Marcus Bustamante Smolka

List of Publications by Year
in descending order

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	A Multidimensional Chromatography Technology for In-depth Phosphoproteome Analysis. Molecular and Cellular Proteomics, 2008, 7, 1389-1396.	3.8	472
2	Proteome-wide identification of in vivo targets of DNA damage checkpoint kinases. Proceedings of the National Academy of Sciences of the United States of America, 2007, 104, 10364-10369.	7.1	378
3	The ALS/FTLD associated protein C9orf72 associates with SMCR8 and WDR41 to regulate the autophagy-lysosome pathway. Acta Neuropathologica Communications, 2016, 4, 51.	5.2	243
4	Optimization of the Isotope-Coded Affinity Tag-Labeling Procedure for Quantitative Proteome Analysis. Analytical Biochemistry, 2001, 297, 25-31.	2.4	198
5	TORC1 Regulates Endocytosis via Npr1-Mediated Phosphoinhibition of a Ubiquitin Ligase Adaptor. Cell, 2011, 147, 1104-1117.	28.9	194
6	<scp>DNA</scp> damage kinase signaling: checkpoint and repair at 30Âyears. EMBO Journal, 2019, 38, e101801.	7.8	178
7	Prosaposin facilitates sortilin-independent lysosomal trafficking of progranulin. Journal of Cell Biology, 2015, 210, 991-1002.	5.2	158
8	Quantitative Protein Profiling Using Two-dimensional Gel Electrophoresis, Isotope-coded Affinity Tag Labeling, and Mass Spectrometry. Molecular and Cellular Proteomics, 2002, 1, 19-29.	3.8	106
9	Phosphoproteomics Reveals Distinct Modes of Mec1/ATR Signaling during DNA Replication. Molecular Cell, 2015, 57, 1124-1132.	9.7	106
10	Checkpoint Responses to DNA Double-Strand Breaks. Annual Review of Biochemistry, 2020, 89, 103-133.	11.1	99
11	Inâ€depth and 3â€dimensional exploration of the budding yeast phosphoproteome. EMBO Reports, 2021, 22, e51121.	4.5	99
12	The Legionella effector SidC defines a unique family of ubiquitin ligases important for bacterial phagosomal remodeling. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 10538-10543.	7.1	98
13	Local phosphocycling mediated by LOK/SLK restricts ezrin function to the apical aspect of epithelial cells. Journal of Cell Biology, 2012, 199, 969-984.	5.2	96
14	DNA Damage Signaling Recruits the Rtt107-Slx4 Scaffolds via Dpb11 to Mediate Replication Stress Response. Molecular Cell, 2010, 39, 300-306.	9.7	93
15	Proteome analysis of the plant pathogen Xylella fastidiosa reveals major cellular and extracellular proteins and a peculiar codon bias distribution. Proteomics, 2003, 3, 224-237.	2.2	87
16	DNA-repair scaffolds dampen checkpoint signalling by counteracting the adaptor Rad9. Nature, 2013, 493, 120-124.	27.8	87
17	An FHA domainâ€“mediated protein interaction network of Rad53 reveals its role in polarized cell growth. Journal of Cell Biology, 2006, 175, 743-753.	5.2	85
18	Checkpoint proteins control morphogenetic events during DNA replication stress in Saccharomyces cerevisiae. Journal of Cell Biology, 2006, 175, 729-741.	5.2	79

#	Article	IF	Citations
19	Dynamic Changes in Protein-Protein Interaction and Protein Phosphorylation Probed with Amine-reactive Isotope Tag. Molecular and Cellular Proteomics, 2005, 4, 1358-1369.	3.8	71
20	Mechanism of Dun1 Activation by Rad53 Phosphorylation in Saccharomyces cerevisiae. Journal of Biological Chemistry, 2007, 282, 986-995.	3.4	68
21	Linking DNA replication checkpoint to MBF cell-cycle transcription reveals a distinct class of G1/S genes. EMBO Journal, 2012, 31, 1798-1810.	7.8	68
22	DNA replication stress differentially regulates G1/S genes via Rad53-dependent inactivation of Nrm1. EMBO Journal, 2012, 31, 1811-1822.	7.8	65
23	Deubiquitination of phosphoribosyl-ubiquitin conjugates by phosphodiesterase-domainâ€“containing Legionella effectors. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 23518-23526.	7.1	64
24	Whi5 Regulation by Site Specific CDK-Phosphorylation in Saccharomyces cerevisiae. PLoS ONE, 2009, 4, e4300.	2.5	61
25	Slx4 and Rtt107 control checkpoint signalling and DNA resection at double-strand breaks. Nucleic Acids Research, 2016, 44, 669-682.	14.5	59
26	Progranulin deficiency leads to reduced glucocerebrosidase activity. PLoS ONE, 2019, 14, e0212382.	2.5	57
27	Protein polyglutamylation catalyzed by the bacterial calmodulin-dependent pseudokinase SidJ. ELife, 2019, 8, .	6.0	56
28	Phosphorylation-Specific MS/MS Scoring for Rapid and Accurate Phosphoproteome Analysis. Journal of Proteome Research, 2008, 7, 3373-3381.	3.7	51
29	TOPBP1Dpb11 plays a conserved role in homologous recombination DNA repair through the coordinated recruitment of 53BP1Rad9. Journal of Cell Biology, 2017, 216, 623-639.	5.2	50
30	A Massively Parallel Pipeline to Clone DNA Variants and Examine Molecular Phenotypes of Human Disease Mutations. PLoS Genetics, 2014, 10, e1004819.	3.5	47
31	ATR-mediated proteome remodeling is a major determinant of homologous recombination capacity in cancer cells. Nucleic Acids Research, 2018, 46, 8311-8325.	14.5	45
32	Dampening <scp>DNA</scp> damage checkpoint signalling via coordinated <scp>BRCT</scp> domain interactions. EMBO Journal, 2015, 34, 1704-1717.	7.8	43
33	Chronic DNA Replication Stress Reduces Replicative Lifespan of Cells by TRP53-Dependent, microRNA-Assisted MCM2-7 Downregulation. PLoS Genetics, 2016, 12, e1005787.	3.5	41
34	Impact of Phosphorylation and Phosphorylation-null Mutants on the Activity and Deamination Specificity of Activation-induced Cytidine Deaminase. Journal of Biological Chemistry, 2008, 283, 17428-17439.	3.4	40
35	Interactome Analysis Reveals Ezrin Can Adopt Multiple Conformational States. Journal of Biological Chemistry, 2013, 288, 35437-35451.	3.4	40
36	Assembly of Slx4 signaling complexes behind <scp>DNA</scp> replication forks. EMBO Journal, 2015, 34, 2182-2197.	7.8	40

#	Article	IF	Citations
37	MaXLinker: Proteome-wide Cross-link Identifications with High Specificity and Sensitivity. Molecular and Cellular Proteomics, 2020, 19, 554-568.	3.8	38
38	Purification and partial characterization of a thrombin-like enzyme, balterobin, from the venom of Bothrops alternatus. Toxicon, 1998, 36, 1059-1063.	1.6	33
39	Separable roles for Mec1/ATR in genome maintenance, DNA replication, and checkpoint signaling. Genes and Development, 2018, 32, 822-835.	5.9	30
40	PLEKHA4/kramer Attenuates Dishevelled Ubiquitination to Modulate Wnt and Planar Cell Polarity Signaling. Cell Reports, 2019, 27, 2157-2170.e8.	6.4	27
41	Next-Generation Sequencing Enables Spatiotemporal Resolution of Human Centromere Replication Timing. Genes, 2019, 10, 269.	2.4	25
42	Structural basis of TRAPPIIIâ€mediated Rab1 activation. EMBO Journal, 2021, 40, e107607.	7.8	24
43	Extraction, purification and biochemical characterization of a peroxidase from Copaifera langsdorffii leaves. Quimica Nova, 2007, 30, 1067-1071.	0.3	22
44	Termination of Replication Stress Signaling via Concerted Action of the Slx4 Scaffold and the PP4 Phosphatase. Genetics, 2015, 201, 937-949.	2.9	21
45	ATR signaling in mammalian meiosis: From upstream scaffolds to downstream signaling. Environmental and Molecular Mutagenesis, 2020, 61, 752-766.	2.2	21
46	Slx4 scaffolding in homologous recombination and checkpoint control: lessons from yeast. Chromosoma, 2017, 126, 45-58.	2.2	20
47	Mec1ATR Autophosphorylation and Ddc2ATRIP Phosphorylation Regulates DNA Damage Checkpoint Signaling. Cell Reports, 2019, 28, 1090-1102.e3.	6.4	19
48	Glucosylation by the Legionella Effector SetA Promotes the Nuclear Localization of the Transcription Factor TFEB. IScience, 2020, 23, 101300.	4.1	18
49	Phosphoproteomics reveals a distinctive Mec1/ATR signaling response upon DNA end hyperâ€resection. EMBO Journal, 2021, 40, e104566.	7.8	17
50	The checkpoint transcriptional response: Make sure to turn it off once you are satisfied. Cell Cycle, 2012, 11, 3166-3174.	2.6	15
51	Quantitative Analysis of DNA Damage Signaling Responses to Chemical and Genetic Perturbations. Methods in Molecular Biology, 2018, 1672, 645-660.	0.9	15
52	Activity of a ubiquitin ligase adaptor is regulated by disordered insertions in its arrestin domain. Molecular Biology of the Cell, 2019, 30, 3057-3072.	2.1	15
53	The Rad53CHK1/CHK2-Spt21NPAT and Tel1ATM axes couple glucose tolerance to histone dosage and subtelomeric silencing. Nature Communications, 2020, 11, 4154.	12.8	14
54	Checkpoint-mediated DNA polymerase Îµ exonuclease activity curbing counteracts resection-driven fork collapse. Molecular Cell, 2021, 81, 2778-2792.e4.	9.7	14

#	Article	IF	Citations
55	Phosphoproteomics of ATR signaling in mouse testes. ELife, 2022, 11, .	6.0	12
56	Intrinsic ATR signaling shapes DNA end resection and suppresses toxic DNA-PKcs signaling. NAR Cancer, 2020, 2, zcaa006.	3.1	10
57	The Co-Repressor SMRT Delays DNA Damage-Induced Caspase Activation by Repressing Pro-Apoptotic Genes and Modulating the Dynamics of Checkpoint Kinase 2 Activation. PLoS ONE, 2013, 8, e59986.	2.5	9
58	Maximized quantitative phosphoproteomics allows high confidence dissection of the DNA damage signaling network. Scientific Reports, 2020, 10, 18056.	3.3	9
59	Comparative analysis of two-dimensional electrophoresis maps (2-DE) of Helicobacter pylori from Brazilian patients with chronic gastritis and duodenal ulcer: a preliminary report. Revista Do Instituto De Medicina Tropical De Sao Paulo, 2006, 48, 175-177.	1.1	8
60	TOPBP1 takes RADical command in recombinational DNA repair. Journal of Cell Biology, 2016, 212, 263-266.	5.2	8
61	Multiple 9-1-1 complexes promote homolog synapsis, DSB repair, and ATR signaling during mammalian meiosis. ELife, 2022, 11, .	6.0	7
62	Absence of Classical Heat Shock Response in the Citrus Pathogen Xylella fastidiosa. Current Microbiology, 2007, 54, 119-123.	2.2	6
63	Comprehensive analysis of DNA replication timing across 184 cell lines suggests a role for MCM10 in replication timing regulation. Human Molecular Genetics, 2022, 31, 2899-2917.	2.9	6
64	Fine-tuning the DNA damage response: Protein Phosphatase 2A checks on CHK2. Cell Cycle, 2010, 9, 861-869.	2.6	3
65	The many roads to checkpoint activation. Cell Cycle, 2012, 11, 4495-4495.	2.6	3
66	Characterization of an anti-FLAG antibody binding protein in V.Âcholerae. Biochemical and Biophysical Research Communications, 2020, 528, 493-498.	2.1	3
67	Primary Structure of a Trypsin Inhibitor (Copaifera langsdorffii Trypsin Inhibitor-1) Obtained from C. langsdorffii Seeds. Journal of Biomolecular Techniques, 2015, 26, 90-102.	1.5	2
68	A field guide to the proteomics of postâ€translational modifications in DNA repair. Proteomics, 2022, 22, .	2.2	2
69	A touching moment for Smc5/6: From ssDNA binding to repair. Cell Cycle, 2011, 10, 1190-1191.	2.6	1
70	Mass Spectrometry-Based Phosphorylation Mapping of Affinity Purified Proteins. Bio-protocol, 2021, 11, e4113.	0.4	1
71	TOPBP1 takes RADical command in recombinational DNA repair. Journal of Experimental Medicine, 2016, 213, 2132OIA2.	8.5	1
72	Fork Slowing and Reversal as an Adaptive Response to Chronic ATR Inhibition. SSRN Electronic Journal, 0, , .	0.4	0

#	Article	IF	Citations
73	FHA domain mediated protein interaction network of Dun1 identifies its novel functions in the DNA damage response. FASEB Journal, 2006, 20, A509.	0.5	0
74	IGF1R-IRS1/2 Pharmacological Inhibitors Act By Distinct Cellular and Molecular Mechanisms and Reveals Vulnerabilities for Treatment of Acute Myeloid Leukemia. Blood, 2021, 138, 1869-1869.	1.4	0
75	PLEKHA5 Regulates Mitotic Progression by Promoting APC/C Localization to Microtubules. FASEB Journal, 2022, 36, .	0.5	0