

Justin L P Benesch

List of Publications by Year in Descending Order

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Version: 2024-04-19

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

107
papers

7,441
citations

46
h-index

85
g-index

133
ext. papers

8,710
ext. citations

9.8
avg, IF

6.06
L-index

#	Paper	IF	Citations
107	Hyperphosphorylated tau self-assembles into amorphous aggregates eliciting TLR4-dependent responses.. <i>Nature Communications</i> , 2022 , 13, 2692	17.4	1
106	Charge Engineering Reveals the Roles of Ionizable Side Chains in Electrospray Ionization Mass Spectrometry.. <i>Jacs Au</i> , 2021 , 1, 2385-2393		2
105	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	13	3
104	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	5.4	3
103	The binding of the small heat-shock protein β -crystallin to fibrils of β -synuclein is driven by entropic forces. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021 , 118,	11.5	2
102	Ion mobility-mass spectrometry shows stepwise protein unfolding under alkaline conditions. <i>Chemical Communications</i> , 2021 , 57, 1450-1453	5.8	1
101	Quantifying Protein-Protein Interactions by Molecular Counting with Mass Photometry. <i>Angewandte Chemie</i> , 2020 , 132, 10866-10871	3.6	4
100	Monitoring protein-metal binding by F NMR - a case study with the New Delhi metallo- β -lactamase 1. <i>RSC Medicinal Chemistry</i> , 2020 , 11, 387-391	3.5	2
99	Origin of complexity in haemoglobin evolution. <i>Nature</i> , 2020 , 581, 480-485	50.4	30
98	Quantifying Protein-Protein Interactions by Molecular Counting with Mass Photometry. <i>Angewandte Chemie - International Edition</i> , 2020 , 59, 10774-10779	16.4	37
97	Conditional Disorder in Small Heat-shock Proteins. <i>Journal of Molecular Biology</i> , 2020 , 432, 3033-3049	6.5	12
96	Small heat-shock proteins and their role in mechanical stress. <i>Cell Stress and Chaperones</i> , 2020 , 25, 601-613		11
95	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	7.8	6
94	Software Requirements for the Analysis and Interpretation of Native Ion Mobility Mass Spectrometry Data. <i>Analytical Chemistry</i> , 2020 , 92, 10881-10890	7.8	8
93	Computational Strategies and Challenges for Using Native Ion Mobility Mass Spectrometry in Biophysics and Structural Biology. <i>Analytical Chemistry</i> , 2020 , 92, 10872-10880	7.8	14
92	Quantifying the heterogeneity of macromolecular machines by mass photometry. <i>Nature Communications</i> , 2020 , 11, 1772	17.4	52
91	Recommendations for reporting ion mobility Mass Spectrometry measurements. <i>Mass Spectrometry Reviews</i> , 2019 , 38, 291-320	11	191

90	Analysis of β -crystallin polydispersity in solution through native microfluidic electrophoresis. <i>Analyst, The</i> , 2019 , 144, 4413-4424	5	3
89	HspB1 phosphorylation regulates its intramolecular dynamics and mechanosensitive molecular chaperone interaction with filamin C. <i>Science Advances</i> , 2019 , 5, eaav8421	14.3	31
88	An ultra-stable gold-coordinated protein cage displaying reversible assembly. <i>Nature</i> , 2019 , 569, 438-442	30.4	72
87	Local unfolding of the HSP27 monomer regulates chaperone activity. <i>Nature Communications</i> , 2019 , 10, 1068	17.4	60
86	Structural and functional consequences of age-related isomerization in β -crystallins. <i>Journal of Biological Chemistry</i> , 2019 , 294, 7546-7555	5.4	21
85	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	8.1	20
84	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	3.5	11
83	Structural principles that enable oligomeric small heat-shock protein paralogs to evolve distinct functions. <i>Science</i> , 2018 , 359, 930-935	33.3	29
82	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	4	5
81	The influence of the N-terminal region proximal to the core domain on the assembly and chaperone activity of β -crystallin. <i>Cell Stress and Chaperones</i> , 2018 , 23, 827-836	4	5
80	Identifying key membrane protein lipid interactions using mass spectrometry. <i>Nature Protocols</i> , 2018 , 13, 1106-1120	18.8	55
79	Real-Time Intrinsic Fluorescence Visualization and Sizing of Proteins and Protein Complexes in Microfluidic Devices. <i>Analytical Chemistry</i> , 2018 , 90, 3849-3855	7.8	29
78	Mass spectrometry beyond the native state. <i>Current Opinion in Chemical Biology</i> , 2018 , 42, 130-137	9.7	31
77	Quantitative mass imaging of single biological macromolecules. <i>Science</i> , 2018 , 360, 423-427	33.3	209
76	Engineering of a Polydisperse Small Heat-Shock Protein Reveals Conserved Motifs of Oligomer Plasticity. <i>Structure</i> , 2018 , 26, 1116-1126.e4	5.2	6
75	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	11.5	21
74	The Jumonji-C oxygenase JMJD7 catalyzes (3S)-lysyl hydroxylation of TRAFAC GTPases. <i>Nature Chemical Biology</i> , 2018 , 14, 688-695	11.7	18
73	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	5.4	23

72	Terminal Regions Confer Plasticity to the Tetrameric Assembly of Human HspB2 and HspB3. <i>Journal of Molecular Biology</i> , 2018 , 430, 3297-3310	6.5	24
71	Integrating mass spectrometry with MD simulations reveals the role of lipids in Na/H antiporters. <i>Nature Communications</i> , 2017 , 8, 13993	17.4	50
70	The Tetrameric Plant Lectin BanLec Neutralizes HIV through Bidentate Binding to Specific Viral Glycans. <i>Structure</i> , 2017 , 25, 773-782.e5	5.2	28
69	Proline isomerization in the C-terminal region of HSP27. <i>Cell Stress and Chaperones</i> , 2017 , 22, 639-651	4	19
68	Accommodating Protein Dynamics in the Modeling of Chemical Crosslinks. <i>Structure</i> , 2017 , 25, 1751-1757.e5	3.5	30
67	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	16.4	19
66	Controlling Protein Orientation in Vacuum Using Electric Fields. <i>Journal of Physical Chemistry Letters</i> , 2017 , 8, 4540-4544	6.4	17
65	Discovery of a Highly Selective Cell-Active Inhibitor of the Histone Lysine Demethylases KDM2/7. <i>Angewandte Chemie</i> , 2017 , 129, 15761-15765	3.6	
64	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	7.8	12
63	Adenosine Monophosphate Binding Stabilizes the KTN Domain of the <i>Shewanella denitrificans</i> Kef Potassium Efflux System. <i>Biochemistry</i> , 2017 , 56, 4219-4234	3.2	4
62	GlycoMob: an ion mobility-mass spectrometry collision cross section database for glycomics. <i>Glycoconjugate Journal</i> , 2016 , 33, 399-404	3	59
61	Protein Aggregate-Ligand Binding Assays Based on Microfluidic Diffusional Separation. <i>ChemBioChem</i> , 2016 , 17, 1920-1924	3.8	10
60	Infrared Laser Activation of Soluble and Membrane Protein Assemblies in the Gas Phase. <i>Analytical Chemistry</i> , 2016 , 88, 7060-7	7.8	22
59	The Human 343delT HSPB5 Chaperone Associated with Early-onset Skeletal Myopathy Causes Defects in Protein Solubility. <i>Journal of Biological Chemistry</i> , 2016 , 291, 14939-53	5.4	15
58	EM?IM: software for relating ion mobility mass spectrometry and electron microscopy data. <i>Analyst, The</i> , 2016 , 141, 70-5	5	13
57	Optimal Synthetic Glycosylation of a Therapeutic Antibody. <i>Angewandte Chemie - International Edition</i> , 2016 , 55, 2361-7	16.4	92
56	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, 749-66	4.1	48
55	Negative Ions Enhance Survival of Membrane Protein Complexes. <i>Journal of the American Society for Mass Spectrometry</i> , 2016 , 27, 1099-104	3.5	15

54	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	7.8	28
53	Phosphomimics destabilize Hsp27 oligomeric assemblies and enhance chaperone activity. <i>Chemistry and Biology</i> , 2015 , 22, 186-95		82
52	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	1.9	13
51	Dynamics-Function Relationships of the Small Heat-Shock Proteins. <i>Heat Shock Proteins</i> , 2015 , 87-100	0.2	4
50	Collision cross sections for structural proteomics. <i>Structure</i> , 2015 , 23, 791-9	5.2	169
49	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, 4577-81	16.4	97
48	Bayesian deconvolution of mass and ion mobility spectra: from binary interactions to polydisperse ensembles. <i>Analytical Chemistry</i> , 2015 , 87, 4370-6	7.8	373
47	Studying the active-site loop movement of the S _B Paolo metallo-β-lactamase-1 Electronic supplementary information (ESI) available: Procedures for protein expression and purification, F-labelling, crystallisation, data collection, and structure determination, table of crystallographic data, table of crystallographic parameters and refinement statistics, figures showing binding mode	9.4	34
46	The Role of the Detergent Micelle in Preserving the Structure of Membrane Proteins in the Gas Phase. <i>Angewandte Chemie</i> , 2015 , 127, 4660-4664 <i>Chemistry</i> , 2015 , 6, 956-963	3.6	5
45	Native mass spectrometry: towards high-throughput structural proteomics. <i>Methods in Molecular Biology</i> , 2015 , 1261, 349-71	1.4	22
44	Dynamical structure of B-crystallin. <i>Progress in Biophysics and Molecular Biology</i> , 2014 , 115, 11-20	4.7	65
43	Ejection of structural zinc leads to inhibition of Ebutyrobetaine hydroxylase. <i>Bioorganic and Medicinal Chemistry Letters</i> , 2014 , 24, 4954-7	2.9	10
42	Mass-selective soft-landing of protein assemblies with controlled landing energies. <i>Analytical Chemistry</i> , 2014 , 86, 8321-8	7.8	42
41	The structured core domain of 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	11.5	154
40	Detergent-free mass spectrometry of membrane protein complexes. <i>Nature Methods</i> , 2013 , 10, 1206-8	21.6	131
39	C-terminal interactions mediate the quaternary dynamics of B-crystallin. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2013 , 368, 20110405	5.8	63
38	Small heat-shock proteins: paramedics of the cell. <i>Topics in Current Chemistry</i> , 2013 , 328, 69-98		95
37	Hsp70 oligomerization is mediated by an interaction between the interdomain linker and the substrate-binding domain. <i>PLoS ONE</i> , 2013 , 8, e67961	3.7	60

36	Probing dynamic conformations of the high-molecular-weight B-crystallin heat shock protein ensemble by NMR spectroscopy. <i>Journal of the American Chemical Society</i> , 2012 , 134, 15343-50	16.4	56
35	Dissecting heterogeneous molecular chaperone complexes using a mass spectrum deconvolution approach. <i>Chemistry and Biology</i> , 2012 , 19, 599-607		61
34	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, 801-16	4.1	113
33	B-crystallin polydispersity is a consequence of unbiased quaternary dynamics. <i>Journal of Molecular Biology</i> , 2011 , 413, 297-309	6.5	96
32	Quaternary dynamics of B-crystallin as a direct consequence of localised tertiary fluctuations in the C-terminus. <i>Journal of Molecular Biology</i> , 2011 , 413, 310-20	6.5	76
31	The polydispersity of B-crystallin is rationalized by an interconverting polyhedral architecture. <i>Structure</i> , 2011 , 19, 1855-63	5.2	95
30	Mass spectrometry: come of age for structural and dynamical biology. <i>Current Opinion in Structural Biology</i> , 2011 , 21, 641-9	8.1	214
29	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, 2007-12	11.5	205
28	Separating and visualising protein assemblies by means of preparative mass spectrometry and microscopy. <i>Journal of Structural Biology</i> , 2010 , 172, 161-8	3.4	54
27	The quaternary organization and dynamics of the molecular chaperone HSP26 are thermally regulated. <i>Chemistry and Biology</i> , 2010 , 17, 1008-17		41
26	Crystal structures of truncated alphaA and alphaB crystallins reveal structural mechanisms of polydispersity important for eye lens function. <i>Protein Science</i> , 2010 , 19, 1031-43	6.3	244
25	Defining the structural basis of human plasminogen binding by streptococcal surface enolase. <i>Journal of Biological Chemistry</i> , 2009 , 284, 17129-17137	5.4	52
24	Coupling microdroplet microreactors with mass spectrometry: reading the contents of single droplets online. <i>Angewandte Chemie - International Edition</i> , 2009 , 48, 3665-8	16.4	146
23	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	1.9	25
22	Collisional activation of protein complexes: picking up the pieces. <i>Journal of the American Society for Mass Spectrometry</i> , 2009 , 20, 341-8	3.5	156
21	Quadrupole-time-of-flight mass spectrometer modified for higher-energy dissociation reduces protein assemblies to peptide fragments. <i>Analytical Chemistry</i> , 2009 , 81, 1270-4	7.8	46
20	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, 1022-32	6.5	40
19	Ion mobility-mass spectrometry analysis of large protein complexes. <i>Nature Protocols</i> , 2008 , 3, 1139-52	18.8	843

18	Small heat shock protein activity is regulated by variable oligomeric substructure. <i>Journal of Biological Chemistry</i> , 2008 , 283, 28513-7	5.4	85
17	Real-time monitoring of protein complexes reveals their quaternary organization and dynamics. <i>Chemistry and Biology</i> , 2008 , 15, 246-53		64
16	Mimicking phosphorylation of alphaB-crystallin affects its chaperone activity. <i>Biochemical Journal</i> , 2007 , 401, 129-41	3.8	147
15	Protein complexes in the gas phase: technology for structural genomics and proteomics. <i>Chemical Reviews</i> , 2007 , 107, 3544-67	68.1	342
14	Mass spectrometry of macromolecular assemblies: preservation and dissociation. <i>Current Opinion in Structural Biology</i> , 2006 , 16, 245-51	8.1	190
13	All three chaperonin genes in the archaeon <i>Haloferax volcanii</i> are individually dispensable. <i>Molecular Microbiology</i> , 2006 , 61, 1583-97	4.1	25
12	Tandem mass spectrometry reveals the quaternary organization of macromolecular assemblies. <i>Chemistry and Biology</i> , 2006 , 13, 597-605		191
11	Subunit exchange of polydisperse proteins: mass spectrometry reveals consequences of alphaA-crystallin truncation. <i>Journal of Biological Chemistry</i> , 2005 , 280, 14485-91	5.4	94
10	Dodecameric structure of the small heat shock protein Acr1 from <i>Mycobacterium tuberculosis</i> . <i>Journal of Biological Chemistry</i> , 2005 , 280, 33419-25	5.4	82
9	Phosphorylation of alphaB-crystallin alters chaperone function through loss of dimeric substructure. <i>Journal of Biological Chemistry</i> , 2004 , 279, 28675-80	5.4	128
8	Polydispersity of a mammalian chaperone: mass spectrometry reveals the population of oligomers in alphaB-crystallin. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2003 , 100, 10611-6	11.5	206
7	Thermal dissociation of multimeric protein complexes by using nanoelectrospray mass spectrometry. <i>Analytical Chemistry</i> , 2003 , 75, 2208-14	7.8	135
6	Subunit exchange of multimeric protein complexes. Real-time monitoring of subunit exchange between small heat shock proteins by using electrospray mass spectrometry. <i>Journal of Biological Chemistry</i> , 2002 , 277, 38921-9	5.4	161
5	Mass-selective and ice-free cryo-EM protein sample preparation via native electrospray ion-beam deposition		2
4	Single-molecule fluorescence-based approach reveals novel mechanistic insights into small heat shock protein chaperone function		1
3	B-crystallin inhibits amyloidogenesis by disassembling aggregation nuclei		1
2	Dysregulated interactions triggered by a neuropathy-causing mutation in the IPV motif of HSP27		2
1	Quantifying the heterogeneity of macromolecular machines by mass photometry		2

