

# Sonia Longhi

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/5664341/publications.pdf>

Version: 2024-02-01

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  | DisProt in 2022: improved quality and accessibility of protein intrinsic disorder annotation. <i>Nucleic Acids Research</i> , 2022, 50, D480-D487.  | 14.5 | 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.  | 4.1  | 6         |
| 3  | Distribution of Charged Residues Affects the Average Size and Shape of Intrinsically Disordered Proteins. <i>Biomolecules</i> , 2022, 12, 561.  | 4.0  | 11        |
| 4  | Predicting Protein Conformational Disorder and Disordered Binding Sites. <i>Methods in Molecular Biology</i> , 2022, 2449, 95-147.  | 0.9  | 4         |
| 5  | 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        |
| 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. | 4.1  | 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.  | 3.7  | 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, .   | 6.5  | 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.   | 4.0  | 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.  | 14.5 | 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.  | 4.0  | 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.   | 4.1  | 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.   | 4.1  | 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.  | 3.3  | 13        |
| 15 | Predicting substitutions to modulate disorder and stability in coiled-coils. <i>BMC Bioinformatics</i> , 2020, 21, 573.   | 2.6  | 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.  | 3.0  | 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.   | 3.0  | 37        |
| 18 | Regulation of measles virus gene expression by P protein coiled-coil properties. <i>Science Advances</i> , 2019, 5, eaaw3702.   | 10.3 | 31        |

| #  | ARTICLE   | IF   | CITATIONS |
|----|---|------|-----------|
| 19 | Understanding Intramolecular Crosstalk in an Intrinsically Disordered Protein. ACS Chemical Biology, 2019, 14, 337-341.   | 3.4  | 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.                            | 2.8  | 4         |
| 22 | Modulation of Measles Virus NTAIL Interactions through Fuzziness and Sequence Features of Disordered Binding Sites. Biomolecules, 2019, 9, 8.   | 4.0  | 17        |
| 23 | Exploration of nucleoprotein $\hat{\pm}$ -MoRE and XD interactions of Nipah and Hendra viruses. Journal of Molecular Modeling, 2018, 24, 113.   | 1.8  | 2         |
| 24 | How Robust Is the Mechanism of Folding-Upon-Binding for an Intrinsically Disordered Protein?. Biophysical Journal, 2018, 114, 1889-1894.  | 0.5  | 39        |
| 25 | Partner-Mediated Polymorphism of an Intrinsically Disordered Protein. Journal of Molecular Biology, 2018, 430, 2493-2507.   | 4.2  | 18        |
| 26 | Experimental Characterization of Fuzzy Protein Assemblies: Interactions of Paramyxoviral NTAIL Domains With Their Functional Partners. Methods in Enzymology, 2018, 611, 137-192.                               | 1.0  | 8         |
| 27 | InSiDD: A Server for Designing Artificial Disordered Proteins. International Journal of Molecular Sciences, 2018, 19, 91.   | 4.1  | 10        |
| 28 | Conformational response to charge clustering in synthetic intrinsically disordered proteins. Biochimica Et Biophysica Acta - General Subjects, 2018, 1862, 2204-2214.   | 2.4  | 16        |
| 29 | Folding Mechanism of the SH3 Domain from Grb2. Journal of Physical Chemistry B, 2018, 122, 11166-11173.   | 2.6  | 9         |
| 30 | The Folding Pathway of the KIX Domain. ACS Chemical Biology, 2017, 12, 1683-1690.   | 3.4  | 6         |
| 31 | DisProt 7.0: a major update of the database of disordered proteins. Nucleic Acids Research, 2017, 45, D219-D227.  | 14.5 | 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. | 5.4  | 30        |
| 33 | Simultaneous quantification of protein order and disorder. Nature Chemical Biology, 2017, 13, 339-342.  | 8.0  | 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.   | 2.5  | 28        |
| 36 | Interfacial Properties of NTAIL, an Intrinsically Disordered Protein. Biophysical Journal, 2017, 113, 2723-2735.  | 0.5  | 8         |

| #  | ARTICLE  | IF   | CITATIONS |
|----|--|------|-----------|
| 37 | Structural disorder and induced folding within two cereal, ABA stress and ripening (ASR) proteins. <i>Scientific Reports</i> , 2017, 7, 15544.   | 3.3  | 47        |
| 38 | 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        |
| 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.   | 4.7  | 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.   | 3.4  | 18        |
| 42 | Predicting Conformational Disorder. <i>Methods in Molecular Biology</i> , 2016, 1415, 265-299.   | 0.9  | 10        |
| 43 | Fuzzy regions in an intrinsically disordered protein impair protein-protein interactions. <i>FEBS Journal</i> , 2016, 283, 576-594.  | 4.7  | 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.  | 4.1  | 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. | 2.3  | 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.  | 2.4  | 12        |
| 47 | Structural disorder within paramyxoviral nucleoproteins. <i>FEBS Letters</i> , 2015, 589, 2649-2659.   | 2.8  | 19        |
| 48 | Order and Disorder in the Replicative Complex of Paramyxoviruses. <i>Advances in Experimental Medicine and Biology</i> , 2015, 870, 351-381.   | 1.6  | 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.   | 2.6  | 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.   | 2.8  | 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.  | 3.4  | 63        |
| 52 | Sequence of Events in Measles Virus Replication: Role of Phosphoprotein-Nucleocapsid Interactions. <i>Journal of Virology</i> , 2014, 88, 10851-10863.   | 3.4  | 44        |
| 53 | Structural Disorder in Viral Proteins. <i>Chemical Reviews</i> , 2014, 114, 6880-6911.   | 47.7 | 181       |
| 54 | Introducing Protein Intrinsic Disorder. <i>Chemical Reviews</i> , 2014, 114, 6561-6588.  | 47.7 | 628       |

| #  | ARTICLE   | IF  | CITATIONS |
|----|---|-----|-----------|
| 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.  | 2.8 | 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.         | 7.1 | 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.                  | 3.1 | 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.   | 2.4 | 23        |
| 61 | 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        |
| 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.                     | 3.5 | 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.   | 4.7 | 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.  | 3.4 | 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. | 7.1 | 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.  | 3.4 | 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.  | 7.6 | 15        |
| 71 | One-step generation of error-prone PCR libraries using Gateway <sup>®</sup> technology. <i>Microbial Cell Factories</i> , 2012, 11, 14.   | 4.0 | 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         |

| #  | ARTICLE  | IF  | CITATIONS |
|----|--|-----|-----------|
| 73 | 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        |
| 74 | Monitoring Structural Transitions in IDPs by Vibrational Spectroscopy of Cyanylated Cysteine. <i>Methods in Molecular Biology</i> , 2012, 895, 245-270.  | 0.9 | 3         |
| 75 | Monitoring Structural Transitions in IDPs by Site-Directed Spin Labeling EPR Spectroscopy. <i>Methods in Molecular Biology</i> , 2012, 895, 361-386.   | 0.9 | 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.   | 6.5 | 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.   | 1.4 | 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.   | 3.4 | 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.  | 7.1 | 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.  | 2.1 | 48        |
| 84 | Editorial [Hot topic: Structural Disorder in Viral Proteins (Guest Editor: Sonia Longhi)]. <i>Protein and Peptide Letters</i> , 2010, 17, 930-931.   | 0.9 | 11        |
| 85 | Structural Disorder within the Measles Virus Nucleoprotein and Phosphoprotein. <i>Protein and Peptide Letters</i> , 2010, 17, 961-978.   | 0.9 | 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. | 2.1 | 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.   | 4.7 | 18        |
| 88 | Structural Disorder within Henipavirus Nucleoprotein and Phosphoprotein: From Predictions to Experimental Assessment. <i>PLoS ONE</i> , 2010, 5, e11684.   | 2.5 | 78        |
| 89 | Structural Disorder Within Henipavirus Nucleoprotein and Phosphoprotein. <i>Biophysical Journal</i> , 2010, 98, 256a.  | 0.5 | 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.   | 0.5 | 59        |

| #   | ARTICLE  | IF  | CITATIONS |
|-----|--|-----|-----------|
| 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.                             | 0.5 | 47        |
| 92  | Conformational Disorder. <i>Methods in Molecular Biology</i> , 2010, 609, 307-325.   | 0.9 | 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.   | 2.8 | 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.                         | 2.4 | 87        |
| 95  | Modular Organization of Rabies Virus Phosphoprotein. <i>Journal of Molecular Biology</i> , 2009, 388, 978-996.   | 4.2 | 104       |
| 96  | Intrinsic disorder in Viral Proteins Genome-Linked: experimental and predictive analyses. <i>Virology Journal</i> , 2009, 6, 23.   | 3.4 | 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.  | 3.4 | 23        |
| 98  | Nucleocapsid Structure and Function. <i>Current Topics in Microbiology and Immunology</i> , 2009, 329, 103-128.  | 1.1 | 58        |
| 99  | Rules Governing Selective Protein Carbonylation. <i>PLoS ONE</i> , 2009, 4, e7269.   | 2.5 | 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. | 2.6 | 101       |
| 101 | MeDor: a metasever for predicting protein disorder. <i>BMC Genomics</i> , 2008, 9, S25.  | 2.8 | 88        |
| 102 | Ebola Virus VP30 Is an RNA Binding Protein. <i>Journal of Virology</i> , 2007, 81, 8967-8976.  | 3.4 | 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.   | 1.4 | 69        |
| 104 | Protein Engineering. <i>Methods in Molecular Biology</i> , 2007, 363, 59-90.   | 0.9 | 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.  | 2.5 | 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.   | 2.6 | 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.   | 2.6 | 241       |

| #   | ARTICLE   | IF  | CITATIONS |
|-----|---|-----|-----------|
| 109 | Structural disorder within the replicative complex of measles virus: Functional implications. <i>Virology</i> , 2006, 344, 94-110.  | 2.4 | 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.   | 2.9 | 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.             | 7.6 | 139       |
| 112 | Hsp72 recognizes a P binding motif in the measles virus N protein C-terminus. <i>Virology</i> , 2005, 337, 162-174.   | 2.4 | 90        |
| 113 | Assessing protein disorder and induced folding. <i>Proteins: Structure, Function and Bioinformatics</i> , 2005, 62, 24-45.  | 2.6 | 388       |
| 114 | VaZyMoLO: a tool to define and classify modularity in viral proteins. <i>Journal of General Virology</i> , 2005, 86, 743-749.   | 2.9 | 45        |
| 115 | Measles virus nucleoprotein induces cell-proliferation arrest and apoptosis through NTA $\alpha$ -NR and NCOE $\alpha$ -Fc $\beta$ RIIB1 interactions, respectively. <i>Journal of General Virology</i> , 2005, 86, 1771-1784.                                    | 2.9 | 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.   | 3.4 | 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. | 7.1 | 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.  | 2.2 | 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.  | 2.9 | 156       |
| 121 | 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        |
| 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.                                      | 3.4 | 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.  | 3.4 | 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.  | 7.5 | 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.  | 2.4 | 95        |
| 126 | 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        |



| #   | ARTICLE  | IF  | CITATIONS |
|-----|--|-----|-----------|
| 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.  | 3.4 | 29        |
| 128 | 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        |
| 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.   | 2.4 | 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.  | 2.6 | 168       |
| 134 | Packing forces in nine crystal forms of cutinase. <i>Proteins: Structure, Function and Bioinformatics</i> , 1998, 31, 320-333.   | 2.6 | 34        |
| 135 | Messages from ultrahigh resolution crystal structures. <i>Current Opinion in Structural Biology</i> , 1998, 8, 730-737.  | 5.7 | 63        |
| 136 | Exploring hydrophobic sites in proteins with xenon or krypton. <i>Proteins: Structure, Function and Bioinformatics</i> , 1998, 30, 61-73.  | 2.6 | 41        |
| 137 | Packing forces in nine crystal forms of cutinase. <i>Proteins: Structure, Function and Bioinformatics</i> , 1998, 31, 320-33.  | 2.6 | 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.  | 4.2 | 211       |
| 139 | Crystal structure of cutinase covalently inhibited by a triglyceride analogue. <i>Protein Science</i> , 1997, 6, 275-286.  | 7.6 | 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.  | 4.5 | 8         |
| 141 | Acyl glycerol hydrolases: inhibitors, interface and catalysis. <i>Current Opinion in Structural Biology</i> , 1996, 6, 449-455.  | 5.7 | 53        |
| 142 | Contribution of Cutinase Serine 42 Side Chain to the Stabilization of the Oxyanion Transition State. <i>Biochemistry</i> , 1996, 35, 398-410.  | 2.5 | 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. | 2.6 | 57        |
| 144 | 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 | 1         |

| #   | ARTICLE   | IF  | CITATIONS |
|-----|---|-----|-----------|
| 145 | Variability within the <i>Candida rugosa</i> Lipase family. <i>Protein Engineering, Design and Selection</i> , 1994, 7, 531-535.  | 2.1 | 97        |
| 146 | Cloning and analysis of <i>Candida cylindracea</i> lipase sequences. <i>Gene</i> , 1993, 124, 45-55.  | 2.2 | 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        |