

Vladislav V. Khrustalev

List of Publications by Year in descending order

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52
papers

431
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840776

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#	ARTICLE	IF	CITATIONS
1	Mutational Pressure in Zika Virus: Local ADAR-Editing Areas Associated with Pauses in Translation and Replication. <i>Frontiers in Cellular and Infection Microbiology</i> , 2017, 7, 44.	3.9	34
2	Magnesium and manganese binding sites on proteins have the same predominant motif of secondary structure. <i>Journal of Theoretical Biology</i> , 2016, 395, 174-185.	1.7	26
3	Stabilization of secondary structure elements by specific combinations of hydrophilic and hydrophobic amino acid residues is more important for proteins encoded by GC-poor genes. <i>Biochimie</i> , 2012, 94, 2706-2715.	2.6	24
4	Random coil structures in bacterial proteins. Relationships of their amino acid compositions to flanking structures and corresponding genic base compositions. <i>Biochimie</i> , 2013, 95, 1745-1754.	2.6	17
5	Ethanol binding sites on proteins. <i>Journal of Molecular Graphics and Modelling</i> , 2017, 78, 187-194.	2.4	15
6	Mutational pressure is a cause of inter- and intragenomic differences in GC-content of simplex and varicello viruses. <i>Computational Biology and Chemistry</i> , 2009, 33, 295-302.	2.3	14
7	Study of Completed Archaeal Genomes and Proteomes: Hypothesis of Strong Mutational AT Pressure Existed in Their Common Predecessor. <i>Genomics, Proteomics and Bioinformatics</i> , 2010, 8, 22-32.	6.9	14
8	The Influence of Flanking Secondary Structures on Amino Acid Content and Typical Lengths of 3/10 Helices. <i>International Journal of Proteomics</i> , 2014, 2014, 1-13.	2.0	14
9	Unusual nucleotide content of Rubella virus genome as a consequence of biased RNA-editing: comparison with Alphaviruses. <i>International Journal of Bioinformatics Research and Applications</i> , 2011, 7, 82.	0.2	12
10	Low rates of synonymous mutations in sequences of <i>Mycobacterium tuberculosis</i> GyrA and KatG genes. <i>Tuberculosis</i> , 2012, 92, 333-344.	1.9	12
11	Microenvironment of tryptophan residues in proteins of four structural classes: applications for fluorescence and circular dichroism spectroscopy. <i>European Biophysics Journal</i> , 2019, 48, 523-537.	2.2	12
12	Translation-Associated Mutational U-Pressure in the First ORF of SARS-CoV-2 and Other Coronaviruses. <i>Frontiers in Microbiology</i> , 2020, 11, 559165.	3.5	12
13	“Protoisochores” in certain archaeal species are formed by replication-associated mutational pressure. <i>Biochimie</i> , 2011, 93, 160-167.	2.6	11
14	A Blueprint for a Mutationist Theory of Replicative Strand Asymmetries Formation. <i>Current Genomics</i> , 2012, 13, 55-64.	1.6	11
15	Amino acid content of beta strands and alpha helices depends on their flanking secondary structure elements. <i>BioSystems</i> , 2018, 168, 45-54.	2.0	11
16	Anin-silico study of alphaherpesviruses ICPO genes: Positive selection or strong mutational GC-pressure?. <i>IUBMB Life</i> , 2008, 60, 456-460.	3.4	10
17	The probability of nonsense mutation caused by replication-associated mutational pressure is much higher for bacterial genes from lagging than from leading strands. <i>Genomics</i> , 2010, 96, 173-180.	2.9	10
18	Percent of highly immunogenic amino acid residues forming B-cell epitopes is higher in homologous proteins encoded by GC-rich genes. <i>Journal of Theoretical Biology</i> , 2011, 282, 71-79.	1.7	10

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19	The level of cytosine is usually much higher than the level of guanine in two-fold degenerated sites from third codon positions of genes from Simplex- and Varicelloviruses with G+C higher than 50%. <i>Journal of Theoretical Biology</i> , 2010, 266, 88-98.	1.7	9
20	Mutational pressure makes HIV1 gp120 linear B-cell epitopes shorter and may lead to their disappearance. <i>Molecular Immunology</i> , 2010, 47, 1635-1639.	2.2	9
21	Intragenic isochores (intrachores) in the platelet phosphofructokinase gene of Passeriform birds. <i>Gene</i> , 2014, 546, 16-24.	2.2	9
22	The alpha helix 1 from the first conserved region of HIV1 gp120 is reconstructed in the short NQ21 peptide. <i>Archives of Biochemistry and Biophysics</i> , 2018, 638, 66-75.	3.0	9
23	The history of mutational pressure changes during the evolution of adeno-associated viruses: A message to gene therapy and DNA-vaccine vectors designers. <i>Infection, Genetics and Evolution</i> , 2020, 77, 104100.	2.3	9
24	Levels of HIV1 gp120 3D B-cell Epitopes Mutability and Variability: Searching for Possible Vaccine Epitopes. <i>Immunological Investigations</i> , 2010, 39, 551-569.	2.0	8
25	Structural and antigenic features of the synthetic SF23 peptide corresponding to the receptor binding fragment of diphtheria toxin. <i>Molecular Immunology</i> , 2015, 63, 235-244.	2.2	8
26	The part of a long beta hairpin from the scrapie form of the human prion protein is reconstructed in the synthetic CC36 protein. <i>Proteins: Structure, Function and Bioinformatics</i> , 2016, 84, 1462-1479.	2.6	8
27	Cobalt(ii) cation binding by proteins. <i>Metallomics</i> , 2019, 11, 1743-1752.	2.4	8
28	Differential S-acylation of Enveloped Viruses. <i>Protein and Peptide Letters</i> , 2019, 26, 588-600.	0.9	8
29	Main Pathways of Proteome Simplification in Alphaherpesviruses Under the Influence of the Strong Mutational GC-pressure. <i>Journal of Proteomics and Bioinformatics</i> , 2009, 02, 088-096.	0.4	8
30	Can Mutational GC-Pressure Create New Linear B-cell Epitopes in Herpes Simplex Virus Type 1 Glycoprotein B?. <i>Immunological Investigations</i> , 2009, 38, 613-623.	2.0	6
31	Local Mutational Pressures in Genomes of Zaire Ebolavirus and Marburg Virus. <i>Advances in Bioinformatics</i> , 2015, 2015, 1-14.	5.7	6
32	Mutational pressure and natural selection in epidermal growth factor receptor gene during germline and somatic mutagenesis in cancer cells. <i>Mutation Research - Fundamental and Molecular Mechanisms of Mutagenesis</i> , 2019, 815, 1-9.	1.0	6
33	The cytoplasmic tail of influenza A/H1N1 virus hemagglutinin is β -structural. <i>Journal of Biomolecular Structure and Dynamics</i> , 2022, 40, 4642-4661.	3.5	5
34	HIV1 V3 Loop Hypermutability is Enhanced by the Guanine Usage Bias in the Part of env Gene Coding for it. <i>In Silico Biology</i> , 2009, 9, 255-269.	0.9	4
35	Inverse correlation between the GC content of bacterial genomes and their level of preterminal codon usage. <i>Molecular Genetics, Microbiology and Virology</i> , 2009, 24, 17-23.	0.3	4
36	Inhibition of Rat Muscle and Liver Phosphofructokinases by High Doses of Ethanol. <i>Biochemistry Research International</i> , 2013, 2013, 1-8.	3.3	4

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37	Opposite nucleotide usage biases in different parts of the <i>Corynebacterium diphtheriae</i> spaC gene. <i>International Journal of Bioinformatics Research and Applications</i> , 2015, 11, 347.	0.2	4
38	Random Coils of Proteins Situated Between a Beta Strand and an Alpha Helix Demonstrate Decreased Solvent Accessibility. <i>Protein Journal</i> , 2020, 39, 308-317.	1.6	4
39	Short repeats in the spa gene of <i>Staphylococcus aureus</i> are prone to nonsense mutations: stop codons can be found in strains isolated from patients with generalized infection. <i>Research in Microbiology</i> , 2013, 164, 913-922.	2.1	3
40	Transcription-associated mutational pressure in the Parvovirus B19 genome: Reactivated genomes contribute to the variability of viral populations. <i>Journal of Theoretical Biology</i> , 2017, 435, 199-207.	1.7	3
41	Selection and structural analysis of the NY25 peptide – A vaccine candidate from hemagglutinin of swine-origin Influenza H1N1. <i>Microbial Pathogenesis</i> , 2018, 125, 72-83.	2.9	3
42	Comprehensive surveillance data suggest a prominent role of parvovirus B19 infection in Belarus and the presence of a third subtype within subgenotype 1a. <i>Scientific Reports</i> , 2021, 11, 1225.	3.3	3
43	The PentUnFOLD algorithm as a tool to distinguish the dark and the light sides of the structural instability of proteins. <i>Amino Acids</i> , 2022, 54, 1155-1171.	2.7	3
44	Mutational pressure in genomes of human \pm -herpesviruses. <i>Molecular Genetics, Microbiology and Virology</i> , 2008, 23, 94-100.	0.3	2
45	Filamentous versus Spherical Morphology: A Case Study of the Recombinant A/WSN/33 (H1N1) Virus. <i>Microscopy and Microanalysis</i> , 2020, 26, 297-309.	0.4	2
46	The PentaFOLD 3.0 Algorithm for the Selection of Stable Elements of Secondary Structure to be Included in Vaccine Peptides. <i>Protein and Peptide Letters</i> , 2021, 28, 573-588.	0.9	2
47	A method for estimation of immunogenic determinants mutability: case studies of HIV1 gp120 and diphtheria toxin. <i>Journal of Integrated OMICS</i> , 2011, 1, .	0.5	2
48	Zebra Finch Glucokinase Containing Two Homologous Halves Is an In Silico Chimera. <i>ISRN Computational Biology</i> , 2013, 2013, 1-6.	0.3	1
49	In silico directed mutagenesis using software for glycosylation sites prediction as a new step in antigen design. <i>Journal of Integrated OMICS</i> , 2012, 2, .	0.5	1
50	Equilibrium Between Dimeric and Monomeric Forms of Human Epidermal Growth Factor is Shifted Towards Dimers in a Solution. <i>Protein Journal</i> , 2022, , 1.	1.6	1
51	Thyroid cancer in persons as a result of the Chernobyl accident. , 0, , 01-11.		0
52	HIV1 V3 loop hypermutability is enhanced by the guanine usage bias in the part of env gene coding for it. <i>In Silico Biology</i> , 2009, 9, 255-69.	0.9	0