Thomas A Kunkel

List of Publications by Year
in descending order

361 papers	52,243 citations	1606 105 h-index	1589 216 g-index
366 all docs	366 docs citations	366 times ranked	23727 citing authors

#	Article	IF	Citations
1	Rapid and efficient site-specific mutagenesis without phenotypic selection.. Proceedings of the National Academy of Sciences of the United States of America, 1985, 82, 488-492.	3.3	6,825
2	[19] Rapid and efficient site-specific mutagenesis without phenotypic selection. Methods in Enzymology, 1987, 154, 367-382.	0.4	5,691
3	Incidence and functional consequences of hMLH1 promoter hypermethylation in colorectal carcinoma. Proceedings of the National Academy of Sciences of the United States of America, 1998, 95, 6870-6875.	3.3	1,708
4	DNA MISMATCH REPAIR. Annual Review of Biochemistry, 2005, 74, 681-710.	5.0	1,174
5	The accuracy of reverse transcriptase from HIV-1. Science, 1988, 242, 1171-1173.	6.0	917
6	DNA Replication Fidelity. Annual Review of Biochemistry, 2000, 69, 497-529.	5.0	896
7	Fidelity of DNA synthesis by the Thermus aquaticus DNA polymerase. Biochemistry, 1988, 27, 6008-6013.	1.2	817
8	The Y-Family of DNA Polymerases. Molecular Cell, 2001, 8, 7-8.	4.5	798
9	[6] Efficient site-directed mutagenesis using uracil-containing DNA. Methods in Enzymology, 1991, 204, 125-139.	0.4	656
10	DNA Replication Fidelity. Journal of Biological Chemistry, 2004, 279, 16895-16898.	1.6	592
11	Requirement for PCNA in DNA Mismatch Repair at a Step Preceding DNA Resynthesis. Cell, 1996, 87, 65-73.	13.5	539
12	Meiotic Pachytene Arrest in MLH1-Deficient Mice. Cell, 1996, 85, 1125-1134.	13.5	528
13	Fidelity of DNA Synthesis. Annual Review of Biochemistry, 1982, 51, 429-457.	5.0	511
14	Yeast DNA Polymerase Îµ Participates in Leading-Strand DNA Replication. Science, 2007, 317, 127-130.	6.0	479
15	A sensitive genetic assay for the detection of cytosine deamination: determination of rate constants and the activation energy. Biochemistry, 1990, 29, 2532-2537.	1.2	461
16	The fidelity of DNA synthesis by eukaryotic replicative and translesion synthesis polymerases. Cell Research, 2008, 18, 148-161.	5.7	446
17	Cadmium is a mutagen that acts by inhibiting mismatch repair. Nature Genetics, 2003, 34, 326-329.	9.4	440
18	Biochemical Basis of DNA Replication Fidelity. Critical Reviews in Biochemistry and Molecular Biology, 1993, 28, 83-126.	2.3	428

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19	Division of Labor at the Eukaryotic Replication Fork. Molecular Cell, 2008, 30, 137-144.	4.5	412
20	High fidelity DNA synthesis by theThermus aquaticusDNA polymerase. Nucleic Acids Research, 1990, 18, 3739-3744.	6.5	408
21	DNA polymerase fidelity and the polymerase chain reaction.. Genome Research, 1991, 1, 17-24.	2.4	389
22	Abundant ribonucleotide incorporation into DNA by yeast replicative polymerases. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 4949-4954.	3.3	367
23	Eukaryotic DNA Replication Fork. Annual Review of Biochemistry, 2017, 86, 417-438.	5.0	365
24	Low fidelity DNA synthesis by human DNA polymerase-Î·. Nature, 2000, 404, 1011-1013.	13.7	356
25	Misalignment-mediated DNA synthesis errors. Biochemistry, 1990, 29, 8003-8011.	1.2	354
26	Mutational specificity of depurination.. Proceedings of the National Academy of Sciences of the United States of America, 1984, 81, 1494-1498.	3.3	350
27	Genome instability due to ribonucleotide incorporation into DNA. Nature Chemical Biology, 2010, 6, 774-781.	3.9	346
28	Eukaryotic Mismatch Repair in Relation to DNA Replication. Annual Review of Genetics, 2015, 49, 291-313.	3.2	342
29	Mutation in the Mismatch Repair Gene Msh6 Causes Cancer Susceptibility. Cell, 1997, 91, 467-477.	13.5	326
30	A Genetic Screen Identifies FAN1, a Fanconi Anemia-Associated Nuclease Necessary for DNA Interstrand Crosslink Repair. Molecular Cell, 2010, 39, 36-47.	4.5	306
31	Infidelity of DNA synthesis associated with bypass of apurinic sites.. Proceedings of the National Academy of Sciences of the United States of America, 1983, 80, 487-491.	3.3	297
32	A Gradient of Template Dependence Defines Distinct Biological Roles for Family X Polymerases in Nonhomologous End Joining. Molecular Cell, 2005, 19, 357-366.	4.5	294
33	Eukaryotic DNA polymerase amino acid sequence required for 3'----5' exonuclease activity.. Proceedings of the National Academy of Sciences of the United States of America, 1991, 88, 9473-9477.	3.3	287
34	A function for cyclin D1 in DNA repair uncovered by protein interactome analyses in human cancers. Nature, 2011, 474, 230-234.	13.7	287
35	RNase H2-Initiated Ribonucleotide Excision Repair. Molecular Cell, 2012, 47, 980-986.	4.5	284
36	Somatic mutation hotspots correlate with DNA polymerase Î· error spectrum. Nature Immunology, 2001, 2, 530-536.	7.0	282

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37	Inactivation of Exonuclease 1 in mice results in DNA mismatch repair defects, increased cancer susceptibility, and male and female sterility. Genes and Development, 2003, 17, 603-614.	2.7	282
38	Mutagenic Processing of Ribonucleotides in DNA by Yeast Topoisomerase I. Science, 2011, 332, 1561-1564.	6.0	251
39	Dividing the workload at a eukaryotic replication fork. Trends in Cell Biology, 2008, 18, 521-527.	3.6	243
40	Preferential cisâ€"syn thymine dimer bypass by DNA polymerase Î· occurs with biased fidelity. Nature, 2004, 428, 97-100.	13.7	241
41	Passing the baton in base excision repair. , 2000, 7, 176-178.		228
42	Functions of DNA Polymerases. Advances in Protein Chemistry, 2004, 69, 137-165.	4.4	225
43	Slippery DNA and diseases. Nature, 1993, 365, 207-208.	13.7	222
44	The Fidelity of Human DNA Polymerase Î³ with and without Exonucleolytic Proofreading and the p55 Accessory Subunit. Journal of Biological Chemistry, 2001, 276, 38555-38562.	1.6	218
45	Saccharomyces cerevisiae MutLÎ± Is a Mismatch Repair Endonuclease. Journal of Biological Chemistry, 2007, 282, 37181-37190.	1.6	217
46	Identification of an Intrinsic 5â€²-Deoxyribose-5-phosphate Lyase Activity in Human DNA Polymerase Î». Journal of Biological Chemistry, 2001, 276, 34659-34663.	1.6	215
47	Fidelity and Processivity of DNA Synthesis by DNA Polymerase Îº, the Product of the Human DINB1 Gene. Journal of Biological Chemistry, 2000, 275, 39678-39684.	1.6	208
48	Repeat expansion â€" all in flap?. Nature Genetics, 1997, 16, 116-118.	9.4	201
49	Structural basis for the dual coding potential of 8-oxoguanosine by a high-fidelity DNA polymerase. EMBO Journal, 2004, 23, 3452-3461.	3.5	200
50	Fidelity of two retroviral reverse transcriptases during DNA-dependent DNA synthesis in vitro.. Molecular and Cellular Biology, 1989, 9, 469-476.	1.1	199
51	Deoxyribonucleoside triphosphate levels: A critical factor in the maintenance of genetic stability. Mutation Research - Reviews in Genetic Toxicology, 1994, 318, 1-64.	3.0	199
52	RNA-templated DNA repair. Nature, 2007, 447, 338-341.	13.7	194
53	[18] Analyzing fidelity of DNA polymerases. Methods in Enzymology, 1995, 262, 217-232.	0.4	191
54	DNA-replication Fidelity, Mismatch Repair and Genome Instability in Cancer Cells. FEBS Journal, 1996, 238, 297-307.	0.2	190

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55	5'-Deoxyribose Phosphate Lyase Activity of Human DNA Polymerase &igr; in Vitro. Science, 2001, 291, 2156-2159.	6.0	187
56	Functional Interaction of Proliferating Cell Nuclear Antigen with MSH2-MSH6 and MSH2-MSH3 Complexes. Journal of Biological Chemistry, 2000, 275, 36498-36501.	1.6	185
57	Implication of DNA Polymerase Î» in Alignment-based Gap Filling for Nonhomologous DNA End Joining in Human Nuclear Extracts. Journal of Biological Chemistry, 2004, 279, 805-811.	1.6	184
58	Mechanisms of mutagenesis in vivo due to imbalanced dNTP pools. Nucleic Acids Research, 2011, 39, 1360-1371.	6.5	178
59	Error rate and specificity of human and murine DNA polymerase Î·. Journal of Molecular Biology, 2001, 312, 335-346.	2.0	171
60	Fidelity of mammalian DNA polymerases. Science, 1981, 213, 765-767.	6.0	170
61	Mutator Phenotypes Conferred by <i>MLH1</i>Overexpression and by Heterozygosity for <i>mlh1</i>Mutations. Molecular and Cellular Biology, 1999, 19, 3177-3183.	1.1	169
62	Evolving Views of DNA Replication (In)Fidelity. Cold Spring Harbor Symposia on Quantitative Biology, 2009, 74, 91-101.	2.0	169
63	Tracking replication enzymology in vivo by genome-wide mapping of ribonucleotide incorporation. Nature Structural and Molecular Biology, 2015, 22, 185-191.	3.6	167
64	DNA Polymerase Î», a Novel DNA Repair Enzyme in Human Cells. Journal of Biological Chemistry, 2002, 277, 13184-13191.	1.6	166
65	Ribonucleotides Are Signals for Mismatch Repair of Leading-Strand Replication Errors. Molecular Cell, 2013, 50, 437-443.	4.5	166
66	Exonucleolytic proofreading. Cell, 1988, 53, 837-840.	13.5	165
67	An Msh2 Point Mutation Uncouples DNA Mismatch Repair and Apoptosis. Cancer Research, 2004, 64, 517-522.	0.4	165
68	Evidence that Errors Made by DNA Polymerase Î± are Corrected by DNA Polymerase Î´. Current Biology, 2006, 16, 202-207.	1.8	162
69	The X family portrait: Structural insights into biological functions of X family polymerases. DNA Repair, 2007, 6, 1709-1725.	1.3	158
70	Depurination-induced infidelity of DNA synthesis with purified DNA replication proteins in vitro. Biochemistry, 1983, 22, 2378-2384.	1.2	153
71	Enzyme-DNA Interactions Required for Efficient Nucleotide Incorporation and Discrimination in Human DNA Polymerase Î². Journal of Biological Chemistry, 1996, 271, 12141-12144.	1.6	153
72	RNase H and Postreplication Repair Protect Cells from Ribonucleotides Incorporated in DNA. Molecular Cell, 2012, 45, 99-110.	4.5	153

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73	Processing ribonucleotides incorporated during eukaryotic DNA replication. Nature Reviews Molecular Cell Biology, 2016, 17, 350-363.	16.1	152
74	Unequal human immunodeficiency virus type 1 reverse transcriptase error rates with RNA and DNA templates.. Proceedings of the National Academy of Sciences of the United States of America, 1992, 89, 6919-6923.	3.3	151
75	Mutation of MSH3 in endometrial cancer and evidence for its functional role in heteroduplex repair. Nature Genetics, 1996, 14, 102-105.	9.4	149
76	DNA precursor asymmetries in mammalian tissue mitochondria and possible contribution to mutagenesis through reduced replication fidelity. Proceedings of the National Academy of Sciences of the United States of America, 2005, 102, 4990-4995.	3.3	148
77	Replication infidelity via a mismatch with Watsonâ€"Crick geometry. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 1862-1867.	3.3	148
78	The 3'->5' exonuclease of DNA polymerase Â can substitute for the 5' flap endonuclease Rad27/Fen1 in processing Okazaki fragments and preventing genome instability. Proceedings of the National Academy of Sciences of the United States of America, 2001, 98, 5122-5127.	3.3	147
79	Mechanism of a genetic glissando*: structural biology of indel mutations. Trends in Biochemical Sciences, 2006, 31, 206-214.	3.7	146
80	DNA Replication Fidelity with 8-Oxodeoxyguanosine Triphosphate. Biochemistry, 1994, 33, 4695-4701.	1.2	143
81	Heterogeneous polymerase fidelity and mismatch repair bias genome variation and composition. Genome Research, 2014, 24, 1751-1764.	2.4	141
82	Exonuclease-1 Deletion Impairs DNA Damage Signaling and Prolongs Lifespan of Telomere-Dysfunctional Mice. Cell, 2007, 130, 863-877.	13.5	139
83	A closed conformation for the Pol Î» catalytic cycle. Nature Structural and Molecular Biology, 2005, 12, 97-98.	3.6	138
84	The Major Roles of DNA Polymerases Epsilon and Delta at the Eukaryotic Replication Fork Are Evolutionarily Conserved. PLoS Genetics, 2011, 7, e1002407.	1.5	137
85	Ribonucleotides in DNA: Origins, repair and consequences. DNA Repair, 2014, 19, 27-37.	1.3	137
86	Active Site Mutation in DNA Polymerase Î³ Associated with Progressive External Ophthalmoplegia Causes Error-prone DNA Synthesis. Journal of Biological Chemistry, 2002, 277, 15225-15228.	1.6	136
87	DNA loop repair by human cell extracts. Science, 1994, 266, 814-816.	6.0	135
88	Evidence for Preferential Mismatch Repair of Lagging Strand DNA Replication Errors in Yeast. Current Biology, 2003, 13, 744-748.	1.8	135
89	Frameshift errors initiated by nucleotide misincorporation.. Proceedings of the National Academy of Sciences of the United States of America, 1990, 87, 4946-4950.	3.3	133
90	Topoisomerase 1-Mediated Removal of Ribonucleotides from Nascent Leading-Strand DNA. Molecular Cell, 2013, 49, 1010-1015.	4.5	130

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91	Functional Overlap in Mismatch Repair by Human MSH3 and MSH6. Genetics, 1998, 148, 1637-1646.	1.2	130
92	Low-fidelity DNA synthesis by human DNA polymerase theta. Nucleic Acids Research, 2008, 36, 3847-3856.	6.5	126
93	Reduced Frameshift Fidelity and Processivity of HIV-1 Reverse Transcriptase Mutants Containing Alanine Substitutions in Helix H of the Thumb Subdomain. Journal of Biological Chemistry, 1995, 270, 19516-19523.	1.6	125
94	The Fidelity of DNA Polymerase Î² during Distributive and Processive DNA Synthesis. Journal of Biological Chemistry, 1999, 274, 3642-3650.	1.6	125
95	DNA Polymerases Divide the Labor of Genome Replication. Trends in Cell Biology, 2016, 26, 640-654.	3.6	123
96	Investigating the Role of the Little Finger Domain of Y-family DNA Polymerases in Low Fidelity Synthesis and Translesion Replication. Journal of Biological Chemistry, 2004, 279, 32932-32940.	1.6	122
97	Side Chains That Influence Fidelity at the Polymerase Active Site of Escherichia coli DNA Polymerase I (Klenow Fragment). Journal of Biological Chemistry, 1999, 274, 3067-3075.	1.6	121
98	Correlation of somatic hypermutation specificity and A-T base pair substitution errors by DNA polymerase Â during copying of a mouse immunoglobulin Â light chain transgene. Proceedings of the National Academy of Sciences of the United States of America, 2002, 99, 9954-9959.	3.3	121
99	A Structural Solution for the DNA Polymerase Î»-Dependent Repair of DNA Gaps with Minimal Homology. Molecular Cell, 2004, 13, 561-572.	4.5	119
100	Direct Visualization of Asymmetric Adenine Nucleotide-Induced Conformational Changes in MutLÎ±. Molecular Cell, 2008, 29, 112-121.	4.5	117
101	Functions of human DNA polymerases Î·, Îº and Î¹ suggested by their properties, including fidelity with undamaged DNA templates. DNA Repair, 2003, 2, 135-149.	1.3	116
102	The Efficiency and Specificity of Apurinic/Apyrimidinic Site Bypass by Human DNA Polymerase Î· and Sulfolobus solfataricus Dpo4. Journal of Biological Chemistry, 2003, 278, 50537-50545.	1.6	116
103	Saccharomyces cerevisiae DNA Polymerase Î´. Journal of Biological Chemistry, 2005, 280, 29980-29987.	1.6	116
104	Exonucleolytic Proofreading during Replication of Repetitive DNA. Biochemistry, 1996, 35, 1046-1053.	1.2	113
105	A minor groove binding track in reverse transcriptase. Nature Structural Biology, 1997, 4, 194-197.	9.7	111
106	<i>In Vivo</i> Consequences of Putative Active Site Mutations in Yeast DNA Polymerases Î±, Îµ, Î´, and Î¶. Genetics, 2001, 159, 47-64.	1.2	111
107	Fidelity of mammalian DNA replication and replicative DNA polymerases. Biochemistry, 1991, 30, 11751-11759.	1.2	109
108	Unique Error Signature of the Four-subunit Yeast DNA Polymerase Ïµ. Journal of Biological Chemistry, 2003, 278, 43770-43780.	1.6	109

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109	The fidelity of DNA synthesis by yeast DNA polymerase zeta alone and with accessory proteins. Nucleic Acids Research, 2006, 34, 4731-4742.	6.5	108
110	Ribonucleotide incorporation, proofreading and bypass by human DNA polymerase Î´. DNA Repair, 2013, 12, 121-127.	1.3	108
111	Deoxynucleoside [1-thio]triphosphates prevent proofreading during in vitro DNA synthesis.. Proceedings of the National Academy of Sciences of the United States of America, 1981, 78, 6734-6738.	3.3	107
112	Participation of mouse DNA polymerase Â in strand-biased mutagenic bypass of UV photoproducts and suppression of skin cancer. Proceedings of the National Academy of Sciences of the United States of America, 2006, 103, 18083-18088.	3.3	107
113	Mismatch Repair Balances Leading and Lagging Strand DNA Replication Fidelity. PLoS Genetics, 2012, 8, e1003016.	1.5	107
114	Exonucleolytic proofreading by calf thymus DNA polymerase delta.. Proceedings of the National Academy of Sciences of the United States of America, 1987, 84, 4865-4869.	3.3	103
115	Error-prone replication of repeated DNA sequences by T7 DNA polymerase in the absence of its processivity subunit.. Proceedings of the National Academy of Sciences of the United States of America, 1994, 91, 6830-6834.	3.3	103
116	Low Fidelity DNA Synthesis by a Y Family DNA Polymerase Due to Misalignment in the Active Site. Journal of Biological Chemistry, 2002, 277, 19633-19638.	1.6	103
117	Biological asymmetries and the fidelity of eukaryotic DNA replication. BioEssays, 1992, 14, 303-308.	1.2	102
118	Yeast Origins Establish a Strand Bias for Replicational Mutagenesis. Molecular Cell, 2002, 10, 207-213.	4.5	102
119	The Frameshift Infidelity of Human DNA Polymerase Î». Journal of Biological Chemistry, 2003, 278, 34685-34690.	1.6	101
120	Altered spectra of hypermutation in antibodies from mice deficient for the DNA mismatch repair protein PMS2. Proceedings of the National Academy of Sciences of the United States of America, 1998, 95, 6953-6958.	3.3	95
121	Increased Susceptibility to UV-Induced Skin Carcinogenesis in Polymerase Î·â€"deficient Mice. Cancer Research, 2006, 66, 87-94.	0.4	95
122	Structural Analysis of Strand Misalignment during DNA Synthesis by a Human DNA Polymerase. Cell, 2006, 124, 331-342.	13.5	94
123	The efficiency and fidelity of 8-oxo-guanine bypass by DNA polymerases Â and Â. Nucleic Acids Research, 2009, 37, 2830-2840.	6.5	93
124	Aprataxin resolves adenylated RNAâ€"DNA junctions to maintain genome integrity. Nature, 2014, 506, 111-115.	13.7	93
125	The Bloom's Syndrome Protein (BLM) Interacts with MLH1 but Is Not Required for DNA Mismatch Repair. Journal of Biological Chemistry, 2001, 276, 30031-30035.	1.6	91
126	Role of glutamic acid-181 in DNA-sequence recognition by the catabolite gene activator protein (CAP) of Escherichia coli: altered DNA-sequence-recognition properties of [Val181]CAP and [Leu181]CAP.. Proceedings of the National Academy of Sciences of the United States of America, 1987, 84, 6083-6087.	3.3	90

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127	Mutagenesis in vitro by DNA polymerase from an RNA tumour virus. Nature, 1979, 278, 857-859.	13.7	89
128	Cytosine deamination in mismatched base pairs. Biochemistry, 1993, 32, 6523-6530.	1.2	89
129	High affinity cooperative DNA binding by the yeast Mlh1-Pms1 heterodimer 1 1Edited by M. Belfort. Journal of Molecular Biology, 2001, 312, 637-647.	2.0	89
130	Structural insight into the substrate specificity of DNA Polymerase Î¼. Nature Structural and Molecular Biology, 2007, 14, 45-53.	3.6	89
131	An Msh2 Conditional Knockout Mouse for Studying Intestinal Cancer and Testing Anticancer Agents. Gastroenterology, 2010, 138, 993-1002.e1.	0.6	89
132	SnapShot: DNA Mismatch Repair. Cell, 2010, 141, 730-730.e1.	13.5	89
133	Recent studies of the fidelity of DNA synthesis. Biochimica Et Biophysica Acta Gene Regulatory Mechanisms, 1988, 951, 1-15.	2.4	88
134	Genome-wide model for the normal eukaryotic DNA replication fork. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 17674-17679.	3.3	88
135	Mutator phenotypes of yeast strains heterozygous for mutations in the MSH2 gene. Proceedings of the National Academy of Sciences of the United States of America, 1999, 96, 2970-2975.	3.3	86
136	Polymerase Î´ replicates both strands after homologous recombinationâ€"dependent fork restart. Nature Structural and Molecular Biology, 2015, 22, 932-938.	3.6	84
137	Inefficient Proofreading and Biased Error Rates during Inaccurate DNA Synthesis by a Mutant Derivative of Saccharomyces cerevisiae DNA Polymerase Î´. Journal of Biological Chemistry, 2007, 282, 2324-2332.	1.6	82
138	Enzymatic switching for efficient and accurate translesion DNA replication. Nucleic Acids Research, 2004, 32, 4665-4675.	6.5	81
139	Mutator phenotypes due to DNA replication infidelity. Seminars in Cancer Biology, 2010, 20, 304-311.	4.3	81
140	Single-strand binding protein enhances fidelity of DNA synthesis in vitro.. Proceedings of the National Academy of Sciences of the United States of America, 1979, 76, 6331-6335.	3.3	80
141	Fidelity of a human cell DNA replication complex.. Proceedings of the National Academy of Sciences of the United States of America, 1988, 85, 7064-7068.	3.3	80
142	Evidence for sequential action of two ATPase active sites in yeast Msh2â€"Msh6. DNA Repair, 2002, 1, 743-753.	1.3	80
143	A Thumb Subdomain Mutant of the Large Fragment of Escherichia coli DNA Polymerase I with Reduced DNA Binding Affinity, Processivity, and Frameshift Fidelity. Journal of Biological Chemistry, 1996, 271, 24954-24961.	1.6	79
144	Fidelity of DNA polymerase I and the DNA polymerase I-DNA primase complex from Saccharomyces cerevisiae.. Molecular and Cellular Biology, 1989, 9, 4447-4458.	1.1	78

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145	Identification of In-Gel Digested Proteins by Complementary Peptide Mass Fingerprinting and Tandem Mass Spectrometry Data Obtained on an Electrospray Ionization Quadrupole Time-of-Flight Mass Spectrometer. Analytical Chemistry, 2000, 72, 1163-1168.	3.2	78
146	Evidence that DNA polymerase Î´ contributes to initiating leading strand DNA replication in Saccharomyces cerevisiae. Nature Communications, 2018, 9, 858.	5.8	77
147	Exonucleolytic proofreading by a mammalian DNA polymerase .gamma.. Biochemistry, 1989, 28, 988-995.	1.2	73
148	Proofreading of DNA Polymerase Î·-dependent Replication Errors. Journal of Biological Chemistry, 2001, 276, 2317-2320.	1.6	73
149	DNA Polymerase Îµ: A Polymerase of Unusual Size (and Complexity). Progress in Molecular Biology and Translational Science, 2008, 82, 101-145.	1.9	73
150	Differential correction of lagging-strand replication errors made by DNA polymerases Î± and Î´. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 21070-21075.	3.3	73
151	A hPMS2 Mutant Cell Line Is Defective in Strand-specific Mismatch Repair. Journal of Biological Chemistry, 1995, 270, 18183-18186.	1.6	72
152	Trace amounts of 8-oxo-dGTP in mitochondrial dNTP pools reduce DNA polymerase Â replication fidelity. Nucleic Acids Research, 2008, 36, 2174-2181.	6.5	72
153	Purification and Properties of Wild-type and Exonuclease-deficient DNA Polymerase II from Escherichia coli. Journal of Biological Chemistry, 1995, 270, 15327-15335.	1.6	71
154	The Multiple Biological Roles of the 3â€²â†’5â€² Exonuclease of Saccharomyces cerevisiae DNA Polymerase Î´ Require Switching between the Polymerase and Exonuclease Domains. Molecular and Cellular Biology, 2005, 25, 461-471.	1.1	71
155	Increased and Imbalanced dNTP Pools Symmetrically Promote Both Leading and Lagging Strand Replication Infidelity. PLoS Genetics, 2014, 10, e1004846.	1.5	71
156	5-ASA Affects Cell Cycle Progression in Colorectal Cells by Reversibly Activating a Replication Checkpoint. Gastroenterology, 2007, 132, 221-235.	0.6	69
157	Base Miscoding and Strand Misalignment Errors by Mutator Klenow Polymerases with Amino Acid Substitutions at Tyrosine 766 in the O Helix of the Fingers Subdomain. Journal of Biological Chemistry, 1997, 272, 7345-7351.	1.6	68
158	Roles of Saccharomyces cerevisiae DNA polymerases PolÂ and PolÂ in response to irradiation by simulated sunlight. Nucleic Acids Research, 2003, 31, 4541-4552.	6.5	68
159	Mammalian<i>Exo1</i>encodes both structural and catalytic functions that play distinct roles in essential biological processes. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, E2470-9.	3.3	68
160	Roles for DNA polymerase Î´ in initiating and terminating leading strand DNA replication. Nature Communications, 2019, 10, 3992.	5.8	68
161	Asymmetric Recognition of DNA Local Distortion. Journal of Biological Chemistry, 2001, 276, 46225-46229.	1.6	67
162	Aromatic hydrogen bond in sequence-specific protein DNA recognition. Nature Structural and Molecular Biology, 1996, 3, 837-841.	3.6	66

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163	Resistance to 6-thioguanine in mismatch repair-deficient human cancer cell lines correlates with an increase in induced mutations at the HPRT locus. Carcinogenesis, 1998, 19, 1931-1937.	1.3	66
164	RPA and PCNA suppress formation of large deletion errors by yeast DNA polymerase Î´. Nucleic Acids Research, 2006, 34, 4335-4341.	6.5	66
165	Mismatch Repairâ€“Independent Increase in Spontaneous Mutagenesis in Yeast Lacking Non-Essential Subunits of DNA Polymerase Îµ. PLoS Genetics, 2010, 6, e1001209.	1.5	66
166	Localization of the Deoxyribose Phosphate Lyase Active Site in Human DNA Polymerase Î¹ by Controlled Proteolysis. Journal of Biological Chemistry, 2003, 278, 29649-29654.	1.6	65
167	DNA Polymerase Delta Synthesizes Both Strands during Break-Induced Replication. Molecular Cell, 2019, 76, 371-381.e4.	4.5	65
168	Mutagenesis in vitro by depurination of Î¦X174 DNA. Nature, 1981, 291, 349-351.	13.7	64
169	Streisinger Revisited: DNA Synthesis Errors Mediated by Substrate Misalignments. Cold Spring Harbor Symposia on Quantitative Biology, 2000, 65, 81-92.	2.0	64
170	Rearrangements of DNA mediated by terminal transferase.. Proceedings of the National Academy of Sciences of the United States of America, 1986, 83, 1867-1871.	3.3	62
171	Structureâ€“function studies of DNA polymerase lambda. DNA Repair, 2005, 4, 1358-1367.	1.3	62
172	Role of the catalytic metal during polymerization by DNA polymerase lambda. DNA Repair, 2007, 6, 1333-1340.	1.3	62
173	Genome-wide analysis of the specificity and mechanisms of replication infidelity driven by imbalanced dNTP pools. Nucleic Acids Research, 2016, 44, 1669-1680.	6.5	62
174	Exonucleolytic proofreading of leading and lagging strand DNA replication errors.. Proceedings of the National Academy of Sciences of the United States of America, 1991, 88, 3465-3469.	3.3	59
175	Alternative solutions and new scenarios for translesion DNA synthesis by human PrimPol. DNA Repair, 2015, 29, 127-138.	1.3	59
176	Topoisomerase Iâ€mediated cleavage at unrepaired ribonucleotides generates DNA doubleâ€strand breaks. EMBO Journal, 2017, 36, 361-373.	3.5	59
177	The use of native T7 DNA polymerase for site-directed mutagenesis. Nucleic Acids Research, 1989, 17, 5408-5408.	6.5	58
178	Differential ATP Binding and Intrinsic ATP Hydrolysis by Amino-terminal Domains of the Yeast Mlh1 and Pms1 Proteins. Journal of Biological Chemistry, 2002, 277, 3673-3679.	1.6	58
179	Molecular breeding of polymerases for resistance to environmental inhibitors. Nucleic Acids Research, 2011, 39, e51-e51.	6.5	58
180	Functional analysis of human MutSÂ and MutSÂ complexes in yeast. Nucleic Acids Research, 1999, 27, 736-742.	6.5	57

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