

# Dmitry M Korzhnev

## List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

49 papers	2,519 citations	27 h-index	50 g-index
53 ext. papers	2,761 ext. citations	8.1 avg, IF	4.91 L-index

#	Paper	IF	Citations
49	Backbone and ILV side-chain NMR resonance assignments of the catalytic domain of human deubiquitinating enzyme USP7.. <i>Biomolecular NMR Assignments</i> , <b>2022</b> , 1	0.7	0
48	NMR resonance assignments for the nucleotide binding domains of the E. coli clamp loader complex $\beta$ subunit. <i>Biomolecular NMR Assignments</i> , <b>2021</b> , 15, 281-285	0.7	
47	Structure-Based Drug Design of Phenazopyridine Derivatives as Inhibitors of Rev1 Interactions in Translesion Synthesis. <i>ChemMedChem</i> , <b>2021</b> , 16, 1126-1132	3.7	4
46	Targeting protein-protein interactions in the DNA damage response pathways for cancer chemotherapy. <i>RSC Chemical Biology</i> , <b>2021</b> , 2, 1167-1195	3	2
45	Dynamics of the E. coli $\beta$ Clamp Dimer Interface and Its Influence on DNA Loading. <i>Biophysical Journal</i> , <b>2019</b> , 117, 587-601	2.9	6
44	Virtual Pharmacophore Screening Identifies Small-Molecule Inhibitors of the Rev1-CT/RIR Protein-Protein Interaction. <i>ChemMedChem</i> , <b>2019</b> , 14, 1610-1617	3.7	9
43	The Rev1-Pol $\eta$ Translesion synthesis mutasome: Structure, interactions and inhibition. <i>The Enzymes</i> , <b>2019</b> , 45, 139-181	2.3	6
42	Small molecule scaffolds that disrupt the Rev1-CT/RIR protein-protein interaction. <i>Bioorganic and Medicinal Chemistry</i> , <b>2018</b> , 26, 4301-4309	3.4	9
41	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> , <b>2018</b> , 115, E8191-E8200	11.5	23
40	Structural Approach To Identify a Lead Scaffold That Targets the Translesion Synthesis Polymerase Rev1. <i>Journal of Chemical Information and Modeling</i> , <b>2018</b> , 58, 2266-2277	6.1	13
39	Conformational Dynamics of a Cysteine-Stabilized Plant Defensin Reveals an Evolutionary Mechanism to Expose Hydrophobic Residues. <i>Biochemistry</i> , <b>2018</b> , 57, 5797-5806	3.2	11
38	Structural Characterization of the Early Events in the Nucleation-Condensation Mechanism in a Protein Folding Process. <i>Journal of the American Chemical Society</i> , <b>2017</b> , 139, 6899-6910	16.4	15
37	Identification of Small Molecule Translesion Synthesis Inhibitors That Target the Rev1-CT/RIR Protein-Protein Interaction. <i>ACS Chemical Biology</i> , <b>2017</b> , 12, 1903-1912	4.9	35
36	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> , <b>2017</b> , 11, 169-173	0.7	1
35	Protein folding by NMR. <i>Progress in Nuclear Magnetic Resonance Spectroscopy</i> , <b>2017</b> , 100, 52-77	10.4	30
34	Targeting the Translesion Synthesis Pathway for the Development of Anti-Cancer Chemotherapeutics. <i>Journal of Medicinal Chemistry</i> , <b>2016</b> , 59, 9321-9336	8.3	37
33	Solution NMR structure of the HLTF HIRAN domain: a conserved module in SWI2/SNF2 DNA damage tolerance proteins. <i>Journal of Biomolecular NMR</i> , <b>2016</b> , 66, 209-219	3	11

32	Interaction between the Rev1 C-Terminal Domain and the PolD3 Subunit of PolII Suggests a Mechanism of Polymerase Exchange upon Rev1/PolII-Dependent Translesion Synthesis. <i>Biochemistry</i> , <b>2016</b> , 55, 2043-53	3.2	44
31	HLTF's Ancient HIRAN Domain Binds 3' DNA Ends to Drive Replication Fork Reversal. <i>Molecular Cell</i> , <b>2015</b> , 58, 1090-100	17.6	127
30	Structural Characterization of Interaction between Human Ubiquitin-specific Protease 7 and Immediate-Early Protein ICP0 of Herpes Simplex Virus-1. <i>Journal of Biological Chemistry</i> , <b>2015</b> , 290, 22907-18	5.4	26
29	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> , <b>2015</b> , 54, 4611-22	3.2	4
28	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> , <b>2014</b> , 53, 5895-906	3.2	20
27	PHD domain from human SHPRH. <i>Journal of Biomolecular NMR</i> , <b>2013</b> , 56, 393-9	3	5
26	Loss of structure-gain of function. <i>Journal of Molecular Biology</i> , <b>2013</b> , 425, 17-8	6.5	3
25	NMR mapping of PCNA interaction with translesion synthesis DNA polymerase Rev1 mediated by Rev1-BRCT domain. <i>Journal of Molecular Biology</i> , <b>2013</b> , 425, 3091-105	6.5	35
24	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> , <b>2012</b> , 109, 17777-82	11.5	13
23	The C-terminal domain of human Rev1 contains independent binding sites for DNA polymerase $\eta$ and Rev7 subunit of polymerase $\eta$ . <i>FEBS Letters</i> , <b>2012</b> , 586, 3051-6	3.8	35
22	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> , <b>2012</b> , 116, 6637-44	3.4	13
21	NMR structure and dynamics of the C-terminal domain from human Rev1 and its complex with Rev1 interacting region of DNA polymerase $\eta$ . <i>Biochemistry</i> , <b>2012</b> , 51, 5506-20	3.2	60
20	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> , <b>2011</b> , 133, 10974-82	16.4	32
19	A transient and low-populated protein-folding intermediate at atomic resolution. <i>Science</i> , <b>2010</b> , 329, 1312-6	33.3	242
18	Measurement of signs of chemical shift differences between ground and excited protein states: a comparison between H(S/M)QC and R1rho methods. <i>Journal of Biomolecular NMR</i> , <b>2010</b> , 46, 205-16	3	20
17	Alternate binding modes for a ubiquitin-SH3 domain interaction studied by NMR spectroscopy. <i>Journal of Molecular Biology</i> , <b>2009</b> , 386, 391-405	6.5	34
16	Probing invisible, low-populated States of protein molecules by relaxation dispersion NMR spectroscopy: an application to protein folding. <i>Accounts of Chemical Research</i> , <b>2008</b> , 41, 442-51	24.3	212
15	The folding pathway of an FF domain: characterization of an on-pathway intermediate state under folding conditions by $(^{15}\text{N})$ , $(^{13}\text{C}(\alpha))$ and $(^{13}\text{C})$ -methyl relaxation dispersion and $(^1\text{H})/(^2\text{H})$ -exchange NMR spectroscopy. <i>Journal of Molecular Biology</i> , <b>2007</b> , 372, 497-512	6.5	51

14	Probing the transition state ensemble of a protein folding reaction by pressure-dependent NMR relaxation dispersion. <i>Journal of the American Chemical Society</i> , <b>2006</b> , 128, 5262-9	16.4	41
13	Abp1p and Fyn SH3 domains fold through similar low-populated intermediate states. <i>Biochemistry</i> , <b>2006</b> , 45, 10175-83	3.2	37
12	Hydration and packing along the folding pathway of SH3 domains by pressure-dependent NMR. <i>Biochemistry</i> , <b>2006</b> , 45, 4711-9	3.2	27
11	Off-resonance R(1rho) 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> , <b>2005</b> , 127, 713-21	16.4	103
10	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> , <b>2005</b> , 127, 15602-11	16.4	84
9	Side-chain interactions in the folding pathway of a Fyn SH3 domain mutant studied by relaxation dispersion NMR spectroscopy. <i>Biochemistry</i> , <b>2005</b> , 44, 15430-6	3.2	28
8	Cross-correlated spin relaxation effects in methyl <sup>1</sup> H CPMG-based relaxation dispersion experiments: complications and a simple solution. <i>Journal of Biomolecular NMR</i> , <b>2005</b> , 31, 337-42	3	13
7	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> , <b>2004</b> , 101, 7954-9	11.5	74
6	Low-populated folding intermediates of Fyn SH3 characterized by relaxation dispersion NMR. <i>Nature</i> , <b>2004</b> , 430, 586-90	50.4	410
5	Multiple-quantum relaxation dispersion NMR spectroscopy probing millisecond time-scale dynamics in proteins: theory and application. <i>Journal of the American Chemical Society</i> , <b>2004</b> , 126, 7320-9	16.4	88
4	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> , <b>2004</b> , 126, 3964-73	16.4	177
3	Double- and zero-quantum NMR relaxation dispersion experiments sampling millisecond time scale dynamics in proteins. <i>Journal of the American Chemical Society</i> , <b>2004</b> , 126, 1886-91	16.4	84
2	Off-resonance R1rho relaxation outside of the fast exchange limit: an experimental study of a cavity mutant of T4 lysozyme. <i>Journal of Biomolecular NMR</i> , <b>2003</b> , 26, 39-48	3	41
1	An NMR experiment for the accurate measurement of heteronuclear spin-lock relaxation rates. <i>Journal of the American Chemical Society</i> , <b>2002</b> , 124, 10743-53	16.4	114