

JosÃ© M Valpuesta

List of Publications by Year in descending order

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174
papers

9,640
citations

29994

54
h-index

46693

89
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180
all docs

180
docs citations

180
times ranked

10034
citing authors

#	ARTICLE	IF	CITATIONS
1	Structural characterization of toxic oligomers that are kinetically trapped during α -synuclein fibril formation. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, E1994-2003.	3.3	384
2	Polymerization of β , into Filaments in the Presence of Heparin: The Minimal Sequence Required for β , α interaction. Journal of Neurochemistry, 1996, 67, 1183-1190.	2.1	352
3	Coexistence of multivalent and monovalent TCRs explains high sensitivity and wide range of response. Journal of Experimental Medicine, 2005, 202, 493-503.	4.2	288
4	The Structure of Native Influenza Virion Ribonucleoproteins. Science, 2012, 338, 1634-1637.	6.0	254
5	Eukaryotic type II chaperonin CCT interacts with actin through specific subunits. Nature, 1999, 402, 693-696.	13.7	247
6	Detailed architecture of a DNA translocating machine: the high-resolution structure of the bacteriophage ϕ 29 connector particle 1 Edited by R. Huber. Journal of Molecular Biology, 2002, 315, 663-676.	2.0	205
7	Structure of the Hsp110:Hsc70 Nucleotide Exchange Machine. Molecular Cell, 2008, 31, 232-243.	4.5	202
8	Eukaryotic chaperonin CCT stabilizes actin and tubulin folding intermediates in open quasi-native conformations. EMBO Journal, 2000, 19, 5971-5979.	3.5	193
9	Structure and function of a protein folding machine: the eukaryotic cytosolic chaperonin CCT. FEBS Letters, 2002, 529, 11-16.	1.3	193
10	The Structure of a Biologically Active Influenza Virus Ribonucleoprotein Complex. PLoS Pathogens, 2009, 5, e1000491.	2.1	186
11	Structure of eukaryotic prefoldin and of its complexes with unfolded actin and the cytosolic chaperonin CCT. EMBO Journal, 2002, 21, 6377-6386.	3.5	184
12	Hsp70 α a master regulator in protein degradation. FEBS Letters, 2017, 591, 2648-2660.	1.3	176
13	Structure of viral connectors and their function in bacteriophage assembly and DNA packaging. Quarterly Reviews of Biophysics, 1994, 27, 107-155.	2.4	157
14	Increased Sensitivity of Antigen-Experienced T Cells through the Enrichment of Oligomeric T Cell Receptor Complexes. Immunity, 2011, 35, 375-387.	6.6	153
15	Analysis of Electron Microscope Images and Electron Diffraction Patterns of Thin Crystals of ϕ 29 Connectors in Ice. Journal of Molecular Biology, 1994, 240, 281-287.	2.0	151
16	Chaperonins: two rings for folding. Trends in Biochemical Sciences, 2011, 36, 424-432.	3.7	140
17	Mechanical Identities of RNA and DNA Double Helices Unveiled at the Single-Molecule Level. Journal of the American Chemical Society, 2013, 135, 122-131.	6.6	139
18	Structure and thermal denaturation of crystalline and noncrystalline cytochrome oxidase as studied by infrared spectroscopy. Biochemistry, 1994, 33, 11650-11655.	1.2	132

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19	The 'sequential allosteric ring' mechanism in the eukaryotic chaperonin-assisted folding of actin and tubulin. <i>EMBO Journal</i> , 2001, 20, 4065-4075.	3.5	130
20	Modulation of the Hsp90 Chaperone Cycle by a Stringent Client Protein. <i>Molecular Cell</i> , 2014, 53, 941-953.	4.5	129
21	Crystal structure of the open conformation of the mammalian chaperonin CCT in complex with tubulin. <i>Nature Structural and Molecular Biology</i> , 2011, 18, 14-19.	3.6	128
22	Interaction of p53 with the CCT Complex Promotes Protein Folding and Wild-Type p53 Activity. <i>Molecular Cell</i> , 2013, 50, 805-817.	4.5	121
23	Maturation of phage T7 involves structural modification of both shell and inner core components. <i>EMBO Journal</i> , 2005, 24, 3820-3829.	3.5	118
24	3D structure of the influenza virus polymerase complex: Localization of subunit domains. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2004, 101, 308-313.	3.3	116
25	Ultrastructural and Functional Analyses of Recombinant Influenza Virus Ribonucleoproteins Suggest Dimerization of Nucleoprotein during Virus Amplification. <i>Journal of Virology</i> , 2000, 74, 156-163.	1.5	111
26	Changes in Microtubule Protofilament Number Induced by Taxol Binding to an Easily Accessible Site. <i>Journal of Biological Chemistry</i> , 1998, 273, 33803-33810.	1.6	104
27	Structural characterization of the substrate transfer mechanism in Hsp70/Hsp90 folding machinery mediated by Hop. <i>Nature Communications</i> , 2014, 5, 5484.	5.8	104
28	Hsp70 chaperone: a master player in protein homeostasis. <i>F1000Research</i> , 2018, 7, 1497.	0.8	103
29	3D reconstruction of the ATP-bound form of CCT reveals the asymmetric folding conformation of a type II chaperonin. <i>Nature Structural Biology</i> , 1999, 6, 639-642.	9.7	102
30	Energetics and Geometry of FtsZ Polymers: Nucleated Self-Assembly of Single Protofilaments. <i>Biophysical Journal</i> , 2008, 94, 1796-1806.	0.2	100
31	Structure of the Connector of Bacteriophage T7 at 8Å... Resolution: Structural Homologies of a Basic Component of a DNA Translocating Machinery. <i>Journal of Molecular Biology</i> , 2005, 347, 895-902.	2.0	99
32	Characterization of ATP and DNA Binding Activities of TrwB, the Coupling Protein Essential in Plasmid R388 Conjugation. <i>Journal of Biological Chemistry</i> , 1999, 274, 36117-36124.	1.6	97
33	The formation of symmetrical GroEL-GroES complexes in the presence of ATP. <i>FEBS Letters</i> , 1994, 345, 181-186.	1.3	86
34	Assembly of Archaeal Cell Division Protein FtsZ and a GTPase-inactive Mutant into Double-stranded Filaments. <i>Journal of Biological Chemistry</i> , 2003, 278, 33562-33570.	1.6	86
35	Three-dimensional reconstruction of a recombinant influenza virus ribonucleoprotein particle. <i>EMBO Reports</i> , 2001, 2, 313-317.	2.0	85
36	The structure of CCT-Hsc70NBD suggests a mechanism for Hsp70 delivery of substrates to the chaperonin. <i>Nature Structural and Molecular Biology</i> , 2008, 15, 858-864.	3.6	85

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37	Dynamics, flexibility, and allostery in molecular chaperonins. <i>FEBS Letters</i> , 2015, 589, 2522-2532.	1.3	83
38	β -Peptide Nanotube Templating of One-Dimensional Parallel Fullerene Arrangements. <i>Journal of the American Chemical Society</i> , 2009, 131, 11335-11337.	6.6	81
39	Architecture and nucleic acids recognition mechanism of the THO complex, an mRNP assembly factor. <i>EMBO Journal</i> , 2012, 31, 1605-1616.	3.5	79
40	Structural Characterization of the Bacteriophage T7 Tail Machinery. <i>Journal of Biological Chemistry</i> , 2013, 288, 26290-26299.	1.6	75
41	SADB phosphorylation of β -tubulin regulates centrosome duplication. <i>Nature Cell Biology</i> , 2009, 11, 1081-1092.	4.6	73
42	The substrate recognition mechanisms in chaperonins. <i>Journal of Molecular Recognition</i> , 2004, 17, 85-94.	1.1	71
43	Topology of the components of the DNA packaging machinery in the phage ϕ 29 prohead. <i>Journal of Molecular Biology</i> , 2000, 298, 807-815.	2.0	70
44	Analysis of the Interaction between the Eukaryotic Chaperonin CCT and Its Substrates Actin and Tubulin. <i>Journal of Structural Biology</i> , 2001, 135, 205-218.	1.3	70
45	PhLP3 Modulates CCT-mediated Actin and Tubulin Folding via Ternary Complexes with Substrates. <i>Journal of Biological Chemistry</i> , 2006, 281, 7012-7021.	1.6	69
46	Arc is a flexible modular protein capable of reversible self-oligomerization. <i>Biochemical Journal</i> , 2015, 468, 145-158.	1.7	69
47	Active DNA unwinding dynamics during processive DNA replication. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 8115-8120.	3.3	67
48	Clathrin-coat disassembly illuminates the mechanisms of Hsp70 force generation. <i>Nature Structural and Molecular Biology</i> , 2016, 23, 821-829.	3.6	67
49	The Hexameric Structure of a Conjugative VirB4 Protein ATPase Provides New Insights for a Functional and Phylogenetic Relationship with DNA Translocases. <i>Journal of Biological Chemistry</i> , 2012, 287, 39925-39932.	1.6	66
50	Structure of the complex between the cytosolic chaperonin CCT and phospho-ucin-like protein. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2004, 101, 17410-17415.	3.3	65
51	Reversible interaction of beta-actin along the channel of the TCP-1 cytoplasmic chaperonin. <i>Biophysical Journal</i> , 1994, 67, 364-368.	0.2	64
52	Purification and Properties of TrwB, a Hexameric, ATP-binding Integral Membrane Protein Essential for R388 Plasmid Conjugation. <i>Journal of Biological Chemistry</i> , 2002, 277, 46456-46462.	1.6	63
53	The three-dimensional structure of an eukaryotic glutamine synthetase: Functional implications of its oligomeric structure. <i>Journal of Structural Biology</i> , 2006, 156, 469-479.	1.3	61
54	Electron cryo-microscopic analysis of crystalline cytochrome oxidase. <i>Journal of Molecular Biology</i> , 1990, 214, 237-251.	2.0	60

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55	Molecular clamp mechanism of substrate binding by hydrophobic coiled-coil residues of the archaeal chaperone prefoldin. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2004, 101, 4367-4372.	3.3	57
56	Segregated ordered lipid phases and protein-promoted membrane cohesivity are required for pulmonary surfactant films to stabilize and protect the respiratory surface. <i>Faraday Discussions</i> , 2013, 161, 535-548.	1.6	57
57	Divergent Substrate-Binding Mechanisms Reveal an Evolutionary Specialization of Eukaryotic Prefoldin Compared to Its Archaeal Counterpart. <i>Structure</i> , 2007, 15, 101-110.	1.6	55
58	Molecular Rearrangements Involved in the Capsid Shell Maturation of Bacteriophage T7. <i>Journal of Biological Chemistry</i> , 2011, 286, 234-242.	1.6	55
59	ATP Binding Induces Large Conformational Changes in the Apical and Equatorial Domains of the Eukaryotic Chaperonin Containing TCP-1 Complex. <i>Journal of Biological Chemistry</i> , 1998, 273, 10091-10094.	1.6	54
60	The three-dimensional structure of a DNA translocating machine at 10 Å... resolution. <i>Structure</i> , 1999, 7, 289-296.	1.6	52
61	GroEL under Heat-Shock. <i>Journal of Biological Chemistry</i> , 1998, 273, 32587-32594.	1.6	49
62	Structures of the GÎ²-CCT and PhLP1-Î²-CCT complexes reveal a mechanism for G-protein Î²-subunit folding and GÎ²Î³ dimer assembly. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 2413-2418.	3.3	49
63	Mechano-chemical kinetics of DNA replication: identification of the translocation step of a replicative DNA polymerase. <i>Nucleic Acids Research</i> , 2015, 43, 3643-3652.	6.5	48
64	The chaperonin CCT inhibits assembly of Î±-synuclein amyloid fibrils by a specific, conformation-dependent interaction. <i>Scientific Reports</i> , 2017, 7, 40859.	1.6	48
65	Elevated levels of Secreted-Frizzled-Related-Protein 1 contribute to Alzheimer's disease pathogenesis. <i>Nature Neuroscience</i> , 2019, 22, 1258-1268.	7.1	48
66	The architecture of the <i>Schizosaccharomyces pombe</i> CCR4-NOT complex. <i>Nature Communications</i> , 2016, 7, 10433.	5.8	47
67	Structural and functional analysis of the role of the chaperonin CCT in mTOR complex assembly. <i>Nature Communications</i> , 2019, 10, 2865.	5.8	47
68	Three-dimensional structure of T3 connector purified from overexpressing bacteria. <i>Journal of Molecular Biology</i> , 1992, 224, 103-112.	2.0	45
69	HYDROMIC: prediction of hydrodynamic properties of rigid macromolecular structures obtained from electron microscopy images. <i>European Biophysics Journal</i> , 2001, 30, 457-462.	1.2	45
70	Prefoldin 5 Is Required for Normal Sensory and Neuronal Development in a Murine Model. <i>Journal of Biological Chemistry</i> , 2011, 286, 726-736.	1.6	45
71	The Broadly Neutralizing Anti-Human Immunodeficiency Virus Type 1 4E10 Monoclonal Antibody Is Better Adapted to Membrane-Bound Epitope Recognition and Blocking than 2F5. <i>Journal of Virology</i> , 2008, 82, 8986-8996.	1.5	44
72	Structural comparison of prokaryotic and eukaryotic chaperonins. <i>Micron</i> , 2001, 32, 43-50.	1.1	43

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73	High resolution atomic force microscopy of double-stranded RNA. <i>Nanoscale</i> , 2016, 8, 11818-11826.	2.8	42
74	Biochemical Characterization of Symmetric GroEL-GroES Complexes. <i>Journal of Biological Chemistry</i> , 1996, 271, 68-76.	1.6	40
75	Crystallographic analysis reveals the 12-fold symmetry of the bacteriophage ϕ 29 connector particle. <i>Journal of Molecular Biology</i> , 1998, 281, 219-225.	2.0	39
76	Conformational Changes in the GroEL Oligomer during the Functional Cycle. <i>Journal of Structural Biology</i> , 1997, 118, 31-42.	1.3	38
77	Structural Analysis of the Bacteriophage T3 Head-to-Tail Connector. <i>Journal of Structural Biology</i> , 2000, 131, 146-155.	1.3	38
78	Excluded Volume Effects on the Refolding and Assembly of an Oligomeric Protein. <i>Journal of Biological Chemistry</i> , 2001, 276, 957-964.	1.6	38
79	Purification and functional characterization of p16, the ATPase of the bacteriophage Phi29 packaging machinery. <i>Nucleic Acids Research</i> , 2001, 29, 4264-4273.	6.5	38
80	The cochaperone CHIP marks Hsp70- and Hsp90-bound substrates for degradation through a very flexible mechanism. <i>Scientific Reports</i> , 2019, 9, 5102.	1.6	38
81	The interring arrangement of the cytosolic chaperonin CCT. <i>EMBO Reports</i> , 2007, 8, 252-257.	2.0	37
82	Interactions of the HIV-1 fusion peptide with large unilamellar vesicles and monolayers. A cryo-TEM and spectroscopic study. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 2000, 1467, 153-164.	1.4	36
83	Point Mutations in a Hinge Linking the Small and Large Domains of β -Actin Result in Trapped Folding Intermediates Bound to Cytosolic Chaperonin CCT. <i>Journal of Structural Biology</i> , 2001, 135, 198-204.	1.3	35
84	Bacterial Tubulin Distinct Loop Sequences and Primitive Assembly Properties Support Its Origin from a Eukaryotic Tubulin Ancestor. <i>Journal of Biological Chemistry</i> , 2011, 286, 19789-19803.	1.6	35
85	Symmetric GroEL-GroES complexes can contain substrate simultaneously in both GroEL rings. <i>FEBS Letters</i> , 1997, 405, 195-199.	1.3	33
86	Domain architecture of the bacteriophage ϕ 29 connector protein. <i>Journal of Molecular Biology</i> , 1999, 288, 899-909.	2.0	33
87	Condensation Prevails over B-A Transition in the Structure of DNA at Low Humidity. <i>Biophysical Journal</i> , 2011, 100, 2006-2015.	0.2	33
88	Large Terminase Conformational Change Induced by Connector Binding in Bacteriophage T7. <i>Journal of Biological Chemistry</i> , 2013, 288, 16998-17007.	1.6	33
89	Interbilayer lipid mixing induced by the human immunodeficiency virus type-1 fusion peptide on large unilamellar vesicles: the nature of the nonlamellar intermediates. <i>Chemistry and Physics of Lipids</i> , 1999, 103, 11-20.	1.5	31
90	Partial Occlusion of Both Cavities of the Eukaryotic Chaperonin with Antibody Has No Effect upon the Rates of β -Actin or α -Tubulin Folding. <i>Journal of Biological Chemistry</i> , 2000, 275, 4587-4591.	1.6	31

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91	All three chaperonin genes in the archaeon <i>Haloferax volcanii</i> are individually dispensable. <i>Molecular Microbiology</i> , 2006, 61, 1583-1597.	1.2	31
92	Microcin E492 Amyloid Formation Is Retarded by Posttranslational Modification. <i>Journal of Bacteriology</i> , 2013, 195, 3995-4004.	1.0	31
93	Programmed Cell Death Protein 5 Interacts with the Cytosolic Chaperonin Containing Tailless Complex Polypeptide 1 (CCT) to Regulate β -Tubulin Folding. <i>Journal of Biological Chemistry</i> , 2014, 289, 4490-4502.	1.6	31
94	Infrared spectroscopic studies of detergent-solubilized uncoupling protein from brown-adipose-tissue mitochondria. <i>FEBS Journal</i> , 1990, 188, 83-89.	0.2	30
95	Nucleoplasmin Binds Histone H2A-H2B Dimers through Its Distal Face*. <i>Journal of Biological Chemistry</i> , 2010, 285, 33771-33778.	1.6	29
96	Stress-induced recrystallization of a protein crystal by electron irradiation. <i>Nature</i> , 1999, 399, 51-54.	13.7	27
97	The structure of the TBCE/TBCB chaperones and β -tubulin complex shows a tubulin dimer dissociation mechanism. <i>Journal of Cell Science</i> , 2015, 128, 1824-34.	1.2	27
98	The Interaction of DNA with Bacteriophage ϕ 29 Connector: A Study by AFM and TEM. <i>Journal of Structural Biology</i> , 1996, 116, 390-398.	1.3	25
99	Gold Nanoparticles Generated in Ethosome Bilayers, As Revealed by Cryo-Electron-Tomography. <i>Journal of Physical Chemistry B</i> , 2009, 113, 3051-3057.	1.2	25
100	Identification of Key Amino Acid Residues Modulating Intracellular and In vitro Microcin E492 Amyloid Formation. <i>Frontiers in Microbiology</i> , 2016, 7, 35.	1.5	25
101	Structure and Non-Structure of Centrosomal Proteins. <i>PLoS ONE</i> , 2013, 8, e62633.	1.1	25
102	Conformational Changes Generated in GroEL during ATP Hydrolysis as Seen by Time-resolved Infrared Spectroscopy. <i>Journal of Biological Chemistry</i> , 1999, 274, 5508-5513.	1.6	24
103	IHF protein inhibits cleavage but not assembly of plasmid R388 relaxosomes. <i>Molecular Microbiology</i> , 1999, 31, 1643-1652.	1.2	24
104	GroEL Stability and Function. <i>Journal of Biological Chemistry</i> , 2003, 278, 32083-32090.	1.6	24
105	Sequential Action of ATP-dependent Subunit Conformational Change and Interaction between Helical Protrusions in the Closure of the Built-in Lid of Group II Chaperonins. <i>Journal of Biological Chemistry</i> , 2008, 283, 34773-34784.	1.6	24
106	Structural characterization of the NAP; the major adhesion complex of the human pathogen <i>Mycoplasma genitalium</i> . <i>Molecular Microbiology</i> , 2017, 105, 869-879.	1.2	24
107	The chaperonin CCT controls T cell receptor-driven 3D configuration of centrioles. <i>Science Advances</i> , 2020, 6, .	4.7	23
108	Structural mechanism for tyrosine hydroxylase inhibition by dopamine and reactivation by Ser40 phosphorylation. <i>Nature Communications</i> , 2022, 13, 74.	5.8	23

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109	Selection of antibody probes to correlate protein sequence domains with their structural distribution. <i>Protein Science</i> , 1999, 8, 883-889.	3.1	22
110	Single Centrosome Manipulation Reveals Its Electric Charge and Associated Dynamic Structure. <i>Biophysical Journal</i> , 2009, 97, 1022-1030.	0.2	22
111	Structural characterization of microcin E492 amyloid formation: Identification of the precursors. <i>Journal of Structural Biology</i> , 2012, 178, 54-60.	1.3	22
112	The chaperonin CCT promotes the formation of fibrillar aggregates of β -tubulin. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2018, 1866, 519-526.	1.1	22
113	Salt Bridges at the Inter-ring Interface Regulate the Thermostat of GroEL. <i>Journal of Biological Chemistry</i> , 2002, 277, 34024-34029.	1.6	21
114	Structural Insights into the Chaperone Activity of the 40-kDa Heat Shock Protein DnaJ. <i>Journal of Biological Chemistry</i> , 2013, 288, 15065-15074.	1.6	21
115	Molecular determinants of the ATP hydrolysis asymmetry of the CCT chaperonin complex. <i>Proteins: Structure, Function and Bioinformatics</i> , 2014, 82, 703-707.	1.5	21
116	Effect of the nonionic detergent Triton X-100 on mitochondrial succinate-oxidizing enzymes. <i>Archives of Biochemistry and Biophysics</i> , 1984, 228, 560-568.	1.4	20
117	Effects of the Inter-ring Communication in GroEL Structural and Functional Asymmetry. <i>Journal of Biological Chemistry</i> , 1997, 272, 32925-32932.	1.6	20
118	Mechanical Properties of High-GC Content DNA with A-Type Base-Stacking. <i>Biophysical Journal</i> , 2011, 100, 1996-2005.	0.2	20
119	Modulation of the Chaperone DnaK Allosterism by the Nucleotide Exchange Factor GrpE. <i>Journal of Biological Chemistry</i> , 2015, 290, 10083-10092.	1.6	20
120	Structure and Function of the Cochaperone Prefoldin. <i>Advances in Experimental Medicine and Biology</i> , 2018, 1106, 119-131.	0.8	20
121	Structural characterization of the TCR complex by electron microscopy. <i>International Immunology</i> , 2010, 22, 897-903.	1.8	19
122	Structure of GroEL in Complex with an Early Folding Intermediate of Alanine Glyoxylate Aminotransferase. <i>Journal of Biological Chemistry</i> , 2010, 285, 6371-6376.	1.6	19
123	Phosphorylation Dependence and Stoichiometry of the Complex Formed by Tyrosine Hydroxylase and 14-3-3 β . <i>Molecular and Cellular Proteomics</i> , 2014, 13, 2017-2030.	2.5	19
124	A new side opening on prolyl oligopeptidase revealed by electron microscopy. <i>FEBS Letters</i> , 2009, 583, 3344-3348.	1.3	17
125	The intrinsically disordered distal face of nucleoplasmin recognizes distinct oligomerization states of histones. <i>Nucleic Acids Research</i> , 2014, 42, 1311-1325.	6.5	17
126	Engineering protein assemblies with allosteric control via monomer fold-switching. <i>Nature Communications</i> , 2019, 10, 5703.	5.8	17

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127	DNA conformational change induced by the bacteriophage λ 29 connector. <i>Nucleic Acids Research</i> , 1992, 20, 5549-5554.	6.5	15
128	Beyond the known functions of the CCR4-NOT complex in gene expression regulatory mechanisms. <i>BioEssays</i> , 2016, 38, 1048-1058.	1.2	15
129	Chaperonin Mechanisms: Multiple and (Mis)Understood?. <i>Annual Review of Biophysics</i> , 2022, 51, 115-133.	4.5	15
130	An infrared spectroscopic study of specifically deuterated fatty-acyl methyl groups in phosphatidylcholine liposomes. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 1991, 1065, 29-34.	1.4	14
131	Prediction of the structure of GroES and its interaction with GroEL. <i>Proteins: Structure, Function and Bioinformatics</i> , 1995, 22, 199-209.	1.5	14
132	Characterization by atomic force microscopy and cryoelectron microscopy of tau polymers assembled in Alzheimer's disease1. <i>Journal of Alzheimer's Disease</i> , 2001, 3, 443-451.	1.2	14
133	The yeast THO complex forms a 5-subunit assembly that directly interacts with active chromatin. <i>Bioarchitecture</i> , 2012, 2, 134-137.	1.5	14
134	Folding, Stability and Polymerization Properties of FtsZ Chimeras with Inserted Tubulin Loops Involved in the Interaction with the Cytosolic Chaperonin CCT and in Microtubule Formation. <i>Journal of Molecular Biology</i> , 2005, 346, 319-330.	2.0	13
135	Mechanical stability of low-humidity single DNA molecules. <i>Biopolymers</i> , 2012, 97, 199-208.	1.2	13
136	Assisted protein folding at low temperature: evolutionary adaptation of the Antarctic fish chaperonin CCT and its client proteins. <i>Biology Open</i> , 2014, 3, 261-270.	0.6	12
137	Phosphoinositide 3-Kinase Beta Protects Nuclear Envelope Integrity by Controlling RCC1 Localization and Ran Activity. <i>Molecular and Cellular Biology</i> , 2015, 35, 249-263.	1.1	12
138	Structural Analysis of the Interactions Between Hsp70 Chaperones and the Yeast DNA Replication Protein Orc4p. <i>Journal of Molecular Biology</i> , 2010, 403, 24-39.	2.0	11
139	Lipid-protein interactions. The mitochondrial complex III-phosphatidylcholine-water system. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 1988, 942, 341-352.	1.4	10
140	ATP hydrolysis induces an intermediate conformational state in GroEL. <i>FEBS Journal</i> , 1999, 259, 347-355.	0.2	10
141	Assisted assembly of bacteriophage T7 core components for genome translocation across the bacterial envelope. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	3.3	10
142	Purification, crystallization and preliminary X-ray diffraction studies of the bacteriophage λ 29 connector particle. <i>FEBS Letters</i> , 1998, 430, 283-287.	1.3	9
143	Manipulation of single polymerase-DNA complexes: A mechanical view of DNA unwinding during replication. <i>Cell Cycle</i> , 2012, 11, 2967-2968.	1.3	9
144	Molecular chaperones: functional mechanisms and nanotechnological applications. <i>Nanotechnology</i> , 2016, 27, 324004.	1.3	9

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145	Molecular architecture of the Bardet-Biedl syndrome protein 2-7-9 subcomplex. <i>Journal of Biological Chemistry</i> , 2019, 294, 16385-16399.	1.6	9
146	Recognition of Membrane-Bound Fusion-Peptide/MPER Complexes by the HIV-1 Neutralizing 2F5 Antibody: Implications for Anti-2F5 Immunogenicity. <i>PLoS ONE</i> , 2012, 7, e52740.	1.1	9
147	Laser light-scattering characterization of mitochondrial complex III-Triton X-100-phospholipid mixed micelles. <i>Biochimica Et Biophysica Acta - Bioenergetics</i> , 1985, 807, 96-99.	0.5	8
148	Ionic interactions at both inter-ring contact sites of GroEL are involved in transmission of the allosteric signal: A time-resolved infrared difference study. <i>Protein Science</i> , 2005, 14, 2267-2274.	3.1	8
149	Size-selective recognition of gold nanoparticles by a molecular chaperone. <i>Chemical Physics Letters</i> , 2010, 501, 108-112.	1.2	8
150	Structural insights into the ability of nucleoplasmin to assemble and chaperone histone octamers for DNA deposition. <i>Scientific Reports</i> , 2019, 9, 9487.	1.6	8
151	Tryptophan fluorescence of mitochondrial complex III reconstituted in phosphatidylcholine bilayers. <i>Archives of Biochemistry and Biophysics</i> , 1987, 257, 285-292.	1.4	7
152	A structural model for the GroEL chaperonin. <i>FEMS Microbiology Letters</i> , 1993, 106, 301-308.	0.7	7
153	Characterization of the structure and self-recognition of the human centrosomal protein NA14: implications for stability and function. <i>Protein Engineering, Design and Selection</i> , 2011, 24, 883-892.	1.0	7
154	Yeast mitochondrial RNAP conformational changes are regulated by interactions with the mitochondrial transcription factor. <i>Nucleic Acids Research</i> , 2014, 42, 11246-11260.	6.5	7
155	Folding for the Immune Synapse: CCT Chaperonin and the Cytoskeleton. <i>Frontiers in Cell and Developmental Biology</i> , 2021, 9, 658460.	1.8	7
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