

# Dmitry M Korzhnev

## List of Publications by Year in descending order

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53  
papers

2,951  
citations

186265

28  
h-index

182427

51  
g-index

53  
all docs

53  
docs citations

53  
times ranked

2521  
citing authors

#	ARTICLE	IF	CITATIONS
1	Architecture of the two metal-binding sites in $\beta$ -prolactin. <i>Biophysical Journal</i> , 2022, 121, 1312-1321.	0.5	2
2	Backbone and ILV side-chain NMR resonance assignments of the catalytic domain of human deubiquitinating enzyme USP7. <i>Biomolecular NMR Assignments</i> , 2022, , 1.	0.8	3
3	DNA Sequence Specificity Reveals a Role of the HLTF HIRAN Domain in the Recognition of Trinucleotide Repeats. <i>Biochemistry</i> , 2022, 61, 992-1004.	2.5	2
4	Structure-Based Drug Design of Phenazopyridine Derivatives as Inhibitors of Rev1 Interactions in Translesion Synthesis. <i>ChemMedChem</i> , 2021, 16, 1126-1132.	3.2	5
5	Targeting protein-protein interactions in the DNA damage response pathways for cancer chemotherapy. <i>RSC Chemical Biology</i> , 2021, 2, 1167-1195.	4.1	14
6	NMR resonance assignments for the nucleotide binding domains of the E. coli clamp loader complex $\beta$ subunit. <i>Biomolecular NMR Assignments</i> , 2021, 15, 281-285.	0.8	0
7	REV1 Inhibition Enhances Radioresistance and Autophagy. <i>Cancers</i> , 2021, 13, 5290.	3.7	7
8	Virtual Pharmacophore Screening Identifies Small Molecule Inhibitors of the Rev1-CT/RIR Protein-Protein Interaction. <i>ChemMedChem</i> , 2019, 14, 1610-1617.	3.2	11
9	Dynamics of the E. coli $\beta$ -Clamp Dimer Interface and Its Influence on DNA Loading. <i>Biophysical Journal</i> , 2019, 117, 587-601.	0.5	12
10	The Rev1-Pol $\eta$ translesion synthesis mutasome: Structure, interactions and inhibition. <i>The Enzymes</i> , 2019, 45, 139-181.	1.7	16
11	Structural Approach To Identify a Lead Scaffold That Targets the Translesion Synthesis Polymerase Rev1. <i>Journal of Chemical Information and Modeling</i> , 2018, 58, 2266-2277.	5.4	14
12	Conformational Dynamics of a Cysteine-Stabilized Plant Defensin Reveals an Evolutionary Mechanism to Expose Hydrophobic Residues. <i>Biochemistry</i> , 2018, 57, 5797-5806.	2.5	15
13	Small molecule scaffolds that disrupt the Rev1-CT/RIR protein-protein interaction. <i>Bioorganic and Medicinal Chemistry</i> , 2018, 26, 4301-4309.	3.0	9
14	Rev7 dimerization is important for assembly and function of the Rev1/Pol $\eta$ translesion synthesis complex. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, E8191-E8200.	7.1	44
15	Structural Characterization of the Early Events in the Nucleation-Condensation Mechanism in a Protein Folding Process. <i>Journal of the American Chemical Society</i> , 2017, 139, 6899-6910.	13.7	18
16	Identification of Small Molecule Translesion Synthesis Inhibitors That Target the Rev1-CT/RIR Protein-Protein Interaction. <i>ACS Chemical Biology</i> , 2017, 12, 1903-1912.	3.4	44
17	NMR resonance assignments for the N-terminal domain of the $\beta$ subunit of the E. coli $\beta$ clamp loader complex. <i>Biomolecular NMR Assignments</i> , 2017, 11, 169-173.	0.8	1
18	Protein folding by NMR. <i>Progress in Nuclear Magnetic Resonance Spectroscopy</i> , 2017, 100, 52-77.	7.5	48

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19	Targeting the Translesion Synthesis Pathway for the Development of Anti-Cancer Chemotherapeutics. <i>Journal of Medicinal Chemistry</i> , 2016, 59, 9321-9336.	6.4	46
20	Solution NMR structure of the HLTf HIRAN domain: a conserved module in SWI2/SNF2 DNA damage tolerance proteins. <i>Journal of Biomolecular NMR</i> , 2016, 66, 209-219.	2.8	13
21	Interaction between the Rev1 C-Terminal Domain and the PolD3 Subunit of Pol $\eta$ Suggests a Mechanism of Polymerase Exchange upon Rev1/Pol $\eta$ -Dependent Translesion Synthesis. <i>Biochemistry</i> , 2016, 55, 2043-2053.	2.5	50
22	Probing the Residual Structure of the Low Populated Denatured State of ADA2h under Folding Conditions by Relaxation Dispersion Nuclear Magnetic Resonance Spectroscopy. <i>Biochemistry</i> , 2015, 54, 4611-4622.	2.5	5
23	HLTF's Ancient HIRAN Domain Binds 3' DNA Ends to Drive Replication Fork Reversal. <i>Molecular Cell</i> , 2015, 58, 1090-1100.	9.7	163
24	Structural Characterization of Interaction between Human Ubiquitin-specific Protease 7 and Immediate-Early Protein ICPO of Herpes Simplex Virus-1. <i>Journal of Biological Chemistry</i> , 2015, 290, 22907-22918.	3.4	34
25	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. <i>Biochemistry</i> , 2014, 53, 5895-5906.	2.5	27
26	PHD domain from human SHPRH. <i>Journal of Biomolecular NMR</i> , 2013, 56, 393-399.	2.8	6
27	Loss of Structure "Gain of Function. <i>Journal of Molecular Biology</i> , 2013, 425, 17-18.	4.2	3
28	NMR Mapping of PCNA Interaction with Translesion Synthesis DNA Polymerase Rev1 Mediated by Rev1-BRCT Domain. <i>Journal of Molecular Biology</i> , 2013, 425, 3091-3105.	4.2	42
29	Transiently populated intermediate functions as a branching point of the FF domain folding pathway. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 17777-17782.	7.1	16
30	The C-terminal domain of human Rev1 contains independent binding sites for DNA polymerase $\delta$ and Rev7 subunit of polymerase $\eta$ . <i>FEBS Letters</i> , 2012, 586, 3051-3056.	2.8	42
31	Cross-Validation of the Structure of a Transiently Formed and Low Populated FF Domain Folding Intermediate Determined by Relaxation Dispersion NMR and CS-Rosetta. <i>Journal of Physical Chemistry B</i> , 2012, 116, 6637-6644.	2.6	14
32	NMR Structure and Dynamics of the C-Terminal Domain from Human Rev1 and Its Complex with Rev1 Interacting Region of DNA Polymerase $\delta$ . <i>Biochemistry</i> , 2012, 51, 5506-5520.	2.5	69
33	Nonnative Interactions in the FF Domain Folding Pathway from an Atomic Resolution Structure of a Sparsely Populated Intermediate: An NMR Relaxation Dispersion Study. <i>Journal of the American Chemical Society</i> , 2011, 133, 10974-10982.	13.7	37
34	Measurement of signs of chemical shift differences between ground and excited protein states: a comparison between H(S/M)QC and R $\nu$ methods. <i>Journal of Biomolecular NMR</i> , 2010, 46, 205-216.	2.8	22
35	A Transient and Low-Populated Protein-Folding Intermediate at Atomic Resolution. <i>Science</i> , 2010, 329, 1312-1316.	12.6	282
36	Alternate Binding Modes for a Ubiquitin-SH3 Domain Interaction Studied by NMR Spectroscopy. <i>Journal of Molecular Biology</i> , 2009, 386, 391-405.	4.2	36

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37	Probing Invisible, Low-Populated States of Protein Molecules by Relaxation Dispersion NMR Spectroscopy: An Application to Protein Folding. <i>Accounts of Chemical Research</i> , 2008, 41, 442-451.	15.6	241
38	The Folding Pathway of an FF domain: Characterization of an On-pathway Intermediate State Under Folding Conditions by $^{15}\text{N}$ , $^{13}\text{C}$ and $^{13}\text{C}$ -methyl Relaxation Dispersion and $^1\text{H}/^2\text{H}$ -exchange NMR Spectroscopy. <i>Journal of Molecular Biology</i> , 2007, 372, 497-512.	4.2	60
39	Probing the Transition State Ensemble of a Protein Folding Reaction by Pressure-Dependent NMR Relaxation Dispersion. <i>Journal of the American Chemical Society</i> , 2006, 128, 5262-5269.	13.7	48
40	Abp1p and Fyn SH3 Domains Fold through Similar Low-Populated Intermediate States. <i>Biochemistry</i> , 2006, 45, 10175-10183.	2.5	41
41	Hydration and Packing along the Folding Pathway of SH3 Domains by Pressure-Dependent NMR. <i>Biochemistry</i> , 2006, 45, 4711-4719.	2.5	31
42	Cross-correlated spin relaxation effects in methyl $^1\text{H}$ CPMG-based relaxation dispersion experiments: Complications and a simple solution. <i>Journal of Biomolecular NMR</i> , 2005, 31, 337-342.	2.8	15
43	Off-Resonance $R_1$ NMR Studies of Exchange Dynamics in Proteins with Low Spin-Lock Fields: An Application to a Fyn SH3 Domain. <i>Journal of the American Chemical Society</i> , 2005, 127, 713-721.	13.7	122
44	Multiple-Site Exchange in Proteins Studied with a Suite of Six NMR Relaxation Dispersion Experiments: An Application to the Folding of a Fyn SH3 Domain Mutant. <i>Journal of the American Chemical Society</i> , 2005, 127, 15602-15611.	13.7	93
45	Side-Chain Interactions in the Folding Pathway of a Fyn SH3 Domain Mutant Studied by Relaxation Dispersion NMR Spectroscopy. <i>Biochemistry</i> , 2005, 44, 15430-15436.	2.5	30
46	Dramatic acceleration of protein folding by stabilization of a nonnative backbone conformation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2004, 101, 7954-7959.	7.1	79
47	Low-populated folding intermediates of Fyn SH3 characterized by relaxation dispersion NMR. <i>Nature</i> , 2004, 430, 586-590.	27.8	445
48	Multiple-Quantum Relaxation Dispersion NMR Spectroscopy Probing Millisecond Time-Scale Dynamics in Proteins: Theory and Application. <i>Journal of the American Chemical Society</i> , 2004, 126, 7320-7329.	13.7	100
49	Probing Slow Dynamics in High Molecular Weight Proteins by Methyl-TROSY NMR Spectroscopy: Application to a 723-Residue Enzyme. <i>Journal of the American Chemical Society</i> , 2004, 126, 3964-3973.	13.7	210
50	Double- and Zero-Quantum NMR Relaxation Dispersion Experiments Sampling Millisecond Time Scale Dynamics in Proteins. <i>Journal of the American Chemical Society</i> , 2004, 126, 1886-1891.	13.7	91
51	Off-resonance $R_1\rho$ relaxation outside of the fast exchange limit: an experimental study of a cavity mutant of T4 lysozyme. <i>Journal of Biomolecular NMR</i> , 2003, 26, 39-48.	2.8	42
52	An NMR Experiment for the Accurate Measurement of Heteronuclear Spin-Lock Relaxation Rates. <i>Journal of the American Chemical Society</i> , 2002, 124, 10743-10753.	13.7	130
53	ILV methyl NMR resonance assignments of the 81 kDa E. coli $\hat{\rho}$ -clamp. <i>Biomolecular NMR Assignments</i> , 0, ,	0.8	1