

Konstantin Pervushin

List of Publications by Year in descending order

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Version: 2024-02-01

89
papers

4,150
citations

136740

32
h-index

118652

62
g-index

91
all docs

91
docs citations

91
times ranked

4497
citing authors

#	ARTICLE	IF	CITATIONS
1	Molecular mechanisms of amyloid disaggregation. <i>Journal of Advanced Research</i> , 2022, 36, 113-132.	4.4	14
2	Anticholinergic Drugs Interact With Neuroprotective Chaperone L-PGDS and Modulate Cytotoxicity of A β Amyloids. <i>Frontiers in Pharmacology</i> , 2020, 11, 862.	1.6	4
3	Amyloid β chaperone α lipocalin-type prostaglandin D synthase acts as a peroxidase in the presence of heme. <i>Biochemical Journal</i> , 2020, 477, 1227-1240.	1.7	8
4	A Short Peptide Hydrogel with High Stiffness Induced by 3×10^6 Helices to β Sheet Transition in Water. <i>Advanced Science</i> , 2019, 6, 1901173.	5.6	36
5	Abundant neuroprotective chaperone Lipocalin-type prostaglandin D synthase (L-PGDS) disassembles the Amyloid- β fibrils. <i>Scientific Reports</i> , 2019, 9, 12579.	1.6	31
6	Three-dimensional structure of <i>Megabalanus rosa</i> Cement Protein 20 revealed by multi-dimensional NMR and molecular dynamics simulations. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2019, 374, 20190198.	1.8	22
7	Hydrogen bond guidance and aromatic stacking drive liquid-liquid phase separation of intrinsically disordered histidine-rich peptides. <i>Nature Communications</i> , 2019, 10, 5465.	5.8	105
8	Matrix-Assisted Laser Desorption Ionization Mass Spectrometry Imaging of Key Proteins in Corneal Samples from Lattice Dystrophy Patients with TGFBI H626R and TGFBI R124C Mutations. <i>Proteomics - Clinical Applications</i> , 2019, 13, 1800053.	0.8	7
9	Antimicrobial activity profiles of Amphiphilic Xanthone derivatives are a function of their molecular Oligomerization. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 2018, 1860, 2281-2298.	1.4	18
10	Structure and Dynamics in the Nucleosome Revealed by Solid-State NMR. <i>Angewandte Chemie - International Edition</i> , 2018, 57, 9734-9738.	7.2	30
11	Binding of a small molecule water channel inhibitor to aquaporin Z examined by solid-state MAS NMR. <i>Journal of Biomolecular NMR</i> , 2018, 71, 91-100.	1.6	2
12	Effect of position-specific single-point mutations and biophysical characterization of amyloidogenic peptide fragments identified from lattice corneal dystrophy patients. <i>Biochemical Journal</i> , 2017, 474, 1705-1725.	1.7	14
13	Utf1 contributes to intergenerational epigenetic inheritance of pluripotency. <i>Scientific Reports</i> , 2017, 7, 14612.	1.6	7
14	Structural characterization of eRF1 mutants indicate a complex mechanism of stop codon recognition. <i>Scientific Reports</i> , 2016, 6, 18644.	1.6	1
15	Modular peptides from the thermoplastic squid sucker ring teeth form amyloid-like cross- β supramolecular networks. <i>Acta Biomaterialia</i> , 2016, 46, 41-54.	4.1	29
16	Efficiency of High Magnetic Fields in Solid-state NMR. <i>Chemistry Letters</i> , 2016, 45, 209-210.	0.7	11
17	Allotides: Proline-Rich Cystine Knot β -Amylase Inhibitors from <i>Allamanda cathartica</i> . <i>Journal of Natural Products</i> , 2015, 78, 695-704.	1.5	29
18	A novel fragment based strategy for membrane active antimicrobials against MRSA. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 2015, 1848, 1023-1031.	1.4	36

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19	DNA-mediated cooperativity facilitates the co-selection of cryptic enhancer sequences by SOX2 and PAX6 transcription factors. <i>Nucleic Acids Research</i> , 2015, 43, 1513-1528.	6.5	37
20	Amino Acid Modified Xanthone Derivatives: Novel, Highly Promising Membrane-Active Antimicrobials for Multidrug-Resistant Gram-Positive Bacterial Infections. <i>Journal of Medicinal Chemistry</i> , 2015, 58, 739-752.	2.9	109
21	Extended Structure of Rat Islet Amyloid Polypeptide in Solution. <i>Advances in Experimental Medicine and Biology</i> , 2015, 827, 85-92.	0.8	0
22	Collaborative development for setup, execution, sharing and analytics of complex NMR experiments. <i>Journal of Magnetic Resonance</i> , 2014, 239, 121-129.	1.2	2
23	Polychromatic frequency encoding in indirect dimensions in NMR spectroscopy. <i>Molecular Physics</i> , 2013, 111, 765-770.	0.8	0
24	Molecular simulations suggest how a branched antimicrobial peptide perturbs a bacterial membrane and enhances permeability. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 2013, 1828, 1112-1121.	1.4	56
25	Structural and dynamic insights into substrate binding and catalysis of human lipocalin prostaglandin D synthase. <i>Journal of Lipid Research</i> , 2013, 54, 1630-1643.	2.0	24
26	Solution Structure of the PAS Domain of a Thermophilic YybT Protein Homolog Reveals a Potential Ligand-binding Site. <i>Journal of Biological Chemistry</i> , 2013, 288, 11949-11959.	1.6	27
27	Comprehensive Analysis and Identification of the Human STIM1 Domains for Structural and Functional Studies. <i>PLoS ONE</i> , 2013, 8, e53979.	1.1	3
28	Progressive Structuring of a Branched Antimicrobial Peptide on the Path to the Inner Membrane Target. <i>Journal of Biological Chemistry</i> , 2012, 287, 26606-26617.	1.6	32
29	Selectivity of stop codon recognition in translation termination is modulated by multiple conformations of GTS loop in eRF1. <i>Nucleic Acids Research</i> , 2012, 40, 5751-5765.	6.5	15
30	The Small Hydrophobic Protein of the Human Respiratory Syncytial Virus Forms Pentameric Ion Channels. <i>Journal of Biological Chemistry</i> , 2012, 287, 24671-24689.	1.6	106
31	Molecular dynamics simulations of a new branched antimicrobial peptide: A comparison of force fields. <i>Journal of Chemical Physics</i> , 2012, 137, 215101.	1.2	26
32	Expression and purification of coronavirus envelope proteins using a modified \hat{I}^2 -barrel construct. <i>Protein Expression and Purification</i> , 2012, 85, 133-141.	0.6	31
33	Structural basis of RNA binding by leucine zipper GCN4. <i>Protein Science</i> , 2012, 21, 667-676.	3.1	6
34	Identification of a Polyoxometalate Inhibitor of the DNA Binding Activity of Sox2. <i>ACS Chemical Biology</i> , 2011, 6, 573-581.	1.6	48
35	Alternate rRNA secondary structures as regulators of translation. <i>Nature Structural and Molecular Biology</i> , 2011, 18, 169-176.	3.6	44
36	The Molecular Basis of Distinct Aggregation Pathways of Islet Amyloid Polypeptide. <i>Journal of Biological Chemistry</i> , 2011, 286, 6291-6300.	1.6	104

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37	Benchmarking NMR experiments: A relational database of protein pulse sequences. <i>Journal of Magnetic Resonance</i> , 2010, 203, 129-137.	1.2	9
38	The Leucine Zipper Domains of the Transcription Factors GCN4 and c-Jun Have Ribonuclease Activity. <i>PLoS ONE</i> , 2010, 5, e10765.	1.1	23
39	pH-Dependent Interactions of Human Islet Amyloid Polypeptide Segments with Insulin Studied by Replica Exchange Molecular Dynamics Simulations. <i>Journal of Physical Chemistry B</i> , 2010, 114, 10176-10183.	1.2	12
40	Residual Structure in Islet Amyloid Polypeptide Mediates Its Interactions with Soluble Insulin. <i>Biochemistry</i> , 2009, 48, 2368-2376.	1.2	42
41	Domain Features of the Peripheral Stalk Subunit H of the Methanogenic A1AO ATP Synthase and the NMR Solution Structure of H1-47. <i>Biophysical Journal</i> , 2009, 97, 286-294.	0.2	6
42	Structure and Inhibition of the SARS Coronavirus Envelope Protein Ion Channel. <i>PLoS Pathogens</i> , 2009, 5, e1000511.	2.1	216
43	Structure-Dependent Charge Density as a Determinant of Antimicrobial Activity of Peptide Analogues of Defensin. <i>Biochemistry</i> , 2009, 48, 7229-7239.	1.2	64
44	Automatic assignment of protein backbone resonances by direct spectrum inspection in targeted acquisition of NMR data. <i>Journal of Biomolecular NMR</i> , 2008, 42, 77-86.	1.6	5
45	Probing the rotor subunit interface of the ATP synthase from <i>llyobacterâ€ftartaricus</i> . <i>FEBS Journal</i> , 2008, 275, 4850-4862.	2.2	28
46	Structural Flexibility of the Pentameric SARS Coronavirus Envelope Protein Ion Channel. <i>Biophysical Journal</i> , 2008, 95, L39-L41.	0.2	71
47	The Cytoplasmic Domain of the Chloride Channel ClC-0: Structural and Dynamic Characterization of Flexible Regions. <i>Journal of Molecular Biology</i> , 2007, 369, 1163-1169.	2.0	17
48	A Minimal Transmembrane β -Barrel Platform Protein Studied by Nuclear Magnetic Resonance. <i>Biochemistry</i> , 2007, 46, 1128-1140.	1.2	31
49	NMR Spin State Exchange Spectroscopy Reveals Equilibrium of Two Distinct Conformations of Leucine Zipper GCN4 in Solution. <i>Journal of the American Chemical Society</i> , 2007, 129, 6461-6469.	6.6	21
50	Structure and dynamics of a molten globular enzyme. <i>Nature Structural and Molecular Biology</i> , 2007, 14, 1202-1206.	3.6	102
51	Structural Plasticity of Peptidyl [~] Prolyl Isomerase sFkpA Is a Key to Its Chaperone Function As Revealed by Solution NMR. <i>Biochemistry</i> , 2006, 45, 11983-11991.	1.2	33
52	SideLink: Automated side-chain assignment of biopolymers from NMR data by relative-hypothesis-prioritization-based simulated logic. <i>Journal of Magnetic Resonance</i> , 2006, 181, 45-67.	1.2	14
53	Measuring $^1\text{H}\text{--}^1\text{H}$ and $^1\text{H}\text{--}^{13}\text{C}$ RDCs in methyl groups: example of pulse sequences with numerically optimized coherence transfer schemes. <i>Journal of Magnetic Resonance</i> , 2005, 172, 36-47.	1.2	3
54	Side-chain H and C resonance assignment in protonated/partially deuterated proteins using an improved 3D ^{13}C -detected HCC ^{13}C -TOCSY. <i>Journal of Magnetic Resonance</i> , 2005, 174, 200-208.	1.2	9

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55	Simultaneous ^1H - or ^2H -, ^{15}N - and multiple-band-selective ^{13}C -decoupling during acquisition in ^{13}C -detected experiments with proteins and oligonucleotides. <i>Journal of Biomolecular NMR</i> , 2005, 31, 1-9.	1.6	24
56	Detection of ^1H , ^{13}C correlations in proteins using a new time- and sensitivity-optimal experiment. <i>Journal of Biomolecular NMR</i> , 2005, 31, 273-278.	1.6	33
57	Investigation of Ligand Binding and Protein Dynamics in <i>Bacillus subtilis</i> Chorismate Mutase by Transverse Relaxation Optimized Spectroscopy ^1H Nuclear Magnetic Resonance. <i>Biochemistry</i> , 2005, 44, 6788-6799.	1.2	29
58	Unusual Heme ^1H -Histidine Bond in the Active Site of a Chaperone. <i>Journal of the American Chemical Society</i> , 2005, 127, 3716-3717.	6.6	55
59	Polychromatic Selective Population Inversion for TROSY Experiments with Large Proteins. <i>Journal of the American Chemical Society</i> , 2005, 127, 405-411.	6.6	13
60	An enzymatic molten globule: Efficient coupling of folding and catalysis. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2004, 101, 12860-12864.	3.3	128
61	Letter to the Editor: Backbone ^1H , ^{15}N , ^{13}C , ^1H and ^{13}C chemical shift assignments and secondary structure of FkpA, a 245-residue peptidyl-prolyl cis/trans isomerase with chaperone activity. <i>Journal of Biomolecular NMR</i> , 2004, 28, 405-406.	1.6	4
62	Measurements of Side-Chain ^{13}C ^1H Residual Dipolar Couplings in Uniformly Deuterated Proteins. <i>Journal of the American Chemical Society</i> , 2004, 126, 2414-2420.	6.6	23
63	NMR Structures of Salt-Rerefolded Forms of the 434-Repressor DNA-Binding Domain in 6 M Urea. <i>Biochemistry</i> , 2004, 43, 13937-13943.	1.2	5
64	Backbone resonance assignment in large protonated proteins using a combination of new 3D TROSY-HN(CA)HA, 4D TROSY-HACANH and ^{13}C -detected HACACO experiments. <i>Journal of Biomolecular NMR</i> , 2003, 26, 69-77.	1.6	20
65	A novel strategy for the assignment of side-chain resonances in completely deuterated large proteins using ^{13}C spectroscopy. <i>Journal of Biomolecular NMR</i> , 2003, 26, 167-179.	1.6	88
66	Sequence-specific ^1H , ^{13}C and ^{15}N resonance assignments of the rat liver fructose-2,6-bisphosphatase domain. <i>Journal of Biomolecular NMR</i> , 2003, 27, 281-282.	1.6	1
67	A new strategy for backbone resonance assignment in large proteins using a MQ-HACACO experiment. <i>Journal of Biomolecular NMR</i> , 2003, 25, 147-152.	1.6	47
68	Observation of Individual Transitions in Magnetically Equivalent Spin Systems. <i>Journal of the American Chemical Society</i> , 2003, 125, 9566-9567.	6.6	10
69	Longitudinal ^1H Relaxation Optimization in TROSY NMR Spectroscopy. <i>Journal of the American Chemical Society</i> , 2002, 124, 12898-12902.	6.6	166
70	NMR Structure of the Heme Chaperone CcmE Reveals a Novel Functional Motif. <i>Structure</i> , 2002, 10, 1551-1557.	1.6	61
71	Trans-Hydrogen-Bond Scalar Couplings as a Source of Structural Constraints in NMR of Proteins: DFT Analysis. <i>Helvetica Chimica Acta</i> , 2002, 85, 3984-3993.	1.0	8
72	Direct NMR observation and DFT calculations of a hydrogen bond at the active site of a 44 kDa enzyme. <i>Journal of Biomolecular NMR</i> , 2002, 24, 31-39.	1.6	16

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73	TROSY experiment for refinement of backbone psi and phi by simultaneous measurements of cross-correlated relaxation rates and $3,4J(\text{H}\alpha\text{HN})$ coupling constants. <i>Journal of Biomolecular NMR</i> , 2002, 24, 291-300.	1.6	13
74	Solution NMR studies of the integral membrane proteins OmpX and OmpA from <i>Escherichia coli</i> . <i>FEBS Letters</i> , 2001, 504, 173-178.	1.3	123
75	[$^{13}\text{C},^{13}\text{C}$]- and [$^{13}\text{C},^1\text{H}$]-TROSY in a Triple Resonance Experiment for Ribose-Base and Intrabase Correlations in Nucleic Acids. <i>Journal of the American Chemical Society</i> , 2001, 123, 658-664.	6.6	61
76	The use of TROSY for detection and suppression of conformational exchange NMR line broadening in biological macromolecules. <i>Journal of Biomolecular NMR</i> , 2001, 20, 275-285.		34
77	TROSY NMR with partially deuterated proteins. <i>Journal of Biomolecular NMR</i> , 2001, 20, 177-180.	1.6	67
78	Improved TROSY-HNCA experiment with suppression of conformational exchange induced relaxation. <i>Journal of Biomolecular NMR</i> , 2001, 21, 161-166.	1.6	9
79	Impact of Transverse Relaxation Optimized Spectroscopy (TROSY) on NMR as a technique in structural biology. <i>Quarterly Reviews of Biophysics</i> , 2000, 33, 161-197.	2.4	150
80	TROSY and CRINEPT: NMR with large molecular and supramolecular structures in solution. <i>Trends in Biochemical Sciences</i> , 2000, 25, 462-468.	3.7	159
81	Determination of $^2J(\text{NN})$ and $^1J(\text{HN})$ coupling constants across Watson-Crick base pairs in the Antennapedia homeodomain-DNA complex using TROSY. <i>Journal of Biomolecular NMR</i> , 2000, 16, 39-46.	1.6	43
82	[$^{15}\text{N},^1\text{H}$]/[$^{13}\text{C},^1\text{H}$]-TROSY for simultaneous detection of backbone $^{15}\text{N}-^1\text{H}$, aromatic $^{13}\text{C}-^1\text{H}$ and side-chain $^{15}\text{N}-^1\text{H}_2$ correlations in large proteins. <i>Journal of Biomolecular NMR</i> , 2000, 17, 195-202.	1.6	35
83	NMR Assignment and Secondary Structure Determination of an Octameric 110 kDa Protein Using TROSY in Triple Resonance Experiments. <i>Journal of the American Chemical Society</i> , 2000, 122, 7543-7548.	6.6	121
84	[^{13}C]-constant-time [$^{15}\text{N},^1\text{H}$]-TROSY-HNCA for sequential assignments of large proteins. <i>Journal of Biomolecular NMR</i> , 1999, 14, 85-88.	1.6	56
85	Improved sensitivity and coherence selection for [$^{15}\text{N},^1\text{H}$]-TROSY elements in triple resonance experiments. <i>Journal of Biomolecular NMR</i> , 1999, 15, 181-184.	1.6	94
86	TROSY-type Triple-Resonance Experiments for Sequential NMR Assignments of Large Proteins. <i>Journal of the American Chemical Society</i> , 1999, 121, 844-848.	6.6	315
87	Transverse Relaxation-Optimized Spectroscopy (TROSY) for NMR Studies of Aromatic Spin Systems in ^{13}C -Labeled Proteins. <i>Journal of the American Chemical Society</i> , 1998, 120, 6394-6400.	6.6	288
88	Deuterium Relaxation in a Uniformly ^{15}N -Labeled Homeodomain and Its DNA Complex. <i>Journal of the American Chemical Society</i> , 1997, 119, 3842-3843.	6.6	26
89	Structural Role of a Buried Salt Bridge in the 434 Repressor DNA-binding Domain. <i>Journal of Molecular Biology</i> , 1996, 264, 1002-1012.	2.0	45