

# Marcus Bustamante Smolka

## List of Publications by Year in descending order

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Version: 2024-02-01

75  
papers

4,329  
citations

109321

35  
h-index

123424

61  
g-index

92  
all docs

92  
docs citations

92  
times ranked

5856  
citing authors

#	ARTICLE	IF	CITATIONS
1	Multiple 9-1-1 complexes promote homolog synapsis, DSB repair, and ATR signaling during mammalian meiosis. <i>ELife</i> , 2022, 11, .	6.0	7
2	Phosphoproteomics of ATR signaling in mouse testes. <i>ELife</i> , 2022, 11, .	6.0	12
3	Comprehensive analysis of DNA replication timing across 184 cell lines suggests a role for MCM10 in replication timing regulation. <i>Human Molecular Genetics</i> , 2022, 31, 2899-2917.	2.9	6
4	PLEKHA5 Regulates Mitotic Progression by Promoting APC/C Localization to Microtubules. <i>FASEB Journal</i> , 2022, 36, .	0.5	0
5	A field guide to the proteomics of post-translational modifications in DNA repair. <i>Proteomics</i> , 2022, 22, .	2.2	2
6	Mass Spectrometry-Based Phosphorylation Mapping of Affinity Purified Proteins. <i>Bio-protocol</i> , 2021, 11, e4113.	0.4	1
7	Phosphoproteomics reveals a distinctive Mec1/ATR signaling response upon DNA end hyper-resection. <i>EMBO Journal</i> , 2021, 40, e104566.	7.8	17
8	Checkpoint-mediated DNA polymerase $\delta$ exonuclease activity curbing counteracts resection-driven fork collapse. <i>Molecular Cell</i> , 2021, 81, 2778-2792.e4.	9.7	14
9	Structural basis of TRAPPIII-mediated Rab1 activation. <i>EMBO Journal</i> , 2021, 40, e107607.	7.8	24
10	In-depth and 3-dimensional exploration of the budding yeast phosphoproteome. <i>EMBO Reports</i> , 2021, 22, e51121.	4.5	99
11	IGF1R-IRS1/2 Pharmacological Inhibitors Act By Distinct Cellular and Molecular Mechanisms and Reveals Vulnerabilities for Treatment of Acute Myeloid Leukemia. <i>Blood</i> , 2021, 138, 1869-1869.	1.4	0
12	Glucosylation by the Legionella Effector SetA Promotes the Nuclear Localization of the Transcription Factor TFEB. <i>IScience</i> , 2020, 23, 101300.	4.1	18
13	ATR signaling in mammalian meiosis: From upstream scaffolds to downstream signaling. <i>Environmental and Molecular Mutagenesis</i> , 2020, 61, 752-766.	2.2	21
14	Intrinsic ATR signaling shapes DNA end resection and suppresses toxic DNA-PKcs signaling. <i>NAR Cancer</i> , 2020, 2, zcaa006.	3.1	10
15	Maximized quantitative phosphoproteomics allows high confidence dissection of the DNA damage signaling network. <i>Scientific Reports</i> , 2020, 10, 18056.	3.3	9
16	The Rad53CHK1/CHK2-Spt21NPAT and Tel1ATM axes couple glucose tolerance to histone dosage and subtelomeric silencing. <i>Nature Communications</i> , 2020, 11, 4154.	12.8	14
17	Characterization of an anti-FLAG antibody binding protein in <i>V. Cholerae</i> . <i>Biochemical and Biophysical Research Communications</i> , 2020, 528, 493-498.	2.1	3
18	Checkpoint Responses to DNA Double-Strand Breaks. <i>Annual Review of Biochemistry</i> , 2020, 89, 103-133.	11.1	99

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19	MaXLinker: Proteome-wide Cross-link Identifications with High Specificity and Sensitivity. <i>Molecular and Cellular Proteomics</i> , 2020, 19, 554-568.	3.8	38
20	Progranulin deficiency leads to reduced glucocerebrosidase activity. <i>PLoS ONE</i> , 2019, 14, e0212382.	2.5	57
21	Mec1ATR Autophosphorylation and Ddc2ATRIP Phosphorylation Regulates DNA Damage Checkpoint Signaling. <i>Cell Reports</i> , 2019, 28, 1090-1102.e3.	6.4	19
22	Activity of a ubiquitin ligase adaptor is regulated by disordered insertions in its arrestin domain. <i>Molecular Biology of the Cell</i> , 2019, 30, 3057-3072.	2.1	15
23	Deubiquitination of phosphoribosyl-ubiquitin conjugates by phosphodiesterase-domain-containing <i>Legionella</i> effectors. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 23518-23526.	7.1	64
24	DNA damage kinase signaling: checkpoint and repair at 30 years. <i>EMBO Journal</i> , 2019, 38, e101801.	7.8	178
25	PLEKHA4 Attenuates Dishevelled Ubiquitination to Modulate Wnt and Planar Cell Polarity Signaling. <i>Cell Reports</i> , 2019, 27, 2157-2170.e8.	6.4	27
26	Next-Generation Sequencing Enables Spatiotemporal Resolution of Human Centromere Replication Timing. <i>Genes</i> , 2019, 10, 269.	2.4	25
27	Protein polyglutamylation catalyzed by the bacterial calmodulin-dependent pseudokinase SidJ. <i>ELife</i> , 2019, 8, .	6.0	56
28	Quantitative Analysis of DNA Damage Signaling Responses to Chemical and Genetic Perturbations. <i>Methods in Molecular Biology</i> , 2018, 1672, 645-660.	0.9	15
29	ATR-mediated proteome remodeling is a major determinant of homologous recombination capacity in cancer cells. <i>Nucleic Acids Research</i> , 2018, 46, 8311-8325.	14.5	45
30	Separable roles for Mec1/ATR in genome maintenance, DNA replication, and checkpoint signaling. <i>Genes and Development</i> , 2018, 32, 822-835.	5.9	30
31	Slx4 scaffolding in homologous recombination and checkpoint control: lessons from yeast. <i>Chromosoma</i> , 2017, 126, 45-58.	2.2	20
32	TOPBP1 Dpb11 plays a conserved role in homologous recombination DNA repair through the coordinated recruitment of 53BP1 Rad9. <i>Journal of Cell Biology</i> , 2017, 216, 623-639.	5.2	50
33	The ALS/FTLD associated protein C9orf72 associates with SMCR8 and WDR41 to regulate the autophagy-lysosome pathway. <i>Acta Neuropathologica Communications</i> , 2016, 4, 51.	5.2	243
34	Chronic DNA Replication Stress Reduces Replicative Lifespan of Cells by TRP53-Dependent, microRNA-Assisted MCM2-7 Downregulation. <i>PLoS Genetics</i> , 2016, 12, e1005787.	3.5	41
35	TOPBP1 takes RADical command in recombinational DNA repair. <i>Journal of Cell Biology</i> , 2016, 212, 263-266.	5.2	8
36	Slx4 and Rtt107 control checkpoint signalling and DNA resection at double-strand breaks. <i>Nucleic Acids Research</i> , 2016, 44, 669-682.	14.5	59

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37	TOPBP1 takes RADical command in recombinational DNA repair. <i>Journal of Experimental Medicine</i> , 2016, 213, 2132OIA2.	8.5	1
38	Assembly of Slx4 signaling complexes behind <scp>DNA</scp> replication forks. <i>EMBO Journal</i> , 2015, 34, 2182-2197.	7.8	40
39	Primary Structure of a Trypsin Inhibitor ( <i>Copaifera langsdorffii</i> Trypsin Inhibitor-1) Obtained from <i>C. langsdorffii</i> Seeds. <i>Journal of Biomolecular Techniques</i> , 2015, 26, 90-102.	1.5	2
40	Phosphoproteomics Reveals Distinct Modes of Mec1/ATR Signaling during DNA Replication. <i>Molecular Cell</i> , 2015, 57, 1124-1132.	9.7	106
41	Dampening <scp>DNA</scp> damage checkpoint signalling via coordinated <scp>BRCT</scp> domain interactions. <i>EMBO Journal</i> , 2015, 34, 1704-1717.	7.8	43
42	Termination of Replication Stress Signaling via Concerted Action of the Slx4 Scaffold and the PP4 Phosphatase. <i>Genetics</i> , 2015, 201, 937-949.	2.9	21
43	Prosaposin facilitates sortilin-independent lysosomal trafficking of progranulin. <i>Journal of Cell Biology</i> , 2015, 210, 991-1002.	5.2	158
44	A Massively Parallel Pipeline to Clone DNA Variants and Examine Molecular Phenotypes of Human Disease Mutations. <i>PLoS Genetics</i> , 2014, 10, e1004819.	3.5	47
45	The <i>Legionella</i> effector SidC defines a unique family of ubiquitin ligases important for bacterial phagosomal remodeling. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 10538-10543.	7.1	98
46	Interactome Analysis Reveals Ezrin Can Adopt Multiple Conformational States. <i>Journal of Biological Chemistry</i> , 2013, 288, 35437-35451.	3.4	40
47	DNA-repair scaffolds dampen checkpoint signalling by counteracting the adaptor Rad9. <i>Nature</i> , 2013, 493, 120-124.	27.8	87
48	The Co-Repressor SMRT Delays DNA Damage-Induced Caspase Activation by Repressing Pro-Apoptotic Genes and Modulating the Dynamics of Checkpoint Kinase 2 Activation. <i>PLoS ONE</i> , 2013, 8, e59986.	2.5	9
49	Linking DNA replication checkpoint to MBF cell-cycle transcription reveals a distinct class of G1/S genes. <i>EMBO Journal</i> , 2012, 31, 1798-1810.	7.8	68
50	DNA replication stress differentially regulates G1/S genes via Rad53-dependent inactivation of Nrm1. <i>EMBO Journal</i> , 2012, 31, 1811-1822.	7.8	65
51	The many roads to checkpoint activation. <i>Cell Cycle</i> , 2012, 11, 4495-4495.	2.6	3
52	Local phosphocycling mediated by LOK/SLK restricts ezrin function to the apical aspect of epithelial cells. <i>Journal of Cell Biology</i> , 2012, 199, 969-984.	5.2	96
53	The checkpoint transcriptional response: Make sure to turn it off once you are satisfied. <i>Cell Cycle</i> , 2012, 11, 3166-3174.	2.6	15
54	TORC1 Regulates Endocytosis via Npr1-Mediated Phosphoinhibition of a Ubiquitin Ligase Adaptor. <i>Cell</i> , 2011, 147, 1104-1117.	28.9	194

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55	A touching moment for Smc5/6: From ssDNA binding to repair. <i>Cell Cycle</i> , 2011, 10, 1190-1191.	2.6	1
56	Fine-tuning the DNA damage response: Protein Phosphatase 2A checks on CHK2. <i>Cell Cycle</i> , 2010, 9, 861-869.	2.6	3
57	DNA Damage Signaling Recruits the Rtt107-Slx4 Scaffolds via Dpb11 to Mediate Replication Stress Response. <i>Molecular Cell</i> , 2010, 39, 300-306.	9.7	93
58	Whi5 Regulation by Site Specific CDK-Phosphorylation in <i>Saccharomyces cerevisiae</i> . <i>PLoS ONE</i> , 2009, 4, e4300.	2.5	61
59	Phosphorylation-Specific MS/MS Scoring for Rapid and Accurate Phosphoproteome Analysis. <i>Journal of Proteome Research</i> , 2008, 7, 3373-3381.	3.7	51
60	A Multidimensional Chromatography Technology for In-depth Phosphoproteome Analysis. <i>Molecular and Cellular Proteomics</i> , 2008, 7, 1389-1396.	3.8	472
61	Impact of Phosphorylation and Phosphorylation-null Mutants on the Activity and Deamination Specificity of Activation-induced Cytidine Deaminase. <i>Journal of Biological Chemistry</i> , 2008, 283, 17428-17439.	3.4	40
62	Proteome-wide identification of in vivo targets of DNA damage checkpoint kinases. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007, 104, 10364-10369.	7.1	378
63	Mechanism of Dun1 Activation by Rad53 Phosphorylation in <i>Saccharomyces cerevisiae</i> . <i>Journal of Biological Chemistry</i> , 2007, 282, 986-995.	3.4	68
64	Extraction, purification and biochemical characterization of a peroxidase from <i>Copaifera langsdorffii</i> leaves. <i>Quimica Nova</i> , 2007, 30, 1067-1071.	0.3	22
65	Absence of Classical Heat Shock Response in the Citrus Pathogen <i>Xylella fastidiosa</i> . <i>Current Microbiology</i> , 2007, 54, 119-123.	2.2	6
66	Comparative analysis of two-dimensional electrophoresis maps (2-DE) of <i>Helicobacter pylori</i> from Brazilian patients with chronic gastritis and duodenal ulcer: a preliminary report. <i>Revista Do Instituto De Medicina Tropical De Sao Paulo</i> , 2006, 48, 175-177.	1.1	8
67	An FHA domain-mediated protein interaction network of Rad53 reveals its role in polarized cell growth. <i>Journal of Cell Biology</i> , 2006, 175, 743-753.	5.2	85
68	Checkpoint proteins control morphogenetic events during DNA replication stress in <i>Saccharomyces cerevisiae</i> . <i>Journal of Cell Biology</i> , 2006, 175, 729-741.	5.2	79
69	FHA domain mediated protein interaction network of Dun1 identifies its novel functions in the DNA damage response. <i>FASEB Journal</i> , 2006, 20, A509.	0.5	0
70	Dynamic Changes in Protein-Protein Interaction and Protein Phosphorylation Probed with Amine-reactive Isotope Tag. <i>Molecular and Cellular Proteomics</i> , 2005, 4, 1358-1369.	3.8	71
71	Proteome analysis of the plant pathogen <i>Xylella fastidiosa</i> reveals major cellular and extracellular proteins and a peculiar codon bias distribution. <i>Proteomics</i> , 2003, 3, 224-237.	2.2	87
72	Quantitative Protein Profiling Using Two-dimensional Gel Electrophoresis, Isotope-coded Affinity Tag Labeling, and Mass Spectrometry. <i>Molecular and Cellular Proteomics</i> , 2002, 1, 19-29.	3.8	106

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73	Optimization of the Isotope-Coded Affinity Tag-Labeling Procedure for Quantitative Proteome Analysis. Analytical Biochemistry, 2001, 297, 25-31.	2.4	198
74	Purification and partial characterization of a thrombin-like enzyme, balterobin, from the venom of Bothrops alternatus. Toxicon, 1998, 36, 1059-1063.	1.6	33
75	Fork Slowing and Reversal as an Adaptive Response to Chronic ATR Inhibition. SSRN Electronic Journal, 0, , .	0.4	0