.3	5
50	AN EXPERIMENTAL STUDY OF THE EFFECT OF RARE POLYMORPHISMS OF HUMAN HBB, HBD AND F9 PROMOTER TATA BOXES ON THE KINETICS OF INTERACTION WITH THE TATA-BINDING PROTEIN. Vavilovskii Zhurnal Genetiki i Selektcii, 2018, 22, 145-152.	1.1	5
51	Candidate SNP Markers of Atherosclerosis That May Significantly Change the Affinity of the TATA-Binding Protein for the Human Gene Promoters. Russian Journal of Genetics, 2019, 55, 1137-1151.	0.6	4
52	Unannotated single nucleotide polymorphisms in the TATA box of erythropoiesis genes show in vitro positive involvements in cognitive and mental disorders. BMC Medical Genetics, 2020, 21, 165.	2.1	4
53	Methods for integration of heterogeneous information resources in molecular biology in the digital library GeneExpress. Programming and Computer Software, 2000, 26, 170-176.	0.9	3
54	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. Frontiers in Genetics, 2013, 4, 122.	2.3	3

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55	Point mutations at positions 663 and 666 associated with mental disorders alter the binding site for transcription factor YY1 in the human tryptophan dioxygenase gene intron 6. <i>Molecular Biology</i> , 2000, 34, 186-193.	1.3	2
56	MINING GENOME VARIATION TO ASSOCIATE GENETIC DISEASE WITH MUTATION ALTERATIONS AND ORTHO/PARALOGOUS POLIMORPHYSMS IN TRANSCRIPTION FACTOR BINDING SITE. <i>International Journal on Artificial Intelligence Tools</i> , 2005, 14, 599-619.	1.0	2
57	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.	0.9	2
58	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.	0.9	2
59	Prediction and verification of the influence of the rs367781716 SNP on the interaction of the TBP-binding protein with the promoter of the human NOS1 gene. <i>Russian Journal of Genetics: Applied Research</i> , 2016, 6, 785-791.	0.4	2
60	An experimental study of the effects of SNPs in the TATA boxes of the <i>GRIN1</i> , <i>ASCL3</i> and <i>NOS1</i> genes on interactions with the TATA-binding protein. <i>Vavilovskii Zhurnal Genetiki I Seleksii</i> , 2022, 26, 227-233.	1.1	2
61	Specific features of the mature microRNA nucleotide sequences can influence the affinity for the human Ago2 and Ago3 proteins. <i>Molecular Biology</i> , 2011, 45, 327-336.	1.3	1
62	Flanking monomer repeats determine decreased context complexity of single nucleotide polymorphism sites in the human genome. <i>Russian Journal of Genetics: Applied Research</i> , 2016, 6, 809-815.	0.4	1
63	Candidate SNP-markers of rheumatoid arthritis that can significantly alter the affinity of the TATA-binding protein for human gene promoters. <i>Vavilovskii Zhurnal Genetiki I Seleksii</i> , 2020, 23, 1047-1058.	1.1	1
64	A bioinformatic search for correspondence between differentially expressed genes of domestic versus wild animals and orthologous human genes altering reproductive potential. <i>Vavilovskii Zhurnal Genetiki I Seleksii</i> , 2022, 26, 96-108.	1.1	1
65	Mining genome variation to associate disease with transcription factor binding site alteration. , 2001, , .		0
66	Possibility spaces and evolution. <i>Paleontological Journal</i> , 2010, 44, 1491-1499.	0.5	0
67	Effects of SNPs in the positioning regions of RNA polymerase II on the TBP/promoter affinity in genes of the human circadian clock. <i>Russian Journal of Genetics: Applied Research</i> , 2016, 6, 759-770.	0.4	0
68	Biomedical and candidate SNP markers of chronopathologies can significantly change the affinity of the TBP-binding protein to the promoters of human genes. <i>Russian Journal of Genetics: Applied Research</i> , 2016, 6, 738-748.	0.4	0
69	Initiation Factors $\hat{\tau}$. , 2018, , .		0