

# Sonia Longhi

## List of Publications by Year in descending order

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148  
papers

9,349  
citations

26630

56  
h-index

45317

90  
g-index

187  
all docs

187  
docs citations

187  
times ranked

7702  
citing authors

#	ARTICLE	IF	CITATIONS
1	Introducing Protein Intrinsic Disorder. <i>Chemical Reviews</i> , 2014, 114, 6561-6588.	47.7	628
2	Assessing protein disorder and induced folding. <i>Proteins: Structure, Function and Bioinformatics</i> , 2005, 62, 24-45.	2.6	388
3	The C-terminal Domain of the Measles Virus Nucleoprotein Is Intrinsically Disordered and Folds upon Binding to the C-terminal Moiety of the Phosphoprotein. <i>Journal of Biological Chemistry</i> , 2003, 278, 18638-18648.	3.4	260
4	The severe acute respiratory syndrome-coronavirus replicative protein nsp9 is a single-stranded RNA-binding subunit unique in the RNA virus world. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2004, 101, 3792-3796.	7.1	254
5	DisProt 7.0: a major update of the database of disordered proteins. <i>Nucleic Acids Research</i> , 2017, 45, D219-D227.	14.5	242
6	A practical overview of protein disorder prediction methods. <i>Proteins: Structure, Function and Bioinformatics</i> , 2006, 65, 1-14.	2.6	241
7	Whatâ€™s in a name? Why these proteins are intrinsically disordered. <i>Intrinsically Disordered Proteins</i> , 2013, 1, e24157.	1.9	226
8	Atomic resolution (1.0 Å..) crystal structure of <i>Fusarium solani</i> cutinase: stereochemical analysis. <i>Journal of Molecular Biology</i> , 1997, 268, 779-799.	4.2	211
9	Structural Disorder in Viral Proteins. <i>Chemical Reviews</i> , 2014, 114, 6880-6911.	47.7	181
10	Intrinsic disorder in measles virus nucleocapsids. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 9839-9844.	7.1	179
11	Exploring hydrophobic sites in proteins with xenon or krypton. <i>Proteins: Structure, Function and Bioinformatics</i> , 1998, 30, 61-73.	2.6	168
12	Cytosolic 5â€™-Triphosphate Ended Viral Leader Transcript of Measles Virus as Activator of the RIG I-Mediated Interferon Response. <i>PLoS ONE</i> , 2007, 2, e279.	2.5	159
13	Structural disorder and modular organization in Paramyxovirinae N and P. <i>Journal of General Virology</i> , 2003, 84, 3239-3252.	2.9	156
14	The C-terminal domain of measles virus nucleoprotein belongs to the class of intrinsically disordered proteins that fold upon binding to their physiological partner. <i>Virus Research</i> , 2004, 99, 157-167.	2.2	156
15	Crystal Structure of the Measles Virus Phosphoprotein Domain Responsible for the Induced Folding of the C-terminal Domain of the Nucleoprotein. <i>Journal of Biological Chemistry</i> , 2003, 278, 44567-44573.	3.4	143
16	The intrinsically disordered C-terminal domain of the measles virus nucleoprotein interacts with the C-terminal domain of the phosphoprotein via two distinct sites and remains predominantly unfolded. <i>Protein Science</i> , 2005, 14, 1975-1992.	7.6	139
17	Cloning and analysis of <i>Candida cylindracea</i> lipase sequences. <i>Gene</i> , 1993, 124, 45-55.	2.2	131
18	Rules Governing Selective Protein Carbonylation. <i>PLoS ONE</i> , 2009, 4, e7269.	2.5	123

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19	DisProt in 2022: improved quality and accessibility of protein intrinsic disorder annotation. <i>Nucleic Acids Research</i> , 2022, 50, D480-D487.	14.5	117
20	Simultaneous quantification of protein order and disorder. <i>Nature Chemical Biology</i> , 2017, 13, 339-342.	8.0	113
21	Liquidâ€“Liquid Phase Separation by Intrinsically Disordered Protein Regions of Viruses: Roles in Viral Life Cycle and Control of Virusâ€“Host Interactions. <i>International Journal of Molecular Sciences</i> , 2020, 21, 9045.	4.1	110
22	Molecular cloning of the cDNA encoding laccase from <i>Pycnoporus cinnabarinus</i> I-937 and expression in <i>Pichiaâ€“pastoris</i> . <i>FEBS Journal</i> , 2000, 267, 1619-1625.	0.2	105
23	Structure-activity of cutinase, a small lipolytic enzyme. <i>Biochimica Et Biophysica Acta - Molecular and Cell Biology of Lipids</i> , 1999, 1441, 185-196.	2.4	104
24	Modular Organization of Rabies Virus Phosphoprotein. <i>Journal of Molecular Biology</i> , 2009, 388, 978-996.	4.2	104
25	Multiscaled exploration of coupled folding and binding of an intrinsically disordered molecular recognition element in measles virus nucleoprotein. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, E3743-52.	7.1	102
26	Mapping Î±â€“helical induced folding within the intrinsically disordered Câ€“terminal domain of the measles virus nucleoprotein by siteâ€“directed spinâ€“labeling EPR spectroscopy. <i>Proteins: Structure, Function and Bioinformatics</i> , 2008, 73, 973-988.	2.6	101
27	Assessing Induced Folding of an Intrinsically Disordered Protein by Site-Directed Spin-Labeling Electron Paramagnetic Resonance Spectroscopy. <i>Journal of Physical Chemistry B</i> , 2006, 110, 20596-20608.	2.6	99
28	Variability within the <i>Candida rugosa</i> Upases family. <i>Protein Engineering, Design and Selection</i> , 1994, 7, 531-535.	2.1	97
29	The N-Terminal Domain of the Phosphoprotein of Morbilliviruses Belongs to the Natively Unfolded Class of Proteins. <i>Virology</i> , 2002, 296, 251-262.	2.4	95
30	PED in 2021: a major update of the protein ensemble database for intrinsically disordered proteins. <i>Nucleic Acids Research</i> , 2021, 49, D404-D411.	14.5	95
31	Contribution of Cutinase Serine 42 Side Chain to the Stabilization of the Oxyanion Transition Stateâ€“,â€“. <i>Biochemistry</i> , 1996, 35, 398-410.	2.5	94
32	Viral RNA-polymerases â€“ a predicted 2â€“O-ribose methyltransferase domain shared by all Mononegavirales. <i>Trends in Biochemical Sciences</i> , 2002, 27, 222-224.	7.5	92
33	Hsp72 recognizes a P binding motif in the measles virus N protein C-terminus. <i>Virology</i> , 2005, 337, 162-174.	2.4	90
34	MeDor: a metasever for predicting protein disorder. <i>BMC Genomics</i> , 2008, 9, S25.	2.8	88
35	Structural disorder within the replicative complex of measles virus: Functional implications. <i>Virology</i> , 2006, 344, 94-110.	2.4	87
36	First evidence for the salt-dependent folding and activity of an esterase from the halophilic archaea <i>Haloarcula marismortui</i> . <i>Biochimica Et Biophysica Acta - Molecular and Cell Biology of Lipids</i> , 2009, 1791, 719-729.	2.4	87

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37	How disordered is my protein and what is its disorder for? A guide through the "dark side" of the protein universe. <i>Intrinsically Disordered Proteins</i> , 2016, 4, e1259708.	1.9	87
38	Measles Virus (MV) Nucleoprotein Binds to a Novel Cell Surface Receptor Distinct from Fc $\beta$ RII via Its C-Terminal Domain: Role in MV-Induced Immunosuppression. <i>Journal of Virology</i> , 2003, 77, 11332-11346.	3.4	81
39	Solution structure of the C-terminal X domain of the measles virus phosphoprotein and interaction with the intrinsically disordered C-terminal domain of the nucleoprotein. <i>Journal of Molecular Recognition</i> , 2010, 23, 435-447.	2.1	81
40	Intrinsic disorder in Viral Proteins Genome-Linked: experimental and predictive analyses. <i>Virology Journal</i> , 2009, 6, 23.	3.4	80
41	Substitution of Two Residues in the Measles Virus Nucleoprotein Results in an Impaired Self-Association. <i>Virology</i> , 2002, 302, 420-432.	2.4	78
42	Structural Disorder within Henipavirus Nucleoprotein and Phosphoprotein: From Predictions to Experimental Assessment. <i>PLoS ONE</i> , 2010, 5, e11684.	2.5	78
43	Cloning and nucleotide sequences of two lipase genes from <i>Candida cylindracea</i> . <i>Biochimica Et Biophysica Acta Gene Regulatory Mechanisms</i> , 1992, 1131, 227-232.	2.4	77
44	Crystal structure of cutinase covalently inhibited by a triglyceride analogue. <i>Protein Science</i> , 1997, 6, 275-286.	7.6	77
45	Predicting Protein Disorder and Induced Folding: From Theoretical Principles to Practical Applications. <i>Current Protein and Peptide Science</i> , 2007, 8, 135-149.	1.4	69
46	Structural and dynamics analysis of intrinsically disordered proteins by high-speed atomic force microscopy. <i>Nature Nanotechnology</i> , 2021, 16, 181-189.	31.5	69
47	Atomic Resolution Description of the Interaction between the Nucleoprotein and Phosphoprotein of Hendra Virus. <i>PLoS Pathogens</i> , 2013, 9, e1003631.	4.7	68
48	Measles virus nucleoprotein induces cell-proliferation arrest and apoptosis through N-TAIL $\beta$ -NR and N-CORE $\beta$ -Fc $\beta$ RIIB1 interactions, respectively. <i>Journal of General Virology</i> , 2005, 86, 1771-1784.	2.9	65
49	Structural analysis of the human respiratory syncytial virus phosphoprotein: characterization of an $\alpha$ -helical domain involved in oligomerization. <i>Journal of General Virology</i> , 2006, 87, 159-169.	2.9	65
50	Characterization of the Interactions between the Nucleoprotein and the Phosphoprotein of Henipavirus. <i>Journal of Biological Chemistry</i> , 2011, 286, 13583-13602.	3.4	65
51	Messages from ultrahigh resolution crystal structures. <i>Current Opinion in Structural Biology</i> , 1998, 8, 730-737.	5.7	63
52	Demonstration of a Folding after Binding Mechanism in the Recognition between the Measles Virus N-TAIL and X Domains. <i>ACS Chemical Biology</i> , 2015, 10, 795-802.	3.4	63
53	Structural disorder within paramyxovirus nucleoproteins and phosphoproteins. <i>Molecular BioSystems</i> , 2012, 8, 69-81.	2.9	62
54	Relevance of Electrostatic Charges in Compactness, Aggregation, and Phase Separation of Intrinsically Disordered Proteins. <i>International Journal of Molecular Sciences</i> , 2020, 21, 6208.	4.1	61

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55	Ebola Virus VP30 Is an RNA Binding Protein. <i>Journal of Virology</i> , 2007, 81, 8967-8976.	3.4	60
56	Conformational Analysis of the Partially Disordered Measles Virus NTAIL-XD Complex by SDSL EPR Spectroscopy. <i>Biophysical Journal</i> , 2010, 98, 1055-1064.	0.5	59
57	Nucleocapsid Structure and Function. <i>Current Topics in Microbiology and Immunology</i> , 2009, 329, 103-128.	1.1	58
58	Dynamics of <i>Fusarium solani</i> cutinase investigated through structural comparison among different crystal forms of its variants. <i>Proteins: Structure, Function and Bioinformatics</i> , 1996, 26, 442-458.	2.6	57
59	Acyl glycerol hydrolases: inhibitors, interface and catalysis. <i>Current Opinion in Structural Biology</i> , 1996, 6, 449-455.	5.7	53
60	An Integrated System to Study Multiply Substituted Human Immunodeficiency Virus Type 1 Reverse Transcriptase. <i>Analytical Biochemistry</i> , 2001, 292, 139-147.	2.4	52
61	High affinity binding between Hsp70 and the C-terminal domain of the measles virus nucleoprotein requires an Hsp40 co-chaperone. <i>Journal of Molecular Recognition</i> , 2010, 23, 301-315.	2.1	48
62	Probing Structural Transitions in the Intrinsically Disordered C-Terminal Domain of the Measles Virus Nucleoprotein by Vibrational Spectroscopy of $\gamma$ -Cyanylated Cysteines. <i>Biophysical Journal</i> , 2010, 99, 1676-1683.	0.5	47
63	Structural disorder and induced folding within two cereal, ABA stress and ripening (ASR) proteins. <i>Scientific Reports</i> , 2017, 7, 15544.	3.3	47
64	VaZyMolO: a tool to define and classify modularity in viral proteins. <i>Journal of General Virology</i> , 2005, 86, 743-749.	2.9	45
65	Molecular Basis for Structural Heterogeneity of an Intrinsically Disordered Protein Bound to a Partner by Combined ESI-IM-MS and Modeling. <i>Journal of the American Society for Mass Spectrometry</i> , 2015, 26, 472-481.	2.8	45
66	Sequence of Events in Measles Virus Replication: Role of Phosphoprotein-Nucleocapsid Interactions. <i>Journal of Virology</i> , 2014, 88, 10851-10863.	3.4	44
67	Essential Amino Acids of the Hantaan Virus N Protein in Its Interaction with RNA. <i>Journal of Virology</i> , 2005, 79, 10032-10039.	3.4	43
68	Compaction and binding properties of the intrinsically disordered C-terminal domain of Henipavirus nucleoprotein as unveiled by deletion studies. <i>Molecular BioSystems</i> , 2012, 8, 392-410.	2.9	43
69	hsp70 and a Novel Axis of Type I Interferon-Dependent Antiviral Immunity in the Measles Virus-Infected Brain. <i>Journal of Virology</i> , 2013, 87, 998-1009.	3.4	43
70	Modulation of Re-initiation of Measles Virus Transcription at Intergenic Regions by PXD to NTAIL Binding Strength. <i>PLoS Pathogens</i> , 2016, 12, e1006058.	4.7	43
71	Fuzzy regions in an intrinsically disordered protein impair protein-protein interactions. <i>FEBS Journal</i> , 2016, 283, 576-594.	4.7	43
72	Interaction between the C-terminal domains of N and P proteins of measles virus investigated by NMR. <i>FEBS Letters</i> , 2009, 583, 1084-1089.	2.8	42

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73	Recombinant pheromone binding protein 1 from <i>Mamestra brassicae</i> (MbraPBP1) . Functional and structural characterization. <i>FEBS Journal</i> , 1999, 264, 707-716.	0.2	41
74	Exploring hydrophobic sites in proteins with xenon or krypton. <i>Proteins: Structure, Function and Bioinformatics</i> , 1998, 30, 61-73.	2.6	41
75	How Robust Is the Mechanism of Folding-Upon-Binding for an Intrinsically Disordered Protein?. <i>Biophysical Journal</i> , 2018, 114, 1889-1894.	0.5	39
76	Assessing induced folding within the intrinsically disordered C-terminal domain of the <i>Henipavirus</i> nucleoproteins by site-directed spin labeling EPR spectroscopy. <i>Journal of Biomolecular Structure and Dynamics</i> , 2013, 31, 453-471.	3.5	38
77	An arsenal of methods for the experimental characterization of intrinsically disordered proteins – How to choose and combine them?. <i>Archives of Biochemistry and Biophysics</i> , 2019, 676, 108055.	3.0	37
78	Probing structural transitions in both structured and disordered proteins using site-directed spin-labeling EPR spectroscopy. <i>Journal of Peptide Science</i> , 2011, 17, 315-328.	1.4	36
79	Plasticity in Structural and Functional Interactions between the Phosphoprotein and Nucleoprotein of Measles Virus. <i>Journal of Biological Chemistry</i> , 2012, 287, 11951-11967.	3.4	36
80	Molecular cloning and bacterial expression of a general odorant-binding protein from the cabbage armyworm <i>Mamestra brassicae</i> . <i>FEBS Journal</i> , 1998, 258, 768-774.	0.2	34
81	Packing forces in nine crystal forms of cutinase. <i>Proteins: Structure, Function and Bioinformatics</i> , 1998, 31, 320-333.	2.6	34
82	Structural genomics of the SARS coronavirus: cloning, expression, crystallization and preliminary crystallographic study of the Nsp9 protein. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2003, 59, 1628-1631.	2.5	34
83	Extracting structural information from charge-state distributions of intrinsically disordered proteins by non-denaturing electrospray-ionization mass spectrometry. <i>Intrinsically Disordered Proteins</i> , 2013, 1, e25068.	1.9	33
84	Structural Disorder within the Measles Virus Nucleoprotein and Phosphoprotein. <i>Protein and Peptide Letters</i> , 2010, 17, 961-978.	0.9	32
85	Dynamics of the Intrinsically Disordered C-terminal Domain of the Nipah Virus Nucleoprotein and Interaction with the X Domain of the Phosphoprotein as Unveiled by NMR Spectroscopy. <i>ChemBioChem</i> , 2015, 16, 268-276.	2.6	31
86	Regulation of measles virus gene expression by P protein coiled-coil properties. <i>Science Advances</i> , 2019, 5, eaaw3702.	10.3	31
87	How order and disorder within paramyxoviral nucleoproteins and phosphoproteins orchestrate the molecular interplay of transcription and replication. <i>Cellular and Molecular Life Sciences</i> , 2017, 74, 3091-3118.	5.4	30
88	The Valine-to-Threonine 75 Substitution in Human Immunodeficiency Virus Type 1 Reverse Transcriptase and Its Relation with Stavudine Resistance. <i>Journal of Biological Chemistry</i> , 2001, 276, 13965-13974.	3.4	29
89	Coiled-coil deformations in crystal structures: the measles virus phosphoprotein multimerization domain as an illustrative example. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2014, 70, 1589-1603.	2.5	29
90	Analyzing the Folding and Binding Steps of an Intrinsically Disordered Protein by Protein Engineering. <i>Biochemistry</i> , 2017, 56, 3780-3786.	2.5	28

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91	Dissecting Partner Recognition by an Intrinsically Disordered Protein Using Descriptive Random Mutagenesis. <i>Journal of Molecular Biology</i> , 2013, 425, 3495-3509.	4.2	25
92	Bioinformatic Analysis of Lytic Polysaccharide Monooxygenases Reveals the Pan-Families Occurrence of Intrinsically Disordered C-Terminal Extensions. <i>Biomolecules</i> , 2021, 11, 1632.	4.0	25
93	The interaction between the measles virus nucleoprotein and the Interferon Regulator Factor 3 relies on a specific cellular environment. <i>Virology Journal</i> , 2009, 6, 59.	3.4	23
94	Biochemical and structural studies of the oligomerization domain of the Nipah virus phosphoprotein: Evidence for an elongated coiled-coil homotrimer. <i>Virology</i> , 2013, 446, 162-172.	2.4	23
95	The Measles Virus NTAIL-XD Complex: An Illustrative Example of Fuzziness. <i>Advances in Experimental Medicine and Biology</i> , 2012, 725, 126-141.	1.6	20
96	Identification of a Region in the Common Amino-terminal Domain of Hendra Virus P, V, and W Proteins Responsible for Phase Transition and Amyloid Formation. <i>Biomolecules</i> , 2021, 11, 1324.	4.0	20
97	SPINE bioinformatics and data-management aspects of high-throughput structural biology. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2006, 62, 1184-1195.	2.5	19
98	Structural Disorder within Paramyxoviral Nucleoproteins and Phosphoproteins in Their Free and Bound Forms: From Predictions to Experimental Assessment. <i>International Journal of Molecular Sciences</i> , 2015, 16, 15688-15726.	4.1	19
99	Structural disorder within paramyxoviral nucleoproteins. <i>FEBS Letters</i> , 2015, 589, 2649-2659.	2.8	19
100	Probing Conformational Changes and Interfacial Recognition Site of Lipases With Surfactants and Inhibitors. <i>Methods in Enzymology</i> , 2017, 583, 279-307.	1.0	19
101	Conformational Disorder. <i>Methods in Molecular Biology</i> , 2010, 609, 307-325.	0.9	19
102	How disorder influences order and vice versa—mutual effects in fusion proteins containing an intrinsically disordered and a globular protein. <i>FEBS Journal</i> , 2010, 277, 4438-4451.	4.7	18
103	Identification and Structural Characterization of an Intermediate in the Folding of the Measles Virus X Domain. <i>Journal of Biological Chemistry</i> , 2016, 291, 10886-10892.	3.4	18
104	The Henipavirus V protein is a prevalently unfolded protein with a zinc-finger domain involved in binding to DDB1. <i>Molecular BioSystems</i> , 2017, 13, 2254-2267.	2.9	18
105	Partner-Mediated Polymorphism of an Intrinsically Disordered Protein. <i>Journal of Molecular Biology</i> , 2018, 430, 2493-2507.	4.2	18
106	Understanding Intramolecular Crosstalk in an Intrinsically Disordered Protein. <i>ACS Chemical Biology</i> , 2019, 14, 337-341.	3.4	18
107	Modulation of Measles Virus NTAIL Interactions through Fuzziness and Sequence Features of Disordered Binding Sites. <i>Biomolecules</i> , 2019, 9, 8.	4.0	17
108	Transcription et répllication des Mononegavirales: une machine moléculaire originale. <i>Virologie</i> , 2012, 16, 225-257.	0.1	17

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109	Conformational response to charge clustering in synthetic intrinsically disordered proteins. <i>Biochimica Et Biophysica Acta - General Subjects</i> , 2018, 1862, 2204-2214.	2.4	16
110	Comprehensive Intrinsic Disorder Analysis of 6108 Viral Proteomes: From the Extent of Intrinsic Disorder Penetration to Functional Annotation of Disordered Viral Proteins. <i>Journal of Proteome Research</i> , 2021, 20, 2704-2713.	3.7	16
111	Interaction between the C-terminal domains of measles virus nucleoprotein and phosphoprotein: A tight complex implying one binding site. <i>Protein Science</i> , 2012, 21, 1577-1585.	7.6	15
112	Insights into the Hendra virus N TAIL $\alpha$ -XD complex: Evidence for a parallel organization of the helical MoRE at the XD surface stabilized by a combination of hydrophobic and polar interactions. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2015, 1854, 1038-1053.	2.3	15
113	One-step generation of error-prone PCR libraries using Gateway <sup>®</sup> technology. <i>Microbial Cell Factories</i> , 2012, 11, 14.	4.0	13
114	Monitoring Structural Transitions in IDPs by Site-Directed Spin Labeling EPR Spectroscopy. <i>Methods in Molecular Biology</i> , 2012, 895, 361-386.	0.9	13
115	Diversification of EPR signatures in site directed spin labeling using a $\hat{1}^2$ -phosphorylated nitroxide. <i>Physical Chemistry Chemical Physics</i> , 2014, 16, 4202.	2.8	13
116	Ensemble description of the intrinsically disordered N-terminal domain of the Nipah virus P/V protein from combined NMR and SAXS. <i>Scientific Reports</i> , 2020, 10, 19574.	3.3	13
117	Insights into the coiled-coil organization of the Hendra virus phosphoprotein from combined biochemical and SAXS studies. <i>Virology</i> , 2015, 477, 42-55.	2.4	12
118	Editorial [Hot topic: Structural Disorder in Viral Proteins (Guest Editor: Sonia Longhi)]. <i>Protein and Peptide Letters</i> , 2010, 17, 930-931.	0.9	11
119	Distribution of Charged Residues Affects the Average Size and Shape of Intrinsically Disordered Proteins. <i>Biomolecules</i> , 2022, 12, 561.	4.0	11
120	Homology-derived three-dimensional structure prediction of <i>Candida cylindracea</i> lipase. <i>Lipids and Lipid Metabolism</i> , 1992, 1165, 129-133.	2.6	10
121	Dividing To Unveil Protein Microheterogeneities: Traveling Wave Ion Mobility Study. <i>Analytical Chemistry</i> , 2011, 83, 7306-7315.	6.5	10
122	Order and Disorder in the Replicative Complex of Paramyxoviruses. <i>Advances in Experimental Medicine and Biology</i> , 2015, 870, 351-381.	1.6	10
123	Predicting Conformational Disorder. <i>Methods in Molecular Biology</i> , 2016, 1415, 265-299.	0.9	10
124	InSiDDe: A Server for Designing Artificial Disordered Proteins. <i>International Journal of Molecular Sciences</i> , 2018, 19, 91.	4.1	10
125	Folding Mechanism of the SH3 Domain from Grb2. <i>Journal of Physical Chemistry B</i> , 2018, 122, 11166-11173.	2.6	9
126	Binding induced folding: Lessons from the kinetics of interaction between NTAIL and XD. <i>Archives of Biochemistry and Biophysics</i> , 2019, 671, 255-261.	3.0	9



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127	Structural and Functional Characterization of the ABA-Water Deficit Stress Domain from Wheat and Barley: An Intrinsically Disordered Domain behind the Versatile Functions of the Plant Abscisic Acid, Stress and Ripening Protein Family. <i>International Journal of Molecular Sciences</i> , 2021, 22, 2314.	4.1	9
128	Insights into the evolutionary forces that shape the codon usage in the viral genome segments encoding intrinsically disordered protein regions. <i>Briefings in Bioinformatics</i> , 2021, 22, .	6.5	9
129	Accuracy of Structural Information Obtained at the European Synchrotron Radiation Facility from Very Rapid Laue Data Collection on Macromolecules. <i>Journal of Applied Crystallography</i> , 1997, 30, 153-163.	4.5	8
130	Solution conformational features and interfacial properties of an intrinsically disordered peptide coupled to alkyl chains: a new class of peptide amphiphiles. <i>Molecular BioSystems</i> , 2013, 9, 1401.	2.9	8
131	Elevated antibody reactivity to measles virus N CORE protein among patients with multiple sclerosis and their healthy siblings with intrathecal oligoclonal immunoglobulin G production. <i>Journal of Clinical Virology</i> , 2014, 61, 107-112.	3.1	8
132	Interfacial Properties of NTAIL, an Intrinsically Disordered Protein. <i>Biophysical Journal</i> , 2017, 113, 2723-2735.	0.5	8
133	Experimental Characterization of Fuzzy Protein Assemblies: Interactions of Paramyxoviral NTAIL Domains With Their Functional Partners. <i>Methods in Enzymology</i> , 2018, 611, 137-192.	1.0	8
134	Structural Disorder within the Measles Virus Nucleoprotein and Phosphoprotein: Functional Implications for Transcription and Replication. , 2011, , 95-125.		6
135	The Folding Pathway of the KIX Domain. <i>ACS Chemical Biology</i> , 2017, 12, 1683-1690.	3.4	6
136	Experimental Evidence of Intrinsic Disorder and Amyloid Formation by the Henipavirus W Proteins. <i>International Journal of Molecular Sciences</i> , 2022, 23, 923.	4.1	6
137	Protein Engineering. <i>Methods in Molecular Biology</i> , 2007, 363, 59-90.	0.9	4
138	Mutual effects of disorder and order in fusion proteins between intrinsically disordered domains and fluorescent proteins. <i>Molecular BioSystems</i> , 2012, 8, 105-113.	2.9	4
139	Probing the dynamic properties of two sites simultaneously in a proteinâ€“protein interaction process: a SDSL-EPR study. <i>Physical Chemistry Chemical Physics</i> , 2019, 21, 22584-22588.	2.8	4
140	Packing forces in nine crystal forms of cutinase. <i>Proteins: Structure, Function and Bioinformatics</i> , 1998, 31, 320-33.	2.6	4
141	Predicting Protein Conformational Disorder and Disordered Binding Sites. <i>Methods in Molecular Biology</i> , 2022, 2449, 95-147.	0.9	4
142	Monitoring Structural Transitions in IDPs by Vibrational Spectroscopy of Cyanylated Cysteine. <i>Methods in Molecular Biology</i> , 2012, 895, 245-270.	0.9	3
143	Extracellular HSP70, Neuroinflammation and Protection Against Viral Virulence. <i>Heat Shock Proteins</i> , 2019, , 23-55.	0.2	3
144	Reply to Jensen and Blackledge: Dual quantifications of intrinsically disordered proteins by NMR ensembles and molecular dynamics simulations. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, E1559.	7.1	2

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145	Exploration of nucleoprotein $\hat{I}\pm$ -MoRE and XD interactions of Nipah and Hendra viruses. Journal of Molecular Modeling, 2018, 24, 113.	1.8	2
146	Structural Disorder Within Henipavirus Nucleoprotein and Phosphoprotein. Biophysical Journal, 2010, 98, 256a.	0.5	1
147	Dynamics of Fusarium solani cutinase investigated through structural comparison among different crystal forms of its variants. Proteins: Structure, Function and Bioinformatics, 1996, 26, 442-458.	2.6	1
148	Predicting substitutions to modulate disorder and stability in coiled-coils. BMC Bioinformatics, 2020, 21, 573.	2.6	0