Sergiy O Garbuzynskiy

List of Publications by Year
in descending order

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	Calculation of Crystal-Solution Dissociation Constants. Biomolecules, 2022, 12, 147.	4.0	0
2	How Can Ice Emerge at 0 Â°C?. Biomolecules, 2022, 12, 981.	4.0	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. Physics of Life Reviews, 2017, 21, 56-71.	2.8	33
5	Sublimation Entropy and Dissociation Constants Prediction by Quantitative Evaluation of Molecular Mobility in Crystals. Journal of Physical Chemistry Letters, 2017, 8, 2758-2763.	4.6	4
6	Calculation of mobility and entropy of the binding of molecules by crystals. Molecular Biology, 2016, 50, 452-461.	1.3	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 Levinthalâ€²s Paradox. ChemPhysChem, 2015, 16, 3375-3378.	2.1	16
8	Restrictions to protein folding determined by the protein size. FEBS Letters, 2013, 587, 1884-1890.	2.8	19
9	Levinthalâ€™s question answered â€¦ again?. Journal of Biomolecular Structure and Dynamics, 2013, 31, 1013-1015.	3.5	7
10	Golden triangle for folding rates of globular proteins. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 147-150.	7.1	58
11	Statistical analysis of unstructured amino acid residues in protein structures. Biochemistry (Moscow), 2010, 75, 192-200.	1.5	9
12	ComSin: database of protein structures in bound (complex) and unbound (single) states in relation to their intrinsic disorder. Nucleic Acids Research, 2010, 38, D283-D287.	14.5	31
13	FoldAmyloid: a method of prediction of amyloidogenic regions from protein sequence. Bioinformatics, 2010, 26, 326-332.	4.1	338
14	Intrinsic Disorder in Protein Interactions: Insights From a Comprehensive Structural Analysis. PLoS Computational Biology, 2009, 5, e1000316.	3.2	104
15	Prediction of amino acid residues protected from hydrogen-deuterium exchange in a protein chain. Biochemistry (Moscow), 2009, 74, 888-897.	1.5	9
16	More compact protein globules exhibit slower folding rates. Proteins: Structure, Function and Bioinformatics, 2008, 70, 329-332.	2.6	32
17	To be folded or to be unfolded?. Protein Science, 2008, 13, 2871-2877.	7.6	69
18	Structural features of protein folding nuclei. FEBS Letters, 2008, 582, 768-772.	2.8	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. Bioinformatics, 2007, 23, 2231-2238.	4.1	89
21	Understanding the Folding Rates and Folding Nuclei of Globular Proteins. Current Protein and Peptide Science, 2007, 8, 521-536.	1.4	18
22	Expected packing density allows prediction of both amyloidogenic and disordered regions in protein chains. Journal of Physics Condensed Matter, 2007, 19, 285225.	1.8	6
23	Backbone Carbonyl Group Basicities Are Related to Gas-Phase Fragmentation of Peptides and Protein Folding. Angewandte Chemie - International Edition, 2007, 46, 1481-1484.	13.8	25
24	FoldUnfold: web server for the prediction of disordered regions in protein chain. Bioinformatics, 2006, 22, 2948-2949.	4.1	148
25	Entropy capacity determines protein folding. Proteins: Structure, Function and Bioinformatics, 2006, 63, 144-154.	2.6	31
26	A search for amyloidogenic regions in protein chains. Molecular Biology, 2006, 40, 821-828.	1.3	15
27	Prediction of Amyloidogenic and Disordered Regions in Protein Chains. PLoS Computational Biology, 2006, 2, e177.	3.2	155
28	IS IT POSSIBLE TO PREDICT AMYLOIDOGENIC REGIONS FROM SEQUENCE ALONE?. Journal of Bioinformatics and Computational Biology, 2006, 04, 373-388.	0.8	26
29	The difference between protein structures obtained by x-ray analysis and nuclear magnetic resonance. Molecular Biology, 2005, 39, 113-122.	1.3	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?. Proteins: Structure, Function and Bioinformatics, 2005, 60, 139-147.	2.6	78
31	Theoretical study of protein folding: outlining folding nuclei and estimation of protein folding rates. Journal of Physics Condensed Matter, 2005, 17, S1539-S1551.	1.8	10
32	Outlining Folding Nuclei in Globular Proteins. Journal of Molecular Biology, 2004, 336, 509-525.	4.2	57
33	Chain length is the main determinant of the folding rate for proteins with three-state folding kinetics. Proteins: Structure, Function and Bioinformatics, 2003, 51, 162-166.	2.6	140
34	Contact order revisited: Influence of protein size on the folding rate. Protein Science, 2003, 12, 2057-2062.	7.6	327