

Justin L P Benesch

List of Publications by Year in descending order

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108
papers

9,716
citations

38742

50
h-index

39675

94
g-index

133
all docs

133
docs citations

133
times ranked

8201
citing authors

#	ARTICLE	IF	CITATIONS
1	Ion mobility mass spectrometry analysis of large protein complexes. <i>Nature Protocols</i> , 2008, 3, 1139-1152.	12.0	973
2	Bayesian Deconvolution of Mass and Ion Mobility Spectra: From Binary Interactions to Polydisperse Ensembles. <i>Analytical Chemistry</i> , 2015, 87, 4370-4376.	6.5	663
3	Quantitative mass imaging of single biological macromolecules. <i>Science</i> , 2018, 360, 423-427.	12.6	453
4	Protein Complexes in the Gas Phase: Technology for Structural Genomics and Proteomics. <i>Chemical Reviews</i> , 2007, 107, 3544-3567.	47.7	376
5	Recommendations for reporting ion mobility Mass Spectrometry measurements. <i>Mass Spectrometry Reviews</i> , 2019, 38, 291-320.	5.4	315
6	Crystal structures of truncated alphaA and alphaB crystallins reveal structural mechanisms of polydispersity important for eye lens function. <i>Protein Science</i> , 2010, 19, 1031-1043.	7.6	264
7	Mass spectrometry: come of age for structural and dynamical biology. <i>Current Opinion in Structural Biology</i> , 2011, 21, 641-649.	5.7	240
8	Polydispersity of a mammalian chaperone: Mass spectrometry reveals the population of oligomers in α B-crystallin. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2003, 100, 10611-10616.	7.1	235
9	Quaternary dynamics and plasticity underlie small heat shock protein chaperone function. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 2007-2012.	7.1	231
10	Collision Cross Sections for Structural Proteomics. <i>Structure</i> , 2015, 23, 791-799.	3.3	231
11	Tandem Mass Spectrometry Reveals the Quaternary Organization of Macromolecular Assemblies. <i>Chemistry and Biology</i> , 2006, 13, 597-605.	6.0	206
12	Mass spectrometry of macromolecular assemblies: preservation and dissociation. <i>Current Opinion in Structural Biology</i> , 2006, 16, 245-251.	5.7	199
13	The structured core domain of α B-crystallin can prevent amyloid fibrillation and associated toxicity. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, E1562-70.	7.1	181
14	Subunit Exchange of Multimeric Protein Complexes. <i>Journal of Biological Chemistry</i> , 2002, 277, 38921-38929.	3.4	180
15	Collisional activation of protein complexes: Picking up the pieces. <i>Journal of the American Society for Mass Spectrometry</i> , 2009, 20, 341-348.	2.8	177
16	Coupling Microdroplet Microreactors with Mass Spectrometry: Reading the Contents of Single Droplets Online. <i>Angewandte Chemie - International Edition</i> , 2009, 48, 3665-3668.	13.8	162
17	Thermal Dissociation of Multimeric Protein Complexes by Using Nanoelectrospray Mass Spectrometry. <i>Analytical Chemistry</i> , 2003, 75, 2208-2214.	6.5	161
18	Mimicking phosphorylation of α B-crystallin affects its chaperone activity. <i>Biochemical Journal</i> , 2007, 401, 129-141.	3.7	159

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19	Detergent-free mass spectrometry of membrane protein complexes. <i>Nature Methods</i> , 2013, 10, 1206-1208.	19.0	152
20	Quantifying the heterogeneity of macromolecular machines by mass photometry. <i>Nature Communications</i> , 2020, 11, 1772.	12.8	146
21	Phosphorylation of $\hat{1}\pm$ B-Crystallin Alters Chaperone Function through Loss of Dimeric Substructure. <i>Journal of Biological Chemistry</i> , 2004, 279, 28675-28680.	3.4	144
22	Two decades of studying non-covalent biomolecular assemblies by means of electrospray ionization mass spectrometry. <i>Journal of the Royal Society Interface</i> , 2012, 9, 801-816.	3.4	125
23	An ultra-stable gold-coordinated protein cage displaying reversible assembly. <i>Nature</i> , 2019, 569, 438-442.	27.8	124
24	$\hat{1}\pm$ B-Crystallin Polydispersity Is a Consequence of Unbiased Quaternary Dynamics. <i>Journal of Molecular Biology</i> , 2011, 413, 297-309.	4.2	122
25	Optimal Synthetic Glycosylation of a Therapeutic Antibody. <i>Angewandte Chemie - International Edition</i> , 2016, 55, 2361-2367.	13.8	122
26	The Role of the Detergent Micelle in Preserving the Structure of Membrane Proteins in the Gas Phase. <i>Angewandte Chemie - International Edition</i> , 2015, 54, 4577-4581.	13.8	117
27	The Polydispersity of $\hat{1}\pm$ B-Crystallin Is Rationalized by an Interconverting Polyhedral Architecture. <i>Structure</i> , 2011, 19, 1855-1863.	3.3	116
28	Small Heat-Shock Proteins: Paramedics of the Cell. <i>Topics in Current Chemistry</i> , 2012, 328, 69-98.	4.0	116
29	Phosphomimics Destabilize Hsp27 Oligomeric Assemblies and Enhance Chaperone Activity. <i>Chemistry and Biology</i> , 2015, 22, 186-195.	6.0	110
30	Subunit Exchange of Polydisperse Proteins. <i>Journal of Biological Chemistry</i> , 2005, 280, 14485-14491.	3.4	109
31	Small Heat Shock Protein Activity Is Regulated by Variable Oligomeric Substructure. <i>Journal of Biological Chemistry</i> , 2008, 283, 28513-28517.	3.4	99
32	Local unfolding of the HSP27 monomer regulates chaperone activity. <i>Nature Communications</i> , 2019, 10, 1068.	12.8	93
33	Dodecameric Structure of the Small Heat Shock Protein Acr1 from <i>Mycobacterium tuberculosis</i> . <i>Journal of Biological Chemistry</i> , 2005, 280, 33419-33425.	3.4	91
34	Quaternary Dynamics of $\hat{1}\pm$ B-Crystallin as a Direct Consequence of Localised Tertiary Fluctuations in the C-Terminus. <i>Journal of Molecular Biology</i> , 2011, 413, 310-320.	4.2	89
35	Origin of complexity in haemoglobin evolution. <i>Nature</i> , 2020, 581, 480-485.	27.8	89
36	Identifying key membrane protein lipid interactions using mass spectrometry. <i>Nature Protocols</i> , 2018, 13, 1106-1120.	12.0	85

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37	Dynamical structure of α -crystallin. <i>Progress in Biophysics and Molecular Biology</i> , 2014, 115, 11-20.	2.9	74
38	GlycoMob: an ion mobility-mass spectrometry collision cross section database for glycomics. <i>Glycoconjugate Journal</i> , 2016, 33, 399-404.	2.7	73
39	Real-Time Monitoring of Protein Complexes Reveals their Quaternary Organization and Dynamics. <i>Chemistry and Biology</i> , 2008, 15, 246-253.	6.0	72
40	Quantifying Protein-Protein Interactions by Molecular Counting with Mass Photometry. <i>Angewandte Chemie - International Edition</i> , 2020, 59, 10774-10779.	13.8	72
41	Dissecting Heterogeneous Molecular Chaperone Complexes Using a Mass Spectrum Deconvolution Approach. <i>Chemistry and Biology</i> , 2012, 19, 599-607.	6.0	70
42	C-terminal interactions mediate the quaternary dynamics of α -crystallin. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2013, 368, 20110405.	4.0	70
43	Integrating mass spectrometry with MD simulations reveals the role of lipids in Na ⁺ /H ⁺ antiporters. <i>Nature Communications</i> , 2017, 8, 13993.	12.8	68
44	Hsp70 Oligomerization Is Mediated by an Interaction between the Interdomain Linker and the Substrate-Binding Domain. <i>PLoS ONE</i> , 2013, 8, e67961.	2.5	66
45	Separating and visualising protein assemblies by means of preparative mass spectrometry and microscopy. <i>Journal of Structural Biology</i> , 2010, 172, 161-168.	2.8	64
46	Probing Dynamic Conformations of the High-Molecular-Weight α -Crystallin Heat Shock Protein Ensemble by NMR Spectroscopy. <i>Journal of the American Chemical Society</i> , 2012, 134, 15343-15350.	13.7	63
47	Characterisation of <i>Shigella</i> Spa33 and <i>Thermotoga</i> FliM/N reveals a new model for C-ring assembly in T3SS. <i>Molecular Microbiology</i> , 2016, 99, 749-766.	2.5	62
48	Defining the Structural Basis of Human Plasminogen Binding by Streptococcal Surface Enolase. <i>Journal of Biological Chemistry</i> , 2009, 284, 17129-17137.	3.4	61
49	Mass-Selective Soft-Landing of Protein Assemblies with Controlled Landing Energies. <i>Analytical Chemistry</i> , 2014, 86, 8321-8328.	6.5	61
50	HspB1 phosphorylation regulates its intramolecular dynamics and mechanosensitive molecular chaperone interaction with filamin C. <i>Science Advances</i> , 2019, 5, eaav8421.	10.3	52
51	Structural principles that enable oligomeric small heat-shock protein paralogs to evolve distinct functions. <i>Science</i> , 2018, 359, 930-935.	12.6	51
52	Quadrupole-Time-of-Flight Mass Spectrometer Modified for Higher-Energy Dissociation Reduces Protein Assemblies to Peptide Fragments. <i>Analytical Chemistry</i> , 2009, 81, 1270-1274.	6.5	50
53	The Small Heat-Shock Proteins HSPB2 and HSPB3 Form Well-defined Heterooligomers in a Unique 3 to 1 Subunit Ratio. <i>Journal of Molecular Biology</i> , 2009, 393, 1022-1032.	4.2	50
54	The Quaternary Organization and Dynamics of the Molecular Chaperone HSP26 Are Thermally Regulated. <i>Chemistry and Biology</i> , 2010, 17, 1008-1017.	6.0	45

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55	Mass spectrometry beyond the native state. <i>Current Opinion in Chemical Biology</i> , 2018, 42, 130-137.	6.1	43
56	Real-Time Intrinsic Fluorescence Visualization and Sizing of Proteins and Protein Complexes in Microfluidic Devices. <i>Analytical Chemistry</i> , 2018, 90, 3849-3855.	6.5	42
57	It takes a dimer to tango: Oligomeric small heat shock proteins dissociate to capture substrate. <i>Journal of Biological Chemistry</i> , 2018, 293, 19511-19521.	3.4	41
58	The Tetrameric Plant Lectin BanLec Neutralizes HIV through Bidentate Binding to Specific Viral Glycans. <i>Structure</i> , 2017, 25, 773-782.e5.	3.3	39
59	Lipid binding attenuates channel closure of the outer membrane protein OmpF. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, 6691-6696.	7.1	39
60	Terminal Regions Confer Plasticity to the Tetrameric Assembly of Human HspB2 and HspB3. <i>Journal of Molecular Biology</i> , 2018, 430, 3297-3310.	4.2	37
61	Studying the active-site loop movement of the SÃo Paolo metallo-Î²-lactamase-1. <i>Chemical Science</i> , 2015, 6, 956-963.	7.4	36
62	Accommodating Protein Dynamics in the Modeling of Chemical Crosslinks. <i>Structure</i> , 2017, 25, 1751-1757.e5.	3.3	36
63	Dehydrated but unharmed. <i>Nature</i> , 2009, 462, 576-577.	27.8	35
64	Discovery of a Highly Selective Cell-Active Inhibitor of the Histone Lysine Demethylases KDM2/7. <i>Angewandte Chemie - International Edition</i> , 2017, 56, 15555-15559.	13.8	32
65	All three chaperonin genes in the archaeon <i>Haloferax volcanii</i> are individually dispensable. <i>Molecular Microbiology</i> , 2006, 61, 1583-1597.	2.5	31
66	The Jumonji-C oxygenase JMJD7 catalyzes (3S)-lysyl hydroxylation of TRAFAC GTPases. <i>Nature Chemical Biology</i> , 2018, 14, 688-695.	8.0	31
67	Native Mass Spectrometry: Towards High-Throughput Structural Proteomics. <i>Methods in Molecular Biology</i> , 2015, 1261, 349-371.	0.9	31
68	Low Charge and Reduced Mobility of Membrane Protein Complexes Has Implications for Calibration of Collision Cross Section Measurements. <i>Analytical Chemistry</i> , 2016, 88, 5879-5884.	6.5	30
69	Small heat-shock proteins and their role in mechanical stress. <i>Cell Stress and Chaperones</i> , 2020, 25, 601-613.	2.9	30
70	Controlling Protein Orientation in Vacuum Using Electric Fields. <i>Journal of Physical Chemistry Letters</i> , 2017, 8, 4540-4544.	4.6	29
71	Weighing-up protein dynamics: the combination of native mass spectrometry and molecular dynamics simulations. <i>Current Opinion in Structural Biology</i> , 2019, 54, 50-58.	5.7	29
72	A Monte Carlo approach for assessing the specificity of protein oligomers observed in nano-electrospray mass spectra. <i>International Journal of Mass Spectrometry</i> , 2009, 283, 169-177.	1.5	28

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73	Infrared Laser Activation of Soluble and Membrane Protein Assemblies in the Gas Phase. <i>Analytical Chemistry</i> , 2016, 88, 7060-7067.	6.5	28
74	Structural and functional consequences of age-related isomerization in α -crystallins. <i>Journal of Biological Chemistry</i> , 2019, 294, 7546-7555.	3.4	27
75	Proline isomerization in the C-terminal region of HSP27. <i>Cell Stress and Chaperones</i> , 2017, 22, 639-651.	2.9	24
76	Computational Strategies and Challenges for Using Native Ion Mobility Mass Spectrometry in Biophysics and Structural Biology. <i>Analytical Chemistry</i> , 2020, 92, 10872-10880.	6.5	24
77	Negative Ions Enhance Survival of Membrane Protein Complexes. <i>Journal of the American Society for Mass Spectrometry</i> , 2016, 27, 1099-1104.	2.8	21
78	Conditional Disorder in Small Heat-shock Proteins. <i>Journal of Molecular Biology</i> , 2020, 432, 3033-3049.	4.2	21
79	Hyperphosphorylated tau self-assembles into amorphous aggregates eliciting TLR4-dependent responses. <i>Nature Communications</i> , 2022, 13, 2692.	12.8	21
80	Software Requirements for the Analysis and Interpretation of Native Ion Mobility Mass Spectrometry Data. <i>Analytical Chemistry</i> , 2020, 92, 10881-10890.	6.5	17
81	Combining tandem mass spectrometry with ion mobility separation to determine the architecture of polydisperse proteins. <i>International Journal of Mass Spectrometry</i> , 2015, 377, 663-671.	1.5	16
82	The Human 343delT HSPB5 Chaperone Associated with Early-onset Skeletal Myopathy Causes Defects in Protein Solubility. <i>Journal of Biological Chemistry</i> , 2016, 291, 14939-14953.	3.4	16
83	EM ² IM: software for relating ion mobility mass spectrometry and electron microscopy data. <i>Analyst</i> , 2016, 141, 70-75.	3.5	16
84	Evaluating the Effect of Phosphorylation on the Structure and Dynamics of Hsp27 Dimers by Means of Ion Mobility Mass Spectrometry. <i>Analytical Chemistry</i> , 2017, 89, 13275-13282.	6.5	16
85	Probing the Dissociation of Protein Complexes by Means of Gas-Phase H/D Exchange Mass Spectrometry. <i>Journal of the American Society for Mass Spectrometry</i> , 2019, 30, 45-57.	2.8	16
86	The binding of the small heat-shock protein α -B-crystallin to fibrils of α -synuclein is driven by entropic forces. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	7.1	15
87	A weakened interface in the P182L variant of HSP27 associated with severe Charcot-Marie-Tooth neuropathy causes aberrant binding to interacting proteins. <i>EMBO Journal</i> , 2021, 40, e103811.	7.8	14
88	Complementing machine learning-based structure predictions with native mass spectrometry. <i>Protein Science</i> , 2022, 31, .	7.6	13
89	Single-molecule fluorescence-based approach reveals novel mechanistic insights into human small heat shock protein chaperone function. <i>Journal of Biological Chemistry</i> , 2021, 296, 100161.	3.4	12
90	Charge Engineering Reveals the Roles of Ionizable Side Chains in Electrospray Ionization Mass Spectrometry. <i>Jacs Au</i> , 2021, 1, 2385-2393.	7.9	12

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91	Ejection of structural zinc leads to inhibition of Î³-butyrobetaine hydroxylase. <i>Bioorganic and Medicinal Chemistry Letters</i> , 2014, 24, 4954-4957.	2.2	11
92	Protein Aggregate-Ligand Binding Assays Based on Microfluidic Diffusional Separation. <i>ChemBioChem</i> , 2016, 17, 1920-1924.	2.6	11
93	Quantifying Protein-Protein Interactions by Molecular Counting with Mass Photometry. <i>Angewandte Chemie</i> , 2020, 132, 10866-10871.	2.0	11
94	Adenosine Monophosphate Binding Stabilizes the KTN Domain of the <i>Shewanella denitrificans</i> Kef Potassium Efflux System. <i>Biochemistry</i> , 2017, 56, 4219-4234.	2.5	9
95	Engineering of a Polydisperse Small Heat-Shock Protein Reveals Conserved Motifs of Oligomer Plasticity. <i>Structure</i> , 2018, 26, 1116-1126.e4.	3.3	9
96	Trajectory Taken by Dimeric Cu/Zn Superoxide Dismutase through the Protein Unfolding and Dissociation Landscape Is Modulated by Salt Bridge Formation. <i>Analytical Chemistry</i> , 2020, 92, 1702-1711.	6.5	9
97	Ion mobility-mass spectrometry shows stepwise protein unfolding under alkaline conditions. <i>Chemical Communications</i> , 2021, 57, 1450-1453.	4.1	8
98	The influence of the N-terminal region proximal to the core domain on the assembly and chaperone activity of Î±B-crystallin. <i>Cell Stress and Chaperones</i> , 2018, 23, 827-836.	2.9	7
99	Analysis of Î±B-crystallin polydispersity in solution through native microfluidic electrophoresis. <i>Analyst</i> , 2019, 144, 4413-4424.	3.5	6
100	Shape-Morphing of an Artificial Protein Cage with Unusual Geometry Induced by a Single Amino Acid Change. <i>ACS Nanoscience Au</i> , 2022, 2, 404-413.	4.8	6
101	Dynamics-Function Relationships of the Small Heat-Shock Proteins. <i>Heat Shock Proteins</i> , 2015, , 87-100.	0.2	5
102	Structural and functional aspects of the interaction partners of the small heat-shock protein in <i>Synechocystis</i> . <i>Cell Stress and Chaperones</i> , 2018, 23, 723-732.	2.9	5
103	Monitoring protein-metal binding by 19F NMR - a case study with the New Delhi metallo-Î²-lactamase 1. <i>RSC Medicinal Chemistry</i> , 2020, 11, 387-391.	3.9	2
104	Biobox: a toolbox for biomolecular modelling. <i>Bioinformatics</i> , 2022, 38, 1149-1151.	4.1	2
105	Aggregation in the spotlight. <i>ELife</i> , 2021, 10, .	6.0	1
106	Discovery of a Highly Selective Cell-Active Inhibitor of the Histone Lysine Demethylases KDM2/7. <i>Angewandte Chemie</i> , 2017, 129, 15761-15765.	2.0	0
107	Frontispiz: Quantifying Protein-Protein Interactions by Molecular Counting with Mass Photometry. <i>Angewandte Chemie</i> , 2020, 132, .	2.0	0
108	Frontispiece: Quantifying Protein-Protein Interactions by Molecular Counting with Mass Photometry. <i>Angewandte Chemie - International Edition</i> , 2020, 59, .	13.8	0