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List of Publications by Year
in descending order

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180 papers	9,669 citations	26630 56 h-index	49909 87 g-index
190 all docs	190 docs citations	190 times ranked	7170 citing authors

#	Article	IF	Citations
1	Modulation of the monomer-dimer equilibrium and catalytic activity of SARS-CoV-2 main protease by a transition-state analog inhibitor. Communications Biology, 2022, 5, 160.	4.4	20
2	Covalent narlaprevir- and boceprevir-derived hybrid inhibitors of SARS-CoV-2 main protease. Nature Communications, 2022, 13, 2268.	12.8	69
3	Real-time Exchange of the Lipid-bound Intermediate and Post-fusion States of the HIV-1 gp41 Ectodomain. Journal of Molecular Biology, 2022, 434, 167683.	4.2	2
4	Concentrationâ€Dependent Structural Transition of the HIVâ€1 gp41 MPER Peptide into Î±â€Helical Trimers. Angewandte Chemie, 2021, 133, 168-172.	2.0	0
5	Concentrationâ€Dependent Structural Transition of the HIVâ€1 gp41 MPER Peptide into Î±â€Helical Trimers. Angewandte Chemie - International Edition, 2021, 60, 166-170.	13.8	5
6	A weakened interface in the P182L variant of HSP27 associated with severe Charcotâ€Marieâ€Tooth neuropathy causes aberrant binding to interacting proteins. EMBO Journal, 2021, 40, e103811.	7.8	14
7	MWC allosteric model explains unusual hemoglobin-oxygen binding curves from sickle cell drug binding. Biophysical Journal, 2021, 120, 2543-2551.	0.5	11
8	Constraints on the Structure of Fibrils Formed by a Racemic Mixture of Amyloid-Î² Peptides from Solid-State NMR, Electron Microscopy, and Theory. Journal of the American Chemical Society, 2021, 143, 13299-13313.	13.7	17
9	Michaelis-like complex of SARS-CoV-2 main protease visualized by room-temperature X-ray crystallography. IUCrJ, 2021, 8, 973-979.	2.2	25
10	Transient lipid-bound states of spike protein heptad repeats provide insights into SARS-CoV-2 membrane fusion. Science Advances, 2021, 7, eabk2226.	10.3	28
11	Structural, Electronic, and Electrostatic Determinants for Inhibitor Binding to Subsites S1 and S2 in SARS-CoV-2 Main Protease. Journal of Medicinal Chemistry, 2021, 64, 17366-17383.	6.4	32
12	Probing the Interaction between HIVâ€1 Protease and the Homodimeric p66/p66â€™ Reverse Transcriptase Precursor by Double Electronâ€Electron Resonance EPR Spectroscopy. ChemBioChem, 2020, 21, 3051-3055.	2.6	3
13	Allosteric control of hemoglobin S fiber formation by oxygen and its relation to the pathophysiology of sickle cell disease. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 15018-15027.	7.1	26
14	Visualizing Tetrahedral Oxyanion Bound in HIV-1 Protease Using Neutrons: Implications for the Catalytic Mechanism and Drug Design. ACS Omega, 2020, 5, 11605-11617.	3.5	6
15	Fast three-color single-molecule FRET using statistical inference. Nature Communications, 2020, 11, 3336.	12.8	27
16	Effects of an HIV-1 maturation inhibitor on the structure and dynamics of CA-SP1 junction helices in virus-like particles. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 10286-10293.	7.1	19
17	Proton transfer and drug binding details revealed in neutron diffraction studies of wild-type and drug resistant HIV-1 protease. Methods in Enzymology, 2020, 634, 257-279.	1.0	4
18	Importance of time-ordered non-uniform sampling of multi-dimensional NMR spectra of AÎ²1â€“42 peptide under aggregating conditions. Journal of Biomolecular NMR, 2019, 73, 429-441.	2.8	15

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19	Observation of Î²-Amyloid Peptide Oligomerization by Pressure-Jump NMR Spectroscopy. Journal of the American Chemical Society, 2019, 141, 13762-13766.	13.7	36
20	Diverse Folding Pathways of HIV-1 Protease Monomer on a Rugged Energy Landscape. Biophysical Journal, 2019, 117, 1456-1466.	0.5	5
21	Inhibition of HIV Maturation via Selective Unfolding and Cross-Linking of Gag Polyprotein by a Mercaptobenzamide Acetylator. Journal of the American Chemical Society, 2019, 141, 8327-8338.	13.7	4
22	Coâ€Evolutionary Fitness Landscapes for Sequence Design. Angewandte Chemie - International Edition, 2018, 57, 5674-5678.	13.8	58
23	Coâ€Evolutionary Fitness Landscapes for Sequence Design. Angewandte Chemie, 2018, 130, 5776-5780.	2.0	5
24	InnenrÃ¼cktitelbild: Co-Evolutionary Fitness Landscapes for Sequence Design (Angew. Chem. 20/2018). Angewandte Chemie, 2018, 130, 6061-6061.	2.0	1
25	Tilted, Uninterrupted, Monomeric HIV-1 gp41 Transmembrane Helix from Residual Dipolar Couplings. Journal of the American Chemical Society, 2018, 140, 34-37.	13.7	39
26	Probing the mechanism of inhibition of amyloid-Î²(1â€“42)â€“induced neurotoxicity by the chaperonin GroEL. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, E11924-E11932.	7.1	29
27	Three-Color Single-Molecule FRET and Fluorescence Lifetime Analysis of Fast Protein Folding. Journal of Physical Chemistry B, 2018, 122, 11702-11720.	2.6	33
28	Room Temperature Neutron Crystallography of Drug Resistant HIV-1 Protease Uncovers Limitations of X-ray Structural Analysis at 100 K. Journal of Medicinal Chemistry, 2017, 60, 2018-2025.	6.4	25
29	Binding kinetics and substrate selectivity in HIV-1 proteaseâ^'Gag interactions probed at atomic resolution by chemical exchange NMR. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, E9855-E9862.	7.1	35
30	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.	7.1	45
31	Longâ€Range Electrostaticsâ€Induced Twoâ€Proton Transfer Captured by Neutron Crystallography in an Enzyme Catalytic Site. Angewandte Chemie, 2016, 128, 5008-5011.	2.0	6
32	Longâ€Range Electrostaticsâ€Induced Twoâ€Proton Transfer Captured by Neutron Crystallography in an Enzyme Catalytic Site. Angewandte Chemie - International Edition, 2016, 55, 4924-4927.	13.8	42
33	Binding of Clinical Inhibitors to a Model Precursor of a Rationally Selected Multidrug Resistant HIV-1 Protease Is Significantly Weaker Than That to the Released Mature Enzyme. Biochemistry, 2016, 55, 2390-2400.	2.5	21
34	Transient HIV-1 Gagâ€“protease interactions revealed by paramagnetic NMR suggest origins of compensatory drug resistance mutations. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, 12456-12461.	7.1	25
35	Evolution under Drug Pressure Remodels the Folding Free-Energy Landscape of Mature HIV-1 Protease. Journal of Molecular Biology, 2016, 428, 2780-2792.	4.2	15
36	Analysis of Fluorescence Lifetime and Energy Transfer Efficiency in Single-Molecule Photon Trajectories of Fast-Folding Proteins. Journal of Physical Chemistry B, 2016, 120, 680-699.	2.6	34

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37	Insights into the Conformation of the Membrane Proximal Regions Critical to the Trimerization of the HIV-1 gp41 Ectodomain Bound to Dodecyl Phosphocholine Micelles. PLoS ONE, 2016, 11, e0160597.	2.5	13
38	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.	2.5	39
39	Testing Landscape Theory for Biomolecular Processes with Single Molecule Fluorescence Spectroscopy. Physical Review Letters, 2015, 115, 018101.	7.8	57
40	Pressureâ€induced structural transition of mature <scp>HIV</scp>â€1 protease from a combined <scp>NMR/MD</scp> simulation approach. Proteins: Structure, Function and Bioinformatics, 2015, 83, 2117-2123.	2.6	21
41	Substituted Bis-THF Protease Inhibitors with Improved Potency against Highly Resistant Mature HIV-1 Protease PR20. Journal of Medicinal Chemistry, 2015, 58, 5088-5095.	6.4	8
42	Dependence of Distance Distributions Derived from Double Electronâ€“Electron Resonance Pulsed EPR Spectroscopy on Pulseâ€Sequence Time. Angewandte Chemie - International Edition, 2015, 54, 5336-5339.	13.8	38
43	The C34 Peptide Fusion Inhibitor Binds to the Six-Helix Bundle Core Domain of HIV-1 gp41 by Displacement of the C-Terminal Helical Repeat Region. Biochemistry, 2015, 54, 6796-6805.	2.5	11
44	Complete dissociation of the HIV-1 gp41 ectodomain and membrane proximal regions upon phospholipid binding. Journal of Biomolecular NMR, 2015, 61, 235-248.	2.8	15
45	Evidence of Distinct Channel Conformations and Substrate Binding Affinities for the Mitochondrial Outer Membrane Protein Translocase Pore Tom40. Journal of Biological Chemistry, 2015, 290, 26204-26217.	3.4	30
46	Mutations Proximal to Sites of Autoproteolysis and the Î±-Helix That Co-evolve under Drug Pressure Modulate the Autoprocessing and Vitality of HIV-1 Protease. Biochemistry, 2015, 54, 5414-5424.	2.5	11
47	Conformation of Inhibitorâ€Free HIVâ€1 Protease Derived from NMR Spectroscopy in a Weakly Oriented Solution. ChemBioChem, 2015, 16, 214-218.	2.6	25
48	Binding of HIV-1 gp41-Directed Neutralizing and Non-Neutralizing Fragment Antibody Binding Domain (Fab) and Single Chain Variable Fragment (ScFv) Antibodies to the Ectodomain of gp41 in the Pre-Hairpin and Six-Helix Bundle Conformations. PLoS ONE, 2014, 9, e104683.	2.5	7
49	Dissociation of the trimeric gp41 ectodomain at the lipidâ€“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.	7.1	41
50	Structures of Darunavir-Resistant HIV-1 Protease Mutant Reveal Atypical Binding of Darunavir to Wide Open Flaps. ACS Chemical Biology, 2014, 9, 1351-1358.	3.4	26
51	Modulating alignment of membrane proteins in liquid-crystalline and oriented gel media by changing the size and charge of phospholipid bicelles. Journal of Biomolecular NMR, 2013, 55, 369-377.	2.8	13
52	Enhanced Stability of Monomer Fold Correlates with Extreme Drug Resistance of HIV-1 Protease. Biochemistry, 2013, 52, 7678-7688.	2.5	9
53	Measuring ultrafast protein folding rates from photon-by-photon analysis of single molecule fluorescence trajectories. Chemical Physics, 2013, 422, 229-237.	1.9	43
54	Internal Dynamics of the Homotrimeric HIVâ€1 Viral Coat Protein gp41 on Multiple Time Scales. Angewandte Chemie - International Edition, 2013, 52, 3911-3915.	13.8	57

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55	Extreme Multidrug Resistant HIV-1 Protease with 20 Mutations Is Resistant to Novel Protease Inhibitors with P1â€²-Pyrrolidinone or P2-Tris-tetrahydrofuran. Journal of Medicinal Chemistry, 2013, 56, 4017-4027.	6.4	34
56	The impact of influenza hemagglutinin fusion peptide length and viral subtype on its structure and dynamics. Biopolymers, 2013, 99, 189-195.	2.4	26
57	Complexes of Neutralizing and Non-Neutralizing Affinity Matured Fabs with a Mimetic of the Internal Trimeric Coiled-Coil of HIV-1 gp41. PLoS ONE, 2013, 8, e78187.	2.5	17
58	Terminal Interface Conformations Modulate Dimer Stability Prior to Amino Terminal Autoprocessing of HIV-1 Protease. Biochemistry, 2012, 51, 1041-1050.	2.5	29
59	Mechanism of Dissociative Inhibition of HIV Protease and Its Autoprocessing from a Precursor. Journal of Molecular Biology, 2012, 422, 230-244.	4.2	7
60	pH-triggered, activated-state conformations of the influenza hemagglutinin fusion peptide revealed by NMR. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 19994-19999.	7.1	71
61	Critical differences in HIVâ€1 and HIVâ€2 protease specificity for clinical inhibitors. Protein Science, 2012, 21, 339-350.	7.6	38
62	HIV-1 Protease with 20 Mutations Exhibits Extreme Resistance to Clinical Inhibitors through Coordinated Structural Rearrangements. Biochemistry, 2012, 51, 2819-2828.	2.5	78
63	Single-Molecule Fluorescence Experiments Determine Protein Folding Transition Path Times. Science, 2012, 335, 981-984.	12.6	360
64	Helical Hairpin Structure of Influenza Hemagglutinin Fusion Peptide Stabilized by Chargeâ^'Dipole Interactions between the N-Terminal Amino Group and the Second Helix. Journal of the American Chemical Society, 2011, 133, 2824-2827.	13.7	36
65	Whole-Body Rocking Motion of a Fusion Peptide in Lipid Bilayers from Size-Dispersed ¹⁵N NMR Relaxation. Journal of the American Chemical Society, 2011, 133, 14184-14187.	13.7	29
66	The L76V Drug Resistance Mutation Decreases the Dimer Stability and Rate of Autoprocessing of HIV-1 Protease by Reducing Internal Hydrophobic Contacts. Biochemistry, 2011, 50, 4786-4795.	2.5	25
67	Extracting Rate Coefficients from Single-Molecule Photon Trajectories and FRET Efficiency Histograms for a Fast-Folding Protein. Journal of Physical Chemistry A, 2011, 115, 3642-3656.	2.5	95
68	NMR solution structure of a cyanovirin homolog from wheat head blight fungus. Proteins: Structure, Function and Bioinformatics, 2011, 79, 1538-1549.	2.6	16
69	Evolution of cyclic peptide protease inhibitors. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 11052-11056.	7.1	118
70	Inhibition of autoprocessing of natural variants and multidrug resistant mutant precursors of HIV-1 protease by clinical inhibitors. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 9072-9077.	7.1	63
71	Autocatalytic maturation, physical/chemical properties, and crystal structure of group N HIVâ€1 protease: Relevance to drug resistance. Protein Science, 2010, 19, 2055-2072.	7.6	22
72	Highly conserved glycine 86 and arginine 87 residues contribute differently to the structure and activity of the mature HIVâ€1 protease. Proteins: Structure, Function and Bioinformatics, 2010, 78, 1015-1025.	2.6	18

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73	Structural Basis of HIV-1 Neutralization by Affinity Matured Fabs Directed against the Internal Trimeric Coiled-Coil of gp41. PLoS Pathogens, 2010, 6, e1001182.	4.7	44
74	Distinguishing between Protein Dynamics and Dye Photophysics inÂSingle-Molecule FRET Experiments. Biophysical Journal, 2010, 98, 696-706.	0.5	55
75	The complete influenza hemagglutinin fusion domain adopts a tight helical hairpin arrangement at the lipid:water interface. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 11341-11346.	7.1	142
76	Experimental determination of upper bound for transition path times in protein folding from single-molecule photon-by-photon trajectories. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 11837-11844.	7.1	262
77	Modulation of Human Immunodeficiency Virus Type 1 Protease Autoprocessing by Charge Properties of Surface Residue 69. Journal of Virology, 2009, 83, 7789-7793.	3.4	13
78	Affinity maturation by targeted diversification of the CDR-H2 loop of a monoclonal Fab derived from a synthetic naÃ¯ve 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. Virology, 2009, 393, 112-119.	2.4	22
79	Interactions of different inhibitors with activeâ€site aspartyl residues of HIVâ€1 protease and possible relevance to pepsin. Proteins: Structure, Function and Bioinformatics, 2009, 75, 556-568.	2.6	21
80	Revealing the dimer dissociation and existence of a folded monomer of the mature HIVâ€2 protease. Protein Science, 2009, 18, 2442-2453.	7.6	22
81	Rapid structural fluctuations of the free HIV protease flaps in solution: Relationship to crystal structures and comparison with predictions of dynamics calculations. Protein Science, 2009, 11, 221-232.	7.6	186
82	A diverse view of protein dynamics from NMR studies of HIVâ€1 protease flaps. Proteins: Structure, Function and Bioinformatics, 2008, 70, 1408-1415.	2.6	40
83	The point mutation A34F causes dimerization of GB1. Proteins: Structure, Function and Bioinformatics, 2008, 71, 1420-1431.	2.6	41
84	Visualizing transient events in amino-terminal autoprocessing of HIV-1 protease. Nature, 2008, 455, 693-696.	27.8	123
85	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. Virology, 2008, 377, 170-183.	2.4	50
86	Structural Evidence for Effectiveness of Darunavir and Two Related Antiviral Inhibitors against HIV-2 Protease. Journal of Molecular Biology, 2008, 384, 178-192.	4.2	44
87	Effect of the Active Site D25N Mutation on the Structure, Stability, and Ligand Binding of the Mature HIV-1 Protease. Journal of Biological Chemistry, 2008, 283, 13459-13470.	3.4	73
88	Novel macromolecular inhibitors of human immunodeficiency virus-1 protease. Protein Engineering, Design and Selection, 2008, 21, 453-461.	2.1	9
89	Mutational and Structural Studies Aimed at Characterizing the Monomer of HIV-1 Protease and Its Precursor. Journal of Biological Chemistry, 2007, 282, 17190-17199.	3.4	51
90	Solution NMR Structure of the Barrier-to-Autointegration Factor-Emerin Complex. Journal of Biological Chemistry, 2007, 282, 14525-14535.	3.4	75

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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. Journal of Virology, 2007, 81, 12946-12953.	3.4	37
92	Dimerization of the class A G protein-coupled neurotensin receptor NTS1 alters G protein interaction. Proceedings of the National Academy of Sciences of the United States of America, 2007, 104, 12199-12204.	7.1	134
93	Characterizing the unfolded states of proteins using single-molecule FRET spectroscopy and molecular simulations. Proceedings of the National Academy of Sciences of the United States of America, 2007, 104, 1528-1533.	7.1	327
94	Local and global structure of the monomeric subunit of the potassium channel KcsA probed by NMR. Biochimica Et Biophysica Acta - Biomembranes, 2007, 1768, 3260-3270.	2.6	33
95	HIVâ€1 Protease: Structure, Dynamics, and Inhibition. Advances in Pharmacology, 2007, 55, 261-298.	2.0	95
96	Caught in the Act:â€‰ The 1.5 Ã… Resolution Crystal Structures of the HIV-1 Protease and the I54V Mutant Reveal a Tetrahedral Reaction Intermediate. Biochemistry, 2007, 46, 14854-14864.	2.5	44
97	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. Virology, 2007, 363, 79-90.	2.4	57
98	Mixed-time parallel evolution in multiple quantum NMR experiments: sensitivity and resolution enhancement in heteronuclear NMR. Journal of Biomolecular NMR, 2007, 37, 195-204.	2.8	22
99	NMR study of the tetrameric KcsA potassium channel in detergent micelles. Protein Science, 2006, 15, 684-698.	7.6	165
100	Mechanism of Drug Resistance Revealed by the Crystal Structure of the Unliganded HIV-1 Protease with F53L Mutation. Journal of Molecular Biology, 2006, 358, 1191-1199.	4.2	48
101	Ultra-high Resolution Crystal Structure of HIV-1 Protease Mutant Reveals Two Binding Sites for Clinical Inhibitor TMC114. Journal of Molecular Biology, 2006, 363, 161-173.	4.2	136
102	Synergistic Inhibition of HIV-1 Envelope-Mediated Membrane Fusion by Inhibitors Targeting the N and C-Terminal Heptad Repeats of gp41. Journal of Molecular Biology, 2006, 364, 283-289.	4.2	23
103	Measurement of 15N relaxation in the detergent-solubilized tetrameric KcsA potassium channel. Journal of Biomolecular NMR, 2006, 36, 123-136.	2.8	86
104	Conformational Changes in HIV-1 gp41 in the Course of HIV-1 Envelope Glycoprotein-Mediated Fusion and Inactivationâ€. Biochemistry, 2005, 44, 12471-12479.	2.5	59
105	Mapping the Binding of the N-terminal Extracellular Tail of the CXCR4 Receptor to Stromal Cell-derived Factor-1Î±. Journal of Molecular Biology, 2005, 345, 651-658.	4.2	58
106	The GB1 Amyloid Fibril: Recruitment of the Peripheral Î²-Strands of the Domain Swapped Dimer into the Polymeric Interface. Journal of Molecular Biology, 2005, 348, 687-698.	4.2	45
107	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. Journal of Molecular Biology, 2005, 353, 945-951.	4.2	27
108	Kinetic, Stability, and Structural Changes in High-resolution Crystal Structures of HIV-1 Protease with Drug-resistant Mutations L24I, I50V, and G73S. Journal of Molecular Biology, 2005, 354, 789-800.	4.2	68

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109	Crystal structures of HIV protease V82A and L90M mutants reveal changes in the indinavir-binding site. FEBS Journal, 2004, 271, 1516-1524.	0.2	71
110	Letter to the Editor: The C-terminal Domain of Viral IAP Associated Factor (cVIAF) is a Structural Homologue of Phosducin: Resonance Assignments and Secondary Structure of the C-Terminal Domain of VIAF. Journal of Biomolecular NMR, 2004, 28, 197-198.	2.8	2
111	Carbonyl carbon transverse relaxation dispersion measurements and ms-Î¼s timescale motion in a protein hydrogen bond network. Journal of Biomolecular NMR, 2004, 29, 187-198.	2.8	73
112	In Vitro Processing of HIV-1 Nucleocapsid Protein by the Viral Proteinase:â€‰ Effects of Amino Acid Substitutions at the Scissile Bond in the Proximal Zinc Finger Sequence. Biochemistry, 2004, 43, 4304-4312.	2.5	5
113	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. Biochemistry, 2004, 43, 8230-8233.	2.5	22
114	Insights into Conformation and Dynamics of Protein GB1 During Folding and Unfolding by NMR. Journal of Molecular Biology, 2004, 335, 1299-1307.	4.2	75
115	High Resolution Crystal Structures of HIV-1 Protease with a Potent Non-peptide Inhibitor (UIC-94017) Active Against Multi-drug-resistant Clinical Strains. Journal of Molecular Biology, 2004, 338, 341-352.	4.2	205
116	A Captured Folding Intermediate Involved in Dimerization and Domain-swapping of GB1. Journal of Molecular Biology, 2004, 340, 615-625.	4.2	49
117	A rapid method to attain isotope labeled small soluble peptides for NMR studies. Journal of Biomolecular NMR, 2003, 26, 193-202.	2.8	39
118	A solution NMR study of the binding kinetics and the internal dynamics of an HIV-1 protease-substrate complex. Protein Science, 2003, 12, 1376-1385.	7.6	84
119	Solution Structure of a Circular-permuted Variant of the Potent HIV-inactivating Protein Cyanovirin-N: Structural Basis for Protein Stability and Oligosaccharide Interaction. Journal of Molecular Biology, 2003, 325, 211-223.	4.2	32
120	A Protein Contortionist: Core Mutations of GB1 that Induce Dimerization and Domain Swapping. Journal of Molecular Biology, 2003, 333, 141-152.	4.2	78
121	Solution Structure of the Mature HIV-1 Protease Monomer. Journal of Biological Chemistry, 2003, 278, 43311-43319.	3.4	76
122	Revisiting Monomeric HIV-1 Protease. Journal of Biological Chemistry, 2003, 278, 6085-6092.	3.4	51
123	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. Journal of Biological Chemistry, 2003, 278, 20278-20285.	3.4	94
124	Design of a Novel Peptide Inhibitor of HIV Fusion That Disrupts the Internal Trimeric Coiled-coil of gp41. Journal of Biological Chemistry, 2002, 277, 14238-14245.	3.4	125
125	The structure of a replication initiator unites diverse aspects of nucleic acid metabolism. Proceedings of the National Academy of Sciences of the United States of America, 2002, 99, 10310-10315.	7.1	123
126	Structure and Orientation of a G Protein Fragment in the Receptor Bound State from Residual Dipolar Couplings. Journal of Molecular Biology, 2002, 322, 441-461.	4.2	95

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127	Solution Structure and Dynamics of the Humanâ"Escherichia coliThioredoxin Chimera:Â Insights into Thermodynamic Stabilityâ€,â€¡. Biochemistry, 2002, 41, 9376-9388.	2.5	10
128	The Domain-Swapped Dimer of Cyanovirin-N Is in a Metastable Folded State. Structure, 2002, 10, 673-686.	3.3	123
129	Effect of sequence polymorphism and drug resistance on two HIV-1 Gag processing sites. FEBS Journal, 2002, 269, 4114-4120.	0.2	64
130	Design and initial characterization of a circular permuted variant of the potent HIV-inactivating protein cyanovirin-N. Proteins: Structure, Function and Bioinformatics, 2002, 46, 153-160.	2.6	17
131	Combining mutations in HIV-1 protease to understand mechanisms of resistance. Proteins: Structure, Function and Bioinformatics, 2002, 48, 107-116.	2.6	46
132	Structure and dynamics of KH domains from FBP bound to single-stranded DNA. Nature, 2002, 415, 1051-1056.	27.8	150
133	1H, 13C, and 15N assignment of the N-terminal, catalytic domain of the replication initiation protein from the geminivirus TYLCV. Journal of Biomolecular NMR, 2002, 24, 73-74.	2.8	7
134	Biosynthetically directed fractional 13C labeling facilitates identification of Phe and Tyr aromatic signals in proteins. Journal of Biomolecular NMR, 2002, 24, 231-235.	2.8	10
135	Characterization of two hydrophobic methyl clusters in HIV-1 protease by NMR spin relaxation in solution11Edited by P. E. Wright. Journal of Molecular Biology, 2001, 305, 515-521.	4.2	47
136	Structural Basis for SRY-dependent 46-X,Y Sex Reversal: Modulation of DNA Bending by a Naturally Occurring Point Mutation. Journal of Molecular Biology, 2001, 312, 481-499.	4.2	132
137	Structure and dynamics of MarA-DNA complexes: an NMR investigation. Journal of Molecular Biology, 2001, 314, 113-127.	4.2	27
138	Comparison of Methyl Rotation Axis Order Parameters Derived from Model-Free Analyses of2H and13C Longitudinal and Transverse Relaxation Rates Measured in the Same Protein Sample. Journal of the American Chemical Society, 2001, 123, 6164-6171.	13.7	100
139	Probing the Structure and Stability of a Hybrid Protein:â€‰ The Humanâ"E. coli Thioredoxin Chimera. Biochemistry, 2001, 40, 11184-11192.	2.5	11
140	Structural implications of drug-resistant mutants of HIV-1 protease: High-resolution crystal structures of the mutant protease/substrate analogue complexes. Proteins: Structure, Function and Bioinformatics, 2001, 43, 455-464.	2.6	125
141	Characterization of the Cholesteric Phase of Filamentous Bacteriophage fd for Molecular Alignment. Journal of Magnetic Resonance, 2001, 149, 154-158.	2.1	21
142	1H, 13C, 15N resonance assignments and fold verification of a circular permuted variant of the potent HIV-inactivating protein cyanovirin-N. Journal of Biomolecular NMR, 2001, 19, 289-290.	2.8	15
143	Optimized labeling of 13CHD2 methyl isotopomers in perdeuterated proteins: potential advantages for 13C relaxation studies of methyl dynamics of larger proteins. Journal of Biomolecular NMR, 2001, 21, 167-171.	2.8	30
144	A simple apparatus for generating stretched polyacrylamide gels, yielding uniform alignment of proteins and detergent micelles. Journal of Biomolecular NMR, 2001, 21, 377-382.	2.8	223

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145	Folded Monomer of HIV-1 Protease. Journal of Biological Chemistry, 2001, 276, 49110-49116.	3.4	85
146	Design and Properties of NCCG-gp41, a Chimeric gp41 Molecule with Nanomolar HIV Fusion Inhibitory Activity. Journal of Biological Chemistry, 2001, 276, 29485-29489.	3.4	88
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