

Dmitry N Ivankov

List of Publications by Year in descending order

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Version: 2024-02-01

31
papers

1,880
citations

393982

19
h-index

476904

29
g-index

37
all docs

37
docs citations

37
times ranked

1857
citing authors

#	ARTICLE	IF	CITATIONS
1	Local fitness landscape of the green fluorescent protein. <i>Nature</i> , 2016, 533, 397-401.	13.7	438
2	Contact order revisited: Influence of protein size on the folding rate. <i>Protein Science</i> , 2003, 12, 2057-2062.	3.1	327
3	Prediction of protein folding rates from the amino acid sequence-predicted secondary structure. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2004, 101, 8942-8944.	3.3	171
4	Chain length is the main determinant of the folding rate for proteins with three-state folding kinetics. <i>Proteins: Structure, Function and Bioinformatics</i> , 2003, 51, 162-166.	1.5	140
5	Folding nuclei in proteins. <i>FEBS Letters</i> , 2001, 489, 113-118.	1.3	72
6	An experimental assay of the interactions of amino acids from orthologous sequences shaping a complex fitness landscape. <i>PLoS Genetics</i> , 2019, 15, e1008079.	1.5	71
7	Self-consistency test reveals systematic bias in programs for prediction change of stability upon mutation. <i>Bioinformatics</i> , 2018, 34, 3653-3658.	1.8	70
8	Coupling between Properties of the Protein Shape and the Rate of Protein Folding. <i>PLoS ONE</i> , 2009, 4, e6476.	1.1	62
9	Golden triangle for folding rates of globular proteins. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 147-150.	3.3	58
10	KineticDB: a database of protein folding kinetics. <i>Nucleic Acids Research</i> , 2009, 37, D342-D346.	6.5	57
11	A structural perspective of compensatory evolution. <i>Current Opinion in Structural Biology</i> , 2014, 26, 104-112.	2.6	42
12	There and back again: Two views on the protein folding puzzle. <i>Physics of Life Reviews</i> , 2017, 21, 56-71.	1.5	33
13	More compact protein globules exhibit slower folding rates. <i>Proteins: Structure, Function and Bioinformatics</i> , 2008, 70, 329-332.	1.5	32
14	Unexpected Diversity of Signal Peptides in Prokaryotes. <i>MBio</i> , 2012, 3, .	1.8	30
15	How many signal peptides are there in bacteria?. <i>Environmental Microbiology</i> , 2013, 15, 983-990.	1.8	29
16	Theoretical Study of a Landscape of Protein Folding~Unfolding Pathways. <i>Folding Rates at Midtransition</i> . <i>Biochemistry</i> , 2001, 40, 9957-9961.	1.2	25
17	COMPACTNESS DETERMINES PROTEIN FOLDING TYPE. <i>Journal of Bioinformatics and Computational Biology</i> , 2008, 06, 667-680.	0.3	21
18	Solution of Levinthal's Paradox and a Physical Theory of Protein Folding Times. <i>Biomolecules</i> , 2020, 10, 250.	1.8	21

#	ARTICLE	IF	CITATIONS
19	QARIP: a web server for quantitative proteomic analysis of regulated intramembrane proteolysis. <i>Nucleic Acids Research</i> , 2013, 41, W459-W464.	6.5	20
20	Understanding the Folding Rates and Folding Nuclei of Globular Proteins. <i>Current Protein and Peptide Science</i> , 2007, 8, 521-536.	0.7	18
21	The relationship between the solvent-accessible surface area of a protein and the number of native contacts in its structure. <i>Molecular Biology</i> , 2008, 42, 932-938.	0.4	17
22	Machine Learning: How Much Does It Tell about Protein Folding Rates?. <i>PLoS ONE</i> , 2015, 10, e0143166.	1.1	16
23	Rate of sequence divergence under constant selection. <i>Biology Direct</i> , 2010, 5, 5.	1.9	12
24	Evolutionary Interplay between Symbiotic Relationships and Patterns of Signal Peptide Gain and Loss. <i>Genome Biology and Evolution</i> , 2018, 10, 928-938.	1.1	9
25	Protein Folding as Flow across a Network of Folding~Unfolding Pathways. 1. The Mid-Transition Case. <i>Journal of Physical Chemistry B</i> , 2010, 114, 7920-7929.	1.2	6
26	Protein Folding as Flow across a Network of Folding~Unfolding Pathways. 2. The "In-Water" Case. <i>Journal of Physical Chemistry B</i> , 2010, 114, 7930-7934.	1.2	6
27	Inhibition of hyaluronan secretion by novel coumarin compounds and chitin synthesis inhibitors. <i>Glycobiology</i> , 2021, 31, 959-974.	1.3	6
28	Exact correspondence between walk in nucleotide and protein sequence spaces. <i>PLoS ONE</i> , 2017, 12, e0182525.	1.1	3
29	HypercubeME: two hundred million combinatorially complete datasets from a single experiment. <i>Bioinformatics</i> , 2020, 36, 1960-1962.	1.8	1
30	Two Views on the Protein Folding Puzzle. , 2018, , 391-412.		0
31	Protein Structure and Its Folding Rate. , 2008, , 273-301.		0