

Majid Masso

List of Publications by Year in descending order

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42
papers

604
citations

932766

10
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642321

23
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44
all docs

44
docs citations

44
times ranked

680
citing authors

#	ARTICLE	IF	CITATIONS
1	Active Participation in Current Faculty Research Inspires Student Achievement. <i>Primus</i> , 2022, 32, 468-484.	0.3	0
2	Structure-based functional analysis of BRCA1 RING domain variants: Concordance of computational mutagenesis, experimental assay, and clinical data. <i>Biophysical Chemistry</i> , 2020, 266, 106442.	1.5	4
3	Functional analysis of BRCA1 RING domain variants: computationally derived structural data can improve upon experimental features for training predictive models. <i>Integrative Biology (United Tj ETQq1 1 0.7843b4rgBT /Overlock</i>	1.0	2
4	Accurate and efficient structure-based computational mutagenesis for modeling fluorescence levels of <i>Aequorea victoria</i> green fluorescent protein mutants. <i>Protein Engineering, Design and Selection</i> , 2020, 33, .	1.0	2
5	Fitness of unregulated human Ras mutants modeled by implementing computational mutagenesis and machine learning techniques. <i>Heliyon</i> , 2019, 5, e01884.	1.4	3
6	Cancer-MI: Modeling Fitness of Unregulated RAS Mutants using Computational Mutagenesis and Machine Learning. <i>Biophysical Journal</i> , 2019, 116, 561a.	0.2	1
7	All-atom four-body knowledge-based statistical potential to distinguish native tertiary RNA structures from nonnative folds. <i>Journal of Theoretical Biology</i> , 2018, 453, 58-67.	0.8	10
8	Modeling transcriptional activation changes to Gal4 variants via structure-based computational mutagenesis. <i>PeerJ</i> , 2018, 6, e4844.	0.9	3
9	All-Atom Four-Body Knowledge-Based Statistical Potentials to Distinguish Native Protein Structures from Nonnative Folds. <i>BioMed Research International</i> , 2017, 2017, 1-17.	0.9	7
10	Sequence-Based Predictive Models of Resistance to HIV-1 Integrase Inhibitors: An n-Grams Approach to Phenotype Assessment. <i>Current HIV Research</i> , 2015, 13, 497-502.	0.2	6
11	Modeling functional changes to <i>Escherichia coli</i> thymidylate synthase upon single residue replacements: a structure-based approach. <i>PeerJ</i> , 2015, 3, e721.	0.9	3
12	AUTO-MUTE 2.0: A Portable Framework with Enhanced Capabilities for Predicting Protein Functional Consequences upon Mutation. <i>Advances in Bioinformatics</i> , 2014, 2014, 1-7.	5.7	53
13	Structure-based predictors of resistance to the HIV-1 integrase inhibitor Elvitegravir. <i>Antiviral Research</i> , 2014, 106, 5-12.	1.9	6
14	Sequence and structure based models of HIV-1 protease and reverse transcriptase drug resistance. <i>BMC Genomics</i> , 2013, 14, S3.	1.2	19
15	Four-body atomic potential for modeling protein-ligand binding affinity: application to enzyme-inhibitor binding energy prediction. <i>BMC Structural Biology</i> , 2013, 13, S1.	2.3	3
16	Fast and Accurate Structure-Based Prediction of Resistance to the HIV-1 Integrase Inhibitor Raltegravir. , 2013, , .		1
17	Prediction of human immunodeficiency virus type 1 drug resistance: Representation of target sequence mutational patterns via an n-grams approach. , 2012, , .		4
18	Knowledge-based scoring function derived from atomic tessellation of macromolecular structures for prediction of protein-ligand binding affinity. , 2012, , .		2

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19	A multibody atomic statistical potential for the prediction of enzyme-inhibitor binding energy. , 2012, 2012, 5526-9.		1
20	Generation of atomic four-body statistical potentials derived from the delaunay tessellation of protein structures. , 2012, 2012, 6321-4.		0
21	A combined sequenceâ€“structure approach for predicting resistance to the non-nucleoside HIV-1 reverse transcriptase inhibitor Nevirapine. Biophysical Chemistry, 2011, 153, 168-172.	1.5	10
22	Sequence-based prediction of HIV-1 coreceptor usage. , 2011, , .		0
23	Structure-based prediction of protein activity changes: Assessing the impact of single residue replacements. , 2011, 2011, 3221-4.		6
24	A structure-based computational mutagenesis elucidates the spectrum of stability-activity relationships in proteins. , 2011, 2011, 3225-8.		5
25	Accurate and efficient gp120 V3 loop structure based models for the determination of HIV-1 co-receptor usage. BMC Bioinformatics, 2010, 11, 494.	1.2	17
26	Knowledge-based computational mutagenesis for predicting the disease potential of human non-synonymous single nucleotide polymorphisms. Journal of Theoretical Biology, 2010, 266, 560-568.	0.8	52
27	Overcoming the Curse of Dimensionality in a Statistical Geometry Based Computational Protein Mutagenesis. , 2010, , .		0
28	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.	1.0	75
29	Improving Prediction Accuracy via Subspace Modeling in a Statistical Geometry Based Computational Protein Mutagenesis. International Journal of Knowledge Discovery in Bioinformatics, 2010, 1, 54-68.	0.8	0
30	Accurate Prediction of Stability Changes in Bacteriophage T4 Lysozyme upon Single Amino Acid Replacements. , 2009, , .		1
31	Modeling the functional consequences of single residue replacements in bacteriophage f1 gene V protein. Protein Engineering, Design and Selection, 2009, 22, 665-671.	1.0	5
32	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.	1.5	33
33	Structure Based Functional Analysis of Bacteriophage f1 Gene V Protein. , 2008, , .		2
34	Computational Mutagenesis of E. coli Lac Repressor: Insight into Structure-Function Relationships and Accurate Prediction of Mutant Activity. , 2008, , 390-401.		5
35	Accurate prediction of stability changes in protein mutants by combining machine learning with structure based computational mutagenesis. Bioinformatics, 2008, 24, 2002-2009.	1.8	153
36	A Novel Sequence-Structure Approach for Accurate Prediction of Resistance to HIV-1 Protease Inhibitors. , 2007, , .		3

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37	Accurate prediction of enzyme mutant activity based on a multibody statistical potential. <i>Bioinformatics</i> , 2007, 23, 3155-3161.	1.8	50
38	Computational mutagenesis studies of protein structureâ€function correlations. <i>Proteins: Structure, Function and Bioinformatics</i> , 2006, 64, 234-245.	1.5	25
39	Comprehensive mutagenesis of HIV-1 protease: a computational geometry approach. <i>Biochemical and Biophysical Research Communications</i> , 2003, 305, 322-326.	1.0	28
40	DC-SIGN points the way to a novel mechanism for HIV-1 transmission. <i>MedGenMed: Medscape General Medicine</i> , 2003, 5, 2.	0.2	5
41	Improving Prediction Accuracy via Subspace Modeling. , 0, , 33-48.		0
42	Improving Prediction Accuracy via Subspace Modeling in a Statistical Geometry Based Computational Protein Mutagenesis. , 0, , 1010-1024.		0