

Peter H L Krijger

List of Publications by Year in descending order

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33
papers

3,557
citations

304743

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h-index

395702

33
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36
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docs citations

36
times ranked

5720
citing authors

#	ARTICLE	IF	CITATIONS
1	The Cohesin Release Factor WAPL Restricts Chromatin Loop Extension. <i>Cell</i> , 2017, 169, 693-707.e14.	28.9	636
2	CTCF Binding Polarity Determines Chromatin Looping. <i>Molecular Cell</i> , 2015, 60, 676-684.	9.7	537
3	Regulation of disease-associated gene expression in the 3D genome. <i>Nature Reviews Molecular Cell Biology</i> , 2016, 17, 771-782.	37.0	294
4	The pluripotent genome in three dimensions is shaped around pluripotency factors. <i>Nature</i> , 2013, 501, 227-231.	27.8	236
5	Targeted sequencing by proximity ligation for comprehensive variant detection and local haplotyping. <i>Nature Biotechnology</i> , 2014, 32, 1019-1025.	17.5	231
6	Enhancer hubs and loop collisions identified from single-allele topologies. <i>Nature Genetics</i> , 2018, 50, 1151-1160.	21.4	189
7	Cell-of-Origin-Specific 3D Genome Structure Acquired during Somatic Cell Reprogramming. <i>Cell Stem Cell</i> , 2016, 18, 597-610.	11.1	187
8	YAP Partially Reprograms Chromatin Accessibility to Directly Induce Adult Cardiogenesis In Vivo. <i>Developmental Cell</i> , 2019, 48, 765-779.e7.	7.0	171
9	A/T mutagenesis in hypermutated immunoglobulin genes strongly depends on PCNAK164 modification. <i>Journal of Experimental Medicine</i> , 2007, 204, 1989-1998.	8.5	144
10	Discovery and validation of sub-threshold genome-wide association study loci using epigenomic signatures. <i>ELife</i> , 2016, 5, .	6.0	115
11	PCNA Ubiquitination Is Important, But Not Essential for Translesion DNA Synthesis in Mammalian Cells. <i>PLoS Genetics</i> , 2011, 7, e1002262.	3.5	113
12	4C-seq from beginning to end: A detailed protocol for sample preparation and data analysis. <i>Methods</i> , 2020, 170, 17-32.	3.8	107
13	Cause and Consequence of Tethering a SubTAD to Different Nuclear Compartments. <i>Molecular Cell</i> , 2016, 61, 461-473.	9.7	73
14	Analysis of somatic hypermutation in X-linked hyper-IgM syndrome shows specific deficiencies in mutational targeting. <i>Blood</i> , 2009, 113, 3706-3715.	1.4	60
15	HLTF and SHPRH are not essential for PCNA polyubiquitination, survival and somatic hypermutation: Existence of an alternative E3 ligase. <i>DNA Repair</i> , 2011, 10, 438-444.	2.8	53
16	Dependence of nucleotide substitutions on Ung2, Msh2, and PCNA-Ub during somatic hypermutation. <i>Journal of Experimental Medicine</i> , 2009, 206, 2603-2611.	8.5	52
17	Building regulatory landscapes reveals that an enhancer can recruit cohesin to create contact domains, engage CTCF sites and activate distant genes. <i>Nature Structural and Molecular Biology</i> , 2022, 29, 563-574.	8.2	49
18	PCNA ubiquitination-independent activation of polymerase δ during somatic hypermutation and DNA damage tolerance. <i>DNA Repair</i> , 2011, 10, 1051-1059.	2.8	43

#	ARTICLE	IF	CITATIONS
19	Identical cells with different 3D genomes; cause and consequences?. <i>Current Opinion in Genetics and Development</i> , 2013, 23, 191-196.	3.3	42
20	Rev1 is essential in generating G to C transversions downstream of the Ung2 pathway but not the Msh2+Ung2 hybrid pathway. <i>European Journal of Immunology</i> , 2013, 43, 2765-2770.	2.9	36
21	Mice deficient for CD137 ligand are predisposed to develop germinal centerâ€derived B-cell lymphoma. <i>Blood</i> , 2009, 114, 2280-2289.	1.4	35
22	Genetic Dissection of a Super Enhancer Controlling the <i>Nppa-Nppb</i> Cluster in the Heart. <i>Circulation Research</i> , 2021, 128, 115-129.	4.5	32
23	Interplay between CTCF boundaries and a super enhancer controls cohesin extrusion trajectories and gene expression. <i>Molecular Cell</i> , 2021, 81, 3082-3095.e6.	9.7	29
24	Multi-contact 4C: long-molecule sequencing of complex proximity ligation products to uncover local cooperative and competitive chromatin topologies. <i>Nature Protocols</i> , 2020, 15, 364-397.	12.0	25
25	Robust detection of translocations in lymphoma FFPE samples using targeted locus capture-based sequencing. <i>Nature Communications</i> , 2021, 12, 3361.	12.8	19
26	Somatic hypermutation of immunoglobulin genes: lessons from proliferating cell nuclear antigen K164R mutant mice. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2009, 364, 621-629.	4.0	11
27	Can We Just Say: Transcription Second?. <i>Cell</i> , 2017, 169, 184-185.	28.9	10
28	Role of the cellular factor CTCF in the regulation of bovine leukemia virus latency and three-dimensional chromatin organization. <i>Nucleic Acids Research</i> , 2022, 50, 3190-3202.	14.5	5
29	The Fanconi Anemia Core Complex Is Dispensable during Somatic Hypermutation and Class Switch Recombination. <i>PLoS ONE</i> , 2010, 5, e15236.	2.5	4
30	A publicâ€private partnership model for COVID-19 diagnostics. <i>Nature Biotechnology</i> , 2021, 39, 1182-1184.	17.5	4
31	Lysine Residue 185 of Rad1 Is a Topological but Not a Functional Counterpart of Lysine Residue 164 of PCNA. <i>PLoS ONE</i> , 2011, 6, e16669.	2.5	3
32	The Ig heavy chain protein but not its message controls early B cell development. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 31343-31352.	7.1	2
33	Error-Prone and Error-Free Resolution of AID Lesions in SHM. <i>Molecular Medicine and Medicinal</i> , 2010, , 97-126.	0.4	1