# Vladimir R PeroviÄ

List of Publications by Year
in descending order



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|---|---|---|---|
| 47 papers | 1,024 citations | 516710 16 h-index | 454955 30 g-index |
| 54 all docs | 54 docs citations | 54 times ranked | 1343 citing authors |

| # | Article | IF | Citations |
|---|---|---|---|
| 1 | The CAFA challenge reports improved protein function prediction and new functional annotations for hundreds of genes through experimental screens. Genome Biology, 2019, 20, 244. | 8.8 | 261 |
| 2 | Characterization of conserved properties of hemagglutinin of H5N1 and human influenza viruses: possible consequences for therapy and infection control. BMC Structural Biology, 2009, 9, 21. | 2.3 | 67 |
| 3 | Identification of hemagglutinin structural domain and polymorphisms which may modulate swine H1N1 interactions with human receptor. BMC Structural Biology, 2009, 9, 62. | 2.3 | 62 |
| 4 | Influenza vaccine as prevention for cardiovascular diseases: Possible molecular mechanism. Vaccine, 2014, 32, 6569-6575. | 3.8 | 51 |
| 5 | Drug Repurposing for Candidate SARS-CoV-2 Main Protease Inhibitors by a Novel In Silico Method. Molecules, 2020, 25, 3830. | 3.8 | 49 |
| 6 | Virtual screen for repurposing approved and experimental drugs for candidate inhibitors of EBOLA virus infection. F1000Research, 2015, 4, 34. | 1.6 | 41 |
| 7 | Discovery of New Therapeutic Targets by the Informational Spectrum Method. Current Protein and Peptide Science, 2008, 9, 493-506. | 1.4 | 34 |
| 8 | Novel Phylogenetic Algorithm to Monitor Human Tropism in Egyptian H5N1-HPAIV Reveals Evolution toward Efficient Human-to-Human Transmission. PLoS ONE, 2013, 8, e61572. | 2.5 | 33 |
| 9 | Novel Virtual Screening Protocol Based on the Combined Use of Molecular Modeling and Electron-Ion Interaction Potential Techniques To Design HIV-1 Integrase Inhibitors. Journal of Chemical Information and Modeling, 2007, 47, 1536-1544. | 5.4 | 32 |
| 10 | Natural Products as Promising Therapeutics for Treatment of Influenza Disease. Current Pharmaceutical Design, 2015, 21, 5573-5588. | 1.9 | 27 |
| 11 | The role of long-range intermolecular interactions in discovery of new drugs. Expert Opinion on Drug Discovery, 2011, 6, 1263-1270. | 5.0 | 26 |
| 12 | In silico analysis suggests interaction between Ebola virus and the extracellular matrix. Frontiers in Microbiology, 2015, 6, 135. | 3.5 | 24 |
| 13 | Arginase Flavonoid Anti-Leishmanial in Silico Inhibitors Flagged against Anti-Targets. Molecules, 2016, 21, 589. | 3.8 | 24 |
| 14 | Ibuprofen as a template molecule for drug design against Ebola virus. Frontiers in Bioscience - Landmark, 2018, 23, 947-953. | 3.0 | 23 |
| 15 | In silico analysis suggests repurposing of ibuprofen for prevention and treatment of EBOLA virus disease. F1000Research, 2015, 4, 104. | 1.6 | 23 |
| 16 | Virtual Screen for Repurposing of Drugs for Candidate Influenza a M2 Ion-Channel Inhibitors. Frontiers in Cellular and Infection Microbiology, 2019, 9, 67. | 3.9 | 19 |
| 17 | IDPpi: Protein-Protein Interaction Analyses of Human Intrinsically Disordered Proteins. Scientific Reports, 2018, 8, 10563. | 3.3 | 18 |
| 18 | Automated feature engineering improves prediction of proteinâ€“protein interactions. Amino Acids, 2019, 51, 1187-1200. | 2.7 | 18 |

| # | Article | IF | Citations |
|---|---|---|---|
| 19 | TRI_tool: a web-tool for prediction of proteinâ€“protein interactions in human transcriptional regulation. Bioinformatics, 2017, 33, 289-291. | 4.1 | 17 |
| 20 | Lipoprotein lipase: A bioinformatics criterion for assessment of mutations as a risk factor for cardiovascular disease. Proteins: Structure, Function and Bioinformatics, 2008, 70, 855-862. | 2.6 | 15 |
| 21 | A combined ligand- and structure-based approach for the identification of rilmenidine-derived compounds which synergize the antitumor effects of doxorubicin. Bioorganic and Medicinal Chemistry, 2016, 24, 3174-3183. | 3.0 | 15 |
| 22 | Evolution of 2014/15 H3N2 Influenza Viruses Circulating in US: Consequences for Vaccine Effectiveness and Possible New Pandemic. Frontiers in Microbiology, 2015, 6, 1456. | 3.5 | 13 |
| 23 | Simple and General Criterion for â€œin silicoâ€•Screening of Candidate HIV Drugs. Current Pharmaceutical Biotechnology, 2013, 14, 561-569. | 1.6 | 13 |
| 24 | Rilmenidine suppresses proliferation and promotes apoptosis via the mitochondrial pathway in human leukemic K562 cells. European Journal of Pharmaceutical Sciences, 2016, 81, 172-180. | 4.0 | 11 |
| 25 | Biological Rationale for the Repurposing of BCG Vaccine against SARS-CoV-2. Journal of Proteome Research, 2020, 19, 4649-4654. | 3.7 | 11 |
| 26 | Mapping of Protein-Protein Interactions: Web-Based Resources for Revealing Interactomes. Current Medicinal Chemistry, 2019, 26, 3890-3910. | 2.4 | 11 |
| 27 | Novel algorithm for phylogenetic analysis of proteins: application to analysis of the evolution of H5N1 influenza viruses. Journal of Mathematical Chemistry, 2013, 51, 2238-2255. | 1.5 | 10 |
| 28 | Assessment of Hepatitis C Virus Protein Sequences with Regard to Interferon/Ribavirin Combination Therapy Response in Patients with HCV Genotype 1b. Protein Journal, 2012, 31, 129-136. | 1.6 | 8 |
| 29 | Identification of Candidate Allosteric Modulators of the M1 Muscarinic Acetylcholine Receptor Which May Improve Vagus Nerve Stimulation in Chronic Tinnitus. Frontiers in Neuroscience, 2017, 11, 636. | 2.8 | 8 |
| 30 | Identification of SARSâ€CoVâ€2 Papainâ€like Protease (PLpro) Inhibitors Using Combined Computational Approach**. ChemistryOpen, 2022, 11, e202100248. | 1.9 | 8 |
| 31 | Virtual screen for repurposing approved and experimental drugs for candidate inhibitors of EBOLA virus infection. F1000Research, 0, 4, 34. | 1.6 | 7 |
| 32 | New in silico and conventional in vitro approaches to advance HIV drug discovery and design. Expert Opinion on Drug Discovery, 2013, 8, 83-92. | 5.0 | 5 |
| 33 | Feature-Based Classification of Amino Acid Substitutions outside Conserved Functional Protein Domains. Scientific World Journal, The, 2013, 2013, 1-10. | 2.1 | 5 |
| 34 | 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. BMC Bioinformatics, 2016, 17, 139. | 2.6 | 5 |
| 35 | Prediction of the effectiveness of COVID-19 vaccine candidates. F1000Research, 0, 9, 365. | 1.6 | 5 |
| 36 | In Silico Screening of Natural Compounds for Candidates 5HT6 Receptor Antagonists against Alzheimerâ€™s Disease. Molecules, 2022, 27, 2626. | 3.8 | 4 |

| # | ARTICLE | IF | CITATIONS |
|---|---|---|---|
| 37 | Improving attrition rates in Ebola virus drug discovery. Expert Opinion on Drug Discovery, 2015, 10, 1025-1032. | 5.0 | 3 |
| 38 | In Silico Criterion for Prediction of Effects of p53 Gene Missense Mutations on p53-Mdm2 Feedback Loop. Protein and Peptide Letters, 2006, 13, 807-814. | 0.9 | 2 |
| 39 | In silico Therapeutics for Neurogenic Hypertension and Vasovagal Syncope. Frontiers in Neuroscience, 2016, 9, 520. | 2.8 | 2 |
| 40 | DiNGO: standalone application for Gene Ontology and Human Phenotype Ontology term enrichment analysis. Bioinformatics, 2020, 36, 1981-1982. | 4.1 | 2 |
| 41 | Tally-2.0: upgraded validator of tandem repeat detection in protein sequences. Bioinformatics, 2020, 36, 3260-3262. | 4.1 | 2 |
| 42 | Evolution of SARS-CoV-2 virus and assessment of the effectiveness of COVID-19 vaccine. F1000Research, 0, 10, 28. | 1.6 | 2 |
| 43 | A simple method for calculation of basic molecular properties of nutrients and their use as a criterion for a healthy diet. F1000Research, 2017, 6, 13. | 1.6 | 2 |
| 44 | Predicted Enhanced Human Propensity of Current Avian-Like H1N1 Swine Influenza Virus from China. PLoS ONE, 2016, 11, e0165451. | 2.5 | 2 |
| 45 | Alignment-free method for functional annotation of amino acid substitutions: Application on epigenetic factors involved in hematologic malignancies. PLoS ONE, 2021, 16, e0244948. | 2.5 | 0 |
| 46 | Role of genetic markers in sport and recreational physical activity. FiziÄka Kultura, 2016, 70, 5-13. | 0.2 | 0 |
| 47 | Simple Chemoinformatics Criterion Using Electron Donor-Acceptor Molecular Characteristics for Selection of Antibiotics Against Multi-Drug-Resistant Bacteria. Discoveries, 2016, 4, e64. | 2.3 | 0 |