

Veronika Csizmák

List of Publications by Year in descending order

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Version: 2024-02-01

21
papers

3,901
citations

430442

18
h-index

713013

21
g-index

22
all docs

22
docs citations

22
times ranked

5596
citing authors

#	ARTICLE	IF	CITATIONS
1	IUPred: web server for the prediction of intrinsically unstructured regions of proteins based on estimated energy content. <i>Bioinformatics</i> , 2005, 21, 3433-3434.	1.8	1,832
2	The Pairwise Energy Content Estimated from Amino Acid Composition Discriminates between Folded and Intrinsically Unstructured Proteins. <i>Journal of Molecular Biology</i> , 2005, 347, 827-839.	2.0	911
3	Dynamic Protein Interaction Networks and New Structural Paradigms in Signaling. <i>Chemical Reviews</i> , 2016, 116, 6424-6462.	23.0	161
4	Pan-cancer analysis of advanced patient tumors reveals interactions between therapy and genomic landscapes. <i>Nature Cancer</i> , 2020, 1, 452-468.	5.7	103
5	Primary Contact Sites in Intrinsically Unstructured Proteins: The Case of Calpastatin and Microtubule-Associated Protein 2. <i>Biochemistry</i> , 2005, 44, 3955-3964.	1.2	97
6	Transient structure and dynamics in the disordered c-Myc transactivation domain affect Bin1 binding. <i>Nucleic Acids Research</i> , 2012, 40, 6353-6366.	6.5	97
7	H-start for exclusively heteronuclear NMR spectroscopy: The case of intrinsically disordered proteins. <i>Journal of Magnetic Resonance</i> , 2009, 198, 275-281.	1.2	90
8	Complex regulatory mechanisms mediated by the interplay of multiple post-translational modifications. <i>Current Opinion in Structural Biology</i> , 2018, 48, 58-67.	2.6	90
9	NMR Relaxation Studies on the Hydrate Layer of Intrinsically Unstructured Proteins. <i>Biophysical Journal</i> , 2005, 88, 2030-2037.	0.2	89
10	Structural and Dynamic Characterization of Intrinsically Disordered Human Securin by NMR Spectroscopy. <i>Journal of the American Chemical Society</i> , 2008, 130, 16873-16879.	6.6	67
11	A Novel Two-dimensional Electrophoresis Technique for the Identification of Intrinsically Unstructured Proteins. <i>Molecular and Cellular Proteomics</i> , 2006, 5, 265-273.	2.5	65
12	High levels of structural disorder in scaffold proteins as exemplified by a novel neuronal protein, CASK-interactive protein1. <i>FEBS Journal</i> , 2009, 276, 3744-3756.	2.2	65
13	Composite low affinity interactions dictate recognition of the cyclin-dependent kinase inhibitor Sic1 by the SCF ^{Cdc4} ubiquitin ligase. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 3287-3292.	3.3	55
14	The Effect of Intrachain Electrostatic Repulsion on Conformational Disorder and Dynamics of the Sic1 Protein. <i>Journal of Physical Chemistry B</i> , 2014, 118, 4088-4097.	1.2	55
15	An allosteric conduit facilitates dynamic multisite substrate recognition by the SCF ^{Cdc4} ubiquitin ligase. <i>Nature Communications</i> , 2017, 8, 13943.	5.8	33
16	Multivalent Interactions with Fbw7 and Pin1 Facilitate Recognition of c-Jun by the SCF ^{Fbw7} Ubiquitin Ligase. <i>Structure</i> , 2018, 26, 28-39.e2.	1.6	29
17	Towards Proteomic Approaches for the Identification of Structural Disorder. <i>Current Protein and Peptide Science</i> , 2007, 8, 173-179.	0.7	20
18	GAP43 shows partial co-localisation but no strong physical interaction with prolyl oligopeptidase. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2010, 1804, 2162-2176.	1.1	20

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19	E3 ubiquitin-protein ligase TRIM21-mediated lysine capture by UBE2E1 reveals substrate-targeting mode of a ubiquitin-conjugating E2. <i>Journal of Biological Chemistry</i> , 2019, 294, 11404-11419.	1.6	16
20	Structural Disorder and Its Connection with Misfolding Diseases. <i>Focus on Structural Biology</i> , 2009, 1-19.	0.1	4
21	Whole-genome and transcriptome analysis of advanced adrenocortical cancer highlights multiple alterations affecting epigenome and DNA repair pathways.. <i>Cold Spring Harbor Molecular Case Studies</i> , 2022, 8, .	0.7	2