

Oscar Llorca

List of Publications by Year in descending order

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124
papers

6,770
citations

50276

46
h-index

74163

75
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132
all docs

132
docs citations

132
times ranked

8618
citing authors

#	ARTICLE	IF	CITATIONS
1	CryoEM of RUVBL1-RUVBL2-ZNHIT2, a complex that interacts with pre-mRNA-processing-splicing factor 8. <i>Nucleic Acids Research</i> , 2022, 50, 1128-1146.	14.5	6
2	RUVBL1-RUVBL2 AAA-ATPase: a versatile scaffold for multiple complexes and functions. <i>Current Opinion in Structural Biology</i> , 2021, 67, 78-85.	5.7	29
3	Type VII secretion systems: structure, functions and transport models. <i>Nature Reviews Microbiology</i> , 2021, 19, 567-584.	28.6	44
4	Structure of the TELO2-TTI1-TTI2 complex and its function in TOR recruitment to the R2TP chaperone. <i>Cell Reports</i> , 2021, 36, 109317.	6.4	20
5	Long Noncoding RNA NIHCOLE Promotes Ligation Efficiency of DNA Double-Strand Breaks in Hepatocellular Carcinoma. <i>Cancer Research</i> , 2021, 81, 4910-4925.	0.9	30
6	Structural basis for substrate specificity of heteromeric transporters of neutral amino acids. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	7.1	11
7	Assembly of the asymmetric human β -tubulin ring complex by RUVBL1-RUVBL2 AAA ATPase. <i>Science Advances</i> , 2020, 6, .	10.3	34
8	RPAP3 C-Terminal Domain: A Conserved Domain for the Assembly of R2TP Co-Chaperone Complexes. <i>Cells</i> , 2020, 9, 1139.	4.1	10
9	Modeling of a 14 kDa RUVBL2-Binding Domain with Medium Resolution Cryo-EM Density. <i>Journal of Chemical Information and Modeling</i> , 2020, 60, 2541-2551.	5.4	3
10	Structural basis of Focal Adhesion Kinase activation on lipid membranes. <i>EMBO Journal</i> , 2020, 39, e104743.	7.8	47
11	Regulation of RUVBL1-RUVBL2 AAA-ATPases by the nonsense-mediated mRNA decay factor DHX34, as evidenced by Cryo-EM. <i>ELife</i> , 2020, 9, .	6.0	9
12	Structural mechanism for regulation of the AAA-ATPases RUVBL1-RUVBL2 in the R2TP co-chaperone revealed by cryo-EM. <i>Science Advances</i> , 2019, 5, eaaw1616.	10.3	33
13	Recurrent Germline DLST Mutations in Individuals with Multiple Pheochromocytomas and Paragangliomas. <i>American Journal of Human Genetics</i> , 2019, 104, 651-664.	6.2	51
14	Architecture of the mycobacterial type VII secretion system. <i>Nature</i> , 2019, 576, 321-325.	27.8	89
15	RPAP3 provides a flexible scaffold for coupling HSP90 to the human R2TP co-chaperone complex. <i>Nature Communications</i> , 2018, 9, 1501.	12.8	54
16	How novel structures inform understanding of complement function. <i>Seminars in Immunopathology</i> , 2018, 40, 3-14.	6.1	6
17	Advances on the Structure of the R2TP/Prefoldin-like Complex. <i>Advances in Experimental Medicine and Biology</i> , 2018, 1106, 73-83.	1.6	15
18	Functional and structural characterization of four mouse monoclonal antibodies to complement C3 with potential therapeutic and diagnostic applications. <i>European Journal of Immunology</i> , 2017, 47, 504-515.	2.9	5

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19	Ionic tethering contributes to the conformational stability and function of complement C3b. <i>Molecular Immunology</i> , 2017, 85, 137-147.	2.2	5
20	Self-Organization of FtsZ Polymers in Solution Reveals Spacer Role of the Disordered C-Terminal Tail. <i>Biophysical Journal</i> , 2017, 113, 1831-1844.	0.5	35
21	TubZ filament assembly dynamics requires the flexible C-terminal tail. <i>Scientific Reports</i> , 2017, 7, 43342.	3.3	3
22	The Structure of the R2TP Complex Defines a Platform for Recruiting Diverse Client Proteins to the HSP90 Molecular Chaperone System. <i>Structure</i> , 2017, 25, 1145-1152.e4.	3.3	48
23	The RNA helicase DHX34 functions as a scaffold for SMG1-mediated UPF1 phosphorylation. <i>Nature Communications</i> , 2016, 7, 10585.	12.8	39
24	Human nonsense-mediated mRNA decay factor UPF2 interacts directly with eRF3 and the SURF complex. <i>Nucleic Acids Research</i> , 2016, 44, 1909-1923.	14.5	50
25	Structural insights on complement activation. <i>FEBS Journal</i> , 2015, 282, 3883-3891.	4.7	22
26	The AAA+ proteins Pontin and Reptin enter adult age: from understanding their basic biology to the identification of selective inhibitors. <i>Frontiers in Molecular Biosciences</i> , 2015, 2, 17.	3.5	37
27	Amyloidogenesis of Bacterial Prionoid RepA-WH1 Recapitulates Dimer to Monomer Transitions of RepA in DNA Replication Initiation. <i>Structure</i> , 2015, 23, 183-189.	3.3	26
28	Modulation of the Chaperone DnaK Allosterism by the Nucleotide Exchange Factor GrpE. <i>Journal of Biological Chemistry</i> , 2015, 290, 10083-10092.	3.4	20
29	The molecular and structural bases for the association of complement C3 mutations with atypical hemolytic uremic syndrome. <i>Molecular Immunology</i> , 2015, 66, 263-273.	2.2	47
30	Structure and Assembly of the PI3K-like Protein Kinases (PIKKs) Revealed by Electron Microscopy. <i>AIMS Biophysics</i> , 2015, 2, 36-57.	0.6	10
31	A Novel Antibody against Human Factor B that Blocks Formation of the C3bB Proconvertase and Inhibits Complement Activation in Disease Models. <i>Journal of Immunology</i> , 2014, 193, 5567-5575.	0.8	14
32	The C-Terminal SH3 Domain Contributes to the Intramolecular Inhibition of Vav Family Proteins. <i>Science Signaling</i> , 2014, 7, ra35.	3.6	41
33	Structure of Yin Yang 1 Oligomers That Cooperate with RuvBL1-RuvBL2 ATPases. <i>Journal of Biological Chemistry</i> , 2014, 289, 22614-22629.	3.4	36
34	A Humanized Antibody That Regulates the Alternative Pathway Convertase: Potential for Therapy of Renal Disease Associated with Nephritic Factors. <i>Journal of Immunology</i> , 2014, 192, 4844-4851.	0.8	29
35	Structures of SMG1-UPFs Complexes: SMG1 Contributes to Regulate UPF2-Dependent Activation of UPF1 in NMD. <i>Structure</i> , 2014, 22, 1105-1119.	3.3	74
36	Iterative Elastic 3D-to-2D Alignment Method Using Normal Modes for Studying Structural Dynamics of Large Macromolecular Complexes. <i>Structure</i> , 2014, 22, 496-506.	3.3	90

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37	The structures of cytosolic and plastid-located glutamine synthetases from <i>Medicago truncatula</i> reveal a common and dynamic architecture. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2014, 70, 981-993.	2.5	25
38	Structural basis for the stabilization of the complement alternative pathway C3 convertase by properdin. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 13504-13509.	7.1	86
39	Structural insights into nonsense-mediated mRNA decay (NMD) by electron microscopy. <i>Current Opinion in Structural Biology</i> , 2013, 23, 161-167.	5.7	4
40	C3 glomerulopathy-associated CFHR1 mutation alters FHR oligomerization and complement regulation. <i>Journal of Clinical Investigation</i> , 2013, 123, 2434-2446.	8.2	176
41	Conformational transitions regulate the exposure of a DNA-binding domain in the RuvBL1-RuvBL2 complex. <i>Nucleic Acids Research</i> , 2012, 40, 11086-11099.	14.5	47
42	Caveolar domain organization and trafficking is regulated by Abl kinases and mDia1. <i>Journal of Cell Science</i> , 2012, 125, 3097-113.	2.0	57
43	Caveolar domain organization and trafficking is regulated by Abl kinases and mDia1. <i>Journal of Cell Science</i> , 2012, 125, 4413-4413.	2.0	10
44	Electron microscopy reveals coexistence of distinct conformations of iC3b. <i>Immunobiology</i> , 2012, 217, 1166.	1.9	0
45	Reconstitution of the Escherichia coli cell division ZipA-FtsZ complexes in nanodiscs as revealed by electron microscopy. <i>Journal of Structural Biology</i> , 2012, 180, 531-538.	2.8	18
46	Flexible tethering of primase and DNA Pol δ in the eukaryotic primosome. <i>Nucleic Acids Research</i> , 2012, 40, 4726-4726.	14.5	0
47	The cryo-EM structure of the UPF-EJC complex shows UPF1 poised toward the RNA 3' end. <i>Nature Structural and Molecular Biology</i> , 2012, 19, 498-505.	8.2	68
48	Assembly and Regulation of the Membrane Attack Complex Based on Structures of C5b6 and sC5b9. <i>Cell Reports</i> , 2012, 1, 200-207.	6.4	161
49	Flexible tethering of primase and DNA Pol δ in the eukaryotic primosome. <i>Nucleic Acids Research</i> , 2011, 39, 8187-8199.	14.5	72
50	Structural and Functional Studies of LRP6 Ectodomain Reveal a Platform for Wnt Signaling. <i>Developmental Cell</i> , 2011, 21, 848-861.	7.0	109
51	Lessons from functional and structural analyses of disease-associated genetic variants in the complement alternative pathway. <i>Biochimica Et Biophysica Acta - Molecular Basis of Disease</i> , 2011, 1812, 12-22.	3.8	33
52	Gene vectors based on DOEPC/DOPE mixed cationic liposomes: a physicochemical study. <i>Soft Matter</i> , 2011, 7, 5991.	2.7	31
53	Structure of Human Complement C8, a Precursor to Membrane Attack. <i>Journal of Molecular Biology</i> , 2011, 405, 325-330.	4.2	30
54	Molecular Architecture and Structural Transitions of a Clostridium thermocellum Mini-Cellulosome. <i>Journal of Molecular Biology</i> , 2011, 407, 571-580.	4.2	28

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55	The nonsense-mediated mRNA decay SMG-1 kinase is regulated by large-scale conformational changes controlled by SMG-8. <i>Genes and Development</i> , 2011, 25, 153-164.	5.9	72
56	Characterization of SMG-9, an essential component of the nonsense-mediated mRNA decay SMG1C complex. <i>Nucleic Acids Research</i> , 2011, 39, 347-358.	14.5	384
57	Unique structure of iC3b resolved at a resolution of 24 Å... by 3D-electron microscopy. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 13236-13240.	7.1	49
58	Evidence for a remodelling of DNA-PK upon autophosphorylation from electron microscopy studies. <i>Nucleic Acids Research</i> , 2011, 39, 5757-5767.	14.5	20
59	Structural and Functional Characterization of an Influenza Virus RNA Polymerase-Genomic RNA Complex. <i>Journal of Virology</i> , 2010, 84, 10477-10487.	3.4	39
60	The Antibacterial Cell Division Inhibitor PC190723 Is an FtsZ Polymer-stabilizing Agent That Induces Filament Assembly and Condensation. <i>Journal of Biological Chemistry</i> , 2010, 285, 14239-14246.	3.4	152
61	Cyclopentenone Prostaglandins with Dienone Structure Promote Cross-Linking of the Chemoresistance-Inducing Enzyme Glutathione Transferase P1-1. <i>Molecular Pharmacology</i> , 2010, 78, 723-733.	2.3	39
62	Biochemical Characterization of the Transcriptional Regulator BzdR from <i>Azoarcus</i> sp. CIB. <i>Journal of Biological Chemistry</i> , 2010, 285, 35694-35705.	3.4	33
63	Human C3 mutation reveals a mechanism of dense deposit disease pathogenesis and provides insights into complement activation and regulation. <i>Journal of Clinical Investigation</i> , 2010, 120, 3702-3712.	8.2	195
64	Coexistence of Closed and Open Conformations of Complement Factor B in the Alternative Pathway C3bB(Mg ²⁺) Proconvertase. <i>Journal of Immunology</i> , 2009, 183, 7347-7351.	0.8	35
65	Electron microscopy of Xrcc4 and the DNA ligase IV Xrcc4 DNA repair complex. <i>DNA Repair</i> , 2009, 8, 1380-1389.	2.8	24
66	Plasmid replication initiator RepB forms a hexamer reminiscent of ring helicases and has mobile nuclease domains. <i>EMBO Journal</i> , 2009, 28, 1666-1678.	7.8	45
67	Conformational rearrangements upon Syk auto-phosphorylation. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2009, 1794, 1211-1217.	2.3	19
68	A Theoretical and Experimental Approach to the Compaction Process of DNA by Dioctadecyldimethylammonium Bromide/Zwitterionic Mixed Liposomes. <i>Journal of Physical Chemistry B</i> , 2009, 113, 15648-15661.	2.6	42
69	3D structure of the C3bB complex provides insights into the activation and regulation of the complement alternative pathway convertase. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 882-887.	7.1	76
70	3D architecture of DNA Pol δ reveals the functional core of multi-subunit replicative polymerases. <i>EMBO Journal</i> , 2009, 28, 1978-1987.	7.8	112
71	Extended and bent conformations of the mannose receptor family. <i>Cellular and Molecular Life Sciences</i> , 2008, 65, 1302-1310.	5.4	63
72	A Physicochemical Characterization of the Interaction between DC-Chol/DOPE Cationic Liposomes and DNA. <i>Journal of Physical Chemistry B</i> , 2008, 112, 12555-12565.	2.6	48

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73	Structure of Epac2 in complex with a cyclic AMP analogue and RAP1B. <i>Nature</i> , 2008, 455, 124-127.	27.8	155
74	Architecture of the Pontin/Reptin Complex, Essential in the Assembly of Several Macromolecular Complexes. <i>Structure</i> , 2008, 16, 1511-1520.	3.3	63
75	Energetics and Geometry of FtsZ Polymers: Nucleated Self-Assembly of Single Protofilaments. <i>Biophysical Journal</i> , 2008, 94, 1796-1806.	0.5	100
76	Structure of the Hsp110:Hsc70 Nucleotide Exchange Machine. <i>Molecular Cell</i> , 2008, 31, 232-243.	9.7	202
77	Compaction Process of Calf Thymus DNA by Mixed Cationic/Zwitterionic Liposomes: A Physicochemical Study. <i>Journal of Physical Chemistry B</i> , 2008, 112, 2187-2197.	2.6	45
78	Three-dimensional model for the isolated recombinant influenza virus polymerase heterotrimer. <i>Nucleic Acids Research</i> , 2007, 35, 3774-3783.	14.5	71
79	Structural Model of Human Endoglin, a Transmembrane Receptor Responsible for Hereditary Hemorrhagic Telangiectasia. <i>Journal of Molecular Biology</i> , 2007, 365, 694-705.	4.2	88
80	Structure of TOR and Its Complex with KOG1. <i>Molecular Cell</i> , 2007, 27, 509-516.	9.7	69
81	3D structure of Syk kinase determined by single-particle electron microscopy. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2007, 1774, 1493-1499.	2.3	21
82	Structural model of full-length human Ku70/Ku80 heterodimer and its recognition of DNA and DNA-PKcs. <i>EMBO Reports</i> , 2007, 8, 56-62.	4.5	111
83	Electron microscopy reconstructions of DNA repair complexes. <i>Current Opinion in Structural Biology</i> , 2007, 17, 215-220.	5.7	9
84	Electrochemical, Microscopic, and Spectroscopic Characterization of Prevesicle Nanostructures and Vesicles on Mixed Cationic Surfactant Systems. <i>Langmuir</i> , 2006, 22, 4027-4036.	3.5	29
85	Cationic Prevesicle and Vesicle Nanoaggregates: An Experimental and Theoretical Study. <i>Journal of Physical Chemistry B</i> , 2006, 110, 23524-23539.	2.6	6
86	Addition of electrophilic lipids to actin alters filament structure. <i>Biochemical and Biophysical Research Communications</i> , 2006, 349, 1387-1393.	2.1	30
87	Three-Dimensional Structure of the Human DNA-PKcs/Ku70/Ku80 Complex Assembled on DNA and Its Implications for DNA DSB Repair. <i>Molecular Cell</i> , 2006, 22, 511-519.	9.7	223
88	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.	2.8	61
89	Structural Model for the Mannose Receptor Family Uncovered by Electron Microscopy of Endo180 and the Mannose Receptor. <i>Journal of Biological Chemistry</i> , 2006, 281, 8780-8787.	3.4	76
90	Global conformational rearrangements during the activation of the GDP/GTP exchange factor Vav3. <i>EMBO Journal</i> , 2005, 24, 1330-1340.	7.8	41

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91	Introduction to 3D reconstruction of macromolecules using single particle electron microscopy1. <i>Acta Pharmacologica Sinica</i> , 2005, 26, 1153-1164.	6.1	15
92	Three-Dimensional Structure and Regulation of the DNA-Dependent Protein Kinase Catalytic Subunit (DNA-PKcs). <i>Structure</i> , 2005, 13, 243-255.	3.3	98
93	Three-Dimensional Structure and Regulation of the DNA-Dependent Protein Kinase Catalytic Subunit (DNA-PKcs). <i>Structure</i> , 2005, 13, 495.	3.3	1
94	Structural Analysis of Tobacco Etch Potyvirus HC-Pro Oligomers Involved in Aphid Transmission. <i>Journal of Virology</i> , 2005, 79, 3758-3765.	3.4	61
95	Aggregation Phenomena on the Ternary Ionic/Nonionic Surfactant System: Didodecyldimethylammonium Bromide/Octyl- β -D-glucopyranoside/Water. Mixed Microaggregates, Vesicles, and Micelles. <i>Langmuir</i> , 2005, 21, 1795-1801.	3.5	18
96	Electron microscopy studies on DNA recognition by DNA-PK. <i>Micron</i> , 2004, 35, 625-633.	2.2	14
97	Three-dimensional interplay among the ligand-binding domains of the urokinase-plasminogen-activator-receptor-associated protein. <i>EMBO Reports</i> , 2003, 4, 807-812.	4.5	28
98	Electron microscopy and 3D reconstructions reveal that human ATM kinase uses an arm-like domain to clamp around double-stranded DNA. <i>Oncogene</i> , 2003, 22, 3867-3874.	5.9	48
99	Visualization of DNA-induced conformational changes in the DNA repair kinase DNA-PKcs. <i>EMBO Journal</i> , 2003, 22, 5875-5882.	7.8	67
100	Three-dimensional reconstruction of a recombinant influenza virus ribonucleoprotein particle. <i>EMBO Reports</i> , 2001, 2, 313-317.	4.5	85
101	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.	2.8	70
102	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.	2.8	35
103	HYDROMIC: prediction of hydrodynamic properties of rigid macromolecular structures obtained from electron microscopy images. <i>European Biophysics Journal</i> , 2001, 30, 457-462.	2.2	45
104	Structural comparison of prokaryotic and eukaryotic chaperonins. <i>Micron</i> , 2001, 32, 43-50.	2.2	43
105	The 'sequential allosteric ring' mechanism in the eukaryotic chaperonin-assisted folding of actin and tubulin. <i>EMBO Journal</i> , 2001, 20, 4065-4075.	7.8	130
106	Excluded Volume Effects on the Refolding and Assembly of an Oligomeric Protein. <i>Journal of Biological Chemistry</i> , 2001, 276, 957-964.	3.4	38
107	Eukaryotic chaperonin CCT stabilizes actin and tubulin folding intermediates in open quasi-native conformations. <i>EMBO Journal</i> , 2000, 19, 5971-5979.	7.8	193
108	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.	3.4	31

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109	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.	4.2	70
110	pH-controlled quaternary states of hexameric DnaB helicase. <i>Journal of Molecular Biology</i> , 2000, 303, 383-393.	4.2	27
111	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.	3.4	24
112	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
113	Eukaryotic type II chaperonin CCT interacts with actin through specific subunits. <i>Nature</i> , 1999, 402, 693-696.	27.8	247
114	ATP hydrolysis induces an intermediate conformational state in GroEL. <i>FEBS Journal</i> , 1999, 259, 347-355.	0.2	10
115	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.	3.4	54
116	GroEL under Heat-Shock. <i>Journal of Biological Chemistry</i> , 1998, 273, 32587-32594.	3.4	49
117	Effects of the Inter-ring Communication in GroEL Structural and Functional Asymmetry. <i>Journal of Biological Chemistry</i> , 1997, 272, 32925-32932.	3.4	20
118	Conformational Changes in the GroEL Oligomer during the Functional Cycle. <i>Journal of Structural Biology</i> , 1997, 118, 31-42.	2.8	38
119	Symmetric GroEL-GroES complexes can contain substrate simultaneously in both GroEL rings. <i>FEBS Letters</i> , 1997, 405, 195-199.	2.8	33
120	Role of the amino terminal domain in GroES oligomerization. <i>BBA - Proteins and Proteomics</i> , 1997, 1337, 47-56.	2.1	6
121	Biochemical Characterization of Symmetric GroEL-GroES Complexes. <i>Journal of Biological Chemistry</i> , 1996, 271, 68-76.	3.4	40
122	Prediction of the structure of GroES and its interaction with GroEL. <i>Proteins: Structure, Function and Bioinformatics</i> , 1995, 22, 199-209.	2.6	14
123	The formation of symmetrical GroEL-GroES complexes in the presence of ATP. <i>FEBS Letters</i> , 1994, 345, 181-186.	2.8	86
124	Structure of the TELO2-TTI1-TTI2 Complex and its Function in TOR Recruitment to the R2TP Chaperone. <i>SSRN Electronic Journal</i> , 0, , .	0.4	0