

Mikel Valle

List of Publications by Year in descending order

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71
papers

6,281
citations

87888

38
h-index

102487

66
g-index

73
all docs

73
docs citations

73
times ranked

6415
citing authors

#	ARTICLE	IF	CITATIONS
1	A switch from α -helical to β -strand conformation during co-translational protein folding. EMBO Journal, 2022, 41, e109175.	7.8	21
2	Autophagy protein LC3C binding to phospholipid and interaction with lipid membranes. International Journal of Biological Macromolecules, 2022, 212, 432-441.	7.5	3
3	3D architecture and structural flexibility revealed in the subfamily of large glutamate dehydrogenases by a mycobacterial enzyme. Communications Biology, 2021, 4, 684.	4.4	3
4	Structural Characterization of N-Linked Glycans in the Receptor Binding Domain of the SARS-CoV-2 Spike Protein and their Interactions with Human Lectins. Angewandte Chemie - International Edition, 2020, 59, 23763-23771.	13.8	81
5	Photoacoustic effect applied on model membranes and living cells: direct observation with multiphoton excitation microscopy and long-term viability analysis. Scientific Reports, 2020, 10, 299.	3.3	9
6	Structure of Turnip mosaic virus and its viral-like particles. Scientific Reports, 2019, 9, 15396.	3.3	36
7	Structural Homology Between Nucleoproteins of ssRNA Viruses. Sub-Cellular Biochemistry, 2018, 88, 129-145.	2.4	11
8	Incorporation of aminoacyl-tRNA into the ribosome as seen by cryo-electron microscopy. journal of hand surgery Asian-Pacific volume, The, 2018, , 339-346.	0.4	0
9	A twisted tRNA intermediate sets the threshold for decoding. journal of hand surgery Asian-Pacific volume, The, 2018, , 359-360.	0.4	0
10	Locking and Unlocking of Ribosomal Motions. journal of hand surgery Asian-Pacific volume, The, 2018, , 347-358.	0.4	0
11	α -Pyruvate Carboxylase, Structure and Function. Sub-Cellular Biochemistry, 2017, 83, 291-322.	2.4	19
12	Ribosome rearrangements at the onset of translational bypassing. Science Advances, 2017, 3, e1700147.	10.3	31
13	Does Ceramide Form Channels? The Ceramide-Induced Membrane Permeabilization Mechanism. Biophysical Journal, 2017, 113, 860-868.	0.5	24
14	Potyvirus virion structure shows conserved protein fold and RNA binding site in ssRNA viruses. Science Advances, 2017, 3, eaao2182.	10.3	84
15	Coating Graphene Oxide with Lipid Bilayers Greatly Decreases Its Hemolytic Properties. Langmuir, 2017, 33, 8181-8191.	3.5	20
16	Real-time and decision taking selection of single-particles during automated cryo-EM sessions based on neuro-fuzzy method. Expert Systems With Applications, 2016, 55, 403-416.	7.6	2
17	Identification of a Membrane-bound Prepore Species Clarifies the Lytic Mechanism of Actinoporins. Journal of Biological Chemistry, 2016, 291, 19210-19219.	3.4	23
18	Lipid Geometry and Bilayer Curvature Modulate LC3/GABARAP-Mediated Model Autophagosomal Elongation. Biophysical Journal, 2016, 110, 411-422.	0.5	54

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19	Histones Cause Aggregation and Fusion of Lipid Vesicles Containing Phosphatidylinositol-4-Phosphate. <i>Biophysical Journal</i> , 2015, 108, 863-871.	0.5	7
20	Structural Insights into tRNA Dynamics on the Ribosome. <i>International Journal of Molecular Sciences</i> , 2015, 16, 9866-9895.	4.1	10
21	The hexameric structure of the human mitochondrial replicative helicase Twinkle. <i>Nucleic Acids Research</i> , 2015, 43, 4284-4295.	14.5	40
22	Fuzzy inference system as decision-maker to automate cryo-EM data acquisition on a transmission electron microscope. , 2015, , .		0
23	Lipidic nanovesicles stabilize suspensions of metal oxide nanoparticles. <i>Chemistry and Physics of Lipids</i> , 2015, 191, 84-90.	3.2	15
24	The near-atomic cryoEM structure of a flexible filamentous plant virus shows homology of its coat protein with nucleoproteins of animal viruses. <i>ELife</i> , 2015, 4, e11795.	6.0	61
25	High-Melting Lipid Mixtures and the Origin of Detergent-Resistant Membranes Studied with Temperature-Solubilization Diagrams. <i>Biophysical Journal</i> , 2014, 107, 2828-2837.	0.5	11
26	Functional Conformations for Pyruvate Carboxylase during Catalysis Explored by Cryoelectron Microscopy. <i>Structure</i> , 2014, 22, 911-922.	3.3	23
27	The ribosome triggers the stringent response by RelA via a highly distorted tRNA. <i>EMBO Reports</i> , 2013, 14, 811-816.	4.5	52
28	Pores of the toxin FraC assemble into 2D hexagonal clusters in both crystal structures and model membranes. <i>Journal of Structural Biology</i> , 2012, 180, 312-317.	2.8	7
29	Model Systems of Precursor Cellular Membranes: Long-Chain Alcohols Stabilize Spontaneously Formed Oleic Acid Vesicles. <i>Biophysical Journal</i> , 2012, 102, 278-286.	0.5	52
30	Structural Insights into the Oligomerization and Architecture of Eukaryotic Membrane Pore-Forming Toxins. <i>Structure</i> , 2011, 19, 181-191.	3.3	99
31	Almost lost in translation. Cryo-EM of a dynamic macromolecular complex: the ribosome. <i>European Biophysics Journal</i> , 2011, 40, 589-597.	2.2	8
32	Electron microscopy studies on the quaternary structure of p53 reveal different binding modes for p53 tetramers in complex with DNA. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 557-562.	7.1	65
33	The Cryo-EM Structure of a Complete 30S Translation Initiation Complex from <i>Escherichia coli</i> . <i>PLoS Biology</i> , 2011, 9, e1001095.	5.6	102
34	Reconstitution of Proapoptotic BAK Function in Liposomes Reveals a Dual Role for Mitochondrial Lipids in the BAK-driven Membrane Permeabilization Process. <i>Journal of Biological Chemistry</i> , 2011, 286, 8213-8230.	3.4	66
35	Cryo-EM Analysis Reveals New Insights into the Mechanism of Action of Pyruvate Carboxylase. <i>Structure</i> , 2010, 18, 1300-1310.	3.3	27
36	Candidate biomarkers in exosome-like vesicles purified from rat and mouse urine samples. <i>Proteomics - Clinical Applications</i> , 2010, 4, 416-425.	1.6	116

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37	A Symmetrical Tetramer for <i>S. aureus</i> Pyruvate Carboxylase in Complex with Coenzyme A. <i>Structure</i> , 2009, 17, 823-832.	3.3	55
38	Averaging of Electron Subtomograms and Random Conical Tilt Reconstructions through Likelihood Optimization. <i>Structure</i> , 2009, 17, 1563-1572.	3.3	112
39	Maximum likelihood refinement of electron microscopy data with normalization errors. <i>Journal of Structural Biology</i> , 2009, 166, 234-240.	2.8	33
40	Characterization and Comprehensive Proteome Profiling of Exosomes Secreted by Hepatocytes. <i>Journal of Proteome Research</i> , 2008, 7, 5157-5166.	3.7	530
41	Structure of ratcheted ribosomes with tRNAs in hybrid states. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008, 105, 16924-16927.	7.1	161
42	Quaternary structures of tumor suppressor p53 and a specific p53-DNA complex. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007, 104, 12324-12329.	7.1	184
43	Disentangling conformational states of macromolecules in 3D-EM through likelihood optimization. <i>Nature Methods</i> , 2007, 4, 27-29.	19.0	387
44	Structural Basis for the Cooperative Assembly of Large T Antigen on the Origin of Replication. <i>Journal of Molecular Biology</i> , 2006, 357, 1295-1305.	4.2	45
45	Flexible Fitting in 3D-EM Guided by the Structural Variability of Protein Superfamilies. <i>Structure</i> , 2006, 14, 1115-1126.	3.3	45
46	Fast maximum-likelihood refinement of electron microscopy images. <i>Bioinformatics</i> , 2005, 21, ii243-ii244.	4.1	54
47	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.	4.2	99
48	Maximum-likelihood Multi-reference Refinement for Electron Microscopy Images. <i>Journal of Molecular Biology</i> , 2005, 348, 139-149.	4.2	239
49	Mechanism for the Disassembly of the Posttermination Complex Inferred from Cryo-EM Studies. <i>Molecular Cell</i> , 2005, 18, 663-674.	9.7	117
50	The role of tRNA as a molecular spring in decoding, accommodation, and peptidyl transfer. <i>FEBS Letters</i> , 2005, 579, 959-962.	2.8	93
51	Dynamics of EF-G interaction with the ribosome explored by classification of a heterogeneous cryo-EM dataset. <i>Journal of Structural Biology</i> , 2004, 147, 283-290.	2.8	88
52	Incorporation of aminoacyl-tRNA into the ribosome as seen by cryo-electron microscopy. <i>Nature Structural and Molecular Biology</i> , 2003, 10, 899-906.	8.2	317
53	A cryo-electron microscopic study of ribosome-bound termination factor RF2. <i>Nature</i> , 2003, 421, 87-90.	27.8	234
54	Large T antigen on the simian virus 40 origin of replication: a 3D snapshot prior to DNA replication. <i>EMBO Journal</i> , 2003, 22, 6205-6213.	7.8	55

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55	Visualizing tmRNA Entry into a Stalled Ribosome. <i>Science</i> , 2003, 300, 127-130.	12.6	141
56	Study of the Structural Dynamics of the E. coli 70S Ribosome Using Real-Space Refinement. <i>Cell</i> , 2003, 113, 789-801.	28.9	273
57	Locking and Unlocking of Ribosomal Motions. <i>Cell</i> , 2003, 114, 123-134.	28.9	579
58	A twisted tRNA intermediate sets the threshold for decoding. <i>Rna</i> , 2003, 9, 384-385.	3.5	38
59	Dynamic reorganization of the functionally active ribosome explored by normal mode analysis and cryo-electron microscopy. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2003, 100, 9319-9323.	7.1	332
60	Problems with the transorientation hypothesis. <i>Rna</i> , 2002, 8, 1093-1094.	3.5	4
61	Cryo-EM reveals an active role for aminoacyl-tRNA in the accommodation process. <i>EMBO Journal</i> , 2002, 21, 3557-3567.	7.8	272
62	A Novel Neural Network Technique for Analysis and Classification of EM Single-Particle Images. <i>Journal of Structural Biology</i> , 2001, 133, 233-245.	2.8	72
63	The Polypeptide Tunnel System in the Ribosome and Its Gating in Erythromycin Resistance Mutants of L4 and L22. <i>Molecular Cell</i> , 2001, 8, 181-188.	9.7	187
64	Large T-Antigen Double Hexamers Imaged at the Simian Virus 40 Origin of Replication. <i>Molecular and Cellular Biology</i> , 2000, 20, 34-41.	2.3	82
65	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
66	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.	3.4	97
67	IHF protein inhibits cleavage but not assembly of plasmid R388 relaxosomes. <i>Molecular Microbiology</i> , 1999, 31, 1643-1652.	2.5	24
68	Domain architecture of the bacteriophage ϕ 29 connector protein. <i>Journal of Molecular Biology</i> , 1999, 288, 899-909.	4.2	33
69	Selection of antibody probes to correlate protein sequence domains with their structural distribution. <i>Protein Science</i> , 1999, 8, 883-889.	7.6	22
70	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.	2.8	25
71	Structure and Dynamics of the Ribosome as Revealed by Cryo-Electron Microscopy. , 0, , 117-141.		0