

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	Restoring Cystic Fibrosis Transmembrane Conductance Regulator Function Reduces Airway Bacteria and Inflammation in People with Cystic Fibrosis and Chronic Lung Infections. <i>American Journal of Respiratory and Critical Care Medicine</i> , 2017, 195, 1617-1628.	5.6	317
2	Regional Isolation Drives Bacterial Diversification within Cystic Fibrosis Lungs. <i>Cell Host and Microbe</i> , 2015, 18, 307-319.	11.0	278
3	Normalization of NAD ⁺ Redox Balance as a Therapy for Heart Failure. <i>Circulation</i> , 2016, 134, 883-894.	1.6	250
4	Mass Spectrometry Identifiable Cross-Linking Strategy for Studying Protein-Protein Interactions. <i>Analytical Chemistry</i> , 2005, 77, 311-318.	6.5	189
5	Mitochondrial protein interactome elucidated by chemical cross-linking mass spectrometry. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, 1732-1737.	7.1	165
6	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
7	<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
8	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
9	Chemical Crosslinking Mass Spectrometry Analysis of Protein Conformations and Supercomplexes in Heart Tissue. <i>Cell Systems</i> , 2018, 6, 136-141.e5.	6.2	118
10	Chemical cross-linking with mass spectrometry: a tool for systems structural biology. <i>Current Opinion in Chemical Biology</i> , 2019, 48, 8-18.	6.1	116
11	Identification of intrinsic order and disorder in the DNA repair protein XPA. <i>Protein Science</i> , 2001, 10, 560-571.	7.6	108
12	Host-Microbe Protein Interactions during Bacterial Infection. <i>Chemistry and Biology</i> , 2015, 22, 1521-1530.	6.0	103
13	Protein Interactions, Post-translational Modifications and Topologies in Human Cells. <i>Molecular and Cellular Proteomics</i> , 2013, 12, 1451-1467.	3.8	102
14	First Community-Wide, Comparative Cross-Linking Mass Spectrometry Study. <i>Analytical Chemistry</i> , 2019, 91, 6953-6961.	6.5	100
15	Unlocking the Secrets of Mitochondria in the Cardiovascular System. <i>Circulation</i> , 2019, 140, 1205-1216.	1.6	91
16	Mitochondrial protein interaction landscape of SS-31. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 15363-15373.	7.1	88
17	Accurate Peptide Fragment Mass Analysis: Multiplexed Peptide Identification and Quantification. <i>Journal of Proteome Research</i> , 2012, 11, 1621-1632.	3.7	86
18	Cross-linking Measurements of In Vivo Protein Complex Topologies. <i>Molecular and Cellular Proteomics</i> , 2011, 10, M110.006841.	3.8	81

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19	In vivo protein interaction network analysis reveals porin-localized antibiotic inactivation in <i>Acinetobacter baumannii</i> strain AB5075. <i>Nature Communications</i> , 2016, 7, 13414.	12.8	81
20	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
21	Quantitative interactome analysis reveals a chemoresistant edgotype. <i>Nature Communications</i> , 2015, 6, 7928.	12.8	77
22	In Vivo Conformational Dynamics of Hsp90 and Its Interactors. <i>Cell Chemical Biology</i> , 2016, 23, 716-726.	5.2	73
23	In vivo protein complex topologies: Sights through a cross-linking lens. <i>Proteomics</i> , 2012, 12, 1565-1575.	2.2	71
24	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
25	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
26	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
27	XLinkDB 2.0: integrated, large-scale structural analysis of protein crosslinking data. <i>Bioinformatics</i> , 2016, 32, 2716-2718.	4.1	54
28	Systems structural biology measurements by in vivo cross-linking with mass spectrometry. <i>Nature Protocols</i> , 2019, 14, 2318-2343.	12.0	53
29	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
30	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
31	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
32	Informatics Strategies for Large-Scale Novel Cross-Linking Analysis. <i>Journal of Proteome Research</i> , 2007, 6, 3412-3421.	3.7	49
33	A Photocleavable and Mass Spectrometry Identifiable Cross-Linker for Protein Interaction Studies. <i>Analytical Chemistry</i> , 2010, 82, 3556-3566.	6.5	49
34	A General Method for Targeted Quantitative Cross-Linking Mass Spectrometry. <i>PLoS ONE</i> , 2016, 11, e0167547.	2.5	46
35	Cellular Interactome Dynamics during Paclitaxel Treatment. <i>Cell Reports</i> , 2019, 29, 2371-2383.e5.	6.4	45
36	Ageing and hypoxia cause protein aggregation in mitochondria. <i>Cell Death and Differentiation</i> , 2017, 24, 1730-1738.	11.2	40

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37	Mango: A General Tool for Collision Induced Dissociation-Cleavable Cross-Linked Peptide Identification. <i>Analytical Chemistry</i> , 2018, 90, 6028-6034.	6.5	39
38	Hsp90 middle domain phosphorylation initiates a complex conformational program to recruit the ATPase-stimulating cochaperone Aha1. <i>Nature Communications</i> , 2019, 10, 2574.	12.8	39
39	Visualization of Host-Poliovirus Interaction Topologies Using Protein Interaction Reporter Technology. <i>Journal of Virology</i> , 2016, 90, 1973-1987.	3.4	38
40	Large-Scale and Targeted Quantitative Cross-Linking MS Using Isotope-Labeled Protein Interaction Reporter (PIR) Cross-Linkers. <i>Journal of Proteome Research</i> , 2017, 16, 720-727.	3.7	38
41	Quantitative Proteomic and Interaction Network Analysis of Cisplatin Resistance in HeLa Cells. <i>PLoS ONE</i> , 2011, 6, e19892.	2.5	37
42	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
43	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
44	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
45	Crosslinking mass spectrometry: A link between structural biology and systems biology. <i>Protein Science</i> , 2021, 30, 773-784.	7.6	30
46	In Vivo Application of Photocleavable Protein Interaction Reporter Technology. <i>Journal of Proteome Research</i> , 2012, 11, 1027-1041.	3.7	29
47	A novel high-performance Fourier transform ion cyclotron resonance cell for improved biopolymer characterization. , 2000, 35, 85-94.		27
48	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
49	Tools for 3D Interactome Visualization. <i>Journal of Proteome Research</i> , 2019, 18, 753-758.	3.7	26
50	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
51	Increased sensitivity with automated validation of XL-MS cleavable peptide crosslinks. <i>Bioinformatics</i> , 2019, 35, 895-897.	4.1	25
52	Prediction of an Upper Limit for the Fraction of Interprotein Cross-Links in Large-Scale In Vivo Cross-Linking Studies. <i>Journal of Proteome Research</i> , 2019, 18, 3077-3085.	3.7	25
53	Longitudinal Transcriptomic, Proteomic, and Metabolomic Analysis of <i>Citrus limon</i> Response to Graft Inoculation by <i>Candidatus Liberibacter asiaticus</i> . <i>Journal of Proteome Research</i> , 2020, 19, 2247-2263.	3.7	25
54	In Vivo Proteome of <i>Pseudomonas aeruginosa</i> in Airways of Cystic Fibrosis Patients. <i>Journal of Proteome Research</i> , 2019, 18, 2601-2612.	3.7	23

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55	Isobaric Quantitative Protein Interaction Reporter Technology for Comparative Interactome Studies. <i>Analytical Chemistry</i> , 2020, 92, 14094-14102.	6.5	23
56	Integrating Cross-Linking Experiments with Ab Initio Proteinâ€“Protein Docking. <i>Journal of Molecular Biology</i> , 2018, 430, 1814-1828.	4.2	22
57	Analysis of the <i>Campylobacter jejuni</i> Genome by SMRT DNA Sequencing Identifies Restriction-Modification Motifs. <i>PLoS ONE</i> , 2015, 10, e0118533.	2.5	20
58	Quantitative interactome analysis with chemical cross-linking and mass spectrometry. <i>Current Opinion in Chemical Biology</i> , 2022, 66, 102076.	6.1	18
59	XLmap: an R package to visualize and score protein structure models based on sites of protein cross-linking. <i>Bioinformatics</i> , 2016, 32, 306-308.	4.1	17
60	Insights in luteovirid structural biology guided by chemical cross-linking and high resolution mass spectrometry. <i>Virus Research</i> , 2017, 241, 42-52.	2.2	17
61	In-Cell Labeling and Mass Spectrometry for Systems-Level Structural Biology. <i>Chemical Reviews</i> , 2022, 122, 7647-7689.	47.7	17
62	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
63	Parallel Detection of Fundamental and Sixth Harmonic Signals Using an ICR Cell with Dipole and Sixth Harmonic Detectors. <i>Journal of the American Society for Mass Spectrometry</i> , 2020, 31, 719-726.	2.8	15
64	Parallel Spectral Acquisition with an Ion Cyclotron Resonance Cell Array. <i>Analytical Chemistry</i> , 2016, 88, 1162-1168.	6.5	13
65	In Vivo Cross-Linking MS Reveals Conservation in OmpA Linkage to Different Classes of Î²-Lactamase Enzymes. <i>Journal of the American Society for Mass Spectrometry</i> , 2020, 31, 190-195.	2.8	13
66	Spectral Library Searching To Identify Cross-Linked Peptides. <i>Journal of Proteome Research</i> , 2016, 15, 1725-1731.	3.7	12
67	Acetylation of muscle creatine kinase negatively impacts high-energy phosphotransfer in heart failure. <i>JCI Insight</i> , 2021, 6, .	5.0	12
68	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
69	Characterization of Harmonic Signal Acquisition with Parallel Dipole and Multipole Detectors. <i>Journal of the American Society for Mass Spectrometry</i> , 2018, 29, 1394-1402.	2.8	9
70	Multiplexed Cross-Linking with Isobaric Quantitative Protein Interaction Reporter Technology. <i>Analytical Chemistry</i> , 2021, 93, 16759-16768.	6.5	9
71	Evidence for lysine acetylation in the coat protein of a poliovirus. <i>Journal of General Virology</i> , 2014, 95, 2321-2327.	2.9	8
72	Parallel Spectral Acquisition with Orthogonal ICR Cells. <i>Journal of the American Society for Mass Spectrometry</i> , 2017, 28, 515-524.	2.8	8

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73	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
74	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
75	Applications and advancements of FT-ICR MS for interactome studies. <i>Mass Spectrometry Reviews</i> , 2022, 41, 248-261.	5.4	5
76	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
77	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
78	Parallel detection in a single ICR cell: Spectral averaging and improved S/N without increased acquisition time. <i>International Journal of Mass Spectrometry</i> , 2018, 427, 29-34.	1.5	4
79	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
80	Deciphering the architecture and interactome of hnRNP proteins and enigmRBPs. <i>Molecular Omics</i> , 2021, 17, 503-516.	2.8	1
81	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
82	Elusive Conformational Dynamics of PPAR β Inactivation Tied Down by Chemical Cross-Linking. <i>Structure</i> , 2018, 26, 1425-1427.	3.3	0