

Pietro Sormanni

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/5376488/publications.pdf>

Version: 2024-02-01

56
papers

2,951
citations

218677
26
h-index

189892
50
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. Journal of Molecular Biology, 2015, 427, 478-490.	4.2	341
2	A natural product inhibits the initiation of β -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
3	MobiDB 3.0: more annotations for intrinsic disorder, conformational diversity and interactions in proteins. Nucleic Acids Research, 2018, 46, D471-D476.	14.5	190
4	Different soluble aggregates of A β 242 can give rise to cellular toxicity through different mechanisms. Nature Communications, 2019, 10, 1541.	12.8	140
5	Parapred: antibody paratope prediction using convolutional and recurrent neural networks. Bioinformatics, 2018, 34, 2944-2950.	4.1	124
6	Selective targeting of primary and secondary nucleation pathways in A β 242 aggregation using a rational antibody scanning method. Science Advances, 2017, 3, e1700488.	10.3	116
7	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
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, 9902-9907.	7.1	113
9	Simultaneous quantification of protein order and disorder. Nature Chemical Biology, 2017, 13, 339-342.	8.0	113
10	Rapid and accurate in silico solubility screening of a monoclonal antibody library. Scientific Reports, 2017, 7, 8200.	3.3	97
11	Third generation antibody discovery methods: <i>in silico</i> rational design. Chemical Society Reviews, 2018, 47, 9137-9157.	38.1	94
12	Targeting disordered proteins with small molecules using entropy. Trends in Biochemical Sciences, 2015, 40, 491-496.	7.5	87
13	A protein homeostasis signature in healthy brains recapitulates tissue vulnerability to Alzheimer's disease. Science Advances, 2016, 2, e1600947.	10.3	84
14	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
15	In vitro and in silico assessment of the developability of a designed monoclonal antibody library. MAbs, 2019, 11, 388-400.	5.2	72
16	Rational design of a conformation-specific antibody for the quantification of A β 2 oligomers. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 13509-13518.	7.1	61
17	Quantifying misfolded protein oligomers as drug targets and biomarkers in Alzheimer and Parkinson diseases. Nature Reviews Chemistry, 2021, 5, 277-294.	30.2	56
18	Conformational dynamics in crystals reveal the molecular bases for D76N beta-2 microglobulin aggregation propensity. Nature Communications, 2018, 9, 1658.	12.8	53

#	ARTICLE	IF	CITATIONS
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.	2.5	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.	4.6	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.	3.2	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.	3.3	47
23	Attentive Cross-Modal Paratope Prediction. <i>Journal of Computational Biology</i> , 2019, 26, 536-545.	1.6	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.	7.1	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.	5.5	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.	13.8	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.	5.2	35
28	Inherent Biophysical Properties Modulate the Toxicity of Soluble Amyloidogenic Light Chains. <i>Journal of Molecular Biology</i> , 2020, 432, 845-860.	4.2	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.	0.9	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.	2.5	25
31	Supersaturated proteins are enriched at synapses and underlie cell and tissue vulnerability in Alzheimer's disease. <i>Heliyon</i> , 2019, 5, e02589.	3.2	23
32	Identifying A- and P-site locations on ribosome-protected mRNA fragments using Integer Programming. <i>Scientific Reports</i> , 2019, 9, 6256.	3.3	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.	4.2	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.	3.3	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.	3.3	16
36	Fibrillogenic propensity of the GroEL apical domain: A Janus-faced minichaperone. <i>FEBS Letters</i> , 2012, 586, 1120-1127.	2.8	15

#	ARTICLE	IF	CITATIONS
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.	3.3	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.	5.2	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.	4.1	14
40	MonteGrappa: An iterative Monte Carlo program to optimize biomolecular potentials in simplified models. <i>Computer Physics Communications</i> , 2015, 186, 93-104.	7.5	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.	4.1	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.	3.7	12
43	Biochemical and biophysical comparison of human and mouse beta β 2 microglobulin reveals the molecular determinants of low amyloid propensity. <i>FEBS Journal</i> , 2020, 287, 546-560.	4.7	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, .	7.1	11
45	Subdomain Architecture and Stability of a Giant Repeat Protein. <i>Journal of Physical Chemistry B</i> , 2013, 117, 13029-13037.	2.6	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.	2.0	10
47	Neuroserpin and transthyretin are extracellular chaperones that preferentially inhibit amyloid formation. <i>Science Advances</i> , 2021, 7, eabf7606.	10.3	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.	4.2	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.	13.7	9
50	Conformational Entropy as a Potential Liability of Computationally Designed Antibodies. <i>Biomolecules</i> , 2022, 12, 718.	4.0	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.	3.0	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.	3.3	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.	2.8	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.	7.1	5

#	ARTICLE	IF	CITATIONS
55	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
56	Computational maturation of a single-domain antibody against A β 42 aggregation. Chemical Science, 2021, 12, 13940-13948.	7.4	4