

# Benjamin T Walters

## List of Publications by Year in descending order

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Version: 2024-02-01

25  
papers

1,614  
citations

471509

17  
h-index

580821

25  
g-index

25  
all docs

25  
docs citations

25  
times ranked

2917  
citing authors

#	ARTICLE	IF	CITATIONS
1	High-Throughput Kinetic Characterization of Irreversible Covalent Inhibitors of KRAS <sup>G12C</sup> by Intact Protein MS and Targeted MRM. <i>Analytical Chemistry</i> , 2022, 94, 1230-1239.	6.5	11
2	Identification of Agitation-Induced Unfolding Events Causing Aggregation of Monoclonal Antibodies Using Hydrogen Exchange-Mass Spectrometry. <i>Journal of Pharmaceutical Sciences</i> , 2022, 111, 2210-2216.	3.3	3
3	Dissecting the molecular basis of high viscosity of monospecific and bispecific IgG antibodies. <i>MAbs</i> , 2020, 12, 1692764.	5.2	27
4	Activation of the IRE1 RNase through remodeling of the kinase front pocket by ATP-competitive ligands. <i>Nature Communications</i> , 2020, 11, 6387.	12.8	24
5	Highland games: A benchmarking exercise in predicting biophysical and drug properties of monoclonal antibodies from amino acid sequences. <i>Biotechnology and Bioengineering</i> , 2020, 117, 2100-2115.	3.3	9
6	Multiscale Coarse-Grained Approach to Investigate Self-Association of Antibodies. <i>Biophysical Journal</i> , 2020, 118, 2741-2754.	0.5	28
7	Bivalent antibody pliers inhibit $\beta$ -tryptase by an allosteric mechanism dependent on the IgG hinge. <i>Nature Communications</i> , 2020, 11, 6435.	12.8	18
8	Structures of autoinhibited and polymerized forms of CARD9 reveal mechanisms of CARD9 and CARD11 activation. <i>Nature Communications</i> , 2019, 10, 3070.	12.8	33
9	Recommendations for performing, interpreting and reporting hydrogen deuterium exchange mass spectrometry (HDX-MS) experiments. <i>Nature Methods</i> , 2019, 16, 595-602.	19.0	452
10	Hydrogen-Deuterium Exchange Mass Spectrometry (HDX-MS) Centroid Data Measured between 3.6 $\text{\AA}^\circ\text{C}$ and 25.4 $\text{\AA}^\circ\text{C}$ for the Fab Fragment of NISTmAb. <i>Journal of Research of the National Institute of Standards and Technology</i> , 2019, 124, 1-7.	1.2	3
11	An Allosteric Anti-tryptase Antibody for the Treatment of Mast Cell-Mediated Severe Asthma. <i>Cell</i> , 2019, 179, 417-431.e19.	28.9	76
12	Optimizing the Formulation and Lyophilization Process for a Fragment Antigen Binding (Fab) Protein Using Solid-State Hydrogen-Deuterium Exchange Mass Spectrometry (ssHDX-MS). <i>Molecular Pharmaceutics</i> , 2019, 16, 4485-4495.	4.6	8
13	Interlaboratory Comparison of Hydrogen-Deuterium Exchange Mass Spectrometry Measurements of the Fab Fragment of NISTmAb. <i>Analytical Chemistry</i> , 2019, 91, 7336-7345.	6.5	44
14	Solid-State Hydrogen-Deuterium Exchange Mass Spectrometry: Correlation of Deuterium Uptake and Long-Term Stability of Lyophilized Monoclonal Antibody Formulations. <i>Molecular Pharmaceutics</i> , 2018, 15, 1-11.	4.6	39
15	Structure-Based Correlation of Light-Induced Histidine Reactivity in A Model Protein. <i>Analytical Chemistry</i> , 2017, 89, 7225-7231.	6.5	14
16	Empirical Method To Accurately Determine Peptide-Averaged Protection Factors from Hydrogen Exchange MS Data. <i>Analytical Chemistry</i> , 2017, 89, 1049-1053.	6.5	16
17	Mutational landscape of antibody variable domains reveals a switch modulating the interdomain conformational dynamics and antigen binding. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, E486-E495.	7.1	72
18	Conformational Destabilization of Immunoglobulin G Increases the Low pH Binding Affinity with the Neonatal Fc Receptor. <i>Journal of Biological Chemistry</i> , 2016, 291, 1817-1825.	3.4	35

#	ARTICLE	IF	CITATIONS
19	Folding of a large protein at high structural resolution. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 18898-18903.	7.1	85
20	Stepwise protein folding at near amino acid resolution by hydrogen exchange and mass spectrometry. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 7684-7689.	7.1	158
21	Protein hydrogen exchange at residue resolution by proteolytic fragmentation mass spectrometry analysis. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 16438-16443.	7.1	131
22	Minimizing Back Exchange in the Hydrogen Exchange-Mass Spectrometry Experiment. Journal of the American Society for Mass Spectrometry, 2012, 23, 2132-2139.	2.8	136
23	Many Overlapping Peptides for Protein Hydrogen Exchange Experiments by the Fragment Separation-Mass Spectrometry Method. Journal of the American Society for Mass Spectrometry, 2011, 22, 1898-905.	2.8	112
24	AMORE-HX: a multidimensional optimization of radial enhanced NMR-sampled hydrogen exchange. Journal of Biomolecular NMR, 2009, 45, 233-239.	2.8	8
25	An Efficient Organic Solvent Based Extraction Method for the Proteomic Analysis of <i>Arabidopsis</i> Plasma Membranes. Journal of Proteome Research, 2009, 8, 2752-2767.	3.7	72