

Sergiy O Garbuzynskiy

List of Publications by Year in descending order

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34
papers

1,875
citations

430442

18
h-index

433756

31
g-index

35
all docs

35
docs citations

35
times ranked

1942
citing authors

#	ARTICLE	IF	CITATIONS
1	Calculation of Crystal-Solution Dissociation Constants. <i>Biomolecules</i> , 2022, 12, 147.	1.8	0
2	How Can Ice Emerge at 0 Å°C?. <i>Biomolecules</i> , 2022, 12, 981.	1.8	3
3	Two Views on the Protein Folding Puzzle. , 2018, , 391-412.		0
4	There and back again: Two views on the protein folding puzzle. <i>Physics of Life Reviews</i> , 2017, 21, 56-71.	1.5	33
5	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.	2.1	4
6	Calculation of mobility and entropy of the binding of molecules by crystals. <i>Molecular Biology</i> , 2016, 50, 452-461.	0.4	5
7	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.	1.0	16
8	Restrictions to protein folding determined by the protein size. <i>FEBS Letters</i> , 2013, 587, 1884-1890.	1.3	19
9	Levinthal's question answered again?. <i>Journal of Biomolecular Structure and Dynamics</i> , 2013, 31, 1013-1015.	2.0	7
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.	3.3	58
11	Statistical analysis of unstructured amino acid residues in protein structures. <i>Biochemistry (Moscow)</i> , 2010, 75, 192-200.	0.7	9
12	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.	6.5	31
13	FoldAmyloid: a method of prediction of amyloidogenic regions from protein sequence. <i>Bioinformatics</i> , 2010, 26, 326-332.	1.8	338
14	Intrinsic Disorder in Protein Interactions: Insights From a Comprehensive Structural Analysis. <i>PLoS Computational Biology</i> , 2009, 5, e1000316.	1.5	104
15	Prediction of amino acid residues protected from hydrogen-deuterium exchange in a protein chain. <i>Biochemistry (Moscow)</i> , 2009, 74, 888-897.	0.7	9
16	More compact protein globules exhibit slower folding rates. <i>Proteins: Structure, Function and Bioinformatics</i> , 2008, 70, 329-332.	1.5	32
17	To be folded or to be unfolded?. <i>Protein Science</i> , 2008, 13, 2871-2877.	3.1	69
18	Structural features of protein folding nuclei. <i>FEBS Letters</i> , 2008, 582, 768-772.	1.3	7

#	ARTICLE	IF	CITATIONS
19	Protein Structure and Its Folding Rate. , 2008, , 273-301.		0
20	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.	1.8	89
21	Understanding the Folding Rates and Folding Nuclei of Globular Proteins. <i>Current Protein and Peptide Science</i> , 2007, 8, 521-536.	0.7	18
22	Expected packing density allows prediction of both amyloidogenic and disordered regions in protein chains. <i>Journal of Physics Condensed Matter</i> , 2007, 19, 285225.	0.7	6
23	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.	7.2	25
24	FoldUnfold: web server for the prediction of disordered regions in protein chain. <i>Bioinformatics</i> , 2006, 22, 2948-2949.	1.8	148
25	Entropy capacity determines protein folding. <i>Proteins: Structure, Function and Bioinformatics</i> , 2006, 63, 144-154.	1.5	31
26	A search for amyloidogenic regions in protein chains. <i>Molecular Biology</i> , 2006, 40, 821-828.	0.4	15
27	Prediction of Amyloidogenic and Disordered Regions in Protein Chains. <i>PLoS Computational Biology</i> , 2006, 2, e177.	1.5	155
28	IS IT POSSIBLE TO PREDICT AMYLOIDOGENIC REGIONS FROM SEQUENCE ALONE?. <i>Journal of Bioinformatics and Computational Biology</i> , 2006, 04, 373-388.	0.3	26
29	The difference between protein structures obtained by x-ray analysis and nuclear magnetic resonance. <i>Molecular Biology</i> , 2005, 39, 113-122.	0.4	6
30	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.	1.5	78
31	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.	0.7	10
32	Outlining Folding Nuclei in Globular Proteins. <i>Journal of Molecular Biology</i> , 2004, 336, 509-525.	2.0	57
33	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
34	Contact order revisited: Influence of protein size on the folding rate. <i>Protein Science</i> , 2003, 12, 2057-2062.	3.1	327