

Amelie Stein

List of Publications by Year in descending order

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37
papers

3,038
citations

279798

23
h-index

361022

35
g-index

56
all docs

56
docs citations

56
times ranked

3856
citing authors

#	ARTICLE	IF	CITATIONS
1	Predicting and interpreting large-scale mutagenesis data using analyses of protein stability and conservation. <i>Cell Reports</i> , 2022, 38, 110207.	6.4	62
2	Co-evolution of drug resistance and broadened substrate recognition in HIV protease variants isolated from an <i>Escherichia coli</i> genetic selection system. <i>Biochemical Journal</i> , 2022, 479, 479-501.	3.7	1
3	Disease-linked mutations cause exposure of a protein quality control degran. <i>Structure</i> , 2022, 30, 1245-1253.e5.	3.3	14
4	Disorder in a two-domain neuronal Ca ²⁺ -binding protein regulates domain stability and dynamics using ligand mimicry. <i>Cellular and Molecular Life Sciences</i> , 2021, 78, 2263-2278.	5.4	4
5	Understanding the Origins of Loss of Protein Function by Analyzing the Effects of Thousands of Variants on Activity and Abundance. <i>Molecular Biology and Evolution</i> , 2021, 38, 3235-3246.	8.9	65
6	Multiplexed assays reveal effects of missense variants in MSH2 and cancer predisposition. <i>PLoS Genetics</i> , 2021, 17, e1009496.	3.5	13
7	Mapping the degradation pathway of a disease-linked aspartoacylase variant. <i>PLoS Genetics</i> , 2021, 17, e1009539.	3.5	12
8	Ensuring scientific reproducibility in bio-macromolecular modeling via extensive, automated benchmarks. <i>Nature Communications</i> , 2021, 12, 6947.	12.8	16
9	Novel HARS2 missense variants identified in individuals with sensorineural hearing impairment and Perrault syndrome. <i>European Journal of Medical Genetics</i> , 2020, 63, 103733.	1.3	9
10	Classifying disease-associated variants using measures of protein activity and stability. , 2020, , 91-107.		21
11	Co-Chaperones in Targeting and Delivery of Misfolded Proteins to the 26S Proteasome. <i>Biomolecules</i> , 2020, 10, 1141.	4.0	29
12	Macromolecular modeling and design in Rosetta: recent methods and frameworks. <i>Nature Methods</i> , 2020, 17, 665-680.	19.0	513
13	Protein destabilization and degradation as a mechanism for hereditary disease. , 2020, , 111-125.		5
14	Folliculin variants linked to Birt-Hogg-Dubé syndrome are targeted for proteasomal degradation. <i>PLoS Genetics</i> , 2020, 16, e1009187.	3.5	16
15	Biophysical and Mechanistic Models for Disease-Causing Protein Variants. <i>Trends in Biochemical Sciences</i> , 2019, 44, 575-588.	7.5	143
16	Toward mechanistic models for genotype-phenotype correlations in phenylketonuria using protein stability calculations. <i>Human Mutation</i> , 2019, 40, 444-457.	2.5	56
17	Protein stability and degradation in health and disease. <i>Advances in Protein Chemistry and Structural Biology</i> , 2019, 114, 61-83.	2.3	31
18	Computational and cellular studies reveal structural destabilization and degradation of MLH1 variants in Lynch syndrome. <i>ELife</i> , 2019, 8, .	6.0	49

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19	Random Mutagenesis Analysis of the Influenza A M2 Proton Channel Reveals Novel Resistance Mutants. <i>Biochemistry</i> , 2018, 57, 5957-5968.	2.5	11
20	Blocking protein quality control to counter hereditary cancers. <i>Genes Chromosomes and Cancer</i> , 2017, 56, 823-831.	2.8	23
21	Predicting the impact of Lynch syndrome-causing missense mutations from structural calculations. <i>PLoS Genetics</i> , 2017, 13, e1006739.	3.5	90
22	Combined Covalent-Electrostatic Model of Hydrogen Bonding Improves Structure Prediction with Rosetta. <i>Journal of Chemical Theory and Computation</i> , 2015, 11, 609-622.	5.3	204
23	3did: a catalog of domain-based interactions of known three-dimensional structure. <i>Nucleic Acids Research</i> , 2014, 42, D374-D379.	14.5	249
24	Improvements to Robotics-Inspired Conformational Sampling in Rosetta. <i>PLoS ONE</i> , 2013, 8, e63090.	2.5	176
25	Control of protein signaling using a computationally designed GTPase/GEF orthogonal pair. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 5277-5282.	7.1	73
26	3did: identification and classification of domain-based interactions of known three-dimensional structure. <i>Nucleic Acids Research</i> , 2011, 39, D718-D723.	14.5	134
27	A Systematic Study of the Energetics Involved in Structural Changes upon Association and Connectivity in Protein Interaction Networks. <i>Structure</i> , 2011, 19, 881-889.	3.3	42
28	Three-dimensional modeling of protein interactions and complexes is going omics. <i>Current Opinion in Structural Biology</i> , 2011, 21, 200-208.	5.7	86
29	Uncovering new substrates for Aurora A kinase. <i>EMBO Reports</i> , 2010, 11, 977-984.	4.5	59
30	Structure of the FoxM1 DNA-recognition domain bound to a promoter sequence. <i>Nucleic Acids Research</i> , 2010, 38, 4527-4538.	14.5	109
31	Novel Peptide-Mediated Interactions Derived from High-Resolution 3-Dimensional Structures. <i>PLoS Computational Biology</i> , 2010, 6, e1000789.	3.2	56
32	3did Update: domain-domain and peptide-mediated interactions of known 3D structure. <i>Nucleic Acids Research</i> , 2009, 37, D300-D304.	14.5	67
33	Dynamic interactions of proteins in complex networks: a more structured view. <i>FEBS Journal</i> , 2009, 276, 5390-5405.	4.7	104
34	A molecular interpretation of genetic interactions in yeast. <i>FEBS Letters</i> , 2008, 582, 1245-1250.	2.8	12
35	Approved Drug Mimics of Short Peptide Ligands from Protein Interaction Motifs. <i>Journal of Chemical Information and Modeling</i> , 2008, 48, 1943-1948.	5.4	35
36	Contextual Specificity in Peptide-Mediated Protein Interactions. <i>PLoS ONE</i> , 2008, 3, e2524.	2.5	140

#	ARTICLE	IF	CITATIONS
37	3did: interacting protein domains of known three-dimensional structure. Nucleic Acids Research, 2004, 33, D413-D417.	14.5	160