Pietro Sormanni

List of Publications by Year in Descending Order

56 papers	1,838 citations	24 h-index	42 g-index
61 ext. papers	2,481 ext. citations	9 avg, IF	5.14 L-index

#	Paper	IF	Citations
56	Current advances in biopharmaceutical informatics: guidelines, impact and challenges in the computational developability assessment of antibody therapeutics.. *MAbs*, **2022**, 14, 2020082	6.6	6
55	Assessment of Therapeutic Antibody Developability by Combinations of In Vitro and In Silico Methods. *Methods in Molecular Biology*, **2022**, 2313, 57-113	1.4	8
54	An aggregation inhibitor specific to oligomeric intermediates of A42 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	11.5	1
53	Conformational Entropy as a Potential Liability of Computationally Designed Antibodies. *Biomolecules*, **2022**, 12, 718	5.9	2
52	An open-source automated PEG precipitation assay to measure the relative solubility of proteins with low material requirement. *Scientific Reports*, **2021**, 11, 21932	4.9	3
51	Computational maturation of a single-domain antibody against A42 aggregation.. *Chemical Science*, **2021**, 12, 13940-13948	9.4	2
50	Comparative Studies in the A30P and A53T Synuclein Strains to Investigate the Molecular Origins of Parkinsonbs Disease. *Frontiers in Cell and Developmental Biology*, **2021**, 9, 552549	5.7	5
49	Systematic Activity Maturation of a Single-Domain Antibody with Non-canonical Amino Acids through Chemical Mutagenesis. *Cell Chemical Biology*, **2021**, 28, 70-77.e5	8.2	6
48	Rationally Designed Bicyclic Peptides Prevent the Conversion of A42 Assemblies Into Fibrillar Structures. *Frontiers in Neuroscience*, **2021**, 15, 623097	5.1	1
47	Quantifying misfolded protein oligomers as drug targets and biomarkers in Alzheimer and Parkinson diseases. *Nature Reviews Chemistry*, **2021**, 5, 277-294	34.6	10
46	Neuroserpin and transthyretin are extracellular chaperones that preferentially inhibit amyloid formation. *Science Advances*, **2021**, 7, eabf7606	14.3	4
45	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	6.5	3
44	Rational design of a conformation-specific antibody for the quantification of A oligomers. *Proceedings of the National Academy of Sciences of the United States of America*, **2020**, 117, 13509-13518	11.5	26
43	Rationally Designed Antibodies as Research Tools to Study the Structure-Toxicity Relationship of Amyloid- Oligomers. *International Journal of Molecular Sciences*, **2020**, 21,	6.3	7
42	Inherent Biophysical Properties Modulate the Toxicity of Soluble Amyloidogenic Light Chains. *Journal of Molecular Biology*, **2020**, 432, 845-860	6.5	10
41	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	11.5	52
40	A rationally designed bicyclic peptide remodels A42 aggregation in vitro and reduces its toxicity in a worm model of Alzheimerbs disease. *Scientific Reports*, **2020**, 10, 15280	4.9	4

39	Biochemical and biophysical comparison of human and mouse beta-2 microglobulin reveals the molecular determinants of low amyloid propensity. *FEBS Journal*, **2020**, 287, 546-560	5.7	6
38	A chemical kinetic basis for measuring translation initiation and elongation rates from ribosome profiling data. *PLoS Computational Biology*, **2019**, 15, e1007070	5	26
37	Identifying A- and P-site locations on ribosome-protected mRNA fragments using Integer Programming. *Scientific Reports*, **2019**, 9, 6256	4.9	11
36	A method of predicting the in vitro fibril formation propensity of A□40 mutants based on their inclusion body levels in E. coli. *Scientific Reports*, **2019**, 9, 3680	4.9	4
35	Protein Solubility Predictions Using the CamSol Method in the Study of Protein Homeostasis. *Cold Spring Harbor Perspectives in Biology*, **2019**, 11,	10.2	22
34	Different soluble aggregates of A□42 can give rise to cellular toxicity through different mechanisms. *Nature Communications*, **2019**, 10, 1541	17.4	71
33	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	2.7	2
32	Supersaturated proteins are enriched at synapses and underlie cell and tissue vulnerability in Alzheimer□s disease. *Heliyon*, **2019**, 5, e02589	3.6	17
31	Attentive Cross-Modal Paratope Prediction. *Journal of Computational Biology*, **2019**, 26, 536-545	1.7	24
30	In vitro and in silico assessment of the developability of a designed monoclonal antibody library. *MAbs*, **2019**, 11, 388-400	6.6	43
29	Parapred: antibody paratope prediction using convolutional and recurrent neural networks. *Bioinformatics*, **2018**, 34, 2944-2950	7.2	62
28	Massively parallel C. elegans tracking provides multi-dimensional fingerprints for phenotypic discovery. *Journal of Neuroscience Methods*, **2018**, 306, 57-67	3	35
27	Conformational dynamics in crystals reveal the molecular bases for D76N beta-2 microglobulin aggregation propensity. *Nature Communications*, **2018**, 9, 1658	17.4	35
26	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	6.5	12
25	A Rationally Designed Hsp70 Variant Rescues the Aggregation-Associated Toxicity of Human IAPP in Cultured Pancreatic Islet □Cells. *International Journal of Molecular Sciences*, **2018**, 19,	6.3	11
24	MobiDB 3.0: more annotations for intrinsic disorder, conformational diversity and interactions in proteins. *Nucleic Acids Research*, **2018**, 46, D471-D476	20.1	143
23	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	5.6	33
22	Third generation antibody discovery methods: in silico rational design. *Chemical Society Reviews*, **2018**, 47, 9137-9157	58.5	64

21	A natural product inhibits the initiation of α-synuclein aggregation and suppresses its toxicity. *Proceedings of the National Academy of Sciences of the United States of America*, **2017**, 114, E1009-E1017	11.5	177
20	Selective targeting of primary and secondary nucleation pathways in Aβ42 aggregation using a rational antibody scanning method. *Science Advances*, **2017**, 3, e1700488	14.3	81
19	Simultaneous quantification of protein order and disorder. *Nature Chemical Biology*, **2017**, 13, 339-342	11.7	83
18	Oxetane Grafts Installed Site-Selectively on Native Disulfides to Enhance Protein Stability and Activity In Vivo. *Angewandte Chemie - International Edition*, **2017**, 56, 14963-14967	16.4	32
17	Oxetane Grafts Installed Site-Selectively on Native Disulfides to Enhance Protein Stability and Activity In Vivo. *Angewandte Chemie*, **2017**, 129, 15159-15163	3.6	8
16	Rapid and accurate in silico solubility screening of a monoclonal antibody library. *Scientific Reports*, **2017**, 7, 8200	4.9	63
15	Delivery of Native Proteins into C. elegans Using a Transduction Protocol Based on Lipid Vesicles. *Scientific Reports*, **2017**, 7, 15045	4.9	11
14	A protein homeostasis signature in healthy brains recapitulates tissue vulnerability to Alzheimer's disease. *Science Advances*, **2016**, 2, e1600947	14.3	68
13	Rational design of mutations that change the aggregation rate of a protein while maintaining its native structure and stability. *Scientific Reports*, **2016**, 6, 25559	4.9	41
12	Targeting disordered proteins with small molecules using entropy. *Trends in Biochemical Sciences*, **2015**, 40, 491-6	10.3	58
11	A Rational Design Strategy for the Selective Activity Enhancement of a Molecular Chaperone toward a Target Substrate. *Biochemistry*, **2015**, 54, 5103-12	3.2	22
10	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	6.5	60
9	MonteGrappa: An iterative Monte Carlo program to optimize biomolecular potentials in simplified models. *Computer Physics Communications*, **2015**, 186, 93-104	4.2	10
8	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, 9902-7	11.5	78
7	The CamSol method of rational design of protein mutants with enhanced solubility. *Journal of Molecular Biology*, **2015**, 427, 478-90	6.5	208
6	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, 14141-6	11.5	36
5	Iterative derivation of effective potentials to sample the conformational space of proteins at atomistic scale. *Journal of Chemical Physics*, **2014**, 140, 195101	3.9	4
4	Subdomain architecture and stability of a giant repeat protein. *Journal of Physical Chemistry B*, **2013**, 117, 13029-37	3.4	8

List of Publications

3	Fibrillogenic propensity of the GroEL apical domain: a Janus-faced minichaperone. *FEBS Letters*, **2012**, 586, 1120-7	3.8	13
2	Paratope Prediction using Convolutional and Recurrent Neural Networks		1
1	Fragment-based computational design of antibodies targeting structured epitopes		3