

# 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  
g-index

180  
all docs

180  
docs citations

180  
times ranked

10034  
citing authors

| #  | ARTICLE   | IF  | CITATIONS |
|----|---|-----|-----------|
| 1  | The Molecular Chaperone CCT Sequesters Gelsolin and Protects it from Cleavage by Caspase-3. <i>Journal of Molecular Biology</i> , 2022, 434, 167399.  | 2.0 | 5         |
| 2  | Structural mechanism for tyrosine hydroxylase inhibition by dopamine and reactivation by Ser40 phosphorylation. <i>Nature Communications</i> , 2022, 13, 74.  | 5.8 | 23        |
| 3  | Chaperonin Mechanisms: Multiple and (Mis)Understood?. <i>Annual Review of Biophysics</i> , 2022, 51, 115-133.   | 4.5 | 15        |
| 4  | Combining Electron Microscopy (EM) and Cross-Linking Mass Spectrometry (XL-MS) for Structural Characterization of Protein Complexes. <i>Methods in Molecular Biology</i> , 2022, 2420, 217-232.                     | 0.4 | 0         |
| 5  | Chaperonins: Nanocarriers with Biotechnological Applications. <i>Nanomaterials</i> , 2021, 11, 503.   | 1.9 | 4         |
| 6  | Folding for the Immune Synapse: CCT Chaperonin and the Cytoskeleton. <i>Frontiers in Cell and Developmental Biology</i> , 2021, 9, 658460.  | 1.8 | 7         |
| 7  | Globular Aggregates Stemming from the Self-Assembly of an Amphiphilic N-Annulated Perylene Bisimide in Aqueous Media. <i>Nanomaterials</i> , 2021, 11, 1457.  | 1.9 | 4         |
| 8  | 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        |
| 9  | T cell asymmetry and metabolic crosstalk can fine-tune immunological synapses. <i>Trends in Immunology</i> , 2021, 42, 649-653.   | 2.9 | 4         |
| 10 | Truncation-Driven Lateral Association of Î±-Synuclein Hinders Amyloid Clearance by the Hsp70-Based Disaggregase. <i>International Journal of Molecular Sciences</i> , 2021, 22, 12983.                              | 1.8 | 4         |
| 11 | The chaperonin CCT controls T cell receptorâ€”driven 3D configuration of centrioles. <i>Science Advances</i> , 2020, 6, .   | 4.7 | 23        |
| 12 | 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         |
| 13 | Elevated levels of Secreted-Frizzled-Related-Protein 1 contribute to Alzheimerâ€™s disease pathogenesis. <i>Nature Neuroscience</i> , 2019, 22, 1258-1268.  | 7.1 | 48        |
| 14 | 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        |
| 15 | 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        |
| 16 | Molecular architecture of the Bardetâ€”Biedl syndrome protein 2-7-9 subcomplex. <i>Journal of Biological Chemistry</i> , 2019, 294, 16385-16399.  | 1.6 | 9         |
| 17 | Engineering protein assemblies with allosteric control via monomer fold-switching. <i>Nature Communications</i> , 2019, 10, 5703.   | 5.8 | 17        |
| 18 | The chaperonin CCT promotes the formation of fibrillar aggregates of Î³-tubulin. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2018, 1866, 519-526.  | 1.1 | 22        |

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|----|---|-----|-----------|
| 19 | Hsp70 chaperone: a master player in protein homeostasis. <i>F1000Research</i> , 2018, 7, 1497.  | 0.8 | 103       |
| 20 | Structure and Function of the Cochaperone Prefoldin. <i>Advances in Experimental Medicine and Biology</i> , 2018, 1106, 119-131.  | 0.8 | 20        |
| 21 | Expression, Functional Characterization, and Preliminary Crystallization of the Cochaperone Prefoldin from the Thermophilic Fungus <i>Chaetomium thermophilum</i> . <i>International Journal of Molecular Sciences</i> , 2018, 19, 2452.  | 1.8 | 4         |
| 22 | The chaperonin CCT inhibits assembly of $\alpha$ -synuclein amyloid fibrils by a specific, conformation-dependent interaction. <i>Scientific Reports</i> , 2017, 7, 40859.  | 1.6 | 48        |
| 23 | Domain topology of human Rasal. <i>Biological Chemistry</i> , 2017, 399, 63-72.   | 1.2 | 2         |
| 24 | Hsp70 a master regulator in protein degradation. <i>FEBS Letters</i> , 2017, 591, 2648-2660.  | 1.3 | 176       |
| 25 | 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        |
| 26 | 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        |
| 27 | Molecular chaperones: functional mechanisms and nanotechnological applications. <i>Nanotechnology</i> , 2016, 27, 324004.   | 1.3 | 9         |
| 28 | Clathrin-coat disassembly illuminates the mechanisms of Hsp70 force generation. <i>Nature Structural and Molecular Biology</i> , 2016, 23, 821-829.   | 3.6 | 67        |
| 29 | Beyond the known functions of the CCR4-NOT complex in gene expression regulatory mechanisms. <i>BioEssays</i> , 2016, 38, 1048-1058.  | 1.2 | 15        |
| 30 | High resolution atomic force microscopy of double-stranded RNA. <i>Nanoscale</i> , 2016, 8, 11818-11826.  | 2.8 | 42        |
| 31 | The architecture of the <i>Schizosaccharomyces pombe</i> CCR4-NOT complex. <i>Nature Communications</i> , 2016, 7, 10433.   | 5.8 | 47        |
| 32 | The structure of the TBCE/TBCB chaperones and $\beta$ -tubulin complex shows a tubulin dimer dissociation mechanism. <i>Journal of Cell Science</i> , 2015, 128, 1824-34.   | 1.2 | 27        |
| 33 | Structures of the $\beta$ -CCT and PhLP1- $\beta$ -CCT complexes reveal a mechanism for G-protein $\beta$ -subunit folding and $\beta$ - $\beta$ dimer assembly. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 2413-2418. | 3.3 | 49        |
| 34 | Electron microscopy: the coming of age of a structural biology technique. <i>Archives of Biochemistry and Biophysics</i> , 2015, 581, 1-2.  | 1.4 | 3         |
| 35 | Modulation of the Chaperone DnaK Allostereism by the Nucleotide Exchange Factor GrpE. <i>Journal of Biological Chemistry</i> , 2015, 290, 10083-10092.  | 1.6 | 20        |
| 36 | Arc is a flexible modular protein capable of reversible self-oligomerization. <i>Biochemical Journal</i> , 2015, 468, 145-158.  | 1.7 | 69        |

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|----|--|-----|-----------|
| 37 | Structural characterization of toxic oligomers that are kinetically trapped during $\alpha$ -synuclein fibril formation. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, E1994-2003. | 3.3 | 384       |
| 38 | Dynamics, flexibility, and allostery in molecular chaperonins. FEBS Letters, 2015, 589, 2522-2532.   | 1.3 | 83        |
| 39 | Mechano-chemical kinetics of DNA replication: identification of the translocation step of a replicative DNA polymerase. Nucleic Acids Research, 2015, 43, 3643-3652.   | 6.5 | 48        |
| 40 | Phosphoinositide 3-Kinase Beta Protects Nuclear Envelope Integrity by Controlling RCC1 Localization and Ran Activity. Molecular and Cellular Biology, 2015, 35, 249-263.   | 1.1 | 12        |
| 41 | Assisted protein folding at low temperature: evolutionary adaptation of the Antarctic fish chaperonin CCT and its client proteins. Biology Open, 2014, 3, 261-270.   | 0.6 | 12        |
| 42 | Phosphorylation Dependence and Stoichiometry of the Complex Formed by Tyrosine Hydroxylase and 14-3-3 $\beta$ . Molecular and Cellular Proteomics, 2014, 13, 2017-2030.  | 2.5 | 19        |
| 43 | The intrinsically disordered distal face of nucleoplasmin recognizes distinct oligomerization states of histones. Nucleic Acids Research, 2014, 42, 1311-1325.   | 6.5 | 17        |
| 44 | Yeast mitochondrial RNAP conformational changes are regulated by interactions with the mitochondrial transcription factor. Nucleic Acids Research, 2014, 42, 11246-11260.  | 6.5 | 7         |
| 45 | Modulation of the Hsp90 Chaperone Cycle by a Stringent Client Protein. Molecular Cell, 2014, 53, 941-953.  | 4.5 | 129       |
| 46 | Programmed Cell Death Protein 5 Interacts with the Cytosolic Chaperonin Containing Tailless Complex Polypeptide 1 (CCT) to Regulate $\beta$ -Tubulin Folding. Journal of Biological Chemistry, 2014, 289, 4490-4502.             | 1.6 | 31        |
| 47 | Molecular determinants of the ATP hydrolysis asymmetry of the CCT chaperonin complex. Proteins: Structure, Function and Bioinformatics, 2014, 82, 703-707.   | 1.5 | 21        |
| 48 | Structural characterization of the substrate transfer mechanism in Hsp70/Hsp90 folding machinery mediated by Hop. Nature Communications, 2014, 5, 5484.  | 5.8 | 104       |
| 49 | Identification of the Translocation Step of a Replicative DNA Polymerase. Biophysical Journal, 2014, 106, 229a.  | 0.2 | 0         |
| 50 | Structural Characterization of the Bacteriophage T7 Tail Machinery. Journal of Biological Chemistry, 2013, 288, 26290-26299.   | 1.6 | 75        |
| 51 | 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       |
| 52 | Interaction of p53 with the CCT Complex Promotes Protein Folding and Wild-Type p53 Activity. Molecular Cell, 2013, 50, 805-817.  | 4.5 | 121       |
| 53 | Segregated ordered lipid phases and protein-promoted membrane cohesivity are required for pulmonary surfactant films to stabilize and protect the respiratory surface. Faraday Discussions, 2013, 161, 535-548.                  | 1.6 | 57        |
| 54 | Structural Insights into the Chaperone Activity of the 40-kDa Heat Shock Protein DnaJ. Journal of Biological Chemistry, 2013, 288, 15065-15074.  | 1.6 | 21        |

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|----|--|-----|-----------|
| 55 | Microcin E492 Amyloid Formation Is Retarded by Posttranslational Modification. <i>Journal of Bacteriology</i> , 2013, 195, 3995-4004.  | 1.0 | 31        |
| 56 | Phosphoinositide 3-kinase beta controls replication factor C assembly and function. <i>Nucleic Acids Research</i> , 2013, 41, 855-868.   | 6.5 | 6         |
| 57 | Large Terminase Conformational Change Induced by Connector Binding in Bacteriophage T7. <i>Journal of Biological Chemistry</i> , 2013, 288, 16998-17007.   | 1.6 | 33        |
| 58 | Structure and Non-Structure of Centrosomal Proteins. <i>PLoS ONE</i> , 2013, 8, e62633.  | 1.1 | 25        |
| 59 | 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        |
| 60 | 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        |
| 61 | 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         |
| 62 | 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        |
| 63 | 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        |
| 64 | The Structure of Native Influenza Virion Ribonucleoproteins. <i>Science</i> , 2012, 338, 1634-1637.  | 6.0 | 254       |
| 65 | Structural characterization of microcin E492 amyloid formation: Identification of the precursors. <i>Journal of Structural Biology</i> , 2012, 178, 54-60.   | 1.3 | 22        |
| 66 | Mechanical stability of low-humidity single DNA molecules. <i>Biopolymers</i> , 2012, 97, 199-208.   | 1.2 | 13        |
| 67 | 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         |
| 68 | 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        |
| 69 | Mechanical Properties of High-GC Content DNA with A-Type Base-Stacking. <i>Biophysical Journal</i> , 2011, 100, 1996-2005.   | 0.2 | 20        |
| 70 | Dna Unwinding Dynamics of a Processive DNA Polymerase. <i>Biophysical Journal</i> , 2011, 100, 239a.   | 0.2 | 0         |
| 71 | Increased Sensitivity of Antigen-Experienced T Cells through the Enrichment of Oligomeric T Cell Receptor Complexes. <i>Immunity</i> , 2011, 35, 375-387.  | 6.6 | 153       |
| 72 | 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       |

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|----|--|-----|-----------|
| 73 | Chaperonins: two rings for folding. <i>Trends in Biochemical Sciences</i> , 2011, 36, 424-432.   | 3.7 | 140       |
| 74 | Molecular Rearrangements Involved in the Capsid Shell Maturation of Bacteriophage T7. <i>Journal of Biological Chemistry</i> , 2011, 286, 234-242.   | 1.6 | 55        |
| 75 | 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         |
| 76 | 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        |
| 77 | 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        |
| 78 | Size-selective recognition of gold nanoparticles by a molecular chaperone. <i>Chemical Physics Letters</i> , 2010, 501, 108-112.   | 1.2 | 8         |
| 79 | Structural characterization of the TCR complex by electron microscopy. <i>International Immunology</i> , 2010, 22, 897-903.  | 1.8 | 19        |
| 80 | 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        |
| 81 | Nucleoplasmin Binds Histone H2A-H2B Dimers through Its Distal Face*. <i>Journal of Biological Chemistry</i> , 2010, 285, 33771-33778.  | 1.6 | 29        |
| 82 | 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        |
| 83 | The Structure of a Biologically Active Influenza Virus Ribonucleoprotein Complex. <i>PLoS Pathogens</i> , 2009, 5, e1000491.   | 2.1 | 186       |
| 84 | A new side opening on prolyl oligopeptidase revealed by electron microscopy. <i>FEBS Letters</i> , 2009, 583, 3344-3348.   | 1.3 | 17        |
| 85 | SADB phosphorylation of $\beta$ -tubulin regulates centrosome duplication. <i>Nature Cell Biology</i> , 2009, 11, 1081-1092.   | 4.6 | 73        |
| 86 | Single Centrosome Manipulation Reveals Its Electric Charge and Associated Dynamic Structure. <i>Biophysical Journal</i> , 2009, 97, 1022-1030.   | 0.2 | 22        |
| 87 | 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        |
| 88 | $\beta$ -Peptide Nanotube Templating of One-Dimensional Parallel Fullerene Arrangements. <i>Journal of the American Chemical Society</i> , 2009, 131, 11335-11337.   | 6.6 | 81        |
| 89 | The structure of CCT $\alpha$ -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        |
| 90 | Energetics and Geometry of FtsZ Polymers: Nucleated Self-Assembly of Single Protofilaments. <i>Biophysical Journal</i> , 2008, 94, 1796-1806.  | 0.2 | 100       |

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|-----|---|-----|-----------|
| 91  | Structure of the Hsp110:Hsc70 Nucleotide Exchange Machine. <i>Molecular Cell</i> , 2008, 31, 232-243.   | 4.5 | 202       |
| 92  | 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        |
| 93  | 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        |
| 94  | The interring arrangement of the cytosolic chaperonin CCT. <i>EMBO Reports</i> , 2007, 8, 252-257.  | 2.0 | 37        |
| 95  | 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        |
| 96  | 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        |
| 97  | 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        |
| 98  | 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        |
| 99  | 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         |
| 100 | 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       |
| 101 | Coexistence of multivalent and monovalent TCRs explains high sensitivity and wide range of response. <i>Journal of Experimental Medicine</i> , 2005, 202, 493-503.  | 4.2 | 288       |
| 102 | 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        |
| 103 | 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        |
| 104 | Structure of the complex between the cytosolic chaperonin CCT and phosphoducin-like protein. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2004, 101, 17410-17415.                                       | 3.3 | 65        |
| 105 | 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        |
| 106 | 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       |
| 107 | The substrate recognition mechanisms in chaperonins. <i>Journal of Molecular Recognition</i> , 2004, 17, 85-94.   | 1.1 | 71        |
| 108 | GroEL Stability and Function. <i>Journal of Biological Chemistry</i> , 2003, 278, 32083-32090.  | 1.6 | 24        |

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|-----|--|-----|-----------|
| 109 | 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        |
| 110 | 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        |
| 111 | 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        |
| 112 | Detailed architecture of a DNA translocating machine: the high-resolution structure of the bacteriophage $\phi$ 29 connector particle 1. Edited by R. Huber. <i>Journal of Molecular Biology</i> , 2002, 315, 663-676.                     | 2.0 | 205       |
| 113 | Structure and function of a protein folding machine: the eukaryotic cytosolic chaperonin CCT. <i>FEBS Letters</i> , 2002, 529, 11-16.  | 1.3 | 193       |
| 114 | Note to the Paper by Guasch et al. (2002) Detailed Architecture of a DNA Translocating Machine: The High-resolution Structure of the Bacteriophage $\phi$ 29 Connector Particle. <i>Journal of Molecular Biology</i> , 2002, 321, 379-380. | 2.0 | 2         |
| 115 | Structure of eukaryotic prefoldin and of its complexes with unfolded actin and the cytosolic chaperonin CCT. <i>EMBO Journal</i> , 2002, 21, 6377-6386.  | 3.5 | 184       |
| 116 | Three-dimensional reconstruction of a recombinant influenza virus ribonucleoprotein particle. <i>EMBO Reports</i> , 2001, 2, 313-317.  | 2.0 | 85        |
| 117 | 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        |
| 118 | Point Mutations in a Hinge Linking the Small and Large Domains of $\beta$ -Actin Result in Trapped Folding Intermediates Bound to Cytosolic Chaperonin CCT. <i>Journal of Structural Biology</i> , 2001, 135, 198-204.                     | 1.3 | 35        |
| 119 | Chaperonins: Folding in the Hole. <i>Journal of Structural Biology</i> , 2001, 135, 83.  | 1.3 | 1         |
| 120 | Characterization by atomic force microscopy and cryoelectron microscopy of tau polymers assembled in Alzheimer's disease. <i>Journal of Alzheimer's Disease</i> , 2001, 3, 443-451.  | 1.2 | 14        |
| 121 | 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        |
| 122 | Structural comparison of prokaryotic and eukaryotic chaperonins. <i>Micron</i> , 2001, 32, 43-50.  | 1.1 | 43        |
| 123 | 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       |
| 124 | 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        |
| 125 | Purification and functional characterization of p16, the ATPase of the bacteriophage $\phi$ 29 packaging machinery. <i>Nucleic Acids Research</i> , 2001, 29, 4264-4273.   | 6.5 | 38        |
| 126 | Eukaryotic chaperonin CCT stabilizes actin and tubulin folding intermediates in open quasi-native conformations. <i>EMBO Journal</i> , 2000, 19, 5971-5979.  | 3.5 | 193       |



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|-----|--|------|-----------|
| 127 | Partial Occlusion of Both Cavities of the Eukaryotic Chaperonin with Antibody Has No Effect upon the Rates of $\beta$ -Actin or $\beta$ -Tubulin Folding. <i>Journal of Biological Chemistry</i> , 2000, 275, 4587-4591.           | 1.6  | 31        |
| 128 | Topology of the components of the DNA packaging machinery in the phage $\phi$ 29 prohead. <i>Journal of Molecular Biology</i> , 2000, 298, 807-815.  | 2.0  | 70        |
| 129 | Structural Analysis of the Bacteriophage T3 Head-to-Tail Connector. <i>Journal of Structural Biology</i> , 2000, 131, 146-155.   | 1.3  | 38        |
| 130 | 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        |
| 131 | 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       |
| 132 | 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        |
| 133 | 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        |
| 134 | IHF protein inhibits cleavage but not assembly of plasmid R388 relaxosomes. <i>Molecular Microbiology</i> , 1999, 31, 1643-1652.   | 1.2  | 24        |
| 135 | 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       |
| 136 | Stress-induced recrystallization of a protein crystal by electron irradiation. <i>Nature</i> , 1999, 399, 51-54.   | 13.7 | 27        |
| 137 | Eukaryotic type II chaperonin CCT interacts with actin through specific subunits. <i>Nature</i> , 1999, 402, 693-696.  | 13.7 | 247       |
| 138 | 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        |
| 139 | The three-dimensional structure of a DNA translocating machine at 10 Å... resolution. <i>Structure</i> , 1999, 7, 289-296.   | 1.6  | 52        |
| 140 | ATP hydrolysis induces an intermediate conformational state in GroEL. <i>FEBS Journal</i> , 1999, 259, 347-355.  | 0.2  | 10        |
| 141 | Domain architecture of the bacteriophage $\phi$ 29 connector protein. <i>Journal of Molecular Biology</i> , 1999, 288, 899-909.  | 2.0  | 33        |
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