Primo SchÃ¤r

List of Publications by Year
in descending order

62 papers	4,868 citations	109321 35 h-index	128289 60 g-index
63 all docs	63 docs citations	63 times ranked	5413 citing authors

#	Article	IF	Citations
1	Longitudinal analysis of healthy colon establishes aspirin as a suppressor of cancer-related epigenetic aging. Clinical Epigenetics, 2020, 12, 164.	4.1	5
2	Assessment of Genotoxicity in Human Cells Exposed to Modulated Electromagnetic Fields of Wireless Communication Devices. Genes, 2020, 11, 347.	2.4	7
3	Inducible TDG knockout models to study epigenetic regulation. F1000Research, 2020, 9, 1112.	1.6	4
4	Aberrant regulation of epigenetic modifiers contributes to the pathogenesis in patients with selenoprotein N â€ related myopathies. Human Mutation, 2019, 40, 962-974.	2.5	13
5	DNA methylation instability by BRAF-mediated TET silencing and lifestyle-exposure divides colon cancer pathways. Clinical Epigenetics, 2019, 11, 196.	4.1	22
6	Tumor Initiation Capacity and Therapy Resistance Are Differential Features of EMT-Related Subpopulations in the NSCLC Cell Line A549. Neoplasia, 2019, 21, 185-196.	5.3	38
7	SUMOylation coordinates BERosome assembly inÂactive DNA demethylation during cellÂdifferentiation. EMBO Journal, 2019, 38, .	7.8	28
8	ELF-MF exposure affects the robustness of epigenetic programming during granulopoiesis. Scientific Reports, 2017, 7, 43345.	3.3	15
9	Active DNA demethylation by DNA repair: Facts and uncertainties. DNA Repair, 2016, 44, 92-102.	2.8	70
10	Biochemical reconstitution of TET1â€“TDGâ€“BER-dependent active DNA demethylation reveals a highly coordinated mechanism. Nature Communications, 2016, 7, 10806.	12.8	166
11	Oestrogen receptor Î² regulates epigenetic patterns at specific genomic loci through interaction with thymine DNA glycosylase. Epigenetics and Chromatin, 2016, 9, 7.	3.9	25
12	Extremely lowâ€frequency magnetic fields and risk of childhood leukemia: A risk assessment by the ARIMMORA consortium. Bioelectromagnetics, 2016, 37, 183-189.	1.6	31
13	3CAPS â€“ a structural APâ€“site analogue as a tool to investigate DNA base excision repair. Nucleic Acids Research, 2016, 44, 2187-2198.	14.5	18
14	Gadd45a promotes DNA demethylation through TDG. Nucleic Acids Research, 2015, 43, 3986-3997.	14.5	77
15	Versatile Recombinant SUMOylation System for the Production of SUMO-Modified Protein. PLoS ONE, 2014, 9, e102157.	2.5	20
16	Reversible Top1 cleavage complexes are stabilized strand-specifically at the ribosomal replication fork barrier and contribute to ribosomal DNA stability. Nucleic Acids Research, 2014, 42, 4985-4995.	14.5	22
17	Tet oxidizes thymine to 5-hydroxymethyluracil in mouse embryonic stem cell DNA. Nature Chemical Biology, 2014, 10, 574-581.	8.0	270
18	Modulation of Age- and Cancer-Associated DNA Methylation Change in the Healthy Colon by Aspirin and Lifestyle. Journal of the National Cancer Institute, 2014, 106, .	6.3	68

#	Article	IF	Citations
19	ELF exposure system for live cell imaging. Bioelectromagnetics, 2013, 34, 231-239.	1.6	5
20	7,8-dihydro-8-oxoadenine, a highly mutagenic adduct, is repaired by Escherichia coli and human mismatch-specific uracil/thymine-DNA glycosylases. Nucleic Acids Research, 2013, 41, 912-923.	14.5	23
21	Resources for methylome analysis suitable for gene knockout studies of potential epigenome modifiers. GigaScience, 2012, 1, 3.	6.4	39
22	DNA glycosylases: in DNA repair and beyond. Chromosoma, 2012, 121, 1-20.	2.2	292
23	DNA Repair and the Control of DNA Methylation. , 2011, 67, 51-68.		30
24	Embryonic lethal phenotype reveals a function of TDG in maintaining epigenetic stability. Nature, 2011, 470, 419-423.	27.8	323
25	DNA fragmentation in human fibroblasts under extremely low frequency electromagnetic field exposure. Mutation Research - Fundamental and Molecular Mechanisms of Mutagenesis, 2010, 683, 74-83.	1.0	92
26	DNA ligase 4 stabilizes the ribosomal DNA array upon fork collapse at the replication fork barrier. DNA Repair, 2010, 9, 879-888.	2.8	16
27	Base Excision by Thymine DNA Glycosylase Mediates DNA-Directed Cytotoxicity of 5-Fluorouracil. PLoS Biology, 2009, 7, e1000091.	5.6	100
28	Sumoylation of poly(ADPâ€ribose) polymerase 1 inhibits its acetylation and restrains transcriptional coactivator function. FASEB Journal, 2009, 23, 3978-3989.	0.5	66
29	DNA Repair in Mammalian Cells. Cellular and Molecular Life Sciences, 2009, 66, 1021-1038.	5.4	73
30	Normal colorectal mucosa exhibits sex- and segment-specific susceptibility to DNA methylation at the hMLH1 and MGMT promoters. Oncogene, 2009, 28, 899-909.	5.9	67
31	Conserved interactions of the splicing factor Ntr1/Spp382 with proteins involved in DNA double-strand break repair and telomere metabolism. Nucleic Acids Research, 2007, 35, 2321-2332.	14.5	15
32	Cell cycle regulation as a mechanism for functional separation of the apparently redundant uracil DNA glycosylases TDG and UNG2. Nucleic Acids Research, 2007, 35, 3859-3867.	14.5	78
33	The enigmatic thymine DNA glycosylase. DNA Repair, 2007, 6, 489-504.	2.8	164
34	O6-methylguanine-DNA methyltransferase promoter hypermethylation in colorectal carcinogenesis. Oncology Reports, 2007, 17, 1421-7.	2.6	11
35	Arginine Methylation Regulates DNA Polymerase Î². Molecular Cell, 2006, 22, 51-62.	9.7	161
36	Functionality of Human Thymine DNA Glycosylase Requires SUMO-Regulated Changes in Protein Conformation. Current Biology, 2005, 15, 616-623.	3.9	143

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37	Homologous Recombination Rescues Mismatch-Repair-Dependent Cytotoxicity of SN1-Type Methylating Agents in S. cerevisiae. Current Biology, 2005, 15, 1395-1400.	3.9	33
38	T:G mismatch-specific thymine-DNA glycosylase (TDG) as a coregulator of transcription interacts with SRC1 family members through a novel tyrosine repeat motif. Nucleic Acids Research, 2005, 33, 6393-6404.	14.5	44
39	Immunohistochemical Analysis Reveals High Frequency of PMS2 Defects in Colorectal Cancer. Gastroenterology, 2005, 128, 1160-1171.	1.3	166
40	Mismatch dependent uracil/thymine-DNA glycosylases excise exocyclic hydroxyethano and hydroxypropano cytosine adducts.. Acta Biochimica Polonica, 2005, 52, 149-165.	0.5	10
41	SMC1 coordinates DNA double-strand break repair pathways. Nucleic Acids Research, 2004, 32, 3921-3929.	14.5	67
42	Lack of mismatch correction facilitates genome evolution in mycobacteria. Molecular Microbiology, 2004, 53, 1601-1609.	2.5	70
43	Translesion DNA Synthesis: Little Fingers Teach Tolerance. Current Biology, 2004, 14, R389-R391.	3.9	25
44	Meiotic Recombination: Sealing the Partnership at the Junction. Current Biology, 2004, 14, R962-R964.	3.9	15
45	T:G Mismatch-specific Thymine-DNA Glycosylase Potentiates Transcription of Estrogen-regulated Genes through Direct Interaction with Estrogen Receptor Î±. Journal of Biological Chemistry, 2003, 278, 38586-38592.	3.4	108
46	Rad52-Independent Accumulation of Joint Circular Minichromosomes during S Phase in Saccharomyces cerevisiae. Molecular and Cellular Biology, 2003, 23, 6363-6372.	2.3	21
47	The versatile thymine DNA-glycosylase: a comparative characterization of the human, Drosophila and fission yeast orthologs. Nucleic Acids Research, 2003, 31, 2261-2271.	14.5	123
48	Acetylation Regulates the DNA End-Trimming Activity of DNA Polymerase Î². Molecular Cell, 2002, 10, 1213-1222.	9.7	110
49	Modification of the human thymine-DNA glycosylase by ubiquitin-like proteins facilitates enzymatic turnover. EMBO Journal, 2002, 21, 1456-1464.	7.8	263
50	Spontaneous DNA Damage, Genome Instability, and Cancerâ€"When DNA Replication Escapes Control. Cell, 2001, 104, 329-332.	28.9	115
51	NEJ1 controls non-homologous end joining in Saccharomyces cerevisiae. Nature, 2001, 414, 666-669.	27.8	213
52	Biochemical Characterization of Uracil Processing Activities in the Hyperthermophilic Archaeon Pyrobaculum aerophilum. Journal of Biological Chemistry, 2001, 276, 29979-29986.	3.4	48
53	Thymine DNA glycosylase. Progress in Molecular Biology and Translational Science, 2001, 68, 235-253.	1.9	80
54	Separating Substrate Recognition from Base Hydrolysis in Human Thymine DNA Glycosylase by Mutational Analysis. Journal of Biological Chemistry, 2000, 275, 33449-33456.	3.4	115

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55	Identification of hMutLÎ², a Heterodimer of hMLH1 and hPMS1. Journal of Biological Chemistry, 1999, 274, 32368-32375.	3.4	156
56	Involvement of nucleotide-excision repair in msh2 pms1-independent mismatch repair. Nature Genetics, 1999, 21, 314-317.	21.4	76
57	Recognition of DNA alterations by the mismatch repair system. Biochemical Journal, 1999, 338, 1.	3.7	39
58	Saccharomyces cerevisiae LIF1: a function involved in DNA double-strand break repair related to mammalian XRCC4. EMBO Journal, 1998, 17, 4188-4198.	7.8	155
59	A newly identified DNA ligase of Saccharomyces cerevisiaeinvolved in RAD52-independent repair of DNA double-strandâ€‰breaks. Genes and Development, 1997, 11, 1912-1924.	5.9	175
60	Regulation of DNA metabolic enzymes upon induction of preB cell development and V(D)J recombination: up-regulation of DNA polymerase delta. Nucleic Acids Research, 1997, 25, 289-296.	14.5	13
61	Mismatch Repair in Schizosacchromyces pombe Requires the mutL Homologous Gene pms1: Molecular Cloning and Functional Analysis. Genetics, 1997, 146, 1275-1286.	2.9	30
62	Inducible TDG knockout models to study epigenetic regulation. F1000Research, 0, 9, 1112.	1.6	1