

Jean-Yves Masson

List of Publications by Year in descending order

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131
papers

8,660
citations

50276

46
h-index

49909

87
g-index

138
all docs

138
docs citations

138
times ranked

10916
citing authors

#	ARTICLE	IF	CITATIONS
1	A DNA repair-independent role for alkyladenine DNA glycosylase in alkylation-induced unfolded protein response. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022, 119, .	7.1	5
2	Common Variant in ALDH2 Modifies the Risk of Breast Cancer Among Carriers of the p.K3326* Variant in BRCA2. <i>JCO Precision Oncology</i> , 2022, 6, e2100450.	3.0	1
3	The Genetic and Molecular Analyses of RAD51C and RAD51D Identifies Rare Variants Implicated in Hereditary Ovarian Cancer from a Genetically Unique Population. <i>Cancers</i> , 2022, 14, 2251.	3.7	4
4	PALB2 Variants: Protein Domains and Cancer Susceptibility. <i>Trends in Cancer</i> , 2021, 7, 188-197.	7.4	13
5	SUMOylation mediates CtIP's functions in DNA end resection and replication fork protection. <i>Nucleic Acids Research</i> , 2021, 49, 928-953.	14.5	13
6	FAN1, a DNA Repair Nuclease, as a Modifier of Repeat Expansion Disorders. <i>Journal of Huntington's Disease</i> , 2021, 10, 95-122.	1.9	34
7	Synergistic effects of type I PRMT and PARP inhibitors against non-small cell lung cancer cells. <i>Clinical Epigenetics</i> , 2021, 13, 54.	4.1	28
8	Assessment of Global DNA Double-Strand End Resection using BrdU-DNA Labeling coupled with Cell Cycle Discrimination Imaging. <i>Journal of Visualized Experiments</i> , 2021, , .	0.3	2
9	Addressing the dark matter of gene therapy: technical and ethical barriers to clinical application. <i>Human Genetics</i> , 2021, , 1.	3.8	4
10	Animal models of Fanconi anemia: A developmental and therapeutic perspective on a multifaceted disease. <i>Seminars in Cell and Developmental Biology</i> , 2021, 113, 113-131.	5.0	10
11	Personalized Risk Assessment for Prevention and Early Detection of Breast Cancer: Integration and Implementation (PERSPECTIVE I&#amp;l). <i>Journal of Personalized Medicine</i> , 2021, 11, 511.	2.5	59
12	ZNF768 links oncogenic RAS to cellular senescence. <i>Nature Communications</i> , 2021, 12, 4841.	12.8	11
13	Molecular Determinant of DIDS Analogs Targeting RAD51 Activity. <i>Molecules</i> , 2021, 26, 5460.	3.8	5
14	XAB2 promotes Ku eviction from single-ended DNA double-strand breaks independently of the ATM kinase. <i>Nucleic Acids Research</i> , 2021, 49, 9906-9925.	14.5	8
15	Functions of the CSB Protein at Topoisomerase 2 Inhibitors-Induced DNA Lesions. <i>Frontiers in Cell and Developmental Biology</i> , 2021, 9, 727836.	3.7	0
16	Starvation-induced proteasome assemblies in the nucleus link amino acid supply to apoptosis. <i>Nature Communications</i> , 2021, 12, 6984.	12.8	29
17	FAN1 exo- not endo-nuclease pausing on disease-associated slipped-DNA repeats: A mechanism of repeat instability. <i>Cell Reports</i> , 2021, 37, 110078.	6.4	19
18	Cockayne syndrome group B protein regulates fork restart, fork progression and MRE11-dependent fork degradation in BRCA1/2-deficient cells. <i>Nucleic Acids Research</i> , 2021, 49, 12836-12854.	14.5	5

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19	A functionally impaired missense variant identified in French Canadian families implicates FANCI as a candidate ovarian cancer-predisposing gene. <i>Genome Medicine</i> , 2021, 13, 186.	8.2	12
20	Functional characterization of 84 PALB2 variants of uncertain significance. <i>Genetics in Medicine</i> , 2020, 22, 622-632.	2.4	40
21	DDX5 resolves R-loops at DNA double-strand breaks to promote DNA repair and avoid chromosomal deletions. <i>NAR Cancer</i> , 2020, 2, zcaa028.	3.1	44
22	Development of a 3D functional assay and identification of biomarkers, predictive for response of high-grade serous ovarian cancer (HGSOC) patients to poly-ADP ribose polymerase inhibitors (PARPis): targeted therapy. <i>Journal of Translational Medicine</i> , 2020, 18, 439.	4.4	15
23	Limiting the DNA Double-Strand Break Resectosome for Genome Protection. <i>Trends in Biochemical Sciences</i> , 2020, 45, 779-793.	7.5	27
24	Variants of uncertain clinical significance in hereditary breast and ovarian cancer genes: best practices in functional analysis for clinical annotation. <i>Journal of Medical Genetics</i> , 2020, 57, 509-518.	3.2	33
25	The Canadian Rare Diseases Models and Mechanisms (RDMM) Network: Connecting Understudied Genes to Model Organisms. <i>American Journal of Human Genetics</i> , 2020, 106, 143-152.	6.2	30
26	Missense PALB2 germline variant disrupts nuclear localization of PALB2 in a patient with breast cancer. <i>Familial Cancer</i> , 2020, 19, 123-131.	1.9	3
27	A slipped-CAG DNA-binding small molecule induces trinucleotide-repeat contractions in vivo. <i>Nature Genetics</i> , 2020, 52, 146-159.	21.4	110
28	Genome-wide R-loop analysis defines unique roles for DDX5, XRN2, and PRMT5 in DNA/RNA hybrid resolution. <i>Life Science Alliance</i> , 2020, 3, e202000762.	2.8	43
29	Perturbing cohesin dynamics drives MRE11 nuclease-dependent replication fork slowing. <i>Nucleic Acids Research</i> , 2019, 47, 1294-1310.	14.5	38
30	Arginine methylation of the <sc>DDX</sc> 5 helicase <sc>RGG</sc> / <sc>RG</sc> motif by <sc>PRMT</sc> 5 regulates resolution of RNA:DNA hybrids. <i>EMBO Journal</i> , 2019, 38, e100986.	7.8	117
31	Poly(ADP-ribose) polymerase-1 antagonizes DNA resection at double-strand breaks. <i>Nature Communications</i> , 2019, 10, 2954.	12.8	122
32	Interactions of the Rad51 inhibitor DIDS with human and bovine serum albumins: Optical spectroscopy and isothermal calorimetry approaches. <i>Biochimie</i> , 2019, 167, 187-197.	2.6	3
33	MRE11-RAD50-NBS1 promotes Fanconi Anemia R-loop suppression at transcription"replication conflicts. <i>Nature Communications</i> , 2019, 10, 4265.	12.8	55
34	CSB interacts with BRCA1 in late S/G2 to promote MRN- and CtIP-mediated DNA end resection. <i>Nucleic Acids Research</i> , 2019, 47, 10678-10692.	14.5	20
35	PRMT7 methylates eukaryotic translation initiation factor 2Î± and regulates its role in stress granule formation. <i>Molecular Biology of the Cell</i> , 2019, 30, 778-793.	2.1	31
36	A Fanci knockout mouse model reveals common and distinct functions for FANCI and FANCD2. <i>Nucleic Acids Research</i> , 2019, 47, 7532-7547.	14.5	36

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37	Emerging roles of eraser enzymes in the dynamic control of protein ADP-ribosylation. <i>Nature Communications</i> , 2019, 10, 1182.	12.8	113
38	SAM68 interaction with U1A modulates U1 snRNP recruitment and regulates mTor pre-mRNA splicing. <i>Nucleic Acids Research</i> , 2019, 47, 4181-4197.	14.5	19
39	BRN2 suppresses apoptosis, reprograms DNA damage repair, and is associated with a high somatic mutation burden in melanoma. <i>Genes and Development</i> , 2019, 33, 310-332.	5.9	35
40	A global functional analysis of missense mutations reveals two major hotspots in the PALB2 tumor suppressor. <i>Nucleic Acids Research</i> , 2019, 47, 10662-10677.	14.5	39
41	Functional analysis of genetic variants in the high-risk breast cancer susceptibility gene PALB2. <i>Nature Communications</i> , 2019, 10, 5296.	12.8	45
42	The Tumor Suppressor PALB2: Inside Out. <i>Trends in Biochemical Sciences</i> , 2019, 44, 226-240.	7.5	83
43	Novel RNA and DNA strand exchange activity of the PALB2 DNA binding domain and its critical role for DNA repair in cells. <i>ELife</i> , 2019, 8, .	6.0	18
44	Phospho-dependent recruitment of the yeast NuA4 acetyltransferase complex by MRX at DNA breaks regulates RPA dynamics during resection. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, 10028-10033.	7.1	25
45	A <sc>RAD</sc> 51 assay feasible in routine tumor samples calls <sc>PARP</sc> inhibitor response beyond <sc>BRCA</sc> mutation. <i>EMBO Molecular Medicine</i> , 2018, 10, .	6.9	169
46	DYNLL1 binds to MRE11 to limit DNA end resection in BRCA1-deficient cells. <i>Nature</i> , 2018, 563, 522-526.	27.8	156
47	<sc>SHLD</sc> 2/ <sc>FAM</sc> 35A co-operates with <sc>REV</sc> 7 to coordinate <sc>DNA</sc> double-strand break repair pathway choice. <i>EMBO Journal</i> , 2018, 37, .	7.8	111
48	Replication Protein A Availability during DNA Replication Stress Is a Major Determinant of Cisplatin Resistance in Ovarian Cancer Cells. <i>Cancer Research</i> , 2018, 78, 5561-5573.	0.9	45
49	Targeting Allostery with Avatars to Design Inhibitors Assessed by Cell Activity: Dissecting MRE11 Endo- and Exonuclease Activities. <i>Methods in Enzymology</i> , 2018, 601, 205-241.	1.0	20
50	CRISPR/Cas9 Gene Editing: From Basic Mechanisms to Improved Strategies for Enhanced Genome Engineering In Vivo. <i>Current Gene Therapy</i> , 2018, 17, 263-274.	2.0	14
51	Coupling of Homologous Recombination and the Checkpoint by ATR. <i>Molecular Cell</i> , 2017, 65, 336-346.	9.7	133
52	RECQ-like helicases Sgs1 and BLM regulate R-loop-associated genome instability. <i>Journal of Cell Biology</i> , 2017, 216, 3991-4005.	5.2	90
53	The identification of FANCD2 DNA binding domains reveals nuclear localization sequences. <i>Nucleic Acids Research</i> , 2017, 45, 8341-8357.	14.5	20
54	Cancer-causing mutations in the tumor suppressor PALB2 reveal a novel cancer mechanism using a hidden nuclear export signal in the WD40 repeat motif. <i>Nucleic Acids Research</i> , 2017, 45, 2644-2657.	14.5	30

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55	Cumulative defects in DNA repair pathways drive the PARP inhibitor response in high-grade serous epithelial ovarian cancer cell lines. <i>Oncotarget</i> , 2017, 8, 40152-40168.	1.8	25
56	Lysine methylation of FEN1 by SET7 is essential for its cellular response to replicative stress. <i>Oncotarget</i> , 2017, 8, 64918-64931.	1.8	10
57	A PALB2-interacting domain in RNF168 couples homologous recombination to DNA break-induced chromatin ubiquitylation. <i>ELife</i> , 2017, 6, .	6.0	65
58	Chromosomal Translocations in the Parasite <i>Leishmania</i> by a MRE11/RAD50-Independent Microhomology-Mediated End Joining Mechanism. <i>PLoS Genetics</i> , 2016, 12, e1006117.	3.5	28
59	ABRAXAS (FAM175A) and Breast Cancer Susceptibility: No Evidence of Association in the Breast Cancer Family Registry. <i>PLoS ONE</i> , 2016, 11, e0156820.	2.5	5
60	Roles for APRIN (PDS5B) in homologous recombination and in ovarian cancer prediction. <i>Nucleic Acids Research</i> , 2016, 44, 10879-10897.	14.5	47
61	Special AT-rich Sequence-binding Protein 1 (SATB1) Functions as an Accessory Factor in Base Excision Repair. <i>Journal of Biological Chemistry</i> , 2016, 291, 22769-22780.	3.4	22
62	HELB Is a Feedback Inhibitor of DNA End Resection. <i>Molecular Cell</i> , 2016, 61, 405-418.	9.7	119
63	Different non-synonymous polymorphisms modulate the interaction of the WRN protein to its protein partners and its enzymatic activities. <i>Oncotarget</i> , 2016, 7, 85680-85696.	1.8	3
64	E4F1 Is a Master Regulator of CHK1-Mediated Functions. <i>Cell Reports</i> , 2015, 11, 210-219.	6.4	19
65	Roles of Rad51 paralogs for promoting homologous recombination in <i>Leishmania infantum</i> . <i>Nucleic Acids Research</i> , 2015, 43, 2701-2715.	14.5	23
66	DNA Damage Signalling and Repair Inhibitors: The Long-Sought-After Achilles™ Heel of Cancer. <i>Biomolecules</i> , 2015, 5, 3204-3259.	4.0	85
67	The RNF138 E3 ligase displaces Ku to promote DNA end resection and regulate DNA repair pathway choice. <i>Nature Cell Biology</i> , 2015, 17, 1446-1457.	10.3	113
68	CRB3A Controls the Morphology and Cohesion of Cancer Cells through Ehm2/p114RhoGEF-Dependent Signaling. <i>Molecular and Cellular Biology</i> , 2015, 35, 3423-3435.	2.3	19
69	Synthesis and biological evaluation of novel N-phenyl ureidobenzenesulfonate derivatives as potential anticancer agents. Part 2. Modulation of the ring B. <i>European Journal of Medicinal Chemistry</i> , 2015, 103, 563-573.	5.5	7
70	Formation of Linear Amplicons with Inverted Duplications in <i>Leishmania</i> Requires the MRE11 Nuclease. <i>PLoS Genetics</i> , 2014, 10, e1004805.	3.5	23
71	DNA Repair Pathways in Trypanosomatids: from DNA Repair to Drug Resistance. <i>Microbiology and Molecular Biology Reviews</i> , 2014, 78, 40-73.	6.6	79
72	Tumor suppressor and deubiquitinase BAP1 promotes DNA double-strand break repair. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 285-290.	7.1	300

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73	DNA Double-Strand Break Repair Pathway Choice Is Directed by Distinct MRE11 Nuclease Activities. <i>Molecular Cell</i> , 2014, 53, 7-18.	9.7	466
74	Exploring the roles of PALB2 at the crossroads of DNA repair and cancer. <i>Biochemical Journal</i> , 2014, 460, 331-342.	3.7	33
75	Breast Cancer Proteins PALB2 and BRCA2 Stimulate Polymerase γ in Recombination-Associated DNA Synthesis at Blocked Replication Forks. <i>Cell Reports</i> , 2014, 6, 553-564.	6.4	72
76	The RAD51 paralogs ensure cellular protection against mitotic defects and aneuploidy. <i>Journal of Cell Science</i> , 2013, 126, 348-359.	2.0	47
77	Reprogramming cellular events by poly(ADP-ribose)-binding proteins. <i>Molecular Aspects of Medicine</i> , 2013, 34, 1066-1087.	6.4	141
78	Mammalian Protein Arginine Methyltransferase 7 (PRMT7) Specifically Targets RXR Sites in Lysine- and Arginine-rich Regions. <i>Journal of Biological Chemistry</i> , 2013, 288, 37010-37025.	3.4	143
79	Fanconi Anemia Group J Helicase and MRE11 Nuclease Interact To Facilitate the DNA Damage Response. <i>Molecular and Cellular Biology</i> , 2013, 33, 2212-2227.	2.3	51
80	Detection of the HIV-1 Minus-Strand-Encoded Antisense Protein and Its Association with Autophagy. <i>Journal of Virology</i> , 2013, 87, 5089-5105.	3.4	38
81	PARP activation regulates the RNA-binding protein NONO in the DNA damage response to DNA double-strand breaks. <i>Nucleic Acids Research</i> , 2012, 40, 10287-10301.	14.5	136
82	CBX4-mediated SUMO modification regulates BMI1 recruitment at sites of DNA damage. <i>Nucleic Acids Research</i> , 2012, 40, 5497-5510.	14.5	117
83	The microRNA pathway controls germ cell proliferation and differentiation in <i>C. elegans</i> . <i>Cell Research</i> , 2012, 22, 1034-1045.	12.0	56
84	Interactions between BRCA2 and RAD51 for promoting homologous recombination in <i>Leishmania infantum</i> . <i>Nucleic Acids Research</i> , 2012, 40, 6570-6584.	14.5	32
85	PALB2 self-interaction controls homologous recombination. <i>Nucleic Acids Research</i> , 2012, 40, 10312-10323.	14.5	48
86	ChAM, a novel motif that mediates PALB2 intrinsic chromatin binding and facilitates DNA repair. <i>EMBO Reports</i> , 2012, 13, 135-141.	4.5	49
87	The MRE11 GAR motif regulates DNA double-strand break processing and ATR activation. <i>Cell Research</i> , 2012, 22, 305-320.	12.0	68
88	Synthesis, Biological Evaluation, and Structure-Activity Relationships of Novel Substituted <i>N</i> -Phenyl Ureidobenzenesulfonate Derivatives Blocking Cell Cycle Progression in S-Phase and Inducing DNA Double-Strand Breaks. <i>Journal of Medicinal Chemistry</i> , 2012, 55, 6194-6208.	6.4	18
89	Irinotecan and DNA-PKcs inhibitors synergize in killing of colon cancer cells. <i>Investigational New Drugs</i> , 2012, 30, 1248-1256.	2.6	45
90	Proteome-wide Identification of WRN-Interacting Proteins in Untreated and Nuclease-Treated Samples. <i>Journal of Proteome Research</i> , 2011, 10, 1216-1227.	3.7	39

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91	The Effect of a DNA Repair Gene on Cellular Invasiveness: Xrcc3 Over-Expression in Breast Cancer Cells. PLoS ONE, 2011, 6, e16394.	2.5	20
92	Lactococcal phage p2 ORF35 is an ATPase involved in DNA recombination and AbiK mechanism. Molecular Microbiology, 2011, 80, 102-116.	2.5	23
93	Partners apart: Smc6-independent DNA binding activity of Smc5 on single-strand DNA. Cell Cycle, 2011, 10, 1025-1030.	2.6	1
94	A Key Role for Poly(ADP-Ribose) Polymerase 3 in Ectodermal Specification and Neural Crest Development. PLoS ONE, 2011, 6, e15834.	2.5	17
95	Cooperation of breast cancer proteins PALB2 and piccolo BRCA2 in stimulating homologous recombination. Nature Structural and Molecular Biology, 2010, 17, 1247-1254.	8.2	268
96	FANCD2: A DNA binding protein regulated by MRE11-RAD50-NBS1. Cell Cycle, 2010, 9, 209-210.	2.6	1
97	The Werner syndrome protein affects the expression of genes involved in adipogenesis and inflammation in addition to cell cycle and DNA damage responses. Cell Cycle, 2009, 8, 2080-2092.	2.6	48
98	Recovery of deficient homologous recombination in Brca2-depleted mouse cells by wild-type Rad51 expression. DNA Repair, 2009, 8, 170-181.	2.8	31
99	Structure and function of phage p2 ORF34, a new type of single-stranded DNA binding protein. Molecular Microbiology, 2009, 73, 1156-1170.	2.5	15
100	MRE11-RAD50-NBS1 is a critical regulator of FANCD2 stability and function during DNA double-strand break repair. EMBO Journal, 2009, 28, 2400-2413.	7.8	56
101	Functional and Structural Basis for a Bacteriophage Homolog of Human RAD52. Current Biology, 2008, 18, 1142-1146.	3.9	66
102	PARP1-dependent Kinetics of Recruitment of MRE11 and NBS1 Proteins to Multiple DNA Damage Sites. Journal of Biological Chemistry, 2008, 283, 1197-1208.	3.4	469
103	A Glycine-Arginine Domain in Control of the Human MRE11 DNA Repair Protein. Molecular and Cellular Biology, 2008, 28, 3058-3069.	2.3	76
104	Stimulation of fission yeast and mouse Hop2-Mnd1 of the Dmc1 and Rad51 recombinases. Nucleic Acids Research, 2007, 35, 2719-2733.	14.5	42
105	Twists and turns in the function of DNA damage signaling and repair proteins by post-translational modifications. DNA Repair, 2007, 6, 561-577.	2.8	24
106	Interplay between human DNA repair proteins at a unique double-strand break in vivo. EMBO Journal, 2006, 25, 222-231.	7.8	172
107	The Transcriptional Histone Acetyltransferase Cofactor TRRAP Associates with the MRN Repair Complex and Plays a Role in DNA Double-Strand Break Repair. Molecular and Cellular Biology, 2006, 26, 402-412.	2.3	68
108	The Hop2 and Mnd1 proteins act in concert with Rad51 and Dmc1 in meiotic recombination. Nature Structural and Molecular Biology, 2005, 12, 449-453.	8.2	163

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109	Fission Yeast Rad51 and Dmc1, Two Efficient DNA Recombinases Forming Helical Nucleoprotein Filaments. <i>Molecular and Cellular Biology</i> , 2005, 25, 4377-4387.	2.3	44
110	Arginine methylation of MRE11 by PRMT1 is required for DNA damage checkpoint control. <i>Genes and Development</i> , 2005, 19, 671-676.	5.9	181
111	Methylation of MRE11 Regulates its Nuclear Compartmentalization. <i>Cell Cycle</i> , 2005, 4, 981-989.	2.6	70
112	Direct interaction of FANCD2 with BRCA2 in DNA damage response pathways. <i>Human Molecular Genetics</i> , 2004, 13, 1241-1248.	2.9	190
113	RAD51C Is Required for Holliday Junction Processing in Mammalian Cells. <i>Science</i> , 2004, 303, 243-246.	12.6	289
114	Exploring the multiple facets of the meiotic recombinase Dmc1. <i>BioEssays</i> , 2004, 26, 1151-1155.	2.5	6
115	Conformational Changes Modulate the Activity of Human RAD51 Protein. <i>Journal of Molecular Biology</i> , 2004, 337, 817-827.	4.2	53
116	XRCC3 and Rad51 Modulate Replication Fork Progression on Damaged Vertebrate Chromosomes. <i>Molecular Cell</i> , 2003, 11, 1109-1117.	9.7	148
117	Role of Mammalian RAD51L2 (RAD51C) in Recombination and Genetic Stability. <i>Journal of Biological Chemistry</i> , 2002, 277, 19322-19330.	3.4	88
118	Role of BRCA2 in Control of the RAD51 Recombination and DNA Repair Protein. <i>Molecular Cell</i> , 2001, 7, 273-282.	9.7	617
119	The Rad51 and Dmc1 recombinases: a non-identical twin relationship. <i>Trends in Biochemical Sciences</i> , 2001, 26, 131-136.	7.5	158
120	Reconstitution of the strand invasion step of double-strand break repair using human Rad51 Rad52 and RPA proteins. <i>Journal of Molecular Biology</i> , 2000, 304, 151-164.	4.2	104
121	The meiosis-specific recombinase hDmc1 forms ring structures and interacts with hRad51. <i>EMBO Journal</i> , 1999, 18, 6552-6560.	7.8	123
122	A Yeast Homologue of the Human Phosphotyrosyl Phosphatase Activator PTPA Is Implicated in Protection against Oxidative DNA Damage Induced by the Model Carcinogen 4-Nitroquinoline 1-Oxide. <i>Journal of Biological Chemistry</i> , 1998, 273, 21489-21496.	3.4	54
123	The Transcriptional Activator Imp2p Maintains Ion Homeostasis in <i>Saccharomyces cerevisiae</i> . <i>Genetics</i> , 1998, 149, 893-901.	2.9	15
124	Normal processing of AP sites in <i>Apn1</i> deficient <i>Saccharomyces cerevisiae</i> is restored by <i>Escherichia coli</i> genes expressing either exonuclease III or endonuclease III. <i>Molecular Microbiology</i> , 1997, 24, 711-721.	2.5	30
125	The <i>Schizosaccharomyces pombe</i> <i>spqM</i> gene is a new member of the Qm transcription factor family. <i>Gene</i> , 1996, 170, 153-154.	2.2	4
126	The <i>Caenorhabditis elegans</i> gene <i>CeAPN1</i> encodes a homolog of <i>Escherichia coli</i> and yeast apurinic/aprimidinic endonuclease. <i>Gene</i> , 1996, 179, 291-293.	2.2	27

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127	A <i>Saccharomyces cerevisiae</i> mutant defines a new locus essential for resistance to the antitumour drug bleomycin. <i>Canadian Journal of Microbiology</i> , 1996, 42, 835-843.	1.7	13
128	Functional mitochondria are essential for <i>Saccharomyces cerevisiae</i> cellular resistance to bleomycin. <i>Current Genetics</i> , 1996, 30, 279-283.	1.7	14
129	A <i>Saccharomyces cerevisiae</i> bleomycin-sensitive mutant, phl40, is defective in the <i>RAD6</i> DNA repair gene. <i>Canadian Journal of Microbiology</i> , 1996, 42, 1263-1266.	1.7	16
130	Primary sequence of the chitosanase from <i>Streptomyces</i> sp. strain N174 and comparison with other endoglycosidases. <i>Gene</i> , 1994, 140, 103-107.	2.2	51
131	<i>Saccharomyces cerevisiae</i> DNA repair processes: an update. <i>Molecular and Cellular Biochemistry</i> , 1979, 158, 65-75.	3.1	10