Martijn S Luijsterburg

List of Publications by Year
in descending order

58	4,153	109137 35	128067 60
papers	citations	h-index	g-index

67	67	67	5323
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	HI-NESS: a family of genetically encoded DNA labels based on a bacterial nucleoid-associated protein. Nucleic Acids Research, 2022, 50, e10-e10.	6.5	4
2	SCAI promotes errorâ€free repair of DNA interstrand crosslinks via the Fanconi anemia pathway. EMBO Reports, 2022, 23, e53639.	2.0	12
3	ZMYM2 restricts 53BP1 at DNA double-strand breaks to favor BRCA1 loading and homologous recombination. Nucleic Acids Research, 2022, 50, 3922-3943.	6.5	16
4	A CSB-PAF1C axis restores processive transcription elongation after DNA damage repair. Nature Communications, 2021, 12, 1342.	5.8	31
5	Poly(ADP-ribosyl)ation temporally confines SUMO-dependent ataxin-3 recruitment to control DNA double-strand break repair. Journal of Cell Science, 2021, 134, .	1.2	8
6	Transcription-Coupled DNA Repair: From Mechanism to Human Disorder. Trends in Cell Biology, 2021, 31, 359-371.	3.6	49
7	ELOF1 is a transcription-coupled DNA repair factor that directs RNA polymerase II ubiquitylation. Nature Cell Biology, 2021, 23, 595-607.	4.6	38
8	Dealing with transcription-blocking DNA damage: Repair mechanisms, RNA polymerase II processing and human disorders. DNA Repair, 2021, 106, 103192.	1.3	25
9	ERCC1mutations impede DNA damage repair and cause liver and kidney dysfunction in patients. Journal of Experimental Medicine, 2021, 218, .	4.2	18
10	Nucleotide excision repair leaves a mark on chromatin: DNA damage detection in nucleosomes. Cellular and Molecular Life Sciences, 2021, 78, 7925-7942.	2.4	20
11	Transcription-coupled nucleotide excision repair is coordinated by ubiquitin and SUMO in response to ultraviolet irradiation. Nucleic Acids Research, 2020, 48, 231-248.	6.5	10
12	CHD7 and 53BP1 regulate distinct pathways for the re-ligation of DNA double-strand breaks. Nature Communications, 2020, 11, 5775.	5.8	28
13	Loss of ZBTB24 impairs nonhomologous end-joining and class-switch recombination in patients with ICF syndrome. Journal of Experimental Medicine, 2020, 217, .	4.2	27
14	VolcaNoseR is a web app for creating, exploring, labeling and sharing volcano plots. Scientific Reports, 2020, 10, 20560.	1.6	301
15	The cooperative action of CSB, CSA, and UVSSA target TFIIH to DNA damage-stalled RNA polymerase II. Nature Communications, 2020, 11, 2104.	5.8	91
16	Human HMGN1 and HMGN2 are not required for transcription-coupled DNA repair. Scientific Reports, 2020, 10, 4332.	1.6	6
17	Ubiquitination of DNA Damage-Stalled RNAPII Promotes Transcription-Coupled Repair. Cell, 2020, 180, 1228-1244.e24.	13.5	132
18	Structural Basis of BRCC36 Function in DNA Repair and Immune Regulation. Molecular Cell, 2019, 75, 483-497.e9.	4.5	50

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19	WWP2 ubiquitylates RNA polymerase II for DNA-PK-dependent transcription arrest and repair at DNA breaks. Genes and Development, 2019, 33, 684-704.	2.7	71
20	The CHD6 chromatin remodeler is an oxidative DNA damage response factor. Nature Communications, 2019, 10, 241.	5.8	45
21	TRiC controls transcription resumption after UV damage by regulating Cockayne syndrome protein A. Nature Communications, 2018, 9, 1040.	5.8	27
22	Aging and drug discovery. Aging, 2018, 10, 3079-3088.	1.4	25
23	Ataxinâ€3 consolidates the <scp>MDC</scp>1â€dependent <scp>DNA</scp> doubleâ€strand break response by counteracting the <scp>SUMO</scp>â€targeted ubiquitin ligase <scp>RNF</scp>4. EMBO Journal, 2017, 36, 1066-1083.	3.5	60
24	A PALB2-interacting domain in RNF168 couples homologous recombination to DNA break-induced chromatin ubiquitylation. ELife, 2017, 6, .	2.8	65
25	Functional Analysis of Missense Variants in the Putative Breast Cancer Susceptibility GeneXRCC2. Human Mutation, 2016, 37, 914-925.	1.1	12
26	PARP1 Links CHD2-Mediated Chromatin Expansion and H3.3 Deposition to DNA Repair by Non-homologous End-Joining. Molecular Cell, 2016, 61, 547-562.	4.5	214
27	ZMYND8 Co-localizes with NuRD on Target Genes and Regulates Poly(ADP-Ribose)-Dependent Recruitment of GATAD2A/NuRD to Sites of DNA Damage. Cell Reports, 2016, 17, 783-798.	2.9	100
28	Antisense oligonucleotide-mediated exon skipping as a strategy to reduce proteolytic cleavage of ataxin-3. Scientific Reports, 2016, 6, 35200.	1.6	31
29	<scp>SUMO</scp> ylation and <scp>PAR</scp> ylation cooperate to recruit and stabilize <scp>SLX</scp> 4 at <scp>DNA</scp> damage sites. EMBO Reports, 2015, 16, 512-519.	2.0	51
30	The de-ubiquitylating enzymes USP26 and USP37 regulate homologous recombination by counteracting RAP80. Nucleic Acids Research, 2015, 43, 6919-6933.	6.5	64
31	Differential binding kinetics of replication protein A during replication and the pre- and post-incision steps of nucleotide excision repair. DNA Repair, 2014, 24, 46-56.	1.3	3
32	Opposing ISWI- and CHD-class chromatin remodeling activities orchestrate heterochromatic DNA repair. Journal of Cell Biology, 2014, 207, 717-733.	2.3	65
33	Should I stay or should I go: VCP/p97-mediated chromatin extraction in the DNA damage response. Experimental Cell Research, 2014, 329, 9-17.	1.2	41
34	Poly(ADP-ribosyl)ation links the chromatin remodeler SMARCA5/SNF2H to RNF168-dependent DNA damage signaling. Journal of Cell Science, 2013, 126, 889-903.	1.2	113
35	Touching base with PARPs: moonlighting in the repair of UV lesions and double-strand breaks. Trends in Biochemical Sciences, 2013, 38, 321-330.	3.7	45
36	The Epsteinâ€“Barr virus nuclear antigen-1 reprograms transcription by mimicry of high mobility group A proteins. Nucleic Acids Research, 2013, 41, 2950-2962.	6.5	40

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37	Remodeling and spacing factor 1 (RSF1) deposits centromere proteins at DNA double-strand breaks to promote non-homologous end-joining. Cell Cycle, 2013, 12, 3070-3082.	1.3	50
38	A Role for MeCP2 in Switching Gene Activity via Chromatin Unfolding and HP1Î³ Displacement. PLoS ONE, 2013, 8, e69347.	1.1	13
39	A new non-catalytic role for ubiquitin ligase RNF8 in unfolding higher-order chromatin structure. EMBO Journal, 2012, 31, 2511-2527.	3.5	94
40	Recognition of DNA damage by XPC coincides with disruption of the XPCâ€“RAD23 complex. Journal of Cell Biology, 2012, 196, 681-688.	2.3	65
41	PARP1 promotes nucleotide excision repair through DDB2 stabilization and recruitment of ALC1. Journal of Cell Biology, 2012, 199, 235-249.	2.3	197
42	DDB2 promotes chromatin decondensation at UV-induced DNA damage. Journal of Cell Biology, 2012, 197, 267-281.	2.3	132
43	Close encounters of the RNF8th kind: when chromatin meets DNA repair. Current Opinion in Cell Biology, 2012, 24, 439-447.	2.6	29
44	Chromatin and the DNA damage response: The cancer connection. Molecular Oncology, 2011, 5, 349-367.	2.1	107
45	The AAA-ATPase VCP/p97 promotes 53BP1 recruitment by removing L3MBTL1 from DNA double-strand breaks. Nature Structural and Molecular Biology, 2011, 18, 1345-1350.	3.6	242
46	Stochastic and reversible assembly of a multiprotein DNA repair complex ensures accurate target site recognition and efficient repair. Journal of Cell Biology, 2010, 189, 445-463.	2.3	114
47	The Emerging Role of HP1 in the DNA Damage Response. Molecular and Cellular Biology, 2009, 29, 6335-6340.	1.1	104
48	Spatial organization of nucleotide excision repair proteins after UV-induced DNA damage in the human cell nucleus. Journal of Cell Science, 2009, 122, 83-91.	1.2	35
49	Heterochromatin protein 1 is recruited to various types of DNA damage. Journal of Cell Biology, 2009, 185, 577-586.	2.3	228
50	Assembly of multiprotein complexes that control genome function. Journal of Cell Biology, 2009, 185, 21-26.	2.3	41
51	The Major Architects of Chromatin: Architectural Proteins in Bacteria, Archaea and Eukaryotes. Critical Reviews in Biochemistry and Molecular Biology, 2008, 43, 393-418.	2.3	194
52	Cellular Concentrations of DDB2 Regulate Dynamic Binding of DDB1 at UV-Induced DNA Damage. Molecular and Cellular Biology, 2008, 28, 7402-7413.	1.1	33
53	Versatile DNA damage detection by the global genome nucleotide excision repair protein XPC. Journal of Cell Science, 2008, 121, 2850-2859.	1.2	109
54	Dynamic in vivo interaction of DDB2 E3 ubiquitin ligase with UV-damaged DNA is independent of damage-recognition protein XPC. Journal of Cell Science, 2007, 120, 2706-2716.	1.2	95

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55	DNA double-strand breaks are not sufficient to initiate recruitment of TRF2. Nature Genetics, 2007, 39, 696-698.	9.4	48
56	Recruitment of the Nucleotide Excision Repair Endonuclease XPG to Sites of UV-Induced DNA Damage Depends on Functional TFIIH. Molecular and Cellular Biology, 2006, 26, 8868-8879.	1.1	88
57	DNA Bridging: a Property Shared among H-NS-Like Proteins. Journal of Bacteriology, 2005, 187, 1845-1848.	1.0	133
58	Analysis of scanning force microscopy images of protein-induced DNA bending using simulations. Nucleic Acids Research, 2005, 33, e68-e68.	6.5	32