

Rebecca Beveridge

List of Publications by Year in descending order

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Version: 2024-02-01

19
papers

993
citations

623734

14
h-index

794594

19
g-index

24
all docs

24
docs citations

24
times ranked

1418
citing authors

#	ARTICLE	IF	CITATIONS
1	Intranasally administered S-MGB-364 displays antitubercular activity and modulates the host immune response to <i>Mycobacterium tuberculosis</i> infection. <i>Journal of Antimicrobial Chemotherapy</i> , 2022, 77, 1061-1071.	3.0	5
2	Structural Proteomics Methods to Interrogate the Conformations and Dynamics of Intrinsically Disordered Proteins. <i>Frontiers in Chemistry</i> , 2021, 9, 603639.	3.6	19
3	The oxidoreductase PYROXD1 uses NAD(P) ⁺ as an antioxidant to sustain tRNA ligase activity in pre-tRNA splicing and unfolded protein response. <i>Molecular Cell</i> , 2021, 81, 2520-2532.e16.	9.7	21
4	Native Mass Spectrometry Can Effectively Predict PROTAC Efficacy. <i>ACS Central Science</i> , 2020, 6, 1223-1230.	11.3	37
5	A synthetic peptide library for benchmarking crosslinking-mass spectrometry search engines for proteins and protein complexes. <i>Nature Communications</i> , 2020, 11, 742.	12.8	62
6	A cross-kingdom conserved ER-phagy receptor maintains endoplasmic reticulum homeostasis during stress. <i>ELife</i> , 2020, 9, .	6.0	139
7	Ion Mobility Mass Spectrometry Measures the Conformational Landscape of p27 and its Domains and how this is Modulated upon Interaction with Cdk2/cyclinA. <i>Angewandte Chemie</i> , 2019, 131, 3146-3150.	2.0	1
8	Structure of McsB, a protein kinase for regulated arginine phosphorylation. <i>Nature Chemical Biology</i> , 2019, 15, 510-518.	8.0	36
9	Ion Mobility Mass Spectrometry Uncovers the Impact of the Patterning of Oppositely Charged Residues on the Conformational Distributions of Intrinsically Disordered Proteins. <i>Journal of the American Chemical Society</i> , 2019, 141, 4908-4918.	13.7	62
10	Ion Mobility Mass Spectrometry Measures the Conformational Landscape of p27 and its Domains and how this is Modulated upon Interaction with Cdk2/cyclinA. <i>Angewandte Chemie - International Edition</i> , 2019, 58, 3114-3118.	13.8	11
11	Structural prediction of protein models using distance restraints derived from cross-linking mass spectrometry data. <i>Nature Protocols</i> , 2018, 13, 478-494.	12.0	56
12	Reply to "Defining distance restraints in HADDOCK". <i>Nature Protocols</i> , 2018, 13, 1503-1505.	12.0	1
13	The replicative helicase MCM recruits cohesin acetyltransferase ESCO2 to mediate centromeric sister chromatid cohesion. <i>EMBO Journal</i> , 2018, 37, .	7.8	50
14	Electron transfer with no dissociation ion mobility mass spectrometry (ETnoD IM-MS). The effect of charge reduction on protein conformation. <i>International Journal of Mass Spectrometry</i> , 2017, 413, 43-51.	1.5	27
15	Mass spectrometry locates local and allosteric conformational changes that occur on cofactor binding. <i>Nature Communications</i> , 2016, 7, 12163.	12.8	53
16	Relating gas phase to solution conformations: Lessons from disordered proteins. <i>Proteomics</i> , 2015, 15, 2872-2883.	2.2	42
17	New cofactor supports \hat{I}^{\pm}, \hat{I}^2 -unsaturated acid decarboxylation via 1,3-dipolar cycloaddition. <i>Nature</i> , 2015, 522, 497-501.	27.8	197
18	A Mass-Spectrometry-Based Framework To Define the Extent of Disorder in Proteins. <i>Analytical Chemistry</i> , 2014, 86, 10979-10991.	6.5	91

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19	Mass spectrometry methods for intrinsically disordered proteins. <i>Analyst, The</i> , 2013, 138, 32-42.	3.5	76