John M Louis

List of Publications by Year in Descending Order

181 papers	8,414 citations	53 h-index	83 g-index
190 ext. papers	9,096 ext. citations	6.8 avg, IF	5.87 L-index

#	Paper	IF	Citations
181	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	6.7	2
180	Covalent narlaprevir- and boceprevir-derived hybrid inhibitors of SARS-CoV-2 main protease.. *Nature Communications*, **2022**, 13, 2268	17.4	10
179	Michaelis-like complex of SARS-CoV-2 main protease visualized by room-temperature X-ray crystallography. *IUCrJ*, **2021**, 8, 973-979	4.7	5
178	Transient lipid-bound states of spike protein heptad repeats provide insights into SARS-CoV-2 membrane fusion. *Science Advances*, **2021**, 7, eabk2226	14.3	0
177	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	8.3	7
176	A weakened interface in the P182L variant of HSP27 associated with severe Charcot-Marie-Tooth neuropathy causes aberrant binding to interacting proteins. *EMBO Journal*, **2021**, 40, e103811	13	3
175	MWC allosteric model explains unusual hemoglobin-oxygen binding curves from sickle cell drug binding. *Biophysical Journal*, **2021**, 120, 2543-2551	2.9	3
174	Concentration-Dependent Structural Transition of the HIV-1 gp41 MPER Peptide into Helical Trimers. *Angewandte Chemie*, **2021**, 133, 168-172	3.6	
173	Concentration-Dependent Structural Transition of the HIV-1 gp41 MPER Peptide into Helical Trimers. *Angewandte Chemie - International Edition*, **2021**, 60, 166-170	16.4	5
172	Constraints on the Structure of Fibrils Formed by a Racemic Mixture of Amyloid- Peptides from Solid-State NMR, Electron Microscopy, and Theory. *Journal of the American Chemical Society*, **2021**, 143, 13299-13313	16.4	3
171	Probing the Interaction between HIV-1 Protease and the Homodimeric p66/p66TReverse Transcriptase Precursor by Double Electron-Electron Resonance EPR Spectroscopy. *ChemBioChem*, **2020**, 21, 3051-3055	3.8	2
170	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	11.5	14
169	Visualizing Tetrahedral Oxyanion Bound in HIV-1 Protease Using Neutrons: Implications for the Catalytic Mechanism and Drug Design. *ACS Omega*, **2020**, 5, 11605-11617	3.9	2
168	Fast three-color single-molecule FRET using statistical inference. *Nature Communications*, **2020**, 11, 3336	17.4	12
167	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	11.5	10
166	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	1.7	1
165	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	16.4	1

164	Importance of time-ordered non-uniform sampling of multi-dimensional NMR spectra of A peptide under aggregating conditions. *Journal of Biomolecular NMR*, **2019**, 73, 429-441	3	10
163	Observation of Amyloid Peptide Oligomerization by Pressure-Jump NMR Spectroscopy. *Journal of the American Chemical Society*, **2019**, 141, 13762-13766	16.4	21
162	Diverse Folding Pathways of HIV-1 Protease Monomer on a Rugged Energy Landscape. *Biophysical Journal*, **2019**, 117, 1456-1466	2.9	3
161	Co-Evolutionary Fitness Landscapes for Sequence Design. *Angewandte Chemie - International Edition*, **2018**, 57, 5674-5678	16.4	37
160	Co-Evolutionary Fitness Landscapes for Sequence Design. *Angewandte Chemie*, **2018**, 130, 5776-5780	3.6	1
159	Innenrücktitelbild: Co-Evolutionary Fitness Landscapes for Sequence Design (Angew. Chem. 20/2018). *Angewandte Chemie*, **2018**, 130, 6061-6061	3.6	1
158	Tilted, Uninterrupted, Monomeric HIV-1 gp41 Transmembrane Helix from Residual Dipolar Couplings. *Journal of the American Chemical Society*, **2018**, 140, 34-37	16.4	33
157	Probing the mechanism of inhibition of amyloid-(1-42)-induced neurotoxicity by the chaperonin GroEL. *Proceedings of the National Academy of Sciences of the United States of America*, **2018**, 115, E11924-E11932	11.5	19
156	Three-Color Single-Molecule FRET and Fluorescence Lifetime Analysis of Fast Protein Folding. *Journal of Physical Chemistry B*, **2018**, 122, 11702-11720	3.4	24
155	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	8.3	20
154	Binding kinetics and substrate selectivity in HIV-1 protease-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	11.5	23
153	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	11.5	35
152	Transient HIV-1 Gag-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	11.5	19
151	Evolution under Drug Pressure Remodels the Folding Free-Energy Landscape of Mature HIV-1 Protease. *Journal of Molecular Biology*, **2016**, 428, 2780-92	6.5	13
150	Analysis of Fluorescence Lifetime and Energy Transfer Efficiency in Single-Molecule Photon Trajectories of Fast-Folding Proteins. *Journal of Physical Chemistry B*, **2016**, 120, 680-99	3.4	28
149	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	3.7	10
148	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	3.7	25
147	Long-Range Electrostatics-Induced Two-Proton Transfer Captured by Neutron Crystallography in an Enzyme Catalytic Site. *Angewandte Chemie*, **2016**, 128, 5008-5011	3.6	6

146	Long-Range Electrostatics-Induced Two-Proton Transfer Captured by Neutron Crystallography in an Enzyme Catalytic Site. *Angewandte Chemie - International Edition*, **2016**, 55, 4924-7	16.4	34
145	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, 2390-400	3.2	19
144	Complete dissociation of the HIV-1 gp41 ectodomain and membrane proximal regions upon phospholipid binding. *Journal of Biomolecular NMR*, **2015**, 61, 235-48	3	13
143	Evidence of Distinct Channel Conformations and Substrate Binding Affinities for the Mitochondrial Outer Membrane Protein Translocase Pore Tom40. *Journal of Biological Chemistry*, **2015**, 290, 26204-17	5.4	22
142	Mutations Proximal to Sites of Autoproteolysis and the Helix That Co-evolve under Drug Pressure Modulate the Autoprocessing and Vitality of HIV-1 Protease. *Biochemistry*, **2015**, 54, 5414-24	3.2	8
141	Conformation of inhibitor-free HIV-1 protease derived from NMR spectroscopy in a weakly oriented solution. *ChemBioChem*, **2015**, 16, 214-8	3.8	22
140	Testing Landscape Theory for Biomolecular Processes with Single Molecule Fluorescence Spectroscopy. *Physical Review Letters*, **2015**, 115, 018101	7.4	49
139	Pressure-induced structural transition of mature HIV-1 protease from a combined NMR/MD simulation approach. *Proteins: Structure, Function and Bioinformatics*, **2015**, 83, 2117-23	4.2	17
138	Substituted Bis-THF Protease Inhibitors with Improved Potency against Highly Resistant Mature HIV-1 Protease PR20. *Journal of Medicinal Chemistry*, **2015**, 58, 5088-95	8.3	8
137	Dependence of distance distributions derived from double electron-electron resonance pulsed EPR spectroscopy on pulse-sequence time. *Angewandte Chemie - International Edition*, **2015**, 54, 5336-9	16.4	28
136	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, 6796-805	3.2	5
135	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, 3425-30	11.5	36
134	Structures of darunavir-resistant HIV-1 protease mutant reveal atypical binding of darunavir to wide open flaps. *ACS Chemical Biology*, **2014**, 9, 1351-8	4.9	19
133	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	3.7	6
132	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, 369-77	3	8
131	Enhanced stability of monomer fold correlates with extreme drug resistance of HIV-1 protease. *Biochemistry*, **2013**, 52, 7678-88	3.2	9
130	Measuring ultrafast protein folding rates from photon-by-photon analysis of single molecule fluorescence trajectories. *Chemical Physics*, **2013**, 422, 229-237	2.3	38
129	Internal dynamics of the homotrimeric HIV-1 viral coat protein gp41 on multiple time scales. *Angewandte Chemie - International Edition*, **2013**, 52, 3911-5	16.4	54

128	Extreme multidrug resistant HIV-1 protease with 20 mutations is resistant to novel protease inhibitors with P1Tpyrrolidinone or P2-tris-tetrahydrofuran. *Journal of Medicinal Chemistry*, **2013**, 56, 4017-27	8.3	29
127	The impact of influenza hemagglutinin fusion peptide length and viral subtype on its structure and dynamics. *Biopolymers*, **2013**, 99, 189-95	2.2	23
126	Internal Dynamics of the Homotrimeric HIV-1 Viral Coat Protein gp41 on Multiple Time Scales. *Angewandte Chemie*, **2013**, 125, 4003-4007	3.6	7
125	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	3.7	16
124	Terminal interface conformations modulate dimer stability prior to amino terminal autoprocessing of HIV-1 protease. *Biochemistry*, **2012**, 51, 1041-50	3.2	27
123	Mechanism of dissociative inhibition of HIV protease and its autoprocessing from a precursor. *Journal of Molecular Biology*, **2012**, 422, 230-44	6.5	7
122	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, 19994-9	11.5	65
121	Critical differences in HIV-1 and HIV-2 protease specificity for clinical inhibitors. *Protein Science*, **2012**, 21, 339-50	6.3	35
120	HIV-1 protease with 20 mutations exhibits extreme resistance to clinical inhibitors through coordinated structural rearrangements. *Biochemistry*, **2012**, 51, 2819-28	3.2	69
119	Single-molecule fluorescence experiments determine protein folding transition path times. *Science*, **2012**, 335, 981-4	33.3	312
118	Extracting rate coefficients from single-molecule photon trajectories and FRET efficiency histograms for a fast-folding protein. *Journal of Physical Chemistry A*, **2011**, 115, 3642-56	2.8	82
117	NMR solution structure of a cyanovirin homolog from wheat head blight fungus. *Proteins: Structure, Function and Bioinformatics*, **2011**, 79, 1538-49	4.2	13
116	Helical hairpin structure of influenza hemagglutinin fusion peptide stabilized by charge-dipole interactions between the N-terminal amino group and the second helix. *Journal of the American Chemical Society*, **2011**, 133, 2824-7	16.4	32
115	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, 14184-7	16.4	27
114	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, 4786-95	3.2	21
113	Evolution of cyclic peptide protease inhibitors. *Proceedings of the National Academy of Sciences of the United States of America*, **2011**, 108, 11052-6	11.5	100
112	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, 9072-7	11.5	56
111	Structural basis of HIV-1 neutralization by affinity matured Fabs directed against the internal trimeric coiled-coil of gp41. *PLoS Pathogens*, **2010**, 6, e1001182	7.6	37

110	Distinguishing between protein dynamics and dye photophysics in single-molecule FRET experiments. *Biophysical Journal*, **2010**, 98, 696-706	2.9	52
109	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, 11341-6	11.5	123
108	Autocatalytic maturation, physical/chemical properties, and crystal structure of group N HIV-1 protease: relevance to drug resistance. *Protein Science*, **2010**, 19, 2055-72	6.3	22
107	Highly conserved glycine 86 and arginine 87 residues contribute differently to the structure and activity of the mature HIV-1 protease. *Proteins: Structure, Function and Bioinformatics*, **2010**, 78, 1015-25	4.2	18
106	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, 11837-44	11.5	236
105	Modulation of human immunodeficiency virus type 1 protease autoprocessing by charge properties of surface residue 69. *Journal of Virology*, **2009**, 83, 7789-93	6.6	13
104	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. *Virology*, **2009**, 393, 112-9	3.6	19
103	Interactions of different inhibitors with active-site aspartyl residues of HIV-1 protease and possible relevance to pepsin. *Proteins: Structure, Function and Bioinformatics*, **2009**, 75, 556-68	4.2	19
102	Revealing the dimer dissociation and existence of a folded monomer of the mature HIV-2 protease. *Protein Science*, **2009**, 18, 2442-53	6.3	19
101	Visualizing transient events in amino-terminal autoprocessing of HIV-1 protease. *Nature*, **2008**, 455, 693-6	30.4	111
100	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, 170-83	3.6	45
99	Structural evidence for effectiveness of darunavir and two related antiviral inhibitors against HIV-2 protease. *Journal of Molecular Biology*, **2008**, 384, 178-92	6.5	40
98	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, 13459-70	5.4	65
97	Novel macromolecular inhibitors of human immunodeficiency virus-1 protease. *Protein Engineering, Design and Selection*, **2008**, 21, 453-61	1.9	7
96	A diverse view of protein dynamics from NMR studies of HIV-1 protease flaps. *Proteins: Structure, Function and Bioinformatics*, **2008**, 70, 1408-15	4.2	36
95	The point mutation A34F causes dimerization of GB1. *Proteins: Structure, Function and Bioinformatics*, **2008**, 71, 1420-31	4.2	31
94	Caught in the Act: the 1.5 A resolution crystal structures of the HIV-1 protease and the I54V mutant reveal a tetrahedral reaction intermediate. *Biochemistry*, **2007**, 46, 14854-64	3.2	40
93	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	3.6	55

92	Mixed-time parallel evolution in multiple quantum NMR experiments: sensitivity and resolution enhancement in heteronuclear NMR. *Journal of Biomolecular NMR*, **2007**, 37, 195-204	3	21
91	Mutational and structural studies aimed at characterizing the monomer of HIV-1 protease and its precursor. *Journal of Biological Chemistry*, **2007**, 282, 17190-9	5.4	48
90	Solution NMR structure of the barrier-to-autointegration factor-Emerin complex. *Journal of Biological Chemistry*, **2007**, 282, 14525-35	5.4	63
89	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, 12946-53	6.6	35
88	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, 12199-204	11.5	129
87	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, 1528-33	11.5	305
86	Local and global structure of the monomeric subunit of the potassium channel KcsA probed by NMR. *Biochimica Et Biophysica Acta - Biomembranes*, **2007**, 1768, 3260-70	3.8	27
85	HIV-1 protease: structure, dynamics, and inhibition. *Advances in Pharmacology*, **2007**, 55, 261-98	5.7	82
84	NMR study of the tetrameric KcsA potassium channel in detergent micelles. *Protein Science*, **2006**, 15, 684-98	6.3	156
83	Mechanism of drug resistance revealed by the crystal structure of the unliganded HIV-1 protease with F53L mutation. *Journal of Molecular Biology*, **2006**, 358, 1191-9	6.5	45
82	Ultra-high resolution crystal structure of HIV-1 protease mutant reveals two binding sites for clinical inhibitor TMC114. *Journal of Molecular Biology*, **2006**, 363, 161-73	6.5	117
81	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, 283-9	6.5	22
80	Measurement of 15N relaxation in the detergent-solubilized tetrameric KcsA potassium channel. *Journal of Biomolecular NMR*, **2006**, 36, 123-36	3	76
79	Conformational changes in HIV-1 gp41 in the course of HIV-1 envelope glycoprotein-mediated fusion and inactivation. *Biochemistry*, **2005**, 44, 12471-9	3.2	57
78	Mapping the binding of the N-terminal extracellular tail of the CXCR4 receptor to stromal cell-derived factor-1alpha. *Journal of Molecular Biology*, **2005**, 345, 651-8	6.5	53
77	The GB1 amyloid fibril: recruitment of the peripheral beta-strands of the domain swapped dimer into the polymeric interface. *Journal of Molecular Biology*, **2005**, 348, 687-98	6.5	39
76	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, 945-51	6.5	27
75	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	6.5	62

74	Crystal structures of HIV protease V82A and L90M mutants reveal changes in the indinavir-binding site. *FEBS Journal*, **2004**, 271, 1516-24		66
73	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, 197-8	3	2
72	Carbonyl carbon transverse relaxation dispersion measurements and ms-micros timescale motion in a protein hydrogen bond network. *Journal of Biomolecular NMR*, **2004**, 29, 187-98	3	72
71	In vitro processing of HIV-1 nucleocapsid protein by the viral proteinase: effects of amino acid substitutions at the scissile bond in the proximal zinc finger sequence. *Biochemistry*, **2004**, 43, 4304-12	3.2	4
70	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, 8230-3	3.2	20
69	Insights into conformation and dynamics of protein GB1 during folding and unfolding by NMR. *Journal of Molecular Biology*, **2004**, 335, 1299-307	6.5	72
68	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, 341-52	6.5	182
67	A captured folding intermediate involved in dimerization and domain-swapping of GB1. *Journal of Molecular Biology*, **2004**, 340, 615-25	6.5	39
66	Solution structure of the mature HIV-1 protease monomer: insight into the tertiary fold and stability of a precursor. *Journal of Biological Chemistry*, **2003**, 278, 43311-9	5.4	69
65	Revisiting monomeric HIV-1 protease. Characterization and redesign for improved properties. *Journal of Biological Chemistry*, **2003**, 278, 6085-92	5.4	49
64	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, 20278-85	5.4	80
63	A rapid method to attain isotope labeled small soluble peptides for NMR studies. *Journal of Biomolecular NMR*, **2003**, 26, 193-202	3	38
62	A solution NMR study of the binding kinetics and the internal dynamics of an HIV-1 protease-substrate complex. *Protein Science*, **2003**, 12, 1376-85	6.3	79
61	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, 211-23	6.5	30
60	A protein contortionist: core mutations of GB1 that induce dimerization and domain swapping. *Journal of Molecular Biology*, **2003**, 333, 141-52	6.5	66
59	Rapid structural fluctuations of the free HIV protease flaps in solution: relationship to crystal structures and comparison with predictions of dynamics calculations. *Protein Science*, **2002**, 11, 221-32	6.3	166
58	The domain-swapped dimer of cyanovirin-N is in a metastable folded state: reconciliation of X-ray and NMR structures. *Structure*, **2002**, 10, 673-86	5.2	115
57	Effect of sequence polymorphism and drug resistance on two HIV-1 Gag processing sites. *FEBS Journal*, **2002**, 269, 4114-20		57

56	Design and initial characterization of a circular permuted variant of the potent HIV-inactivating protein cyanovirin-N. *Proteins: Structure, Function and Bioinformatics*, **2002**, 46, 153-60	4.2	17
55	Combining mutations in HIV-1 protease to understand mechanisms of resistance. *Proteins: Structure, Function and Bioinformatics*, **2002**, 48, 107-16	4.2	45
54	Structure and dynamics of KH domains from FBP bound to single-stranded DNA. *Nature*, **2002**, 415, 1051-6	36.4	141
53	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, 73-4	3	7
52	Biosynthetically directed fractional 13C labeling facilitates identification of Phe and Tyr aromatic signals in proteins. *Journal of Biomolecular NMR*, **2002**, 24, 231-5	3	10
51	Design of a novel peptide inhibitor of HIV fusion that disrupts the internal trimeric coiled-coil of gp41. *Journal of Biological Chemistry*, **2002**, 277, 14238-45	5.4	111
50	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, 10310-5	11.5	105
49	Structure and orientation of a G protein fragment in the receptor bound state from residual dipolar couplings. *Journal of Molecular Biology*, **2002**, 322, 441-61	6.5	93
48	Solution structure and dynamics of the human-Escherichia coli thioredoxin chimera: insights into thermodynamic stability. *Biochemistry*, **2002**, 41, 9376-88	3.2	10
47	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, 455-64	4.2	111
46	Characterization of the cholesteric phase of filamentous bacteriophage fd for molecular alignment. *Journal of Magnetic Resonance*, **2001**, 149, 154-8	3	19
45	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, 289-90	3	13
44	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, 167-71	3	25
43	A simple apparatus for generating stretched polyacrylamide gels, yielding uniform alignment of proteins and detergent micelles. *Journal of Biomolecular NMR*, **2001**, 21, 377-82	3	194
42	Folded monomer of HIV-1 protease. *Journal of Biological Chemistry*, **2001**, 276, 49110-6	5.4	81
41	Design and properties of N(CCG)-gp41, a chimeric gp41 molecule with nanomolar HIV fusion inhibitory activity. *Journal of Biological Chemistry*, **2001**, 276, 29485-9	5.4	80
40	Characterization of two hydrophobic methyl clusters in HIV-1 protease by NMR spin relaxation in solution. *Journal of Molecular Biology*, **2001**, 305, 515-21	6.5	46
39	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, 481-99	6.5	114

38	Structure and dynamics of MarA-DNA complexes: an NMR investigation. *Journal of Molecular Biology*, **2001**, 314, 113-27	6.5	25
37	Comparison of methyl rotation axis order parameters derived from model-free analyses of (2)H and (13)C longitudinal and transverse relaxation rates measured in the same protein sample. *Journal of the American Chemical Society*, **2001**, 123, 6164-71	16.4	89
36	Probing the structure and stability of a hybrid protein: the human-E. coli thioredoxin chimera. *Biochemistry*, **2001**, 40, 11184-92	3.2	10
35	Comparison of the substrate specificity of the human T-cell leukemia virus and human immunodeficiency virus proteinases. *FEBS Journal*, **2000**, 267, 6287-95		52
34	Cloning of the bovine leukemia virus proteinase in Escherichia coli and comparison of its specificity to that of human T-cell leukemia virus proteinase. *BBA - Proteins and Proteomics*, **2000**, 1478, 1-8		12
33	Biophysical characterization of gp41 aggregates suggests a model for the molecular mechanism of HIV-associated neurological damage and dementia. *Journal of Biological Chemistry*, **2000**, 275, 19877-82	5.4	26
32	HIV-1 protease: maturation, enzyme specificity, and drug resistance. *Advances in Pharmacology*, **2000**, 49, 111-46	5.7	60
31	Antiviral agent based on the non-structural protein targeting the maturation process of HIV-1: expression and susceptibility of chimeric Vpr as a substrate for cleavage by HIV-1 protease. *Protein Engineering, Design and Selection*, **2000**, 13, 431-6	1.9	4
30	Is human thioredoxin monomeric or dimeric?. *Protein Science*, **1999**, 8, 426-9	6.3	17
29	Stabilization from autoproteolysis and kinetic characterization of the human T-cell leukemia virus type 1 proteinase. *Journal of Biological Chemistry*, **1999**, 274, 6660-6	5.4	46
28	Proteolytic processing of HIV-1 protease precursor, kinetics and mechanism. *Journal of Biological Chemistry*, **1999**, 274, 23437-42	5.4	50
27	Effect of substrate residues on the P2Tpreference of retroviral proteinases. *FEBS Journal*, **1999**, 264, 921-9		36
26	Effect of serine and tyrosine phosphorylation on retroviral proteinase substrates. *FEBS Journal*, **1999**, 265, 423-9		11
25	Autoprocessing of HIV-1 protease is tightly coupled to protein folding. *Nature Structural Biology*, **1999**, 6, 868-75		150
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