Dmitry M Korzhnev

List of Publications by Year
in descending order

53	2,951	186265 28	182427 51
papers	citations	h-index	g-index

53	53	53	2521
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Low-populated folding intermediates of Fyn SH3 characterized by relaxation dispersion NMR. Nature, 2004, 430, 586-590.	27.8	445
2	A Transient and Low-Populated Protein-Folding Intermediate at Atomic Resolution. Science, 2010, 329, 1312-1316.	12.6	282
3	Probing Invisible, Low-Populated States of Protein Molecules by Relaxation Dispersion NMR Spectroscopy: An Application to Protein Folding. Accounts of Chemical Research, 2008, 41, 442-451.	15.6	241
4	Probing Slow Dynamics in High Molecular Weight Proteins by Methyl-TROSY NMR Spectroscopy:Â Application to a 723-Residue Enzyme. Journal of the American Chemical Society, 2004, 126, 3964-3973.	13.7	210
5	HLTFâ€™s Ancient HIRAN Domain Binds 3â€² DNA Ends to Drive Replication Fork Reversal. Molecular Cell, 2015, 58, 1090-1100.	9.7	163
6	An NMR Experiment for the Accurate Measurement of Heteronuclear Spin-Lock Relaxation Rates. Journal of the American Chemical Society, 2002, 124, 10743-10753.	13.7	130
7	Off-Resonance R1ÏNMR Studies of Exchange Dynamics in Proteins with Low Spin-Lock Fields:Â An Application to a Fyn SH3 Domain. Journal of the American Chemical Society, 2005, 127, 713-721.	13.7	122
8	Multiple-Quantum Relaxation Dispersion NMR Spectroscopy Probing Millisecond Time-Scale Dynamics in Proteins:â€‰ Theory and Application. Journal of the American Chemical Society, 2004, 126, 7320-7329.	13.7	100
9	Multiple-Site Exchange in Proteins Studied with a Suite of Six NMR Relaxation Dispersion Experiments:â€‰ An Application to the Folding of a Fyn SH3 Domain Mutant. Journal of the American Chemical Society, 2005, 127, 15602-15611.	13.7	93
10	Double- and Zero-Quantum NMR Relaxation Dispersion Experiments Sampling Millisecond Time Scale Dynamics in Proteins. Journal of the American Chemical Society, 2004, 126, 1886-1891.	13.7	91
11	Dramatic acceleration of protein folding by stabilization of a nonnative backbone conformation. Proceedings of the National Academy of Sciences of the United States of America, 2004, 101, 7954-7959.	7.1	79
12	NMR Structure and Dynamics of the C-Terminal Domain from Human Rev1 and Its Complex with Rev1 Interacting Region of DNA Polymerase Î·. Biochemistry, 2012, 51, 5506-5520.	2.5	69
13	The Folding Pathway of an FF domain: Characterization of an On-pathway Intermediate State Under Folding Conditions by 15N, 13CÎ± and 13C-methyl Relaxation Dispersion and 1H/2H-exchange NMR Spectroscopy. Journal of Molecular Biology, 2007, 372, 497-512.	4.2	60
14	Interaction between the Rev1 C-Terminal Domain and the PolD3 Subunit of PolÎ¶ Suggests a Mechanism of Polymerase Exchange upon Rev1/PolÎ¶-Dependent Translesion Synthesis. Biochemistry, 2016, 55, 2043-2053.	2.5	50
15	Probing the Transition State Ensemble of a Protein Folding Reaction by Pressure-Dependent NMR Relaxation Dispersion. Journal of the American Chemical Society, 2006, 128, 5262-5269.	13.7	48
16	Protein folding by NMR. Progress in Nuclear Magnetic Resonance Spectroscopy, 2017, 100, 52-77.	7.5	48
17	Targeting the Translesion Synthesis Pathway for the Development of Anti-Cancer Chemotherapeutics. Journal of Medicinal Chemistry, 2016, 59, 9321-9336.	6.4	46
18	Identification of Small Molecule Translesion Synthesis Inhibitors That Target the Rev1-CT/RIR Proteinâ^'Protein Interaction. ACS Chemical Biology, 2017, 12, 1903-1912.	3.4	44

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19	Rev7 dimerization is important for assembly and function of the Rev1/PolÎ¶ translesion synthesis complex. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, E8191-E8200.	7.1	44
20	Off-resonance R1rho relaxation outside of the fast exchange limit: an experimental study of a cavity mutant of T4 lysozyme. Journal of Biomolecular NMR, 2003, 26, 39-48.	2.8	42
21	The Câ€terminal domain of human Rev1 contains independent binding sites for DNA polymerase Î· and Rev7 subunit of polymerase Î¶. FEBS Letters, 2012, 586, 3051-3056.	2.8	42
22	NMR Mapping of PCNA Interaction with Translesion Synthesis DNA Polymerase Rev1 Mediated by Rev1-BRCT Domain. Journal of Molecular Biology, 2013, 425, 3091-3105.	4.2	42
23	Abp1p and Fyn SH3 Domains Fold through Similar Low-Populated Intermediate Statesâ€. Biochemistry, 2006, 45, 10175-10183.	2.5	41
24	Nonnative Interactions in the FF Domain Folding Pathway from an Atomic Resolution Structure of a Sparsely Populated Intermediate: An NMR Relaxation Dispersion Study. Journal of the American Chemical Society, 2011, 133, 10974-10982.	13.7	37
25	Alternate Binding Modes for a Ubiquitinâ€“SH3 Domain Interaction Studied by NMR Spectroscopy. Journal of Molecular Biology, 2009, 386, 391-405.	4.2	36
26	Structural Characterization of Interaction between Human Ubiquitin-specific Protease 7 and Immediate-Early Protein ICP0 of Herpes Simplex Virus-1. Journal of Biological Chemistry, 2015, 290, 22907-22918.	3.4	34
27	Hydration and Packing along the Folding Pathway of SH3 Domains by Pressure-Dependent NMR. Biochemistry, 2006, 45, 4711-4719.	2.5	31
28	Side-Chain Interactions in the Folding Pathway of a Fyn SH3 Domain Mutant Studied by Relaxation Dispersion NMR Spectroscopyâ€. Biochemistry, 2005, 44, 15430-15436.	2.5	30
29	NMR Structure of the Human Rad18 Zinc Finger in Complex with Ubiquitin Defines a Class of UBZ Domains in Proteins Linked to the DNA Damage Response. Biochemistry, 2014, 53, 5895-5906.	2.5	27
30	Measurement of signs of chemical shift differences between ground and excited protein states: a comparison between H(S/M)QC and R 1Ï•methods. Journal of Biomolecular NMR, 2010, 46, 205-216.	2.8	22
31	Structural Characterization of the Early Events in the Nucleationâ€“Condensation Mechanism in a Protein Folding Process. Journal of the American Chemical Society, 2017, 139, 6899-6910.	13.7	18
32	Transiently populated intermediate functions as a branching point of the FF domain folding pathway. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 17777-17782.	7.1	16
33	The Rev1-PolÎ¶ translesion synthesis mutasome: Structure, interactions and inhibition. The Enzymes, 2019, 45, 139-181.	1.7	16
34	Cross-correlated spin relaxation effects in methyl 1H CPMG-based relaxation dispersion experiments: Complications and a simple solution. Journal of Biomolecular NMR, 2005, 31, 337-342.	2.8	15
35	Conformational Dynamics of a Cysteine-Stabilized Plant Defensin Reveals an Evolutionary Mechanism to Expose Hydrophobic Residues. Biochemistry, 2018, 57, 5797-5806.	2.5	15
36	Cross-Validation of the Structure of a Transiently Formed and Low Populated FF Domain Folding Intermediate Determined by Relaxation Dispersion NMR and CS-Rosetta. Journal of Physical Chemistry B, 2012, 116, 6637-6644.	2.6	14

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37	Structural Approach To Identify a Lead Scaffold That Targets the Translesion Synthesis Polymerase Rev1. Journal of Chemical Information and Modeling, 2018, 58, 2266-2277.	5.4	14
38	Targeting proteinâ€“protein interactions in the DNA damage response pathways for cancer chemotherapy. RSC Chemical Biology, 2021, 2, 1167-1195.	4.1	14
39	Solution NMR structure of the HLTF HIRAN domain: a conserved module in SWI2/SNF2 DNA damage tolerance proteins. Journal of Biomolecular NMR, 2016, 66, 209-219.	2.8	13
40	Dynamics of the E.Âcoli Î²-Clamp Dimer Interface and Its Influence on DNA Loading. Biophysical Journal, 2019, 117, 587-601.	0.5	12
41	Virtual Pharmacophore Screening Identifies Smallâ€Molecule Inhibitors of the Rev1â€CT/RIR Proteinâ€“Protein Interaction. ChemMedChem, 2019, 14, 1610-1617.	3.2	11
42	Small molecule scaffolds that disrupt the Rev1-CT/RIR protein-protein interaction. Bioorganic and Medicinal Chemistry, 2018, 26, 4301-4309.	3.0	9
43	REV1 Inhibition Enhances Radioresistance and Autophagy. Cancers, 2021, 13, 5290.	3.7	7
44	PHD domain from human SHPRH. Journal of Biomolecular NMR, 2013, 56, 393-399.	2.8	6
45	Probing the Residual Structure of the Low Populated Denatured State of ADA2h under Folding Conditions by Relaxation Dispersion Nuclear Magnetic Resonance Spectroscopy. Biochemistry, 2015, 54, 4611-4622.	2.5	5
46	Structureâ€Based Drug Design of Phenazopyridine Derivatives as Inhibitors of Rev1 Interactions in Translesion Synthesis. ChemMedChem, 2021, 16, 1126-1132.	3.2	5
47	Loss of Structureâ€”Gain of Function. Journal of Molecular Biology, 2013, 425, 17-18.	4.2	3
48	Backbone and ILV side-chain NMR resonance assignments of the catalytic domain of human deubiquitinating enzyme USP7. Biomolecular NMR Assignments, 2022, , 1.	0.8	3
49	Architecture of the two metal-binding sites inÂprolactin. Biophysical Journal, 2022, 121, 1312-1321.	0.5	2
50	DNA Sequence Specificity Reveals a Role of the HLTF HIRAN Domain in the Recognition of Trinucleotide Repeats. Biochemistry, 2022, 61, 992-1004.	2.5	2
51	NMR resonance assignments for the N-terminal domain of the Î´ subunit of the E. coli Î³ clamp loader complex. Biomolecular NMR Assignments, 2017, 11, 169-173.	0.8	1
52	ILV methyl NMR resonance assignments of the 81ÂkDa E. coli Î²-clamp. Biomolecular NMR Assignments, 0, , .	0.8	1
53	NMR resonance assignments for the nucleotide binding domains of the E. coli clamp loader complex Î³ subunit. Biomolecular NMR Assignments, 2021, 15, 281-285.	0.8	0