Majid Masso

List of Publications by Year
in descending order

Source: https://exaly.com/author-pdf/2203925/publications.pdf

Version: 2024-02-01

42	604	932766	642321
papers	citations	10 h-index	23 g-index

44	44	44	680
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	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
2	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
3	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
4	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
5	Accurate prediction of enzyme mutant activity based on a multibody statistical potential. Bioinformatics, 2007, 23, 3155-3161.	1.8	50
6	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
7	Comprehensive mutagenesis of HIV-1 protease: a computational geometry approach. Biochemical and Biophysical Research Communications, 2003, 305, 322-326.	1.0	28
8	Computational mutagenesis studies of protein structureâ€function correlations. Proteins: Structure, Function and Bioinformatics, 2006, 64, 234-245.	1.5	25
9	Sequence and structure based models of HIV-1 protease and reverse transcriptase drug resistance. BMC Genomics, 2013, 14, S3.	1.2	19
10	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
11	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
12	All-atom four-body knowledge-based statistical potential to distinguish native tertiary RNA structures from nonnative folds. Journal of Theoretical Biology, 2018, 453, 58-67.	0.8	10
13	All-Atom Four-Body Knowledge-Based Statistical Potentials to Distinguish Native Protein Structures from Nonnative Folds. BioMed Research International, 2017, 2017, 1-17.	0.9	7
14	Structure-based prediction of protein activity changes: Assessing the impact of single residue replacements. , 2011, 2011, 3221-4.		6
15	Structure-based predictors of resistance to the HIV-1 integrase inhibitor Elvitegravir. Antiviral Research, 2014, 106, 5-12.	1.9	6
16	Sequence-Based Predictive Models of Resistance to HIV-1 Integrase Inhibitors: An n-Grams Approach to Phenotype Assessment. Current HIV Research, 2015, 13, 497-502.	0.2	6
17	Computational Mutagenesis of E. coli Lac Repressor: Insight into Structure-Function Relationships and Accurate Prediction of Mutant Activity. , 2008, , 390-401.		5
18	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

#	Article	IF	Citations
19	A structure-based computational mutagenesis elucidates the spectrum of stability-activity relationships in proteins. , 2011, 2011, 3225-8.		5
20	DC-SIGN points the way to a novel mechanism for HIV-1 transmission. MedGenMed: Medscape General Medicine, 2003, 5, 2.	0.2	5
21	Prediction of human immunodeficiency virus type 1 drug resistance: Representation of target sequence mutational patterns via an n-grams approach. , 2012, , .		4
22	Structure-based functional analysis of BRCA1 RING domain variants: Concordance of computational mutagenesis, experimental assay, and clinical data. Biophysical Chemistry, 2020, 266, 106442.	1.5	4
23	A Novel Sequence-Structure Approach for Accurate Prediction of Resistance to HIV-1 Protease Inhibitors. , 2007, , .		3
24	Four-body atomic potential for modeling protein-ligand binding affinity: application to enzyme-inhibitor binding energy prediction. BMC Structural Biology, 2013, 13, S1.	2.3	3
25	Fitness of unregulated human Ras mutants modeled by implementing computational mutagenesis and machine learning techniques. Heliyon, 2019, 5, e01884.	1.4	3
26	Modeling transcriptional activation changes to Gal4 variants via structure-based computational mutagenesis. PeerJ, 2018, 6, e4844.	0.9	3
27	Modeling functional changes toEscherichia colithymidylate synthase upon single residue replacements: a structure-based approach. PeerJ, 2015, 3, e721.	0.9	3
28	Structure Based Functional Analysis of Bacteriophage f1 Gene V Protein. , 2008, , .		2
29	Knowledge-based scoring function derived from atomic tessellation of macromolecular structures for prediction of protein-ligand binding affinity. , 2012, , .		2
30	Accurate and efficient structure-based computational mutagenesis for modeling fluorescence levels of Aequorea victoria green fluorescent protein mutants. Protein Engineering, Design and Selection, 2020, 33, .	1.0	2
31	Accurate Prediction of Stability Changes in Bacteriophage T4 Lysozyme upon Single Amino Acid Replacements. , 2009, , .		1
32	A multibody atomic statistical potential for the prediction of enzyme-inhibitor binding energy. , 2012, 2012, 5526-9.		1
33	Fast and Accurate Structure-Based Prediction of Resistance to the HIV-1 Integrase Inhibitor Raltegravir. , 2013, , .		1
34	Cancer-MI: Modeling Fitness of Unregulated RAS Mutants using Computational Mutagenesis and Machine Learning. Biophysical Journal, 2019, 116, 561a.	0.2	1
35	Functional analysis of BRCA1 RING domain variants: computationally derived structural data can improve upon experimental features for training predictive models. Integrative Biology (United) Tj ETQq1 1 0.784314 rgBT /Overlock		0
36	Overcoming the Curse of Dimensionality in a Statistical Geometry Based Computational Protein Mutagenesis. , 2010, , .		0

#	Article	IF	Citations
37	Sequence-based prediction of HIV-1 coreceptor usage. , 2011, , .		0
38	Generation of atomic four-body statistical potentials derived from the delaunay tessellation of protein structures. , 2012, 2012, 6321-4.		0
39	Active Participation in Current Faculty Research Inspires Student Achievement. Primus, 2022, 32, 468-484.	0.3	0
40	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
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