Nevena Veljkovic

List of Publications by Year
in descending order

22 papers	730 citations	840776 11 h-index	713466 21 g-index
22 all docs	22 docs citations	22 times ranked	1018 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	DisProt: intrinsic protein disorder annotation in 2020. Nucleic Acids Research, 2020, 48, D269-D276.	14.5	141
3	DisProt in 2022: improved quality and accessibility of protein intrinsic disorder annotation. Nucleic Acids Research, 2022, 50, D480-D487.	14.5	117
4	Discovery of New Therapeutic Targets by the Informational Spectrum Method. Current Protein and Peptide Science, 2008, 9, 493-506.	1.4	34
5	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
6	Cytoplasmatic compartmentalization by Bcr–Abl promotes TET2 loss–of–function in chronic myeloid leukemia. Journal of Cellular Biochemistry, 2012, 113, 2765-2774.	2.6	18
7	IDPpi: Protein-Protein Interaction Analyses of Human Intrinsically Disordered Proteins. Scientific Reports, 2018, 8, 10563.	3.3	18
8	Automated feature engineering improves prediction of protein–protein interactions. Amino Acids, 2019, 51, 1187-1200.	2.7	18
9	AIDS epidemic at the beginning of the third millennium: time for a new AIDS vaccine strategy. Vaccine, 2001, 19, 1855-1862.	3.8	15
10	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
11	The Presence of Antibodies Recognizing a Peptide Derived from the Second Conserved Region of HIV-1 gp120 Correlates with Non-Progressive HIV Infection. Current HIV Research, 2007, 5, 443-448.	0.5	13
12	Genetic Markers for Coronary Artery Disease. Medicina (Lithuania), 2018, 54, 36.	2.0	9
13	Meta-Analysis of Circulating Cell-Free DNA's Role in the Prognosis of Pancreatic Cancer. Cancers, 2021, 13, 3378.	3.7	9
14	Antibodies reactive with C-terminus of the second conserved region of HIV-1gp120 as possible prognostic marker and therapeutic agent for HIV disease. Journal of Clinical Virology, 2004, 31, 39-44.	3.1	8
15	Identification of an active Chi recombinational hot spot within the HIV-1 envelope gene: consequences for development of AIDS vaccines. Vaccine, 1999, 17, 1462-1467.	3.8	7
16	Feature-Based Classification of Amino Acid Substitutions outside Conserved Functional Protein Domains. Scientific World Journal, The, 2013, 2013, 1-10.	2.1	5
17	Natural autoantibodies in healthy neonatals recognizing a peptide derived from the second conserved region of HIV-1 GP120. Vojnosanitetski Pregled, 2014, 71, 352-361.	0.2	3
18	DiNGO: standalone application for Gene Ontology and Human Phenotype Ontology term enrichment analysis. Bioinformatics, 2020, 36, 1981-1982.	4.1	2

#	Article	IF	Citations
19	Tally-2.0: upgraded validator of tandem repeat detection in protein sequences. Bioinformatics, 2020, 36, 3260-3262.	4.1	2
20	Deciphering Imidazoline Off‐targets by Fishing in the Class A of GPCR field. Molecular Informatics, 2020, 39, 1900165.	2.5	1
21	Molecular mimicry of HIV gp120: Possible implications on prevention and therapy of AIDS. Archive of Oncology, 2005, 13, 126-130.	0.2	1
22	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