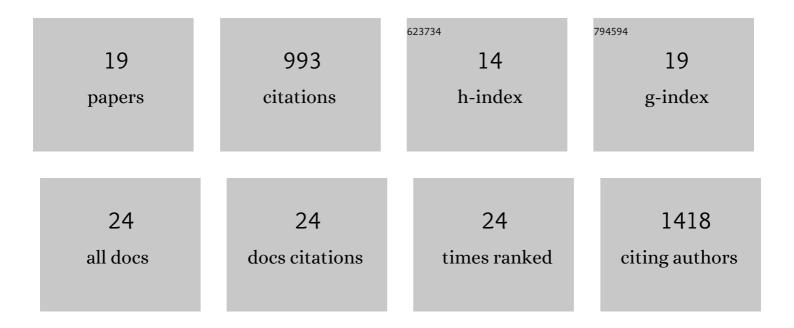
## Rebecca Beveridge

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/7334160/publications.pdf Version: 2024-02-01



#	Article	IF	CITATIONS
1	Intranasally administered S-MGB-364 displays antitubercular activity and modulates the host immune response to <i>Mycobacterium tuberculosis</i> infection. Journal of Antimicrobial Chemotherapy, 2022, 77, 1061-1071.	3.0	5
2	Structural Proteomics Methods to Interrogate the Conformations and Dynamics of Intrinsically Disordered Proteins. Frontiers in Chemistry, 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. Molecular Cell, 2021, 81, 2520-2532.e16.	9.7	21
4	Native Mass Spectrometry Can Effectively Predict PROTAC Efficacy. ACS Central Science, 2020, 6, 1223-1230.	11.3	37
5	A synthetic peptide library for benchmarking crosslinking-mass spectrometry search engines for proteins and protein complexes. Nature Communications, 2020, 11, 742.	12.8	62
6	A cross-kingdom conserved ER-phagy receptor maintains endoplasmic reticulum homeostasis during stress. ELife, 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/cyclinâ€A. Angewandte Chemie, 2019, 131, 3146-3150.	2.0	1
8	Structure of McsB, a protein kinase for regulated arginine phosphorylation. Nature Chemical Biology, 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. Journal of the American Chemical Society, 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/cyclinâ€A. Angewandte Chemie - International Edition, 2019, 58, 3114-3118.	13.8	11
11	Structural prediction of protein models using distance restraints derived from cross-linking mass spectrometry data. Nature Protocols, 2018, 13, 478-494.	12.0	56
12	Reply to â€~Defining distance restraints in HADDOCK'. Nature Protocols, 2018, 13, 1503-1505.	12.0	1
13	The replicative helicase MCM recruits cohesin acetyltransferase ESCO2 to mediate centromeric sister chromatid cohesion. EMBO Journal, 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. International Journal of Mass Spectrometry, 2017, 413, 43-51.	1.5	27
15	Mass spectrometry locates local and allosteric conformational changes that occur on cofactor binding. Nature Communications, 2016, 7, 12163.	12.8	53
16	Relating gas phase to solution conformations: Lessons from disordered proteins. Proteomics, 2015, 15, 2872-2883.	2.2	42
17	New cofactor supports α,β-unsaturated acid decarboxylation via 1,3-dipolar cycloaddition. Nature, 2015, 522, 497-501.	27.8	197
18	A Mass-Spectrometry-Based Framework To Define the Extent of Disorder in Proteins. Analytical Chemistry, 2014, 86, 10979-10991.	6.5	91

#	Article	IF	CITATIONS
19	Mass spectrometry methods for intrinsically disordered proteins. Analyst, The, 2013, 138, 32-42.	3.5	76