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	Machine Learning Prediction of Antimicrobial Peptides. Methods in Molecular Biology, 2022, 2405, 1-37.	0.9	22
2	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
3	<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
4	Fitness of unregulated human Ras mutants modeled by implementing computational mutagenesis and machine learning techniques. Heliyon, 2019, 5, e01884.	3.2	3
5	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
6	Structure-Based Predictors of Resistance to the HIV-1 Integrase Inhibitor Elvitegravir. Biophysical Journal, 2014, 106, 409a.	0.5	0
7	Structure-based predictors of resistance to the HIV-1 integrase inhibitor Elvitegravir. Antiviral Research, 2014, 106, 5-12.	4.1	6
8	Sequence and structure based models of HIV-1 protease and reverse transcriptase drug resistance. BMC Genomics, 2013, 14, S3.	2.8	19
9	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
10	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
11	Structure-based prediction of protein activity changes: Assessing the impact of single residue replacements. , 2011, 2011, 3221-4.		6
12	A structure-based computational mutagenesis elucidates the spectrum of stability-activity relationships in proteins. , 2011, 2011, 3225-8.		5
13	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
14	Novel Approach for Clustering Zeolite Crystal Structures. Molecular Informatics, 2010, 29, 297-301.	2.5	9
15	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
16	Discrimination of thermophilic and mesophilic proteins. BMC Structural Biology, 2010, 10, S5.	2.3	109
17	Framework-Type Determination for Zeolite Structures in the Inorganic Crystal Structure Database. Journal of Physical and Chemical Reference Data, 2010, 39, .	4.2	17
18	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

#	Article	IF	Citations
19	Accurate Prediction of Stability Changes in Bacteriophage T4 Lysozyme upon Single Amino Acid Replacements. , 2009, , .		1
20	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
21	Machine learning approach for structure-based zeolite classification. Microporous and Mesoporous Materials, 2009, 117, 339-349.	4.4	49
22	Identifying Zeolite Frameworks with a Machine Learning Approach. Journal of Physical Chemistry C, 2009, 113, 21721-21725.	3.1	36
23	A Cheminformatics Approach for Zeolite Framework Determination. Lecture Notes in Computer Science, 2009, , 160-168.	1.3	2
24	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
25	Structure Based Functional Analysis of Bacteriophage f1 Gene V Protein. , 2008, , .		2
26	Computational Mutagenesis of E. coli Lac Repressor: Insight into Structure-Function Relationships and Accurate Prediction of Mutant Activity. , 2008, , 390-401.		5
27	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
28	Charge Transport Phenomena in Peptide Molecular Junctions. Research Letters in Nanotechnology, 2008, 2008, 1-5.	0.3	1
29	Decoy Discrimination Using Contact Potentials Based on Delaunay Tessellation of Hydrated Proteins. , 2007, , .		1
30	A Novel Sequence-Structure Approach for Accurate Prediction of Resistance to HIV-1 Protease Inhibitors. , 2007, , .		3
31	Discrimination and Classification of Thermophilic and Mesophilic Proteins. , 2007, , .		0
32	Accurate prediction of enzyme mutant activity based on a multibody statistical potential. Bioinformatics, 2007, 23, 3155-3161.	4.1	50
33	Computational mutagenesis studies of protein structureâ€function correlations. Proteins: Structure, Function and Bioinformatics, 2006, 64, 234-245.	2.6	25
34	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
35	Graph theoretic properties of networks formed by the Delaunay tessellation of protein structures. Physical Review E, 2006, 73, 041925.	2.1	25
36	Protein Structural Domain Assignment with a Delaunay Tessellation Derived Lattice. , 2006, , .		1

#	Article	IF	Citations
37	Statistical Geometry and Topology of Real and Model Protein Structures. , 2006, , .		0
38	Statistical geometry approach to the study of functional effects of human nonsynonymous SNPs. Human Mutation, 2005, 26, 471-476.	2.5	9
39	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
40	Cell Surface Expression of CD147/EMMPRIN Is Regulated by Cyclophilin 60. Journal of Biological Chemistry, 2005, 280, 27866-27871.	3.4	66
41	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
42	A new topological method to measure protein structure similarity. Biochemical and Biophysical Research Communications, 2003, 304, 320-325.	2.1	27
43	Comprehensive mutagenesis of HIV-1 protease: a computational geometry approach. Biochemical and Biophysical Research Communications, 2003, 305, 322-326.	2.1	28
44	Simplicial Neighborhood Analysis of Protein Packing (SNAPP): A Computational Geometry Approach to Studying Proteins. Methods in Enzymology, 2003, 374, 509-544.	1.0	36
45	SECOST: sequence-conformation-structure database for amino acid residues in proteins. Bioinformatics, 1999, 15, 525-526.	4.1	1
46	Delaunay Tessellation of Proteins: Four Body Nearest-Neighbor Propensities of Amino Acid Residues. Journal of Computational Biology, 1996, 3, 213-221.	1.6	152
47	Pseudotorsional OCCO backbone angle as a single descriptor of protein secondary structure. Protein Science, 1995, 4, 1633-1643.	7.6	11
48	Rapid protein structure classification using one-dimensional structure profiles on the BioSCAN parallel computer. Bioinformatics, 1995, 11, 675-679.	4.1	1
49	Distance Dependence of Water Structure around Model Solutes. The Journal of Physical Chemistry, 1994, 98, 5559-5564.	2.9	59
50	Mobility of stretched water. Journal of Chemical Physics, 1993, 98, 9859-9862.	3.0	25
51	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