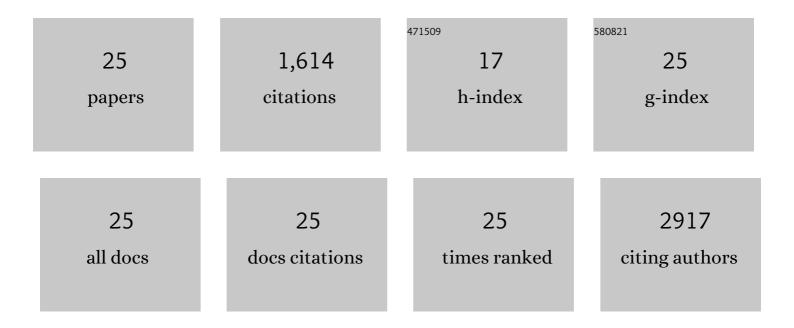
## Benjamin T Walters

List of Publications by Year in descending order

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#	Article	lF	CITATIONS
1	Recommendations for performing, interpreting and reporting hydrogen deuterium exchange mass spectrometry (HDX-MS) experiments. Nature Methods, 2019, 16, 595-602.	19.0	452
2	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
3	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
4	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
5	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
6	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
7	An Allosteric Anti-tryptase Antibody for the Treatment of Mast Cell-Mediated Severe Asthma. Cell, 2019, 179, 417-431.e19.	28.9	76
8	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
9	Mutational landscape of antibody variable domains reveals a switch modulating the interdomain conformational dynamics and antigen binding. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, E486-E495.	7.1	72
10	Interlaboratory Comparison of Hydrogen–Deuterium Exchange Mass Spectrometry Measurements of the Fab Fragment of NISTmAb. Analytical Chemistry, 2019, 91, 7336-7345.	6.5	44
11	Solid-State Hydrogen–Deuterium Exchange Mass Spectrometry: Correlation of Deuterium Uptake and Long-Term Stability of Lyophilized Monoclonal Antibody Formulations. Molecular Pharmaceutics, 2018, 15, 1-11.	4.6	39
12	Conformational Destabilization of Immunoglobulin G Increases the Low pH Binding Affinity with the Neonatal Fc Receptor. Journal of Biological Chemistry, 2016, 291, 1817-1825.	3.4	35
13	Structures of autoinhibited and polymerized forms of CARD9 reveal mechanisms of CARD9 and CARD11 activation. Nature Communications, 2019, 10, 3070.	12.8	33
14	Multiscale Coarse-Grained Approach to Investigate Self-Association of Antibodies. Biophysical Journal, 2020, 118, 2741-2754.	0.5	28
15	Dissecting the molecular basis of high viscosity of monospecific and bispecific IgG antibodies. MAbs, 2020, 12, 1692764.	5.2	27
16	Activation of the IRE1 RNase through remodeling of the kinase front pocket by ATP-competitive ligands. Nature Communications, 2020, 11, 6387.	12.8	24
17	Bivalent antibody pliers inhibit β-tryptase by an allosteric mechanism dependent on the IgG hinge. Nature Communications, 2020, 11, 6435.	12.8	18
18	Empirical Method To Accurately Determine Peptide-Averaged Protection Factors from Hydrogen Exchange MS Data. Analytical Chemistry, 2017, 89, 1049-1053.	6.5	16

#	Article	IF	CITATIONS
19	Structure-Based Correlation of Light-Induced Histidine Reactivity in A Model Protein. Analytical Chemistry, 2017, 89, 7225-7231.	6.5	14
20	High-Throughput Kinetic Characterization of Irreversible Covalent Inhibitors of KRAS <sup>G12C</sup> by Intact Protein MS and Targeted MRM. Analytical Chemistry, 2022, 94, 1230-1239.	6.5	11
21	Highland games: A benchmarking exercise in predicting biophysical and drug properties of monoclonal antibodies from amino acid sequences. Biotechnology and Bioengineering, 2020, 117, 2100-2115.	3.3	9
22	AMORE-HX: a multidimensional optimization of radial enhanced NMR-sampled hydrogen exchange. Journal of Biomolecular NMR, 2009, 45, 233-239.	2.8	8
23	Optimizing the Formulation and Lyophilization Process for a Fragment Antigen Binding (Fab) Protein Using Solid-State Hydrogen–Deuterium Exchange Mass Spectrometry (ssHDX-MS). Molecular Pharmaceutics, 2019, 16, 4485-4495.	4.6	8
24	Hydrogen-Deuterium Exchange Mass Spectrometry (HDX-MS) Centroid Data Measured between 3.6 °C and 25.4 °C for the Fab Fragment of NISTmAb. Journal of Research of the National Institute of Standards and Technology, 2019, 124, 1-7.	1.2	3
25	Identification of Agitation-Induced Unfolding Events Causing Aggregation of Monoclonal Antibodies Using Hydrogen Exchange-Mass Spectrometry. Journal of Pharmaceutical Sciences, 2022, 111, 2210-2216.	3.3	3