

Borries Demeler

List of Publications by Year in descending order

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155
papers

6,734
citations

53660

45
h-index

82410

72
g-index

166
all docs

166
docs citations

166
times ranked

8387
citing authors

#	ARTICLE	IF	CITATIONS
1	Structural Bases of Unphosphorylated STAT1 Association and Receptor Binding. <i>Molecular Cell</i> , 2005, 17, 761-771.	4.5	250
2	Sedimentation velocity analysis of highly heterogeneous systems. <i>Analytical Biochemistry</i> , 2004, 335, 279-288.	1.1	232
3	Structural basis of HIV-1 capsid recognition by PF74 and CPSF6. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 18625-18630.	3.3	215
4	Structure of the Hsp110:Hsc70 Nucleotide Exchange Machine. <i>Molecular Cell</i> , 2008, 31, 232-243.	4.5	202
5	A two-dimensional spectrum analysis for sedimentation velocity experiments of mixtures with heterogeneity in molecular weight and shape. <i>European Biophysics Journal</i> , 2010, 39, 405-414.	1.2	198
6	Direct Sedimentation Analysis of Interference Optical Data in Analytical Ultracentrifugation. <i>Biophysical Journal</i> , 1999, 76, 2288-2296.	0.2	168
7	Ag ₄₄ (SR) ₃₀₄ ²⁻ : a silver-thiolate superatom complex. <i>Nanoscale</i> , 2012, 4, 4269.	2.8	154
8	Dissociation of Human Copper-Zinc Superoxide Dismutase Dimers Using Chaotrope and Reductant. <i>Journal of Biological Chemistry</i> , 2004, 279, 54558-54566.	1.6	149
9	Neural network optimization for E. coli promoter prediction. <i>Nucleic Acids Research</i> , 1991, 19, 1593-1599.	6.5	134
10	Analytical Ultracentrifugation of Complex Macromolecular Systems. <i>Biochemistry</i> , 1994, 33, 13155-13163.	1.2	126
11	Gene Selection, Alternative Splicing, and Post-translational Processing Regulate Neuroligin Selectivity for Î²-Neurexins. <i>Biochemistry</i> , 2006, 45, 12816-12827.	1.2	117
12	Monte Carlo analysis of sedimentation experiments. <i>Colloid and Polymer Science</i> , 2008, 286, 129-137.	1.0	117
13	Deamidation destabilizes and triggers aggregation of a lens protein, Î²A3-crystallin. <i>Protein Science</i> , 2008, 17, 1565-1575.	3.1	115
14	The implementation of SOMO (Solution MOdeller) in the UltraScan analytical ultracentrifugation data analysis suite: enhanced capabilities allow the reliable hydrodynamic modeling of virtually any kind of biomacromolecule. <i>European Biophysics Journal</i> , 2010, 39, 423-435.	1.2	111
15	Determination of Molecular Parameters by Fitting Sedimentation Data to Finite-Element Solutions of the Lamm Equation. <i>Biophysical Journal</i> , 1998, 74, 444-454.	0.2	107
16	Molecular details of a starch utilization pathway in the human gut symbiont <i>Escherichia coli</i> bacterium rectale. <i>Molecular Microbiology</i> , 2015, 95, 209-230.	1.2	104
17	Chaperone activity of cytosolic small heat shock proteins from wheat. <i>FEBS Journal</i> , 2004, 271, 1426-1436.	0.2	96
18	Cytotoxic Cell Granule-mediated Apoptosis. <i>Journal of Biological Chemistry</i> , 2002, 277, 49523-49530.	1.6	93

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19	Precision Templating with DNA of a Virus-like Particle with Peptide Nanostructures. <i>Journal of the American Chemical Society</i> , 2013, 135, 6211-6219.	6.6	90
20	Structure of the Polycomb Group Protein PCGF1 in Complex with BCOR Reveals Basis for Binding Selectivity of PCGF Homologs. <i>Structure</i> , 2013, 21, 665-671.	1.6	89
21	Cryo-EM reveals a novel octameric integrase structure for betaretroviral intasome function. <i>Nature</i> , 2016, 530, 358-361.	13.7	88
22	Methods for the Design and Analysis of Sedimentation Velocity and Sedimentation Equilibrium Experiments with Proteins. <i>Current Protocols in Protein Science</i> , 2010, 60, Unit 7.13.	2.8	82
23	Mechanism of Rab Geranylgeranylation: Formation of the Catalytic Ternary Complex. <i>Biochemistry</i> , 1998, 37, 12559-12568.	1.2	81
24	Polycomb Group Targeting through Different Binding Partners of RING1B C-Terminal Domain. <i>Structure</i> , 2010, 18, 966-975.	1.6	81
25	Modeling Analytical Ultracentrifugation Experiments with an Adaptive Space-Time Finite Element Solution of the Lamm Equation. <i>Biophysical Journal</i> , 2005, 89, 1589-1602.	0.2	75
26	Characterization of Size, Anisotropy, and Density Heterogeneity of Nanoparticles by Sedimentation Velocity. <i>Analytical Chemistry</i> , 2014, 86, 7688-7695.	3.2	74
27	Macrocyclic β -Sheet Peptides That Mimic Protein Quaternary Structure through Intermolecular β -Sheet Interactions. <i>Journal of the American Chemical Society</i> , 2007, 129, 5558-5569.	6.6	73
28	RING Dimerization Links Higher-Order Assembly of TRIM5 to Synthesis of K63-Linked Polyubiquitin. <i>Cell Reports</i> , 2015, 12, 788-797.	2.9	72
29	Parsimonious regularization using genetic algorithms applied to the analysis of analytical ultracentrifugation experiments. , 2007, , .		69
30	Domain Mapping of the Polycystin-2 C-terminal Tail Using de Novo Molecular Modeling and Biophysical Analysis. <i>Journal of Biological Chemistry</i> , 2008, 283, 28305-28312.	1.6	69
31	Modeling Analytical Ultracentrifugation Experiments with an Adaptive Space-Time Finite Element Solution for Multicomponent Reacting Systems. <i>Biophysical Journal</i> , 2008, 95, 54-65.	0.2	67
32	Divergence of multimodular polyketide synthases revealed by a didomain structure. <i>Nature Chemical Biology</i> , 2012, 8, 615-621.	3.9	66
33	A Locking Mechanism Regulates RNA Synthesis and Host Protein Interaction by the Hepatitis C Virus Polymerase. <i>Journal of Biological Chemistry</i> , 2008, 283, 20535-20546.	1.6	65
34	Analytical Ultracentrifugation Data Analysis with UltraScan-III. , 2016, , 119-143.		62
35	A Parametrically Constrained Optimization Method for Fitting Sedimentation Velocity Experiments. <i>Biophysical Journal</i> , 2014, 106, 1741-1750.	0.2	56
36	Linear Free-Energy Analysis of Mercury(II) and Cadmium(II) Binding to Three-Stranded Coiled Coils. <i>Biochemistry</i> , 2005, 44, 10732-10740.	1.2	55

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37	Binding of Dr adhesins of <i>Escherichia coli</i> to carcinoembryonic antigen triggers receptor dissociation. <i>Molecular Microbiology</i> , 2008, 67, 420-434.	1.2	55
38	Developments in the USâ€šSOMO Bead Modeling Suite: New Features in the Direct Residueâ€šBead Method, Improved Grid Routines, and Influence of Accessible Surface Area Screening. <i>Macromolecular Bioscience</i> , 2010, 10, 746-753.	2.1	55
39	N-terminal Residues of the <i>Vibrio cholerae</i> Virulence Regulatory Protein ToxT Involved in Dimerization and Modulation by Fatty Acids. <i>Journal of Biological Chemistry</i> , 2011, 286, 28644-28655.	1.6	55
40	The Open AUC Project. <i>European Biophysics Journal</i> , 2010, 39, 347-359.	1.2	54
41	The Growth-Suppressive Function of the Polycomb Group Protein Polyhomeotic Is Mediated by Polymerization of Its Sterile Alpha Motif (SAM) Domain. <i>Journal of Biological Chemistry</i> , 2012, 287, 8702-8713.	1.6	54
42	Controlling Self-Assembly of a Peptide-Based Material via Metal-Ion Induced Registry Shift. <i>Journal of the American Chemical Society</i> , 2013, 135, 10278-10281.	6.6	54
43	Matrix cell adhesion activation by non-adhesion proteins. <i>Journal of Cell Science</i> , 2005, 118, 2965-2974.	1.2	52
44	Blocking Hepatitis C Virus Infection with Recombinant Form of Envelope Protein 2 Ectodomain. <i>Journal of Virology</i> , 2009, 83, 11078-11089.	1.5	52
45	BMI1 regulates PRC1 architecture and activity through homo- and hetero-oligomerization. <i>Nature Communications</i> , 2016, 7, 13343.	5.8	52
46	X-ray Crystallographic and Analytical Ultracentrifugation Analyses of Truncated and Full-Length Yeast Copper Chaperones for SOD (LYS7):â€šA Dimerâ€šDimer Model of LYS7â€šSOD Association and Copper Delivery. <i>Biochemistry</i> , 2000, 39, 3611-3623.	1.2	50
47	Disrupted Zinc-Binding Sites in Structures of Pathogenic SOD1 Variants D124V and H80R. <i>Biochemistry</i> , 2010, 49, 5714-5725.	1.2	50
48	Parallel computational techniques for the analysis of sedimentation velocity experiments in UltraScan. <i>Colloid and Polymer Science</i> , 2008, 286, 139-148.	1.0	49
49	Characterization of Reversible Associations by Sedimentation Velocity with UltraScan. <i>Macromolecular Bioscience</i> , 2010, 10, 775-782.	2.1	48
50	Effects of T592 phosphomimetic mutations on tetramer stability and dNTPase activity of SAMHD1 can not explain the retroviral restriction defect. <i>Scientific Reports</i> , 2016, 6, 31353.	1.6	48
51	Dynamic Interactions between Clathrin and Locally Structured Elements in a Disordered Protein Mediate Clathrin Lattice Assembly. <i>Journal of Molecular Biology</i> , 2010, 404, 274-290.	2.0	46
52	Simultaneous Identification of Spectral Properties and Sizes of Multiple Particles in Solution with Subnanometer Resolution. <i>Angewandte Chemie - International Edition</i> , 2016, 55, 11770-11774.	7.2	46
53	A Proteomic Screen of Neuronal Cell-Surface Molecules Reveals IgLONs as Structurally Conserved Interaction Modules at the Synapse. <i>Structure</i> , 2019, 27, 893-906.e9.	1.6	44
54	Domain architecture and oligomerization properties of the paramyxovirus PIV 5 hemagglutinin-neuraminidase (HN) protein. <i>Virology</i> , 2008, 378, 282-291.	1.1	43

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55	Each Monomer of the Dimeric Accessory Protein for Human Mitochondrial DNA Polymerase Has a Distinct Role in Conferring Processivity. <i>Journal of Biological Chemistry</i> , 2010, 285, 1490-1499.	1.6	43
56	Structural and Mechanistic Insights into the Latrophilin3-FLRT3 Complex that Mediates Glutamatergic Synapse Development. <i>Structure</i> , 2015, 23, 1665-1677.	1.6	42
57	The Griffithsin Dimer Is Required for High-Potency Inhibition of HIV-1: Evidence for Manipulation of the Structure of gp120 as Part of the Griffithsin Dimer Mechanism. <i>Antimicrobial Agents and Chemotherapy</i> , 2013, 57, 3976-3989.	1.4	40
58	Geminin Has Dimerization, Cdt1-binding, and Destruction Domains That Are Required for Biological Activity. <i>Journal of Biological Chemistry</i> , 2004, 279, 45957-45968.	1.6	39
59	Design of Thiolate Rich Metal Binding Sites within a Peptidic Framework. <i>Inorganic Chemistry</i> , 2008, 47, 10875-10888.	1.9	39
60	The Role of Individual Carbohydrate-Binding Sites in the Function of the Potent Anti-HIV Lectin Griffithsin. <i>Molecular Pharmaceutics</i> , 2012, 9, 2613-2625.	2.3	39
61	A postreductionist framework for protein biochemistry. <i>Nature Chemical Biology</i> , 2011, 7, 331-334.	3.9	37
62	The Missing Linker: A Dimerization Motif Located within Polyketide Synthase Modules. <i>ACS Chemical Biology</i> , 2013, 8, 1263-1270.	1.6	37
63	Structure-Function Analysis of the Heat Shock Factor-binding Protein Reveals a Protein Composed Solely of a Highly Conserved and Dynamic Coiled-coil Trimerization Domain. <i>Journal of Biological Chemistry</i> , 2002, 277, 735-745.	1.6	36
64	Chapter 4 Analysis of Heterogeneity in Molecular Weight and Shape by Analytical Ultracentrifugation Using Parallel Distributed Computing. <i>Methods in Enzymology</i> , 2009, 454, 87-113.	0.4	35
65	Characterization of the Interaction between the Cohesin Subunits Rad21 and SA1/2. <i>PLoS ONE</i> , 2013, 8, e69458.	1.1	35
66	Structure and Dynamics of the Homodimeric Dynein Light Chain km23. <i>Journal of Molecular Biology</i> , 2005, 352, 338-354.	2.0	34
67	The E2 Domains of APP and APLP1 Share a Conserved Mode of Dimerization. <i>Biochemistry</i> , 2011, 50, 5453-5464.	1.2	34
68	Hidden Components in Aqueous Au-144-Fractionated by PAGE: High-Resolution Orbitrap ESI-MS Identifies the Gold-102 and Higher All-Aromatic Au-MBA Cluster Compounds. <i>Journal of Physical Chemistry B</i> , 2016, 120, 6430-6438.	1.2	34
69	An engineered transforming growth factor β^2 (TGF- β^2) monomer that functions as a dominant negative to block TGF- β^2 signaling. <i>Journal of Biological Chemistry</i> , 2017, 292, 7173-7188.	1.6	34
70	Next-Generation AUC. <i>Methods in Enzymology</i> , 2015, 562, 27-47.	0.4	33
71	Analytical Characterization of Size-Dependent Properties of Larger Aqueous Gold Nanoclusters. <i>Journal of Physical Chemistry C</i> , 2016, 120, 8950-8958.	1.5	33
72	Contribution of oligomerization to the anti-HIV-1 properties of SAMHD1. <i>Retrovirology</i> , 2013, 10, 131.	0.9	32

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73	Next-Generation AUC Adds a Spectral Dimension. <i>Methods in Enzymology</i> , 2015, 562, 1-26.	0.4	32
74	Genetic Algorithm Optimization for Obtaining Accurate Molecular Weight Distributions from Sedimentation Velocity Experiments. , 0, , 33-40.		31
75	The Macromolecular Architecture of Extracellular Domain of Î±NRXN1: Domain Organization, Flexibility, and Insights into Trans-Synaptic Disposition. <i>Structure</i> , 2010, 18, 1044-1053.	1.6	30
76	Substrate interaction defects in histidyl-tRNA synthetase linked to dominant axonal peripheral neuropathy. <i>Human Mutation</i> , 2018, 39, 415-432.	1.1	30
77	Isolation of Novel Large and Aggregating Bacteriophages. <i>Methods in Molecular Biology</i> , 2009, 501, 55-66.	0.4	29
78	The Apache Airavata Application Programming Interface: Overview and Evaluation with the UltraScan Science Gateway. , 2014, , .		29
79	Structural Characterization of the Extracellular Domain of CASPR2 and Insights into Its Association with the Novel Ligand Contactin1. <i>Journal of Biological Chemistry</i> , 2016, 291, 5788-5802.	1.6	29
80	Tetrahedral (<i>T</i>) Closed-Shell Cluster of 29 Silver Atoms & 12 Lipoate Ligands, [Ag₂₉(R-Î±-LA)₁₂]^(3âˆ-): Antibacterial and Antifungal Activity. <i>ACS Applied Nano Materials</i> , 2018, 1, 1595-1602.	2.4	28
81	The Growth-Promoting and Stress Response Activities of the <i>Bacillus subtilis</i> GTP Binding Protein Obg Are Separable by Mutation. <i>Journal of Bacteriology</i> , 2008, 190, 6625-6635.	1.0	27
82	Repurposing Triphenylmethane Dyes to Bind to Trimers Derived from AÎ². <i>Journal of the American Chemical Society</i> , 2018, 140, 11745-11754.	6.6	27
83	Nucleic acid binding by SAMHD1 contributes to the antiretroviral activity and is enhanced by the GpsN modification. <i>Nature Communications</i> , 2021, 12, 731.	5.8	26
84	2D analysis of polydisperse coreâ€™shell nanoparticles using analytical ultracentrifugation. <i>Analyst</i> , The, 2017, 142, 206-217.	1.7	25
85	Sedimentation velocity analysis of macromolecular assemblies. <i>Methods in Enzymology</i> , 2000, 321, 66-80.	0.4	24
86	Computing Large Sparse Multivariate Optimization Problems with an Application in Biophysics. , 2006, , .		24
87	Polymorphism of Oligomers of a Peptide from Î²-Amyloid. <i>Journal of the American Chemical Society</i> , 2014, 136, 5432-5442.	6.6	24
88	Spectral and Hydrodynamic Analysis of West Nile Virus RNAâ€™Protein Interactions by Multiwavelength Sedimentation Velocity in the Analytical Ultracentrifuge. <i>Analytical Chemistry</i> , 2017, 89, 862-870.	3.2	24
89	General Model for Retroviral Capsid Pattern Recognition by TRIM5 Proteins. <i>Journal of Virology</i> , 2018, 92, .	1.5	24
90	Nanometer to Millimeter Scale Peptide-Porphyrin Materials. <i>Biomacromolecules</i> , 2010, 11, 2602-2609.	2.6	22

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91	Pih1p-Tah1p Puts a Lid on Hexameric AAA+ ATPases Rvb1/2p. <i>Structure</i> , 2017, 25, 1519-1529.e4.	1.6	22
92	Structural Transitions of the RING1B C-Terminal Region upon Binding the Polycomb cbox Domain. <i>Biochemistry</i> , 2008, 47, 8007-8015.	1.2	21
93	Structural Characterization of the E2 Domain of APL-1, a <i>Caenorhabditis elegans</i> Homolog of Human Amyloid Precursor Protein, and Its Heparin Binding Site. <i>Journal of Biological Chemistry</i> , 2010, 285, 2165-2173.	1.6	21
94	Density Matching Multi-wavelength Analytical Ultracentrifugation to Measure Drug Loading of Lipid Nanoparticle Formulations. <i>ACS Nano</i> , 2021, 15, 5068-5076.	7.3	21
95	Molecular parameters from sedimentation velocity experiments: Whole boundary fitting using approximate and numerical solutions of lamm equation. <i>Methods in Enzymology</i> , 2000, 321, 38-66.	0.4	20
96	Multi-speed sedimentation velocity implementation in UltraScan-III. <i>European Biophysics Journal</i> , 2018, 47, 825-835.	1.2	20
97	Functionality of Redox-Active Cysteines Is Required for Restriction of Retroviral Replication by SAMHD1. <i>Cell Reports</i> , 2018, 24, 815-823.	2.9	20
98	Moving analytical ultracentrifugation software to a good manufacturing practices (GMP) environment. <i>PLoS Computational Biology</i> , 2020, 16, e1007942.	1.5	20
99	Human DDX17 Unwinds Rift Valley Fever Virus Non-Coding RNAs. <i>International Journal of Molecular Sciences</i> , 2021, 22, 54.	1.8	20
100	Assembly Mechanism of the Sixty-Subunit Nanoparticles via Interaction of RNA with the Reengineered Protein Connector of phi29 DNA-Packaging Motor. <i>ACS Nano</i> , 2010, 4, 3293-3301.	7.3	19
101	Solution-state conformation and stoichiometry of yeast Sir3 heterochromatin fibres. <i>Nature Communications</i> , 2014, 5, 4751.	5.8	19
102	The Usher Syndrome Type IIIB Histidyl-tRNA Synthetase Mutation Confers Temperature Sensitivity. <i>Biochemistry</i> , 2017, 56, 3619-3631.	1.2	19
103	Novel combinations of experimental and computational analysis tested on the binding of metalloprotoporphyrins to albumin. <i>International Journal of Biological Macromolecules</i> , 2019, 134, 445-457.	3.6	19
104	Solution Formation of Holliday Junctions in Inverted-Repeat DNA Sequences. <i>Biochemistry</i> , 2006, 45, 2467-2471.	1.2	18
105	Modulation of aggregate size- and shape-distributions of the amyloid- β peptide by a designed β -sheet breaker. <i>European Biophysics Journal</i> , 2010, 39, 415-422.	1.2	17
106	Detergent-solubilized <i>Escherichia coli</i> cytochrome <i>b</i> ₃ ubiquinol oxidase: a monomeric, not a dimeric complex. <i>FEBS Letters</i> , 1999, 457, 153-156.	1.3	16
107	Multi-wavelength analytical ultracentrifugation of human serum albumin complexed with porphyrin. <i>European Biophysics Journal</i> , 2018, 47, 789-797.	1.2	16
108	The BRPF1 bromodomain is a molecular reader of di-acetyllsine. <i>Current Research in Structural Biology</i> , 2020, 2, 104-115.	1.1	16

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109	Mechanism of NanR gene repression and allosteric induction of bacterial sialic acid metabolism. <i>Nature Communications</i> , 2021, 12, 1988.	5.8	16
110	Adjustable Ellipsoid Nanoparticles Assembled from Re-engineered Connectors of the Bacteriophage Phi29 DNA Packaging Motor. <i>ACS Nano</i> , 2009, 3, 2163-2170.	7.3	14
111	Structural and functional characterisation of the entry point to pyocyanin biosynthesis in <i>Pseudomonas aeruginosa</i> defines a new 3-deoxy- <i>l</i> -arabino-heptulosonate 7-phosphate synthase subclass. <i>Bioscience Reports</i> , 2018, 38, .	1.1	14
112	Analytical Sedimentation of the IIAChb and IIBChb Proteins of the Escherichia coli N ₁ -Diacetylchitobiose Phosphotransferase System. <i>Journal of Biological Chemistry</i> , 2000, 275, 33110-33115.	1.6	13
113	Neuropathy-associated histidyl-tRNA synthetase variants attenuate protein synthesis in vitro and disrupt axon outgrowth in developing zebrafish. <i>FEBS Journal</i> , 2021, 288, 142-159.	2.2	13
114	Kinetic Mechanism and Quaternary Structure of Aminobacter aminovorans NADH:Flavin Oxidoreductase: An Unusual Flavin Reductase with Bound Flavin. <i>Biochemistry</i> , 2004, 43, 1580-1590.	1.2	12
115	Coupled Unfolding and Dimerization by the PAH2 Domain of the Mammalian Sin3A Corepressor. <i>Journal of Molecular Biology</i> , 2006, 360, 7-14.	2.0	12
116	Structure-Function Studies of the Bacillus subtilis Ric Proteins Identify the Fe-S Cluster-Ligating Residues and Their Roles in Development and RNA Processing. <i>MBio</i> , 2019, 10, .	1.8	12
117	Nanoscale Structure Determination of Murray Valley Encephalitis and Powassan Virus Non-Coding RNAs. <i>Viruses</i> , 2020, 12, 190.	1.5	12
118	A new mode of SAM domain mediated oligomerization observed in the CASKIN2 neuronal scaffolding protein. <i>Cell Communication and Signaling</i> , 2016, 14, 17.	2.7	11
119	Multi-speed sedimentation velocity simulations with UltraScan-III. <i>European Biophysics Journal</i> , 2018, 47, 815-823.	1.2	11
120	Structure of a pentameric virion-associated fiber with a potential role in Orsay virus entry to host cells. <i>PLoS Pathogens</i> , 2017, 13, e1006231.	2.1	11
121	Nickel-Dependent Oligomerization of the Alpha Subunit of Acetyl-Coenzyme A Synthase/Carbon Monoxide Dehydrogenase. <i>Biochemistry</i> , 2007, 46, 11606-11613.	1.2	10
122	Routine fluorescence microscopy of single untethered protein molecules confined to a planar zone. <i>Journal of Microscopy</i> , 2007, 226, 256-262.	0.8	10
123	Human Polyhomeotic Homolog 3 (PHC3) Sterile Alpha Motif (SAM) Linker Allows Open-Ended Polymerization of PHC3 SAM. <i>Biochemistry</i> , 2012, 51, 5379-5386.	1.2	10
124	Multi-wavelength analytical ultracentrifugation as a tool to characterise protein-DNA interactions in solution. <i>European Biophysics Journal</i> , 2020, 49, 819-827.	1.2	10
125	The pH-Induced Selectivity Between Cysteine or Histidine Coordinated Heme in an Artificial Helical Metalloprotein. <i>Angewandte Chemie - International Edition</i> , 2021, 60, 3974-3978.	7.2	10
126	Multi-wavelength analytical ultracentrifugation of biopolymer mixtures and interactions. <i>Analytical Biochemistry</i> , 2022, 652, 114728.	1.1	10

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127	Construction and Analyses of Tetrameric Forms of Yeast NAD ⁺ -Specific Isocitrate Dehydrogenase. <i>Biochemistry</i> , 2011, 50, 230-239.	1.2	9
128	Advancements of the UltraScan scientific gateway for open standardsâ€based cyberinfrastructures. <i>Concurrency Computation Practice and Experience</i> , 2014, 26, 2280-2291.	1.4	9
129	A calibration disk for the correction of radial errors from chromatic aberration and rotor stretch in the Optima AUCâ„ analytical ultracentrifuge. <i>European Biophysics Journal</i> , 2020, 49, 701-709.	1.2	9
130	Coordination of Di-Acetylated Histone Ligands by the ATAD2 Bromodomain. <i>International Journal of Molecular Sciences</i> , 2021, 22, 9128.	1.8	9
131	Biology--Computing large sparse multivariate optimization problems with an application in biophysics. , 2006, , .		8
132	Biophysical characterisation of human LincRNA-p21 sense and antisense Alu inverted repeats. <i>Nucleic Acids Research</i> , 2022, 50, 5881-5898.	6.5	8
133	Reversible self-association of recombinant bovine factor B. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2006, 1764, 1741-1749.	1.1	7
134	Sequence Reversal Prevents Chain Collapse and Yields Heat-Sensitive Intrinsic Disorder. <i>Biophysical Journal</i> , 2018, 115, 328-340.	0.2	7
135	Measuring molecular interactions in solution using multi-wavelength analytical ultracentrifugation: combining spectral analysis with hydrodynamics. <i>Biochemist</i> , 2019, 41, 14-18.	0.2	6
136	Performance optimization of large non-negatively constrained least squares problems with an application in biophysics. , 2010, , .		5
137	Characterizing Drugâ€Polymer Interactions in Aqueous Solution with Analytical Ultracentrifugation. <i>Molecular Pharmaceutics</i> , 2021, 18, 246-256.	2.3	5
138	Two-dimensional grid optimization for sedimentation velocity analysis in the analytical ultracentrifuge. <i>European Biophysics Journal</i> , 2018, 47, 837-844.	1.2	4
139	Measuring compressibility in the optima AUCâ„ analytical ultracentrifuge. <i>European Biophysics Journal</i> , 2020, 49, 711-718.	1.2	4
140	Improvements of the UltraScan scientific gateway to enable computational jobs on large-scale and open-standards based cyberinfrastructures. , 2013, , .		4
141	A Disulfide-Stabilized A ¹² that Forms Dimers but Does Not Form Fibrils. <i>Biochemistry</i> , 2022, 61, 252-264.	1.2	4
142	UltraScan gateway enhancements. , 2011, , .		3
143	Conformation-Dependent Human p52Shc Phosphorylation by Human c-Src. <i>Biochemistry</i> , 2015, 54, 3469-3482.	1.2	3
144	Crystallographic Structures of IlvNâˆVal/Ile Complexes: Conformational Selectivity for Feedback Inhibition of Aceto Hydroxy Acid Synthases. <i>Biochemistry</i> , 2019, 58, 1992-2008.	1.2	3

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145	Cardiac Troponin T Forms a Tetramer in Vitro. <i>Biochemistry</i> , 2008, 47, 1970-1976.	1.2	2
146	Intra- and inter-molecular effects of a conserved arginine residue of neuronal and inducible nitric oxide synthases on FMN and calmodulin binding. <i>Archives of Biochemistry and Biophysics</i> , 2013, 533, 88-94.	1.4	2
147	Simultane Bestimmung spektraler Eigenschaften und Größen von multiplen Partikeln in Lösung mit Subnanometer-Auflösung. <i>Angewandte Chemie</i> , 2016, 128, 11944-11949.	1.6	2
148	The pH-Induced Selectivity Between Cysteine or Histidine Coordinated Heme in an Artificial α -Helical Metalloprotein. <i>Angewandte Chemie</i> , 2021, 133, 4020-4024.	1.6	2
149	Probing RNA-Protein Interactions and RNA Compaction by Sedimentation Velocity Analytical Ultracentrifugation. <i>Methods in Molecular Biology</i> , 2020, 2113, 281-317.	0.4	2
150	US-SOMO cluster methods. , 2013, , .		2
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