

Kevin M Downard

List of Publications by Year in descending order

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86
papers

2,219
citations

201385

27
h-index

276539

41
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87
all docs

87
docs citations

87
times ranked

1302
citing authors

#	ARTICLE	IF	CITATIONS
1	Determination of Macromolecular Folding and Structure by Synchrotron X-Ray Radiolysis Techniques. <i>Analytical Biochemistry</i> , 2001, 289, 103-115.	1.1	116
2	Electrospray-assisted modification of proteins: a radical probe of protein structure. , 1999, 13, 2352-2358.		113
3	Radical approaches to probe protein structure, folding, and interactions by mass spectrometry. <i>Mass Spectrometry Reviews</i> , 2001, 20, 388-401.	2.8	111
4	C-terminal specific protein degradation: Activity and substrate specificity of the Tsp protease. <i>Protein Science</i> , 1995, 4, 1507-1515.	3.1	70
5	Antigenic Surveillance of the Influenza Virus by Mass Spectrometry. <i>Biochemistry</i> , 1999, 38, 14185-14191.	1.2	62
6	Direct Identification of Protein Epitopes by Mass Spectrometry without Immobilization of Antibody and Isolation of Antibody~Peptide Complexes. <i>Analytical Chemistry</i> , 1999, 71, 1792-1801.	3.2	61
7	Photochemical and electrophysical production of radicals on millisecond timescales to probe the structure, dynamics and interactions of proteins. <i>Photochemical and Photobiological Sciences</i> , 2004, 3, 741.	1.6	61
8	Study of the Ribonuclease~S-Protein~Peptide Complex Using a Radical Probe and Electrospray Ionization Mass Spectrometry. <i>Analytical Chemistry</i> , 2003, 75, 1557-1563.	3.2	60
9	Hydroxyl radical probe of the calmodulin-melittin complex interface by electrospray ionization mass spectrometry. <i>Journal of the American Society for Mass Spectrometry</i> , 2005, 16, 225-233.	1.2	58
10	Subtyping of the Influenza Virus by High Resolution Mass Spectrometry. <i>Analytical Chemistry</i> , 2009, 81, 3500-3506.	3.2	56
11	Advances in radical probe mass spectrometry for protein footprinting in chemical biology applications. <i>Chemical Society Reviews</i> , 2014, 43, 3244.	18.7	54
12	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> , 1994, 5, 966-975.	1.2	51
13	A proteomics approach to survey the antigenicity of the influenza virus by mass spectrometry. <i>Proteomics</i> , 2006, 6, 2034-2041.	1.3	51
14	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> , 2000, 11, 746-750.	1.2	48
15	Binding of a natural anthocyanin inhibitor to influenza neuraminidase by mass spectrometry. <i>Analytical and Bioanalytical Chemistry</i> , 2013, 405, 6563-6572.	1.9	46
16	Unfolding of apomyoglobin helices by synchrotron radiolysis and mass spectrometry. <i>FEBS Journal</i> , 2001, 268, 5578-5588.	0.2	37
17	Catechin inhibition of influenza neuraminidase and its molecular basis with mass spectrometry. <i>Journal of Pharmaceutical and Biomedical Analysis</i> , 2015, 111, 222-230.	1.4	36
18	Proteotyping for the rapid identification of influenza virus and other biopathogens. <i>Chemical Society Reviews</i> , 2013, 42, 8584.	18.7	35

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19	Ions of the interactome: The role of MS in the study of protein interactions in proteomics and structural biology. <i>Proteomics</i> , 2006, 6, 5374-5384.	1.3	34
20	Detection, Mapping, and Proteotyping of SARS-CoV-2 Coronavirus with High Resolution Mass Spectrometry. <i>ACS Infectious Diseases</i> , 2020, 6, 3269-3276.	1.8	34
21	Hydroxyl radical probe of the surface of lysozyme by synchrotron radiolysis and mass spectrometry. <i>Rapid Communications in Mass Spectrometry</i> , 2002, 16, 53-61.	0.7	33
22	Signature peptides of influenza nucleoprotein for the typing and subtyping of the virus by high resolution mass spectrometry. <i>Analyst, The</i> , 2009, 134, 2253.	1.7	33
23	Contributions of mass spectrometry to structural immunology. , 2000, 35, 493-503.		32
24	Onset of oxidative damage in I±-crystallin by radical probe mass spectrometry. <i>Analytical Biochemistry</i> , 2005, 344, 247-256.	1.1	32
25	Antigenic characterisation of H3N2 subtypes of the influenza virus by mass spectrometry. <i>Journal of Virological Methods</i> , 2007, 145, 106-114.	1.0	32
26	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> , 2010, 165, 178-185.	1.0	32
27	Rapid Differentiation of Seasonal and Pandemic H1N1 Influenza through Proteotyping of Viral Neuraminidase with Mass Spectrometry. <i>Analytical Chemistry</i> , 2010, 82, 4584-4590.	3.2	32
28	Mass spectrometry analytical responses to the SARS-CoV2 coronavirus in review. <i>TrAC - Trends in Analytical Chemistry</i> , 2021, 142, 116328.	5.8	31
29	PROXIMO—a new docking algorithm to model protein complexes using data from radical probe mass spectrometry (RP-MS). <i>Bioinformatics</i> , 2006, 22, 1702-1709.	1.8	30
30	Inhibition of influenza hemagglutinin with the antiviral inhibitor arbidol using a proteomics based approach and mass spectrometry. <i>Antiviral Research</i> , 2013, 100, 399-406.	1.9	29
31	Amino acid sequence prerequisites for the formation of cn ions. <i>Journal of the American Society for Mass Spectrometry</i> , 1993, 4, 874-831.	1.2	28
32	Strategy for identifying proteinâ€“protein interactions of gel-separated proteins and complexes by mass spectrometry. <i>Analytical Biochemistry</i> , 2003, 318, 60-70.	1.1	28
33	Mass spectrometry analysis of the influenza virus. <i>Mass Spectrometry Reviews</i> , 2009, 28, 35-49.	2.8	27
34	Francis William Aston: The Man Behind the Mass Spectrograph. <i>European Journal of Mass Spectrometry</i> , 2007, 13, 177-190.	0.5	25
35	Antigenicity of a Type A Influenza Virus Through Comparison of Hemagglutination Inhibition and Mass Spectrometry Immunoassays. <i>Journal of Immunoassay and Immunochemistry</i> , 2009, 30, 245-261.	0.5	25
36	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> , 2012, 26, 226-230.	0.7	25

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37	Mass Trees: A New Phylogenetic Approach and Algorithm to Chart Evolutionary History with Mass Spectrometry. <i>Analytical Chemistry</i> , 2013, 85, 5475-5482.	3.2	24
38	Detection and evolution of SARS-CoV-2 coronavirus variants of concern with mass spectrometry. <i>Analytical and Bioanalytical Chemistry</i> , 2021, 413, 7241-7249.	1.9	23
39	Incorporation of a Proteotyping Approach Using Mass Spectrometry for Surveillance of Influenza Virus in Cell-Cultured Strains. <i>Journal of Clinical Microbiology</i> , 2014, 52, 725-735.	1.8	22
40	Charging behavior of highly basic peptides during electrospray ionization. A predilection for protons. <i>International Journal of Mass Spectrometry and Ion Processes</i> , 1995, 148, 191-202.	1.9	20
41	FluShuffle and FluResort: new algorithms to identify reassorted strains of the influenza virus by mass spectrometry. <i>BMC Bioinformatics</i> , 2012, 13, 208.	1.2	20
42	Proteotyping to establish the lineage of type A H1N1 and type B human influenza virus. <i>Journal of Virological Methods</i> , 2011, 171, 117-122.	1.0	19
43	Rapid Typing and Subtyping of Vaccine Strains of the Influenza Virus with High Resolution Mass Spectrometry. <i>European Journal of Mass Spectrometry</i> , 2010, 16, 321-329.	0.5	18
44	Anti-Viral Inhibitor Binding to Influenza Neuraminidase by MALDI Mass Spectrometry. <i>Analytical Chemistry</i> , 2012, 84, 3725-3730.	3.2	18
45	Evolution of Influenza Neuraminidase and the Detection of Antiviral Resistant Strains Using Mass Trees. <i>Analytical Chemistry</i> , 2014, 86, 629-637.	3.2	18
46	Mutational analysis employing a phylogenetic mass tree approach in a study of the evolution of the influenza virus. <i>Molecular Phylogenetics and Evolution</i> , 2017, 112, 209-217.	1.2	18
47	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> , 2018, 121, 132-138.	1.2	18
48	Ancestral and Compensatory Mutations that Promote Antiviral Resistance in Influenza A H1N1 Neuraminidase Revealed by a Phylonumerics Approach. <i>Journal of Molecular Evolution</i> , 2018, 86, 546-553.	0.8	17
49	Fingerprinting a killer: surveillance of the influenza virus by mass spectrometry. <i>Analyst</i> , 2007, 132, 611.	1.7	16
50	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> , 2007, 18, 563-566.	1.2	16
51	Kinetics of Antigen-Antibody Interactions Employing a MALDI Mass Spectrometry Immunoassay. <i>Analytical Chemistry</i> , 2008, 80, 7720-7726.	3.2	16
52	FluTyper-an algorithm for automated typing and subtyping of the influenza virus from high resolution mass spectral data. <i>BMC Bioinformatics</i> , 2010, 11, 266.	1.2	16
53	Proteotyping of the Parainfluenza Virus with High-Resolution Mass Spectrometry. <i>Analytical Chemistry</i> , 2013, 85, 1097-1105.	3.2	16
54	Quantitation of anthocyanins in elderberry fruit extracts and nutraceutical formulations with paper spray ionization mass spectrometry. <i>Journal of Mass Spectrometry</i> , 2018, 53, 58-64.	0.7	15

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55	Homology-modelled structure of the β 2B3-crystallin heterodimer studied by ion mobility and radical probe MS. FEBS Journal, 2011, 278, 4044-4054.	2.2	14
56	Substituent effects on the binding of natural product anthocyanidin inhibitors to influenza neuraminidase with mass spectrometry. Analytica Chimica Acta, 2014, 828, 61-69.	2.6	14
57	Mechanisms of antiviral resistance in influenza neuraminidase revealed by a mass spectrometry based phylonumerics approach. Molecular Phylogenetics and Evolution, 2019, 135, 286-296.	1.2	14
58	On-plate deposition of oxidized proteins to facilitate protein footprinting studies by radical probe mass spectrometry. Rapid Communications in Mass Spectrometry, 2012, 26, 2311-2318.	0.7	13
59	Subtyping of influenza neuraminidase using mass spectrometry. Analyst, The, 2013, 138, 1787.	1.7	13
60	Interaction between alpha and epsilon-crystallin, common to the eye of the Australian platypus, by radical probe mass spectrometry. Journal of Mass Spectrometry, 2006, 41, 1298-1303.	0.7	12
61	SEQUENCE-FREE PHYLOGENETICS WITH MASS SPECTROMETRY. Mass Spectrometry Reviews, 2020, 41, 3-14.	2.8	12
62	Indirect study of non-covalent protein complexes by MALDI mass spectrometry: Origins, advantages, and applications of the "intensity-fading" approach. Mass Spectrometry Reviews, 2016, 35, 559-573.	2.8	11
63	Methionine specific sequence ions formed by the dissociation of protonated peptides at high collision energies. Journal of Mass Spectrometry, 1995, 30, 25-32.	0.7	9
64	Ability of N-acetylcarnosine to protect lens crystallins from oxidation and oxidative damage by radical probe mass spectrometry (RP-MS). Rapid Communications in Mass Spectrometry, 2010, 24, 2900-2908.	0.7	9
65	Origins of the reassortant 2009 pandemic influenza virus through proteotyping with mass spectrometry. Journal of Mass Spectrometry, 2014, 49, 93-102.	0.7	9
66	Darwin's Tree of Life is Numbered. Resolving the Origins of Species by Mass. Evolutionary Biology, 2020, 47, 325-333.	0.5	9
67	Subtyping of hepatitis C virus with high resolution mass spectrometry. Clinical Mass Spectrometry, 2017, 4-5, 19-24.	1.9	8
68	Reimaging the Tree of Life Using a Mass Based Phylonumerics Approach. Evolutionary Biology, 2020, 47, 76-84.	0.5	8
69	Detection of SARS CoV-2 coronavirus omicron variant with mass spectrometry. Analyst, The, 2022, 147, 1181-1190.	1.7	8
70	Detection and structural features of the β 2B3-crystallin heterodimer by radical probe mass spectrometry (RP-MS). Journal of Mass Spectrometry, 2009, 44, 803-812.	0.7	7
71	Stability of the β 2B3 crystallin heterodimer to increased oxidation by radical probe and ion mobility mass spectrometry. Journal of Structural Biology, 2015, 189, 20-27.	1.3	7
72	Mass spectrometry in structural proteomics: The case for radical probe protein footprinting. TrAC - Trends in Analytical Chemistry, 2019, 110, 293-302.	5.8	7

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73	Molecular basis of influenza hemagglutinin inhibition with an entry-blocker peptide by computational docking and mass spectrometry. <i>Antiviral Chemistry and Chemotherapy</i> , 2015, 24, 109-117.	0.3	6
74	Evolution of SARS CoV-2 Coronavirus Surface Protein Investigated with Mass Spectrometry Based Phylogenetics. <i>Analytical Letters</i> , 0, , 1-13.	1.0	6
75	Characterization of the conformations of antigenic peptides of protein lactate dehydrogenase (LDH-C4) by electrospray ionization mass spectrometry. , 1997, 11, 1853-1858.		5
76	Phylogenetic Analysis Using Protein Mass Spectrometry. <i>Methods in Molecular Biology</i> , 2017, 1549, 135-146.	0.4	5
77	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> , 2016, 408, 6637-6648.	1.9	4
78	Protein phylogenetics with mass spectrometry. A comparison of methods. <i>Analytical Methods</i> , 2021, 13, 1442-1454.	1.3	3
79	New Anthocyanins from Black Elderberry of Inhibitory Potential Revealed by Mass Spectrometry. <i>Natural Products Journal</i> , 2016, 6, 94-102.	0.1	2
80	Molecular basis of benzimidazole inhibitors to hepatitis C virus envelope glycoprotein. <i>Chemical Biology and Drug Design</i> , 2018, 92, 1638-1646.	1.5	2
81	A Molecular Immunoproteomics Approach to Assess the Viral Antigenicity of Influenza. <i>Methods in Molecular Biology</i> , 2019, 2024, 353-369.	0.4	1
82	Concentration of Hydroxyl Radicals during Electrical Discharge for Radical Probe Protein Footprinting Mass Spectrometry. <i>Rapid Communications in Mass Spectrometry</i> , 2019, 33, 1420-1422.	0.7	1
83	Evolution of Type B Influenza Virus Using a Mass Spectrometry Based Phylonumerics Approach. <i>Evolutionary Biology</i> , 2021, 48, 259-268.	0.5	1
84	Mass-Based Protein Phylogenetic Approach to Identify Epistasis. <i>Methods in Molecular Biology</i> , 2021, 2212, 1-15.	0.4	1
85	Joseph John Thomson investigates the paranormal. <i>European Journal of Mass Spectrometry</i> , 2021, 27, 146906672110505.	0.5	0
86	Analysis of bacterial biotyping datasets with a mass-based phylonumerics approach. <i>Analytical and Bioanalytical Chemistry</i> , 2022, , 1.	1.9	0