

Vladimir Ivanisenko

List of Publications by Year in descending order

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Version: 2024-02-01

81
papers

1,251
citations

394421

19
h-index

434195

31
g-index

84
all docs

84
docs citations

84
times ranked

1462
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.	2.4	4
2	Plant Biology and Biotechnology: Focus on Genomics and Bioinformatics. <i>International Journal of Molecular Sciences</i> , 2022, 23, 6759.	4.1	4
3	Correlation of Metabolic Profiles of Plasma and Cerebrospinal Fluid of High-Grade Glioma Patients. <i>Metabolites</i> , 2021, 11, 133.	2.9	13
4	Long and short isoforms of c-FLIP act as control checkpoints of DED filament assembly. <i>Oncogene</i> , 2020, 39, 1756-1772.	5.9	22
5	The role of death domain proteins in host response upon SARS-CoV-2 infection: modulation of programmed cell death and translational applications. <i>Cell Death Discovery</i> , 2020, 6, 101.	4.7	41
6	Young «oil site» of the Uzon Caldera as a habitat for unique microbial life. <i>BMC Microbiology</i> , 2020, 20, 349.	3.3	4
7	Pharmacological targeting of c-FLIPL and Bcl-2 family members promotes apoptosis in CD95L-resistant cells. <i>Scientific Reports</i> , 2020, 10, 20823.	3.3	4
8	ANDDigest: a new web-based module of ANDSystem for the search of knowledge in the scientific literature. <i>BMC Bioinformatics</i> , 2020, 21, 228.	2.6	19
9	The story of the lost twins: decoding the genetic identities of the Kumhar and Kurcha populations from the Indian subcontinent. <i>BMC Genetics</i> , 2020, 21, 117.	2.7	5
10	Learning the changes of barnase mutants thermostability from structural fluctuations obtained using anisotropic network modeling. <i>Journal of Molecular Graphics and Modelling</i> , 2020, 97, 107572.	2.4	0
11	Design, Synthesis and Molecular Modeling Study of Conjugates of ADP and Morpholino Nucleosides as A Novel Class of Inhibitors of PARP-1, PARP-2 and PARP-3. <i>International Journal of Molecular Sciences</i> , 2020, 21, 214.	4.1	10
12	Dissecting DISC regulation via pharmacological targeting of caspase-8/c-FLIPL heterodimer. <i>Cell Death and Differentiation</i> , 2020, 27, 2117-2130.	11.2	19
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.	0.9	5
14	Delineating the role of c-FLIP/NEMO interaction in the CD95 network via rational design of molecular probes. <i>BMC Genomics</i> , 2019, 20, 293.	2.8	9
15	The molecular mechanisms driving physiological changes after long duration space flights revealed by quantitative analysis of human blood proteins. <i>BMC Medical Genomics</i> , 2019, 12, 45.	1.5	6
16	Prioritization of genes involved in endothelial cell apoptosis by their implication in lymphedema using an analysis of associative gene networks with ANDSystem. <i>BMC Medical Genomics</i> , 2019, 12, 47.	1.5	18
17	A new version of the ANDSystem tool for automatic extraction of knowledge from scientific publications with expanded functionality for reconstruction of associative gene networks by considering tissue-specific gene expression. <i>BMC Bioinformatics</i> , 2019, 20, 34.	2.6	50
18	Evaluation of cardiovascular system state by urine proteome after manned space flight. <i>Acta Astronautica</i> , 2019, 160, 594-600.	3.2	4

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19	Comorbidity of asthma and hypertension may be mediated by shared genetic dysregulation and drug side effects. <i>Scientific Reports</i> , 2019, 9, 16302.	3.3	20
20	Improved regression model to predict an impact of SOD1 mutations on ALS patients survival time based on analysis of hydrogen bond stability. <i>Journal of Molecular Graphics and Modelling</i> , 2019, 86, 247-255.	2.4	2
21	FunGeneNet: a web tool to estimate enrichment of functional interactions in experimental gene sets. <i>BMC Genomics</i> , 2018, 19, 76.	2.8	7
22	Search for New Candidate Genes Involved in the Comorbidity of Asthma and Hypertension Based on Automatic Analysis of Scientific Literature. <i>Journal of Integrative Bioinformatics</i> , 2018, 15, .	1.5	12
23	GenCoNet – A Graph Database for the Analysis of Comorbidities by Gene Networks. <i>Journal of Integrative Bioinformatics</i> , 2018, 15, .	1.5	10
24	shRNA-Induced Knockdown of a Bioinformatically Predicted Target IL10 Influences Functional Parameters in Spontaneously Hypertensive Rats with Asthma. <i>Journal of Integrative Bioinformatics</i> , 2018, 15, .	1.5	8
25	Integrative Analysis of Co-Morbid Multifactorial Diseases. <i>Journal of Integrative Bioinformatics</i> , 2018, 15, .	1.5	1
26	Molecular Relationships between Bronchial Asthma and Hypertension as Comorbid Diseases. <i>Journal of Integrative Bioinformatics</i> , 2018, 15, .	1.5	12
27	Novel candidate genes important for asthma and hypertension comorbidity revealed from associative gene networks. <i>BMC Medical Genomics</i> , 2018, 11, 15.	1.5	57
28	Molecular mechanisms underlying the impact of mutations in SOD1 on its conformational properties associated with amyotrophic lateral sclerosis as revealed with molecular modelling. <i>BMC Structural Biology</i> , 2018, 18, 1.	2.3	22
29	ANALYSIS OF THE INTERACTIONS OF NEURONAL APOPTOSIS GENES IN THE ASSOCIATIVE GENE NETWORK OF PARKINSON'S DISEASE. <i>Vavilovskii Zhurnal Genetiki i Seleksii</i> , 2018, 22, 153-160.	1.1	3
30	Dynamic properties of SOD1 mutants can predict survival time of patients carrying familial amyotrophic lateral sclerosis. <i>Journal of Biomolecular Structure and Dynamics</i> , 2017, 35, 645-656.	3.5	9
31	A study of structural properties of gene network graphs for mathematical modeling of integrated mosaic gene networks. <i>Journal of Bioinformatics and Computational Biology</i> , 2017, 15, 1650045.	0.8	2
32	SITEX 2.0: Projections of protein functional sites on eukaryotic genes. Extension with orthologous genes. <i>Journal of Bioinformatics and Computational Biology</i> , 2017, 15, 1650044.	0.8	1
33	Molecular mechanisms of the interaction between the processes of the cell response to mechanical stress and neuronal apoptosis in primary open-angle glaucoma. <i>Russian Journal of Genetics: Applied Research</i> , 2017, 7, 558-564.	0.4	1
34	Regression model for predicting pathogenic properties of SOD1 mutants based on the analysis of conformational stability and conservation of hydrogen bonds. <i>Journal of Molecular Graphics and Modelling</i> , 2017, 77, 378-385.	2.4	10
35	Structural modeling of NAD ⁺ binding modes to PARP-1. <i>Russian Journal of Genetics: Applied Research</i> , 2017, 7, 574-579.	0.4	3
36	Mosaic gene network modelling identified new regulatory mechanisms in HCV infection. <i>Virus Research</i> , 2016, 218, 71-78.	2.2	8

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37	Design and experimental validation of small-molecule inhibitors of the FADD protein. Russian Journal of Genetics: Applied Research, 2016, 6, 778-784.	0.4	0
38	Novel tuberculosis susceptibility candidate genes revealed by the reconstruction and analysis of associative networks. Infection, Genetics and Evolution, 2016, 46, 118-123.	2.3	21
39	Computer simulation of the spatial structures of MUC1 peptides capable of inhibiting apoptosis. Russian Journal of Genetics: Applied Research, 2016, 6, 771-777.	0.4	0
40	Interactome of the hepatitis C virus: Literature mining with ANDSystem. Virus Research, 2016, 218, 40-48.	2.2	25
41	NACE: A web-based tool for prediction of intercompartmental efficiency of human molecular genetic networks. Virus Research, 2016, 218, 79-85.	2.2	4
42	Computer analysis of protein functional sites projection on exon structure of genes in Metazoa. BMC Genomics, 2015, 16, S2.	2.8	2
43	Prediction of tissue-specific effects of gene knockout on apoptosis in different anatomical structures of human brain. BMC Genomics, 2015, 16, S3.	2.8	8
44	ANDSystem: an Associative Network Discovery System for automated literature mining in the field of biology. BMC Systems Biology, 2015, 9, S2.	3.0	58
45	Molecular association of pathogenetic contributors to pre-eclampsia (pre-eclampsia associome). BMC Systems Biology, 2015, 9, S4.	3.0	25
46	Permanent proteins in the urine of healthy humans during the Mars-500 experiment. Journal of Bioinformatics and Computational Biology, 2015, 13, 1540001.	0.8	17
47	Structural and dynamic properties of mutant SOD1 proteins associated with amyotrophic lateral sclerosis. Russian Journal of Genetics: Applied Research, 2015, 5, 348-353.	0.4	1
48	A New Stochastic Model for Subgenomic Hepatitis C Virus Replication Considers Drug Resistant Mutants. PLoS ONE, 2014, 9, e91502.	2.5	12
49	Bioinformatics analysis of the genome of Geobacillus stearothermophilus 22 Strain isolated from the Garga hot spring, Baikal Region. Russian Journal of Genetics: Applied Research, 2014, 4, 267-272.	0.4	2
50	Insights into pathophysiology of dystrophy through the analysis of gene networks: an example of bronchial asthma and tuberculosis. Immunogenetics, 2014, 66, 457-465.	2.4	21
51	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
52	Molecular analysis of the benthos microbial community in Zavarzin thermal spring (Uzon Caldera,) Tj ETQq0 0 0 rgBT/Overlock 10 Tf 50	2.8	39
53	Analysis of signaling networks distributed over intracellular compartments based on protein-protein interactions. BMC Genomics, 2014, 15, S7.	2.8	6
54	Time-course human urine proteomics in space-flight simulation experiments. BMC Genomics, 2014, 15, S2.	2.8	35

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55	Exploring Interaction of TNF and Orthopoxviral CrmB Protein by Surface Plasmon Resonance and Free Energy Calculation. <i>Protein and Peptide Letters</i> , 2014, 21, 1273-1281.	0.9	3
56	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
57	Accuracy of protein allergenicity prediction can be improved by taking into account data on allergenic protein discontinuous peptides. <i>Journal of Biomolecular Structure and Dynamics</i> , 2013, 31, 59-64.	3.5	6
58	Computational screening for new inhibitors of <i>M. tuberculosis</i> mycolyltransferases antigen 85 group of proteins as potential drug targets. <i>Journal of Biomolecular Structure and Dynamics</i> , 2013, 31, 30-43.	3.5	10
59	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.	0.8	13
60	Detection of Renal and Urinary Tract Proteins Before and After Spaceflight. <i>Aviation, Space, and Environmental Medicine</i> , 2013, 84, 859-863.	0.5	4
61	Detection of Renal Tissue and Urinary Tract Proteins in the Human Urine after Space Flight. <i>PLoS ONE</i> , 2013, 8, e71652.	2.5	24
62	SitEx: a computer system for analysis of projections of protein functional sites on eukaryotic genes. <i>Nucleic Acids Research</i> , 2012, 40, D278-D283.	14.5	5
63	Finding biomarkers in non-model species: literature mining of transcription factors involved in bovine embryo development. <i>BioData Mining</i> , 2012, 5, 12.	4.0	9
64	Computer analysis of metagenomic data – Prediction of quantitative value of specific activity of proteins. <i>Doklady Biochemistry and Biophysics</i> , 2012, 443, 76-80.	0.9	4
65	Protein allergenicity prediction on the basis of conformational peptides. <i>Russian Journal of Genetics: Applied Research</i> , 2012, 2, 18-22.	0.4	0
66	Application of the ANDCell computer system to reconstruction and analysis of associative networks describing potential relationships between myopia and glaucoma. <i>Russian Journal of Genetics: Applied Research</i> , 2011, 1, 21-28.	0.4	17
67	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, .	1.5	10
68	Functional Divergence of <i>Helicobacter pylori</i> Related to Early Gastric Cancer. <i>Journal of Proteome Research</i> , 2010, 9, 254-267.	3.7	22
69	Characterization of glycoprotein E C-End of West Nile virus and evaluation of its interaction force with $\alpha 2 \beta 3$ integrin as putative cellular receptor. <i>Biochemistry (Moscow)</i> , 2010, 75, 472-480.	1.5	15
70	Expression and molecular characterization of the Mycobacterium tuberculosis PII protein. <i>Journal of Biochemistry</i> , 2010, 147, 279-289.	1.7	12
71	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.	1.5	11
72	C-terminal fragment of human laminin-binding protein contains a receptor domain for Venezuelan equine encephalitis and tick-borne encephalitis viruses. <i>Biochemistry (Moscow)</i> , 2009, 74, 1328-1336.	1.5	32

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73	uORFs, reinitiation and alternative translation start sites in human mRNAs. FEBS Letters, 2008, 582, 1293-1297.	2.8	57
74	Web-based Computational Tools for the Prediction and Analysis of Post-translational Modifications of Proteins. , 2008, 446, 363-384.		0
75	MATHEMATICAL MODEL FOR SUPPRESSION OF SUBGENOMIC HEPATITIS C VIRUS RNA REPLICATION IN CELL CULTURE. Journal of Bioinformatics and Computational Biology, 2007, 05, 593-609.	0.8	10
76	WebProAnalyst: an interactive tool for analysis of quantitative structure-activity relationships in protein families. Nucleic Acids Research, 2005, 33, W99-W104.	14.5	12
77	PDBSite: a database of the 3D structure of protein functional sites. Nucleic Acids Research, 2004, 33, D183-D187.	14.5	71
78	PDBSiteScan: a program for searching for active, binding and posttranslational modification sites in the 3D structures of proteins. Nucleic Acids Research, 2004, 32, W549-W554.	14.5	69
79	Tick-Borne Encephalitis with Hemorrhagic Syndrome, Novosibirsk Region, Russia, 1999. Emerging Infectious Diseases, 2003, 9, 743-746.	4.3	55
80	A fast genetic algorithm for RNA secondary structure analysis. Russian Chemical Bulletin, 2002, 51, 1135-1144.	1.5	21
81	Insertion of foreign epitopes in HBcAg: how to make the chimeric particle assemble. Amino Acids, 2000, 18, 329-337.	2.7	46