

Primo SchÄör

List of Publications by Year in descending order

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Version: 2024-02-01

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	Embryonic lethal phenotype reveals a function of TDG in maintaining epigenetic stability. <i>Nature</i> , 2011, 470, 419-423.	27.8	323
2	DNA glycosylases: in DNA repair and beyond. <i>Chromosoma</i> , 2012, 121, 1-20.	2.2	292
3	Tet oxidizes thymine to 5-hydroxymethyluracil in mouse embryonic stem cell DNA. <i>Nature Chemical Biology</i> , 2014, 10, 574-581.	8.0	270
4	Modification of the human thymine-DNA glycosylase by ubiquitin-like proteins facilitates enzymatic turnover. <i>EMBO Journal</i> , 2002, 21, 1456-1464.	7.8	263
5	NEJ1 controls non-homologous end joining in <i>Saccharomyces cerevisiae</i> . <i>Nature</i> , 2001, 414, 666-669.	27.8	213
6	A newly identified DNA ligase of <i>Saccharomyces cerevisiae</i> involved in RAD52-independent repair of DNA double-strand breaks. <i>Genes and Development</i> , 1997, 11, 1912-1924.	5.9	175
7	Immunohistochemical Analysis Reveals High Frequency of PMS2 Defects in Colorectal Cancer. <i>Gastroenterology</i> , 2005, 128, 1160-1171.	1.3	166
8	Biochemical reconstitution of TET1-TDG-BER-dependent active DNA demethylation reveals a highly coordinated mechanism. <i>Nature Communications</i> , 2016, 7, 10806.	12.8	166
9	The enigmatic thymine DNA glycosylase. <i>DNA Repair</i> , 2007, 6, 489-504.	2.8	164
10	Arginine Methylation Regulates DNA Polymerase β . <i>Molecular Cell</i> , 2006, 22, 51-62.	9.7	161
11	Identification of hMutL β , a Heterodimer of hMLH1 and hPMS1. <i>Journal of Biological Chemistry</i> , 1999, 274, 32368-32375.	3.4	156
12	<i>Saccharomyces cerevisiae</i> LIF1: a function involved in DNA double-strand break repair related to mammalian XRCC4. <i>EMBO Journal</i> , 1998, 17, 4188-4198.	7.8	155
13	Functionality of Human Thymine DNA Glycosylase Requires SUMO-Regulated Changes in Protein Conformation. <i>Current Biology</i> , 2005, 15, 616-623.	3.9	143
14	The versatile thymine DNA-glycosylase: a comparative characterization of the human, <i>Drosophila</i> and fission yeast orthologs. <i>Nucleic Acids Research</i> , 2003, 31, 2261-2271.	14.5	123
15	Separating Substrate Recognition from Base Hydrolysis in Human Thymine DNA Glycosylase by Mutational Analysis. <i>Journal of Biological Chemistry</i> , 2000, 275, 33449-33456.	3.4	115
16	Spontaneous DNA Damage, Genome Instability, and Cancer—When DNA Replication Escapes Control. <i>Cell</i> , 2001, 104, 329-332.	28.9	115
17	Acetylation Regulates the DNA End-Trimming Activity of DNA Polymerase β . <i>Molecular Cell</i> , 2002, 10, 1213-1222.	9.7	110
18	T:G Mismatch-specific Thymine-DNA Glycosylase Potentiates Transcription of Estrogen-regulated Genes through Direct Interaction with Estrogen Receptor β . <i>Journal of Biological Chemistry</i> , 2003, 278, 38586-38592.	3.4	108

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19	Base Excision by Thymine DNA Glycosylase Mediates DNA-Directed Cytotoxicity of 5-Fluorouracil. <i>PLoS Biology</i> , 2009, 7, e1000091.	5.6	100
20	DNA fragmentation in human fibroblasts under extremely low frequency electromagnetic field exposure. <i>Mutation Research - Fundamental and Molecular Mechanisms of Mutagenesis</i> , 2010, 683, 74-83.	1.0	92
21	Thymine DNA glycosylase. <i>Progress in Molecular Biology and Translational Science</i> , 2001, 68, 235-253.	1.9	80
22	Cell cycle regulation as a mechanism for functional separation of the apparently redundant uracil DNA glycosylases TDG and UNG2. <i>Nucleic Acids Research</i> , 2007, 35, 3859-3867.	14.5	78
23	Gadd45a promotes DNA demethylation through TDG. <i>Nucleic Acids Research</i> , 2015, 43, 3986-3997.	14.5	77
24	Involvement of nucleotide-excision repair in msh2 pms1-independent mismatch repair. <i>Nature Genetics</i> , 1999, 21, 314-317.	21.4	76
25	DNA Repair in Mammalian Cells. <i>Cellular and Molecular Life Sciences</i> , 2009, 66, 1021-1038.	5.4	73
26	Lack of mismatch correction facilitates genome evolution in mycobacteria. <i>Molecular Microbiology</i> , 2004, 53, 1601-1609.	2.5	70
27	Active DNA demethylation by DNA repair: Facts and uncertainties. <i>DNA Repair</i> , 2016, 44, 92-102.	2.8	70
28	Modulation of Age- and Cancer-Associated DNA Methylation Change in the Healthy Colon by Aspirin and Lifestyle. <i>Journal of the National Cancer Institute</i> , 2014, 106, .	6.3	68
29	SMC1 coordinates DNA double-strand break repair pathways. <i>Nucleic Acids Research</i> , 2004, 32, 3921-3929.	14.5	67
30	Normal colorectal mucosa exhibits sex- and segment-specific susceptibility to DNA methylation at the hMLH1 and MGMT promoters. <i>Oncogene</i> , 2009, 28, 899-909.	5.9	67
31	Sumoylation of poly(ADP-ribose) polymerase 1 inhibits its acetylation and restrains transcriptional coactivator function. <i>FASEB Journal</i> , 2009, 23, 3978-3989.	0.5	66
32	Biochemical Characterization of Uracil Processing Activities in the Hyperthermophilic Archaeon <i>Pyrobaculum aerophilum</i> . <i>Journal of Biological Chemistry</i> , 2001, 276, 29979-29986.	3.4	48
33	T:G mismatch-specific thymine-DNA glycosylase (TDG) as a coregulator of transcription interacts with SRC1 family members through a novel tyrosine repeat motif. <i>Nucleic Acids Research</i> , 2005, 33, 6393-6404.	14.5	44
34	Recognition of DNA alterations by the mismatch repair system. <i>Biochemical Journal</i> , 1999, 338, 1.	3.7	39
35	Resources for methylome analysis suitable for gene knockout studies of potential epigenome modifiers. <i>GigaScience</i> , 2012, 1, 3.	6.4	39
36	Tumor Initiation Capacity and Therapy Resistance Are Differential Features of EMT-Related Subpopulations in the NSCLC Cell Line A549. <i>Neoplasia</i> , 2019, 21, 185-196.	5.3	38

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37	Homologous Recombination Rescues Mismatch-Repair-Dependent Cytotoxicity of SN1-Type Methylating Agents in <i>S. cerevisiae</i> . <i>Current Biology</i> , 2005, 15, 1395-1400.	3.9	33
38	Extremely low-frequency magnetic fields and risk of childhood leukemia: A risk assessment by the ARIMMORA consortium. <i>Bioelectromagnetics</i> , 2016, 37, 183-189.	1.6	31
39	DNA Repair and the Control of DNA Methylation. , 2011, 67, 51-68.		30
40	Mismatch Repair in <i>Schizosaccharomyces pombe</i> Requires the mutL Homologous Gene <i>pms1</i> : Molecular Cloning and Functional Analysis. <i>Genetics</i> , 1997, 146, 1275-1286.	2.9	30
41	SUMOylation coordinates BERosome assembly in active DNA demethylation during cell differentiation. <i>EMBO Journal</i> , 2019, 38, .	7.8	28
42	Translesion DNA Synthesis: Little Fingers Teach Tolerance. <i>Current Biology</i> , 2004, 14, R389-R391.	3.9	25
43	Oestrogen receptor β regulates epigenetic patterns at specific genomic loci through interaction with thymine DNA glycosylase. <i>Epigenetics and Chromatin</i> , 2016, 9, 7.	3.9	25
44	7,8-dihydro-8-oxoadenine, a highly mutagenic adduct, is repaired by <i>Escherichia coli</i> and human mismatch-specific uracil/thymine-DNA glycosylases. <i>Nucleic Acids Research</i> , 2013, 41, 912-923.	14.5	23
45	Reversible Top1 cleavage complexes are stabilized strand-specifically at the ribosomal replication fork barrier and contribute to ribosomal DNA stability. <i>Nucleic Acids Research</i> , 2014, 42, 4985-4995.	14.5	22
46	DNA methylation instability by BRAF-mediated TET silencing and lifestyle-exposure divides colon cancer pathways. <i>Clinical Epigenetics</i> , 2019, 11, 196.	4.1	22
47	Rad52-Independent Accumulation of Joint Circular Minichromosomes during S Phase in <i>Saccharomyces cerevisiae</i> . <i>Molecular and Cellular Biology</i> , 2003, 23, 6363-6372.	2.3	21
48	Versatile Recombinant SUMOylation System for the Production of SUMO-Modified Protein. <i>PLoS ONE</i> , 2014, 9, e102157.	2.5	20
49	3CAPS – a structural AP site analogue as a tool to investigate DNA base excision repair. <i>Nucleic Acids Research</i> , 2016, 44, 2187-2198.	14.5	18
50	DNA ligase 4 stabilizes the ribosomal DNA array upon fork collapse at the replication fork barrier. <i>DNA Repair</i> , 2010, 9, 879-888.	2.8	16
51	Meiotic Recombination: Sealing the Partnership at the Junction. <i>Current Biology</i> , 2004, 14, R962-R964.	3.9	15
52	Conserved interactions of the splicing factor Ntr1/Spp382 with proteins involved in DNA double-strand break repair and telomere metabolism. <i>Nucleic Acids Research</i> , 2007, 35, 2321-2332.	14.5	15
53	ELF-MF exposure affects the robustness of epigenetic programming during granulopoiesis. <i>Scientific Reports</i> , 2017, 7, 43345.	3.3	15
54	Regulation of DNA metabolic enzymes upon induction of preB cell development and V(D)J recombination: up-regulation of DNA polymerase delta. <i>Nucleic Acids Research</i> , 1997, 25, 289-296.	14.5	13

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55	Aberrant regulation of epigenetic modifiers contributes to the pathogenesis in patients with selenoprotein N related myopathies. <i>Human Mutation</i> , 2019, 40, 962-974.	2.5	13
56	O6-methylguanine-DNA methyltransferase promoter hypermethylation in colorectal carcinogenesis. <i>Oncology Reports</i> , 2007, 17, 1421-7.	2.6	11
57	Mismatch dependent uracil/thymine-DNA glycosylases excise exocyclic hydroxyethano and hydroxypropano cytosine adducts.. <i>Acta Biochimica Polonica</i> , 2005, 52, 149-165.	0.5	10
58	Assessment of Genotoxicity in Human Cells Exposed to Modulated Electromagnetic Fields of Wireless Communication Devices. <i>Genes</i> , 2020, 11, 347.	2.4	7
59	ELF exposure system for live cell imaging. <i>Bioelectromagnetics</i> , 2013, 34, 231-239.	1.6	5
60	Longitudinal analysis of healthy colon establishes aspirin as a suppressor of cancer-related epigenetic aging. <i>Clinical Epigenetics</i> , 2020, 12, 164.	4.1	5
61	Inducible TDG knockout models to study epigenetic regulation. <i>F1000Research</i> , 2020, 9, 1112.	1.6	4
62	Inducible TDG knockout models to study epigenetic regulation. <i>F1000Research</i> , 0, 9, 1112.	1.6	1