Mikhail P Ponomarenko

List of Publications by Year
in descending order

69	1,133	331670 21	434195 31
papers	citations	h-index	g-index

71	71	71	621
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	A bioinformatic search for correspondence between differentially expressed genes of domestic versus wild animals and orthologous human genes altering reproductive potential. Vavilovskii Zhurnal Genetiki I Selektsii, 2022, 26, 96-108.	1.1	1
2	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
3	An experimental study of the effects of SNPs in the TATA boxes of the <i>GRIN1, ASCL3</i> and <i>NOS1</i> genes on interactions with the TATA-binding protein. Vavilovskii Zhurnal Genetiki I Selektsii, 2022, 26, 227-233.	1.1	2
4	A Bioinformatics Model of Human Diseases on the Basis of Differentially Expressed Genes (of Domestic) Tj ETQq0 0 0 rgBT /Overlock 10 Changes. International Journal of Molecular Sciences, 2021, 22, 2346.	4.1	7
5	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
6	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
7	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
8	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
9	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
10	Ð¡andidate SNP-markers of rheumatoid arthritis that can significantly alter the affinity of the TATA-binding protein for human gene promoters. Vavilovskii Zhurnal Genetiki I Selektsii, 2020, 23, 1047-1058.	1.1	1
11	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
12	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. Frontiers in Genetics, 2019, 10, 73.	2.3	14
13	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
14	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.	2.8	22
15	Evolution of Brain Active Gene Promoters in Human Lineage Towards the Increased Plasticity of Gene Regulation. Molecular Neurobiology, 2018, 55, 1871-1904.	4.0	12
16	Initiation Factors â˜†. , 2018, , .		0
17	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 Selektsii, 2018, 22, 145-152.	1.1	5
18	Candidate SNP markers of social dominance, which may affect the affinity of the TATA-binding protein for human gene promoters. Russian Journal of Genetics: Applied Research, 2017, 7, 523-537.	0.4	12

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19	SNP TATA Comparator genomewide landmarks for preventive personalized medicine. Frontiers in Bioscience - Scholar, 2017, 9, 276-306.	2.1	19
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. Frontiers in Aging Neuroscience, 2017, 9, 231.	3.4	23
21	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.	1.9	21
22	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.	4.8	17
23	Flanking monomer repeats determine decreased context complexity of single nucleotide polymorphism sites in the human genome. Russian Journal of Genetics: Applied Research, 2016, 6, 809-815.	0.4	1
24	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. BMC Genomics, 2016, 17, 995.	2.8	20
25	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
26	Prediction and verification of the influence of the rs367781716 SNP on the interaction of the Đ¢ĐĐ¢Đ•binding protein with the promoter of the human ĐĐ'Đ¡Đ9 gene. Russian Journal of Genetics: Applied Research, 2016, 6, 785-791.	0.4	2
27	Effects of SNPs in the positioning regions of RNA polymerase II on the TBP/promoter affinity in genes of the human circadian clock. Russian Journal of Genetics: Applied Research, 2016, 6, 759-770.	0.4	0
28	Biomedical and candidate SNP markers of chronopathologies can significantly change the affinity of the Đ¢ĐĐ¢Đ•binding protein to the promoters of human genes. Russian Journal of Genetics: Applied Research, 2016, 6, 738-748.	0.4	0
29	Obesity-related known and candidate SNP markers can significantly change affinity of TATA-binding protein for human gene promoters. BMC Genomics, 2015, 16, S5.	2.8	24
30	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
31	How to Use SNP_TATA_Comparator to Find a Significant Change in Gene Expression Caused by the Regulatory SNP of This Geneâ€™s Promoter via a Change in Affinity of the TATA-Binding Protein for This Promoter. BioMed Research International, 2015, 2015, 1-17.	1.9	34
32	Sequence-based prediction of transcription upregulation by auxin in plants. Journal of Bioinformatics and Computational Biology, 2015, 13, 1540009.	0.8	14
33	The Mechanism by which TATA-Box Polymorphisms Associated with Human Hereditary Diseases Influence Interactions with the TATA-Binding Protein. Human Mutation, 2014, 35, 601-608.	2.5	41
34	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
35	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
36	HOW MULTIPLE AUXIN RESPONSIVE ELEMENTS MAY INTERACT IN PLANT PROMOTERS: A REVERSE PROBLEM SOLUTION. Journal of Bioinformatics and Computational Biology, 2013, 11, 1340011.	0.8	11

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37	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. PLoS ONE, 2013, 8, e54626.	2.5	55
38	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
39	Contextual DNA features significant for the DNA damage by the 193-nm ultraviolet laser beam. Doklady Biochemistry and Biophysics, 2012, 447, 267-272.	0.9	2
40	Specific features of the mature microrna nucleotide sequences can influence the affinity for the human Ago2 and Ago3 proteins. Molecular Biology, 2011, 45, 327-336.	1.3	1
41	Thermodynamic and kinetic basis for recognition and repair of 8-oxoguanine in DNA by human 8-oxoguanine-DNA glycosylase. Nucleic Acids Research, 2011, 39, 4836-4850.	14.5	18
42	Possibility spaces and evolution. Paleontological Journal, 2010, 44, 1491-1499.	0.5	0
43	TATA box polymorphisms in genes of commercial and laboratory animals and plants associated with selectively valuable traits. Russian Journal of Genetics, 2010, 46, 394-403.	0.6	19
44	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
45	A precise equation of equilibrium of four steps of TBP binding with the TATA box for prognosis of phenotypic manifestation of mutations. Biophysics (Russian Federation), 2010, 55, 358-369.	0.7	19
46	SNPS IN THE HIV-1 TATA BOX AND THE AIDS PANDEMIC. Journal of Bioinformatics and Computational Biology, 2010, 08, 607-625.	0.8	19
47	TATA box polymorphisms in human gene promoters and associated hereditary pathologies. Biochemistry (Moscow), 2009, 74, 117-129.	1.5	54
48	Prediction of the affinity of the TATA-binding protein to TATA boxes with single nucleotide polymorphisms. Molecular Biology, 2009, 43, 472-479.	1.3	25
49	A step-by-step model of TBP/TATA box binding allows predicting human hereditary diseases by single nucleotide polymorphism. Doklady Biochemistry and Biophysics, 2008, 419, 88-92.	0.9	42
50	The abundance of microRNA in Arabidopsis thaliana correlates with the presence of tetranucleotides WRHW and DRYD in their sequences. Doklady Biochemistry and Biophysics, 2008, 420, 150-154.	0.9	2
51	MINING GENOME VARIATION TO ASSOCIATE GENETIC DISEASE WITH MUTATION ALTERATIONS AND ORTHO/PARALOGOUS POLIMORPHYSMS IN TRANSCRIPTION FACTOR BINDING SITE. International Journal on Artificial Intelligence Tools, 2005, 14, 599-619.	1.0	2
52	rSNP_Guide, a database system for analysis of transcription factor binding to DNA with variations: application to genome annotation. Nucleic Acids Research, 2003, 31, 118-121.	14.5	27
53	ASPD (Artificially Selected Proteins/Peptides Database): a database of proteins and peptides evolved in vitro. Nucleic Acids Research, 2002, 30, 200-202.	14.5	29
54	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

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55	rSNP_Guide: An integrated database-tools system for studying SNPs and site-directed mutations in transcription factor binding sites. Human Mutation, 2002, 20, 239-248.	2.5	49
56	Mining DNA sequences to predict sites which mutations cause genetic diseases. Knowledge-Based Systems, 2002, 15, 225-233.	7.1	9
57	Mining genome variation to associate disease with transcription factor binding site alteration. , 2001, , .		0
58	rSNP_Guide, a database system for analysis of transcription factor binding to target sequences: application to SNPs and site-directed mutations. Nucleic Acids Research, 2001, 29, 312-316.	14.5	28
59	ACTIVITY: a database on DNA/RNA sites activity adapted to apply sequence-activity relationships from one system to another. Nucleic Acids Research, 2001, 29, 284-287.	14.5	25
60	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
61	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. Molecular Biology, 2000, 34, 186-193.	1.3	2
62	SELEX_DB: an activated database on selected randomized DNA/RNA sequences addressed to genomic sequence annotation. Nucleic Acids Research, 2000, 28, 205-208.	14.5	21
63	Conformational and physicochemical DNA features specific for transcription factor binding sites. Bioinformatics, 1999, 15, 654-668.	4.1	67
64	Identification of sequence-dependent DNA features correlating to activity of DNA sites interacting with proteins. Bioinformatics, 1999, 15, 687-703.	4.1	46
65	Integrated databases and computer systems for studying eukaryotic gene expression. Bioinformatics, 1999, 15, 669-686.	4.1	21
66	Oligonucleotide frequency matrices addressed to recognizing functional DNA sites. Bioinformatics, 1999, 15, 631-643.	4.1	39
67	Prediction of eukaryotic mRNA translational properties. Bioinformatics, 1999, 15, 704-712.	4.1	23
68	Nucleosomal DNA property database. Bioinformatics, 1999, 15, 582-592.	4.1	24
69	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.	2.8	32