

# Kevin M Downard

## List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

86

papers

1,851

citations

26

h-index

38

g-index

87

ext. papers

2,005

ext. citations

5.7

avg, IF

5.31

L-index

#	Paper	IF	Citations
86	SEQUENCE-FREE PHYLOGENETICS WITH MASS SPECTROMETRY. <i>Mass Spectrometry Reviews</i> , <b>2022</b> , 41, 3-14	11	6
85	Detection of SARS CoV-2 coronavirus omicron variant with mass spectrometry.. <i>Analyst, The</i> , <b>2022</b> , 147, 1181-1190	5	0
84	Analysis of bacterial biotyping datasets with a mass-based phylonumerics approach.. <i>Analytical and Bioanalytical Chemistry</i> , <b>2022</b> , 1	4.4	
83	Joseph John Thomson investigates the paranormal. <i>European Journal of Mass Spectrometry</i> , <b>2021</b> , 27, 151-157	1.1	
82	Evolution of Type B Influenza Virus Using a Mass Spectrometry Based Phylonumerics Approach. <i>Evolutionary Biology</i> , <b>2021</b> , 48, 259-268	3	
81	Protein phylogenetics with mass spectrometry. A comparison of methods. <i>Analytical Methods</i> , <b>2021</b> , 13, 1442-1454	3.2	1
80	Mass spectrometry analytical responses to the SARS-CoV2 coronavirus in review. <i>TrAC - Trends in Analytical Chemistry</i> , <b>2021</b> , 142, 116328	14.6	9
79	Detection and evolution of SARS-CoV-2 coronavirus variants of concern with mass spectrometry. <i>Analytical and Bioanalytical Chemistry</i> , <b>2021</b> , 413, 7241-7249	4.4	9
78	Mass-Based Protein Phylogenetic Approach to Identify Epistasis. <i>Methods in Molecular Biology</i> , <b>2021</b> , 2212, 1-15	1.4	1
77	Reimaging the Tree of Life Using a Mass Based Phylonumerics Approach. <i>Evolutionary Biology</i> , <b>2020</b> , 47, 76-84	3	6
76	Detection, Mapping, and Proteotyping of SARS-CoV-2 Coronavirus with High Resolution Mass Spectrometry. <i>ACS Infectious Diseases</i> , <b>2020</b> , 6, 3269-3276	5.5	11
75	Darwin's Tree of Life is Numbered. Resolving the Origins of Species by Mass. <i>Evolutionary Biology</i> , <b>2020</b> , 47, 325-333	3	7
74	Concentration of hydroxyl radicals during electrical discharge for radical probe protein footprinting mass spectrometry. <i>Rapid Communications in Mass Spectrometry</i> , <b>2019</b> , 33, 1420-1422	2.2	1
73	Mechanisms of antiviral resistance in influenza neuraminidase revealed by a mass spectrometry based phylonumerics approach. <i>Molecular Phylogenetics and Evolution</i> , <b>2019</b> , 135, 286-296	4.1	9
72	A Molecular Immunoproteomics Approach to Assess the Viral Antigenicity of Influenza. <i>Methods in Molecular Biology</i> , <b>2019</b> , 2024, 353-369	1.4	
71	Mass spectrometry in structural proteomics: The case for radical probe protein footprinting. <i>TrAC - Trends in Analytical Chemistry</i> , <b>2019</b> , 110, 293-302	14.6	5
70	Identification of epistatic mutations and insights into the evolution of the influenza virus using a mass-based protein phylogenetic approach. <i>Molecular Phylogenetics and Evolution</i> , <b>2018</b> , 121, 132-138	4.1	13

69	Quantitation of anthocyanins in elderberry fruit extracts and nutraceutical formulations with paper spray ionization mass spectrometry. <i>Journal of Mass Spectrometry</i> , <b>2018</b> , 53, 58-64	2.2	12
68	Molecular basis of benzimidazole inhibitors to hepatitis C virus envelope glycoprotein. <i>Chemical Biology and Drug Design</i> , <b>2018</b> , 92, 1638-1646	2.9	2
67	Ancestral and Compensatory Mutations that Promote Antiviral Resistance in Influenza N1 Neuraminidase Revealed by a Phylonumerics Approach. <i>Journal of Molecular Evolution</i> , <b>2018</b> , 86, 546-553	3.1	12
66	Mutational analysis employing a phylogenetic mass tree approach in a study of the evolution of the influenza virus. <i>Molecular Phylogenetics and Evolution</i> , <b>2017</b> , 112, 209-217	4.1	15
65	Subtyping of hepatitis C virus with high resolution mass spectrometry. <i>Clinical Mass Spectrometry</i> , <b>2017</b> , 4-5, 19-24	1.9	6
64	Phylogenetic Analysis Using Protein Mass Spectrometry. <i>Methods in Molecular Biology</i> , <b>2017</b> , 1549, 135-146	1.4	3
63	Effect of charge on the conformation of highly basic peptides including the tail regions of histone proteins by ion mobility mass spectrometry. <i>Analytical and Bioanalytical Chemistry</i> , <b>2016</b> , 408, 6637-48	4.4	4
62	New Anthocyanins from Black Elderberry of Inhibitory Potential Revealed by Mass Spectrometry. <i>Natural Products Journal</i> , <b>2016</b> , 6, 94-102	0.6	2
61	Indirect study of non-covalent protein complexes by MALDI mass spectrometry: Origins, advantages, and applications of the "intensity-fading" approach. <i>Mass Spectrometry Reviews</i> , <b>2016</b> , 35, 559-73	11	7
60	Catechin inhibition of influenza neuraminidase and its molecular basis with mass spectrometry. <i>Journal of Pharmaceutical and Biomedical Analysis</i> , <b>2015</b> , 111, 222-30	3.5	30
59	Stability of the B2B3 crystallin heterodimer to increased oxidation by radical probe and ion mobility mass spectrometry. <i>Journal of Structural Biology</i> , <b>2015</b> , 189, 20-7	3.4	6
58	Molecular basis of influenza hemagglutinin inhibition with an entry-blocker peptide by computational docking and mass spectrometry. <i>Antiviral Chemistry and Chemotherapy</i> , <b>2015</b> , 24, 109-17	3.5	3
57	Advances in radical probe mass spectrometry for protein footprinting in chemical biology applications. <i>Chemical Society Reviews</i> , <b>2014</b> , 43, 3244-58	58.5	48
56	Evolution of influenza neuraminidase and the detection of antiviral resistant strains using mass trees. <i>Analytical Chemistry</i> , <b>2014</b> , 86, 629-37	7.8	15
55	Origins of the reassortant 2009 pandemic influenza virus through proteotyping with mass spectrometry. <i>Journal of Mass Spectrometry</i> , <b>2014</b> , 49, 93-102	2.2	6
54	Substituent effects on the binding of natural product anthocyanidin inhibitors to influenza neuraminidase with mass spectrometry. <i>Analytica Chimica Acta</i> , <b>2014</b> , 828, 61-9	6.6	12
53	Incorporation of a proteotyping approach using mass spectrometry for surveillance of influenza virus in cell-cultured strains. <i>Journal of Clinical Microbiology</i> , <b>2014</b> , 52, 725-35	9.7	16
52	Binding of a natural anthocyanin inhibitor to influenza neuraminidase by mass spectrometry. <i>Analytical and Bioanalytical Chemistry</i> , <b>2013</b> , 405, 6563-72	4.4	34

51	Proteotyping for the rapid identification of influenza virus and other biopathogens. <i>Chemical Society Reviews</i> , <b>2013</b> , 42, 8584-95	58.5	26
50	Inhibition of influenza hemagglutinin with the antiviral inhibitor arbidol using a proteomics based approach and mass spectrometry. <i>Antiviral Research</i> , <b>2013</b> , 100, 399-406	10.8	24
49	Subtyping of influenza neuraminidase using mass spectrometry. <i>Analyst, The</i> , <b>2013</b> , 138, 1787-93	5	10
48	Mass trees: a new phylogenetic approach and algorithm to chart evolutionary history with mass spectrometry. <i>Analytical Chemistry</i> , <b>2013</b> , 85, 5475-82	7.8	20
47	Proteotyping of the parainfluenza virus with high-resolution mass spectrometry. <i>Analytical Chemistry</i> , <b>2013</b> , 85, 1097-105	7.8	10
46	Anti-viral inhibitor binding to influenza neuraminidase by MALDI mass spectrometry. <i>Analytical Chemistry</i> , <b>2012</b> , 84, 3725-30	7.8	16
45	FluShuffle and FluResort: new algorithms to identify reassorted strains of the influenza virus by mass spectrometry. <i>BMC Bioinformatics</i> , <b>2012</b> , 13, 208	3.6	17
44	Impact of limited oxidation on protein ion mobility and structure of importance to footprinting by radical probe mass spectrometry. <i>Rapid Communications in Mass Spectrometry</i> , <b>2012</b> , 26, 226-30	2.2	22
43	On-plate deposition of oxidized proteins to facilitate protein footprinting studies by radical probe mass spectrometry. <i>Rapid Communications in Mass Spectrometry</i> , <b>2012</b> , 26, 2311-8	2.2	11
42	Homology-modelled structure of the B2B3-crystallin heterodimer studied by ion mobility and radical probe MS. <i>FEBS Journal</i> , <b>2011</b> , 278, 4044-54	5.7	13
41	Proteotyping to establish the lineage of type A H1N1 and type B human influenza virus. <i>Journal of Virological Methods</i> , <b>2011</b> , 171, 117-22	2.6	15
40	Rapid differentiation of seasonal and pandemic H1N1 influenza through proteotyping of viral neuraminidase with mass spectrometry. <i>Analytical Chemistry</i> , <b>2010</b> , 82, 4584-90	7.8	27
39	Rapid typing and subtyping of vaccine strains of the influenza virus with high resolution mass spectrometry. <i>European Journal of Mass Spectrometry</i> , <b>2010</b> , 16, 321-9	1.1	14
38	Typing of human and animal strains of influenza virus with conserved signature peptides of matrix M1 protein by high resolution mass spectrometry. <i>Journal of Virological Methods</i> , <b>2010</b> , 165, 178-85	2.6	23
37	FluTyper-an algorithm for automated typing and subtyping of the influenza virus from high resolution mass spectral data. <i>BMC Bioinformatics</i> , <b>2010</b> , 11, 266	3.6	16
36	Ability of N-acetylcarnosine to protect lens crystallins from oxidation and oxidative damage by radical probe mass spectrometry (RP-MS). <i>Rapid Communications in Mass Spectrometry</i> , <b>2010</b> , 24, 2900-8 <sup>2.2</sup>	2.2	9
35	Antigenicity of a type A influenza virus through comparison of hemagglutination inhibition and mass spectrometry immunoassays. <i>Journal of Immunoassay and Immunochemistry</i> , <b>2009</b> , 30, 245-61	1.8	22
34	Mass spectrometry analysis of the influenza virus. <i>Mass Spectrometry Reviews</i> , <b>2009</b> , 28, 35-49	11	20

33	Detection and structural features of the betaB2-B3-crystallin heterodimer by radical probe mass spectrometry (RP-MS). <i>Journal of Mass Spectrometry</i> , <b>2009</b> , 44, 803-12	2.2	6
32	Subtyping of the influenza virus by high resolution mass spectrometry. <i>Analytical Chemistry</i> , <b>2009</b> , 81, 3500-6	7.8	48
31	Signature peptides of influenza nucleoprotein for the typing and subtyping of the virus by high resolution mass spectrometry. <i>Analyst, The</i> , <b>2009</b> , 134, 2253-61	5	26
30	Kinetics of antigen-antibody interactions employing a MALDI mass spectrometry immunoassay. <i>Analytical Chemistry</i> , <b>2008</b> , 80, 7720-6	7.8	13
29	Fingerprinting a killer: surveillance of the influenza virus by mass spectrometry. <i>Analyst, The</i> , <b>2007</b> , 132, 611-4	5	15
28	A computer algorithm for the identification of protein interactions from the spectra of masses (PRISM). <i>Journal of the American Society for Mass Spectrometry</i> , <b>2007</b> , 18, 563-6	3.5	13
27	Antigenic characterisation of H3N2 subtypes of the influenza virus by mass spectrometry. <i>Journal of Virological Methods</i> , <b>2007</b> , 145, 106-14	2.6	27
26	Historical account: Francis William Aston: the man behind the mass spectrograph. <i>European Journal of Mass Spectrometry</i> , <b>2007</b> , 13, 177-90	1.1	17
25	Interaction between alpha and upsilon-crystallin, common to the eye of the Australian platypus, by radical probe mass spectrometry. <i>Journal of Mass Spectrometry</i> , <b>2006</b> , 41, 1298-303	2.2	11
24	PROXIMO--a new docking algorithm to model protein complexes using data from radical probe mass spectrometry (RP-MS). <i>Bioinformatics</i> , <b>2006</b> , 22, 1702-9	7.2	27
23	A proteomics approach to survey the antigenicity of the influenza virus by mass spectrometry. <i>Proteomics</i> , <b>2006</b> , 6, 2034-41	4.8	45
22	Ions of the interactome: the role of MS in the study of protein interactions in proteomics and structural biology. <i>Proteomics</i> , <b>2006</b> , 6, 5374-84	4.8	28
21	Hydroxyl radical probe of the calmodulin-melittin complex interface by electrospray ionization mass spectrometry. <i>Journal of the American Society for Mass Spectrometry</i> , <b>2005</b> , 16, 225-33	3.5	54
20	Onset of oxidative damage in alpha-crystallin by radical probe mass spectrometry. <i>Analytical Biochemistry</i> , <b>2005</b> , 344, 247-56	3.1	29
19	Photochemical and electrophysical production of radicals on millisecond timescales to probe the structure, dynamics and interactions of proteins. <i>Photochemical and Photobiological Sciences</i> , <b>2004</b> , 3, 741-8	4.2	57
18	Strategy for identifying protein-protein interactions of gel-separated proteins and complexes by mass spectrometry. <i>Analytical Biochemistry</i> , <b>2003</b> , 318, 60-70	3.1	22
17	Study of the ribonuclease-S-protein-peptide complex using a radical probe and electrospray ionization mass spectrometry. <i>Analytical Chemistry</i> , <b>2003</b> , 75, 1557-63	7.8	56
16	Hydroxyl radical probe of the surface of lysozyme by synchrotron radiolysis and mass spectrometry. <i>Rapid Communications in Mass Spectrometry</i> , <b>2002</b> , 16, 53-61	2.2	30

15	Unfolding of apomyoglobin helices by synchrotron radiolysis and mass spectrometry. <i>FEBS Journal</i> , <b>2001</b> , 268, 5578-88		33
14	Radical approaches to probe protein structure, folding, and interactions by mass spectrometry. <i>Mass Spectrometry Reviews</i> , <b>2001</b> , 20, 388-401	11	107
13	Determination of macromolecular folding and structure by synchrotron x-ray radiolysis techniques. <i>Analytical Biochemistry</i> , <b>2001</b> , 289, 103-15	3.1	107
12	Contributions of mass spectrometry to structural immunology. <i>Journal of Mass Spectrometry</i> , <b>2000</b> , 35, 493-503	2.2	29
11	Preservation and detection of specific antibody-peptide complexes by matrix-assisted laser desorption ionization mass spectrometry. <i>Journal of the American Society for Mass Spectrometry</i> , <b>2000</b> , 11, 746-50	3.5	46
10	Electrospray-assisted modification of proteins: a radical probe of protein structure. <i>Rapid Communications in Mass Spectrometry</i> , <b>1999</b> , 13, 2352-8	2.2	99
9	Antigenic surveillance of the influenza virus by mass spectrometry. <i>Biochemistry</i> , <b>1999</b> , 38, 14185-91	3.2	56
8	Direct identification of protein epitopes by mass spectrometry without immobilization of antibody and isolation of antibody-peptide complexes. <i>Analytical Chemistry</i> , <b>1999</b> , 71, 1792-801	7.8	56
7	Characterization of the conformations of antigenic peptides of protein lactate dehydrogenase (LDH-C4) by electrospray ionization mass spectrometry. <i>Rapid Communications in Mass Spectrometry</i> , <b>1997</b> , 11, 1853-8	2.2	4
6	C-terminal specific protein degradation: activity and substrate specificity of the Tsp protease. <i>Protein Science</i> , <b>1995</b> , 4, 1507-15	6.3	58
5	Charging behavior of highly basic peptides during electrospray ionization. A predilection for protons. <i>International Journal of Mass Spectrometry and Ion Processes</i> , <b>1995</b> , 148, 191-202		18
4	Methionine specific sequence ions formed by the dissociation of protonated peptides at high collision energies. <i>Journal of Mass Spectrometry</i> , <b>1995</b> , 30, 25-32	2.2	9
3	The effect of charge state and the localization of charge on the collision-induced dissociation of peptide ions. <i>Journal of the American Society for Mass Spectrometry</i> , <b>1994</b> , 5, 966-75	3.5	49
2	Amino acid sequence prerequisites for the formation of cn ions. <i>Journal of the American Society for Mass Spectrometry</i> , <b>1993</b> , 4, 874-31	3.5	27
1	Evolution of SARS CoV-2 Coronavirus Surface Protein Investigated with Mass Spectrometry Based Phylogenetics. <i>Analytical Letters</i> , 1-13	2.2	3