

# Alexander P Golovanov

## List of Publications by Year in descending order

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64  
papers

2,716  
citations

236612

25  
h-index

182168

51  
g-index

69  
all docs

69  
docs citations

69  
times ranked

4240  
citing authors

#	ARTICLE	IF	CITATIONS
1	Temporal and spatial characterisation of protein liquid-liquid phase separation using NMR spectroscopy. <i>Nature Communications</i> , 2022, 13, 1767.	5.8	11
2	Development of a fast screening method for selecting excipients in formulations using MD simulations, NMR and microscale thermophoresis. <i>European Journal of Pharmaceutics and Biopharmaceutics</i> , 2021, 158, 11-20.	2.0	5
3	Comprehensive Assessment of Protein and Excipient Stability in Biopharmaceutical Formulations Using <sup>1</sup> H NMR Spectroscopy. <i>ACS Pharmacology and Translational Science</i> , 2021, 4, 288-295.	2.5	14
4	Stability of a high-concentration monoclonal antibody solution produced by liquid-liquid phase separation. <i>MAbs</i> , 2021, 13, 1940666.	2.6	11
5	Orthogonal Techniques to Study the Effect of pH, Sucrose, and Arginine Salts on Monoclonal Antibody Physical Stability and Aggregation During Long-Term Storage. <i>Journal of Pharmaceutical Sciences</i> , 2020, 109, 584-594.	1.6	26
6	The Effect of Point Mutations on the Biophysical Properties of an Antimicrobial Peptide: Development of a Screening Protocol for Peptide Stability Screening. <i>Molecular Pharmaceutics</i> , 2020, 17, 3298-3313.	2.3	9
7	Binding of excipients is a poor predictor for aggregation kinetics of biopharmaceutical proteins. <i>European Journal of Pharmaceutics and Biopharmaceutics</i> , 2020, 151, 127-136.	2.0	13
8	Arginine to Lysine Mutations Increase the Aggregation Stability of a Single-Chain Variable Fragment through Unfolded-State Interactions. <i>Biochemistry</i> , 2019, 58, 3413-3421.	1.2	24
9	Detection of the adulteration of fresh coconut water via NMR spectroscopy and chemometrics. <i>Analyst</i> , 2019, 144, 1401-1408.	1.7	14
10	Studies of the oligomerisation mechanism of a cystatin-based engineered protein scaffold. <i>Scientific Reports</i> , 2019, 9, 9067.	1.6	2
11	Interaction of a Macrocycle with an Aggregation-Prone Region of a Monoclonal Antibody. <i>Molecular Pharmaceutics</i> , 2019, 16, 3100-3108.	2.3	7
12	Conformational Stability Study of a Therapeutic Peptide Plectasin Using Molecular Dynamics Simulations in Combination with NMR. <i>Journal of Physical Chemistry B</i> , 2019, 123, 4867-4877.	1.2	14
13	Use of <sup>19</sup> F Differential Labelling for the Simultaneous Detection and Monitoring of Three Individual Proteins in a Serum Environment. <i>ChemPlusChem</i> , 2019, 84, 443-446.	1.3	1
14	<sup>19</sup> F Dark-State Exchange Saturation Transfer NMR Reveals Reversible Formation of Protein-Specific Large Clusters in High-Concentration Protein Mixtures. <i>Analytical Chemistry</i> , 2019, 91, 4702-4708.	3.2	11
15	Molecular Mechanism of SR Protein Kinase 1 Inhibition by the Herpes Virus Protein ICP27. <i>MBio</i> , 2019, 10, .	1.8	17
16	New Disulphide Bond in Cystatin-Based Protein Scaffold Prevents Domain-Swap-Mediated Oligomerization and Stabilizes the Functionally Active Form. <i>ACS Omega</i> , 2019, 4, 18248-18256.	1.6	2
17	Solvation of Pristine Graphene Using Amino Acids: A Molecular Simulation and Experimental Analysis. <i>Journal of Physical Chemistry C</i> , 2019, 123, 30234-30244.	1.5	7
18	Structural identification of conserved RNA binding sites in herpesvirus ORF57 homologs: implications for PAN RNA recognition. <i>Nucleic Acids Research</i> , 2019, 47, 1987-2001.	6.5	4

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19	The ICP27 Homology Domain of the Human Cytomegalovirus Protein UL69 Adopts a Dimer-of-Dimers Structure. <i>MBio</i> , 2018, 9, .	1.8	8
20	Overlapping motifs on the herpes viral proteins ICP27 and ORF57 mediate interactions with the mRNA export adaptors ALYREF and UIF. <i>Scientific Reports</i> , 2018, 8, 15005.	1.6	12
21	<sup>19</sup> F NMR as a Tool for Monitoring Individual Differentially Labeled Proteins in Complex Mixtures. <i>Molecular Pharmaceutics</i> , 2018, 15, 2785-2796.	2.3	10
22	The effect of charge mutations on the stability and aggregation of a human single chain Fv fragment. <i>European Journal of Pharmaceutics and Biopharmaceutics</i> , 2017, 115, 18-30.	2.0	43
23	Investigating Liquidâ€“Liquid Phase Separation of a Monoclonal Antibody Using Solution-State NMR Spectroscopy: Effect of Argâ€“Glu and Argâ€“HCl. <i>Molecular Pharmaceutics</i> , 2017, 14, 2852-2860.	2.3	25
24	The herpes viral transcription factor ICP4 forms a novel DNA recognition complex. <i>Nucleic Acids Research</i> , 2017, 45, 8064-8078.	6.5	23
25	Graphene in therapeutics delivery: Problems, solutions and future opportunities. <i>European Journal of Pharmaceutics and Biopharmaceutics</i> , 2016, 104, 235-250.	2.0	197
26	Characterizing monoclonal antibody formulations in arginine glutamate solutions using <sup>1</sup> H NMR spectroscopy. <i>MAbs</i> , 2016, 8, 1245-1258.	2.6	31
27	Dynamic studies of H-Rasâ€“GTPÎ³S interactions with nucleotide exchange factor Sos reveal a transient ternary complex formation in solution. <i>Scientific Reports</i> , 2016, 6, 29706.	1.6	3
28	Monitoring Ras Interactions with the Nucleotide Exchange Factor Son of Sevenless (Sos) Using Site-specific NMR Reporter Signals and Intrinsic Fluorescence. <i>Journal of Biological Chemistry</i> , 2016, 291, 1703-1718.	1.6	31
29	The effects of arginine glutamate, a promising excipient for protein formulation, on cell viability: Comparisons with NaCl. <i>Toxicology in Vitro</i> , 2016, 33, 88-98.	1.1	14
30	The structure of the folded domain from the signature multifunctional protein ICP27 from herpes simplex virus-1 reveals an intertwined dimer. <i>Scientific Reports</i> , 2015, 5, 11234.	1.6	23
31	Competitive and Cooperative Interactions Mediate RNA Transfer from Herpesvirus Saimiri ORF57 to the Mammalian Export Adaptor ALYREF. <i>PLoS Pathogens</i> , 2014, 10, e1003907.	2.1	23
32	The effect of arginine glutamate on the stability of monoclonal antibodies in solution. <i>International Journal of Pharmaceutics</i> , 2014, 473, 126-133.	2.6	64
33	<sup>1</sup> H, <sup>13</sup> C and <sup>15</sup> N resonance assignment for the human K-Ras at physiological pH. <i>Biomolecular NMR Assignments</i> , 2013, 7, 215-219.	0.4	25
34	The Interaction of the Cellular Export Adaptor Protein Aly/REF with ICP27 Contributes to the Efficiency of Herpes Simplex Virus 1 mRNA Export. <i>Journal of Virology</i> , 2013, 87, 7210-7217.	1.5	18
35	In support of the BMRB. <i>Nature Structural and Molecular Biology</i> , 2012, 19, 854-860.	3.6	6
36	Fingerprinting food: current technologies for the detection of food adulteration and contamination. <i>Chemical Society Reviews</i> , 2012, 41, 5706.	18.7	362

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37	Structural Basis for the Recognition of Cellular mRNA Export Factor REF by Herpes Viral Proteins HSV-1 ICP27 and HVS ORF57. <i>PLoS Pathogens</i> , 2011, 7, e1001244.	2.1	41
38	Graphene as a transparent conductive support for studying biological molecules by transmission electron microscopy. <i>Applied Physics Letters</i> , 2010, 97, .	1.5	138
39	Simultaneous measurement of residual dipolar couplings for proteins in complex using the isotopically discriminated NMR approach. <i>Journal of the American Chemical Society</i> , 2009, 131, 8564-8570.	6.6	11
40	Increasing the sensitivity of cryoprobe protein NMR experiments by using the sole low-conductivity arginine glutamate salt. <i>Journal of Magnetic Resonance</i> , 2008, 191, 335-339.	1.2	24
41	Mutually exclusive interactions drive handover of mRNA from export adaptors to TAP. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008, 105, 5154-5159.	3.3	158
42	Specificity and Autoregulation of Notch Binding by Tandem WW Domains in Suppressor of Deltex. <i>Journal of Biological Chemistry</i> , 2007, 282, 29032-29042.	1.6	33
43	Quantification of casein phosphorylation with conformational interpretation using Raman spectroscopy. <i>Analyst, The</i> , 2007, 132, 1053.	1.7	28
44	Isotopically Discriminated NMR Spectroscopy: A Tool for Investigating Complex Protein Interactions in Vitro. <i>Journal of the American Chemical Society</i> , 2007, 129, 6528-6535.	6.6	28
45	The Solution Structure of a Domain from the <i>Neisseria meningitidis</i> Lipoprotein PilP Reveals a New $\beta$ -Sandwich Fold. <i>Journal of Molecular Biology</i> , 2006, 364, 186-195.	2.0	39
46	Molecular basis of RNA recognition and TAP binding by the SR proteins SRp20 and 9G8. <i>EMBO Journal</i> , 2006, 25, 5126-5137.	3.5	140
47	Assignment of $^1\text{H}$ , $^{13}\text{C}$ , and $^{15}\text{N}$ resonances for the REF2-I mRNA export factor. <i>Journal of Biomolecular NMR</i> , 2006, 36, 41-41.	1.6	3
48	Assignment of $^1\text{H}$ , $^{13}\text{C}$ , and $^{15}\text{N}$ resonances for the PilP pilot protein from <i>Neisseria meningitidis</i> . <i>Journal of Biomolecular NMR</i> , 2006, 36, 68-68.	1.6	3
49	The solution structure of REF2-I reveals interdomain interactions and regions involved in binding mRNA export factors and RNA. <i>Rna</i> , 2006, 12, 1933-1948.	1.6	44
50	The Unstructured N-terminal Tail of ParG Modulates Assembly of a Quaternary Nucleoprotein Complex in Transcription Repression. <i>Journal of Biological Chemistry</i> , 2005, 280, 28683-28691.	1.6	25
51	Distinct Domains of Small Tims Involved in Subunit Interaction and Substrate Recognition. <i>Journal of Molecular Biology</i> , 2005, 351, 839-849.	2.0	40
52	The Structural Basis of the TIM10 Chaperone Assembly. <i>Journal of Biological Chemistry</i> , 2004, 279, 18959-18966.	1.6	54
53	The Structure and Dynamics of Tandem WW Domains in a Negative Regulator of Notch Signaling, Suppressor of Deltex. <i>Journal of Biological Chemistry</i> , 2004, 279, 34991-35000.	1.6	41
54	A Simple Method for Improving Protein Solubility and Long-Term Stability. <i>Journal of the American Chemical Society</i> , 2004, 126, 8933-8939.	6.6	382

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55	ParG, a protein required for active partition of bacterial plasmids, has a dimeric ribbon-helix-helix structure. <i>Molecular Microbiology</i> , 2003, 50, 1141-1153.	1.2	76
56	Structure-activity relationships in flexible protein domains: regulation of rho GTPases by RhoGDI and D4 GDI. <i>Journal of Molecular Biology</i> , 2001, 305, 121-135.	2.0	62
57	Structural consequences of site-directed mutagenesis in flexible protein domains. <i>FEBS Journal</i> , 2001, 268, 2253-2260.	0.2	11
58	Mapping the binding site for the GTP-binding protein Rac-1 on its inhibitor RhoGDI-1. <i>Structure</i> , 2000, 8, 47-56.	1.6	74
59	Stabilization of Proteins by Enhancement of Inter-residue Hydrophobic Contacts: Lessons of T4 Lysozyme and Barnase. <i>Journal of Biomolecular Structure and Dynamics</i> , 2000, 18, 477-491.	2.0	10
60	A New Method to Characterize Hydrophobic Organization of Proteins: Application to Rational Protein Engineering of Barnase. <i>Journal of Biomolecular Structure and Dynamics</i> , 1998, 15, 673-687.	2.0	5
61	Processing of heteronuclear NMR relaxation data with the new software DASHA. <i>Applied Magnetic Resonance</i> , 1995, 9, 581-588.	0.6	81
62	Detailed Assessment of Spatial Hydrophobic and Electrostatic Properties of 2D NMR-Derived Models of Neurotoxin II. <i>Journal of Biomolecular Structure and Dynamics</i> , 1995, 12, 971-991.	2.0	6
63	Amino acid residue: is it structural or functional?. <i>FEBS Letters</i> , 1995, 375, 162-166.	1.3	11
64	Two-dimensional <sup>1</sup> H-NMR study of the spatial structure of neurotoxin II from <i>Naja naja oxiana</i> . <i>FEBS Journal</i> , 1993, 213, 1213-1223.	0.2	37