

Sebastian Hiller

List of Publications by Year in descending order

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117
papers

7,740
citations

87888

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56724

83
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128
all docs

128
docs citations

128
times ranked

9128
citing authors

#	ARTICLE	IF	CITATIONS
1	Acquisition of enzymatic progress curves in real time by quenching-free ion exchange chromatography. <i>Analytical Biochemistry</i> , 2022, 639, 114523.	2.4	3
2	Pseudocontact Shifts in Biomolecular NMR Spectroscopy. <i>Chemical Reviews</i> , 2022, 122, 9422-9467.	47.7	29
3	Monitoring the antibiotic darobactin modulating the β -barrel assembly factor BamA. <i>Structure</i> , 2022, 30, 350-359.e3.	3.3	24
4	Motional clustering in supra- β -barrel assembly factor BamA. <i>Structure</i> , 2022, 30, 350-359.e3.	2.1	4
5	Gasdermin-A3 pore formation propagates along variable pathways. <i>Nature Communications</i> , 2022, 13, 2609.	12.8	25
6	Reciprocal growth control by competitive binding of nucleotide second messengers to a metabolic switch in <i>Caulobacter crescentus</i> . <i>Nature Microbiology</i> , 2021, 6, 59-72.	13.3	23
7	Molecular chaperones and their denaturing effect on client proteins. <i>Journal of Biomolecular NMR</i> , 2021, 75, 1-8.	2.8	8
8	Inositol pyrophosphates promote the interaction of SPX domains with the coiled-coil motif of PHR transcription factors to regulate plant phosphate homeostasis. <i>Nature Communications</i> , 2021, 12, 384.	12.8	105
9	Insights into SusCD-mediated glycan import by a prominent gut symbiont. <i>Nature Communications</i> , 2021, 12, 44.	12.8	42
10	Active membrane rupture spurs a range of cell deaths. <i>Nature</i> , 2021, 591, 36-37.	27.8	11
11	The antibiotic darobactin mimics a β -strand to inhibit outer membrane insertase. <i>Nature</i> , 2021, 593, 125-129.	27.8	112
12	Redefining Molecular Chaperones as Chaotropes. <i>Frontiers in Molecular Biosciences</i> , 2021, 8, 683132.	3.5	12
13	The dynamic mechanism of 4E-BP1 recognition and phosphorylation by mTORC1. <i>Molecular Cell</i> , 2021, 81, 2403-2416.e5.	9.7	32
14	Outer membrane permeability: Antimicrobials and diverse nutrients bypass porins in <i>Pseudomonas aeruginosa</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	7.1	44
15	Identification of a Dps contamination in Mitomycin-C-induced expression of Colicin Ia. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 2021, 1863, 183607.	2.6	0
16	RNA-bound PGC-1 β controls gene expression in liquid-like nuclear condensates. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	7.1	10
17	Sequence-Specific Resonance Assignment of Soluble Nonglobular Proteins by 7D APSY-NMR Spectroscopy. , 2021, , 72-77.		0
18	Multisystem inflammation and susceptibility to viral infections in human ZNF1 deficiency. <i>Journal of Allergy and Clinical Immunology</i> , 2021, 148, 381-393.	2.9	40

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19	Chaperone Spy Protects Outer Membrane Proteins from Folding Stress via Dynamic Complex Formation. <i>MBio</i> , 2021, 12, e0213021.	4.1	10
20	Mutasynthetic Production and Antimicrobial Characterization of Darobactin Analogs. <i>Microbiology Spectrum</i> , 2021, 9, e0153521.	3.0	26
21	Protein NMR Resonanzzuordnung ohne Spektralanalyse: automatisierte Festkörperlaserprojektionspektroskopie in 5D (SOASY). <i>Angewandte Chemie</i> , 2020, 132, 2400-2405.	2.0	0
22	The electrostatic core of the outer membrane protein X from <i>E. coli</i> . <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 2020, 1862, 183031.	2.6	7
23	Protein NMR Resonance Assignment without Spectral Analysis: Solid-State Automated Projection Spectroscopy (SOASY). <i>Angewandte Chemie - International Edition</i> , 2020, 59, 2380-2384.	13.8	23
24	The Structural Basis for Low Conductance in the Membrane Protein VDAC upon \hat{I}^2 -NADH Binding and Voltage Gating. <i>Structure</i> , 2020, 28, 206-214.e4.	3.3	28
25	Regulation of \hat{I}^{\pm} -synuclein by chaperones in mammalian cells. <i>Nature</i> , 2020, 577, 127-132.	27.8	184
26	Regulation of chaperone function by coupled folding and oligomerization. <i>Science Advances</i> , 2020, 6, .	10.3	24
27	Structure of a proton-dependent lipid transporter involved in lipoteichoic acids biosynthesis. <i>Nature Structural and Molecular Biology</i> , 2020, 27, 561-569.	8.2	25
28	Detergent Titration as an Efficient Method for NMR Resonance Assignments of Membrane Proteins in Lipid Bilayer Nanodiscs. <i>Analytical Chemistry</i> , 2020, 92, 7786-7793.	6.5	8
29	Protocol for High-Yield Production of Photo-Leucine-Labeled Proteins in <i>Escherichia coli</i> . <i>Journal of Proteome Research</i> , 2020, 19, 3100-3108.	3.7	3
30	Hybrid histidine kinase activation by cyclic di-GMP mediated domain liberation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 1000-1008.	7.1	28
31	NMR pseudocontact shifts in a symmetric protein homotrimer. <i>Journal of Biomolecular NMR</i> , 2020, 74, 413-419.	2.8	6
32	Precise timing of transcription by c-di-GMP coordinates cell cycle and morphogenesis in <i>Caulobacter</i> . <i>Nature Communications</i> , 2020, 11, 816.	12.8	38
33	Sample Preparation and Technical Setup for NMR Spectroscopy with Integral Membrane Proteins. <i>Methods in Molecular Biology</i> , 2020, 2127, 373-396.	0.9	1
34	A guide to quantifying membrane protein dynamics in lipids and other native-like environments by solution-state NMR spectroscopy. <i>FEBS Journal</i> , 2019, 286, 1610-1623.	4.7	19
35	The Periplasmic Chaperones Skp and SurA. <i>Sub-Cellular Biochemistry</i> , 2019, 92, 169-186.	2.4	30
36	An integrative protocol for the structure determination of the mouse ASC-PYD filament. <i>Methods in Enzymology</i> , 2019, 625, 205-222.	1.0	0

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37	Identification of conformation-selective nanobodies against the membrane protein insertase BamA by an integrated structural biology approach. <i>Journal of Biomolecular NMR</i> , 2019, 73, 375-384.	2.8	20
38	Frustrated Interfaces Facilitate Dynamic Interactions between Native Client Proteins and Holdase Chaperones. <i>ChemBioChem</i> , 2019, 20, 2803-2806.	2.6	17
39	Lipid- and Cholesterol-Mediated Timescale-Specific Modulation of Membrane Protein Dynamics. <i>Biophysical Journal</i> , 2019, 116, 364a.	0.5	0
40	Two-State Folding of the Outer Membrane Protein X into a Lipid Bilayer Membrane. <i>Angewandte Chemie</i> , 2019, 131, 2691-2695.	2.0	1
41	Chimeric peptidomimetic antibiotics against Gram-negative bacteria. <i>Nature</i> , 2019, 576, 452-458.	27.8	231
42	A new antibiotic selectively kills Gram-negative pathogens. <i>Nature</i> , 2019, 576, 459-464.	27.8	456
43	Chaperone-Bound Clients: The Importance of Being Dynamic. <i>Trends in Biochemical Sciences</i> , 2019, 44, 517-527.	7.5	39
44	Two-State Folding of the Outer Membrane Protein X into a Lipid Bilayer Membrane. <i>Angewandte Chemie - International Edition</i> , 2019, 58, 2665-2669.	13.8	5
45	Common Patterns in Chaperone Interactions with a Native Client Protein. <i>Angewandte Chemie - International Edition</i> , 2018, 57, 5921-5924.	13.8	22
46	HtrA1 Mediated Intracellular Effects on Tubulin Using a Polarized RPE Disease Model. <i>EBioMedicine</i> , 2018, 27, 258-274.	6.1	17
47	The Gasdermin pore acts as a conduit for IL-1 β secretion in mice. <i>European Journal of Immunology</i> , 2018, 48, 584-592.	2.9	273
48	Äœbereinstimmende Muster in Chaperon-Interaktionen mit einem nativen Klientenprotein. <i>Angewandte Chemie</i> , 2018, 130, 6024-6027.	2.0	1
49	Chaperone-client complexes: A dynamic liaison. <i>Journal of Magnetic Resonance</i> , 2018, 289, 142-155.	2.1	17
50	Lipid- and Cholesterol-Mediated Time-Scale-Specific Modulation of the Outer Membrane Protein X Dynamics in Lipid Bilayers. <i>Journal of the American Chemical Society</i> , 2018, 140, 15402-15411.	13.7	23
51	Sequence-Specific Solution NMR Assignments of the β -Barrel Insertase BamA to Monitor Its Conformational Ensemble at the Atomic Level. <i>Journal of the American Chemical Society</i> , 2018, 140, 11252-11260.	13.7	45
52	Conformational plasticity of molecular chaperones involved in periplasmic and outer membrane protein folding. <i>FEMS Microbiology Letters</i> , 2018, 365, .	1.8	15
53	Mechanism of membrane pore formation by human gasdermin. <i>EMBO Journal</i> , 2018, 37, .	7.8	178
54	Assay for high-throughput screening of inhibitors of the ASC-PYD inflammasome core filament. <i>Cell Stress</i> , 2018, 2, 82-90.	3.2	4

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55	Maltoporin LamB Unfolds β Hairpins along Mechanical Stress-Dependent Unfolding Pathways. <i>Structure</i> , 2017, 25, 1139-1144.e2.	3.3	22
56	A Spring-Loaded Mechanism Governs the Clamp-like Dynamics of the Skp Chaperone. <i>Structure</i> , 2017, 25, 1079-1088.e3.	3.3	34
57	The dynamic dimer structure of the chaperone Trigger Factor. <i>Nature Communications</i> , 2017, 8, 1992.	12.8	46
58	Monitoring Backbone Hydrogen-Bond Formation in β -Barrel Membrane Protein Folding. <i>Angewandte Chemie - International Edition</i> , 2016, 55, 5952-5955.	13.8	27
59	Monitoring Backbone Hydrogen-Bond Formation in β -Barrel Membrane Protein Folding. <i>Angewandte Chemie</i> , 2016, 128, 6056-6059.	2.0	4
60	<scp>GSDMD</scp> membrane pore formation constitutes the mechanism of pyroptotic cell death. <i>EMBO Journal</i> , 2016, 35, 1766-1778.	7.8	842
61	Germline NLRP1 Mutations Cause Skin Inflammatory and Cancer Susceptibility Syndromes via Inflammasome Activation. <i>Cell</i> , 2016, 167, 187-202.e17.	28.9	317
62	ASC filament formation serves as a signal amplification mechanism for inflammasomes. <i>Nature Communications</i> , 2016, 7, 11929.	12.8	299
63	A molecular mechanism of chaperone-client recognition. <i>Science Advances</i> , 2016, 2, e1601625.	10.3	64
64	Intrinsic regulation of FIC-domain AMP-transferases by oligomerization and automodification. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, E529-37.	7.1	27
65	Sequence-specific solid-state NMR assignments of the mouse ASC PYRIN domain in its filament form. <i>Biomolecular NMR Assignments</i> , 2016, 10, 107-115.	0.8	12
66	Dimeric Structure of the Bacterial Extracellular Foldase PrsA. <i>Journal of Biological Chemistry</i> , 2015, 290, 3278-3292.	3.4	41
67	Characterization of the insertase BamA in three different membrane mimetics by solution NMR spectroscopy. <i>Journal of Biomolecular NMR</i> , 2015, 61, 333-345.	2.8	32
68	Chaperones and chaperone-substrate complexes: Dynamic playgrounds for NMR spectroscopists. <i>Progress in Nuclear Magnetic Resonance Spectroscopy</i> , 2015, 86-87, 41-64.	7.5	31
69	Conserved Omp85 lid-lock structure and substrate recognition in FhaC. <i>Nature Communications</i> , 2015, 6, 7452.	12.8	31
70	Revisiting the Interaction between the Chaperone Skp and Lipopolysaccharide. <i>Biophysical Journal</i> , 2015, 108, 1516-1526.	0.5	12
71	Local Mitochondrial-Endolysosomal Microfusion Cleaves Voltage-Dependent Anion Channel 1 To Promote Survival in Hypoxia. <i>Molecular and Cellular Biology</i> , 2015, 35, 1491-1505.	2.3	40
72	Cyclic di-GMP acts as a cell cycle oscillator to drive chromosome replication. <i>Nature</i> , 2015, 523, 236-239.	27.8	186

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73	Structure and assembly of the mouse ASC inflammasome by combined NMR spectroscopy and cryo-electron microscopy. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 13237-13242.	7.1	133
74	Purification and Bicelle Crystallization for Structure Determination of the E. coli Outer Membrane Protein TamA. <i>Methods in Molecular Biology</i> , 2015, 1329, 259-270.	0.9	4
75	Impact of holdase chaperones Skp and SurA on the folding of β^2 -barrel outer-membrane proteins. <i>Nature Structural and Molecular Biology</i> , 2015, 22, 795-802.	8.2	108
76	STIL binding to Polo-box 3 of PLK4 regulates centriole duplication. <i>ELife</i> , 2015, 4, .	6.0	109
77	<i>Shigella</i> reroutes host cell central metabolism to obtain high-flux nutrient supply for vigorous intracellular growth. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 9929-9934.	7.1	71
78	How Amphipols Embed Membrane Proteins: Global Solvent Accessibility and Interaction with a Flexible Protein Terminus. <i>Journal of Membrane Biology</i> , 2014, 247, 965-970.	2.1	33
79	Structural Mapping of a Chaperone-Substrate Interaction Surface. <i>Angewandte Chemie - International Edition</i> , 2014, 53, 5069-5072.	13.8	28
80	Trypanosomal TAC40 constitutes a novel subclass of mitochondrial β^2 -barrel proteins specialized in mitochondrial genome inheritance. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 7624-7629.	7.1	47
81	The Functional Heart of the M2 Channel. <i>Biophysical Journal</i> , 2013, 104, 1639-1640.	0.5	3
82	The structural basis of autotransporter translocation by TamA. <i>Nature Structural and Molecular Biology</i> , 2013, 20, 1318-1320.	8.2	116
83	Conformation and dynamics of the periplasmic membrane-protein-chaperone complexes OmpA-Skp and tOmpA-Skp. <i>Nature Structural and Molecular Biology</i> , 2013, 20, 1265-1272.	8.2	123
84	Perspectives of solution NMR spectroscopy for structural and functional studies of integral membrane proteins. <i>Molecular Physics</i> , 2013, 111, 843-849.	1.7	5
85	Dynamic nature of heterochromatin highlighted by a HP1 ^{Swi6} -dependent gene silencing mechanism. <i>Cell Cycle</i> , 2012, 11, 3907-3908.	2.6	4
86	Solution NMR Studies of Membrane-Protein-Chaperone Complexes. <i>Chimia</i> , 2012, 66, 759.	0.6	16
87	4D solid-state NMR for protein structure determination. <i>Physical Chemistry Chemical Physics</i> , 2012, 14, 5239.	2.8	42
88	Bacterial Origin of a Mitochondrial Outer Membrane Protein Translocase. <i>Journal of Biological Chemistry</i> , 2012, 287, 31437-31445.	3.4	35
89	HP1 ^{Swi6} Mediates the Recognition and Destruction of Heterochromatic RNA Transcripts. <i>Molecular Cell</i> , 2012, 47, 215-227.	9.7	115
90	Solution NMR spectroscopic characterization of human VDAC-2 in detergent micelles and lipid bilayer nanodiscs. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 2012, 1818, 1562-1569.	2.6	53

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91	Automated Projection Spectroscopy and Its Applications. Topics in Current Chemistry, 2011, 316, 21-47.	4.0	17
92	Automated NMR Resonance Assignment of Large Proteins for Protein-Ligand Interaction Studies. Journal of the American Chemical Society, 2011, 133, 210-213.	13.7	27
93	4D APSY-HCBC(CG)CDHD experiment for automated assignment of aromatic amino acid side chains in proteins. Journal of Biomolecular NMR, 2011, 51, 313-318.	2.8	5
94	A Proton-Detected 4D Solid-State NMR Experiment for Protein Structure Determination. ChemPhysChem, 2011, 12, 915-918.	2.1	160
95	Residual structure in a peptide fragment of the outer membrane protein X under denaturing conditions: a molecular dynamics study. European Biophysics Journal, 2010, 39, 1421-1432.	2.2	7
96	Backbone and ILV side chain methyl group assignments of the integral human membrane protein VDAC-1. Biomolecular NMR Assignments, 2010, 4, 29-32.	0.8	10
97	CACA-TOCSY with alternate ^{13}C - ^{12}C labeling: a ^{13}C direct detection experiment for mainchain resonance assignment, dihedral angle information, and amino acid type identification. Journal of Biomolecular NMR, 2010, 47, 55-63.	2.8	23
98	The 3D structures of VDAC represent a native conformation. Trends in Biochemical Sciences, 2010, 35, 514-521.	7.5	115
99	Nonmicellar systems for solution NMR spectroscopy of membrane proteins. Current Opinion in Structural Biology, 2010, 20, 471-479.	5.7	114
100	VDAC Studied by Solution NMR: Implications for the Native Structure. Biophysical Journal, 2010, 98, 207a.	0.5	0
101	Coupled Decomposition of Four-Dimensional NOESY Spectra. Journal of the American Chemical Society, 2009, 131, 12970-12978.	13.7	51
102	The role of solution NMR in the structure determinations of VDAC-1 and other membrane proteins. Current Opinion in Structural Biology, 2009, 19, 396-401.	5.7	81
103	The T-lock: automated compensation of radio-frequency induced sample heating. Journal of Biomolecular NMR, 2009, 44, 69-76.	2.8	6
104	Structural and Functional Characterization of the Integral Membrane Protein VDAC-1 in Lipid Bilayer Nanodiscs. Journal of the American Chemical Society, 2009, 131, 17777-17779.	13.7	158
105	APSY-NMR with proteins: practical aspects and backbone assignment. Journal of Biomolecular NMR, 2008, 42, 179-195.	2.8	55
106	Interactions with Hydrophobic Clusters in the Urea-Unfolded Membrane Protein OmpX. Angewandte Chemie - International Edition, 2008, 47, 977-981.	13.8	21
107	Automated NMR Assignment of Protein Side Chain Resonances Using Automated Projection Spectroscopy (APSY). Journal of the American Chemical Society, 2008, 130, 12073-12079.	13.7	28
108	Solution Structure of the Integral Human Membrane Protein VDAC-1 in Detergent Micelles. Science, 2008, 321, 1206-1210.	12.6	605

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109	PDCD4 inhibits translation initiation by binding to eIF4A using both its MA3 domains. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 3274-3279.	7.1	125
110	Sequence-Specific Resonance Assignment of Soluble Nonglobular Proteins by 7D APSY-NMR Spectroscopy. Journal of the American Chemical Society, 2007, 129, 10823-10828.	13.7	71
111	NMR assignment of the E. coli type 1 pilus protein FimF. Journal of Biomolecular NMR, 2007, 38, 195-195.	2.8	4
112	Cell-free protein synthesis of perdeuterated proteins for NMR studies. Journal of Biomolecular NMR, 2007, 39, 229-238.	2.8	45
113	Automated Resonance Assignment of Proteins: 6 DAPSY-NMR. Journal of Biomolecular NMR, 2006, 35, 27-37.	2.8	80
114	Managing the solvent water polarization to obtain improved NMR spectra of large molecular structures. Journal of Biomolecular NMR, 2005, 32, 61-70.	2.8	46
115	Automated projection spectroscopy (APSY). Proceedings of the National Academy of Sciences of the United States of America, 2005, 102, 10876-10881.	7.1	232
116	Nonrandom Structure in the Urea-Unfolded Escherichia coli Outer Membrane Protein X (OmpX). Biochemistry, 2004, 43, 860-869.	2.5	49
117	NMR Structure of the Apoptosis- and Inflammation-Related NALP1 Pyrin Domain. Structure, 2003, 11, 1199-1205.	3.3	124