Miguel Garcia-Diaz

List of Publications by Year
in descending order

63	3,271	136950 32	149698 56
papers	citations	h-index	g-index

66	66	66	3019
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	A Gradient of Template Dependence Defines Distinct Biological Roles for Family X Polymerases in Nonhomologous End Joining. Molecular Cell, 2005, 19, 357-366.	9.7	294
2	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.	3.4	184
3	DNA Polymerase Î», a Novel DNA Repair Enzyme in Human Cells. Journal of Biological Chemistry, 2002, 277, 13184-13191.	3.4	166
4	The X family portrait: Structural insights into biological functions of X family polymerases. DNA Repair, 2007, 6, 1709-1725.	2.8	158
5	Mechanism of a genetic glissando*: structural biology of indel mutations. Trends in Biochemical Sciences, 2006, 31, 206-214.	7.5	146
6	A closed conformation for the Pol Î» catalytic cycle. Nature Structural and Molecular Biology, 2005, 12, 97-98.	8.2	138
7	Plastid gene expression and plant development require a plastidic protein of the mitochondrial transcription termination factor family. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 6674-6679.	7.1	134
8	A Structural Solution for the DNA Polymerase Î»-Dependent Repair of DNA Gaps with Minimal Homology. Molecular Cell, 2004, 13, 561-572.	9.7	119
9	The Frameshift Infidelity of Human DNA Polymerase Î». Journal of Biological Chemistry, 2003, 278, 34685-34690.	3.4	101
10	Helix Unwinding and Base Flipping Enable Human MTERF1 to Terminate Mitochondrial Transcription. Cell, 2010, 141, 982-993.	28.9	95
11	Structural Analysis of Strand Misalignment during DNA Synthesis by a Human DNA Polymerase. Cell, 2006, 124, 331-342.	28.9	94
12	Structural insight into the substrate specificity of DNA Polymerase Î¼. Nature Structural and Molecular Biology, 2007, 14, 45-53.	8.2	89
13	Lack of sugar discrimination by human Pol Â requires a single glycine residue. Nucleic Acids Research, 2003, 31, 4441-4449.	14.5	87
14	Multiple Functions of DNA Polymerases. Critical Reviews in Plant Sciences, 2007, 26, 105-122.	5.7	85
15	Structure of human nSMase2 reveals an interdomain allosteric activation mechanism for ceramide generation. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, E5549-E5558.	7.1	82
16	Structure of the Essential MTERF4:NSUN4 Protein Complex Reveals How an MTERF Protein Collaborates to Facilitate rRNA Modification. Structure, 2012, 20, 1940-1947.	3.3	65
17	A Structural and Energetic Model for the Slow-Onset Inhibition of the <i>Mycobacterium tuberculosis</i> Enoyl-ACP Reductase InhA. ACS Chemical Biology, 2014, 9, 986-993.	3.4	63
18	Structureâ€"function studies of DNA polymerase lambda. DNA Repair, 2005, 4, 1358-1367.	2.8	62

#	Article	IF	Citations
19	Role of the catalytic metal during polymerization by DNA polymerase lambda. DNA Repair, 2007, 6, 1333-1340.	2.8	62
20	Biochemical Properties of Saccharomyces cerevisiae DNA Polymerase IV. Journal of Biological Chemistry, 2005, 280, 20051-20058.	3.4	56
21	Catalytic mechanism of human DNA polymerase Î» with Mg2+ and Mn2+ from ab initio quantum mechanical/molecular mechanical studies. DNA Repair, 2008, 7, 1824-1834.	2.8	52
22	A human transcription factor in search mode. Nucleic Acids Research, 2016, 44, 63-74.	14.5	52
23	Template strand scrunching during DNA gap repair synthesis by human polymerase Î». Nature Structural and Molecular Biology, 2009, 16, 967-972.	8.2	49
24	Timeâ€Dependent Diaryl Ether Inhibitors of InhA: Structureâ€"Activity Relationship Studies of Enzyme Inhibition, Antibacterial Activity, and inâ€...vivo Efficacy. ChemMedChem, 2014, 9, 776-791.	3.2	48
25	DNA Polymerase X of African Swine Fever Virus: Insertion Fidelity on Gapped DNA substrates and AP lyase Activity Support a Role in Base Excision Repair of Viral DNA. Journal of Molecular Biology, 2003, 326, 1403-1412.	4.2	47
26	A Distinct MaoC-like Enoyl-CoA Hydratase Architecture Mediates Cholesterol Catabolism in <i>Mycobacterium tuberculosis</i>. ACS Chemical Biology, 2014, 9, 2632-2645.	3.4	47
27	Unraveling Cholesterol Catabolism in <i>Mycobacterium tuberculosis</i>: ChsE4-ChsE5 Î±₂Î²₂ Acyl-CoA Dehydrogenase Initiates Î²-Oxidation of 3-Oxo-cholest-4-en-26-oyl CoA. ACS Infectious Diseases, 2015, 1, 110-125.	3.8	46
28	A unique error signature for human DNA polymerase Î½. DNA Repair, 2007, 6, 213-223.	2.8	44
29	Organization of the human mitochondrial transcription initiation complex. Nucleic Acids Research, 2014, 42, 4100-4112.	14.5	39
30	Promiscuous mismatch extension by human DNA polymerase lambda. Nucleic Acids Research, 2006, 34, 3259-3266.	14.5	38
31	Substrateâ€induced DNA strand misalignment during catalytic cycling by DNA polymerase Î». EMBO Reports, 2008, 9, 459-464.	4.5	36
32	Mitochondrial genetic variation is enriched in G-quadruplex regions that stall DNA synthesis in vitro. Human Molecular Genetics, 2020, 29, 1292-1309.	2.9	36
33	Basis for the Isoform-specific Interaction of Myosin Phosphatase Subunits Protein Phosphatase 1c Î² and Myosin Phosphatase Targeting Subunit 1. Journal of Biological Chemistry, 2010, 285, 6419-6424.	3.4	35
34	Loop 1 modulates the fidelity of DNA polymerase Â. Nucleic Acids Research, 2010, 38, 5419-5431.	14.5	34
35	A fidelity mechanism in <scp>DNA</scp> polymerase lambda promotes errorâ€free bypass of 8â€oxoâ€<scp>dG</scp>. EMBO Journal, 2016, 35, 2045-2059.	7.8	30
36	A specific, low K m ADP-ribose pyrophosphatase from rat liver. FEBS Letters, 1989, 244, 123-126.	2.8	27

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37	Hitting the brakes: Termination of mitochondrial transcription. Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms, 2012, 1819, 939-947.	1.9	21
38	Structural basis for S -adenosylmethionine binding and methyltransferase activity by mitochondrial transcription factor B1. Nucleic Acids Research, 2013, 41, 7947-7959.	14.5	21
39	Mechanisms of mammalian mitochondrial transcription. Protein Science, 2019, 28, 1594-1605.	7.6	19
40	Alcohol esterification reactions and mechanisms of snake venom 5'-nucleotide phosphodiesterase. FEBS Journal, 1993, 213, 1139-1148.	0.2	17
41	Interaction between DNA Polymerase Î» and Anticancer Nucleoside Analogs. Journal of Biological Chemistry, 2010, 285, 16874-16879.	3.4	17
42	Non-stop mRNA decay: a special attribute of trans-translation mediated ribosome rescue. Frontiers in Microbiology, 2014, 5, 93.	3.5	17
43	Biochemical Characterization of the Human Mitochondrial Replicative Twinkle Helicase. Journal of Biological Chemistry, 2016, 291, 14324-14339.	3.4	17
44	Tolerance for 8-oxoguanine but not thymine glycol in alignment-based gap filling of partially complementary double-strand break ends by DNA polymerase Î» in human nuclear extracts. Nucleic Acids Research, 2008, 36, 2895-2905.	14.5	16
45	Nucleotide binding interactions modulate dNTP selectivity and facilitate 8-oxo-dGTP incorporation by DNA polymerase lambda. Nucleic Acids Research, 2015, 43, 8089-8099.	14.5	16
46	Characterization of a Natural Mutator Variant of Human DNA Polymerase Î» which Promotes Chromosomal Instability by Compromising NHEJ. PLoS ONE, 2009, 4, e7290.	2.5	16
47	The juxtamembrane linker in neutral sphingomyelinase-2 functions as an intramolecular allosteric switch that activates the enzyme. Journal of Biological Chemistry, 2019, 294, 7488-7502.	3.4	15
48	Post-translational Succinylation of <i>Mycobacterium tuberculosis</i> Enoyl-CoA Hydratase EchA19 Slows Catalytic Hydration of Cholesterol Catabolite 3-Oxo-chol-4,22-diene-24-oyl-CoA. ACS Infectious Diseases, 2020, 6, 2214-2224.	3.8	15
49	D-MTERF5 is a novel factor modulating transcription in Drosophila mitochondria. Mitochondrion, 2012, 12, 492-499.	3.4	14
50	Methanol esterification reactions catalyzed by snake venom and bovine intestinal 5'-nucleotide phosphodiesterases. Formation of nucleoside 5'-monophosphate methyl esters from guanosine 5'-triphosphate and other nucleoside 5'-polyphosphates. FEBS Journal, 1991, 196, 451-457.	0.2	12
51	Mitochondrial transcription. Transcription, 2011, 2, 32-36.	3.1	12
52	Structural and Biochemical Basis for Intracellular Kinase Inhibition by Src-specific Peptidic Macrocycles. Cell Chemical Biology, 2016, 23, 1103-1112.	5.2	12
53	hnRNPA2 mediated acetylation reduces telomere length in response to mitochondrial dysfunction. PLoS ONE, 2018, 13, e0206897.	2.5	12
54	A minimal motif for sequence recognition by mitochondrial transcription factor A (TFAM). Nucleic Acids Research, 2022, 50, 322-332.	14.5	10

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55	Characterization of Biomolecular Helices and Their Complementarity Using Geometric Analysis. Journal of Chemical Information and Modeling, 2017, 57, 864-874.	5.4	9
56	The active site of TthPolX is adapted to prevent 8-oxo-dGTP misincorporation. Nucleic Acids Research, 2014, 42, 534-543.	14.5	8
57	A Remote Palm Domain Residue of RB69 DNA Polymerase Is Critical for Enzyme Activity and Influences the Conformation of the Active Site. PLoS ONE, 2013, 8, e76700.	2.5	7
58	Enzymatic Î²-Oxidation of the Cholesterol Side Chain in <i>Mycobacterium tuberculosis</i> Bifurcates Stereospecifically at Hydration of 3-Oxo-cholest-4,22-dien-24-oyl-CoA. ACS Infectious Diseases, 2021, 7, 1739-1751.	3.8	7
59	High Efficiency of Glycerol 2-Phosphate and sn -Glycerol 3-Phosphate as Nucleotidyl Acceptors in Snake Venom Phosphodiesterase Esterifications. Formation of Primary and Secondary AMP-O-Glyceryl and AMP-O-Glycerophosphoryl Esters and Evidence for an Acceptor-Binding Enzyme Site. FEBS Journal, 1995, 233, 442-447.	0.2	5
60	Structures of the Leishmania infantum polymerase beta. DNA Repair, 2014, 18, 1-9.	2.8	5
61	A549 cells contain enlarged mitochondria with independently functional clustered mtDNA nucleoids. PLoS ONE, 2021, 16, e0249047.	2.5	5
62	Base Flipping by MTERF1 Can Accommodate Multiple Conformations and Occurs in a Stepwise Fashion. Journal of Molecular Biology, 2016, 428, 2542-2556.	4.2	3
63	Are There Mutator Polymerases?. Scientific World Journal, The, 2003, 3, 422-431.	2.1	2