Alexey K Shaytan

List of Publications by Year
in descending order

40	1,291	430442 18	377514 34
papers	citations	h-index	g-index

44	44	44	2002
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Electron microscopy analysis of ATP-independent nucleosome unfolding by FACT. Communications Biology, 2022, 5, 2.	2.0	16
2	Molecular Mechanisms of Oncogenesis through the Lens of Nucleosomes and Histones. Journal of Physical Chemistry B, 2021, 125, 3963-3976.	1.2	14
3	Design of Nucleic Acid Biosensors Based on CRISPR/Cas Systems and Reporter Split Proteins. Moscow University Biological Sciences Bulletin, 2021, 76, 52-58.	0.1	2
4	Histone dynamics mediate DNA unwrapping and sliding in nucleosomes. Nature Communications, 2021, 12, 2387.	5.8	70
5	Modeling of tandem dCas9 complexes bound to DNA for nucleic acids detection. Microscopy and Microanalysis, 2021, 27, 1696-1698.	0.2	0
6	Integrative Modeling of Nucleosomes and Supranucleosomal Structures. Biophysical Journal, 2020, 118, 64a.	0.2	0
7	Analyzing Nucleosome Plasticity via Atomistic MD Simulations. Biophysical Journal, 2020, 118, 9a.	0.2	0
8	Determining the Binding Constant of LANA Protein Fragment with Nucleosome. Moscow University Biological Sciences Bulletin, 2020, 75, 252-256.	0.1	1
9	Histone Octamer Structure Is Altered Early in ISW2 ATP-Dependent Nucleosome Remodeling. Cell Reports, 2019, 28, 282-294.e6.	2.9	20
10	Linking chromatin composition and structural dynamics at the nucleosome level. Current Opinion in Structural Biology, 2019, 56, 46-55.	2.6	38
11	Structural interpretation of DNAâ€“protein hydroxyl-radical footprinting experiments with high resolution using HYDROID. Nature Protocols, 2018, 13, 2535-2556.	5.5	6
12	Molecular basis of CENP-C association with the CENP-A nucleosome at yeast centromeres. Genes and Development, 2017, 31, 1958-1972.	2.7	45
13	MS_HistoneDB, a manually curated resource for proteomic analysis of human and mouse histones. Epigenetics and Chromatin, 2017, 10, 2.	1.8	40
14	Hydroxyl-radical footprinting combined with molecular modeling identifies unique features of DNA conformation and nucleosome positioning. Nucleic Acids Research, 2017, 45, 9229-9243.	6.5	18
15	Nucleosomal Barrier to Transcription: Structural Determinants and Changes in Chromatin Structure. Biochemistry & Molecular Biology Journal, 2016, 2, .	0.3	14
16	HistoneDB 2.0: a histone database with variantsâ€”an integrated resource to explore histones and their variants. Database: the Journal of Biological Databases and Curation, 2016, 2016, baw014.	1.4	99
17	Genomic profiling of multiple sequentially acquired tumor metastatic sites from an â€œexceptional responderâ€•lung adenocarcinoma patient reveals extensive genomic heterogeneity and novel somatic variants driving treatment response. Journal of Physical Education and Sports Management, 2016, 2, a001263.	0.5	18
18	Nucleosome Dynamics at Microsecond Timescale: DNA-Protein Interactions, Water-Mediated Interactions and Nucleosome Formation. Biophysical Journal, 2016, 110, 405a.	0.2	2

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19	Trajectories of microsecond molecular dynamics simulations of nucleosomes and nucleosome core particles. Data in Brief, 2016, 7, 1678-1681.	0.5	3
20	Structure and functions of linker histones. Biochemistry (Moscow), 2016, 81, 213-223.	0.7	10
21	Large-scale ATP-independent nucleosome unfolding by a histone chaperone. Nature Structural and Molecular Biology, 2016, 23, 1111-1116.	3.6	85
22	Coupling between Histone Conformations and DNA Geometry in Nucleosomes on a Microsecond Timescale: Atomistic Insights into Nucleosome Functions. Journal of Molecular Biology, 2016, 428, 221-237.	2.0	131
23	Polymorphism of Histone Tail Interactions in Nucleosome. Biophysical Journal, 2015, 108, 72a.	0.2	0
24	Direct prediction of residual dipolar couplings of small molecules in a stretched gel by stochastic molecular dynamics simulations. Magnetic Resonance in Chemistry, 2015, 53, 213-217.	1.1	24
25	Structural Perspectives on the Evolutionary Expansion of Unique Protein-Protein Binding Sites. Biophysical Journal, 2015, 109, 1295-1306.	0.2	11
26	Nucleosome adaptability conferred by sequence and structural variations in histone H2Aâ€“H2B dimers. Current Opinion in Structural Biology, 2015, 32, 48-57.	2.6	52
27	Structural analysis of nucleosomal barrier to transcription. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, E5787-95.	3.3	65
28	Analysis of the mechanism of nucleosome survival during transcription. Nucleic Acids Research, 2014, 42, 1619-1627.	6.5	40
29	Physicochemical mechanisms of protein regulation by phosphorylation. Frontiers in Genetics, 2014, 5, 270.	1.1	152
30	Investigation of Ion Permeation through the Cx26 Hemichannel. Biophysical Journal, 2014, 106, 556a.	0.2	0
31	Voltage-gated ion channel modulation by lipids: Insights from molecular dynamics simulations. Biochimica Et Biophysica Acta - Biomembranes, 2014, 1838, 1322-1331.	1.4	32
32	Genome packaging in EL and Lin68, two giant phiKZ-like bacteriophages of P. aeruginosa. Virology, 2014, 468-470, 472-478.	1.1	26
33	Molecular Insights into Electroporation and Electrotransfer through Model Cell Membranes. Biophysical Journal, 2014, 106, 291a.	0.2	0
34	Comparative Computational Study of Interaction of C60-Fullerene and Tris-Malonyl-C60-Fullerene Isomers with Lipid Bilayer: Relation to Their Antioxidant Effect. PLoS ONE, 2014, 9, e102487.	1.1	30
35	Peptide nanofibrils boost retroviral gene transfer and provide a rapid means for concentrating viruses. Nature Nanotechnology, 2013, 8, 130-136.	15.6	125
36	Self-Assembling Nanofibers from Thiopheneâ€“Peptide Diblock Oligomers: A Combined Experimental and Computer Simulations Study. ACS Nano, 2011, 5, 6894-6909.	7.3	41

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37	Self-organizing bioinspired oligothiopheneâ€“oligopeptide hybrids. Beilstein Journal of Nanotechnology, 2011, 2, 525-544.	1.5	10
38	Free energy profiles of amino acid side chain analogs near waterâ€“vapor interface obtained via MD simulations. Journal of Computational Chemistry, 2010, 31, 204-216.	1.5	11
39	Large-scale atomistic simulation of a nanosized fibril formed by thiopheneâ€“peptide â€œmolecular chimerasâ€. Soft Matter, 2010, 6, 1453.	1.2	7
40	Solvent Accessible Surface Area of Amino Acid Residues in Globular Proteins: Correlation of Apparent Transfer Free Energies with Experimental Hydrophobicity Scales. Biomacromolecules, 2009, 10, 1224-1237.	2.6	31