Ivan D Dimitrov

List of Publications by Year
in descending order

46	2,100	471509 17	289244 40
papers	citations	h-index	g-index

47	47	47	2114
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	AllerTOP v.2â€"a server for in silico prediction of allergens. Journal of Molecular Modeling, 2014, 20, 2278.	1.8	663
2	AllergenFP: allergenicity prediction by descriptor fingerprints. Bioinformatics, 2014, 30, 846-851.	4.1	471
3	AllerTOP - a server for in silico prediction of allergens. BMC Bioinformatics, 2013, 14, S4.	2.6	293
4	Antimycobacterial activity of novel hydrazide-hydrazone derivatives with 2 H -chromene and coumarin scaffold. Bioorganic and Medicinal Chemistry Letters, 2017, 27, 223-227.	2.2	62
5	EpiTOPâ€"a proteochemometric tool for MHC class II binding prediction. Bioinformatics, 2010, 26, 2066-2068.	4.1	55
6	Peptide binding prediction for the human class II MHC allele HLA-DP2: a molecular docking approach. BMC Structural Biology, 2011, 11, 32.	2.3	52
7	EpiDOCK: a molecular docking-based tool for MHC class II binding prediction. Protein Engineering, Design and Selection, 2013, 26, 631-634.	2.1	51
8	Approaches to assess IgE mediated allergy risks (sensitization and cross-reactivity) from new or modified dietary proteins. Food and Chemical Toxicology, 2018, 112, 97-107.	3.6	36
9	Curcumin Inhibits the Primary Nucleation of Amyloid-Beta Peptide: A Molecular Dynamics Study. Biomolecules, 2020, 10, 1323.	4.0	36
10	Novel hits for acetylcholinesterase inhibition derived by docking-based screening on ZINC database. Journal of Enzyme Inhibition and Medicinal Chemistry, 2018, 33, 768-776.	5.2	32
11	Peptide binding to the HLA-DRB1 supertype: A proteochemometrics analysis. European Journal of Medicinal Chemistry, 2010, 45, 236-243.	5.5	27
12	Immunogenicity Prediction by VaxiJen: A Ten Year Overview. Journal of Proteomics and Bioinformatics, 2017, 10, .	0.4	26
13	VaxiJen Dataset of Bacterial Immunogens: An Update. Current Computer-Aided Drug Design, 2019, 15, 398-400.	1.2	25
14	Molecular Docking Study on Galantamine Derivatives as Cholinesterase Inhibitors. Molecular Informatics, 2015, 34, 394-403.	2.5	24
15	Totally chlorine-free bleaching of flax pulp. Bioresource Technology, 2002, 85, 79-85.	9.6	23
16	MHC Class II Binding Predictionâ€"A Little Help from a Friend. Journal of Biomedicine and Biotechnology, 2010, 2010, 1-8.	3.0	20
17	Associations between Milk and Egg Allergens and the HLA-DRB1/DQ Polymorphism: A Bioinformatics Approach. International Archives of Allergy and Immunology, 2016, 169, 33-39.	2.1	18
18	Peptide binding to HLA-DP proteins at pH 5.0 and pH 7.0: a quantitative molecular docking study. BMC Structural Biology, 2012, 12, 20.	2.3	17

#	Article	IF	Citations
19	HLAâ€ÐP2 binding prediction by molecular dynamics simulations. Protein Science, 2011, 20, 1918-1928.	7.6	16
20	MHC Class II Binding Prediction by Molecular Docking. Molecular Informatics, 2011, 30, 368-375.	2.5	16
21	Predicting Immunogenicity Risk in Biopharmaceuticals. Symmetry, 2021, 13, 388.	2.2	14
22	Proteochemometrics-Based Prediction of Peptide Binding to HLA-DP Proteins. Journal of Chemical Information and Modeling, 2018, 58, 297-304.	5.4	13
23	Bacterial Immunogenicity Prediction by Machine Learning Methods. Vaccines, 2020, 8, 709.	4.4	12
24	Cellular polyamines condense hyperphosphorylated Tau, triggering Alzheimerâ€™s disease. Scientific Reports, 2020, 10, 10098.	3.3	12
25	Allergenicity prediction by artificial neural networks. Journal of Chemometrics, 2014, 28, 282-286.	1.3	11
26	Effects of Curcumin and Ferulic Acid on the Folding of Amyloid-Î² Peptide. Molecules, 2021, 26, 2815.	3.8	10
27	Virtual Screening and Hit Selection of Natural Compounds as Acetylcholinesterase Inhibitors. Molecules, 2022, 27, 3139.	3.8	10
28	Histidine Hydrogen Bonding in MHC at pH 5 and pH 7 Modeled by Molecular Docking and Molecular Dynamics Simulations. Current Computer-Aided Drug Design, 2014, 10, 41-49.	1.2	9
29	Kinetic Model of Xylanase Action on Kraft Pulp. Reaction Kinetics and Catalysis Letters, 2000, 71, 231-238.	0.6	6
30	A Cohesive and Integrated Platform for Immunogenicity Prediction. Methods in Molecular Biology, 2016, 1404, 761-770.	0.9	6
31	Bridging solvent molecules mediate RNase A â€“ Ligand binding. PLoS ONE, 2019, 14, e0224271.	2.5	6
32	Two Faces of Milk Proteins Peptides with Both Allergenic and Multidimensional Health Beneficial Impactâ€”Integrated In Vitro/In Silico Approach. Foods, 2021, 10, 163.	4.3	5
33	Quantitative Prediction of Peptide Binding to HLA-DP1 Protein. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2013, 10, 811-815.	3.0	4
34	Peptide Binding Prediction to Five Most Frequent HLAâ€ÐQ Proteins â€“ a Proteochemometric Approach. Molecular Informatics, 2015, 34, 467-476.	2.5	4
35	UHPLC-Orbitrap-MS Tentative Identification of 51 Oleraceins (Cyclo-Dopa Amides) in Portulaca oleracea L. Cluster Analysis and MS2 Filtering by Mass Difference. Plants, 2021, 10, 1921.	3.5	4
36	An Alignment-Independent Platform for Allergenicity Prediction. Methods in Molecular Biology, 2020, 2131, 147-153.	0.9	3

#	Article	IF	Citations
37	Topochemical kinetics of xylanase action on kraft pulp. Biocatalysis and Biotransformation, 2005, 23, 33-36.	2.0	2
38	AllerScreener â€“ A Server for Allergenicity and Cross-Reactivity Prediction. Cybernetics and Information Technologies, 2020, 20, 175-184.	1.1	2
39	Proteochemometrics for the Prediction of Binding to the MHC Proteins. Letters in Drug Design and Discovery, 2016, 14, 2-9.	0.7	2
40	Proteochemometrics for the Prediction of Peptide Binding to Multiple HLA Class II Proteins. Methods in Pharmacology and Toxicology, 2018, , 395-404.	0.2	1
41	Clustering of Red/White Wine and Allergen/Non-Allergen Data Sets by Using Descriptor Fingerprints. IOP Conference Series: Materials Science and Engineering, 2021, 1031, 012053.	0.6	0
42	Molecular Dynamics Simulations of Acetylcholinesterase â€“ Beta-Amyloid Peptide Complex. Cybernetics and Information Technologies, 2020, 20, 140-154.	1.1	0
43	Bridging solvent molecules mediate RNase A â€“ Ligand binding. , 2019, 14, e0224271.		0
44	Bridging solvent molecules mediate RNase A â€“ Ligand binding. , 2019, 14, e0224271.		0
45	Bridging solvent molecules mediate RNase A â€“ Ligand binding. , 2019, 14, e0224271.		0
46	Bridging solvent molecules mediate RNase A â€“ Ligand binding. , 2019, 14, e0224271.		0