

# Sonia Longhi

## List of Publications by Year in descending order

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148  
papers

9,349  
citations

26567

56  
h-index

45213

90  
g-index

187  
all docs

187  
docs citations

187  
times ranked

7702  
citing authors

#	ARTICLE	IF	CITATIONS
1	DisProt in 2022: improved quality and accessibility of protein intrinsic disorder annotation. <i>Nucleic Acids Research</i> , 2022, 50, D480-D487.	6.5	117
2	Experimental Evidence of Intrinsic Disorder and Amyloid Formation by the Henipavirus W Proteins. <i>International Journal of Molecular Sciences</i> , 2022, 23, 923.	1.8	6
3	Distribution of Charged Residues Affects the Average Size and Shape of Intrinsically Disordered Proteins. <i>Biomolecules</i> , 2022, 12, 561.	1.8	11
4	Predicting Protein Conformational Disorder and Disordered Binding Sites. <i>Methods in Molecular Biology</i> , 2022, 2449, 95-147.	0.4	4
5	Structural and dynamics analysis of intrinsically disordered proteins by high-speed atomic force microscopy. <i>Nature Nanotechnology</i> , 2021, 16, 181-189.	15.6	69
6	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.	1.8	9
7	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.	1.8	16
8	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, .	3.2	9
9	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.	1.8	20
10	PED in 2021: a major update of the protein ensemble database for intrinsically disordered proteins. <i>Nucleic Acids Research</i> , 2021, 49, D404-D411.	6.5	95
11	Bioinformatic Analysis of Lytic Polysaccharide Monooxygenases Reveals the Pan-Families Occurrence of Intrinsically Disordered C-Terminal Extensions. <i>Biomolecules</i> , 2021, 11, 1632.	1.8	25
12	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.	1.8	110
13	Relevance of Electrostatic Charges in Compactness, Aggregation, and Phase Separation of Intrinsically Disordered Proteins. <i>International Journal of Molecular Sciences</i> , 2020, 21, 6208.	1.8	61
14	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.	1.6	13
15	Predicting substitutions to modulate disorder and stability in coiled-coils. <i>BMC Bioinformatics</i> , 2020, 21, 573.	1.2	0
16	Binding induced folding: Lessons from the kinetics of interaction between NTAIL and XD. <i>Archives of Biochemistry and Biophysics</i> , 2019, 671, 255-261.	1.4	9
17	An arsenal of methods for the experimental characterization of intrinsically disordered proteins â€“ How to choose and combine them?. <i>Archives of Biochemistry and Biophysics</i> , 2019, 676, 108055.	1.4	37
18	Regulation of measles virus gene expression by P protein coiled-coil properties. <i>Science Advances</i> , 2019, 5, eaaw3702.	4.7	31

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19	Understanding Intramolecular Crosstalk in an Intrinsically Disordered Protein. ACS Chemical Biology, 2019, 14, 337-341.	1.6	18
20	Extracellular HSP70, Neuroinflammation and Protection Against Viral Virulence. Heat Shock Proteins, 2019, , 23-55.	0.2	3
21	Probing the dynamic properties of two sites simultaneously in a proteinâ€™protein interaction process: a SDSL-EPR study. Physical Chemistry Chemical Physics, 2019, 21, 22584-22588.	1.3	4
22	Modulation of Measles Virus NTAIL Interactions through Fuzziness and Sequence Features of Disordered Binding Sites. Biomolecules, 2019, 9, 8.	1.8	17
23	Exploration of nucleoprotein $\hat{\pm}$ -MoRE and XD interactions of Nipah and Hendra viruses. Journal of Molecular Modeling, 2018, 24, 113.	0.8	2
24	How Robust Is the Mechanism of Folding-Upon-Binding for an Intrinsically Disordered Protein?. Biophysical Journal, 2018, 114, 1889-1894.	0.2	39
25	Partner-Mediated Polymorphism of an Intrinsically Disordered Protein. Journal of Molecular Biology, 2018, 430, 2493-2507.	2.0	18
26	Experimental Characterization of Fuzzy Protein Assemblies: Interactions of Paramyxoviral NTAIL Domains With Their Functional Partners. Methods in Enzymology, 2018, 611, 137-192.	0.4	8
27	InSiDD: A Server for Designing Artificial Disordered Proteins. International Journal of Molecular Sciences, 2018, 19, 91.	1.8	10
28	Conformational response to charge clustering in synthetic intrinsically disordered proteins. Biochimica Et Biophysica Acta - General Subjects, 2018, 1862, 2204-2214.	1.1	16
29	Folding Mechanism of the SH3 Domain from Grb2. Journal of Physical Chemistry B, 2018, 122, 11166-11173.	1.2	9
30	The Folding Pathway of the KIX Domain. ACS Chemical Biology, 2017, 12, 1683-1690.	1.6	6
31	DisProt 7.0: a major update of the database of disordered proteins. Nucleic Acids Research, 2017, 45, D219-D227.	6.5	242
32	How order and disorder within paramyxoviral nucleoproteins and phosphoproteins orchestrate the molecular interplay of transcription and replication. Cellular and Molecular Life Sciences, 2017, 74, 3091-3118.	2.4	30
33	Simultaneous quantification of protein order and disorder. Nature Chemical Biology, 2017, 13, 339-342.	3.9	113
34	The Henipavirus V protein is a prevalently unfolded protein with a zinc-finger domain involved in binding to DDB1. Molecular BioSystems, 2017, 13, 2254-2267.	2.9	18
35	Analyzing the Folding and Binding Steps of an Intrinsically Disordered Protein by Protein Engineering. Biochemistry, 2017, 56, 3780-3786.	1.2	28
36	Interfacial Properties of NTAIL, an Intrinsically Disordered Protein. Biophysical Journal, 2017, 113, 2723-2735.	0.2	8

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37	Structural disorder and induced folding within two cereal, ABA stress and ripening (ASR) proteins. <i>Scientific Reports</i> , 2017, 7, 15544.	1.6	47
38	Probing Conformational Changes and Interfacial Recognition Site of Lipases With Surfactants and Inhibitors. <i>Methods in Enzymology</i> , 2017, 583, 279-307.	0.4	19
39	Modulation of Re-initiation of Measles Virus Transcription at Intergenic Regions by PXD to NTAIL Binding Strength. <i>PLoS Pathogens</i> , 2016, 12, e1006058.	2.1	43
40	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
41	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.	1.6	18
42	Predicting Conformational Disorder. <i>Methods in Molecular Biology</i> , 2016, 1415, 265-299.	0.4	10
43	Fuzzy regions in an intrinsically disordered protein impair protein-protein interactions. <i>FEBS Journal</i> , 2016, 283, 576-594.	2.2	43
44	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.	1.8	19
45	Insights into the Hendra virus N TAIL "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.	1.1	15
46	Insights into the coiled-coil organization of the Hendra virus phosphoprotein from combined biochemical and SAXS studies. <i>Virology</i> , 2015, 477, 42-55.	1.1	12
47	Structural disorder within paramyxoviral nucleoproteins. <i>FEBS Letters</i> , 2015, 589, 2649-2659.	1.3	19
48	Order and Disorder in the Replicative Complex of Paramyxoviruses. <i>Advances in Experimental Medicine and Biology</i> , 2015, 870, 351-381.	0.8	10
49	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.	1.3	31
50	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.	1.2	45
51	Demonstration of a Folding after Binding Mechanism in the Recognition between the Measles Virus N <sub>TAIL</sub> and X Domains. <i>ACS Chemical Biology</i> , 2015, 10, 795-802.	1.6	63
52	Sequence of Events in Measles Virus Replication: Role of Phosphoprotein-Nucleocapsid Interactions. <i>Journal of Virology</i> , 2014, 88, 10851-10863.	1.5	44
53	Structural Disorder in Viral Proteins. <i>Chemical Reviews</i> , 2014, 114, 6880-6911.	23.0	181
54	Introducing Protein Intrinsic Disorder. <i>Chemical Reviews</i> , 2014, 114, 6561-6588.	23.0	628

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55	Diversification of EPR signatures in site directed spin labeling using a $\hat{I}^2$ -phosphorylated nitroxide. <i>Physical Chemistry Chemical Physics</i> , 2014, 16, 4202.	1.3	13
56	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.	3.3	2
57	Elevated antibody reactivity to measles virus NCORE 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.	1.6	8
58	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
59	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
60	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.	1.1	23
61	Dissecting Partner Recognition by an Intrinsically Disordered Protein Using Descriptive Random Mutagenesis. <i>Journal of Molecular Biology</i> , 2013, 425, 3495-3509.	2.0	25
62	Assessing induced folding within the intrinsically disordered C-terminal domain of the Henipavirus nucleoproteins by site-directed spin labeling EPR spectroscopy. <i>Journal of Biomolecular Structure and Dynamics</i> , 2013, 31, 453-471.	2.0	38
63	What are TMs in a name? Why these proteins are intrinsically disordered. <i>Intrinsically Disordered Proteins</i> , 2013, 1, e24157.	1.9	226
64	Atomic Resolution Description of the Interaction between the Nucleoprotein and Phosphoprotein of Hendra Virus. <i>PLoS Pathogens</i> , 2013, 9, e1003631.	2.1	68
65	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.	1.5	43
66	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
67	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.	3.3	102
68	Plasticity in Structural and Functional Interactions between the Phosphoprotein and Nucleoprotein of Measles Virus. <i>Journal of Biological Chemistry</i> , 2012, 287, 11951-11967.	1.6	36
69	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
70	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.	3.1	15
71	One-step generation of error-prone PCR libraries using Gateway <sup>®</sup> technology. <i>Microbial Cell Factories</i> , 2012, 11, 14.	1.9	13
72	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

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73	The Measles Virus NTAIL-XD Complex: An Illustrative Example of Fuzziness. <i>Advances in Experimental Medicine and Biology</i> , 2012, 725, 126-141.	0.8	20
74	Monitoring Structural Transitions in IDPs by Vibrational Spectroscopy of Cyanylated Cysteine. <i>Methods in Molecular Biology</i> , 2012, 895, 245-270.	0.4	3
75	Monitoring Structural Transitions in IDPs by Site-Directed Spin Labeling EPR Spectroscopy. <i>Methods in Molecular Biology</i> , 2012, 895, 361-386.	0.4	13
76	Structural disorder within paramyxovirus nucleoproteins and phosphoproteins. <i>Molecular BioSystems</i> , 2012, 8, 69-81.	2.9	62
77	Transcription et répllication des Mononegavirales: une machine moléculaire originale. <i>Virologie</i> , 2012, 16, 225-257.	0.1	17
78	Dividing To Unveil Protein Microheterogeneities: Traveling Wave Ion Mobility Study. <i>Analytical Chemistry</i> , 2011, 83, 7306-7315.	3.2	10
79	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.	0.8	36
80	Structural Disorder within the Measles Virus Nucleoprotein and Phosphoprotein: Functional Implications for Transcription and Replication. , 2011, , 95-125.		6
81	Characterization of the Interactions between the Nucleoprotein and the Phosphoprotein of Henipavirus. <i>Journal of Biological Chemistry</i> , 2011, 286, 13583-13602.	1.6	65
82	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.	3.3	179
83	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.	1.1	48
84	Editorial [Hot topic: Structural Disorder in Viral Proteins (Guest Editor: Sonia Longhi)]. <i>Protein and Peptide Letters</i> , 2010, 17, 930-931.	0.4	11
85	Structural Disorder within the Measles Virus Nucleoprotein and Phosphoprotein. <i>Protein and Peptide Letters</i> , 2010, 17, 961-978.	0.4	32
86	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.	1.1	81
87	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.	2.2	18
88	Structural Disorder within Henipavirus Nucleoprotein and Phosphoprotein: From Predictions to Experimental Assessment. <i>PLoS ONE</i> , 2010, 5, e11684.	1.1	78
89	Structural Disorder Within Henipavirus Nucleoprotein and Phosphoprotein. <i>Biophysical Journal</i> , 2010, 98, 256a.	0.2	1
90	Conformational Analysis of the Partially Disordered Measles Virus NTAIL-XD Complex by SDSL EPR Spectroscopy. <i>Biophysical Journal</i> , 2010, 98, 1055-1064.	0.2	59

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91	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.	0.2	47
92	Conformational Disorder. <i>Methods in Molecular Biology</i> , 2010, 609, 307-325.	0.4	19
93	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.	1.3	42
94	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.	1.2	87
95	Modular Organization of Rabies Virus Phosphoprotein. <i>Journal of Molecular Biology</i> , 2009, 388, 978-996.	2.0	104
96	Intrinsic disorder in Viral Proteins Genome-Linked: experimental and predictive analyses. <i>Virology Journal</i> , 2009, 6, 23.	1.4	80
97	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.	1.4	23
98	Nucleocapsid Structure and Function. <i>Current Topics in Microbiology and Immunology</i> , 2009, 329, 103-128.	0.7	58
99	Rules Governing Selective Protein Carbonylation. <i>PLoS ONE</i> , 2009, 4, e7269.	1.1	123
100	Mapping $\alpha$ -helical induced folding within the intrinsically disordered C-terminal domain of the measles virus nucleoprotein by site-directed spin-labeling EPR spectroscopy. <i>Proteins: Structure, Function and Bioinformatics</i> , 2008, 73, 973-988.	1.5	101
101	MeDor: a metasever for predicting protein disorder. <i>BMC Genomics</i> , 2008, 9, S25.	1.2	88
102	Ebola Virus VP30 Is an RNA Binding Protein. <i>Journal of Virology</i> , 2007, 81, 8967-8976.	1.5	60
103	Predicting Protein Disorder and Induced Folding: From Theoretical Principles to Practical Applications. <i>Current Protein and Peptide Science</i> , 2007, 8, 135-149.	0.7	69
104	Protein Engineering. <i>Methods in Molecular Biology</i> , 2007, 363, 59-90.	0.4	4
105	Cytosolic 5'-Triphosphate Ended Viral Leader Transcript of Measles Virus as Activator of the RIG I-Mediated Interferon Response. <i>PLoS ONE</i> , 2007, 2, e279.	1.1	159
106	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.	1.2	99
107	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
108	A practical overview of protein disorder prediction methods. <i>Proteins: Structure, Function and Bioinformatics</i> , 2006, 65, 1-14.	1.5	241

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109	Structural disorder within the replicative complex of measles virus: Functional implications. <i>Virology</i> , 2006, 344, 94-110.	1.1	87
110	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.	1.3	65
111	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.	3.1	139
112	Hsp72 recognizes a P binding motif in the measles virus N protein C-terminus. <i>Virology</i> , 2005, 337, 162-174.	1.1	90
113	Assessing protein disorder and induced folding. <i>Proteins: Structure, Function and Bioinformatics</i> , 2005, 62, 24-45.	1.5	388
114	VaZyMoLO: a tool to define and classify modularity in viral proteins. <i>Journal of General Virology</i> , 2005, 86, 743-749.	1.3	45
115	Measles virus nucleoprotein induces cell-proliferation arrest and apoptosis through N-TAIL $\alpha$ -NR and N-CORE $\alpha$ -Fc $\gamma$ RIIB1 interactions, respectively. <i>Journal of General Virology</i> , 2005, 86, 1771-1784.	1.3	65
116	Essential Amino Acids of the Hantaan Virus N Protein in Its Interaction with RNA. <i>Journal of Virology</i> , 2005, 79, 10032-10039.	1.5	43
117	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.	3.3	254
118	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.	1.1	156
119	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
120	Structural disorder and modular organization in Paramyxovirinae N and P. <i>Journal of General Virology</i> , 2003, 84, 3239-3252.	1.3	156
121	Measles Virus (MV) Nucleoprotein Binds to a Novel Cell Surface Receptor Distinct from Fc $\gamma$ RII via Its C-Terminal Domain: Role in MV-Induced Immunosuppression. <i>Journal of Virology</i> , 2003, 77, 11332-11346.	1.5	81
122	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.	1.6	260
123	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.	1.6	143
124	Viral RNA-polymerases $\alpha$ a predicted 2 $\alpha$ -O-ribose methyltransferase domain shared by all Mononegavirales. <i>Trends in Biochemical Sciences</i> , 2002, 27, 222-224.	3.7	92
125	The N-Terminal Domain of the Phosphoprotein of Morbilliviruses Belongs to the Natively Unfolded Class of Proteins. <i>Virology</i> , 2002, 296, 251-262.	1.1	95
126	Substitution of Two Residues in the Measles Virus Nucleoprotein Results in an Impaired Self-Association. <i>Virology</i> , 2002, 302, 420-432.	1.1	78



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127	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.	1.6	29
128	An Integrated System to Study Multiply Substituted Human Immunodeficiency Virus Type 1 Reverse Transcriptase. <i>Analytical Biochemistry</i> , 2001, 292, 139-147.	1.1	52
129	Molecular cloning of the cDNA encoding laccase from <i>Pycnoporus cinnabarinus</i> I-937 and expression in <i>Pichia pastoris</i> . <i>FEBS Journal</i> , 2000, 267, 1619-1625.	0.2	105
130	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
131	Structure-activity of cutinase, a small lipolytic enzyme. <i>Biochimica Et Biophysica Acta - Molecular and Cell Biology of Lipids</i> , 1999, 1441, 185-196.	1.2	104
132	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
133	Exploring hydrophobic sites in proteins with xenon or krypton. <i>Proteins: Structure, Function and Bioinformatics</i> , 1998, 30, 61-73.	1.5	168
134	Packing forces in nine crystal forms of cutinase. <i>Proteins: Structure, Function and Bioinformatics</i> , 1998, 31, 320-333.	1.5	34
135	Messages from ultrahigh resolution crystal structures. <i>Current Opinion in Structural Biology</i> , 1998, 8, 730-737.	2.6	63
136	Exploring hydrophobic sites in proteins with xenon or krypton. <i>Proteins: Structure, Function and Bioinformatics</i> , 1998, 30, 61-73.	1.5	41
137	Packing forces in nine crystal forms of cutinase. <i>Proteins: Structure, Function and Bioinformatics</i> , 1998, 31, 320-33.	1.5	4
138	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.	2.0	211
139	Crystal structure of cutinase covalently inhibited by a triglyceride analogue. <i>Protein Science</i> , 1997, 6, 275-286.	3.1	77
140	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.	1.9	8
141	Acyl glycerol hydrolases: inhibitors, interface and catalysis. <i>Current Opinion in Structural Biology</i> , 1996, 6, 449-455.	2.6	53
142	Contribution of Cutinase Serine 42 Side Chain to the Stabilization of the Oxyanion Transition State. <i>Biochemistry</i> , 1996, 35, 398-410.	1.2	94
143	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.	1.5	57
144	Dynamics of <i>Fusarium solani</i> cutinase investigated through structural comparison among different crystal forms of its variants. , 1996, 26, 442.		1

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145	Variability within the <i>Candida rugosa</i> Lipase family. <i>Protein Engineering, Design and Selection</i> , 1994, 7, 531-535.	1.0	97
146	Cloning and analysis of <i>Candida cylindracea</i> lipase sequences. <i>Gene</i> , 1993, 124, 45-55.	1.0	131
147	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
148	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