

# Wade M Borchers

## List of Publications by Year in descending order

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Version: 2024-02-01

16  
papers

924  
citations

759233

12  
h-index

996975

15  
g-index

19  
all docs

19  
docs citations

19  
times ranked

916  
citing authors

#	ARTICLE	IF	CITATIONS
1	Deciphering how naturally occurring sequence features impact the phase behaviours of disordered prion-like domains. <i>Nature Chemistry</i> , 2022, 14, 196-207.	13.6	216
2	Disorder and residual helicity alter p53-Mdm2 binding affinity and signaling in cells. <i>Nature Chemical Biology</i> , 2014, 10, 1000-1002.	8.0	167
3	How do intrinsically disordered protein regions encode a driving force for liquid-liquid phase separation?. <i>Current Opinion in Structural Biology</i> , 2021, 67, 41-50.	5.7	162
4	Interaction between p53 N terminus and core domain regulates specific and nonspecific DNA binding. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 8859-8868.	7.1	61
5	Autoinhibition of MDMX by intramolecular p53 mimicry. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 4624-4629.	7.1	43
6	±-Helix-Mimicking Sulfonyl-AApeptide Inhibitors for p53-MDM2/MDMX Protein-Protein Interactions. <i>Journal of Medicinal Chemistry</i> , 2020, 63, 975-986.	6.4	43
7	Conserved Helix-Flanking Prolines Modulate Intrinsically Disordered Protein:Target Affinity by Altering the Lifetime of the Bound Complex. <i>Biochemistry</i> , 2017, 56, 2379-2384.	2.5	40
8	Secondary interaction between MDMX and p53 core domain inhibits p53 DNA binding. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, E2558-63.	7.1	38
9	Optimal Affinity Enhancement by a Conserved Flexible Linker Controls p53 Mimicry in MdmX. <i>Biophysical Journal</i> , 2017, 112, 2038-2042.	0.5	34
10	Uncoupling the Folding and Binding of an Intrinsically Disordered Protein. <i>Journal of Molecular Biology</i> , 2018, 430, 2389-2402.	4.2	18
11	Conserved Glycines Control Disorder and Function in the Cold-Regulated Protein, COR15A. <i>Biomolecules</i> , 2019, 9, 84.	4.0	15
12	Structural divergence is more extensive than sequence divergence for a family of intrinsically disordered proteins. <i>Proteins: Structure, Function and Bioinformatics</i> , 2013, 81, 1686-1698.	2.6	14
13	Using NMR Chemical Shifts to Determine Residue-Specific Secondary Structure Populations for Intrinsically Disordered Proteins. <i>Methods in Enzymology</i> , 2018, 611, 101-136.	1.0	11
14	Using chemical shifts to generate structural ensembles for intrinsically disordered proteins with converged distributions of secondary structure. <i>Intrinsically Disordered Proteins</i> , 2015, 3, e984565.	1.9	10
15	p53 Phosphomimetics Preserve Transient Secondary Structure but Reduce Binding to Mdm2 and MdmX. <i>Biomolecules</i> , 2019, 9, 83.	4.0	4
16	Phase behavior of intrinsically disordered prion-like domains. <i>FASEB Journal</i> , 2022, 36, .	0.5	1