Anton A Polyansky

List of Publications by Year
in descending order

30	997	394421 19	454955 30
papers	citations	h-index	g-index

33	33	33	1430
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	The Structure and Regulation of Human Muscle Î±-Actinin. Cell, 2014, 159, 1447-1460.	28.9	178
2	PREDDIMER: a web server for prediction of transmembrane helical dimers. Bioinformatics, 2014, 30, 889-890.	4.1	77
3	Antimicrobial Peptides Induce Growth of Phosphatidylglycerol Domains in a Model Bacterial Membrane. Journal of Physical Chemistry Letters, 2010, 1, 3108-3111.	4.6	65
4	Multistate Organization of Transmembrane Helical Protein Dimers Governed by the Host Membrane. Journal of the American Chemical Society, 2012, 134, 14390-14400.	13.7	63
5	<scp>RNA</scp>â€protein interactions in an unstructured context. FEBS Letters, 2018, 592, 2901-2916.	2.8	53
6	Evidence of direct complementary interactions between messenger RNAs and their cognate proteins. Nucleic Acids Research, 2013, 41, 8434-8443.	14.5	48
7	Structural mechanism for the recognition and ubiquitination of a single nucleosome residue by Rad6â€“Bre1. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, 10553-10558.	7.1	44
8	Sequence signatures of direct complementarity between mRNAs and cognate proteins on multiple levels. Nucleic Acids Research, 2012, 40, 8874-8882.	14.5	39
9	The Conformation of the Epidermal Growth Factor Receptor Transmembrane Domain Dimer Dynamically Adapts to the Local Membrane Environment. Biochemistry, 2017, 56, 1697-1705.	2.5	39
10	Adaptation of a Membrane-active Peptide to Heterogeneous Environment. I. Structural Plasticity of the Peptide. Journal of Physical Chemistry B, 2009, 113, 1107-1119.	2.6	36
11	Estimation of Conformational Entropy in Proteinâ€“Ligand Interactions: A Computational Perspective. Methods in Molecular Biology, 2012, 819, 327-353.	0.9	34
12	PARENT: A Parallel Software Suite for the Calculation of Configurational Entropy in Biomolecular Systems. Journal of Chemical Theory and Computation, 2016, 12, 2055-2065.	5.3	34
13	Proteome-wide analysis reveals clues of complementary interactions between mRNAs and their cognate proteins as the physicochemical foundation of the genetic code. RNA Biology, 2013, 10, 1248-1254.	3.1	32
14	Protein Electrostatic Properties Predefining the Level of Surface Hydrophobicity Change upon Phosphorylation. Journal of Physical Chemistry Letters, 2012, 3, 973-976.	4.6	30
15	A novel non-canonical PIP-box mediates PARG interaction with PCNA. Nucleic Acids Research, 2017, 45, 9741-9759.	14.5	30
16	Modeling Transmembrane Domain Dimers/Trimers of Plexin Receptors: Implications for Mechanisms of Signal Transmission across the Membrane. PLoS ONE, 2015, 10, e0121513.	2.5	30
17	On the Contribution of Linear Correlations to Quasi-harmonic Conformational Entropy in Proteins. Journal of Chemical Theory and Computation, 2012, 8, 3820-3829.	5.3	23
18	Analogue encoding of physicochemical properties of proteins in their cognate messenger RNAs. Nature Communications, 2013, 4, 2784.	12.8	23

#	Article	IF	Citations
19	Adaptable Lipid Matrix Promotes Proteinâ€“Protein Association in Membranes. Journal of Chemical Theory and Computation, 2015, 11, 4415-4426.	5.3	21
20	Order from disorder in the sarcomere: FATZ forms a fuzzy but tight complex and phase-separated condensates with Î±-actinin. Science Advances, 2021, 7, .	10.3	15
21	Inosine Nucleobase Acts as Guanine in Interactions with Protein Side Chains. Journal of the American Chemical Society, 2016, 138, 5519-5522.	13.7	14
22	Structural, dynamic, and functional aspects of helix association in membranes. Advances in Protein Chemistry and Structural Biology, 2011, 83, 129-161.	2.3	12
23	On the Contribution of Protein Spatial Organization to the Physicochemical Interconnection between Proteins and Their Cognate mRNAs. Life, 2014, 4, 788-799.	2.4	10
24	COMPUTER SIMULATIONS OF MEMBRANE-LYTIC PEPTIDES: PERSPECTIVES IN DRUG DESIGN. Journal of Bioinformatics and Computational Biology, 2007, 05, 611-626.	0.8	9
25	Dependence of Binding Free Energies between RNA Nucleobases and Protein Side Chains on Local Dielectric Properties. Journal of Chemical Theory and Computation, 2017, 13, 4504-4513.	5.3	9
26	Fuento: functional enrichment for bioinformatics. Bioinformatics, 2017, 33, 2604-2606.	4.1	8
27	Atomistic mechanism of the constitutive activation of PDGFRA via its transmembrane domain. Biochimica Et Biophysica Acta - General Subjects, 2019, 1863, 82-95.	2.4	8
28	Self-Consistent Framework Connecting Experimental Proxies of Protein Dynamics with Configurational Entropy. Journal of Chemical Theory and Computation, 2018, 14, 3796-3810.	5.3	5
29	Direct interplay between stereochemistry and conformational preferences in aminoacylated oligoribonucleotides. Nucleic Acids Research, 2019, 47, 11077-11089.	14.5	2
30	Compositional complementarity between genomic RNA and coat proteins in positive-sense single-stranded RNA viruses. Nucleic Acids Research, 2022, 50, 4054-4067.	14.5	1