Iosif I Vaisman

List of Publications by Year
in descending order

51	1,633	304743 22	302126 39
papers	citations	h-index	g-index

54	54	54	1885
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Local structural order and molecular associations in water-DMSO mixtures. Molecular dynamics study. Journal of the American Chemical Society, 1992, 114, 7889-7896.	13.7	298
2	Accurate prediction of stability changes in protein mutants by combining machine learning with structure based computational mutagenesis. Bioinformatics, 2008, 24, 2002-2009.	4.1	153
3	Delaunay Tessellation of Proteins: Four Body Nearest-Neighbor Propensities of Amino Acid Residues. Journal of Computational Biology, 1996, 3, 213-221.	1.6	152
4	Discrimination of thermophilic and mesophilic proteins. BMC Structural Biology, 2010, 10, S5.	2.3	109
5	AUTO-MUTE: web-based tools for predicting stability changes in proteins due to single amino acid replacements. Protein Engineering, Design and Selection, 2010, 23, 683-687.	2.1	75
6	Cell Surface Expression of CD147/EMMPRIN Is Regulated by Cyclophilin 60. Journal of Biological Chemistry, 2005, 280, 27866-27871.	3.4	66
7	Distance Dependence of Water Structure around Model Solutes. The Journal of Physical Chemistry, 1994, 98, 5559-5564.	2.9	59
8	AUTO-MUTE 2.0: A Portable Framework with Enhanced Capabilities for Predicting Protein Functional Consequences upon Mutation. Advances in Bioinformatics, 2014, 2014, 1-7.	5.7	53
9	Knowledge-based computational mutagenesis for predicting the disease potential of human non-synonymous single nucleotide polymorphisms. Journal of Theoretical Biology, 2010, 266, 560-568.	1.7	52
10	Accurate prediction of enzyme mutant activity based on a multibody statistical potential. Bioinformatics, 2007, 23, 3155-3161.	4.1	50
11	Machine learning approach for structure-based zeolite classification. Microporous and Mesoporous Materials, 2009, 117, 339-349.	4.4	49
12	Simplicial Neighborhood Analysis of Protein Packing (SNAPP): A Computational Geometry Approach to Studying Proteins. Methods in Enzymology, 2003, 374, 509-544.	1.0	36
13	Identifying Zeolite Frameworks with a Machine Learning Approach. Journal of Physical Chemistry C, 2009, 113, 21721-21725.	3.1	36
14	Statistical geometry based prediction of nonsynonymous SNP functional effects using random forest and neuroâ€fuzzy classifiers. Proteins: Structure, Function and Bioinformatics, 2008, 71, 1930-1939.	2.6	33
15	Elevated TNFR1 and Serotonin in Bone Metastasis Are Correlated with Poor Survival following Bone Metastasis Diagnosis for Both Carcinoma and Sarcoma Primary Tumors. Clinical Cancer Research, 2013, 19, 2473-2485.	7.0	31
16	Comprehensive mutagenesis of HIV-1 protease: a computational geometry approach. Biochemical and Biophysical Research Communications, 2003, 305, 322-326.	2.1	28
17	A new topological method to measure protein structure similarity. Biochemical and Biophysical Research Communications, 2003, 304, 320-325.	2.1	27
18	A simple topological representation of protein structure: Implications for new, fast, and robust structural classification. Proteins: Structure, Function and Bioinformatics, 2004, 56, 487-501.	2.6	26

#	Article	IF	Citations
19	Mobility of stretched water. Journal of Chemical Physics, 1993, 98, 9859-9862.	3.0	25
20	Computational mutagenesis studies of protein structureâ€function correlations. Proteins: Structure, Function and Bioinformatics, 2006, 64, 234-245.	2.6	25
21	Graph theoretic properties of networks formed by the Delaunay tessellation of protein structures. Physical Review E, 2006, 73, 041925.	2.1	25
22	New method for protein secondary structure assignment based on a simple topological descriptor. Proteins: Structure, Function and Bioinformatics, 2005, 60, 513-524.	2.6	23
23	Machine Learning Prediction of Antimicrobial Peptides. Methods in Molecular Biology, 2022, 2405, 1-37.	0.9	22
24	Predicting the transactivation activity of p53 missense mutants using a four-body potential score derived from Delaunay tessellations. Human Mutation, 2006, 27, 163-172.	2.5	21
25	Sequence and structure based models of HIV-1 protease and reverse transcriptase drug resistance. BMC Genomics, 2013, 14, S3.	2.8	19
26	Accurate and efficient gp120 V3 loop structure based models for the determination of HIV-1 co-receptor usage. BMC Bioinformatics, 2010, 11, 494.	2.6	17
27	Framework-Type Determination for Zeolite Structures in the Inorganic Crystal Structure Database. Journal of Physical and Chemical Reference Data, 2010, 39, .	4.2	17
28	Predictive Models to Identify Small Molecule Activators and Inhibitors of Opioid Receptors. Journal of Chemical Information and Modeling, 2021, 61, 2675-2685.	5.4	14
29	Pseudotorsional OCCO backbone angle as a single descriptor of protein secondary structure. Protein Science, 1995, 4, 1633-1643.	7.6	11
30	A combined sequenceâ€“structure approach for predicting resistance to the non-nucleoside HIV-1 reverse transcriptase inhibitor Nevirapine. Biophysical Chemistry, 2011, 153, 168-172.	2.8	10
31	Statistical geometry approach to the study of functional effects of human nonsynonymous SNPs. Human Mutation, 2005, 26, 471-476.	2.5	9
32	Novel Approach for Clustering Zeolite Crystal Structures. Molecular Informatics, 2010, 29, 297-301.	2.5	9
33	Structure-based prediction of protein activity changes: Assessing the impact of single residue replacements. , 2011, 2011, 3221-4.		6
34	Structure-based predictors of resistance to the HIV-1 integrase inhibitor Elvitegravir. Antiviral Research, 2014, 106, 5-12.	4.1	6
35	Computational Mutagenesis of E. coli Lac Repressor: Insight into Structure-Function Relationships and Accurate Prediction of Mutant Activity. , 2008, , 390-401.		5
36	Modeling the functional consequences of single residue replacements in bacteriophage f1 gene V protein. Protein Engineering, Design and Selection, 2009, 22, 665-671.	2.1	5

#	Article	IF	Citations
37	A structure-based computational mutagenesis elucidates the spectrum of stability-activity relationships in proteins. , 2011, 2011, 3225-8.		5
38	<scp>cnnAlpha</scp>: Protein disordered regions prediction by reduced amino acid alphabets and convolutional neural networks. Proteins: Structure, Function and Bioinformatics, 2020, 88, 1472-1481.	2.6	5
39	A Novel Sequence-Structure Approach for Accurate Prediction of Resistance to HIV-1 Protease Inhibitors. , 2007, , .		3
40	Fitness of unregulated human Ras mutants modeled by implementing computational mutagenesis and machine learning techniques. Heliyon, 2019, 5, e01884.	3.2	3
41	Structure Based Functional Analysis of Bacteriophage f1 Gene V Protein. , 2008, , .		2
42	A Cheminformatics Approach for Zeolite Framework Determination. Lecture Notes in Computer Science, 2009, , 160-168.	1.3	2
43	Rapid protein structure classification using one-dimensional structure profiles on the BioSCAN parallel computer. Bioinformatics, 1995, 11, 675-679.	4.1	1
44	SECOST: sequence-conformation-structure database for amino acid residues in proteins. Bioinformatics, 1999, 15, 525-526.	4.1	1
45	Decoy Discrimination Using Contact Potentials Based on Delaunay Tessellation of Hydrated Proteins. , 2007, , .		1
46	Charge Transport Phenomena in Peptide Molecular Junctions. Research Letters in Nanotechnology, 2008, 2008, 1-5.	0.3	1
47	Accurate Prediction of Stability Changes in Bacteriophage T4 Lysozyme upon Single Amino Acid Replacements. , 2009, , .		1
48	Protein Structural Domain Assignment with a Delaunay Tessellation Derived Lattice. , 2006, , .		1
49	Discrimination and Classification of Thermophilic and Mesophilic Proteins. , 2007, , .		0
50	Structure-Based Predictors of Resistance to the HIV-1 Integrase Inhibitor Elvitegravir. Biophysical Journal, 2014, 106, 409a.	0.5	0
51	Statistical Geometry and Topology of Real and Model Protein Structures. , 2006, , .		0