

Anton A Polyansky

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/2879300/publications.pdf>

Version: 2024-02-01

30
papers

997
citations

394421

19
h-index

454955

30
g-index

33
all docs

33
docs citations

33
times ranked

1430
citing authors

#	ARTICLE	IF	CITATIONS
1	Compositional complementarity between genomic RNA and coat proteins in positive-sense single-stranded RNA viruses. <i>Nucleic Acids Research</i> , 2022, 50, 4054-4067.	14.5	1
2	Order from disorder in the sarcomere: FATZ forms a fuzzy but tight complex and phase-separated condensates with β -actinin. <i>Science Advances</i> , 2021, 7, .	10.3	15
3	Direct interplay between stereochemistry and conformational preferences in aminoacylated oligoribonucleotides. <i>Nucleic Acids Research</i> , 2019, 47, 11077-11089.	14.5	2
4	Atomistic mechanism of the constitutive activation of PDGFRA via its transmembrane domain. <i>Biochimica Et Biophysica Acta - General Subjects</i> , 2019, 1863, 82-95.	2.4	8
5	Self-Consistent Framework Connecting Experimental Proxies of Protein Dynamics with Configurational Entropy. <i>Journal of Chemical Theory and Computation</i> , 2018, 14, 3796-3810.	5.3	5
6	$\langle \text{scp} \rangle \text{RNA} \text{--} \text{protein}$ interactions in an unstructured context. <i>FEBS Letters</i> , 2018, 592, 2901-2916.	2.8	53
7	<i>Fuente</i> : functional enrichment for bioinformatics. <i>Bioinformatics</i> , 2017, 33, 2604-2606.	4.1	8
8	The Conformation of the Epidermal Growth Factor Receptor Transmembrane Domain Dimer Dynamically Adapts to the Local Membrane Environment. <i>Biochemistry</i> , 2017, 56, 1697-1705.	2.5	39
9	A novel non-canonical PIP-box mediates PARC interaction with PCNA. <i>Nucleic Acids Research</i> , 2017, 45, 9741-9759.	14.5	30
10	Dependence of Binding Free Energies between RNA Nucleobases and Protein Side Chains on Local Dielectric Properties. <i>Journal of Chemical Theory and Computation</i> , 2017, 13, 4504-4513.	5.3	9
11	Inosine Nucleobase Acts as Guanine in Interactions with Protein Side Chains. <i>Journal of the American Chemical Society</i> , 2016, 138, 5519-5522.	13.7	14
12	Structural mechanism for the recognition and ubiquitination of a single nucleosome residue by Rad6 β -Bre1. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, 10553-10558.	7.1	44
13	PARENT: A Parallel Software Suite for the Calculation of Configurational Entropy in Biomolecular Systems. <i>Journal of Chemical Theory and Computation</i> , 2016, 12, 2055-2065.	5.3	34
14	Adaptable Lipid Matrix Promotes Protein β -Protein Association in Membranes. <i>Journal of Chemical Theory and Computation</i> , 2015, 11, 4415-4426.	5.3	21
15	Modeling Transmembrane Domain Dimers/Trimers of Plexin Receptors: Implications for Mechanisms of Signal Transmission across the Membrane. <i>PLoS ONE</i> , 2015, 10, e0121513.	2.5	30
16	On the Contribution of Protein Spatial Organization to the Physicochemical Interconnection between Proteins and Their Cognate mRNAs. <i>Life</i> , 2014, 4, 788-799.	2.4	10
17	The Structure and Regulation of Human Muscle β -Actinin. <i>Cell</i> , 2014, 159, 1447-1460.	28.9	178
18	PREDDIMER: a web server for prediction of transmembrane helical dimers. <i>Bioinformatics</i> , 2014, 30, 889-890.	4.1	77

#	ARTICLE	IF	CITATIONS
19	Evidence of direct complementary interactions between messenger RNAs and their cognate proteins. <i>Nucleic Acids Research</i> , 2013, 41, 8434-8443.	14.5	48
20	Analogue encoding of physicochemical properties of proteins in their cognate messenger RNAs. <i>Nature Communications</i> , 2013, 4, 2784.	12.8	23
21	Proteome-wide analysis reveals clues of complementary interactions between mRNAs and their cognate proteins as the physicochemical foundation of the genetic code. <i>RNA Biology</i> , 2013, 10, 1248-1254.	3.1	32
22	Protein Electrostatic Properties Predefining the Level of Surface Hydrophobicity Change upon Phosphorylation. <i>Journal of Physical Chemistry Letters</i> , 2012, 3, 973-976.	4.6	30
23	On the Contribution of Linear Correlations to Quasi-harmonic Conformational Entropy in Proteins. <i>Journal of Chemical Theory and Computation</i> , 2012, 8, 3820-3829.	5.3	23
24	Sequence signatures of direct complementarity between mRNAs and cognate proteins on multiple levels. <i>Nucleic Acids Research</i> , 2012, 40, 8874-8882.	14.5	39
25	Multistate Organization of Transmembrane Helical Protein Dimers Governed by the Host Membrane. <i>Journal of the American Chemical Society</i> , 2012, 134, 14390-14400.	13.7	63
26	Estimation of Conformational Entropy in Protein-Ligand Interactions: A Computational Perspective. <i>Methods in Molecular Biology</i> , 2012, 819, 327-353.	0.9	34
27	Structural, dynamic, and functional aspects of helix association in membranes. <i>Advances in Protein Chemistry and Structural Biology</i> , 2011, 83, 129-161.	2.3	12
28	Antimicrobial Peptides Induce Growth of Phosphatidylglycerol Domains in a Model Bacterial Membrane. <i>Journal of Physical Chemistry Letters</i> , 2010, 1, 3108-3111.	4.6	65
29	Adaptation of a Membrane-active Peptide to Heterogeneous Environment. I. Structural Plasticity of the Peptide. <i>Journal of Physical Chemistry B</i> , 2009, 113, 1107-1119.	2.6	36
30	COMPUTER SIMULATIONS OF MEMBRANE-LYTIC PEPTIDES: PERSPECTIVES IN DRUG DESIGN. <i>Journal of Bioinformatics and Computational Biology</i> , 2007, 05, 611-626.	0.8	9