

Sebastian Hiller

List of Publications by Year in descending order

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117
papers

7,740
citations

87888

38
h-index

56724

83
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128
all docs

128
docs citations

128
times ranked

9128
citing authors

#	ARTICLE	IF	CITATIONS
1	<scp>GSDMD</scp> membrane pore formation constitutes the mechanism of pyroptotic cell death. EMBO Journal, 2016, 35, 1766-1778.	7.8	842
2	Solution Structure of the Integral Human Membrane Protein VDAC-1 in Detergent Micelles. Science, 2008, 321, 1206-1210.	12.6	605
3	A new antibiotic selectively kills Gram-negative pathogens. Nature, 2019, 576, 459-464.	27.8	456
4	Germline NLRP1 Mutations Cause Skin Inflammatory and Cancer Susceptibility Syndromes via Inflammasome Activation. Cell, 2016, 167, 187-202.e17.	28.9	317
5	ASC filament formation serves as a signal amplification mechanism for inflammasomes. Nature Communications, 2016, 7, 11929.	12.8	299
6	The Gasdermin α pore acts as a conduit for IL β secretion in mice. European Journal of Immunology, 2018, 48, 584-592.	2.9	273
7	Automated projection spectroscopy (APSY). Proceedings of the National Academy of Sciences of the United States of America, 2005, 102, 10876-10881.	7.1	232
8	Chimeric peptidomimetic antibiotics against Gram-negative bacteria. Nature, 2019, 576, 452-458.	27.8	231
9	Cyclic di-GMP acts as a cell cycle oscillator to drive chromosome replication. Nature, 2015, 523, 236-239.	27.8	186
10	Regulation of α -synuclein by chaperones in mammalian cells. Nature, 2020, 577, 127-132.	27.8	184
11	Mechanism of membrane pore formation by human gasdermin α . EMBO Journal, 2018, 37, .	7.8	178
12	A Proton-Detected 4D Solid-State NMR Experiment for Protein Structure Determination. ChemPhysChem, 2011, 12, 915-918.	2.1	160
13	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
14	Structure and assembly of the mouse ASC inflammasome by combined NMR spectroscopy and cryo-electron microscopy. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 13237-13242.	7.1	133
15	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
16	NMR Structure of the Apoptosis- and Inflammation-Related NALP1 Pyrin Domain. Structure, 2003, 11, 1199-1205.	3.3	124
17	Conformation and dynamics of the periplasmic membrane-protein α -chaperone complexes OmpX α -Skp and tOmpA α -Skp. Nature Structural and Molecular Biology, 2013, 20, 1265-1272.	8.2	123
18	The structural basis of autotransporter translocation by TamA. Nature Structural and Molecular Biology, 2013, 20, 1318-1320.	8.2	116

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19	The 3D structures of VDAC represent a native conformation. Trends in Biochemical Sciences, 2010, 35, 514-521.	7.5	115
20	HP1Swi6 Mediates the Recognition and Destruction of Heterochromatic RNA Transcripts. Molecular Cell, 2012, 47, 215-227.	9.7	115
21	Nonmicellar systems for solution NMR spectroscopy of membrane proteins. Current Opinion in Structural Biology, 2010, 20, 471-479.	5.7	114
22	The antibiotic darobactin mimics a β -strand to inhibit outer membrane insertase. Nature, 2021, 593, 125-129.	27.8	112
23	STIL binding to Polo-box 3 of PLK4 regulates centriole duplication. ELife, 2015, 4, .	6.0	109
24	Impact of holdase chaperones Skp and SurA on the folding of β -barrel outer-membrane proteins. Nature Structural and Molecular Biology, 2015, 22, 795-802.	8.2	108
25	Inositol pyrophosphates promote the interaction of SPX domains with the coiled-coil motif of PHR transcription factors to regulate plant phosphate homeostasis. Nature Communications, 2021, 12, 384.	12.8	105
26	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
27	Automated Resonance Assignment of Proteins: 6 DAPSY-NMR. Journal of Biomolecular NMR, 2006, 35, 27-37.	2.8	80
28	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
29	<i>Shigella</i> reroutes host cell central metabolism to obtain high-flux nutrient supply for vigorous intracellular growth. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 9929-9934.	7.1	71
30	A molecular mechanism of chaperone-client recognition. Science Advances, 2016, 2, e1601625.	10.3	64
31	APSY-NMR with proteins: practical aspects and backbone assignment. Journal of Biomolecular NMR, 2008, 42, 179-195.	2.8	55
32	Solution NMR spectroscopic characterization of human VDAC-2 in detergent micelles and lipid bilayer nanodiscs. Biochimica Et Biophysica Acta - Biomembranes, 2012, 1818, 1562-1569.	2.6	53
33	Coupled Decomposition of Four-Dimensional NOESY Spectra. Journal of the American Chemical Society, 2009, 131, 12970-12978.	13.7	51
34	Nonrandom Structure in the Urea-Unfolded Escherichia coli Outer Membrane Protein X (OmpX). Biochemistry, 2004, 43, 860-869.	2.5	49
35	Trypanosomal TAC40 constitutes a novel subclass of mitochondrial β -barrel proteins specialized in mitochondrial genome inheritance. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 7624-7629.	7.1	47
36	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

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37	The dynamic dimer structure of the chaperone Trigger Factor. <i>Nature Communications</i> , 2017, 8, 1992.	12.8	46
38	Cell-free protein synthesis of perdeuterated proteins for NMR studies. <i>Journal of Biomolecular NMR</i> , 2007, 39, 229-238.	2.8	45
39	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
40	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
41	4D solid-state NMR for protein structure determination. <i>Physical Chemistry Chemical Physics</i> , 2012, 14, 5239.	2.8	42
42	Insights into SusCD-mediated glycan import by a prominent gut symbiont. <i>Nature Communications</i> , 2021, 12, 44.	12.8	42
43	Dimeric Structure of the Bacterial Extracellular Foldase PrsA. <i>Journal of Biological Chemistry</i> , 2015, 290, 3278-3292.	3.4	41
44	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
45	Multisystem inflammation and susceptibility to viral infections in human ZNFX1 deficiency. <i>Journal of Allergy and Clinical Immunology</i> , 2021, 148, 381-393.	2.9	40
46	Chaperone-Bound Clients: The Importance of Being Dynamic. <i>Trends in Biochemical Sciences</i> , 2019, 44, 517-527.	7.5	39
47	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
48	Bacterial Origin of a Mitochondrial Outer Membrane Protein Translocase. <i>Journal of Biological Chemistry</i> , 2012, 287, 31437-31445.	3.4	35
49	A Spring-Loaded Mechanism Governs the Clamp-like Dynamics of the Skp Chaperone. <i>Structure</i> , 2017, 25, 1079-1088.e3.	3.3	34
50	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
51	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
52	The dynamic mechanism of 4E-BP1 recognition and phosphorylation by mTORC1. <i>Molecular Cell</i> , 2021, 81, 2403-2416.e5.	9.7	32
53	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
54	Conserved Omp85 lid-lock structure and substrate recognition in FhaC. <i>Nature Communications</i> , 2015, 6, 7452.	12.8	31

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55	The Periplasmic Chaperones Skp and SurA. <i>Sub-Cellular Biochemistry</i> , 2019, 92, 169-186.	2.4	30
56	Pseudocontact Shifts in Biomolecular NMR Spectroscopy. <i>Chemical Reviews</i> , 2022, 122, 9422-9467.	47.7	29
57	Automated NMR Assignment of Protein Side Chain Resonances Using Automated Projection Spectroscopy (APSY). <i>Journal of the American Chemical Society</i> , 2008, 130, 12073-12079.	13.7	28
58	Structural Mapping of a Chaperone-Substrate Interaction Surface. <i>Angewandte Chemie - International Edition</i> , 2014, 53, 5069-5072.	13.8	28
59	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
60	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
61	Automated NMR Resonance Assignment of Large Proteins for Protein-Ligand Interaction Studies. <i>Journal of the American Chemical Society</i> , 2011, 133, 210-213.	13.7	27
62	Monitoring Backbone Hydrogen-Bond Formation in \hat{I}^2 -Barrel Membrane Protein Folding. <i>Angewandte Chemie - International Edition</i> , 2016, 55, 5952-5955.	13.8	27
63	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
64	Mutasynthetic Production and Antimicrobial Characterization of Darobactin Analogs. <i>Microbiology Spectrum</i> , 2021, 9, e0153521.	3.0	26
65	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
66	Gasdermin-A3 pore formation propagates along variable pathways. <i>Nature Communications</i> , 2022, 13, 2609.	12.8	25
67	Regulation of chaperone function by coupled folding and oligomerization. <i>Science Advances</i> , 2020, 6, .	10.3	24
68	Monitoring the antibiotic darobactin modulating the \hat{I}^2 -barrel assembly factor BamA. <i>Structure</i> , 2022, 30, 350-359.e3.	3.3	24
69	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. <i>Journal of Biomolecular NMR</i> , 2010, 47, 55-63.	2.8	23
70	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
71	Protein NMR Resonance Assignment without Spectral Analysis: 5D-Solid-State Automated Projection Spectroscopy (SO-APSY). <i>Angewandte Chemie - International Edition</i> , 2020, 59, 2380-2384.	13.8	23
72	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

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73	Maltoporin LamB Unfolds \hat{I}^2 Hairpins along Mechanical Stress-Dependent Unfolding Pathways. <i>Structure</i> , 2017, 25, 1139-1144.e2.	3.3	22
74	Common Patterns in Chaperone Interactions with a Native Client Protein. <i>Angewandte Chemie - International Edition</i> , 2018, 57, 5921-5924.	13.8	22
75	Interactions with Hydrophobic Clusters in the Urea-Unfolded Membrane Protein OmpX. <i>Angewandte Chemie - International Edition</i> , 2008, 47, 977-981.	13.8	21
76	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
77	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
78	Automated Projection Spectroscopy and Its Applications. <i>Topics in Current Chemistry</i> , 2011, 316, 21-47.	4.0	17
79	HtrA1 Mediated Intracellular Effects on Tubulin Using a Polarized RPE Disease Model. <i>EBioMedicine</i> , 2018, 27, 258-274.	6.1	17
80	Chaperone-client complexes: A dynamic liaison. <i>Journal of Magnetic Resonance</i> , 2018, 289, 142-155.	2.1	17
81	Frustrated Interfaces Facilitate Dynamic Interactions between Native Client Proteins and Holdase Chaperones. <i>ChemBioChem</i> , 2019, 20, 2803-2806.	2.6	17
82	Solution NMR Studies of Membrane-Protein-Chaperone Complexes. <i>Chimia</i> , 2012, 66, 759.	0.6	16
83	Conformational plasticity of molecular chaperones involved in periplasmic and outer membrane protein folding. <i>FEMS Microbiology Letters</i> , 2018, 365, .	1.8	15
84	Revisiting the Interaction between the Chaperone Skp and Lipopolysaccharide. <i>Biophysical Journal</i> , 2015, 108, 1516-1526.	0.5	12
85	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
86	Redefining Molecular Chaperones as Chaotropes. <i>Frontiers in Molecular Biosciences</i> , 2021, 8, 683132.	3.5	12
87	Active membrane rupture spurs a range of cell deaths. <i>Nature</i> , 2021, 591, 36-37.	27.8	11
88	Backbone and ILV side chain methyl group assignments of the integral human membrane protein VDAC-1. <i>Biomolecular NMR Assignments</i> , 2010, 4, 29-32.	0.8	10
89	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
90	Chaperone Spy Protects Outer Membrane Proteins from Folding Stress via Dynamic Complex Formation. <i>MBio</i> , 2021, 12, e0213021.	4.1	10

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91	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
92	Molecular chaperones and their denaturing effect on client proteins. <i>Journal of Biomolecular NMR</i> , 2021, 75, 1-8.	2.8	8
93	Residual structure in a peptide fragment of the outer membrane protein X under denaturing conditions: a molecular dynamics study. <i>European Biophysics Journal</i> , 2010, 39, 1421-1432.	2.2	7
94	The electrostatic core of the outer membrane protein X from E. coli. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 2020, 1862, 183031.	2.6	7
95	The T-lock: automated compensation of radio-frequency induced sample heating. <i>Journal of Biomolecular NMR</i> , 2009, 44, 69-76.	2.8	6
96	NMR pseudocontact shifts in a symmetric protein homotrimer. <i>Journal of Biomolecular NMR</i> , 2020, 74, 413-419.	2.8	6
97	4D APSY-HCBCB(CG)CDHD experiment for automated assignment of aromatic amino acid side chains in proteins. <i>Journal of Biomolecular NMR</i> , 2011, 51, 313-318.	2.8	5
98	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
99	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
100	NMR assignment of the E. coli type 1 pilus protein FimF. <i>Journal of Biomolecular NMR</i> , 2007, 38, 195-195.	2.8	4
101	Dynamic nature of heterochromatin highlighted by a HP1 ^{Swi6} -dependent gene silencing mechanism. <i>Cell Cycle</i> , 2012, 11, 3907-3908.	2.6	4
102	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
103	Monitoring Backbone Hydrogen Bond Formation in β -Barrel Membrane Protein Folding. <i>Angewandte Chemie</i> , 2016, 128, 6056-6059.	2.0	4
104	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
105	Motional clustering in supra-molecular clusters of β -barrel membrane proteins: conformational exchange influences NOE cross-relaxation rate. <i>Journal of Magnetic Resonance</i> , 2022, 338, 107196.	2.1	4
106	The Functional Heart of the M2 Channel. <i>Biophysical Journal</i> , 2013, 104, 1639-1640.	0.5	3
107	Protocol for High-Yield Production of Photo-Leucine-Labeled Proteins in Escherichia coli. <i>Journal of Proteome Research</i> , 2020, 19, 3100-3108.	3.7	3
108	Acquisition of enzymatic progress curves in real time by quenching-free ion exchange chromatography. <i>Analytical Biochemistry</i> , 2022, 639, 114523.	2.4	3

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109	Äœbereinstimmende Muster in Chaperonâ€Interaktionen mit einem nativen Klientenprotein. Angewandte Chemie, 2018, 130, 6024-6027.	2.0	1
110	Twoâ€State Folding of the Outer Membrane Protein X into a Lipid Bilayer Membrane. Angewandte Chemie, 2019, 131, 2691-2695.	2.0	1
111	Sample Preparation and Technical Setup for NMR Spectroscopy with Integral Membrane Proteins. Methods in Molecular Biology, 2020, 2127, 373-396.	0.9	1
112	VDAC Studied by Solution NMR: Implications for the Native Structure. Biophysical Journal, 2010, 98, 207a.	0.5	0
113	An integrative protocol for the structure determination of the mouse ASC-PYD filament. Methods in Enzymology, 2019, 625, 205-222.	1.0	0
114	Lipid- and Cholesterol-Mediated Timescale-Specific Modulation of Membrane Protein Dynamics. Biophysical Journal, 2019, 116, 364a.	0.5	0
115	Proteinâ€NMRâ€Resonanzzuordnung ohne Spektralanalyse: automatisierte Festkâ€rperâ€Projektionsspektroskopie in 5D (SOâ€APSY). Angewandte Chemie, 2020, 132, 2400-2405.	2.0	0
116	Identification of a Dps contamination in Mitomycin-Câ€induced expression of Colicin Ia. Biochimica Et Biophysica Acta - Biomembranes, 2021, 1863, 183607.	2.6	0
117	Sequence-Specific Resonance Assignment of Soluble Nonglobular Proteins by 7D APSY-NMR Spectroscopy. , 2021, , 72-77.		0