G Marius Clore

List of Publications by Year in Descending Order

561 papers	60,146 citations	116 h-index	232 g-index
592 ext. papers	62,995 ext. citations	8.8 avg, IF	7.49 L-index

#	Paper	IF	Citations
561	Time-resolved DEER EPR and solid-state NMR afford kinetic and structural elucidation of substrate binding to Ca-ligated calmodulin.. *Proceedings of the National Academy of Sciences of the United States of America*, **2022**, 119,	11.5	2
560	NMR methods for exploring 'dark' states in ligand binding and protein-protein interactions.. *Progress in Nuclear Magnetic Resonance Spectroscopy*, **2022**, 128, 1-24	10.4	2
559	Visualization of Sparsely-populated Lower-order Oligomeric States of Human Mitochondrial Hsp60 by Cryo-electron Microscopy. *Journal of Molecular Biology*, **2021**, 433, 167322	6.5	0
558	Probing Side-Chain Dynamics in Proteins by NMR Relaxation of Isolated C Magnetization Modes in CH Methyl Groups. *Journal of Physical Chemistry B*, **2021**, 125, 3343-3352	3.4	2
557	Probing the Interaction of Huntingtin Exon-1 Polypeptides with the Chaperonin Nanomachine GroEL. *ChemBioChem*, **2021**, 22, 1985-1991	3.8	2
556	Quantitative Exchange NMR-Based Analysis of Huntingtin-SH3 Interactions Suggests an Allosteric Mechanism of Inhibition of Huntingtin Aggregation. *Journal of the American Chemical Society*, **2021**, 143, 9672-9681	16.4	1
555	A simple and cost-effective protocol for high-yield expression of deuterated and selectively isoleucine/leucine/valine methyl protonated proteins in Escherichia coli grown in shaker flasks. *Journal of Biomolecular NMR*, **2021**, 75, 83-87	3	1
554	The measurement of relaxation rates of degenerate H transitions in methyl groups of proteins using acute angle radiofrequency pulses. *Journal of Magnetic Resonance*, **2021**, 330, 107034	3	1
553	Submillisecond Freezing Permits Cryoprotectant-Free EPR Double Electron-Electron Resonance Spectroscopy. *ChemPhysChem*, **2020**, 21, 1224-1229	3.2	12
552	Probing the Interaction between HIV-1 Protease and the Homodimeric p66/p66' Reverse Transcriptase Precursor by Double Electron-Electron Resonance EPR Spectroscopy. *ChemBioChem*, **2020**, 21, 3051-3055	3.8	2
551	Abrogation of prenucleation, transient oligomerization of the Huntingtin exon 1 protein by human profilin I. *Proceedings of the National Academy of Sciences of the United States of America*, **2020**, 117, 5844-5852	11.5	11
550	Kinetics of Fast Tetramerization of the Huntingtin Exon 1 Protein Probed by Concentration-Dependent On-Resonance Measurements. *Journal of Physical Chemistry Letters*, **2020**, 11, 5643-5648	6.4	3
549	Determining methyl sidechain conformations in a CS-ROSETTA model using methyl H-C residual dipolar couplings. *Journal of Biomolecular NMR*, **2020**, 74, 111-118	3	2
548	Magic-Angle-Pulse Driven Separation of Degenerate H Transitions in Methyl Groups of Proteins: Application to Studies of Methyl Axis Dynamics. *ChemPhysChem*, **2020**, 21, 1087-1091	3.2	7
547	Optimized NMR Experiments for the Isolation of I=1/2 Manifold Transitions in Methyl Groups of Proteins. *ChemPhysChem*, **2020**, 21, 13-19	3.2	8
546	XIPP: multi-dimensional NMR analysis software. *Journal of Biomolecular NMR*, **2020**, 74, 9-25	3	1
545	Optimized selection of slow-relaxing C transitions in methyl groups of proteins: application to relaxation dispersion. *Journal of Biomolecular NMR*, **2020**, 74, 673-680	3	6

544	An S/T motif controls reversible oligomerization of the Hsp40 chaperone DNAJB6b through subtle reorganization of a β-sheet backbone. *Proceedings of the National Academy of Sciences of the United States of America*, **2020**, 117, 30441-30450	11.5	7
543	filtering by H-methyl labeling in a deuterated protein for pulsed double electron-electron resonance EPR. *Chemical Communications*, **2020**, 56, 10890-10893	5.8	2
542	A three-dimensional potential of mean force to improve backbone and sidechain hydrogen bond geometry in Xplor-NIH protein structure determination. *Protein Science*, **2020**, 29, 100-110	6.3	7
541	Quantitative Interpretation of Solvent Paramagnetic Relaxation for Probing Protein-Cosolute Interactions. *Journal of the American Chemical Society*, **2020**, 142, 8281-8290	16.4	4
540	Spatial domain organization in the HIV-1 reverse transcriptase p66 homodimer precursor probed by double electron-electron resonance EPR. *Proceedings of the National Academy of Sciences of the United States of America*, **2019**, 116, 17809-17816	11.5	10
539	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
538	Probing initial transient oligomerization events facilitating Huntingtin fibril nucleation at atomic resolution by relaxation-based NMR. *Proceedings of the National Academy of Sciences of the United States of America*, **2019**, 116, 3562-3571	11.5	33
537	Exchange saturation transfer and associated NMR techniques for studies of protein interactions involving high-molecular-weight systems. *Journal of Biomolecular NMR*, **2019**, 73, 461-469	3	8
536	Protein NMR: Boundless opportunities. *Journal of Magnetic Resonance*, **2019**, 306, 187-191	3	21
535	Unraveling the structure and dynamics of the human DNAJB6b chaperone by NMR reveals insights into Hsp40-mediated proteostasis. *Proceedings of the National Academy of Sciences of the United States of America*, **2019**, 116, 21529-21538	11.5	21
534	A simple protocol for expression of isotope-labeled proteins in Escherichia coli grown in shaker flasks at high cell density. *Journal of Biomolecular NMR*, **2019**, 73, 743-748	3	3
533	Probing transient excited states of the bacterial cell division regulator MinE by relaxation dispersion NMR spectroscopy. *Proceedings of the National Academy of Sciences of the United States of America*, **2019**, 116, 25446-25455	11.5	8
532	TiO Nanoparticles Catalyze Oxidation of Huntingtin Exon 1-Derived Peptides Impeding Aggregation: A Quantitative NMR Study of Binding and Kinetics. *Journal of the American Chemical Society*, **2019**, 141, 94-97	16.4	23
531	Targeting a Dark Excited State of HIV-1 Nucleocapsid by Antiretroviral Thioesters Revealed by NMR Spectroscopy. *Angewandte Chemie - International Edition*, **2018**, 57, 2687-2691	16.4	16
530	Targeting a Dark Excited State of HIV-1 Nucleocapsid by Antiretroviral Thioesters Revealed by NMR Spectroscopy. *Angewandte Chemie*, **2018**, 130, 2717-2721	3.6	2
529	Probing Conformational States of the Finger and Thumb Subdomains of HIV-1 Reverse Transcriptase Using Double Electron-Electron Resonance Electron Paramagnetic Resonance Spectroscopy. *Biochemistry*, **2018**, 57, 489-493	3.2	6
528	Interaction of Huntingtin Exon-1 Peptides with Lipid-Based Micellar Nanoparticles Probed by Solution NMR and Q-Band Pulsed EPR. *Journal of the American Chemical Society*, **2018**, 140, 6199-6202	16.4	22
527	Disassembly/reassembly strategy for the production of highly pure GroEL, a tetradecameric supramolecular machine, suitable for quantitative NMR, EPR and mutational studies. *Protein Expression and Purification*, **2018**, 142, 8-15	2	2

526	Extensive Sampling of the Cavity of the GroEL Nanomachine by Protein Substrates Probed by Paramagnetic Relaxation Enhancement. *Journal of Physical Chemistry Letters*, **2018**, 9, 3368-3371	6.4	8
525	Xplor-NIH for molecular structure determination from NMR and other data sources. *Protein Science*, **2018**, 27, 26-40	6.3	96
524	Probing the mechanism of inhibition of amyloid-β(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
523	Decorrelating Kinetic and Relaxation Parameters in Exchange Saturation Transfer NMR: A Case Study of N-Terminal Huntingtin Peptides Binding to Unilamellar Lipid Vesicles. *Journal of Physical Chemistry B*, **2018**, 122, 11271-11278	3.4	12
522	Confinement and Stabilization of Fyn SH3 Folding Intermediate Mimetics within the Cavity of the Chaperonin GroEL Demonstrated by Relaxation-Based NMR. *Biochemistry*, **2017**, 56, 903-906	3.2	16
521	Probing the Binding Modes of a Multidomain Protein to Lipid-based Nanoparticles by Relaxation-based NMR. *Journal of Physical Chemistry Letters*, **2017**, 8, 2535-2540	6.4	7
520	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
519	Structure Determination of Large Macromolecular Complexes Using NMR **2017**, 316-318		
518	Chaperonin GroEL accelerates protofibril formation and decorates fibrils of the Het-s prion protein. *Proceedings of the National Academy of Sciences of the United States of America*, **2017**, 114, 9104-9109	11.5	16
517	Towards interpretation of intermolecular paramagnetic relaxation enhancement outside the fast exchange limit. *Journal of Biomolecular NMR*, **2016**, 66, 1-7	3	5
516	NMR in Structural and Cell Biology **2016**, 98-107		1
515	Long Distance Measurements up to 160 Å in the GroEL Tetradecamer Using Q-Band DEER EPR Spectroscopy. *Angewandte Chemie - International Edition*, **2016**, 55, 15905-15909	16.4	92
514	Long Distance Measurements up to 160 Å in the GroEL Tetradecamer Using Q-Band DEER EPR Spectroscopy. *Angewandte Chemie*, **2016**, 128, 16137-16141	3.6	26
513	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
512	Quantitative Characterization of Configurational Space Sampled by HIV-1 Nucleocapsid Using Solution NMR, X-ray Scattering and Protein Engineering. *ChemPhysChem*, **2016**, 17, 1548-52	3.2	10
511	Hybrid Approaches to Structural Characterization of Conformational Ensembles of Complex Macromolecular Systems Combining NMR Residual Dipolar Couplings and Solution X-ray Scattering. *Chemical Reviews*, **2016**, 116, 6305-22	68.1	30
510	Dynamics of SOX2 Interactions with DNA **2016**, 25-41		1
509	Improving NMR Structures of RNA. *Structure*, **2016**, 24, 806-815	5.2	30

508	Global Dynamics and Exchange Kinetics of a Protein on the Surface of Nanoparticles Revealed by Relaxation-Based Solution NMR Spectroscopy. *Journal of the American Chemical Society*, **2016**, 138, 5789-92	16.4	49
507	A simple and robust protocol for high-yield expression of perdeuterated proteins in Escherichia coli grown in shaker flasks. *Journal of Biomolecular NMR*, **2016**, 66, 85-91	3	30
506	Quantitative Resolution of Monomer-Dimer Populations by Inversion Modulated DEER EPR Spectroscopy. *ChemPhysChem*, **2016**, 17, 2987-2991	3.2	11
505	Visualizing transient dark states by NMR spectroscopy. *Quarterly Reviews of Biophysics*, **2015**, 48, 35-116	7	152
504	Conformation and dynamics of the Gag polyprotein of the human immunodeficiency virus 1 studied by NMR spectroscopy. *Proceedings of the National Academy of Sciences of the United States of America*, **2015**, 112, 3374-9	11.5	35
503	Intrinsic unfoldase/foldase activity of the chaperonin GroEL directly demonstrated using multinuclear relaxation-based NMR. *Proceedings of the National Academy of Sciences of the United States of America*, **2015**, 112, 8817-23	11.5	68
502	Dynamic equilibrium between closed and partially closed states of the bacterial Enzyme I unveiled by solution NMR and X-ray scattering. *Proceedings of the National Academy of Sciences of the United States of America*, **2015**, 112, 11565-70	11.5	24
501	Mutations Proximal to Sites of Autoproteolysis and the α-Helix That Co-evolve under Drug Pressure Modulate the Autoprocessing and Vitality of HIV-1 Protease. *Biochemistry*, **2015**, 54, 5414-24	3.2	8
500	Reply to Marchenko et al.: Flux analysis of GroEL-assisted protein folding/unfolding. *Proceedings of the National Academy of Sciences of the United States of America*, **2015**, 112, E6833-4	11.5	1
499	Dependence of Distance Distributions Derived from Double Electron–Electron Resonance Pulsed EPR Spectroscopy on Pulse-Sequence Time. *Angewandte Chemie*, **2015**, 127, 5426-5429	3.6	2
498	The energetics of a three-state protein folding system probed by high-pressure relaxation dispersion NMR spectroscopy. *Angewandte Chemie - International Edition*, **2015**, 54, 11157-61	16.4	21
497	The Energetics of a Three-State Protein Folding System Probed by High-Pressure Relaxation Dispersion NMR Spectroscopy. *Angewandte Chemie*, **2015**, 127, 11309-11313	3.6	
496	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
495	Practical Aspects of Paramagnetic Relaxation Enhancement in Biological Macromolecules. *Methods in Enzymology*, **2015**, 564, 485-97	1.7	53
494	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
493	Large interdomain rearrangement triggered by suppression of micro- to millisecond dynamics in bacterial Enzyme I. *Nature Communications*, **2015**, 6, 5960	17.4	27
492	Interplay between conformational selection and induced fit in multidomain protein-ligand binding probed by paramagnetic relaxation enhancement. *Biophysical Chemistry*, **2014**, 186, 3-12	3.5	37
491	A NMR experiment for simultaneous correlations of valine and leucine/isoleucine methyls with carbonyl chemical shifts in proteins. *Journal of Biomolecular NMR*, **2014**, 58, 1-8	3	15

490	Characterizing methyl-bearing side chain contacts and dynamics mediating amyloid protofibril interactions using C(methyl)-DEST and lifetime line broadening. *Angewandte Chemie - International Edition*, **2014**, 53, 10345-9	16.4	40
489	Probing the rate-limiting step for intramolecular transfer of a transcription factor between specific sites on the same DNA molecule by (15)Nz-exchange NMR spectroscopy. *Journal of the American Chemical Society*, **2014**, 136, 14369-72	16.4	6
488	Investigation of the Structure and Dynamics of the CapsidSpacer Peptide 1Nucleocapsid Fragment of the HIV-1 Gag Polyprotein by Solution NMR Spectroscopy. *Angewandte Chemie*, **2014**, 126, 1043-1046	3.6	1
487	Investigation of the structure and dynamics of the capsid-spacer peptide 1-nucleocapsid fragment of the HIV-1 gag polyprotein by solution NMR spectroscopy. *Angewandte Chemie - International Edition*, **2014**, 53, 1025-8	16.4	14
486	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
485	Characterizing Methyl-Bearing Side Chain Contacts and Dynamics Mediating Amyloid Protofibril Interactions Using 13Cmethyl-DEST and Lifetime Line Broadening. *Angewandte Chemie*, **2014**, 126, 10513-10517	3.6	2
484	Using small angle solution scattering data in Xplor-NIH structure calculations. *Progress in Nuclear Magnetic Resonance Spectroscopy*, **2014**, 80, 1-11	10.4	43
483	Encounter complexes and dimensionality reduction in protein-protein association. *ELife*, **2014**, 3, e01370	8.9	42
482	Generating accurate contact maps of transient long-range interactions in intrinsically disordered proteins by paramagnetic relaxation enhancement. *Biophysical Journal*, **2013**, 104, 1635-6	2.9	6
481	Structure, dynamics and biophysics of the cytoplasmic protein-protein complexes of the bacterial phosphoenolpyruvate: sugar phosphotransferase system. *Trends in Biochemical Sciences*, **2013**, 38, 515-30	10.3	46
480	Structure and dynamics of full-length HIV-1 capsid protein in solution. *Journal of the American Chemical Society*, **2013**, 135, 16133-47	16.4	95
479	Sequence-specific determination of protein and peptide concentrations by absorbance at 205 nm. *Protein Science*, **2013**, 22, 851-8	6.3	219
478	The length of the calmodulin linker determines the extent of transient interdomain association and target affinity. *Journal of the American Chemical Society*, **2013**, 135, 9648-51	16.4	21
477	Structural basis for enzyme I inhibition by ketoglutarate. *ACS Chemical Biology*, **2013**, 8, 1232-40	4.9	24
476	Seeing the invisible by paramagnetic and diamagnetic NMR. *Biochemical Society Transactions*, **2013**, 41, 1343-54	5.1	16
475	Probing the transient dark state of substrate binding to GroEL by relaxation-based solution NMR. *Proceedings of the National Academy of Sciences of the United States of America*, **2013**, 110, 11361-6	11.5	66
474	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
473	Smooth statistical torsion angle potential derived from a large conformational database via adaptive kernel density estimation improves the quality of NMR protein structures. *Protein Science*, **2012**, 21, 1824-36	6.3	46

472	Peptides from second extracellular loop of C-C chemokine receptor type 5 (CCR5) inhibit diverse strains of HIV-1. *Journal of Biological Chemistry*, **2012**, 287, 15076-86	5.4	20
471	Contrast-matched small-angle X-ray scattering from a heavy-atom-labeled protein in structure determination: application to a lead-substituted calmodulin-peptide complex. *Journal of the American Chemical Society*, **2012**, 134, 14686-9	16.4	32
470	Coupling between internal dynamics and rotational diffusion in the presence of exchange between discrete molecular conformations. *Journal of Chemical Physics*, **2012**, 136, 034108	3.9	18
469	Probing exchange kinetics and atomic resolution dynamics in high-molecular-weight complexes using dark-state exchange saturation transfer NMR spectroscopy. *Nature Protocols*, **2012**, 7, 1523-33	18.8	81
468	An efficient protocol for incorporation of an unnatural amino acid in perdeuterated recombinant proteins using glucose-based media. *Journal of Biomolecular NMR*, **2012**, 52, 191-5	3	13
467	Structure of the Plasmodium 6-cysteine s48/45 domain. *Proceedings of the National Academy of Sciences of the United States of America*, **2012**, 109, 6692-7	11.5	51
466	Solution structure of the IIAChitobiose-HPr complex of the N,N'-diacetylchitobiose branch of the Escherichia coli phosphotransferase system. *Journal of Biological Chemistry*, **2012**, 287, 23819-29	5.4	11
465	Interplay between minor and major groove-binding transcription factors Sox2 and Oct1 in translocation on DNA studied by paramagnetic and diamagnetic NMR. *Journal of Biological Chemistry*, **2012**, 287, 14349-63	5.4	24
464	Impact of protein/protein interactions on global intermolecular translocation rates of the transcription factors Sox2 and Oct1 between DNA cognate sites analyzed by z-exchange NMR spectroscopy. *Journal of Biological Chemistry*, **2012**, 287, 26962-70	5.4	14
463	Conformational selection and substrate binding regulate the monomer/dimer equilibrium of the C-terminal domain of Escherichia coli enzyme I. *Journal of Biological Chemistry*, **2012**, 287, 26989-98	5.4	25
462	Recent Developments in Biomolecular NMR. *RSC Biomolecular Sciences*, **2012**,		5
461	No interaction of barrier-to-autointegration factor (BAF) with HIV-1 MA, cone-rod homeobox (Crx) or MAN1-C in absence of DNA. *PLoS ONE*, **2011**, 6, e25123	3.7	11
460	A short recollection on the paper entitled "A common sense approach to peak picking in two-, three-, and four-dimensional spectra using automatic computer analysis of contour diagrams" by D.S. Garrett, R. Powers, A.M. Gronenborn, and G.M. Clore [J. Magn. Reson. 95 (1991) 214-220]. *Journal of Magnetic Resonance*, **2011**, 213, 364-5	3	13
459	A common sense approach to peak picking in two-, three-, and four-dimensional spectra using automatic computer analysis of contour diagrams. 1991. *Journal of Magnetic Resonance*, **2011**, 213, 357-63	3	126
458	A rigid disulfide-linked nitroxide side chain simplifies the quantitative analysis of PRE data. *Journal of Biomolecular NMR*, **2011**, 51, 105-14	3	49
457	Exploring translocation of proteins on DNA by NMR. *Journal of Biomolecular NMR*, **2011**, 51, 209-19	3	31
456	Automated sequence- and stereo-specific assignment of methyl-labeled proteins by paramagnetic relaxation and methyl-methyl nuclear Overhauser enhancement spectroscopy. *Journal of Biomolecular NMR*, **2011**, 51, 319-28	3	44
455	Exploring sparsely populated states of macromolecules by diamagnetic and paramagnetic NMR relaxation. *Protein Science*, **2011**, 20, 229-46	6.3	55

454	Impact of 15N R2/R1 relaxation restraints on molecular size, shape, and bond vector orientation for NMR protein structure determination with sparse distance restraints. *Journal of the American Chemical Society*, **2011**, 133, 6154-7	16.4	7
453	Transient, sparsely populated compact states of apo and calcium-loaded calmodulin probed by paramagnetic relaxation enhancement: interplay of conformational selection and induced fit. *Journal of the American Chemical Society*, **2011**, 133, 18966-74	16.4	99
452	Combined use of residual dipolar couplings and solution X-ray scattering to rapidly probe rigid-body conformational transitions in a non-phosphorylatable active-site mutant of the 128 kDa enzyme I dimer. *Journal of the American Chemical Society*, **2011**, 133, 424-7	16.4	31
451	Atomic-resolution dynamics on the surface of amyloid-β protofibrils probed by solution NMR. *Nature*, **2011**, 480, 268-72	50.4	320
450	Solution structure of the monovalent lectin microvirin in complex with Man(alpha)(1-2)Man provides a basis for anti-HIV activity with low toxicity. *Journal of Biological Chemistry*, **2011**, 286, 20788-96	5.4	55
449	Intra- and intermolecular translocation of the bi-domain transcription factor Oct1 characterized by liquid crystal and paramagnetic NMR. *Proceedings of the National Academy of Sciences of the United States of America*, **2011**, 108, E169-76	11.5	35
448	Mechanistic details of a protein-protein association pathway revealed by paramagnetic relaxation enhancement titration measurements. *Proceedings of the National Academy of Sciences of the United States of America*, **2010**, 107, 1379-84	11.5	71
447	Solution structure of the IIAChitobiose-IIBChitobiose complex of the N,N'-diacetylchitobiose branch of the Escherichia coli phosphotransferase system. *Journal of Biological Chemistry*, **2010**, 285, 4173-4184	5.4	8
446	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
445	Structure-independent analysis of the breadth of the positional distribution of disordered groups in macromolecules from order parameters for long, variable-length vectors using NMR paramagnetic relaxation enhancement. *Journal of the American Chemical Society*, **2010**, 132, 13346-56	16.4	31
444	Kinetics of amyloid beta monomer-to-oligomer exchange by NMR relaxation. *Journal of the American Chemical Society*, **2010**, 132, 9948-51	16.4	152
443	Direct use of 15N relaxation rates as experimental restraints on molecular shape and orientation for docking of protein-protein complexes. *Journal of the American Chemical Society*, **2010**, 132, 5987-9	16.4	15
442	Solution structure of the 128 kDa enzyme I dimer from Escherichia coli and its 146 kDa complex with HPr using residual dipolar couplings and small- and wide-angle X-ray scattering. *Journal of the American Chemical Society*, **2010**, 132, 13026-45	16.4	100
441	Water in the polar and nonpolar cavities of the protein interleukin-1β. *Journal of Physical Chemistry B*, **2010**, 114, 16290-7	3.4	37
440	Structural basis of the association of HIV-1 matrix protein with DNA. *PLoS ONE*, **2010**, 5, e15675	3.7	19
439	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**	3.6	19
438	Using multiple quantum coherence to increase the 15N resolution in a three-dimensional TROSY HNCO experiment for accurate PRE and RDC measurements. *Journal of Magnetic Resonance*, **2009**, 200, 173-7	3	8
437	Using the experimentally determined components of the overall rotational diffusion tensor to restrain molecular shape and size in NMR structure determination of globular proteins and protein-protein complexes. *Journal of the American Chemical Society*, **2009**, 131, 9522-31	16.4	24

436	Theory, practice, and applications of paramagnetic relaxation enhancement for the characterization of transient low-population states of biological macromolecules and their complexes. *Chemical Reviews*, **2009**, 109, 4108-39	68.1	575
435	Visualizing transient events in amino-terminal autoprocessing of HIV-1 protease. *Nature*, **2008**, 455, 693-6	30.4	111
434	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
433	Visualization of transient ultra-weak protein self-association in solution using paramagnetic relaxation enhancement. *Journal of the American Chemical Society*, **2008**, 130, 4048-56	16.4	73
432	Visualizing lowly-populated regions of the free energy landscape of macromolecular complexes by paramagnetic relaxation enhancement. *Molecular BioSystems*, **2008**, 4, 1058-69		58
431	A pseudopotential for improving the packing of ellipsoidal protein structures determined from NMR data. *Journal of Physical Chemistry B*, **2008**, 112, 6070-3	3.4	21
430	Sequestering of the prehairpin intermediate of gp41 by peptide N36Mut(e,g) potentiates the human immunodeficiency virus type 1 neutralizing activity of monoclonal antibodies directed against the N-terminal helical repeat of gp41. *Journal of Virology*, **2008**, 82, 10032-41	6.6	28
429	Replica exchange simulations of transient encounter complexes in protein-protein association. *Proceedings of the National Academy of Sciences of the United States of America*, **2008**, 105, 12855-60	11.5	94
428	Global jumping and domain-specific intersegment transfer between DNA cognate sites of the multidomain transcription factor Oct-1. *Proceedings of the National Academy of Sciences of the United States of America*, **2008**, 105, 13871-6	11.5	75
427	Impact of phosphorylation on structure and thermodynamics of the interaction between the N-terminal domain of enzyme I and the histidine phosphocarrier protein of the bacterial phosphotransferase system. *Journal of Biological Chemistry*, **2008**, 283, 18980-9	5.4	28
426	Solution NMR structures of productive and non-productive complexes between the A and B domains of the cytoplasmic subunit of the mannose transporter of the Escherichia coli phosphotransferase system. *Journal of Biological Chemistry*, **2008**, 283, 11024-37	5.4	22
425	Automated error-tolerant macromolecular structure determination from multidimensional nuclear Overhauser enhancement spectra and chemical shift assignments: improved robustness and performance of the PASD algorithm. *Journal of Biomolecular NMR*, **2008**, 41, 221-39	3	16
424	Spin-state selective carbon-detected HNCO with TROSY optimization in all dimensions and double echo-antiecho sensitivity enhancement in both indirect dimensions. *Journal of the American Chemical Society*, **2007**, 129, 5484-91	16.4	18
423	A physical picture of atomic motions within the Dickerson DNA dodecamer in solution derived from joint ensemble refinement against NMR and large-angle X-ray scattering data. *Biochemistry*, **2007**, 46, 1152-66	3.2	88
422	Role of electrostatic interactions in transient encounter complexes in protein-protein association investigated by paramagnetic relaxation enhancement. *Journal of the American Chemical Society*, **2007**, 129, 12954-5	16.4	66
421	TROSY-based z-exchange spectroscopy: application to the determination of the activation energy for intermolecular protein translocation between specific sites on different DNA molecules. *Journal of the American Chemical Society*, **2007**, 129, 13232-7	16.4	43
420	Heteronuclear NMR spectroscopy for lysine NH(3) groups in proteins: unique effect of water exchange on (15)N transverse relaxation. *Journal of the American Chemical Society*, **2007**, 129, 2971-80	16.4	79
419	Practical aspects of (1)H transverse paramagnetic relaxation enhancement measurements on macromolecules. *Journal of Magnetic Resonance*, **2007**, 184, 185-95	3	202

418	Open-to-closed transition in apo maltose-binding protein observed by paramagnetic NMR. *Nature*, **2007**, 449, 1078-82	50.4	336
417	Elucidating transient macromolecular interactions using paramagnetic relaxation enhancement. *Current Opinion in Structural Biology*, **2007**, 17, 603-16	8.1	177
416	Solution NMR structure of the barrier-to-autointegration factor-Emerin complex. *Journal of Biological Chemistry*, **2007**, 282, 14525-35	5.4	63
415	Intramolecular domain-domain association/dissociation and phosphoryl transfer in the mannitol transporter of Escherichia coli are not coupled. *Proceedings of the National Academy of Sciences of the United States of America*, **2007**, 104, 3153-8	11.5	21
414	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
413	Solution structure of a post-transition state analog of the phosphotransfer reaction between the A and B cytoplasmic domains of the mannitol transporter IIMannitol of the Escherichia coli phosphotransferase system. *Journal of Biological Chemistry*, **2006**, 281, 8939-49	5.4	26
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