

# John M Louis

## List of Publications by Citations

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190  
ext. papers

9,096  
ext. citations

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L-index

#	Paper	IF	Citations
181	Single-molecule fluorescence experiments determine protein folding transition path times. <i>Science</i> , <b>2012</b> , 335, 981-4	33.3	312
180	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> , <b>2007</b> , 104, 1528-33	11.5	305
179	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> , <b>2009</b> , 106, 11837-44	11.5	236
178	Flap opening and dimer-interface flexibility in the free and inhibitor-bound HIV protease, and their implications for function. <i>Structure</i> , <b>1999</b> , 7, 1047-55	5.2	223
177	A simple apparatus for generating stretched polyacrylamide gels, yielding uniform alignment of proteins and detergent micelles. <i>Journal of Biomolecular NMR</i> , <b>2001</b> , 21, 377-82	3	194
176	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> , <b>2004</b> , 338, 341-52	6.5	182
175	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> , <b>2002</b> , 11, 221-32	6.3	166
174	NMR study of the tetrameric KcsA potassium channel in detergent micelles. <i>Protein Science</i> , <b>2006</b> , 15, 684-98	6.3	156
173	Crystal structure of cyanovirin-N, a potent HIV-inactivating protein, shows unexpected domain swapping. <i>Journal of Molecular Biology</i> , <b>1999</b> , 288, 403-12	6.5	152
172	Autoprocessing of HIV-1 protease is tightly coupled to protein folding. <i>Nature Structural Biology</i> , <b>1999</b> , 6, 868-75		150
171	Structure and dynamics of KH domains from FBP bound to single-stranded DNA. <i>Nature</i> , <b>2002</b> , 415, 1051-5	6.4	141
170	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> , <b>2007</b> , 104, 12199-204	11.5	129
169	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> , <b>2010</b> , 107, 11341-6	11.5	123
168	Ultra-high resolution crystal structure of HIV-1 protease mutant reveals two binding sites for clinical inhibitor TMC114. <i>Journal of Molecular Biology</i> , <b>2006</b> , 363, 161-73	6.5	117
167	The domain-swapped dimer of cyanovirin-N is in a metastable folded state: reconciliation of X-ray and NMR structures. <i>Structure</i> , <b>2002</b> , 10, 673-86	5.2	115
166	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> , <b>2001</b> , 312, 481-99	6.5	114
165	Visualizing transient events in amino-terminal autoprocessing of HIV-1 protease. <i>Nature</i> , <b>2008</b> , 455, 693-6	6.4	111

164	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> , <b>2001</b> , 43, 455-64	4.2	111
163	Design of a novel peptide inhibitor of HIV fusion that disrupts the internal trimeric coiled-coil of gp41. <i>Journal of Biological Chemistry</i> , <b>2002</b> , 277, 14238-45	5.4	111
162	Kinetic and modeling studies of S3-S3Tsubsites of HIV proteinases. <i>Biochemistry</i> , <b>1992</b> , 31, 4793-800	3.2	106
161	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> , <b>2002</b> , 99, 10310-5	11.5	105
160	Structural and kinetic analysis of drug resistant mutants of HIV-1 protease. <i>FEBS Journal</i> , <b>1999</b> , 263, 238-45		104
159	Evolution of cyclic peptide protease inhibitors. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2011</b> , 108, 11052-6	11.5	100
158	Structure and orientation of a G protein fragment in the receptor bound state from residual dipolar couplings. <i>Journal of Molecular Biology</i> , <b>2002</b> , 322, 441-61	6.5	93
157	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. <i>Journal of the American Chemical Society</i> , <b>2001</b> , 123, 6164-71	16.4	89
156	Extracting rate coefficients from single-molecule photon trajectories and FRET efficiency histograms for a fast-folding protein. <i>Journal of Physical Chemistry A</i> , <b>2011</b> , 115, 3642-56	2.8	82
155	HIV-1 protease: structure, dynamics, and inhibition. <i>Advances in Pharmacology</i> , <b>2007</b> , 55, 261-98	5.7	82
154	Folded monomer of HIV-1 protease. <i>Journal of Biological Chemistry</i> , <b>2001</b> , 276, 49110-6	5.4	81
153	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> , <b>2003</b> , 278, 20278-85	5.4	80
152	Design and properties of N(CCG)-gp41, a chimeric gp41 molecule with nanomolar HIV fusion inhibitory activity. <i>Journal of Biological Chemistry</i> , <b>2001</b> , 276, 29485-9	5.4	80
151	A solution NMR study of the binding kinetics and the internal dynamics of an HIV-1 protease-substrate complex. <i>Protein Science</i> , <b>2003</b> , 12, 1376-85	6.3	79
150	Hydrophilic peptides derived from the transframe region of Gag-Pol inhibit the HIV-1 protease. <i>Biochemistry</i> , <b>1998</b> , 37, 2105-10	3.2	79
149	Transverse 13C Relaxation of CHD2 Methyl Isotopomers To Detect Slow Conformational Changes of Protein Side Chains. <i>Journal of the American Chemical Society</i> , <b>1999</b> , 121, 11589-11590	16.4	77
148	Measurement of 15N relaxation in the detergent-solubilized tetrameric KcsA potassium channel. <i>Journal of Biomolecular NMR</i> , <b>2006</b> , 36, 123-36	3	76
147	Carbonyl carbon transverse relaxation dispersion measurements and ms-micros timescale motion in a protein hydrogen bond network. <i>Journal of Biomolecular NMR</i> , <b>2004</b> , 29, 187-98	3	72

146	Insights into conformation and dynamics of protein GB1 during folding and unfolding by NMR. <i>Journal of Molecular Biology</i> , <b>2004</b> , 335, 1299-307	6.5	72
145	HIV-1 protease with 20 mutations exhibits extreme resistance to clinical inhibitors through coordinated structural rearrangements. <i>Biochemistry</i> , <b>2012</b> , 51, 2819-28	3.2	69
144	Solution structure of the mature HIV-1 protease monomer: insight into the tertiary fold and stability of a precursor. <i>Journal of Biological Chemistry</i> , <b>2003</b> , 278, 43311-9	5.4	69
143	Crystal structures of HIV protease V82A and L90M mutants reveal changes in the indinavir-binding site. <i>FEBS Journal</i> , <b>2004</b> , 271, 1516-24		66
142	A protein contortionist: core mutations of GB1 that induce dimerization and domain swapping. <i>Journal of Molecular Biology</i> , <b>2003</b> , 333, 141-52	6.5	66
141	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> , <b>2012</b> , 109, 19994-9	11.5	65
140	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> , <b>2008</b> , 283, 13459-70	5.4	65
139	Solution NMR structure of the barrier-to-autointegration factor-Emerin complex. <i>Journal of Biological Chemistry</i> , <b>2007</b> , 282, 14525-35	5.4	63
138	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> , <b>2005</b> , 354, 789-800	6.5	62
137	HIV-1 protease: maturation, enzyme specificity, and drug resistance. <i>Advances in Pharmacology</i> , <b>2000</b> , 49, 111-46	5.7	60
136	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> , <b>1991</b> , 199, 361-9		59
135	Conformational changes in HIV-1 gp41 in the course of HIV-1 envelope glycoprotein-mediated fusion and inactivation. <i>Biochemistry</i> , <b>2005</b> , 44, 12471-9	3.2	57
134	Effect of sequence polymorphism and drug resistance on two HIV-1 Gag processing sites. <i>FEBS Journal</i> , <b>2002</b> , 269, 4114-20		57
133	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> , <b>2011</b> , 108, 9072-7	11.5	56
132	The effect of salt on the Michaelis Menten constant of the HIV-1 protease correlates with the Hofmeister series. <i>FEBS Letters</i> , <b>1991</b> , 280, 344-6	3.8	56
131	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> , <b>2007</b> , 363, 79-90	3.6	55
130	A transient precursor of the HIV-1 protease. Isolation, characterization, and kinetics of maturation. <i>Journal of Biological Chemistry</i> , <b>1996</b> , 271, 4477-81	5.4	55
129	Internal dynamics of the homotrimeric HIV-1 viral coat protein gp41 on multiple time scales. <i>Angewandte Chemie - International Edition</i> , <b>2013</b> , 52, 3911-5	16.4	54

128	Mapping the binding of the N-terminal extracellular tail of the CXCR4 receptor to stromal cell-derived factor-1alpha. <i>Journal of Molecular Biology</i> , <b>2005</b> , 345, 651-8	6.5	53
127	Distinguishing between protein dynamics and dye photophysics in single-molecule FRET experiments. <i>Biophysical Journal</i> , <b>2010</b> , 98, 696-706	2.9	52
126	Comparison of the substrate specificity of the human T-cell leukemia virus and human immunodeficiency virus proteinases. <i>FEBS Journal</i> , <b>2000</b> , 267, 6287-95		52
125	Preparation of uniformly isotope-labeled DNA oligonucleotides for NMR spectroscopy. <i>Journal of Biological Chemistry</i> , <b>1998</b> , 273, 2374-8	5.4	50
124	Proteolytic processing of HIV-1 protease precursor, kinetics and mechanism. <i>Journal of Biological Chemistry</i> , <b>1999</b> , 274, 23437-42	5.4	50
123	Testing Landscape Theory for Biomolecular Processes with Single Molecule Fluorescence Spectroscopy. <i>Physical Review Letters</i> , <b>2015</b> , 115, 018101	7.4	49
122	Revisiting monomeric HIV-1 protease. Characterization and redesign for improved properties. <i>Journal of Biological Chemistry</i> , <b>2003</b> , 278, 6085-92	5.4	49
121	Mutational and structural studies aimed at characterizing the monomer of HIV-1 protease and its precursor. <i>Journal of Biological Chemistry</i> , <b>2007</b> , 282, 17190-9	5.4	48
120	Chemical synthesis and expression of the HIV-1 protease gene in E. coli. <i>Biochemical and Biophysical Research Communications</i> , <b>1989</b> , 159, 87-94	3.4	48
119	Characterization of two hydrophobic methyl clusters in HIV-1 protease by NMR spin relaxation in solution. <i>Journal of Molecular Biology</i> , <b>2001</b> , 305, 515-21	6.5	46
118	Stabilization from autoproteolysis and kinetic characterization of the human T-cell leukemia virus type 1 proteinase. <i>Journal of Biological Chemistry</i> , <b>1999</b> , 274, 6660-6	5.4	46
117	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> , <b>2008</b> , 377, 170-83	3.6	45
116	Mechanism of drug resistance revealed by the crystal structure of the unliganded HIV-1 protease with F53L mutation. <i>Journal of Molecular Biology</i> , <b>2006</b> , 358, 1191-9	6.5	45
115	Combining mutations in HIV-1 protease to understand mechanisms of resistance. <i>Proteins: Structure, Function and Bioinformatics</i> , <b>2002</b> , 48, 107-16	4.2	45
114	Influence of flanking sequences on the dimer stability of human immunodeficiency virus type 1 protease. <i>Biochemistry</i> , <b>1996</b> , 35, 12957-62	3.2	45
113	Structural basis for specificity of retroviral proteases. <i>Biochemistry</i> , <b>1998</b> , 37, 4518-26	3.2	41
112	Structural evidence for effectiveness of darunavir and two related antiviral inhibitors against HIV-2 protease. <i>Journal of Molecular Biology</i> , <b>2008</b> , 384, 178-92	6.5	40
111	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. <i>Biochemistry</i> , <b>2007</b> , 46, 14854-64	3.2	40

110	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> , <b>2005</b> , 348, 687-98	6.5	39
109	A captured folding intermediate involved in dimerization and domain-swapping of GB1. <i>Journal of Molecular Biology</i> , <b>2004</b> , 340, 615-25	6.5	39
108	Measuring ultrafast protein folding rates from photon-by-photon analysis of single molecule fluorescence trajectories. <i>Chemical Physics</i> , <b>2013</b> , 422, 229-237	2.3	38
107	A rapid method to attain isotope labeled small soluble peptides for NMR studies. <i>Journal of Biomolecular NMR</i> , <b>2003</b> , 26, 193-202	3	38
106	Co-Evolutionary Fitness Landscapes for Sequence Design. <i>Angewandte Chemie - International Edition</i> , <b>2018</b> , 57, 5674-5678	16.4	37
105	Structural basis of HIV-1 neutralization by affinity matured Fabs directed against the internal trimeric coiled-coil of gp41. <i>PLoS Pathogens</i> , <b>2010</b> , 6, e1001182	7.6	37
104	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 P2T position of substrates. <i>FEBS Journal</i> , <b>1997</b> , 249, 523-30		37
103	Dissociation of the trimeric gp41 ectodomain at the lipid-water interface suggests an active role in HIV-1 Env-mediated membrane fusion. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2014</b> , 111, 3425-30	11.5	36
102	A diverse view of protein dynamics from NMR studies of HIV-1 protease flaps. <i>Proteins: Structure, Function and Bioinformatics</i> , <b>2008</b> , 70, 1408-15	4.2	36
101	Effect of substrate residues on the P2T preference of retroviral proteinases. <i>FEBS Journal</i> , <b>1999</b> , 264, 921-9		36
100	Oligomerization of the tetramerization domain of p53 probed by two- and three-color single-molecule FRET. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2017</b> , 114, E6812-E6821	11.5	35
99	Critical differences in HIV-1 and HIV-2 protease specificity for clinical inhibitors. <i>Protein Science</i> , <b>2012</b> , 21, 339-50	6.3	35
98	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> , <b>2007</b> , 81, 12946-53	6.6	35
97	The gag precursor contains a specific HIV-1 protease cleavage site between the NC (P7) and P1 proteins. <i>FEBS Letters</i> , <b>1993</b> , 333, 21-4	3.8	35
96	Long-Range Electrostatics-Induced Two-Proton Transfer Captured by Neutron Crystallography in an Enzyme Catalytic Site. <i>Angewandte Chemie - International Edition</i> , <b>2016</b> , 55, 4924-7	16.4	34
95	Tilted, Uninterrupted, Monomeric HIV-1 gp41 Transmembrane Helix from Residual Dipolar Couplings. <i>Journal of the American Chemical Society</i> , <b>2018</b> , 140, 34-37	16.4	33
94	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> , <b>2011</b> , 133, 2824-7	16.4	32
93	The point mutation A34F causes dimerization of GB1. <i>Proteins: Structure, Function and Bioinformatics</i> , <b>2008</b> , 71, 1420-31	4.2	31

92	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> , <b>2003</b> , 325, 211-23	6.5	30
91	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> , <b>1989</b> , 164, 30-8	3.4	30
90	Extreme multidrug resistant HIV-1 protease with 20 mutations is resistant to novel protease inhibitors with P1Tpyrrolidinone or P2-tris-tetrahydrofuran. <i>Journal of Medicinal Chemistry</i> , <b>2013</b> , 56, 4017-27	8.3	29
89	Analysis of Fluorescence Lifetime and Energy Transfer Efficiency in Single-Molecule Photon Trajectories of Fast-Folding Proteins. <i>Journal of Physical Chemistry B</i> , <b>2016</b> , 120, 680-99	3.4	28
88	Dependence of distance distributions derived from double electron-electron resonance pulsed EPR spectroscopy on pulse-sequence time. <i>Angewandte Chemie - International Edition</i> , <b>2015</b> , 54, 5336-9	16.4	28
87	Terminal interface conformations modulate dimer stability prior to amino terminal autoprocessing of HIV-1 protease. <i>Biochemistry</i> , <b>2012</b> , 51, 1041-50	3.2	27
86	Whole-body rocking motion of a fusion peptide in lipid bilayers from size-dispersed 15N NMR relaxation. <i>Journal of the American Chemical Society</i> , <b>2011</b> , 133, 14184-7	16.4	27
85	Studies on the symmetry and sequence context dependence of the HIV-1 proteinase specificity. <i>Journal of Biological Chemistry</i> , <b>1997</b> , 272, 16807-14	5.4	27
84	Local and global structure of the monomeric subunit of the potassium channel KcsA probed by NMR. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , <b>2007</b> , 1768, 3260-70	3.8	27
83	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> , <b>2005</b> , 353, 945-51	6.5	27
82	The regulation of Dictyostelium development by transmembrane signalling. <i>Journal of Eukaryotic Microbiology</i> , <b>1995</b> , 42, 200-5	3.6	27
81	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> , <b>2000</b> , 275, 19877-82	5.4	26
80	Optimized labeling of 13CHD2 methyl isotopomers in perdeuterated proteins: potential advantages for 13C relaxation studies of methyl dynamics of larger proteins. <i>Journal of Biomolecular NMR</i> , <b>2001</b> , 21, 167-71	3	25
79	Structure and dynamics of MarA-DNA complexes: an NMR investigation. <i>Journal of Molecular Biology</i> , <b>2001</b> , 314, 113-27	6.5	25
78	Structural Studies of a Rationally Selected Multi-Drug Resistant HIV-1 Protease Reveal Synergistic Effect of Distal Mutations on Flap Dynamics. <i>PLoS ONE</i> , <b>2016</b> , 11, e0168616	3.7	25
77	Three-Color Single-Molecule FRET and Fluorescence Lifetime Analysis of Fast Protein Folding. <i>Journal of Physical Chemistry B</i> , <b>2018</b> , 122, 11702-11720	3.4	24
76	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> , <b>2017</b> , 114, E9855-E9862	11.5	23
75	The impact of influenza hemagglutinin fusion peptide length and viral subtype on its structure and dynamics. <i>Biopolymers</i> , <b>2013</b> , 99, 189-95	2.2	23

74	Evidence of Distinct Channel Conformations and Substrate Binding Affinities for the Mitochondrial Outer Membrane Protein Translocase Pore Tom40. <i>Journal of Biological Chemistry</i> , <b>2015</b> , 290, 26204-17	5.4	22
73	Conformation of inhibitor-free HIV-1 protease derived from NMR spectroscopy in a weakly oriented solution. <i>ChemBioChem</i> , <b>2015</b> , 16, 214-8	3.8	22
72	Autocatalytic maturation, physical/chemical properties, and crystal structure of group N HIV-1 protease: relevance to drug resistance. <i>Protein Science</i> , <b>2010</b> , 19, 2055-72	6.3	22
71	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> , <b>2006</b> , 364, 283-9	6.5	22
70	Observation of $\beta$ Amyloid Peptide Oligomerization by Pressure-Jump NMR Spectroscopy. <i>Journal of the American Chemical Society</i> , <b>2019</b> , 141, 13762-13766	16.4	21
69	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> , <b>2011</b> , 50, 4786-95	3.2	21
68	Mixed-time parallel evolution in multiple quantum NMR experiments: sensitivity and resolution enhancement in heteronuclear NMR. <i>Journal of Biomolecular NMR</i> , <b>2007</b> , 37, 195-204	3	21
67	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> , <b>2017</b> , 60, 2018-2025	8.3	20
66	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> , <b>2004</b> , 43, 8230-3	3.2	20
65	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> , <b>2016</b> , 113, 12456-12461	11.5	19
64	Structures of darunavir-resistant HIV-1 protease mutant reveal atypical binding of darunavir to wide open flaps. <i>ACS Chemical Biology</i> , <b>2014</b> , 9, 1351-8	4.9	19
63	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> , <b>2009</b> , 388, 112-8	3.6	19
62	Interactions of different inhibitors with active-site aspartyl residues of HIV-1 protease and possible relevance to pepsin. <i>Proteins: Structure, Function and Bioinformatics</i> , <b>2009</b> , 75, 556-68	4.2	19
61	Revealing the dimer dissociation and existence of a folded monomer of the mature HIV-2 protease. <i>Protein Science</i> , <b>2009</b> , 18, 2442-53	6.3	19
60	Characterization of the cholesteric phase of filamentous bacteriophage fd for molecular alignment. <i>Journal of Magnetic Resonance</i> , <b>2001</b> , 149, 154-8	3	19
59	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. <i>Biochemistry</i> , <b>2016</b> , 55, 2390-400	3.2	19
58	Probing the mechanism of inhibition of amyloid- $\beta$ (1-42)-induced neurotoxicity by the chaperonin GroEL. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2018</b> , 115, E11924-E11932	11.5	19
57	Highly conserved glycine 86 and arginine 87 residues contribute differently to the structure and activity of the mature HIV-1 protease. <i>Proteins: Structure, Function and Bioinformatics</i> , <b>2010</b> , 78, 1015-25	4.2	18



56	Pressure-induced structural transition of mature HIV-1 protease from a combined NMR/MD simulation approach. <i>Proteins: Structure, Function and Bioinformatics</i> , <b>2015</b> , 83, 2117-23	4.2	17
55	Is human thioredoxin monomeric or dimeric?. <i>Protein Science</i> , <b>1999</b> , 8, 426-9	6.3	17
54	Design and initial characterization of a circular permuted variant of the potent HIV-inactivating protein cyanovirin-N. <i>Proteins: Structure, Function and Bioinformatics</i> , <b>2002</b> , 46, 153-60	4.2	17
53	Effect of salt on the kinetic parameters of retroviral and mammalian aspartic acid proteases. <i>Bioorganic Chemistry</i> , <b>1992</b> , 20, 67-76	5.1	17
52	Purification of HIV-1 wild-type protease and characterization of proteolytically inactive HIV-1 protease mutants by pepstatin A affinity chromatography. <i>FEBS Letters</i> , <b>1991</b> , 280, 347-50	3.8	17
51	Beta-adrenergic regulation of c-fos gene expression in an epithelial cell line. <i>FEBS Letters</i> , <b>1988</b> , 240, 118-22	3.8	17
50	Complexes of neutralizing and non-neutralizing affinity matured Fabs with a mimetic of the internal trimeric coiled-coil of HIV-1 gp41. <i>PLoS ONE</i> , <b>2013</b> , 8, e78187	3.7	16
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48	Complete dissociation of the HIV-1 gp41 ectodomain and membrane proximal regions upon phospholipid binding. <i>Journal of Biomolecular NMR</i> , <b>2015</b> , 61, 235-48	3	13
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- 2 Transient lipid-bound states of spike protein heptad repeats provide insights into SARS-CoV-2 membrane fusion. *Science Advances*, **2021**, 7, eabk2226 14.3 ○
- 1 Concentration-Dependent Structural Transition of the HIV-1 gp41 MPER Peptide into  $\beta$ -Helical Trimers. *Angewandte Chemie*, **2021**, 133, 168-172 3.6