Veronika CsizmÃ³k

List of Publications by Year
in descending order

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Version: 2024-02-01

21 papers	3,901 citations	430874 18 h-index	713466 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. Bioinformatics, 2005, 21, 3433-3434.	4.1	1,832
2	The Pairwise Energy Content Estimated from Amino Acid Composition Discriminates between Folded and Intrinsically Unstructured Proteins. Journal of Molecular Biology, 2005, 347, 827-839.	4.2	911
3	Dynamic Protein Interaction Networks and New Structural Paradigms in Signaling. Chemical Reviews, 2016, 116, 6424-6462.	47.7	161
4	Pan-cancer analysis of advanced patient tumors reveals interactions between therapy and genomic landscapes. Nature Cancer, 2020, 1, 452-468.	13.2	103
5	Primary Contact Sites in Intrinsically Unstructured Proteins:Â The Case of Calpastatin and Microtubule-Associated Protein 2â€. Biochemistry, 2005, 44, 3955-3964.	2.5	97
6	Transient structure and dynamics in the disordered c-Myc transactivation domain affect Bin1 binding. Nucleic Acids Research, 2012, 40, 6353-6366.	14.5	97
7	H-start for exclusively heteronuclear NMR spectroscopy: The case of intrinsically disordered proteins. Journal of Magnetic Resonance, 2009, 198, 275-281.	2.1	90
8	Complex regulatory mechanisms mediated by the interplay of multiple post-translational modifications. Current Opinion in Structural Biology, 2018, 48, 58-67.	5.7	90
9	NMR Relaxation Studies on the Hydrate Layer of Intrinsically Unstructured Proteins. Biophysical Journal, 2005, 88, 2030-2037.	0.5	89
10	Structural and Dynamic Characterization of Intrinsically Disordered Human Securin by NMR Spectroscopy. Journal of the American Chemical Society, 2008, 130, 16873-16879.	13.7	67
11	A Novel Two-dimensional Electrophoresis Technique for the Identification of Intrinsically Unstructured Proteins. Molecular and Cellular Proteomics, 2006, 5, 265-273.	3.8	65
12	High levels of structural disorder in scaffold proteins as exemplified by a novel neuronal protein, CASKâ€interactive protein1. FEBS Journal, 2009, 276, 3744-3756.	4.7	65
13	Composite low affinity interactions dictate recognition of the cyclin-dependent kinase inhibitor Sic1 by the SCF ^{Cdc4} ubiquitin ligase. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 3287-3292.	7.1	55
14	The Effect of Intrachain Electrostatic Repulsion on Conformational Disorder and Dynamics of the Sic1 Protein. Journal of Physical Chemistry B, 2014, 118, 4088-4097.	2.6	55
15	An allosteric conduit facilitates dynamic multisite substrate recognition by the SCFCdc4 ubiquitin ligase. Nature Communications, 2017, 8, 13943.	12.8	33
16	Multivalent Interactions with Fbw7 and Pin1 Facilitate Recognition of c-Jun by the SCFFbw7 Ubiquitin Ligase. Structure, 2018, 26, 28-39.e2.	3.3	29
17	Towards Proteomic Approaches for the Identification of Structural Disorder. Current Protein and Peptide Science, 2007, 8, 173-179.	1.4	20
18	GAP43 shows partial co-localisation but no strong physical interaction with prolyl oligopeptidase. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2010, 1804, 2162-2176.	2.3	20

#	Article	IF	Citations
19	E3 ubiquitin-protein ligase TRIM21-mediated lysine capture by UBE2E1 reveals substrate-targeting mode of a ubiquitin-conjugating E2. Journal of Biological Chemistry, 2019, 294, 11404-11419.	3.4	16
20	Structural Disorder and Its Connection with Misfolding Diseases. Focus on Structural Biology, 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.. Cold Spring Harbor Molecular Case Studies, 2022, 8, .	1.0	2