

# 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	Locking and Unlocking of Ribosomal Motions. <i>Cell</i> , 2003, 114, 123-134.	28.9	579
2	Characterization and Comprehensive Proteome Profiling of Exosomes Secreted by Hepatocytes. <i>Journal of Proteome Research</i> , 2008, 7, 5157-5166.	3.7	530
3	Disentangling conformational states of macromolecules in 3D-EM through likelihood optimization. <i>Nature Methods</i> , 2007, 4, 27-29.	19.0	387
4	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
5	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
6	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
7	Cryo-EM reveals an active role for aminoacyl-tRNA in the accommodation process. <i>EMBO Journal</i> , 2002, 21, 3557-3567.	7.8	272
8	Maximum-likelihood Multi-reference Refinement for Electron Microscopy Images. <i>Journal of Molecular Biology</i> , 2005, 348, 139-149.	4.2	239
9	A cryo-electron microscopic study of ribosome-bound termination factor RF2. <i>Nature</i> , 2003, 421, 87-90.	27.8	234
10	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
11	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
12	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
13	Visualizing tmRNA Entry into a Stalled Ribosome. <i>Science</i> , 2003, 300, 127-130.	12.6	141
14	Mechanism for the Disassembly of the Posttermination Complex Inferred from Cryo-EM Studies. <i>Molecular Cell</i> , 2005, 18, 663-674.	9.7	117
15	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
16	Averaging of Electron Subtomograms and Random Conical Tilt Reconstructions through Likelihood Optimization. <i>Structure</i> , 2009, 17, 1563-1572.	3.3	112
17	The Cryo-EM Structure of a Complete 30S Translation Initiation Complex from Escherichia coli. <i>PLoS Biology</i> , 2011, 9, e1001095.	5.6	102
18	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

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19	Structural Insights into the Oligomerization and Architecture of Eukaryotic Membrane Pore-Forming Toxins. <i>Structure</i> , 2011, 19, 181-191.	3.3	99
20	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
21	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
22	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
23	Potyvirus virion structure shows conserved protein fold and RNA binding site in ssRNA viruses. <i>Science Advances</i> , 2017, 3, eaao2182.	10.3	84
24	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
25	Structural Characterization of N-Linked Glycans in the Receptor Binding Domain of the SARS-CoV-2 Spike Protein and their Interactions with Human Lectins. <i>Angewandte Chemie - International Edition</i> , 2020, 59, 23763-23771.	13.8	81
26	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
27	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.	4.2	70
28	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
29	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
30	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
31	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
32	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
33	Fast maximum-likelihood refinement of electron microscopy images. <i>Bioinformatics</i> , 2005, 21, ii243-ii244.	4.1	54
34	Lipid Geometry and Bilayer Curvature Modulate LC3/GABARAP-Mediated Model Autophagosomal Elongation. <i>Biophysical Journal</i> , 2016, 110, 411-422.	0.5	54
35	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
36	The ribosome triggers the stringent response by RelA via a highly distorted tRNA. <i>EMBO Reports</i> , 2013, 14, 811-816.	4.5	52

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37	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
38	Flexible Fitting in 3D-EM Guided by the Structural Variability of Protein Superfamilies. <i>Structure</i> , 2006, 14, 1115-1126.	3.3	45
39	The hexameric structure of the human mitochondrial replicative helicase Twinkle. <i>Nucleic Acids Research</i> , 2015, 43, 4284-4295.	14.5	40
40	A twisted tRNA intermediate sets the threshold for decoding. <i>Rna</i> , 2003, 9, 384-385.	3.5	38
41	Structure of Turnip mosaic virus and its viral-like particles. <i>Scientific Reports</i> , 2019, 9, 15396.	3.3	36
42	Domain architecture of the bacteriophage $\phi$ 29 connector protein. <i>Journal of Molecular Biology</i> , 1999, 288, 899-909.	4.2	33
43	Maximum likelihood refinement of electron microscopy data with normalization errors. <i>Journal of Structural Biology</i> , 2009, 166, 234-240.	2.8	33
44	Ribosome rearrangements at the onset of translational bypassing. <i>Science Advances</i> , 2017, 3, e1700147.	10.3	31
45	Cryo-EM Analysis Reveals New Insights into the Mechanism of Action of Pyruvate Carboxylase. <i>Structure</i> , 2010, 18, 1300-1310.	3.3	27
46	The Interaction of DNA with Bacteriophage $\phi$ 29 Connector: A Study by AFM and TEM. <i>Journal of Structural Biology</i> , 1996, 116, 390-398.	2.8	25
47	IHF protein inhibits cleavage but not assembly of plasmid R388 relaxosomes. <i>Molecular Microbiology</i> , 1999, 31, 1643-1652.	2.5	24
48	Does Ceramide Form Channels? The Ceramide-Induced Membrane Permeabilization Mechanism. <i>Biophysical Journal</i> , 2017, 113, 860-868.	0.5	24
49	Functional Conformations for Pyruvate Carboxylase during Catalysis Explored by Cryoelectron Microscopy. <i>Structure</i> , 2014, 22, 911-922.	3.3	23
50	Identification of a Membrane-bound Prepore Species Clarifies the Lytic Mechanism of Actinoporins. <i>Journal of Biological Chemistry</i> , 2016, 291, 19210-19219.	3.4	23
51	Selection of antibody probes to correlate protein sequence domains with their structural distribution. <i>Protein Science</i> , 1999, 8, 883-889.	7.6	22
52	A switch from $\alpha$ -helical to $\beta$ -strand conformation during co-translational protein folding. <i>EMBO Journal</i> , 2022, 41, e109175.	7.8	21
53	Coating Graphene Oxide with Lipid Bilayers Greatly Decreases Its Hemolytic Properties. <i>Langmuir</i> , 2017, 33, 8181-8191.	3.5	20
54	Pyruvate Carboxylase, Structure and Function. <i>Sub-Cellular Biochemistry</i> , 2017, 83, 291-322.	2.4	19

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55	Lipidic nanovesicles stabilize suspensions of metal oxide nanoparticles. <i>Chemistry and Physics of Lipids</i> , 2015, 191, 84-90.	3.2	15
56	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
57	Structural Homology Between Nucleoproteins of ssRNA Viruses. <i>Sub-Cellular Biochemistry</i> , 2018, 88, 129-145.	2.4	11
58	Structural Insights into tRNA Dynamics on the Ribosome. <i>International Journal of Molecular Sciences</i> , 2015, 16, 9866-9895.	4.1	10
59	Photoacoustic effect applied on model membranes and living cells: direct observation with multiphoton excitation microscopy and long-term viability analysis. <i>Scientific Reports</i> , 2020, 10, 299.	3.3	9
60	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
61	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
62	Histones Cause Aggregation and Fusion of Lipid Vesicles Containing Phosphatidylinositol-4-Phosphate. <i>Biophysical Journal</i> , 2015, 108, 863-871.	0.5	7
63	Problems with the transorientation hypothesis. <i>Rna</i> , 2002, 8, 1093-1094.	3.5	4
64	3D architecture and structural flexibility revealed in the subfamily of large glutamate dehydrogenases by a mycobacterial enzyme. <i>Communications Biology</i> , 2021, 4, 684.	4.4	3
65	Autophagy protein LC3C binding to phospholipid and interaction with lipid membranes. <i>International Journal of Biological Macromolecules</i> , 2022, 212, 432-441.	7.5	3
66	Real-time and decision taking selection of single-particles during automated cryo-EM sessions based on neuro-fuzzy method. <i>Expert Systems With Applications</i> , 2016, 55, 403-416.	7.6	2
67	Fuzzy inference system as decision-maker to automate cryo-EM data acquisition on a transmission electron microscope. , 2015, , .		0
68	Incorporation of aminoacyl-tRNA into the ribosome as seen by cryo-electron microscopy. <i>journal of hand surgery Asian-Pacific volume, The</i> , 2018, , 339-346.	0.4	0
69	A twisted tRNA intermediate sets the threshold for decoding. <i>journal of hand surgery Asian-Pacific volume, The</i> , 2018, , 359-360.	0.4	0
70	Locking and Unlocking of Ribosomal Motions. <i>journal of hand surgery Asian-Pacific volume, The</i> , 2018, , 347-358.	0.4	0
71	Structure and Dynamics of the Ribosome as Revealed by Cryo-Electron Microscopy. , 0, , 117-141.		0