

Pietro Sormanni

List of Publications by Year in descending order

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Version: 2024-02-01

56
papers

2,951
citations

218381

26
h-index

197535

49
g-index

61
all docs

61
docs citations

61
times ranked

4139
citing authors

#	ARTICLE	IF	CITATIONS
1	The CamSol Method of Rational Design of Protein Mutants with Enhanced Solubility. <i>Journal of Molecular Biology</i> , 2015, 427, 478-490.	2.0	341
2	A natural product inhibits the initiation of I \pm -synuclein aggregation and suppresses its toxicity. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, E1009-E1017.	3.3	231
3	MobiDB 3.0: more annotations for intrinsic disorder, conformational diversity and interactions in proteins. <i>Nucleic Acids Research</i> , 2018, 46, D471-D476.	6.5	190
4	Different soluble aggregates of A β 242 can give rise to cellular toxicity through different mechanisms. <i>Nature Communications</i> , 2019, 10, 1541.	5.8	140
5	Parapred: antibody paratope prediction using convolutional and recurrent neural networks. <i>Bioinformatics</i> , 2018, 34, 2944-2950.	1.8	124
6	Selective targeting of primary and secondary nucleation pathways in A β 242 aggregation using a rational antibody scanning method. <i>Science Advances</i> , 2017, 3, e1700488.	4.7	116
7	Proteome-wide observation of the phenomenon of life on the edge of solubility. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 1015-1020.	3.3	115
8	Rational design of antibodies targeting specific epitopes within intrinsically disordered proteins. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 9902-9907.	3.3	113
9	Simultaneous quantification of protein order and disorder. <i>Nature Chemical Biology</i> , 2017, 13, 339-342.	3.9	113
10	Rapid and accurate in silico solubility screening of a monoclonal antibody library. <i>Scientific Reports</i> , 2017, 7, 8200.	1.6	97
11	Third generation antibody discovery methods: <i>in silico</i> rational design. <i>Chemical Society Reviews</i> , 2018, 47, 9137-9157.	18.7	94
12	Targeting disordered proteins with small molecules using entropy. <i>Trends in Biochemical Sciences</i> , 2015, 40, 491-496.	3.7	87
13	A protein homeostasis signature in healthy brains recapitulates tissue vulnerability to Alzheimer's disease. <i>Science Advances</i> , 2016, 2, e1600947.	4.7	84
14	The s2D Method: Simultaneous Sequence-Based Prediction of the Statistical Populations of Ordered and Disordered Regions in Proteins. <i>Journal of Molecular Biology</i> , 2015, 427, 982-996.	2.0	77
15	In vitro and in silico assessment of the developability of a designed monoclonal antibody library. <i>MAbs</i> , 2019, 11, 388-400.	2.6	72
16	Rational design of a conformation-specific antibody for the quantification of A β 2 oligomers. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 13509-13518.	3.3	61
17	Quantifying misfolded protein oligomers as drug targets and biomarkers in Alzheimer and Parkinson diseases. <i>Nature Reviews Chemistry</i> , 2021, 5, 277-294.	13.8	56
18	Conformational dynamics in crystals reveal the molecular bases for D76N beta-2 microglobulin aggregation propensity. <i>Nature Communications</i> , 2018, 9, 1658.	5.8	53

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19	Massively parallel <i>C. elegans</i> tracking provides multi-dimensional fingerprints for phenotypic discovery. <i>Journal of Neuroscience Methods</i> , 2018, 306, 57-67.	1.3	52
20	Developability Assessment of Engineered Monoclonal Antibody Variants with a Complex Self-Association Behavior Using Complementary Analytical and in Silico Tools. <i>Molecular Pharmaceutics</i> , 2018, 15, 5697-5710.	2.3	52
21	A chemical kinetic basis for measuring translation initiation and elongation rates from ribosome profiling data. <i>PLoS Computational Biology</i> , 2019, 15, e1007070.	1.5	50
22	Rational design of mutations that change the aggregation rate of a protein while maintaining its native structure and stability. <i>Scientific Reports</i> , 2016, 6, 25559.	1.6	47
23	Attentive Cross-Modal Paratope Prediction. <i>Journal of Computational Biology</i> , 2019, 26, 536-545.	0.8	45
24	Understanding the frustration arising from the competition between function, misfolding, and aggregation in a globular protein. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 14141-14146.	3.3	43
25	Protein Solubility Predictions Using the CamSol Method in the Study of Protein Homeostasis. <i>Cold Spring Harbor Perspectives in Biology</i> , 2019, 11, a033845.	2.3	42
26	Oxetane Grafts Installed Selectively on Native Disulfides to Enhance Protein Stability and Activity In Vivo. <i>Angewandte Chemie - International Edition</i> , 2017, 56, 14963-14967.	7.2	39
27	Current advances in biopharmaceutical informatics: guidelines, impact and challenges in the computational developability assessment of antibody therapeutics. <i>MAbs</i> , 2022, 14, 2020082.	2.6	35
28	Inherent Biophysical Properties Modulate the Toxicity of Soluble Amyloidogenic Light Chains. <i>Journal of Molecular Biology</i> , 2020, 432, 845-860.	2.0	26
29	Assessment of Therapeutic Antibody Developability by Combinations of In Vitro and In Silico Methods. <i>Methods in Molecular Biology</i> , 2022, 2313, 57-113.	0.4	26
30	A Rational Design Strategy for the Selective Activity Enhancement of a Molecular Chaperone toward a Target Substrate. <i>Biochemistry</i> , 2015, 54, 5103-5112.	1.2	25
31	Supersaturated proteins are enriched at synapses and underlie cell and tissue vulnerability in Alzheimer's disease. <i>Heliyon</i> , 2019, 5, e02589.	1.4	23
32	Identifying A- and P-site locations on ribosome-protected mRNA fragments using Integer Programming. <i>Scientific Reports</i> , 2019, 9, 6256.	1.6	18
33	Corneal Dystrophy Mutations Drive Pathogenesis by Targeting TGFBIp Stability and Solubility in a Latent Amyloid-forming Domain. <i>Journal of Molecular Biology</i> , 2018, 430, 1116-1140.	2.0	17
34	Delivery of Native Proteins into <i>C. elegans</i> Using a Transduction Protocol Based on Lipid Vesicles. <i>Scientific Reports</i> , 2017, 7, 15045.	1.6	16
35	An open-source automated PEG precipitation assay to measure the relative solubility of proteins with low material requirement. <i>Scientific Reports</i> , 2021, 11, 21932.	1.6	16
36	Fibrillogenic propensity of the GroEL apical domain: A Janus-faced minichaperone. <i>FEBS Letters</i> , 2012, 586, 1120-1127.	1.3	15

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37	A rationally designed bicyclic peptide remodels A β 242 aggregation in vitro and reduces its toxicity in a worm model of Alzheimer's disease. <i>Scientific Reports</i> , 2020, 10, 15280.	1.6	15
38	Systematic Activity Maturation of a Single-Domain Antibody with Non-canonical Amino Acids through Chemical Mutagenesis. <i>Cell Chemical Biology</i> , 2021, 28, 70-77.e5.	2.5	15
39	A Rationally Designed Hsp70 Variant Rescues the Aggregation-Associated Toxicity of Human IAPP in Cultured Pancreatic Islet β -Cells. <i>International Journal of Molecular Sciences</i> , 2018, 19, 1443.	1.8	14
40	MonteGrappa: An iterative Monte Carlo program to optimize biomolecular potentials in simplified models. <i>Computer Physics Communications</i> , 2015, 186, 93-104.	3.0	12
41	Rationally Designed Antibodies as Research Tools to Study the Structure-Toxicity Relationship of Amyloid- β Oligomers. <i>International Journal of Molecular Sciences</i> , 2020, 21, 4542.	1.8	12
42	Comparative Studies in the A30P and A53T α -Synuclein <i>C. elegans</i> Strains to Investigate the Molecular Origins of Parkinson's Disease. <i>Frontiers in Cell and Developmental Biology</i> , 2021, 9, 552549.	1.8	12
43	Biochemical and biophysical comparison of human and mouse beta-2 microglobulin reveals the molecular determinants of low amyloid propensity. <i>FEBS Journal</i> , 2020, 287, 546-560.	2.2	11
44	Correlation between the binding affinity and the conformational entropy of nanobody SARS-CoV-2 spike protein complexes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022, 119, .	3.3	11
45	Subdomain Architecture and Stability of a Giant Repeat Protein. <i>Journal of Physical Chemistry B</i> , 2013, 117, 13029-13037.	1.2	10
46	Oxetane Grafts Installed Site-Selectively on Native Disulfides to Enhance Protein Stability and Activity In Vivo. <i>Angewandte Chemie</i> , 2017, 129, 15159-15163.	1.6	10
47	Neuroserpin and transthyretin are extracellular chaperones that preferentially inhibit amyloid formation. <i>Science Advances</i> , 2021, 7, eabf7606.	4.7	10
48	Pairs of amino acids at the P- and A-sites of the ribosome predictably and causally modulate translation-elongation rates. <i>Journal of Molecular Biology</i> , 2020, 432, 166696.	2.0	9
49	β -Clamp-Mediated Homo- and Heterodimerization of Single-Domain Antibodies via Site-Specific Homobifunctional Conjugation. <i>Journal of the American Chemical Society</i> , 2022, 144, 13026-13031.	6.6	9
50	Conformational Entropy as a Potential Liability of Computationally Designed Antibodies. <i>Biomolecules</i> , 2022, 12, 718.	1.8	8
51	Iterative derivation of effective potentials to sample the conformational space of proteins at atomistic scale. <i>Journal of Chemical Physics</i> , 2014, 140, 195101.	1.2	6
52	A method of predicting the in vitro fibril formation propensity of A β 240 mutants based on their inclusion body levels in <i>E. coli</i> . <i>Scientific Reports</i> , 2019, 9, 3680.	1.6	6
53	Rationally Designed Bicyclic Peptides Prevent the Conversion of A β 242 Assemblies Into Fibrillar Structures. <i>Frontiers in Neuroscience</i> , 2021, 15, 623097.	1.4	6
54	An aggregation inhibitor specific to oligomeric intermediates of A β 242 derived from phage display libraries of stable, small proteins. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022, 119, e2121966119.	3.3	5

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55	Modulating the cardiotoxic behaviour of immunoglobulin light chain dimers through point mutations. <i>Amyloid: the International Journal of Experimental and Clinical Investigation: the Official Journal of the International Society of Amyloidosis</i> , 2019, 26, 105-106.	1.4	4
56	Computational maturation of a single-domain antibody against A β 242 aggregation. <i>Chemical Science</i> , 2021, 12, 13940-13948.	3.7	4