Pietro Sormanni

List of Publications by Year
in descending order

56	2,951	218677	189892
papers	citations	26 h-index	50 g-index

61	61	61	4139
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Assessment of Therapeutic Antibody Developability by Combinations of In Vitro and In Silico Methods. Methods in Molecular Biology, 2022, 2313, 57-113.	0.9	26
2	Current advances in biopharmaceutical informatics: guidelines, impact and challenges in the computational developability assessment of antibody therapeutics. MAbs, 2022, 14, 2020082.	5.2	35
3	An aggregation inhibitor specific to oligomeric intermediates of AÎ²42 derived from phage display libraries of stable, small proteins. Proceedings of the National Academy of Sciences of the United States of America, 2022, 119, e2121966119.	7.1	5
4	Conformational Entropy as a Potential Liability of Computationally Designed Antibodies. Biomolecules, 2022, 12, 718.	4.0	8
5	Ï€-Clamp-Mediated Homo- and Heterodimerization of Single-Domain Antibodies via Site-Specific Homobifunctional Conjugation. Journal of the American Chemical Society, 2022, 144, 13026-13031.	13.7	9
6	Correlation between the binding affinity and the conformational entropy of nanobody SARS-CoV-2 spike protein complexes. Proceedings of the National Academy of Sciences of the United States of America, 2022, 119, .	7.1	11
7	Systematic Activity Maturation of a Single-Domain Antibody with Non-canonical Amino Acids through Chemical Mutagenesis. Cell Chemical Biology, 2021, 28, 70-77.e5.	5.2	15
8	Rationally Designed Bicyclic Peptides Prevent the Conversion of AÎ²42 Assemblies Into Fibrillar Structures. Frontiers in Neuroscience, 2021, 15, 623097.	2.8	6
9	Quantifying misfolded protein oligomers as drug targets and biomarkers in Alzheimer and Parkinson diseases. Nature Reviews Chemistry, 2021, 5, 277-294.	30.2	56
10	Comparative Studies in the A30P and A53T Î±-Synuclein C. elegans Strains to Investigate the Molecular Origins of Parkinson's Disease. Frontiers in Cell and Developmental Biology, 2021, 9, 552549.	3.7	12
11	Computational maturation of a single-domain antibody against AÎ²42 aggregation. Chemical Science, 2021, 12, 13940-13948.	7.4	4
12	An open-source automated PEG precipitation assay to measure the relative solubility of proteins with low material requirement. Scientific Reports, 2021, 11, 21932.	3.3	16
13	Neuroserpin and transthyretin are extracellular chaperones that preferentially inhibit amyloid formation. Science Advances, 2021, 7, eabf7606.	10.3	10
14	Biochemical and biophysical comparison of human and mouse betaâ€2 microglobulin reveals the molecular determinants of low amyloid propensity. FEBS Journal, 2020, 287, 546-560.	4.7	11
15	Inherent Biophysical Properties Modulate the Toxicity of Soluble Amyloidogenic Light Chains. Journal of Molecular Biology, 2020, 432, 845-860.	4.2	26
16	Proteome-wide observation of the phenomenon of life on the edge of solubility. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 1015-1020.	7.1	115
17	A rationally designed bicyclic peptide remodels AÎ²42 aggregation in vitro and reduces its toxicity in a worm model of Alzheimerâ€™s disease. Scientific Reports, 2020, 10, 15280.	3.3	15
18	Pairs of amino acids at the P- and A-sites of the ribosome predictably and causally modulate translation-elongation rates. Journal of Molecular Biology, 2020, 432, 166696.	4.2	9

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19	Rational design of a conformation-specific antibody for the quantification of AÎ² oligomers. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 13509-13518.	7.1	61
20	Rationally Designed Antibodies as Research Tools to Study the Structureâ€“Toxicity Relationship of Amyloid-Î² Oligomers. International Journal of Molecular Sciences, 2020, 21, 4542.	4.1	12
21	Modulating the cardiotoxic behaviour of immunoglobulin light chain dimers through point mutations. Amyloid: the International Journal of Experimental and Clinical Investigation: the Official Journal of the International Society of Amyloidosis, 2019, 26, 105-106.	3.0	4
22	A chemical kinetic basis for measuring translation initiation and elongation rates from ribosome profiling data. PLoS Computational Biology, 2019, 15, e1007070.	3.2	50
23	Identifying A- and P-site locations on ribosome-protected mRNA fragments using Integer Programming. Scientific Reports, 2019, 9, 6256.	3.3	18
24	A method of predicting the in vitro fibril formation propensity of AÎ²40 mutants based on their inclusion body levels in E. coli. Scientific Reports, 2019, 9, 3680.	3.3	6
25	Protein Solubility Predictions Using the CamSol Method in the Study of Protein Homeostasis. Cold Spring Harbor Perspectives in Biology, 2019, 11, a033845.	5.5	42
26	Different soluble aggregates of AÎ²42 can give rise to cellular toxicity through different mechanisms. Nature Communications, 2019, 10, 1541.	12.8	140
27	Supersaturated proteins are enriched at synapses and underlie cell and tissue vulnerability in Alzheimer's disease. Heliyon, 2019, 5, e02589.	3.2	23
28	Attentive Cross-Modal Paratope Prediction. Journal of Computational Biology, 2019, 26, 536-545.	1.6	45
29	In vitro and in silico assessment of the developability of a designed monoclonal antibody library. MAbs, 2019, 11, 388-400.	5.2	72
30	Parapred: antibody paratope prediction using convolutional and recurrent neural networks. Bioinformatics, 2018, 34, 2944-2950.	4.1	124
31	Massively parallel C. elegans tracking provides multi-dimensional fingerprints for phenotypic discovery. Journal of Neuroscience Methods, 2018, 306, 57-67.	2.5	52
32	Conformational dynamics in crystals reveal the molecular bases for D76N beta-2 microglobulin aggregation propensity. Nature Communications, 2018, 9, 1658.	12.8	53
33	Corneal Dystrophy Mutations Drive Pathogenesis by Targeting TGFBIp Stability and Solubility in a Latent Amyloid-forming Domain. Journal of Molecular Biology, 2018, 430, 1116-1140.	4.2	17
34	Developability Assessment of Engineered Monoclonal Antibody Variants with a Complex Self-Association Behavior Using Complementary Analytical and in Silico Tools. Molecular Pharmaceutics, 2018, 15, 5697-5710.	4.6	52
35	Third generation antibody discovery methods:in silicorational design. Chemical Society Reviews, 2018, 47, 9137-9157.	38.1	94
36	A Rationally Designed Hsp70 Variant Rescues the Aggregation-Associated Toxicity of Human IAPP in Cultured Pancreatic Islet Î²-Cells. International Journal of Molecular Sciences, 2018, 19, 1443.	4.1	14

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37	MobiDB 3.0: more annotations for intrinsic disorder, conformational diversity and interactions in proteins. Nucleic Acids Research, 2018, 46, D471-D476.	14.5	190
38	A natural product inhibits the initiation of Î±-synuclein aggregation and suppresses its toxicity. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, E1009-E1017.	7.1	231
39	Selective targeting of primary and secondary nucleation pathways in AÎ²42 aggregation using a rational antibody scanning method. Science Advances, 2017, 3, e1700488.	10.3	116
40	Simultaneous quantification of protein order and disorder. Nature Chemical Biology, 2017, 13, 339-342.	8.0	113
41	Oxetane Grafts Installed Siteâ€Selectively on Native Disulfides to Enhance Protein Stability and Activity Inâ€...Vivo. Angewandte Chemie - International Edition, 2017, 56, 14963-14967.	13.8	39
42	Oxetane Grafts Installed Siteâ€Selectively on Native Disulfides to Enhance Protein Stability and Activity Inâ€...Vivo. Angewandte Chemie, 2017, 129, 15159-15163.	2.0	10
43	Rapid and accurate in silico solubility screening of a monoclonal antibody library. Scientific Reports, 2017, 7, 8200.	3.3	97
44	Delivery of Native Proteins into C. elegans Using a Transduction Protocol Based on Lipid Vesicles. Scientific Reports, 2017, 7, 15045.	3.3	16
45	Rational design of mutations that change the aggregation rate of a protein while maintaining its native structure and stability. Scientific Reports, 2016, 6, 25559.	3.3	47
46	A protein homeostasis signature in healthy brains recapitulates tissue vulnerability to Alzheimerâ€™s disease. Science Advances, 2016, 2, e1600947.	10.3	84
47	Rational design of antibodies targeting specific epitopes within intrinsically disordered proteins. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 9902-9907.	7.1	113
48	The CamSol Method of Rational Design of Protein Mutants with Enhanced Solubility. Journal of Molecular Biology, 2015, 427, 478-490.	4.2	341
49	Targeting disordered proteins with small molecules using entropy. Trends in Biochemical Sciences, 2015, 40, 491-496.	7.5	87
50	A Rational Design Strategy for the Selective Activity Enhancement of a Molecular Chaperone toward a Target Substrate. Biochemistry, 2015, 54, 5103-5112.	2.5	25
51	The s2D Method: Simultaneous Sequence-Based Prediction of the Statistical Populations of Ordered and Disordered Regions in Proteins. Journal of Molecular Biology, 2015, 427, 982-996.	4.2	77
52	MonteGrappa: An iterative Monte Carlo program to optimize biomolecular potentials in simplified models. Computer Physics Communications, 2015, 186, 93-104.	7.5	12
53	Iterative derivation of effective potentials to sample the conformational space of proteins at atomistic scale. Journal of Chemical Physics, 2014, 140, 195101.	3.0	6
54	Understanding the frustration arising from the competition between function, misfolding, and aggregation in a globular protein. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 14141-14146.	7.1	43

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55	Subdomain Architecture and Stability of a Giant Repeat Protein. Journal of Physical Chemistry B, 2013, 117, 13029-13037.	2.6	10
56	Fibrillogenic propensity of the GroEL apical domain: A Janusâ€faced minichaperone. FEBS Letters, 2012, 586, 1120-1127.	2.8	15