

Victor Martin Bolanos-Garcia

List of Publications by Year in descending order

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71
papers

2,374
citations

218381

26
h-index

214527

47
g-index

73
all docs

73
docs citations

73
times ranked

3417
citing authors

#	ARTICLE	IF	CITATIONS
1	The Biomolecules Journal Club: Highlights on Recent Papersâ€”1. Biomolecules, 2022, 12, 86.	1.8	0
2	The spindle checkpoint proteins BUB1 and BUBR1: (SLiM)ming down to the basics. Trends in Biochemical Sciences, 2022, 47, 352-366.	3.7	12
3	Identification of Novel Potential Heparanase Inhibitors Using Virtual Screening. Catalysts, 2022, 12, 503.	1.6	3
4	Interfacial Activity of Lipoprotein (a) Isoforms with a Variable Number of Kringle IV Type 2 Repeats: A New Indicator of Cardiovascular Risk?. Annals of Clinical and Laboratory Science, 2021, 51, 795-804.	0.2	0
5	Deregulation of Chromosome Segregation and Cancer. Annual Review of Cancer Biology, 2020, 4, 257-278.	2.3	11
6	Editorial: E3 Ubiquitin Ligases: From Structure to Physiology. Frontiers in Physiology, 2020, 11, 621053.	1.3	1
7	Interfering with mRNA Methylation by the 2â€²O-Methyltransferase (NSP16) from SARS-CoV-2 to Tackle the COVID-19 Disease. Catalysts, 2020, 10, 1023.	1.6	9
8	Pseudokinases: From Allosteric Regulation of Catalytic Domains and the Formation of Macromolecular Assemblies to Emerging Drug Targets. Catalysts, 2019, 9, 778.	1.6	12
9	Combinatorial Use of Chitosan Nanoparticles, Reversine, and Ionising Radiation on Breast Cancer Cells Associated with Mitosis Deregulation. Biomolecules, 2019, 9, 186.	1.8	11
10	A Molecular Modeling Approach to Identify Novel Inhibitors of the Major Facilitator Superfamily of Efflux Pump Transporters. Antibiotics, 2019, 8, 25.	1.5	32
11	The Anaphase Promoting Complex/Cyclosome (APC/C): A Versatile E3 Ubiquitin Ligase. Sub-Cellular Biochemistry, 2019, 93, 539-623.	1.0	6
12	Mps1 Phosphorylates Its N-Terminal Extension to Relieve Autoinhibition and Activate the Spindle Assembly Checkpoint. Current Biology, 2018, 28, 872-883.e5.	1.8	22
13	Co-occurrence of Noonan and Cardiofaciocutaneous Syndrome Features in a Patient with KRAS Variant. Journal of Pediatric Genetics, 2018, 07, 158-163.	0.3	4
14	Cdc20: At the Crossroads between Chromosome Segregation and Mitotic Exit. Trends in Biochemical Sciences, 2017, 42, 193-205.	3.7	109
15	Protein Complexes in the Nucleus: The Control of Chromosome Segregation. Sub-Cellular Biochemistry, 2017, 83, 455-481.	1.0	2
16	BubR1 kinase: protection against aneuploidy and premature aging. Trends in Molecular Medicine, 2015, 21, 364-372.	3.5	48
17	The dynamic protein Knl1 â€” a kinetochore rendezvous. Journal of Cell Science, 2014, 127, 3415-23.	1.2	38
18	The dynamics of signal amplification by macromolecular assemblies for the control of chromosome segregation. Frontiers in Physiology, 2014, 5, 368.	1.3	4

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19	The internal Cdc20 binding site in BubR1 facilitates both spindle assembly checkpoint signalling and silencing. <i>Nature Communications</i> , 2014, 5, 5563.	5.8	55
20	Formation of Multiprotein Assemblies in the Nucleus. <i>International Review of Cell and Molecular Biology</i> , 2014, 307, 151-174.	1.6	3
21	Dynein-dependent transport of spindle assembly checkpoint proteins off kinetochores toward spindle poles. <i>FEBS Letters</i> , 2014, 588, 3265-3273.	1.3	34
22	Structural and Physiological Analyses of the Alkanesulphonate-Binding Protein (SsuA) of the Citrus Pathogen <i>Xanthomonas citri</i> . <i>PLoS ONE</i> , 2013, 8, e80083.	1.1	13
23	Crystal structure, biochemical and biophysical characterisation of NHR1 domain of E3 Ubiquitin ligase neutralized. <i>Advances in Enzyme Research</i> , 2013, 01, 61-75.	0.7	3
24	Structural and functional insights into the role of the N-terminal Mps1 TPR domain in the SAC (spindle assembly checkpoint). <i>Biochemical Journal</i> , 2012, 448, 321-328.	1.7	19
25	Characterization of Spindle Checkpoint Kinase Mps1 Reveals Domain with Functional and Structural Similarities to Tetratricopeptide Repeat Motifs of Bub1 and BubR1 Checkpoint Kinases. <i>Journal of Biological Chemistry</i> , 2012, 287, 5988-6001.	1.6	32
26	The architecture of the BubR1 tetratricopeptide tandem repeat defines a protein motif underlying mitotic checkpoint-kinetochore communication. <i>Bioarchitecture</i> , 2012, 2, 23-27.	1.5	3
27	Difference in lipid packing sensitivity of exchangeable apolipoproteins apoA-I and apoA-II: An important determinant for their distinctive role in lipid metabolism. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 2012, 1818, 2732-2741.	1.4	4
28	Spatial and temporal organization of multi-protein assemblies: achieving sensitive control in information-rich cell-regulatory systems. <i>Philosophical Transactions Series A, Mathematical, Physical, and Engineering Sciences</i> , 2012, 370, 3023-3039.	1.6	28
29	¹ H, ¹³ C and ¹⁵ N resonance assignments of the kinetochore localisation domain of BUBR1, a central component of the spindle assembly checkpoint. <i>Biomolecular NMR Assignments</i> , 2012, 6, 115-118.	0.4	2
30	Structural Insights into the Role of Domain Flexibility in Human DNA Ligase IV. <i>Structure</i> , 2012, 20, 1212-1222.	1.6	44
31	Spatial and Temporal Organisation of Multiprotein Systems of Cell Regulation and Signalling: What Can We Learn from NHEJ System of Double-Strand Break Repair?. <i>NATO Science for Peace and Security Series A: Chemistry and Biology</i> , 2012, , 1-31.	0.5	1
32	Fluid and Condensed ApoA-I/Phospholipid Monolayers Provide Insights into ApoA-I Membrane Insertion. <i>Journal of Molecular Biology</i> , 2011, 410, 60-76.	2.0	13
33	Structure of a Blinkin-BUBR1 Complex Reveals an Interaction Crucial for Kinetochore-Mitotic Checkpoint Regulation via an Unanticipated Binding Site. <i>Structure</i> , 2011, 19, 1691-1700.	1.6	68
34	Structure of a Blinkin-BUBR1 Complex Reveals an Interaction Crucial for Kinetochore-Mitotic Checkpoint Regulation via an Unanticipated Binding Site. <i>Structure</i> , 2011, 19, 1895.	1.6	0
35	BUB1 and BUBR1: multifaceted kinases of the cell cycle. <i>Trends in Biochemical Sciences</i> , 2011, 36, 141-150.	3.7	158
36	CENP-C Is a Structural Platform for Kinetochore Assembly. <i>Current Biology</i> , 2011, 21, 399-405.	1.8	233

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37	Biochemical characterisation of MX-4, a plant cysteine protease of broad specificity and high stability. <i>Food Chemistry</i> , 2011, 126, 543-552.	4.2	5
38	Cell-Cycle Inhibition by <i>Helicobacter pylori</i> L-Asparaginase. <i>PLoS ONE</i> , 2010, 5, e13892.	1.1	54
39	Structural Biology of DNA Repair: Spatial Organisation of the Multicomponent Complexes of Nonhomologous End Joining. <i>Journal of Nucleic Acids</i> , 2010, 2010, 1-19.	0.8	24
40	Defining the Molecular Basis of BubR1 Kinetochore Interactions and APC/C-CDC20 Inhibition. <i>Journal of Biological Chemistry</i> , 2010, 285, 14764-14776.	1.6	37
41	Targeting protein interactions of p53 for therapeutic intervention: Success in a frustrated landscape. <i>Cell Cycle</i> , 2009, 8, 3631-3635.	1.3	2
42	Perspectives on protein crystallisation. <i>Progress in Biophysics and Molecular Biology</i> , 2009, 101, 56-63.	1.4	13
43	New directions in conventional methods of protein crystallization. <i>Progress in Biophysics and Molecular Biology</i> , 2009, 101, 3-12.	1.4	50
44	The Crystal Structure of the N-Terminal Region of BUB1 Provides Insight into the Mechanism of BUB1 Recruitment to Kinetochores. <i>Structure</i> , 2009, 17, 105-116.	1.6	45
45	The alkanesulfonate-binding protein from <i>Xanthomonas axonopodis</i> pv. <i>citri</i> . <i>Acta Crystallographica Section A: Foundations and Advances</i> , 2009, 65, s141-s141.	0.3	0
46	Assessment of the Mitotic Spindle Assembly Checkpoint (SAC) as the Target of Anticancer Therapies. <i>Current Cancer Drug Targets</i> , 2009, 9, 131-141.	0.8	16
47	The N-terminal, TPR-containing domain of the mitotic checkpoint protein BUBR1 does not bind fatty acids. <i>Computational Biology and Chemistry</i> , 2008, 32, 139-140.	1.1	3
48	Crystal structure of human XLF/Cernunnos reveals unexpected differences from XRCC4 with implications for NHEJ. <i>EMBO Journal</i> , 2008, 27, 290-300.	3.5	106
49	Surface Rheology and Adsorption Kinetics Reveal the Relative Amphiphilicity, Interfacial Activity, and Stability of Human Exchangeable Apolipoproteins. <i>Biophysical Journal</i> , 2008, 94, 1735-1745.	0.2	14
50	Characterization of the Tetratricopeptide-Containing Domain of BUB1, BUBR1, and PP5 Proves That Domain Amphiphilicity over Amino Acid Sequence Specificity Governs Protein Adsorption and Interfacial Activity. <i>Journal of Physical Chemistry B</i> , 2008, 112, 7984-7991.	1.2	11
51	Protein kinase CK2 as an ectokinase: The role of the regulatory CK2 β subunit. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008, 105, 5693-5698.	3.3	38
52	Structural analysis and classification of native proteins from <i>E. coli</i> commonly co-purified by immobilised metal affinity chromatography. <i>Biochimica Et Biophysica Acta - General Subjects</i> , 2006, 1760, 1304-1313.	1.1	174
53	Evidence for the Role of the monB Genes in Polyether Ring Formation during Monensin Biosynthesis. <i>Chemistry and Biology</i> , 2006, 13, 453-460.	6.2	109
54	Identifying interaction motifs in CK2 β – a ubiquitous kinase regulatory subunit. <i>Trends in Biochemical Sciences</i> , 2006, 31, 654-661.	3.7	51

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55	Evidence that a Novel Thioesterase is Responsible for Polyketide Chain Release during Biosynthesis of the Polyether Ionophore Monensin. <i>ChemBioChem</i> , 2006, 7, 1435-1442.	1.3	57
56	The tight control of nucleation in counterdiffusive flow regimes by hyperfluorinated oils. <i>Journal of Crystal Growth</i> , 2005, 283, 215-221.	0.7	3
57	MET meet adaptors: Functional and structural implications in downstream signalling mediated by the Met receptor. <i>Molecular and Cellular Biochemistry</i> , 2005, 276, 149-157.	1.4	48
58	Aurora kinases. <i>International Journal of Biochemistry and Cell Biology</i> , 2005, 37, 1572-1577.	1.2	130
59	The Conserved N-Terminal Region of the Mitotic Checkpoint Protein BUBR1: A Putative TPR Motif of High Surface Activity. <i>Biophysical Journal</i> , 2005, 89, 2640-2649.	0.2	22
60	Structure of the regulatory subunit of CK2 in the presence of a p21WAF1 peptide demonstrates flexibility of the acidic loop. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2004, 60, 1698-1704.	2.5	6
61	Cell cycle regulatory protein p27KIP1 is a substrate and interacts with the protein kinase CK2. <i>Journal of Cellular Biochemistry</i> , 2004, 91, 865-879.	1.2	46
62	On the structure and function of apolipoproteins: more than a family of lipid-binding proteins. <i>Progress in Biophysics and Molecular Biology</i> , 2003, 83, 47-68.	1.4	68
63	The use of oil in a counter-diffusive system allows to control nucleation and coarsening during protein crystallization. <i>Journal of Crystal Growth</i> , 2003, 253, 517-523.	0.7	5
64	Amino acid sequence, biochemical characterization, and comparative modeling of a nonspecific lipid transfer protein from <i>Amaranthus hypochondriacus</i> . <i>Archives of Biochemistry and Biophysics</i> , 2003, 415, 24-33.	1.4	24
65	Asymmetry in the Multiprotein Systems of Molecular Biology. <i>Structural Chemistry</i> , 2002, 13, 405-412.	1.0	13
66	Crystallization and Preliminary X-Ray Analysis of Ovocleidin-17 A Major Protein of the Gallus Gallus Eggshell Calcified Layer. <i>Protein and Peptide Letters</i> , 2002, 9, 253-257.	0.4	15
67	Monolayers of Apolipoproteins at the Air/Water Interface. <i>Journal of Physical Chemistry B</i> , 2001, 105, 5757-5765.	1.2	76
68	Phase Transitions in Monolayers of Human Apolipoprotein C-I. <i>Journal of Physical Chemistry B</i> , 1999, 103, 6236-6242.	1.2	27
69	Precrystallization of human apoprotein A-I based on its aggregation behavior in solution studied by dynamic light scattering. <i>Journal of Molecular Structure</i> , 1998, 440, 1-8.	1.8	10
70	Stability of the C-terminal peptide of CETP mediated through an (i, i+4) array. <i>BBA - Proteins and Proteomics</i> , 1998, 1384, 7-15.	2.1	15
71	CETP and exchangeable apoproteins: common features in lipid binding activity. <i>Molecular and Cellular Biochemistry</i> , 1997, 175, 1-10.	1.4	18