

# John M Louis

## List of Publications by Year in descending order

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180  
papers

9,669  
citations

26567

56  
h-index

49773

87  
g-index

190  
all docs

190  
docs citations

190  
times ranked

7170  
citing authors

| #  | ARTICLE   | IF   | CITATIONS |
|----|---|------|-----------|
| 1  | Single-Molecule Fluorescence Experiments Determine Protein Folding Transition Path Times. <i>Science</i> , 2012, 335, 981-984.  | 6.0  | 360       |
| 2  | Characterizing the unfolded states of proteins using single-molecule FRET spectroscopy and molecular simulations. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007, 104, 1528-1533.                            | 3.3  | 327       |
| 3  | Experimental determination of upper bound for transition path times in protein folding from single-molecule photon-by-photon trajectories. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 11837-11844. | 3.3  | 262       |
| 4  | Flap opening and dimer-interface flexibility in the free and inhibitor-bound HIV protease, and their implications for function. <i>Structure</i> , 1999, 7, 1047-S12.   | 1.6  | 243       |
| 5  | A simple apparatus for generating stretched polyacrylamide gels, yielding uniform alignment of proteins and detergent micelles. <i>Journal of Biomolecular NMR</i> , 2001, 21, 377-382.   | 1.6  | 223       |
| 6  | High Resolution Crystal Structures of HIV-1 Protease with a Potent Non-peptide Inhibitor (UIC-94017) Active Against Multi-drug-resistant Clinical Strains. <i>Journal of Molecular Biology</i> , 2004, 338, 341-352.  | 2.0  | 205       |
| 7  | Rapid structural fluctuations of the free HIV protease flaps in solution: Relationship to crystal structures and comparison with predictions of dynamics calculations. <i>Protein Science</i> , 2009, 11, 221-232.  | 3.1  | 186       |
| 8  | Autoprocessing of HIV-1 protease is tightly coupled to protein folding. <i>Nature Structural Biology</i> , 1999, 6, 868-875.  | 9.7  | 168       |
| 9  | NMR study of the tetrameric KcsA potassium channel in detergent micelles. <i>Protein Science</i> , 2006, 15, 684-698.   | 3.1  | 165       |
| 10 | Crystal structure of cyanovirin-N, a potent HIV-inactivating protein, shows unexpected domain swapping. <i>Journal of Molecular Biology</i> , 1999, 288, 403-412.   | 2.0  | 160       |
| 11 | Structure and dynamics of KH domains from FBP bound to single-stranded DNA. <i>Nature</i> , 2002, 415, 1051-1056.   | 13.7 | 150       |
| 12 | The complete influenza hemagglutinin fusion domain adopts a tight helical hairpin arrangement at the lipid:water interface. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 11341-11346.                | 3.3  | 142       |
| 13 | Ultra-high Resolution Crystal Structure of HIV-1 Protease Mutant Reveals Two Binding Sites for Clinical Inhibitor TMC114. <i>Journal of Molecular Biology</i> , 2006, 363, 161-173.   | 2.0  | 136       |
| 14 | Dimerization of the class A G protein-coupled neurotensin receptor NTS1 alters G protein interaction. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007, 104, 12199-12204.                                      | 3.3  | 134       |
| 15 | Structural Basis for SRY-dependent 46-X,Y Sex Reversal: Modulation of DNA Bending by a Naturally Occurring Point Mutation. <i>Journal of Molecular Biology</i> , 2001, 312, 481-499.  | 2.0  | 132       |
| 16 | Structural implications of drug-resistant mutants of HIV-1 protease: High-resolution crystal structures of the mutant protease/substrate analogue complexes. <i>Proteins: Structure, Function and Bioinformatics</i> , 2001, 43, 455-464.                   | 1.5  | 125       |
| 17 | Design of a Novel Peptide Inhibitor of HIV Fusion That Disrupts the Internal Trimeric Coiled-coil of gp41. <i>Journal of Biological Chemistry</i> , 2002, 277, 14238-14245.   | 1.6  | 125       |
| 18 | The structure of a replication initiator unites diverse aspects of nucleic acid metabolism. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2002, 99, 10310-10315.   | 3.3  | 123       |

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|----|--|------|-----------|
| 19 | The Domain-Swapped Dimer of Cyanovirin-N Is in a Metastable Folded State. <i>Structure</i> , 2002, 10, 673-686.  | 1.6  | 123       |
| 20 | Visualizing transient events in amino-terminal autoprocessing of HIV-1 protease. <i>Nature</i> , 2008, 455, 693-696.   | 13.7 | 123       |
| 21 | Evolution of cyclic peptide protease inhibitors. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 11052-11056.  | 3.3  | 118       |
| 22 | Structural and kinetic analysis of drug resistant mutants of HIV-1 protease. <i>FEBS Journal</i> , 1999, 263, 238-244.   | 0.2  | 115       |
| 23 | Kinetic and modeling studies of S3-S3' subsites of HIV proteinases. <i>Biochemistry</i> , 1992, 31, 4793-4800.   | 1.2  | 113       |
| 24 | Comparison of Methyl Rotation Axis Order Parameters Derived from Model-Free Analyses of <sup>2</sup> H and <sup>13</sup> C Longitudinal and Transverse Relaxation Rates Measured in the Same Protein Sample. <i>Journal of the American Chemical Society</i> , 2001, 123, 6164-6171. | 6.6  | 100       |
| 25 | Structure and Orientation of a G Protein Fragment in the Receptor Bound State from Residual Dipolar Couplings. <i>Journal of Molecular Biology</i> , 2002, 322, 441-461.   | 2.0  | 95        |
| 26 | HIV-1 Protease: Structure, Dynamics, and Inhibition. <i>Advances in Pharmacology</i> , 2007, 55, 261-298.  | 1.2  | 95        |
| 27 | Extracting Rate Coefficients from Single-Molecule Photon Trajectories and FRET Efficiency Histograms for a Fast-Folding Protein. <i>Journal of Physical Chemistry A</i> , 2011, 115, 3642-3656.  | 1.1  | 95        |
| 28 | Covalent Trimers of the Internal N-terminal Trimeric Coiled-coil of gp41 and Antibodies Directed against Them Are Potent Inhibitors of HIV Envelope-mediated Cell Fusion. <i>Journal of Biological Chemistry</i> , 2003, 278, 20278-20285.   | 1.6  | 94        |
| 29 | Design and Properties of NCCG-gp41, a Chimeric gp41 Molecule with Nanomolar HIV Fusion Inhibitory Activity. <i>Journal of Biological Chemistry</i> , 2001, 276, 29485-29489.   | 1.6  | 88        |
| 30 | Measurement of <sup>15</sup> N relaxation in the detergent-solubilized tetrameric KcsA potassium channel. <i>Journal of Biomolecular NMR</i> , 2006, 36, 123-136.  | 1.6  | 86        |
| 31 | Hydrophilic Peptides Derived from the Transframe Region of Gag-Pol Inhibit the HIV-1 Protease. <i>Biochemistry</i> , 1998, 37, 2105-2110.  | 1.2  | 85        |
| 32 | Folded Monomer of HIV-1 Protease. <i>Journal of Biological Chemistry</i> , 2001, 276, 49110-49116.   | 1.6  | 85        |
| 33 | A solution NMR study of the binding kinetics and the internal dynamics of an HIV-1 protease-substrate complex. <i>Protein Science</i> , 2003, 12, 1376-1385.   | 3.1  | 84        |
| 34 | Transverse <sup>13</sup> C Relaxation of CHD2 Methyl Isotopomers To Detect Slow Conformational Changes of Protein Side Chains. <i>Journal of the American Chemical Society</i> , 1999, 121, 11589-11590.   | 6.6  | 82        |
| 35 | A Protein Contortionist: Core Mutations of GB1 that Induce Dimerization and Domain Swapping. <i>Journal of Molecular Biology</i> , 2003, 333, 141-152.   | 2.0  | 78        |
| 36 | HIV-1 Protease with 20 Mutations Exhibits Extreme Resistance to Clinical Inhibitors through Coordinated Structural Rearrangements. <i>Biochemistry</i> , 2012, 51, 2819-2828.  | 1.2  | 78        |

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|----|---|-----|-----------|
| 37 | Solution Structure of the Mature HIV-1 Protease Monomer. <i>Journal of Biological Chemistry</i> , 2003, 278, 43311-43319.   | 1.6 | 76        |
| 38 | Insights into Conformation and Dynamics of Protein GB1 During Folding and Unfolding by NMR. <i>Journal of Molecular Biology</i> , 2004, 335, 1299-1307.   | 2.0 | 75        |
| 39 | Solution NMR Structure of the Barrier-to-Autointegration Factor-Emerin Complex. <i>Journal of Biological Chemistry</i> , 2007, 282, 14525-14535.  | 1.6 | 75        |
| 40 | Carbonyl carbon transverse relaxation dispersion measurements and ms- $\mu$ s timescale motion in a protein hydrogen bond network. <i>Journal of Biomolecular NMR</i> , 2004, 29, 187-198.  | 1.6 | 73        |
| 41 | Effect of the Active Site D25N Mutation on the Structure, Stability, and Ligand Binding of the Mature HIV-1 Protease. <i>Journal of Biological Chemistry</i> , 2008, 283, 13459-13470.  | 1.6 | 73        |
| 42 | Autoprocessing of the HIV-1 protease using purified wild-type and mutated fusion proteins expressed at high levels in <i>Escherichia coli</i> . <i>FEBS Journal</i> , 1991, 199, 361-369.   | 0.2 | 71        |
| 43 | Crystal structures of HIV protease V82A and L90M mutants reveal changes in the indinavir-binding site. <i>FEBS Journal</i> , 2004, 271, 1516-1524.  | 0.2 | 71        |
| 44 | pH-triggered, activated-state conformations of the influenza hemagglutinin fusion peptide revealed by NMR. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 19994-19999.                         | 3.3 | 71        |
| 45 | Covalent narpaprevir- and boceprevir-derived hybrid inhibitors of SARS-CoV-2 main protease. <i>Nature Communications</i> , 2022, 13, 2268.  | 5.8 | 69        |
| 46 | Kinetic, Stability, and Structural Changes in High-resolution Crystal Structures of HIV-1 Protease with Drug-resistant Mutations L24I, I50V, and G73S. <i>Journal of Molecular Biology</i> , 2005, 354, 789-800.                                    | 2.0 | 68        |
| 47 | HIV-1 protease: Maturation, enzyme specificity, and drug resistance. <i>Advances in Pharmacology</i> , 2000, 49, 111-146.   | 1.2 | 67        |
| 48 | Effect of sequence polymorphism and drug resistance on two HIV-1 Gag processing sites. <i>FEBS Journal</i> , 2002, 269, 4114-4120.  | 0.2 | 64        |
| 49 | The effect of salt on the Michaelis-Menten constant of the HIV-1 protease correlates with the Hofmeister series. <i>FEBS Letters</i> , 1991, 280, 344-346.  | 1.3 | 63        |
| 50 | Inhibition of autoprocessing of natural variants and multidrug resistant mutant precursors of HIV-1 protease by clinical inhibitors. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 9072-9077. | 3.3 | 63        |
| 51 | Comparison of the substrate specificity of the human T-cell leukemia virus and human immunodeficiency virus proteinases. <i>FEBS Journal</i> , 2000, 267, 6287-6295.  | 0.2 | 59        |
| 52 | Conformational Changes in HIV-1 gp41 in the Course of HIV-1 Envelope Glycoprotein-Mediated Fusion and Inactivation. <i>Biochemistry</i> , 2005, 44, 12471-12479.  | 1.2 | 59        |
| 53 | Preparation of Uniformly Isotope-labeled DNA Oligonucleotides for NMR Spectroscopy. <i>Journal of Biological Chemistry</i> , 1998, 273, 2374-2378.  | 1.6 | 58        |
| 54 | Mapping the Binding of the N-terminal Extracellular Tail of the CXCR4 Receptor to Stromal Cell-derived Factor-1 $\alpha$ . <i>Journal of Molecular Biology</i> , 2005, 345, 651-658.  | 2.0 | 58        |

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|----|--|-----|-----------|
| 55 | Co-evolutionary Fitness Landscapes for Sequence Design. <i>Angewandte Chemie - International Edition</i> , 2018, 57, 5674-5678.  | 7.2 | 58        |
| 56 | A Transient Precursor of the HIV-1 Protease. <i>Journal of Biological Chemistry</i> , 1996, 271, 4477-4481.  | 1.6 | 57        |
| 57 | Cross-reactive HIV-1 neutralizing monoclonal antibodies selected by screening of an immune human phage library against an envelope glycoprotein (gp140) isolated from a patient (R2) with broadly HIV-1 neutralizing antibodies. <i>Virology</i> , 2007, 363, 79-90. | 1.1 | 57        |
| 58 | Internal Dynamics of the Homotrimeric HIV-1 Viral Coat Protein gp41 on Multiple Time Scales. <i>Angewandte Chemie - International Edition</i> , 2013, 52, 3911-3915.   | 7.2 | 57        |
| 59 | Testing Landscape Theory for Biomolecular Processes with Single Molecule Fluorescence Spectroscopy. <i>Physical Review Letters</i> , 2015, 115, 018101.  | 2.9 | 57        |
| 60 | Distinguishing between Protein Dynamics and Dye Photophysics in Single-Molecule FRET Experiments. <i>Biophysical Journal</i> , 2010, 98, 696-706.  | 0.2 | 55        |
| 61 | Proteolytic Processing of HIV-1 Protease Precursor, Kinetics and Mechanism. <i>Journal of Biological Chemistry</i> , 1999, 274, 23437-23442.   | 1.6 | 54        |
| 62 | Chemical synthesis and expression of the HIV-1 protease gene in E.coli. <i>Biochemical and Biophysical Research Communications</i> , 1989, 159, 87-94.   | 1.0 | 52        |
| 63 | Stabilization from Autoproteolysis and Kinetic Characterization of the Human T-cell Leukemia Virus Type 1 Proteinase. <i>Journal of Biological Chemistry</i> , 1999, 274, 6660-6666.   | 1.6 | 52        |
| 64 | Revisiting Monomeric HIV-1 Protease. <i>Journal of Biological Chemistry</i> , 2003, 278, 6085-6092.  | 1.6 | 51        |
| 65 | Mutational and Structural Studies Aimed at Characterizing the Monomer of HIV-1 Protease and Its Precursor. <i>Journal of Biological Chemistry</i> , 2007, 282, 17190-17199.  | 1.6 | 51        |
| 66 | Antibody elicited against the gp41 N-heptad repeat (NHR) coiled-coil can neutralize HIV-1 with modest potency but non-neutralizing antibodies also bind to NHR mimetics. <i>Virology</i> , 2008, 377, 170-183.   | 1.1 | 50        |
| 67 | Influence of Flanking Sequences on the Dimer Stability of Human Immunodeficiency Virus Type 1 Protease. <i>Biochemistry</i> , 1996, 35, 12957-12962.   | 1.2 | 49        |
| 68 | A Captured Folding Intermediate Involved in Dimerization and Domain-swapping of GB1. <i>Journal of Molecular Biology</i> , 2004, 340, 615-625.   | 2.0 | 49        |
| 69 | Mechanism of Drug Resistance Revealed by the Crystal Structure of the Unliganded HIV-1 Protease with F53L Mutation. <i>Journal of Molecular Biology</i> , 2006, 358, 1191-1199.  | 2.0 | 48        |
| 70 | Characterization of two hydrophobic methyl clusters in HIV-1 protease by NMR spin relaxation in solution. Edited by P. E. Wright. <i>Journal of Molecular Biology</i> , 2001, 305, 515-521.  | 2.0 | 47        |
| 71 | Combining mutations in HIV-1 protease to understand mechanisms of resistance. <i>Proteins: Structure, Function and Bioinformatics</i> , 2002, 48, 107-116.   | 1.5 | 46        |
| 72 | The GB1 Amyloid Fibril: Recruitment of the Peripheral $\beta$ -Strands of the Domain Swapped Dimer into the Polymeric Interface. <i>Journal of Molecular Biology</i> , 2005, 348, 687-698.   | 2.0 | 45        |

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|----|---|-----|-----------|
| 73 | Oligomerization of the tetramerization domain of p53 probed by two- and three-color single-molecule FRET. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, E6812-E6821.                                  | 3.3 | 45        |
| 74 | Caught in the Act: The 1.5 Å... Resolution Crystal Structures of the HIV-1 Protease and the I54V Mutant Reveal a Tetrahedral Reaction Intermediate. Biochemistry, 2007, 46, 14854-14864.  | 1.2 | 44        |
| 75 | Structural Evidence for Effectiveness of Darunavir and Two Related Antiviral Inhibitors against HIV-2 Protease. Journal of Molecular Biology, 2008, 384, 178-192.   | 2.0 | 44        |
| 76 | Structural Basis of HIV-1 Neutralization by Affinity Matured Fabs Directed against the Internal Trimeric Coiled-Coil of gp41. PLoS Pathogens, 2010, 6, e1001182.  | 2.1 | 44        |
| 77 | The gag precursor contains a specific HIV-1 protease cleavage site between the NC (P7) and P1 proteins. FEBS Letters, 1993, 333, 21-24.   | 1.3 | 43        |
| 78 | Measuring ultrafast protein folding rates from photon-by-photon analysis of single molecule fluorescence trajectories. Chemical Physics, 2013, 422, 229-237.  | 0.9 | 43        |
| 79 | Long-Range Electrostatics-Induced Two-Proton Transfer Captured by Neutron Crystallography in an Enzyme Catalytic Site. Angewandte Chemie - International Edition, 2016, 55, 4924-4927.  | 7.2 | 42        |
| 80 | Structural Basis for Specificity of Retroviral Proteases. Biochemistry, 1998, 37, 4518-4526.  | 1.2 | 41        |
| 81 | The point mutation A34F causes dimerization of GB1. Proteins: Structure, Function and Bioinformatics, 2008, 71, 1420-1431.  | 1.5 | 41        |
| 82 | Dissociation of the trimeric gp41 ectodomain at the lipid-water interface suggests an active role in HIV-1 Env-mediated membrane fusion. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 3425-3430.     | 3.3 | 41        |
| 83 | A diverse view of protein dynamics from NMR studies of HIV-1 protease flaps. Proteins: Structure, Function and Bioinformatics, 2008, 70, 1408-1415.   | 1.5 | 40        |
| 84 | Crystallographic Analysis of Human Immunodeficiency Virus 1 Protease with an Analog of the Conserved CA-p2 Substrate. Interactions with Frequently Occurring Glutamic Acid Residue at P2' Position of Substrates. FEBS Journal, 1997, 249, 523-530. | 0.2 | 39        |
| 85 | A rapid method to attain isotope labeled small soluble peptides for NMR studies. Journal of Biomolecular NMR, 2003, 26, 193-202.  | 1.6 | 39        |
| 86 | Tilted, Uninterrupted, Monomeric HIV-1 gp41 Transmembrane Helix from Residual Dipolar Couplings. Journal of the American Chemical Society, 2018, 140, 34-37.  | 6.6 | 39        |
| 87 | Structural Studies of a Rationally Selected Multi-Drug Resistant HIV-1 Protease Reveal Synergistic Effect of Distal Mutations on Flap Dynamics. PLoS ONE, 2016, 11, e0168616.   | 1.1 | 39        |
| 88 | Critical differences in HIV-1 and HIV-2 protease specificity for clinical inhibitors. Protein Science, 2012, 21, 339-350.   | 3.1 | 38        |
| 89 | Dependence of Distance Distributions Derived from Double Electron-Electron Resonance Pulsed EPR Spectroscopy on Pulse Sequence Time. Angewandte Chemie - International Edition, 2015, 54, 5336-5339.  | 7.2 | 38        |
| 90 | Effect of substrate residues on the P2' preference of retroviral proteinases. FEBS Journal, 1999, 264, 921-929.   | 0.2 | 37        |

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|-----|--|-----|-----------|
| 91  | A Monoclonal Fab Derived from a Human Nonimmune Phage Library Reveals a New Epitope on gp41 and Neutralizes Diverse Human Immunodeficiency Virus Type 1 Strains. <i>Journal of Virology</i> , 2007, 81, 12946-12953.                                 | 1.5 | 37        |
| 92  | Helical Hairpin Structure of Influenza Hemagglutinin Fusion Peptide Stabilized by Charge-Dipole Interactions between the N-Terminal Amino Group and the Second Helix. <i>Journal of the American Chemical Society</i> , 2011, 133, 2824-2827.        | 6.6 | 36        |
| 93  | Observation of $\beta^2$ -Amyloid Peptide Oligomerization by Pressure-Jump NMR Spectroscopy. <i>Journal of the American Chemical Society</i> , 2019, 141, 13762-13766.   | 6.6 | 36        |
| 94  | Studies on the Symmetry and Sequence Context Dependence of the HIV-1 Proteinase Specificity. <i>Journal of Biological Chemistry</i> , 1997, 272, 16807-16814.  | 1.6 | 35        |
| 95  | Binding kinetics and substrate selectivity in HIV-1 protease-Gag interactions probed at atomic resolution by chemical exchange NMR. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, E9855-E9862. | 3.3 | 35        |
| 96  | Extreme Multidrug Resistant HIV-1 Protease with 20 Mutations Is Resistant to Novel Protease Inhibitors with P1-Pyrrolidinone or P2-Tris-tetrahydrofuran. <i>Journal of Medicinal Chemistry</i> , 2013, 56, 4017-4027.                                | 2.9 | 34        |
| 97  | Analysis of Fluorescence Lifetime and Energy Transfer Efficiency in Single-Molecule Photon Trajectories of Fast-Folding Proteins. <i>Journal of Physical Chemistry B</i> , 2016, 120, 680-699.   | 1.2 | 34        |
| 98  | Local and global structure of the monomeric subunit of the potassium channel KcsA probed by NMR. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 2007, 1768, 3260-3270.  | 1.4 | 33        |
| 99  | Three-Color Single-Molecule FRET and Fluorescence Lifetime Analysis of Fast Protein Folding. <i>Journal of Physical Chemistry B</i> , 2018, 122, 11702-11720.  | 1.2 | 33        |
| 100 | Substitution mutations of the highly conserved arginine 87 of HIV-1 protease result in loss of proteolytic activity. <i>Biochemical and Biophysical Research Communications</i> , 1989, 164, 30-38.  | 1.0 | 32        |
| 101 | Solution Structure of a Circular-permuted Variant of the Potent HIV-inactivating Protein Cyanovirin-N: Structural Basis for Protein Stability and Oligosaccharide Interaction. <i>Journal of Molecular Biology</i> , 2003, 325, 211-223.             | 2.0 | 32        |
| 102 | Structural, Electronic, and Electrostatic Determinants for Inhibitor Binding to Subsites S1 and S2 in SARS-CoV-2 Main Protease. <i>Journal of Medicinal Chemistry</i> , 2021, 64, 17366-17383.   | 2.9 | 32        |
| 103 | Optimized labeling of $^{13}\text{C}$ HD2 methyl isotopomers in perdeuterated proteins: potential advantages for $^{13}\text{C}$ relaxation studies of methyl dynamics of larger proteins. <i>Journal of Biomolecular NMR</i> , 2001, 21, 167-171.   | 1.6 | 30        |
| 104 | Evidence of Distinct Channel Conformations and Substrate Binding Affinities for the Mitochondrial Outer Membrane Protein Translocase Pore Tom40. <i>Journal of Biological Chemistry</i> , 2015, 290, 26204-26217.                                    | 1.6 | 30        |
| 105 | The Regulation of Dictyostelium Development by Transmembrane Signalling. <i>Journal of Eukaryotic Microbiology</i> , 1995, 42, 200-205.  | 0.8 | 29        |
| 106 | Whole-Body Rocking Motion of a Fusion Peptide in Lipid Bilayers from Size-Dispersed $^{15}\text{N}$ NMR Relaxation. <i>Journal of the American Chemical Society</i> , 2011, 133, 14184-14187.  | 6.6 | 29        |
| 107 | Terminal Interface Conformations Modulate Dimer Stability Prior to Amino Terminal Autoprocessing of HIV-1 Protease. <i>Biochemistry</i> , 2012, 51, 1041-1050.   | 1.2 | 29        |
| 108 | Probing the mechanism of inhibition of amyloid- $\beta^2$ (1-42)-induced neurotoxicity by the chaperonin GroEL. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, E11924-E11932.                   | 3.3 | 29        |

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|-----|--|-----|-----------|
| 109 | Biophysical Characterization of gp41 Aggregates Suggests a Model for the Molecular Mechanism of HIV-associated Neurological Damage and Dementia. <i>Journal of Biological Chemistry</i> , 2000, 275, 19877-19882.  | 1.6 | 28        |
| 110 | Transient lipid-bound states of spike protein heptad repeats provide insights into SARS-CoV-2 membrane fusion. <i>Science Advances</i> , 2021, 7, eabk2226.  | 4.7 | 28        |
| 111 | Structure and dynamics of MarA-DNA complexes: an NMR investigation. <i>Journal of Molecular Biology</i> , 2001, 314, 113-127.  | 2.0 | 27        |
| 112 | Characterization and HIV-1 Fusion Inhibitory Properties of Monoclonal Fabs Obtained From a Human Non-immune Phage Library Selected Against Diverse Epitopes of the Ectodomain of HIV-1 gp41. <i>Journal of Molecular Biology</i> , 2005, 353, 945-951.   | 2.0 | 27        |
| 113 | Fast three-color single-molecule FRET using statistical inference. <i>Nature Communications</i> , 2020, 11, 3336.  | 5.8 | 27        |
| 114 | The impact of influenza hemagglutinin fusion peptide length and viral subtype on its structure and dynamics. <i>Biopolymers</i> , 2013, 99, 189-195.   | 1.2 | 26        |
| 115 | Structures of Darunavir-Resistant HIV-1 Protease Mutant Reveal Atypical Binding of Darunavir to Wide Open Flaps. <i>ACS Chemical Biology</i> , 2014, 9, 1351-1358.   | 1.6 | 26        |
| 116 | Allosteric control of hemoglobin S fiber formation by oxygen and its relation to the pathophysiology of sickle cell disease. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 15018-15027.  | 3.3 | 26        |
| 117 | The L76V Drug Resistance Mutation Decreases the Dimer Stability and Rate of Autoprocessing of HIV-1 Protease by Reducing Internal Hydrophobic Contacts. <i>Biochemistry</i> , 2011, 50, 4786-4795.   | 1.2 | 25        |
| 118 | Conformation of Inhibitor-Free HIV-1 Protease Derived from NMR Spectroscopy in a Weakly Oriented Solution. <i>ChemBioChem</i> , 2015, 16, 214-218.   | 1.3 | 25        |
| 119 | Transient HIV-1 Gag-protease interactions revealed by paramagnetic NMR suggest origins of compensatory drug resistance mutations. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, 12456-12461.   | 3.3 | 25        |
| 120 | Room Temperature Neutron Crystallography of Drug Resistant HIV-1 Protease Uncovers Limitations of X-ray Structural Analysis at 100 K. <i>Journal of Medicinal Chemistry</i> , 2017, 60, 2018-2025.   | 2.9 | 25        |
| 121 | Michaelis-like complex of SARS-CoV-2 main protease visualized by room-temperature X-ray crystallography. <i>IUCr</i> , 2021, 8, 973-979.   | 1.0 | 25        |
| 122 | Synergistic Inhibition of HIV-1 Envelope-Mediated Membrane Fusion by Inhibitors Targeting the N and C-Terminal Heptad Repeats of gp41. <i>Journal of Molecular Biology</i> , 2006, 364, 283-289.   | 2.0 | 23        |
| 123 | Temperature-Dependent Intermediates in HIV-1 Envelope Glycoprotein-Mediated Fusion Revealed by Inhibitors that Target N- and C-Terminal Helical Regions of HIV-1 gp41. <i>Biochemistry</i> , 2004, 43, 8230-8233.  | 1.2 | 22        |
| 124 | Mixed-time parallel evolution in multiple quantum NMR experiments: sensitivity and resolution enhancement in heteronuclear NMR. <i>Journal of Biomolecular NMR</i> , 2007, 37, 195-204.  | 1.6 | 22        |
| 125 | Affinity maturation by targeted diversification of the CDR-H2 loop of a monoclonal Fab derived from a synthetic naïve human antibody library and directed against the internal trimeric coiled-coil of gp41 yields a set of Fabs with improved HIV-1 neutralization potency and breadth. <i>Virology</i> , 2009, 393, 112-119. | 1.1 | 22        |
| 126 | Revealing the dimer dissociation and existence of a folded monomer of the mature HIV-2 protease. <i>Protein Science</i> , 2009, 18, 2442-2453.   | 3.1 | 22        |



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|-----|---|-----|-----------|
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