

Vladimir R PeroviÄ

List of Publications by Year in descending order

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47
papers

1,024
citations

516710

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30
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docs citations

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times ranked

1343
citing authors

#	ARTICLE	IF	CITATIONS
1	Identification of SARS-CoV-2 Papain-like Protease (PLpro) Inhibitors Using Combined Computational Approach**. <i>ChemistryOpen</i> , 2022, 11, e202100248.	1.9	8
2	In Silico Screening of Natural Compounds for Candidates 5HT6 Receptor Antagonists against Alzheimer's Disease. <i>Molecules</i> , 2022, 27, 2626.	3.8	4
3	Alignment-free method for functional annotation of amino acid substitutions: Application on epigenetic factors involved in hematologic malignancies. <i>PLoS ONE</i> , 2021, 16, e0244948.	2.5	0
4	DiNGO: standalone application for Gene Ontology and Human Phenotype Ontology term enrichment analysis. <i>Bioinformatics</i> , 2020, 36, 1981-1982.	4.1	2
5	Biological Rationale for the Repurposing of BCG Vaccine against SARS-CoV-2. <i>Journal of Proteome Research</i> , 2020, 19, 4649-4654.	3.7	11
6	Drug Repurposing for Candidate SARS-CoV-2 Main Protease Inhibitors by a Novel In Silico Method. <i>Molecules</i> , 2020, 25, 3830.	3.8	49
7	Tally-2.0: upgraded validator of tandem repeat detection in protein sequences. <i>Bioinformatics</i> , 2020, 36, 3260-3262.	4.1	2
8	Automated feature engineering improves prediction of protein-protein interactions. <i>Amino Acids</i> , 2019, 51, 1187-1200.	2.7	18
9	Virtual Screen for Repurposing of Drugs for Candidate Influenza A M2 Ion-Channel Inhibitors. <i>Frontiers in Cellular and Infection Microbiology</i> , 2019, 9, 67.	3.9	19
10	The CAFA challenge reports improved protein function prediction and new functional annotations for hundreds of genes through experimental screens. <i>Genome Biology</i> , 2019, 20, 244.	8.8	261
11	Mapping of Protein-Protein Interactions: Web-Based Resources for Revealing Interactomes. <i>Current Medicinal Chemistry</i> , 2019, 26, 3890-3910.	2.4	11
12	Ibuprofen as a template molecule for drug design against Ebola virus. <i>Frontiers in Bioscience - Landmark</i> , 2018, 23, 947-953.	3.0	23
13	IDPpi: Protein-Protein Interaction Analyses of Human Intrinsically Disordered Proteins. <i>Scientific Reports</i> , 2018, 8, 10563.	3.3	18
14	TRI_tool: a web-tool for prediction of protein-protein interactions in human transcriptional regulation. <i>Bioinformatics</i> , 2017, 33, 289-291.	4.1	17
15	Identification of Candidate Allosteric Modulators of the M1 Muscarinic Acetylcholine Receptor Which May Improve Vagus Nerve Stimulation in Chronic Tinnitus. <i>Frontiers in Neuroscience</i> , 2017, 11, 636.	2.8	8
16	A simple method for calculation of basic molecular properties of nutrients and their use as a criterion for a healthy diet. <i>F1000Research</i> , 2017, 6, 13.	1.6	2
17	In silico Therapeutics for Neurogenic Hypertension and Vasovagal Syncope. <i>Frontiers in Neuroscience</i> , 2016, 9, 520.	2.8	2
18	Arginase Flavonoid Anti-Leishmanial in Silico Inhibitors Flagged against Anti-Targets. <i>Molecules</i> , 2016, 21, 589.	3.8	24

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19	A combined ligand- and structure-based approach for the identification of rilmenidine-derived compounds which synergize the antitumor effects of doxorubicin. <i>Bioorganic and Medicinal Chemistry</i> , 2016, 24, 3174-3183.	3.0	15
20	Common molecular mechanism of the hepatic lesion and the cardiac parasympathetic regulation in chronic hepatitis C infection: a critical role for the muscarinic receptor type 3. <i>BMC Bioinformatics</i> , 2016, 17, 139.	2.6	5
21	Rilmenidine suppresses proliferation and promotes apoptosis via the mitochondrial pathway in human leukemic K562 cells. <i>European Journal of Pharmaceutical Sciences</i> , 2016, 81, 172-180.	4.0	11
22	Predicted Enhanced Human Propensity of Current Avian-Like H1N1 Swine Influenza Virus from China. <i>PLoS ONE</i> , 2016, 11, e0165451.	2.5	2
23	Role of genetic markers in sport and recreational physical activity. <i>FiziÄŦka Kultura</i> , 2016, 70, 5-13.	0.2	0
24	Simple Chemoinformatics Criterion Using Electron Donor-Acceptor Molecular Characteristics for Selection of Antibiotics Against Multi-Drug-Resistant Bacteria. <i>Discoveries</i> , 2016, 4, e64.	2.3	0
25	Evolution of 2014/15 H3N2 Influenza Viruses Circulating in US: Consequences for Vaccine Effectiveness and Possible New Pandemic. <i>Frontiers in Microbiology</i> , 2015, 6, 1456.	3.5	13
26	In silico analysis suggests interaction between Ebola virus and the extracellular matrix. <i>Frontiers in Microbiology</i> , 2015, 6, 135.	3.5	24
27	Improving attrition rates in Ebola virus drug discovery. <i>Expert Opinion on Drug Discovery</i> , 2015, 10, 1025-1032.	5.0	3
28	Virtual screen for repurposing approved and experimental drugs for candidate inhibitors of EBOLA virus infection. <i>F1000Research</i> , 2015, 4, 34.	1.6	41
29	In silico analysis suggests repurposing of ibuprofen for prevention and treatment of EBOLA virus disease. <i>F1000Research</i> , 2015, 4, 104.	1.6	23
30	Natural Products as Promising Therapeutics for Treatment of Influenza Disease. <i>Current Pharmaceutical Design</i> , 2015, 21, 5573-5588.	1.9	27
31	Influenza vaccine as prevention for cardiovascular diseases: Possible molecular mechanism. <i>Vaccine</i> , 2014, 32, 6569-6575.	3.8	51
32	Novel algorithm for phylogenetic analysis of proteins: application to analysis of the evolution of H5N1 influenza viruses. <i>Journal of Mathematical Chemistry</i> , 2013, 51, 2238-2255.	1.5	10
33	New in silico and conventional in vitro approaches to advance HIV drug discovery and design. <i>Expert Opinion on Drug Discovery</i> , 2013, 8, 83-92.	5.0	5
34	Novel Phylogenetic Algorithm to Monitor Human Tropism in Egyptian H5N1-HPAIV Reveals Evolution toward Efficient Human-to-Human Transmission. <i>PLoS ONE</i> , 2013, 8, e61572.	2.5	33
35	Feature-Based Classification of Amino Acid Substitutions outside Conserved Functional Protein Domains. <i>Scientific World Journal</i> , The, 2013, 2013, 1-10.	2.1	5
36	Simple and General Criterion for â€œin silicoâ€•Screening of Candidate HIV Drugs. <i>Current Pharmaceutical Biotechnology</i> , 2013, 14, 561-569.	1.6	13

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37	Assessment of Hepatitis C Virus Protein Sequences with Regard to Interferon/Ribavirin Combination Therapy Response in Patients with HCV Genotype 1b. <i>Protein Journal</i> , 2012, 31, 129-136.	1.6	8
38	The role of long-range intermolecular interactions in discovery of new drugs. <i>Expert Opinion on Drug Discovery</i> , 2011, 6, 1263-1270.	5.0	26
39	Characterization of conserved properties of hemagglutinin of H5N1 and human influenza viruses: possible consequences for therapy and infection control. <i>BMC Structural Biology</i> , 2009, 9, 21.	2.3	67
40	Identification of hemagglutinin structural domain and polymorphisms which may modulate swine H1N1 interactions with human receptor. <i>BMC Structural Biology</i> , 2009, 9, 62.	2.3	62
41	Lipoprotein lipase: A bioinformatics criterion for assessment of mutations as a risk factor for cardiovascular disease. <i>Proteins: Structure, Function and Bioinformatics</i> , 2008, 70, 855-862.	2.6	15
42	Discovery of New Therapeutic Targets by the Informational Spectrum Method. <i>Current Protein and Peptide Science</i> , 2008, 9, 493-506.	1.4	34
43	Novel Virtual Screening Protocol Based on the Combined Use of Molecular Modeling and Electron-Ion Interaction Potential Techniques To Design HIV-1 Integrase Inhibitors. <i>Journal of Chemical Information and Modeling</i> , 2007, 47, 1536-1544.	5.4	32
44	In Silico Criterion for Prediction of Effects of p53 Gene Missense Mutations on p53-Mdm2 Feedback Loop. <i>Protein and Peptide Letters</i> , 2006, 13, 807-814.	0.9	2
45	Evolution of SARS-CoV-2 virus and assessment of the effectiveness of COVID-19 vaccine. <i>F1000Research</i> , 0, 10, 28.	1.6	2
46	Prediction of the effectiveness of COVID-19 vaccine candidates. <i>F1000Research</i> , 0, 9, 365.	1.6	5
47	Virtual screen for repurposing approved and experimental drugs for candidate inhibitors of EBOLA virus infection. <i>F1000Research</i> , 0, 4, 34.	1.6	7