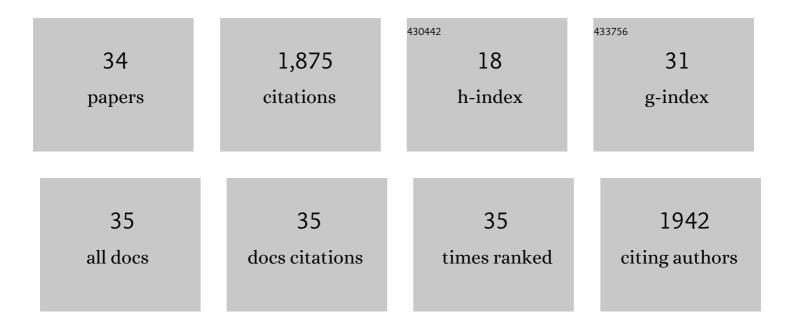
Sergiy O Garbuzynskiy

List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	FoldAmyloid: a method of prediction of amyloidogenic regions from protein sequence. Bioinformatics, 2010, 26, 326-332.	1.8	338
2	Contact order revisited: Influence of protein size on the folding rate. Protein Science, 2003, 12, 2057-2062.	3.1	327
3	Prediction of Amyloidogenic and Disordered Regions in Protein Chains. PLoS Computational Biology, 2006, 2, e177.	1.5	155
4	FoldUnfold: web server for the prediction of disordered regions in protein chain. Bioinformatics, 2006, 22, 2948-2949.	1.8	148
5	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.	1.5	140
6	Intrinsic Disorder in Protein Interactions: Insights From a Comprehensive Structural Analysis. PLoS Computational Biology, 2009, 5, e1000316.	1.5	104
7	Different packing of external residues can explain differences in the thermostability of proteins from thermophilic and mesophilic organisms. Bioinformatics, 2007, 23, 2231-2238.	1.8	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?. Proteins: Structure, Function and Bioinformatics, 2005, 60, 139-147.	1.5	78
9	To be folded or to be unfolded?. Protein Science, 2008, 13, 2871-2877.	3.1	69
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.	3.3	58
11	Outlining Folding Nuclei in Globular Proteins. Journal of Molecular Biology, 2004, 336, 509-525.	2.0	57
12	There and back again: Two views on the protein folding puzzle. Physics of Life Reviews, 2017, 21, 56-71.	1.5	33
13	More compact protein globules exhibit slower folding rates. Proteins: Structure, Function and Bioinformatics, 2008, 70, 329-332.	1.5	32
14	Entropy capacity determines protein folding. Proteins: Structure, Function and Bioinformatics, 2006, 63, 144-154.	1.5	31
15	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.	6.5	31
16	IS IT POSSIBLE TO PREDICT AMYLOIDOGENIC REGIONS FROM SEQUENCE ALONE?. Journal of Bioinformatics and Computational Biology, 2006, 04, 373-388.	0.3	26
17	Backbone Carbonyl Group Basicities Are Related to Gas-Phase Fragmentation of Peptides and Protein Folding. Angewandte Chemie - International Edition, 2007, 46, 1481-1484.	7.2	25
18	Restrictions to protein folding determined by the protein size. FEBS Letters, 2013, 587, 1884-1890.	1.3	19

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#	Article	IF	CITATIONS
19	Understanding the Folding Rates and Folding Nuclei of Globular Proteins. Current Protein and Peptide Science, 2007, 8, 521-536.	0.7	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. ChemPhysChem, 2015, 16, 3375-3378.	1.0	16
21	A search for amyloidogenic regions in protein chains. Molecular Biology, 2006, 40, 821-828.	0.4	15
22	Theoretical study of protein folding: outlining folding nuclei and estimation of protein folding rates. Journal of Physics Condensed Matter, 2005, 17, S1539-S1551.	0.7	10
23	Prediction of amino acid residues protected from hydrogen-deuterium exchange in a protein chain. Biochemistry (Moscow), 2009, 74, 888-897.	0.7	9
24	Statistical analysis of unstructured amino acid residues in protein structures. Biochemistry (Moscow), 2010, 75, 192-200.	0.7	9
25	Structural features of protein folding nuclei. FEBS Letters, 2008, 582, 768-772.	1.3	7
26	Levinthal's question answered … again?. Journal of Biomolecular Structure and Dynamics, 2013, 31, 1013-1015.	2.0	7
27	The difference between protein structures obtained by x-ray analysis and nuclear magnetic resonance. Molecular Biology, 2005, 39, 113-122.	0.4	6
28	Expected packing density allows prediction of both amyloidogenic and disordered regions in protein chains. Journal of Physics Condensed Matter, 2007, 19, 285225.	0.7	6
29	Calculation of mobility and entropy of the binding of molecules by crystals. Molecular Biology, 2016, 50, 452-461.	0.4	5
30	Sublimation Entropy and Dissociation Constants Prediction by Quantitative Evaluation of Molecular Mobility in Crystals. Journal of Physical Chemistry Letters, 2017, 8, 2758-2763.	2.1	4
31	How Can Ice Emerge at 0 °C?. Biomolecules, 2022, 12, 981.	1.8	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. Biomolecules, 2022, 12, 147.	1.8	0