

Christine Ebel

List of Publications by Year in descending order

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127
papers

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citations

66234

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129
all docs

129
docs citations

129
times ranked

5955
citing authors

#	ARTICLE	IF	CITATIONS
1	Interaction of the Mitotic Inhibitor Monastrol with Human Kinesin Eg5. <i>Biochemistry</i> , 2003, 42, 338-349.	1.2	171
2	Hepatitis C Virus Core Protein Is a Dimeric Alpha-Helical Protein Exhibiting Membrane Protein Features. <i>Journal of Virology</i> , 2005, 79, 11353-11365.	1.5	128
3	Two Microtubule-associated Proteins of <i>Arabidopsis</i> MAP65s Promote Antiparallel Microtubule Bundling. <i>Molecular Biology of the Cell</i> , 2008, 19, 4534-4544.	0.9	125
4	NMR Structure and Ion Channel Activity of the p7 Protein from Hepatitis C Virus. <i>Journal of Biological Chemistry</i> , 2010, 285, 31446-31461.	1.6	119
5	Insights into the regulation of the human COP9 signalosome catalytic subunit, CSN5/Jab1. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 1273-1278.	3.3	115
6	Partial specific volume and solvent interactions of amphipol A8-35. <i>Analytical Biochemistry</i> , 2004, 334, 318-334.	1.1	105
7	DC-SIGN Neck Domain Is a pH-sensor Controlling Oligomerization. <i>Journal of Biological Chemistry</i> , 2009, 284, 21229-21240.	1.6	105
8	Mannose hyperbranched dendritic polymers interact with clustered organization of DC-SIGN and inhibit gp120 binding. <i>FEBS Letters</i> , 2006, 580, 2402-2408.	1.3	103
9	Conformation of heparin studied with macromolecular hydrodynamic methods and X-ray scattering. <i>European Biophysics Journal</i> , 2003, 32, 437-449.	1.2	99
10	Well-Defined Nanoparticles Formed by Hydrophobic Assembly of a Short and Polydisperse Random Terpolymer, Amphipol A8-35. <i>Langmuir</i> , 2006, 22, 1281-1290.	1.6	99
11	Bacteriorhodopsin/Amphipol Complexes: Structural and Functional Properties. <i>Biophysical Journal</i> , 2008, 94, 3523-3537.	0.2	97
12	MIB-MIP is a mycoplasma system that captures and cleaves immunoglobulin G. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, 5406-5411.	3.3	97
13	Phosphorylation-induced dimerization of the FixJ receiver domain. <i>Molecular Microbiology</i> , 1999, 34, 504-511.	1.2	96
14	Probing Protein-Sugar Interactions. <i>Biophysical Journal</i> , 2000, 78, 385-393.	0.2	94
15	Non-Ideality by Sedimentation Velocity of Halophilic Malate Dehydrogenase in Complex Solvents. <i>Biophysical Journal</i> , 2001, 81, 1868-1880.	0.2	90
16	Relative Role of Anions and Cations in the Stabilization of Halophilic Malate Dehydrogenase. <i>Biochemistry</i> , 1999, 38, 9039-9047.	1.2	84
17	On the Domain Structure and the Polymerization State of the Sendai Virus P Protein. <i>Virology</i> , 2000, 266, 99-109.	1.1	81
18	Gel chromatography and analytical ultracentrifugation to determine the extent of detergent binding and aggregation, and Stokes radius of membrane proteins using sarcoplasmic reticulum Ca ²⁺ -ATPase as an example. <i>Nature Protocols</i> , 2008, 3, 1782-1795.	5.5	76

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19	Fast Collisional Lipid Transfer Among Polymer-Bounded Nanodiscs. <i>Scientific Reports</i> , 2017, 7, 45875.	1.6	74
20	Oligomeric States of the Detergent-solubilized Human Serum Paraoxonase (PON1). <i>Journal of Biological Chemistry</i> , 2002, 277, 33386-33397.	1.6	71
21	A Multilaboratory Comparison of Calibration Accuracy and the Performance of External References in Analytical Ultracentrifugation. <i>PLoS ONE</i> , 2015, 10, e0126420.	1.1	71
22	Small angle neutron scattering for the study of solubilised membrane proteins. <i>European Physical Journal E</i> , 2013, 36, 71.	0.7	70
23	Virulence Factor of Potato Virus Y, Genome-attached Terminal Protein VPg, Is a Highly Disordered Protein. <i>Journal of Biological Chemistry</i> , 2008, 283, 213-221.	1.6	66
24	Small-Angle X-Ray Scattering Reveals the Solution Structure of the Full-Length DNA Gyrase A Subunit. <i>Structure</i> , 2005, 13, 287-296.	1.6	65
25	Structural Studies of Langerin and Birbeck Granule: A Macromolecular Organization Model. <i>Biochemistry</i> , 2009, 48, 2684-2698.	1.2	64
26	Non-Ionic Amphiphilic Homopolymers: Synthesis, Solution Properties, and Biochemical Validation. <i>Langmuir</i> , 2012, 28, 4625-4639.	1.6	64
27	Micellar and Biochemical Properties of (Hemi)Fluorinated Surfactants Are Controlled by the Size of the Polar Head. <i>Biophysical Journal</i> , 2009, 97, 1077-1086.	0.2	63
28	Biophysical study of halophilic malate dehydrogenase in solution: revised subunit structure and solvent interactions of native and recombinant enzyme. <i>Journal of the Chemical Society, Faraday Transactions</i> , 1993, 89, 2659-2666.	1.7	61
29	Purification of Na ⁺ ,K ⁺ -ATPase Expressed in <i>Pichia pastoris</i> Reveals an Essential Role of Phospholipid-Protein Interactions. <i>Journal of Biological Chemistry</i> , 2005, 280, 16610-16618.	1.6	61
30	Anti-activator ExsD Forms a 1:1 Complex with ExsA to Inhibit Transcription of Type III Secretion Operons. <i>Journal of Biological Chemistry</i> , 2009, 284, 15762-15770.	1.6	61
31	PatA and PatB Form a Functional Heterodimeric ABC Multidrug Efflux Transporter Responsible for the Resistance of <i>Streptococcus pneumoniae</i> to Fluoroquinolones. <i>Biochemistry</i> , 2012, 51, 7755-7765.	1.2	59
32	Solvent Interactions of Halophilic Malate Dehydrogenase. <i>Biochemistry</i> , 2002, 41, 13234-13244.	1.2	58
33	Aggregation of VSV M protein is reversible and mediated by nucleation sites: Implications for viral assembly. <i>Virology</i> , 1995, 206, 28-37.	1.1	57
34	Isolation and Characterisation of the Rabies Virus N ^o -P Complex Produced in Insect Cells. <i>Virology</i> , 2003, 305, 406-414.	1.1	57
35	The Oligomeric States of <i>Haloarcula marismortui</i> Malate Dehydrogenase are Modulated by Solvent Components as Shown by Crystallographic and Biochemical Studies. <i>Journal of Molecular Biology</i> , 2003, 326, 859-873.	2.0	57
36	The ABC transporter BmrA from <i>Bacillus subtilis</i> is a functional dimer when in a detergent-solubilized state. <i>Biochemical Journal</i> , 2006, 395, 345-353.	1.7	57

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37	Reversible Dissociation and Unfolding of Dimeric Creatine Kinase Isoenzyme MM in Guanidine Hydrochloride and Urea. <i>FEBS Journal</i> , 1995, 234, 160-170.	0.2	54
38	Analytical Ultracentrifugation Sedimentation Velocity for the Characterization of Detergent-Solubilized Membrane Proteins Ca ⁺⁺ -ATPase and ExbB. <i>Journal of Biological Physics</i> , 2007, 33, 399-419.	0.7	50
39	Interplay of Protein Disorder in Retinoic Acid Receptor Heterodimer and Its Corepressor Regulates Gene Expression. <i>Structure</i> , 2019, 27, 1270-1285.e6.	1.6	50
40	Density Contrast Sedimentation Velocity for the Determination of Protein Partial-Specific Volumes. <i>PLoS ONE</i> , 2011, 6, e26221.	1.1	49
41	Sedimentation velocity to characterize surfactants and solubilized membrane proteins. <i>Methods</i> , 2011, 54, 56-66.	1.9	47
42	Unique DC-SIGN Clustering Activity of a Small Glycomimetic: A Lesson for Ligand Design. <i>ACS Chemical Biology</i> , 2014, 9, 1377-1385.	1.6	47
43	Insights into the Molecular Relationships between Malate and Lactate Dehydrogenases: A Structural and Biochemical Properties of Monomeric and Dimeric Intermediates of a Mutant of Tetrameric-[LDH-like] Malate Dehydrogenase from the Halophilic Archaeon <i>Haloarcula marismortui</i> . <i>Biochemistry</i> , 2000, 39, 1001-1010.	1.2	45
44	Trapping and Stabilization of Integral Membrane Proteins by Hydrophobically Grafted Glucose-Based Telomers. <i>Biomacromolecules</i> , 2009, 10, 3317-3326.	2.6	44
45	Link between Protein ⁺ Solvent and Weak Protein ⁺ Protein Interactions Gives Insight into Halophilic Adaptation. <i>Biochemistry</i> , 2002, 41, 13245-13252.	1.2	42
46	Characterization of a TET-like Aminopeptidase Complex from the Hyperthermophilic Archaeon <i>Pyrococcus horikoshii</i> . <i>Biochemistry</i> , 2005, 44, 3477-3486.	1.2	42
47	Glucose-Based Amphiphilic Telomers Designed to Keep Membrane Proteins Soluble in Aqueous Solutions: Synthesis and Physicochemical Characterization. <i>Langmuir</i> , 2008, 24, 13581-13590.	1.6	42
48	Assembly and Enzymatic Properties of the Catalytic Domain of Human Complement Protease C1r. <i>Journal of Biological Chemistry</i> , 2001, 276, 36233-36240.	1.6	40
49	Assessing the Conformational Changes of pb5, the Receptor-binding Protein of Phage T5, upon Binding to Its <i>Escherichia coli</i> Receptor FhuA. <i>Journal of Biological Chemistry</i> , 2013, 288, 30763-30772.	1.6	40
50	Lactobionamide Surfactants with Hydrogenated, Perfluorinated or Hemifluorinated Tails: A Physical-Chemical and Biochemical Characterization. <i>Langmuir</i> , 2006, 22, 8881-8890.	1.6	38
51	Mitochondrial Bovine ADP/ATP Carrier in Detergent Is Predominantly Monomeric but Also Forms Multimeric Species. <i>Biochemistry</i> , 2008, 47, 12319-12331.	1.2	38
52	Evidence for Kinetic Intermediate States during the Refolding of GdnHCl-Denatured MM-Creatine Kinase. Characterization of a Trapped Monomeric Species. <i>Biochemistry</i> , 1998, 37, 17579-17589.	1.2	37
53	Characterization of the Yeast Peroxiredoxin Ahp1 in Its Reduced Active and Overoxidized Inactive Forms Using NMR. <i>Biochemistry</i> , 2003, 42, 14139-14149.	1.2	37
54	The oligomer plasticity of the small heat-shock protein Lo18 from <i>Oenococcus oeni</i> influences its role in both membrane stabilization and protein protection. <i>Biochemical Journal</i> , 2012, 444, 97-104.	1.7	36

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55	Functionality of membrane proteins overexpressed and purified from <i>E. coli</i> is highly dependent upon the strain. <i>Scientific Reports</i> , 2019, 9, 2654.	1.6	36
56	An Archaeal Peptidase Assembles into Two Different Quaternary Structures. <i>Journal of Biological Chemistry</i> , 2006, 281, 36327-36337.	1.6	35
57	Modular Structure of the Full-Length DNA Gyrase B Subunit Revealed by Small-Angle X-Ray Scattering. <i>Structure</i> , 2007, 15, 329-339.	1.6	35
58	Oligomerization of the 17-kDa peptide-binding domain of the molecular chaperone HSC70. <i>FEBS Journal</i> , 1999, 259, 379-384.	0.2	34
59	Synergy between Extracellular Modules of Vascular Endothelial Cadherin Promotes Homotypic Hexameric Interactions. <i>Journal of Biological Chemistry</i> , 2002, 277, 12790-12801.	1.6	34
60	Characterization of the elongosome core PBP2 α :MreC complex of <i>Helicobacter pylori</i> . <i>Molecular Microbiology</i> , 2011, 82, 68-86.	1.2	34
61	AUC and Small-Angle Scattering for Membrane Proteins. <i>Methods in Enzymology</i> , 2015, 562, 257-286.	0.4	34
62	New Functional Sulfide Oxidase-Oxygen Reductase Supercomplex in the Membrane of the Hyperthermophilic Bacterium <i>Aquifex aeolicus</i> . <i>Journal of Biological Chemistry</i> , 2010, 285, 41815-41826.	1.6	33
63	The major leucyl aminopeptidase of <i>Trypanosoma cruzi</i> (LAPTc) assembles into a homohexamer and belongs to the M17 family of metallopeptidases. <i>BMC Biochemistry</i> , 2011, 12, 46.	4.4	33
64	Optimized Purification of a Heterodimeric ABC Transporter in a Highly Stable Form Amenable to 2-D Crystallization. <i>PLoS ONE</i> , 2011, 6, e19677.	1.1	32
65	Characterization of a Novel Complex from Halophilic Archaeobacteria, Which Displays Chaperone-like Activities in Vitro. <i>Journal of Biological Chemistry</i> , 2001, 276, 29906-29914.	1.6	31
66	Organic solvent extracted EmrE solubilized in dodecyl maltoside is monomeric and binds drug ligand. <i>Biochemical and Biophysical Research Communications</i> , 2005, 327, 437-445.	1.0	31
67	The RNA-binding region of human TRBP interacts with microRNA precursors through two independent domains. <i>Nucleic Acids Research</i> , 2013, 41, 4241-4252.	6.5	30
68	Micellar and biochemical properties of a propyl-ended fluorinated surfactant designed for membrane-protein study. <i>Journal of Colloid and Interface Science</i> , 2015, 445, 127-136.	5.0	30
69	Low Resolution Structure Determination Shows Procollagen C-Proteinase Enhancer to be an Elongated Multidomain Glycoprotein. <i>Journal of Biological Chemistry</i> , 2003, 278, 7199-7205.	1.6	29
70	Biophysical Characterization of the C-propeptide Trimer from Human Procollagen III Reveals a Tri-lobed Structure. <i>Journal of Biological Chemistry</i> , 2001, 276, 48930-48936.	1.6	28
71	Self-assembly of the Vascular Endothelial Cadherin Ectodomain in a Ca ²⁺ -dependent Hexameric Structure. <i>Journal of Biological Chemistry</i> , 2001, 276, 3581-3588.	1.6	27
72	The BR domain of PsrP interacts with extracellular DNA to promote bacterial aggregation; structural insights into pneumococcal biofilm formation. <i>Scientific Reports</i> , 2016, 6, 32371.	1.6	27

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73	Analytical Ultracentrifuge for the Characterization of Detergent in Solution. , 0, , 74-82.		26
74	The basic keratin 10-binding domain of the virulence-associated pneumococcal serine-rich protein PsrP adopts a novel MSCRAMM fold. <i>Open Biology</i> , 2014, 4, 130090.	1.5	26
75	An Example of Non-Conservation of Oligomeric Structure in Prokaryotic Aminoacyl-tRNA Synthetases. Biochemical and Structural Properties of Glycyl-tRNA Synthetase from <i>Thermus thermophilus</i> . <i>FEBS Journal</i> , 1996, 241, 814-826.	0.2	25
76	Enhancing Potency and Selectivity of a DCâ€SIGN Glycomimetic Ligand by Fragmentâ€Based Design: Structural Basis. <i>Chemistry - A European Journal</i> , 2019, 25, 14659-14668.	1.7	25
77	The <i>Trypanosoma cruzi</i> Virulence Factor Oligopeptidase B (OPBTc) Assembles into an Active and Stable Dimer. <i>PLoS ONE</i> , 2012, 7, e30431.	1.1	24
78	Functional determinants of the Epstein-Barr virus protease. <i>Journal of Molecular Biology</i> , 2001, 311, 217-228.	2.0	23
79	Assemblies of lauryl maltose neopentyl glycol (LMNG) and LMNG-solubilized membrane proteins. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 2019, 1861, 939-957.	1.4	23
80	Salivary apyrases of <i>Triatoma infestans</i> are assembled into homo-oligomers. <i>Biochemical Journal</i> , 2006, 396, 509-515.	1.7	22
81	A Central Role for Water in the Control of the Spin State of Cytochrome P-450 _{sc} . <i>FEBS Journal</i> , 1997, 250, 276-285.	0.2	21
82	Proteinâ€solvent and weak proteinâ€protein interactions in halophilic malate dehydrogenase. <i>Journal of Crystal Growth</i> , 1999, 196, 395-402.	0.7	21
83	A diglycosylated fluorinated surfactant to handle integral membrane proteins in aqueous solution. <i>Journal of Fluorine Chemistry</i> , 2012, 134, 63-71.	0.9	21
84	Comparison of solubility and interactions of aprotinin (BPTI) solutions in H ₂ O and D ₂ O. <i>Journal of Crystal Growth</i> , 2000, 217, 311-319.	0.7	20
85	Understanding the crystallisation of an acidic protein by dilution in the ternary NaClâ€2-methyl-2,4-pentanediolâ€H ₂ O system. <i>Journal of Crystal Growth</i> , 2001, 232, 102-113.	0.7	20
86	Potassium Acts as a GTPase-Activating Element on Each Nucleotide-Binding Domain of the Essential <i>Bacillus subtilis</i> EngA. <i>PLoS ONE</i> , 2012, 7, e46795.	1.1	20
87	Influence of an anion-binding site in the stabilization of halophilic malate dehydrogenase from <i>Haloarcula marismortui</i> . <i>Biochimie</i> , 2007, 89, 981-987.	1.3	19
88	Organization of Human Interferon Î³â€Heparin Complexes from Solution Properties and Hydrodynamicsâ€. <i>Biochemistry</i> , 2006, 45, 13227-13238.	1.2	18
89	Structure and Interactions of Fish Type III Antifreeze Protein inâ€Solution. <i>Biophysical Journal</i> , 2010, 99, 609-618.	0.2	18
90	Sparingly fluorinated maltoside-based surfactants for membrane-protein stabilization. <i>New Journal of Chemistry</i> , 2016, 40, 5364-5378.	1.4	18

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91	Fluorinated diglucose detergents for membrane-protein extraction. <i>Methods</i> , 2018, 147, 84-94.	1.9	18
92	Crowding in extremophiles: linkage between solvation and weak protein-protein interactions, stability and dynamics, provides insight into molecular adaptation. <i>Journal of Molecular Recognition</i> , 2004, 17, 382-389.	1.1	17
93	Sedimentation Velocity Analytical Ultracentrifugation for Intrinsically Disordered Proteins. <i>Methods in Molecular Biology</i> , 2012, 896, 91-105.	0.4	17
94	X-ray structure of full-length human RuvB-Like 2 - mechanistic insights into coupling between ATP binding and mechanical action. <i>Scientific Reports</i> , 2018, 8, 13726.	1.6	17
95	Probing the Conformation of FhaC with Small-Angle Neutron Scattering and Molecular Modeling. <i>Biophysical Journal</i> , 2014, 107, 185-196.	0.2	16
96	The MurG glycosyltransferase provides an oligomeric scaffold for the cytoplasmic steps of peptidoglycan biosynthesis in the human pathogen <i>Bordetella pertussis</i> . <i>Scientific Reports</i> , 2019, 9, 4656.	1.6	15
97	Tail proteins of phage T5: Investigation of the effect of the His6-tag position, from expression to crystallisation. <i>Protein Expression and Purification</i> , 2015, 109, 70-78.	0.6	14
98	Sedimentation Velocity Analytical Ultracentrifugation in Hydrogenated and Deuterated Solvents for the Characterization of Membrane Proteins. <i>Methods in Molecular Biology</i> , 2013, 1033, 219-251.	0.4	14
99	Complex Formation between Mur Enzymes from <i>Streptococcus pneumoniae</i> . <i>Biochemistry</i> , 2019, 58, 3314-3324.	1.2	13
100	TETRALEC, Artificial Tetrameric Lectins: A Tool to Screen Ligand and Pathogen Interactions. <i>International Journal of Molecular Sciences</i> , 2020, 21, 5290.	1.8	13
101	New Amphiphiles to Handle Membrane Proteins: - Between Chemistry, Physical Chemistry, and Biochemistry. , 2014, , 205-251.		13
102	Structural Insights into the Catalytic Cycle of a Bacterial Multidrug ABC Efflux Pump. <i>Journal of Molecular Biology</i> , 2022, 434, 167541.	2.0	13
103	Hydrogenated Diglucose Detergents for Membrane-Protein Extraction and Stabilization. <i>Langmuir</i> , 2019, 35, 4287-4295.	1.6	12
104	The role of polar and dispersive parts of surface tension on the bistability of SmC cells. <i>Ferroelectrics</i> , 1988, 85, 47-56.	0.3	11
105	Active Detergent-solubilized H ⁺ ,K ⁺ -ATPase Is a Monomer*. <i>Journal of Biological Chemistry</i> , 2012, 287, 41963-41978.	1.6	11
106	Hybrid Fluorinated and Hydrogenated Double-Chain Surfactants for Handling Membrane Proteins. <i>Journal of Organic Chemistry</i> , 2016, 81, 681-688.	1.7	11
107	Maltose-Based Fluorinated Surfactants for Membrane-Protein Extraction and Stabilization. <i>Langmuir</i> , 2021, 37, 2111-2122.	1.6	11
108	Self-association of adenine-dependent hairpin ribozymes. <i>European Biophysics Journal</i> , 2008, 37, 173-182.	1.2	10

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109	Role of Phosphorylation in Moesin Interactions with PIP2-Containing Biomimetic Membranes. <i>Biophysical Journal</i> , 2018, 114, 98-112.	0.2	10
110	Oligomeric structure of the repressor of the bacteriophage Mu early operon. <i>FEBS Journal</i> , 1998, 252, 408-415.	0.2	9
111	Thermodynamic relationships between protein-solvent and protein-protein interactions. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2002, 58, 1554-1559.	2.5	9
112	Essential Kinesins: Characterization of <i>Caenorhabditis elegans</i> KLP-15. <i>Biochemistry</i> , 2005, 44, 6526-6536.	1.2	9
113	Interdomain Flexibility within NADPH Oxidase Suggested by SANS Using LMNG Stealth Carrier. <i>Biophysical Journal</i> , 2020, 119, 605-618.	0.2	9
114	Oligomeric Status and Nucleotide Binding Properties of the Plastid ATP/ADP Transporter 1: Toward a Molecular Understanding of the Transport Mechanism. <i>PLoS ONE</i> , 2012, 7, e32325.	1.1	9
115	Cold-induced conformational changes of ribonuclease A as investigated by subzero transverse temperature gradient gel electrophoresis. <i>BBA - Proteins and Proteomics</i> , 1994, 1208, 1-7.	2.1	8
116	Solution Behavior of Amphiphilic Glycodendrimers with a Rod-Like Core. <i>Macromolecular Bioscience</i> , 2016, 16, 896-905.	2.1	8
117	Fine-tuning of intrinsic N-Oct-3 POU domain allostery by regulatory DNA targets. <i>Nucleic Acids Research</i> , 2007, 35, 4420-4432.	6.5	7
118	Solvent Mediated Protein-Protein Interactions. , 2007, , 255-287.		7
119	Small-angle neutron scattering study of halophilic glyceraldehyde 3-phosphate dehydrogenase (hGAPDH). <i>Physica B: Condensed Matter</i> , 1991, 174, 306-308.	1.3	3
120	Molecular Adaptation to High Salt. , 0, , 240-253.		3
121	New ferroelectric materials with high spontaneous polarization: Synthesis, physical properties and electro-optical behaviour of some mixtures. <i>Ferroelectrics</i> , 1988, 85, 441-450.	0.3	2
122	Analytical Ultracentrifugation and Size-Exclusion Chromatography Coupled with Light Scattering for the Characterization of Membrane Proteins in Solution. , 2014, , 267-287.		2
123	Glucose-Based Fluorinated Surfactants as Additives for the Crystallization of Membrane Proteins: Synthesis and Preliminary Physical-Chemical and Biochemical Characterization. <i>ACS Omega</i> , 2021, 6, 24397-24406.	1.6	2
124	Sedimentation Velocity Methods for the Characterization of Protein Heterogeneity and Protein Affinity Interactions. <i>Methods in Molecular Biology</i> , 2021, 2247, 155-171.	0.4	2
125	Assembly of an atypical Γ -macroglobulin complex from <i>Pseudomonas aeruginosa</i> . <i>Scientific Reports</i> , 2018, 8, 527.	1.6	1
126	AUC in the High Concentration of Salts/Cosolvent. , 2016, , 355-373.		0

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127	Examining Membrane Proteins by Neutron Scattering. Methods in Molecular Biology, 2020, 2168, 147-175.	0.4	0