

Sergiy O Garbuzynskiy

List of Publications by Year in descending order

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Version: 2024-02-01

34
papers

1,875
citations

430874

18
h-index

434195

31
g-index

35
all docs

35
docs citations

35
times ranked

1942
citing authors

#	ARTICLE	IF	CITATIONS
1	FoldAmyloid: a method of prediction of amyloidogenic regions from protein sequence. <i>Bioinformatics</i> , 2010, 26, 326-332.	4.1	338
2	Contact order revisited: Influence of protein size on the folding rate. <i>Protein Science</i> , 2003, 12, 2057-2062.	7.6	327
3	Prediction of Amyloidogenic and Disordered Regions in Protein Chains. <i>PLoS Computational Biology</i> , 2006, 2, e177.	3.2	155
4	FoldUnfold: web server for the prediction of disordered regions in protein chain. <i>Bioinformatics</i> , 2006, 22, 2948-2949.	4.1	148
5	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.	2.6	140
6	Intrinsic Disorder in Protein Interactions: Insights From a Comprehensive Structural Analysis. <i>PLoS Computational Biology</i> , 2009, 5, e1000316.	3.2	104
7	Different packing of external residues can explain differences in the thermostability of proteins from thermophilic and mesophilic organisms. <i>Bioinformatics</i> , 2007, 23, 2231-2238.	4.1	89
8	Comparison of X-ray and NMR structures: Is there a systematic difference in residue contacts between X-ray- and NMR-resolved protein structures?. <i>Proteins: Structure, Function and Bioinformatics</i> , 2005, 60, 139-147.	2.6	78
9	To be folded or to be unfolded?. <i>Protein Science</i> , 2008, 13, 2871-2877.	7.6	69
10	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.	7.1	58
11	Outlining Folding Nuclei in Globular Proteins. <i>Journal of Molecular Biology</i> , 2004, 336, 509-525.	4.2	57
12	There and back again: Two views on the protein folding puzzle. <i>Physics of Life Reviews</i> , 2017, 21, 56-71.	2.8	33
13	More compact protein globules exhibit slower folding rates. <i>Proteins: Structure, Function and Bioinformatics</i> , 2008, 70, 329-332.	2.6	32
14	Entropy capacity determines protein folding. <i>Proteins: Structure, Function and Bioinformatics</i> , 2006, 63, 144-154.	2.6	31
15	ComSin: database of protein structures in bound (complex) and unbound (single) states in relation to their intrinsic disorder. <i>Nucleic Acids Research</i> , 2010, 38, D283-D287.	14.5	31
16	IS IT POSSIBLE TO PREDICT AMYLOIDOGENIC REGIONS FROM SEQUENCE ALONE?. <i>Journal of Bioinformatics and Computational Biology</i> , 2006, 04, 373-388.	0.8	26
17	Backbone Carbonyl Group Basicities Are Related to Gas-Phase Fragmentation of Peptides and Protein Folding. <i>Angewandte Chemie - International Edition</i> , 2007, 46, 1481-1484.	13.8	25
18	Restrictions to protein folding determined by the protein size. <i>FEBS Letters</i> , 2013, 587, 1884-1890.	2.8	19

#	ARTICLE	IF	CITATIONS
19	Understanding the Folding Rates and Folding Nuclei of Globular Proteins. <i>Current Protein and Peptide Science</i> , 2007, 8, 521-536.	1.4	18
20	Reduction of the Search Space for the Folding of Proteins at the Level of Formation and Assembly of Secondary Structures: A New View on the Solution of Levinthal's Paradox. <i>ChemPhysChem</i> , 2015, 16, 3375-3378.	2.1	16
21	A search for amyloidogenic regions in protein chains. <i>Molecular Biology</i> , 2006, 40, 821-828.	1.3	15
22	Theoretical study of protein folding: outlining folding nuclei and estimation of protein folding rates. <i>Journal of Physics Condensed Matter</i> , 2005, 17, S1539-S1551.	1.8	10
23	Prediction of amino acid residues protected from hydrogen-deuterium exchange in a protein chain. <i>Biochemistry (Moscow)</i> , 2009, 74, 888-897.	1.5	9
24	Statistical analysis of unstructured amino acid residues in protein structures. <i>Biochemistry (Moscow)</i> , 2010, 75, 192-200.	1.5	9
25	Structural features of protein folding nuclei. <i>FEBS Letters</i> , 2008, 582, 768-772.	2.8	7
26	Levinthal's question answered – again?. <i>Journal of Biomolecular Structure and Dynamics</i> , 2013, 31, 1013-1015.	3.5	7
27	The difference between protein structures obtained by x-ray analysis and nuclear magnetic resonance. <i>Molecular Biology</i> , 2005, 39, 113-122.	1.3	6
28	Expected packing density allows prediction of both amyloidogenic and disordered regions in protein chains. <i>Journal of Physics Condensed Matter</i> , 2007, 19, 285225.	1.8	6
29	Calculation of mobility and entropy of the binding of molecules by crystals. <i>Molecular Biology</i> , 2016, 50, 452-461.	1.3	5
30	Sublimation Entropy and Dissociation Constants Prediction by Quantitative Evaluation of Molecular Mobility in Crystals. <i>Journal of Physical Chemistry Letters</i> , 2017, 8, 2758-2763.	4.6	4
31	How Can Ice Emerge at 0 Å°C?. <i>Biomolecules</i> , 2022, 12, 981.	4.0	3
32	Two Views on the Protein Folding Puzzle. , 2018, , 391-412.		0
33	Protein Structure and Its Folding Rate. , 2008, , 273-301.		0
34	Calculation of Crystal-Solution Dissociation Constants. <i>Biomolecules</i> , 2022, 12, 147.	4.0	0