

# John F Kellie

## List of Publications by Year in Descending Order

**Source:** <https://exaly.com/author-pdf/4650590/john-f-kellie-publications-by-year.pdf>

**Version:** 2024-04-28

This document has been generated based on the publications and citations recorded by exaly.com. For the latest version of this publication list, visit the link given above.

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

25  
papers

1,164  
citations

14  
h-index

27  
g-index

27  
ext. papers

1,294  
ext. citations

5.2  
avg, IF

3.76  
L-index

#	Paper	IF	Citations
25	2021 White Paper on Recent Issues in Bioanalysis: Mass Spec of Proteins, Extracellular Vesicles, CRISPR, Chiral Assays, Oligos; Nanomedicines Bioanalysis; ICH M10 Section 7.1; Non-Liquid & Rare Matrices; Regulatory Inputs [ - Recommendations on Endogenous Compounds, Small Molecules, ...	2.1	2
24	Intact Protein Mass Spectrometry for Therapeutic Protein Quantitation, Pharmacokinetics, and Biotransformation in Preclinical and Clinical Studies: An Industry Perspective. <i>Journal of the American Society for Mass Spectrometry</i> , <b>2021</b> , 32, 1886-1900	3.5	9
23	Cloud solutions for GxP laboratories: considerations for data storage. <i>Bioanalysis</i> , <b>2021</b> , 13, 1313-1321	2.1	
22	Antibody Subunit LC-MS Analysis for Pharmacokinetic and Biotransformation Determination from In-Life Studies for Complex Biotherapeutics. <i>Analytical Chemistry</i> , <b>2020</b> , 92, 8268-8277	7.8	8
21	IQ consortium perspective: complementary LBA and LC-MS in protein therapeutics bioanalysis and biotransformation assessment. <i>Bioanalysis</i> , <b>2020</b> , 12, 257-270	2.1	11
20	Native high-resolution mass spectrometry analysis of noncovalent protein complexes up to 450 kDa. <i>Bioanalysis</i> , <b>2020</b> , 12, 1353-1362	2.1	2
19	Intact mAb LC-MS for drug concentration from pre-clinical studies: bioanalytical method performance and in-life samples. <i>Bioanalysis</i> , <b>2020</b> , 12, 1389-1403	2.1	3
18	Intact protein LCMS for pharmacokinetics. <i>International Journal of Pharmacokinetics</i> , <b>2019</b> , 4, IPK05	0.3	
17	2019 White Paper on Recent Issues in Bioanalysis: Chromatographic Assays (Part 1 - Innovation in Small Molecules and Oligonucleotides & Mass Spectrometric Method Development Strategies for Large Molecule Bioanalysis). <i>Bioanalysis</i> , <b>2019</b> , 11, 2029-2048	2.1	16
16	Biotherapeutic Antibody Subunit LC-MS and Peptide Mapping LC-MS Measurements to Study Possible Biotransformation and Critical Quality Attributes In Vivo. <i>Journal of Pharmaceutical Sciences</i> , <b>2019</b> , 108, 1415-1422	3.9	5
15	Drug monitoring by volumetric absorptive microsampling: method development considerations to mitigate hematocrit effects. <i>Bioanalysis</i> , <b>2018</b> , 10, 241-255	2.1	14
14	Review of approaches and examples for monitoring biotransformation in protein and peptide therapeutics by MS. <i>Bioanalysis</i> , <b>2018</b> ,	2.1	14
13	Toward best practices in data processing and analysis for intact biotherapeutics by MS in quantitative bioanalysis. <i>Bioanalysis</i> , <b>2017</b> , 9, 1883-1893	2.1	19
12	Application of high-resolution MS for development of peptide and large-molecule drug candidates. <i>Bioanalysis</i> , <b>2016</b> , 8, 169-77	2.1	18
11	A whole-molecule immunocapture LC-MS approach for the in vivo quantitation of biotherapeutics. <i>Bioanalysis</i> , <b>2016</b> , 8, 2103-14	2.1	32
10	Mechanism of Inactivation of GABA Aminotransferase by (E)- and (Z)-(1S,3S)-3-Amino-4-fluoromethylenyl-1-cyclopentanoic Acid. <i>ACS Chemical Biology</i> , <b>2015</b> , 10, 2087-98	4.9	8
9	Quantitative measurement of intact alpha-synuclein proteoforms from post-mortem control and Parkinson's disease brain tissue by intact protein mass spectrometry. <i>Scientific Reports</i> , <b>2014</b> , 4, 5797	4.9	89

8	Robust analysis of the yeast proteome under 50 kDa by molecular-mass-based fractionation and top-down mass spectrometry. <i>Analytical Chemistry</i> , <b>2012</b> , 84, 209-15	7.8	54
7	Nano-LC FTICR tandem mass spectrometry for top-down proteomics: routine baseline unit mass resolution of whole cell lysate proteins up to 72 kDa. <i>Analytical Chemistry</i> , <b>2012</b> , 84, 2111-7	7.8	35
6	Mapping intact protein isoforms in discovery mode using top-down proteomics. <i>Nature</i> , <b>2011</b> , 480, 254-8	5.4	520
5	Size-sorting combined with improved nanocapillary liquid chromatography-mass spectrometry for identification of intact proteins up to 80 kDa. <i>Analytical Chemistry</i> , <b>2010</b> , 82, 1234-44	7.8	83
4	The emerging process of Top Down mass spectrometry for protein analysis: biomarkers, protein-therapeutics, and achieving high throughput. <i>Molecular BioSystems</i> , <b>2010</b> , 6, 1532-9		79
3	Insights into aging through measurements of the Drosophila proteome as a function of temperature. <i>Mechanisms of Ageing and Development</i> , <b>2010</b> , 131, 584-90	5.6	7
2	Intact mass detection, interpretation, and visualization to automate Top-Down proteomics on a large scale. <i>Proteomics</i> , <b>2010</b> , 10, 3589-97	4.8	44
1	A robust two-dimensional separation for top-down tandem mass spectrometry of the low-mass proteome. <i>Journal of the American Society for Mass Spectrometry</i> , <b>2009</b> , 20, 2183-91	3.5	81