

Sergiy O Garbuzynskiy

List of Publications by Year in descending order

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Version: 2024-02-01

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 | FoldAmyloid: a method of prediction of amyloidogenic regions from protein sequence. <i>Bioinformatics</i> , 2010, 26, 326-332. | 1.8 | 338 |
| 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 Amyloidogenic and Disordered Regions in Protein Chains. <i>PLoS Computational Biology</i> , 2006, 2, e177. | 1.5 | 155 |
| 4 | FoldUnfold: web server for the prediction of disordered regions in protein chain. <i>Bioinformatics</i> , 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. <i>Proteins: Structure, Function and Bioinformatics</i> , 2003, 51, 162-166. | 1.5 | 140 |
| 6 | Intrinsic Disorder in Protein Interactions: Insights From a Comprehensive Structural Analysis. <i>PLoS Computational Biology</i> , 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. <i>Bioinformatics</i> , 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?. <i>Proteins: Structure, Function and Bioinformatics</i> , 2005, 60, 139-147. | 1.5 | 78 |
| 9 | To be folded or to be unfolded?. <i>Protein Science</i> , 2008, 13, 2871-2877. | 3.1 | 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. | 3.3 | 58 |
| 11 | Outlining Folding Nuclei in Globular Proteins. <i>Journal of Molecular Biology</i> , 2004, 336, 509-525. | 2.0 | 57 |
| 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 | Entropy capacity determines protein folding. <i>Proteins: Structure, Function and Bioinformatics</i> , 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. <i>Nucleic Acids Research</i> , 2010, 38, D283-D287. | 6.5 | 31 |
| 16 | IS IT POSSIBLE TO PREDICT AMYLOIDOGENIC REGIONS FROM SEQUENCE ALONE?. <i>Journal of Bioinformatics and Computational Biology</i> , 2006, 04, 373-388. | 0.3 | 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. | 7.2 | 25 |
| 18 | Restrictions to protein folding determined by the protein size. <i>FEBS Letters</i> , 2013, 587, 1884-1890. | 1.3 | 19 |

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|----|---|-----|-----------|
| 19 | Understanding the Folding Rates and Folding Nuclei of Globular Proteins. <i>Current Protein and Peptide Science</i> , 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. <i>ChemPhysChem</i> , 2015, 16, 3375-3378. | 1.0 | 16 |
| 21 | A search for amyloidogenic regions in protein chains. <i>Molecular Biology</i> , 2006, 40, 821-828. | 0.4 | 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. | 0.7 | 10 |
| 23 | 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 |
| 24 | Statistical analysis of unstructured amino acid residues in protein structures. <i>Biochemistry (Moscow)</i> , 2010, 75, 192-200. | 0.7 | 9 |
| 25 | Structural features of protein folding nuclei. <i>FEBS Letters</i> , 2008, 582, 768-772. | 1.3 | 7 |
| 26 | Levinthal's question answered – again?. <i>Journal of Biomolecular Structure and Dynamics</i> , 2013, 31, 1013-1015. | 2.0 | 7 |
| 27 | 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 |
| 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. | 0.7 | 6 |
| 29 | Calculation of mobility and entropy of the binding of molecules by crystals. <i>Molecular Biology</i> , 2016, 50, 452-461. | 0.4 | 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. | 2.1 | 4 |
| 31 | How Can Ice Emerge at 0 Å°C?. <i>Biomolecules</i> , 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. <i>Biomolecules</i> , 2022, 12, 147. | 1.8 | 0 |