

# James E Bruce

## List of Publications by Year in descending order

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82  
papers

4,505  
citations

109321

35  
h-index

114465

63  
g-index

88  
all docs

88  
docs citations

88  
times ranked

4750  
citing authors

#	ARTICLE	IF	CITATIONS
1	Applications and advancements of FT-ICR-MS for interactome studies. <i>Mass Spectrometry Reviews</i> , 2022, 41, 248-261.	5.4	5
2	In-Cell Labeling and Mass Spectrometry for Systems-Level Structural Biology. <i>Chemical Reviews</i> , 2022, 122, 7647-7689.	47.7	17
3	Quantitative interactome analysis with chemical cross-linking and mass spectrometry. <i>Current Opinion in Chemical Biology</i> , 2022, 66, 102076.	6.1	18
4	Multiplexed Isobaric Quantitative Cross-Linking Reveals Drug-Induced Interactome Changes in Breast Cancer Cells. <i>Analytical Chemistry</i> , 2022, 94, 2713-2722.	6.5	10
5	Quantitative Isotope-Labeled Cross-Linker Proteomics Reveals Developmental Variation in Protein Interactions and Post-Translational Modifications in <i>Diaphorina citri</i> , the Citrus Greening Insect Vector. <i>ACS Agricultural Science and Technology</i> , 2022, 2, 486-500.	2.3	3
6	Upregulation of mitochondrial ATPase inhibitory factor 1 (ATPIF1) mediates increased glycolysis in mouse hearts. <i>Journal of Clinical Investigation</i> , 2022, 132, .	8.2	17
7	Differential proteome and interactome analysis reveal the basis of pleiotropy associated with the histidine methyltransferase Hpm1p. <i>Molecular and Cellular Proteomics</i> , 2022, , 100249.	3.8	1
8	Improved Interpretation of Protein Conformational Differences and Ligand Occupancy in Large-Scale Cross-Link Data. <i>Journal of Proteome Research</i> , 2022, 21, 1475-1484.	3.7	5
9	Leveraging the Entirety of the Protein Data Bank to Enable Improved Structure Prediction Based on Cross-Link Data. <i>Journal of Proteome Research</i> , 2021, 20, 1087-1095.	3.7	6
10	Deciphering the architecture and interactome of hnRNP proteins and enigmRBPs. <i>Molecular Omics</i> , 2021, 17, 503-516.	2.8	1
11	Acetylation of muscle creatine kinase negatively impacts high-energy phosphotransfer in heart failure. <i>JCI Insight</i> , 2021, 6, .	5.0	12
12	Crosslinking mass spectrometry: A link between structural biology and systems biology. <i>Protein Science</i> , 2021, 30, 773-784.	7.6	30
13	Multi-omics Comparison Reveals Landscape of Citrus limon and Citrus sinensis Response to <i>Candidatus Liberibacter asiaticus</i> . <i>PhytoFrontiers</i> , 2021, 1, 76-84.	1.6	8
14	Application of frequency multiple FT-ICR MS signal acquisition for improved proteome research. <i>International Journal of Mass Spectrometry</i> , 2021, 465, 116578.	1.5	5
15	Multiplexed Cross-Linking with Isobaric Quantitative Protein Interaction Reporter Technology. <i>Analytical Chemistry</i> , 2021, 93, 16759-16768.	6.5	9
16	Longitudinal Transcriptomic, Proteomic, and Metabolomic Analyses of <i>Citrus sinensis</i> (L.) Osbeck Graft-Inoculated with <i>Candidatus Liberibacter asiaticus</i> . <i>Journal of Proteome Research</i> , 2020, 19, 719-732.	3.7	31
17	In Vivo Cross-Linking MS Reveals Conservation in OmpA Linkage to Different Classes of $\beta^2$ -Lactamase Enzymes. <i>Journal of the American Society for Mass Spectrometry</i> , 2020, 31, 190-195.	2.8	13
18	Isobaric Quantitative Protein Interaction Reporter Technology for Comparative Interactome Studies. <i>Analytical Chemistry</i> , 2020, 92, 14094-14102.	6.5	23

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19	Mitochondrial protein interaction landscape of SS-31. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 15363-15373.	7.1	88
20	Longitudinal Transcriptomic, Proteomic, and Metabolomic Analysis of <i>Citrus limon</i> Response to Graft Inoculation by <i>Candidatus Liberibacter asiaticus</i> . Journal of Proteome Research, 2020, 19, 2247-2263.	3.7	25
21	Parallel Detection of Fundamental and Sixth Harmonic Signals Using an ICR Cell with Dipole and Sixth Harmonic Detectors. Journal of the American Society for Mass Spectrometry, 2020, 31, 719-726.	2.8	15
22	Increased sensitivity with automated validation of XL-MS cleavable peptide crosslinks. Bioinformatics, 2019, 35, 895-897.	4.1	25
23	Prediction of an Upper Limit for the Fraction of Interprotein Cross-Links in Large-Scale In Vivo Cross-Linking Studies. Journal of Proteome Research, 2019, 18, 3077-3085.	3.7	25
24	Systems structural biology measurements by in vivo cross-linking with mass spectrometry. Nature Protocols, 2019, 14, 2318-2343.	12.0	53
25	Unlocking the Secrets of Mitochondria in the Cardiovascular System. Circulation, 2019, 140, 1205-1216.	1.6	91
26	Hsp90 middle domain phosphorylation initiates a complex conformational program to recruit the ATPase-stimulating cochaperone Aha1. Nature Communications, 2019, 10, 2574.	12.8	39
27	In Vivo Proteome of <i>Pseudomonas aeruginosa</i> in Airways of Cystic Fibrosis Patients. Journal of Proteome Research, 2019, 18, 2601-2612.	3.7	23
28	First Community-Wide, Comparative Cross-Linking Mass Spectrometry Study. Analytical Chemistry, 2019, 91, 6953-6961.	6.5	100
29	Cellular Interactome Dynamics during Paclitaxel Treatment. Cell Reports, 2019, 29, 2371-2383.e5.	6.4	45
30	Chemical cross-linking with mass spectrometry: a tool for systems structural biology. Current Opinion in Chemical Biology, 2019, 48, 8-18.	6.1	116
31	Tools for 3D Interactome Visualization. Journal of Proteome Research, 2019, 18, 753-758.	3.7	26
32	Mango: A General Tool for Collision Induced Dissociation-Cleavable Cross-Linked Peptide Identification. Analytical Chemistry, 2018, 90, 6028-6034.	6.5	39
33	Integrating Cross-Linking Experiments with Ab Initio Protein-Protein Docking. Journal of Molecular Biology, 2018, 430, 1814-1828.	4.2	22
34	Chemical Crosslinking Mass Spectrometry Analysis of Protein Conformations and Supercomplexes in Heart Tissue. Cell Systems, 2018, 6, 136-141.e5.	6.2	118
35	Characterization of Harmonic Signal Acquisition with Parallel Dipole and Multipole Detectors. Journal of the American Society for Mass Spectrometry, 2018, 29, 1394-1402.	2.8	9
36	Parallel detection in a single ICR cell: Spectral averaging and improved S/N without increased acquisition time. International Journal of Mass Spectrometry, 2018, 427, 29-34.	1.5	4

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37	Elusive Conformational Dynamics of PPAR $\beta$ Inactivation Tied Down by Chemical Cross-Linking. Structure, 2018, 26, 1425-1427.	3.3	0
38	Parallel Spectral Acquisition with Orthogonal ICR Cells. Journal of the American Society for Mass Spectrometry, 2017, 28, 515-524.	2.8	8
39	Mitochondrial protein interactome elucidated by chemical cross-linking mass spectrometry. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, 1732-1737.	7.1	165
40	Restoring Cystic Fibrosis Transmembrane Conductance Regulator Function Reduces Airway Bacteria and Inflammation in People with Cystic Fibrosis and Chronic Lung Infections. American Journal of Respiratory and Critical Care Medicine, 2017, 195, 1617-1628.	5.6	317
41	Insights in luteovirid structural biology guided by chemical cross-linking and high resolution mass spectrometry. Virus Research, 2017, 241, 42-52.	2.2	17
42	Ageing and hypoxia cause protein aggregation in mitochondria. Cell Death and Differentiation, 2017, 24, 1730-1738.	11.2	40
43	Large-Scale and Targeted Quantitative Cross-Linking MS Using Isotope-Labeled Protein Interaction Reporter (PIR) Cross-Linkers. Journal of Proteome Research, 2017, 16, 720-727.	3.7	38
44	XLmap: an R package to visualize and score protein structure models based on sites of protein cross-linking. Bioinformatics, 2016, 32, 306-308.	4.1	17
45	XLinkDB 2.0: integrated, large-scale structural analysis of protein crosslinking data. Bioinformatics, 2016, 32, 2716-2718.	4.1	54
46	Spectral Library Searching To Identify Cross-Linked Peptides. Journal of Proteome Research, 2016, 15, 1725-1731.	3.7	12
47	Normalization of NAD <sup>+</sup> Redox Balance as a Therapy for Heart Failure. Circulation, 2016, 134, 883-894.	1.6	250
48	In vivo protein interaction network analysis reveals porin-localized antibiotic inactivation in Acinetobacter baumannii strain AB5075. Nature Communications, 2016, 7, 13414.	12.8	81
49	In Vivo Conformational Dynamics of Hsp90 and Its Interactors. Cell Chemical Biology, 2016, 23, 716-726.	5.2	73
50	Visualization of Host-Poliovirus Interaction Topologies Using Protein Interaction Reporter Technology. Journal of Virology, 2016, 90, 1973-1987.	3.4	38
51	Parallel Spectral Acquisition with an Ion Cyclotron Resonance Cell Array. Analytical Chemistry, 2016, 88, 1162-1168.	6.5	13
52	A General Method for Targeted Quantitative Cross-Linking Mass Spectrometry. PLoS ONE, 2016, 11, e0167547.	2.5	46
53	Analysis of the Campylobacter jejuni Genome by SMRT DNA Sequencing Identifies Restriction-Modification Motifs. PLoS ONE, 2015, 10, e0118533.	2.5	20
54	Quantitative interactome analysis reveals a chemoresistant edgotype. Nature Communications, 2015, 6, 7928.	12.8	77

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55	Dynamic Proteome Response of <i>Pseudomonas aeruginosa</i> to Tobramycin Antibiotic Treatment. <i>Molecular and Cellular Proteomics</i> , 2015, 14, 2126-2137.	3.8	37
56	Probing the Protein Interaction Network of <i>Pseudomonas aeruginosa</i> Cells by Chemical Cross-Linking Mass Spectrometry. <i>Structure</i> , 2015, 23, 762-773.	3.3	71
57	Host-Microbe Protein Interactions during Bacterial Infection. <i>Chemistry and Biology</i> , 2015, 22, 1521-1530.	6.0	103
58	Regional Isolation Drives Bacterial Diversification within Cystic Fibrosis Lungs. <i>Cell Host and Microbe</i> , 2015, 18, 307-319.	11.0	278
59	Evidence for lysine acetylation in the coat protein of a poliovirus. <i>Journal of General Virology</i> , 2014, 95, 2321-2327.	2.9	8
60	Performance evaluation of a dual linear ion trap-Fourier transform ion cyclotron resonance mass spectrometer for proteomics research. <i>Journal of Proteomics</i> , 2013, 88, 109-119.	2.4	25
61	<i>In Vivo</i> Protein Interaction Network Identified with a Novel Real-Time Cross-Linked Peptide Identification Strategy. <i>Journal of Proteome Research</i> , 2013, 12, 1569-1579.	3.7	130
62	XLink-DB: Database and Software Tools for Storing and Visualizing Protein Interaction Topology Data. <i>Journal of Proteome Research</i> , 2013, 12, 1989-1995.	3.7	50
63	Protein Interactions, Post-translational Modifications and Topologies in Human Cells. <i>Molecular and Cellular Proteomics</i> , 2013, 12, 1451-1467.	3.8	102
64	In Vivo Application of Photocleavable Protein Interaction Reporter Technology. <i>Journal of Proteome Research</i> , 2012, 11, 1027-1041.	3.7	29
65	Accurate Peptide Fragment Mass Analysis: Multiplexed Peptide Identification and Quantification. <i>Journal of Proteome Research</i> , 2012, 11, 1621-1632.	3.7	86
66	Cross-linking Measurements of the <i>Potato leafroll virus</i> Reveal Protein Interaction Topologies Required for Virion Stability, Aphid Transmission, and Virus-Plant Interactions. <i>Journal of Proteome Research</i> , 2012, 11, 2968-2981.	3.7	62
67	In vivo protein complex topologies: Sights through a cross-linking lens. <i>Proteomics</i> , 2012, 12, 1565-1575.	2.2	71
68	Quantification of Protein-Protein Interactions with Chemical Cross-Linking and Mass Spectrometry. <i>Journal of Proteome Research</i> , 2011, 10, 1528-1537.	3.7	27
69	Quantitative Proteomic and Interaction Network Analysis of Cisplatin Resistance in HeLa Cells. <i>PLoS ONE</i> , 2011, 6, e19892.	2.5	37
70	Cross-linking Measurements of In Vivo Protein Complex Topologies. <i>Molecular and Cellular Proteomics</i> , 2011, 10, M110.006841.	3.8	81
71	A Photocleavable and Mass Spectrometry Identifiable Cross-Linker for Protein Interaction Studies. <i>Analytical Chemistry</i> , 2010, 82, 3556-3566.	6.5	49
72	Improved Strategies for Rapid Identification of Chemically Cross-Linked Peptides Using Protein Interaction Reporter Technology. <i>Journal of Proteome Research</i> , 2010, 9, 6323-6333.	3.7	32

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73	A new cross-linking strategy: protein interaction reporter (PIR) technology for protein-protein interaction studies. <i>Molecular BioSystems</i> , 2010, 6, 939.	2.9	127
74	Identification of Protein-Protein Interactions and Topologies in Living Cells with Chemical Cross-linking and Mass Spectrometry. <i>Molecular and Cellular Proteomics</i> , 2009, 8, 409-420.	3.8	140
75	In Vivo Identification of the Outer Membrane Protein OmcA-MtrC Interaction Network in <i>Shewanella oneidensis</i> MR-1 Cells Using Novel Hydrophobic Chemical Cross-Linkers. <i>Journal of Proteome Research</i> , 2008, 7, 1712-1720.	3.7	78
76	Profiling the Membrane Proteome of <i>Shewanella oneidensis</i> MR-1 with New Affinity Labeling Probes. <i>Journal of Proteome Research</i> , 2007, 6, 724-734.	3.7	58
77	Informatics Strategies for Large-Scale Novel Cross-Linking Analysis. <i>Journal of Proteome Research</i> , 2007, 6, 3412-3421.	3.7	49
78	Collisionally Activated Dissociation and Electron Capture Dissociation of Several Mass Spectrometry-Identifiable Chemical Cross-Linkers. <i>Analytical Chemistry</i> , 2006, 78, 8183-8193.	6.5	52
79	Mass Spectrometry Identifiable Cross-Linking Strategy for Studying Protein-Protein Interactions. <i>Analytical Chemistry</i> , 2005, 77, 311-318.	6.5	189
80	Identification of intrinsic order and disorder in the DNA repair protein XPA. <i>Protein Science</i> , 2001, 10, 560-571.	7.6	108
81	A novel high-performance Fourier transform ion cyclotron resonance cell for improved biopolymer characterization. <i>Journal of Mass Spectrometry</i> , 2000, 35, 85-94.		27
82	Selected-ion accumulation from an external electrospray ionization source with a fourier-transform ion cyclotron resonance mass spectrometer. <i>Rapid Communications in Mass Spectrometry</i> , 1993, 7, 914-919.	1.5	49