Oxana V Galzitskaya

List of Publications by Year
in descending order

156 papers	3,582 citations	159358 30 h-index	182168 51 g-index
159 all docs	159 docs citations	159 times ranked	3436 citing authors

#	Article	IF	Citations
1	FoldAmyloid: a method of prediction of amyloidogenic regions from protein sequence. Bioinformatics, 2010, 26, 326-332.	1.8	338
2	Prediction of Amyloidogenic and Disordered Regions in Protein Chains. PLoS Computational Biology, 2006, 2, e177.	1.5	155
3	FoldUnfold: web server for the prediction of disordered regions in protein chain. Bioinformatics, 2006, 22, 2948-2949.	1.8	148
4	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
5	Intrinsic Disorder in Protein Interactions: Insights From a Comprehensive Structural Analysis. PLoS Computational Biology, 2009, 5, e1000316.	1.5	104
6	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
7	TREND OF AMINO ACID COMPOSITION OF PROTEINS OF DIFFERENT TAXA. Journal of Bioinformatics and Computational Biology, 2006, 04, 597-608.	0.3	82
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	Folding nuclei in proteins. FEBS Letters, 2001, 489, 113-118.	1.3	72
10	To be folded or to be unfolded?. Protein Science, 2008, 13, 2871-2877.	3.1	69
11	The Ising model for prediction of disordered residues from protein sequence alone. Physical Biology, 2011, 8, 035004.	0.8	64
12	Coupling between Properties of the Protein Shape and the Rate of Protein Folding. PLoS ONE, 2009, 4, e6476.	1.1	62
13	Library of Disordered Patterns in 3D Protein Structures. PLoS Computational Biology, 2010, 6, e1000958.	1.5	60
14	Prediction of protein domain boundaries from sequence alone. Protein Science, 2003, 12, 696-701.	3.1	58
15	Megahertz single-particle imaging at the European XFEL. Communications Physics, 2020, 3, .	2.0	58
16	Outlining Folding Nuclei in Globular Proteins. Journal of Molecular Biology, 2004, 336, 509-525.	2.0	57
17	The role of Î²-amyloid peptide in neurodegenerative diseases. Ageing Research Reviews, 2011, 10, 440-452.	5.0	49
18	IsUnstruct: prediction of the residue status to be ordered or disordered in the protein chain by a method based on the Ising model. Journal of Biomolecular Structure and Dynamics, 2013, 31, 1034-1043.	2.0	48

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19	How to Determine the Size of Folding Nuclei of Protofibrils from the Concentration Dependence of the Rate and Lag-Time of Aggregation. I. Modeling the Amyloid Protofibril Formation. Journal of Physical Chemistry B, 2014, 118, 1189-1197.	1.2	48
20	Antimicrobial and Amyloidogenic Activity of Peptides. Can Antimicrobial Peptides Be Used against SARS-CoV-2?. International Journal of Molecular Sciences, 2020, 21, 9552.	1.8	45
21	Stability and rigidity/flexibilityâ€"Two sides of the same coin?. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2013, 1834, 854-866.	1.1	43
22	Proteome evolution of deep-sea hydrothermal vent alvinellid polychaetes supports the ancestry of thermophily and subsequent adaptation to cold in some lineages. Genome Biology and Evolution, 2017, 9, evw298.	1.1	39
23	Energy landscape of a Î²-hairpin peptide in explicit water studied by multicanonical molecular dynamics. Chemical Physics Letters, 2001, 337, 169-175.	1.2	38
24	One of the possible mechanisms of amyloid fibrils formation based on the sizes of primary and secondary folding nuclei of AÎ²40 and AÎ²42. Journal of Structural Biology, 2016, 194, 404-414.	1.3	37
25	Structure and functions of syndecans in vertebrates. Biochemistry (Moscow), 2013, 78, 1071-1085.	0.7	35
26	There and back again: Two views on the protein folding puzzle. Physics of Life Reviews, 2017, 21, 56-71.	1.5	33
27	To Be Fibrils or To Be Nanofilms? Oligomers Are Building Blocks for Fibril and Nanofilm Formation of Fragments of AÎ² Peptide. Langmuir, 2018, 34, 2332-2343.	1.6	33
28	More compact protein globules exhibit slower folding rates. Proteins: Structure, Function and Bioinformatics, 2008, 70, 329-332.	1.5	32
29	Studies of Polymorphism of Amyloid-Î² 42 Peptide from Different Suppliers. Journal of Alzheimer's Disease, 2015, 47, 583-593.	1.2	32
30	Non-random distribution of homo-repeats: links with biological functions and human diseases. Scientific Reports, 2016, 6, 26941.	1.6	32
31	α-Helix and β-Hairpin Folding from Experiment, Analytical Theory and Molecular Dynamics Simulations. Current Protein and Peptide Science, 2002, 3, 191-200.	0.7	32
32	Entropy capacity determines protein folding. Proteins: Structure, Function and Bioinformatics, 2006, 63, 144-154.	1.5	31
33	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
34	Hyperphosphorylation induces structural modification of tau-protein. FEBS Letters, 1998, 439, 21-25.	1.3	30
35	?-Hairpins, ?-helices, and the intermediates among the secondary structures in the energy landscape of a peptide from a distal ?-hairpin of SH3 domain. Journal of Computational Chemistry, 2003, 24, 310-318.	1.5	30
36	HRaP: database of occurrence of HomoRepeats and patterns in proteomes. Nucleic Acids Research, 2014, 42, D273-D278.	6.5	30

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37	The Mechanism Underlying Amyloid Polymorphism is Opened for Alzheimerâ€™s Disease Amyloid-Î² Peptide. Journal of Alzheimer's Disease, 2016, 54, 821-830.	1.2	30
38	Folding of chains with random and edited sequences: similarities and differences. Protein Engineering, Design and Selection, 1995, 8, 883-892.	1.0	29
39	Optimal region of average sideâ€chain entropy for fast protein folding. Protein Science, 2000, 9, 580-586.	3.1	29
40	Structural polymorphism and possible pathways of amyloid fibril formation on the example of insulin protein. Biochemistry (Moscow), 2012, 77, 1237-1247.	0.7	29
41	How to Determine the Size of Folding Nuclei of Protofibrils from the Concentration Dependence of the Rate and Lag-Time of Aggregation. II. Experimental Application for Insulin and LysPro Insulin: Aggregation Morphology, Kinetics, and Sizes of Nuclei. Journal of Physical Chemistry B, 2014, 118, 1198-1206.	1.2	27
42	IS IT POSSIBLE TO PREDICT AMYLOIDOGENIC REGIONS FROM SEQUENCE ALONE?. Journal of Bioinformatics and Computational Biology, 2006, 04, 373-388.	0.3	26
43	Amyloid-like properties ofSaccharomyces cerevisiaecell wall glucantransferase Bgl2p. Prion, 2008, 2, 91-96.	0.9	26
44	Rosetta Stone for Amyloid Fibrils: The Key Role of Ring-Like Oligomers in Amyloidogenesis. Journal of Alzheimer's Disease, 2017, 59, 785-795.	1.2	26
45	How Common Is Disorder? Occurrence of Disordered Residues in Four Domains of Life. International Journal of Molecular Sciences, 2015, 16, 19490-19507.	1.8	24
46	Haloarcula marismortui archaellin genes as ecoparalogs. Extremophiles, 2014, 18, 341-349.	0.9	22
47	Structural model of amyloid fibrils for amyloidogenic peptide from Bgl2pâ€“glucantransferase of S. cerevisiae cell wall and its modifying analog. New morphology of amyloid fibrils. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2016, 1864, 1489-1499.	1.1	22
48	COMPACTNESS DETERMINES PROTEIN FOLDING TYPE. Journal of Bioinformatics and Computational Biology, 2008, 06, 667-680.	0.3	21
49	Amyloidogenic peptides of yeast cell wall glucantransferase Bgl2p as a model for the investigation of its pH-dependent fibril formation. Prion, 2013, 7, 175-184.	0.9	21
50	Disordered Patterns in Clustered Protein Data Bank and in Eukaryotic and Bacterial Proteomes. PLoS ONE, 2011, 6, e27142.	1.1	20
51	Computational Approaches to Identification of Aggregation Sites and the Mechanism of Amyloid Growth. Advances in Experimental Medicine and Biology, 2015, 855, 213-239.	0.8	19
52	MIRRAGGE â€“ Minimum Information Required for Reproducible AGGregation Experiments. Frontiers in Molecular Neuroscience, 2020, 13, 582488.	1.4	19
53	Understanding the Folding Rates and Folding Nuclei of Globular Proteins. Current Protein and Peptide Science, 2007, 8, 521-536.	0.7	18
54	The binding of monomeric amyloid Î² peptide to serum albumin is affected by major plasma unsaturated fatty acids. Biochemical and Biophysical Research Communications, 2019, 510, 248-253.	1.0	18

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55	The number of domains in the ribosomal protein S1 as a hallmark of the phylogenetic grouping of bacteria. PLoS ONE, 2019, 14, e0221370.	1.1	18
56	Amyloidogenic Propensities of Ribosomal S1 Proteins: Bioinformatics Screening and Experimental Checking. International Journal of Molecular Sciences, 2020, 21, 5199.	1.8	18
57	Antimicrobial and Amyloidogenic Activity of Peptides Synthesized on the Basis of the Ribosomal S1 Protein from Thermus Thermophilus. International Journal of Molecular Sciences, 2020, 21, 6382.	1.8	18
58	<scp>T</scp>axonomic distribution, repeats, and functions of the S1 domainâ€containing proteins as members of the OBâ€fold family. Proteins: Structure, Function and Bioinformatics, 2017, 85, 602-613.	1.5	17
59	Î²-hairpin folds by molecular dynamics simulations. Chemical Physics Letters, 2000, 326, 421-429.	1.2	16
60	Cell communication using intrinsically disordered proteins: what can syndecans say?. Journal of Biomolecular Structure and Dynamics, 2015, 33, 1037-1050.	2.0	16
61	New Mechanism of Amyloid Fibril Formation. Current Protein and Peptide Science, 2019, 20, 630-640.	0.7	16
62	Mechanisms of amyloid fibril formation. Biochemistry (Moscow), 2014, 79, 1515-1527.	0.7	15
63	Repeats in S1 Proteins: Flexibility and Tendency for Intrinsic Disorder. International Journal of Molecular Sciences, 2019, 20, 2377.	1.8	15
64	Oligomers Are Promising Targets for Drug Development in the Treatment of Proteinopathies. Frontiers in Molecular Neuroscience, 2019, 12, 319.	1.4	15
65	Solution conformation of phakellistatin 8 investigated by molecular dynamics simulations. Journal of Molecular Graphics and Modelling, 1999, 17, 19-27.	1.3	14
66	FLEXIBILITY AND MOBILITY IN MESOPHILIC AND THERMOPHILIC HOMOLOGOUS PROTEINS FROM MOLECULAR DYNAMICS AND FOLDUNFOLD METHOD. Journal of Bioinformatics and Computational Biology, 2010, 08, 377-394.	0.3	14
67	Role of Syndecans in Lipid Metabolism and Human Diseases. Advances in Experimental Medicine and Biology, 2015, 855, 241-258.	0.8	14
68	Insulin and Lispro Insulin: What is Common and Different in their Behavior?. Current Protein and Peptide Science, 2016, 18, 57-64.	0.7	14
69	Determination of size of folding nuclei of fibrils formed from recombinant AÎ²(1-40) peptide. Biochemistry (Moscow), 2016, 81, 538-547.	0.7	14
70	Smooth muscle titin formsinÂvitroamyloid aggregates. Bioscience Reports, 2016, 36, .	1.1	14
71	Determination of regions involved in amyloid fibril formation for AÎ²(1-40) peptide. Biochemistry (Moscow), 2016, 81, 762-769.	0.7	14
72	A novel web server predicts amino acid residue protection against hydrogenâ€“deuterium exchange. Bioinformatics, 2013, 29, 1375-1381.	1.8	13

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73	Should the Treatment of Amyloidosis Be Personified? Molecular Mechanism of Amyloid Formation by AÎ² Peptide and Its Fragments. Journal of Alzheimer's Disease Reports, 2018, 2, 181-199.	1.2	13
74	Determination of amyloid core regions of insulin analogues fibrils. Prion, 2020, 14, 149-162.	0.9	13
75	Structural and Functional Peculiarities of Î±-Crystallin. Biology, 2020, 9, 85.	1.3	13
76	Folding rate dependence on the chain length for RNA-like heteropolymers. Folding & Design, 1998, 3, 69-78.	4.5	12
77	Repeats are one of the main characteristics of RNA-binding proteins with prion-like domains. Molecular BioSystems, 2015, 11, 2210-2218.	2.9	12
78	Comparative Analysis of Proteomes of a Number of Nosocomial Pathogens by KEGG Modules and KEGG Pathways. International Journal of Molecular Sciences, 2020, 21, 7839.	1.8	12
79	Multiple Antimicrobial Effects of Hybrid Peptides Synthesized Based on the Sequence of Ribosomal S1 Protein from Staphylococcus aureus. International Journal of Molecular Sciences, 2022, 23, 524.	1.8	12
80	Two-, Three-, and Four-State Events Occur in the Mechanical Unfolding of Small Protein L Using Molecular Dynamics Simulations. Protein and Peptide Letters, 2010, 17, 92-103.	0.4	11
81	Influence of Conformational Entropy on the Protein Folding Rate. Entropy, 2010, 12, 961-982.	1.1	11
82	Accessible Surfaces of Beta Proteins Increase with Increasing Protein Molecular Mass More Rapidly than Those of Other Proteins. PLoS ONE, 2011, 6, e28464.	1.1	11
83	Investigation of the Relationship between the S1 Domain and Its Molecular Functions Derived from Studies of the Tertiary Structure. Molecules, 2019, 24, 3681.	1.7	11
84	Is It Possible to Create Antimicrobial Peptides Based on the Amyloidogenic Sequence of Ribosomal S1 Protein of P. aeruginosa?. International Journal of Molecular Sciences, 2021, 22, 9776.	1.8	11
85	Roughness of the globular protein surface: Analysis of high resolution X-ray data. Proteins: Structure, Function and Bioinformatics, 1997, 28, 194-201.	1.5	10
86	Right- and left-handed three-helix proteins. II. Similarity and differences in mechanical unfolding of proteins. Proteins: Structure, Function and Bioinformatics, 2014, 82, 90-102.	1.5	10
87	Studies of the Process of Amyloid Formation by AÎ² Peptide. Biochemistry (Moscow), 2018, 83, S62-S80.	0.7	10
88	Identification of Amyloidogenic Regions in the Spine of Insulin Fibrils. Biochemistry (Moscow), 2019, 84, 47-55.	0.7	10
89	Prediction of Residue Status to Be Protected or Not Protected From Hydrogen Exchange Using Amino Acid Sequence Only. The Open Biochemistry Journal, 2008, 2, 77-80.	0.3	10
90	Prediction of amino acid residues protected from hydrogen-deuterium exchange in a protein chain. Biochemistry (Moscow), 2009, 74, 888-897.	0.7	9

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91	Statistical analysis of unstructured amino acid residues in protein structures. Biochemistry (Moscow), 2010, 75, 192-200.	0.7	9
92	Nucleationâ€based prediction of the protein folding rate and its correlation with the folding nucleus size. Proteins: Structure, Function and Bioinformatics, 2012, 80, 2711-2727.	1.5	9
93	An N-terminal, 830 residues intrinsically disordered region of the cytoskeleton-regulatory protein supervillin contains Myosin II- and F-actin-binding sites. Journal of Biomolecular Structure and Dynamics, 2013, 31, 1150-1159.	2.0	9
94	Activation of Neuronal Defense Mechanisms in Response to Pathogenic Factors Triggering Induction of Amyloidosis in Alzheimer's Disease. Journal of Alzheimer's Disease, 2014, 40, 19-32.	1.2	9
95	X-ray diffraction and electron microscopy data for amyloid formation of AÎ²40 and AÎ²42. Data in Brief, 2016, 8, 108-113.	0.5	9
96	Î±-Crystallins are small heat shock proteins: Functional and structural properties. Biochemistry (Moscow), 2017, 82, 106-121.	0.7	9
97	Comparative mechanical unfolding studies of spectrin domains R15, R16 and R17. Journal of Structural Biology, 2018, 201, 162-170.	1.3	9
98	Analysis of Insulin Analogs and the Strategy of Their Further Development. Biochemistry (Moscow), 2018, 83, S146-S162.	0.7	9
99	Computer simulation of secondary structure folding of random and â€˜â€˜editedâ€™â€™ RNA chains. Journal of Chemical Physics, 1996, 105, 319-325.	1.2	8
100	General Dynamic Properties of AÂ12-36 Amyloid Peptide Involved in Alzheimer's Disease from Unfolding Simulation. Journal of Biochemistry, 2004, 136, 583-594.	0.9	8
101	PREDICTION OF LOOP REGIONS IN PROTEIN SEQUENCE. Journal of Bioinformatics and Computational Biology, 2008, 06, 1035-1047.	0.3	8
102	Bioinformatics Analysis of Actin Molecules: Why Quantity Does Not Translate Into Quality?. Frontiers in Genetics, 2020, 11, 617763.	1.1	8
103	Comparative Analysis of Aggregation of Thermus thermophilus Ribosomal Protein bS1 and Its Stable Fragment. Biochemistry (Moscow), 2020, 85, 344-354.	0.7	8
104	Identification of Amyloidogenic Regions in Pseudomonas aeruginosa Ribosomal S1 Protein. International Journal of Molecular Sciences, 2021, 22, 7291.	1.8	8
105	Exploring Amyloidogenicity of Peptides From Ribosomal S1 Protein to Develop Novel AMPs. Frontiers in Molecular Biosciences, 2021, 8, 705069.	1.6	8
106	Multiple Unfolding Intermediates Obtained by Molecular Dynamic Simulations under Stretching for Immunoglobulin-Binding Domain of Protein G. The Open Biochemistry Journal, 2009, 3, 66-77.	0.3	8
107	How Quickly Do Proteins Fold and Unfold, and What Structural Parameters Correlate with These Values?. Biomolecules, 2020, 10, 197.	1.8	8
108	Amyloidogenic Peptides: New Class of Antimicrobial Peptides with the Novel Mechanism of Activity. International Journal of Molecular Sciences, 2022, 23, 5463.	1.8	8

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109	Geometrical factor and physical reasons for its influence on the kinetic and thermodynamic properties of RNA-like heteropolymers. Folding & Design, 1997, 2, 193-201.	4.5	7
110	Prediction of Number and Position of Domain Boundaries in Multi-Domain Proteins by Use of Amino Acid Sequence Alone. Current Protein and Peptide Science, 2007, 8, 189-195.	0.7	7
111	Estimation of Protein Folding Rate from Monte Carlo Simulations and Entropy Capacity. Current Protein and Peptide Science, 2010, 11, 523-537.	0.7	7
112	Search for conserved amino acid residues of the Î±-crystallin proteins of vertebrates. Journal of Bioinformatics and Computational Biology, 2016, 14, 1641004.	0.3	7
113	Disordered Residues and Patterns in the Protein Data Bank. Molecules, 2020, 25, 1522.	1.7	7
114	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
115	SEARCH FOR FOLDING INITIATION SITES FROM AMINO ACID SEQUENCE. Journal of Bioinformatics and Computational Biology, 2008, 06, 681-691.	0.3	6
116	A COMPARATIVE ANALYSIS OF FOLDING PATHWAYS OF THERMOPHILIC AND MESOPHILIC PROTEINS BY MONTE CARLO SIMULATIONS. Journal of Bioinformatics and Computational Biology, 2010, 08, 395-411.	0.3	6
117	Rightâ€•and leftâ€handed threeâ€helix proteins. I. Experimental and simulation analysis of differences in folding and structure. Proteins: Structure, Function and Bioinformatics, 2013, 81, 1527-1541.	1.5	6
118	Mechanical stability analysis of the protein L immunoglobulinâ€binding domain by full alanine screening using molecular dynamics simulations. Biotechnology Journal, 2015, 10, 386-394.	1.8	6
119	Proteome-scale understanding of relationship between homo-repeat enrichments and protein aggregation properties. PLoS ONE, 2018, 13, e0206941.	1.1	6
120	New Model for Stacking Monomers in Filamentous Actin from Skeletal Muscles of Oryctolagus cuniculus. International Journal of Molecular Sciences, 2020, 21, 8319.	1.8	6
121	Search for Structural Basis of Interactions of Biogenic Amines with Human TAAR1 and TAAR6 Receptors. International Journal of Molecular Sciences, 2022, 23, 209.	1.8	6
122	Bacterial proteins fold faster than eukaryotic proteins with simple folding kinetics. Biochemistry (Moscow), 2011, 76, 225-235.	0.7	5
123	What is Responsible for Atypical Dependence of the Rate of Amyloid Formation on Protein Concentration: Fibril-Catalyzed Initiation of New Fibrils or Competition with Oligomers?. Journal of Physical Chemistry Letters, 2018, 9, 1002-1006.	2.1	5
124	Sequence and evolutionary analysis of bacterial ribosomal <scp>S1</scp> proteins. Proteins: Structure, Function and Bioinformatics, 2021, 89, 1111-1124.	1.5	5
125	Regions which are Responsible for Swapping are also Responsible for Folding and Misfolding. The Open Biochemistry Journal, 2011, 5, 27-36.	0.3	5
126	Comparison of transition states obtained upon modeling of unfolding of immunoglobulin-binding domains of proteins L and G caused by external action with transition states obtained in the absence of force probed by experiments. Biochemistry (Moscow), 2009, 74, 316-328.	0.7	4

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127	Cunning Simplicity of a Stoichiometry Driven Protein Folding Thesis. Journal of Biomolecular Structure and Dynamics, 2011, 28, 595-598.	2.0	4
128	Comparison of experimental and theoretical data on hydrogen-deuterium exchange for ten globular proteins. Biochemistry (Moscow), 2012, 77, 616-623.	0.7	4
129	Myosin Binding Protein-C Forms Amyloid-Like Aggregates In Vitro. International Journal of Molecular Sciences, 2021, 22, 731.	1.8	4
130	Reversible and Irreversible Aggregation of Proteins from the FET Family: Influence of Repeats in Protein Chain on Its Aggregation Capacity. Current Protein and Peptide Science, 2016, 17, 319-331.	0.7	4
131	Hepatic and Aortic Arch Expression and Serum Levels of Syndecan-1 in ApoE Mice. The Open Biochemistry Journal, 2017, 11, 77-93.	0.3	4
132	Are the same or different amino acid residues responsible for correct and incorrect protein folding?. Biochemistry (Moscow), 2009, 74, 186-193.	0.7	3
133	Experimental and theoretical studies of mechanical unfolding of different proteins. Biochemistry (Moscow), 2013, 78, 1216-1227.	0.7	3
134	Folding of Rightâ€•and Leftâ€Handed Threeâ€Helix Proteins. Israel Journal of Chemistry, 2014, 54, 1126-1136.	1.0	3
135	Peptide AÎ²(16-25) forms nanofilms in the process of its aggregation. Biochemistry (Moscow), 2016, 81, 755-761.	0.7	3
136	Is there an advantageous arrangement of aromatic residues in proteins? Statistical analysis of aromatic interactions in globular proteins. Computational and Structural Biotechnology Journal, 2021, 19, 5960-5968.	1.9	3
137	Is It Possible to Find an Antimicrobial Peptide That Passes the Membrane Bilayer with Minimal Force Resistance? An Attempt at a Predictive Approach by Molecular Dynamics Simulation. International Journal of Molecular Sciences, 2022, 23, 5997.	1.8	3
138	Prediction of folding nuclei in tRNA molecules. Biochemistry (Moscow), 2011, 76, 236-244.	0.7	2
139	What handedness and angles between helices has the studied three-helical protein domain?. Bioinformatics, 2015, 31, 963-965.	1.8	2
140	Dataset of the molecular dynamics simulations of bilayers consisting of short amyloidogenic peptide VDSWNVLVAG from Bgl2pâ€“glucantransferase of S. cerevisiae cell wall. Data in Brief, 2016, 9, 597-601.	0.5	2
141	Is there codon usage bias for poly-Q stretches in the human proteome?. Journal of Bioinformatics and Computational Biology, 2019, 17, 1950010.	0.3	2
142	Search for Functional Flexible Regions in the G-protein Family: New Reading of the FoldUnfold Program. Protein and Peptide Letters, 2018, 25, 589-598.	0.4	2
143	Mechanism of Amyloid Gel Formation by Several Short Amyloidogenic Peptides. Nanomaterials, 2021, 11, 3129.	1.9	2
144	Inâ€depth analysis of amino acid and nucleotide sequences of Hsp60: How conserved is this protein?. Proteins: Structure, Function and Bioinformatics, 2022, 90, 1119-1141.	1.5	2

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145	Determination of the Most Stable Packing of Peptides from Ribosomal S1 Protein, Protein Bgl2p, and AÎ² peptide in Î²-layers During Molecular Dynamics Simulations. Methods in Molecular Biology, 2022, 2340, 221-233.	0.4	2
146	Influence of organization of native protein structure on its folding: Modeling of the folding of Î±-helical proteins. Biochemistry (Moscow), 2010, 75, 995-1005.	0.7	1
147	Modeling amyloid fibril formation. Biochemistry (Moscow), 2011, 76, 366-373.	0.7	1
148	Theoretical Search for RNA Folding Nuclei. Entropy, 2015, 17, 7827-7847.	1.1	1
149	Ile351, Leu355 and Ile461 residues are essential for catalytic activity of bovine cytochrome P450scc (CYP11A1). Steroids, 2019, 143, 80-90.	0.8	1
150	Extended disordered regions of ribosome-associated NAC proteins paralogs belong only to the germline in Drosophila melanogaster. Scientific Reports, 2022, 12, .	1.6	1
151	Is protein folding rate dependent on number of folding stages? Modeling of protein folding with ferredoxin-like fold. Biochemistry (Moscow), 2010, 75, 717-727.	0.7	0
152	Intensive protein synthesis in neurons and phosphorylation of beta-amyloid precursor protein and tau-protein are triggering factors of neuronal amyloidosis and Alzheimerâ€™s disease. Biochemistry (Moscow) Supplement Series B: Biomedical Chemistry, 2013, 7, 278-293.	0.2	0
153	Influence of Repeats in the Protein Chain on its Aggregation Capacity for ALS-Associated Proteins. , 0, , .		0
154	Two Views on the Protein Folding Puzzle. , 2018, , 391-412.		0
155	Search for functions of intrinsically disordered prion-like domains for FET proteins involved in amyotrophic lateral sclerosis and frontotemporal dementia. , 2022, , 117-133.		0
156	Simulations of the Stretching of Two Models of Filamentous Actin at a Constant Velocity Using Method of Molecular Dynamics. Lecture Notes on Data Engineering and Communications Technologies, 2022, , 379-385.	0.5	0