

# Alexey K Shaytan

## List of Publications by Year in descending order

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Version: 2024-02-01

40  
papers

1,291  
citations

430442

18  
h-index

377514

34  
g-index

44  
all docs

44  
docs citations

44  
times ranked

2002  
citing authors

#	ARTICLE	IF	CITATIONS
1	Physicochemical mechanisms of protein regulation by phosphorylation. <i>Frontiers in Genetics</i> , 2014, 5, 270.	1.1	152
2	Coupling between Histone Conformations and DNA Geometry in Nucleosomes on a Microsecond Timescale: Atomistic Insights into Nucleosome Functions. <i>Journal of Molecular Biology</i> , 2016, 428, 221-237.	2.0	131
3	Peptide nanofibrils boost retroviral gene transfer and provide a rapid means for concentrating viruses. <i>Nature Nanotechnology</i> , 2013, 8, 130-136.	15.6	125
4	HistoneDB 2.0: a histone database with variants—an integrated resource to explore histones and their variants. <i>Database: the Journal of Biological Databases and Curation</i> , 2016, 2016, baw014.	1.4	99
5	Large-scale ATP-independent nucleosome unfolding by a histone chaperone. <i>Nature Structural and Molecular Biology</i> , 2016, 23, 1111-1116.	3.6	85
6	Histone dynamics mediate DNA unwrapping and sliding in nucleosomes. <i>Nature Communications</i> , 2021, 12, 2387.	5.8	70
7	Structural analysis of nucleosomal barrier to transcription. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, E5787-95.	3.3	65
8	Nucleosome adaptability conferred by sequence and structural variations in histone H2A–H2B dimers. <i>Current Opinion in Structural Biology</i> , 2015, 32, 48-57.	2.6	52
9	Molecular basis of CENP-C association with the CENP-A nucleosome at yeast centromeres. <i>Genes and Development</i> , 2017, 31, 1958-1972.	2.7	45
10	Self-Assembling Nanofibers from Thiophene–Peptide Diblock Oligomers: A Combined Experimental and Computer Simulations Study. <i>ACS Nano</i> , 2011, 5, 6894-6909.	7.3	41
11	Analysis of the mechanism of nucleosome survival during transcription. <i>Nucleic Acids Research</i> , 2014, 42, 1619-1627.	6.5	40
12	MS_HistoneDB, a manually curated resource for proteomic analysis of human and mouse histones. <i>Epigenetics and Chromatin</i> , 2017, 10, 2.	1.8	40
13	Linking chromatin composition and structural dynamics at the nucleosome level. <i>Current Opinion in Structural Biology</i> , 2019, 56, 46-55.	2.6	38
14	Voltage-gated ion channel modulation by lipids: Insights from molecular dynamics simulations. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 2014, 1838, 1322-1331.	1.4	32
15	Solvent Accessible Surface Area of Amino Acid Residues in Globular Proteins: Correlation of Apparent Transfer Free Energies with Experimental Hydrophobicity Scales. <i>Biomacromolecules</i> , 2009, 10, 1224-1237.	2.6	31
16	Comparative Computational Study of Interaction of C60-Fullerene and Tris-Malonyl-C60-Fullerene Isomers with Lipid Bilayer: Relation to Their Antioxidant Effect. <i>PLoS ONE</i> , 2014, 9, e102487.	1.1	30
17	Genome packaging in EL and Lin68, two giant phiKZ-like bacteriophages of <i>P. aeruginosa</i> . <i>Virology</i> , 2014, 468-470, 472-478.	1.1	26
18	Direct prediction of residual dipolar couplings of small molecules in a stretched gel by stochastic molecular dynamics simulations. <i>Magnetic Resonance in Chemistry</i> , 2015, 53, 213-217.	1.1	24

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19	Histone Octamer Structure Is Altered Early in ISW2 ATP-Dependent Nucleosome Remodeling. <i>Cell Reports</i> , 2019, 28, 282-294.e6.	2.9	20
20	Genomic profiling of multiple sequentially acquired tumor metastatic sites from an "exceptional responder" lung adenocarcinoma patient reveals extensive genomic heterogeneity and novel somatic variants driving treatment response. <i>Journal of Physical Education and Sports Management</i> , 2016, 2, a001263.	0.5	18
21	Hydroxyl-radical footprinting combined with molecular modeling identifies unique features of DNA conformation and nucleosome positioning. <i>Nucleic Acids Research</i> , 2017, 45, 9229-9243.	6.5	18
22	Electron microscopy analysis of ATP-independent nucleosome unfolding by FACT. <i>Communications Biology</i> , 2022, 5, 2.	2.0	16
23	Nucleosomal Barrier to Transcription: Structural Determinants and Changes in Chromatin Structure. <i>Biochemistry &amp; Molecular Biology Journal</i> , 2016, 2, .	0.3	14
24	Molecular Mechanisms of Oncogenesis through the Lens of Nucleosomes and Histones. <i>Journal of Physical Chemistry B</i> , 2021, 125, 3963-3976.	1.2	14
25	Free energy profiles of amino acid side chain analogs near water-vapor interface obtained via MD simulations. <i>Journal of Computational Chemistry</i> , 2010, 31, 204-216.	1.5	11
26	Structural Perspectives on the Evolutionary Expansion of Unique Protein-Protein Binding Sites. <i>Biophysical Journal</i> , 2015, 109, 1295-1306.	0.2	11
27	Self-organizing bioinspired oligothiophene-oligopeptide hybrids. <i>Beilstein Journal of Nanotechnology</i> , 2011, 2, 525-544.	1.5	10
28	Structure and functions of linker histones. <i>Biochemistry (Moscow)</i> , 2016, 81, 213-223.	0.7	10
29	Large-scale atomistic simulation of a nanosized fibril formed by thiophene-peptide "molecular chimeras". <i>Soft Matter</i> , 2010, 6, 1453.	1.2	7
30	Structural interpretation of DNA-protein hydroxyl-radical footprinting experiments with high resolution using HYDROID. <i>Nature Protocols</i> , 2018, 13, 2535-2556.	5.5	6
31	Trajectories of microsecond molecular dynamics simulations of nucleosomes and nucleosome core particles. <i>Data in Brief</i> , 2016, 7, 1678-1681.	0.5	3
32	Nucleosome Dynamics at Microsecond Timescale: DNA-Protein Interactions, Water-Mediated Interactions and Nucleosome Formation. <i>Biophysical Journal</i> , 2016, 110, 405a.	0.2	2
33	Design of Nucleic Acid Biosensors Based on CRISPR/Cas Systems and Reporter Split Proteins. <i>Moscow University Biological Sciences Bulletin</i> , 2021, 76, 52-58.	0.1	2
34	Determining the Binding Constant of LANA Protein Fragment with Nucleosome. <i>Moscow University Biological Sciences Bulletin</i> , 2020, 75, 252-256.	0.1	1
35	Investigation of Ion Permeation through the Cx26 Hemichannel. <i>Biophysical Journal</i> , 2014, 106, 556a.	0.2	0
36	Molecular Insights into Electroporation and Electrotransfer through Model Cell Membranes. <i>Biophysical Journal</i> , 2014, 106, 291a.	0.2	0

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37	Polymorphism of Histone Tail Interactions in Nucleosome. Biophysical Journal, 2015, 108, 72a.	0.2	0
38	Integrative Modeling of Nucleosomes and Supranucleosomal Structures. Biophysical Journal, 2020, 118, 64a.	0.2	0
39	Analyzing Nucleosome Plasticity via Atomistic MD Simulations. Biophysical Journal, 2020, 118, 9a.	0.2	0
40	Modeling of tandem dCas9 complexes bound to DNA for nucleic acids detection. Microscopy and Microanalysis, 2021, 27, 1696-1698.	0.2	0