

Miguel Garcia-Diaz

List of Publications by Year in descending order

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Version: 2024-02-01

63
papers

3,271
citations

156536

32
h-index

169272

56
g-index

66
all docs

66
docs citations

66
times ranked

3362
citing authors

#	ARTICLE	IF	CITATIONS
1	A minimal motif for sequence recognition by mitochondrial transcription factor A (TFAM). <i>Nucleic Acids Research</i> , 2022, 50, 322-332.	6.5	10
2	A549 cells contain enlarged mitochondria with independently functional clustered mtDNA nucleoids. <i>PLoS ONE</i> , 2021, 16, e0249047.	1.1	5
3	Enzymatic β^2 -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. <i>ACS Infectious Diseases</i> , 2021, 7, 1739-1751.	1.8	7
4	Post-translational Succinylation of <i>Mycobacterium tuberculosis</i> Enoyl-CoA Hydratase EchA19 Slows Catalytic Hydration of Cholesterol Catabolite 3-Oxo-chole-4,22-diene-24-oyl-CoA. <i>ACS Infectious Diseases</i> , 2020, 6, 2214-2224.	1.8	15
5	Mitochondrial genetic variation is enriched in G-quadruplex regions that stall DNA synthesis in vitro. <i>Human Molecular Genetics</i> , 2020, 29, 1292-1309.	1.4	36
6	Mechanisms of mammalian mitochondrial transcription. <i>Protein Science</i> , 2019, 28, 1594-1605.	3.1	19
7	The juxtamembrane linker in neutral sphingomyelinase-2 functions as an intramolecular allosteric switch that activates the enzyme. <i>Journal of Biological Chemistry</i> , 2019, 294, 7488-7502.	1.6	15
8	hnRNPA2 mediated acetylation reduces telomere length in response to mitochondrial dysfunction. <i>PLoS ONE</i> , 2018, 13, e0206897.	1.1	12
9	Characterization of Biomolecular Helices and Their Complementarity Using Geometric Analysis. <i>Journal of Chemical Information and Modeling</i> , 2017, 57, 864-874.	2.5	9
10	Structure of human nSMase2 reveals an interdomain allosteric activation mechanism for ceramide generation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, E5549-E5558.	3.3	82
11	Biochemical Characterization of the Human Mitochondrial Replicative Twinkle Helicase. <i>Journal of Biological Chemistry</i> , 2016, 291, 14324-14339.	1.6	17
12	A human transcription factor in search mode. <i>Nucleic Acids Research</i> , 2016, 44, 63-74.	6.5	52
13	Structural and Biochemical Basis for Intracellular Kinase Inhibition by Src-specific Peptidic Macrocycles. <i>Cell Chemical Biology</i> , 2016, 23, 1103-1112.	2.5	12
14	A fidelity mechanism in <i>DNA</i> polymerase lambda promotes error-free bypass of 8-oxo-dG. <i>EMBO Journal</i> , 2016, 35, 2045-2059.	3.5	30
15	Base Flipping by MTERF1 Can Accommodate Multiple Conformations and Occurs in a Stepwise Fashion. <i>Journal of Molecular Biology</i> , 2016, 428, 2542-2556.	2.0	3
16	Nucleotide binding interactions modulate dNTP selectivity and facilitate 8-oxo-dGTP incorporation by DNA polymerase lambda. <i>Nucleic Acids Research</i> , 2015, 43, 8089-8099.	6.5	16
17	Unraveling Cholesterol Catabolism in <i>Mycobacterium tuberculosis</i> : ChsE4-ChsE5 β^2 Acyl-CoA Dehydrogenase Initiates β^2 -Oxidation of 3-Oxo-cholest-4-en-26-oyl CoA. <i>ACS Infectious Diseases</i> , 2015, 1, 110-125.	1.8	46
18	Non-stop mRNA decay: a special attribute of trans-translation mediated ribosome rescue. <i>Frontiers in Microbiology</i> , 2014, 5, 93.	1.5	17

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19	A Distinct MaoC-like Enoyl-CoA Hydratase Architecture Mediates Cholesterol Catabolism in <i>Mycobacterium tuberculosis</i> . ACS Chemical Biology, 2014, 9, 2632-2645.	1.6	47
20	Time-Dependent Diaryl Ether Inhibitors of InhA: Structure-Activity Relationship Studies of Enzyme Inhibition, Antibacterial Activity, and <i>in vivo</i> Efficacy. ChemMedChem, 2014, 9, 776-791.	1.6	48
21	Organization of the human mitochondrial transcription initiation complex. Nucleic Acids Research, 2014, 42, 4100-4112.	6.5	39
22	The active site of TthPolX is adapted to prevent 8-oxo-dGTP misincorporation. Nucleic Acids Research, 2014, 42, 534-543.	6.5	8
23	Structures of the Leishmania infantum polymerase beta. DNA Repair, 2014, 18, 1-9.	1.3	5
24	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.	1.6	63
25	Structural basis for S-adenosylmethionine binding and methyltransferase activity by mitochondrial transcription factor B1. Nucleic Acids Research, 2013, 41, 7947-7959.	6.5	21
26	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.	1.1	7
27	Hitting the brakes: Termination of mitochondrial transcription. Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms, 2012, 1819, 939-947.	0.9	21
28	Structure of the Essential MTERF4:NSUN4 Protein Complex Reveals How an MTERF Protein Collaborates to Facilitate rRNA Modification. Structure, 2012, 20, 1940-1947.	1.6	65
29	D-MTERF5 is a novel factor modulating transcription in Drosophila mitochondria. Mitochondrion, 2012, 12, 492-499.	1.6	14
30	Mitochondrial transcription. Transcription, 2011, 2, 32-36.	1.7	12
31	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.	3.3	134
32	Basis for the Isoform-specific Interaction of Myosin Phosphatase Subunits Protein Phosphatase 1c $\hat{1}$ and Myosin Phosphatase Targeting Subunit 1. Journal of Biological Chemistry, 2010, 285, 6419-6424.	1.6	35
33	Loop 1 modulates the fidelity of DNA polymerase \hat{A} . Nucleic Acids Research, 2010, 38, 5419-5431.	6.5	34
34	Interaction between DNA Polymerase \hat{B} and Anticancer Nucleoside Analogs. Journal of Biological Chemistry, 2010, 285, 16874-16879.	1.6	17
35	Helix Unwinding and Base Flipping Enable Human MTERF1 to Terminate Mitochondrial Transcription. Cell, 2010, 141, 982-993.	13.5	95
36	Template strand scrunching during DNA gap repair synthesis by human polymerase \hat{B} . Nature Structural and Molecular Biology, 2009, 16, 967-972.	3.6	49

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37	Characterization of a Natural Mutator Variant of Human DNA Polymerase ϵ which Promotes Chromosomal Instability by Compromising NHEJ. PLoS ONE, 2009, 4, e7290.	1.1	16
38	Substrate-induced DNA strand misalignment during catalytic cycling by DNA polymerase ϵ . EMBO Reports, 2008, 9, 459-464.	2.0	36
39	Catalytic mechanism of human DNA polymerase ϵ with Mg ²⁺ and Mn ²⁺ from ab initio quantum mechanical/molecular mechanical studies. DNA Repair, 2008, 7, 1824-1834.	1.3	52
40	Tolerance for 8-oxoguanine but not thymine glycol in alignment-based gap filling of partially complementary double-strand break ends by DNA polymerase ϵ in human nuclear extracts. Nucleic Acids Research, 2008, 36, 2895-2905.	6.5	16
41	Multiple Functions of DNA Polymerases. Critical Reviews in Plant Sciences, 2007, 26, 105-122.	2.7	85
42	Structural insight into the substrate specificity of DNA Polymerase δ . Nature Structural and Molecular Biology, 2007, 14, 45-53.	3.6	89
43	A unique error signature for human DNA polymerase δ . DNA Repair, 2007, 6, 213-223.	1.3	44
44	Role of the catalytic metal during polymerization by DNA polymerase lambda. DNA Repair, 2007, 6, 1333-1340.	1.3	62
45	The X family portrait: Structural insights into biological functions of X family polymerases. DNA Repair, 2007, 6, 1709-1725.	1.3	158
46	Structural Analysis of Strand Misalignment during DNA Synthesis by a Human DNA Polymerase. Cell, 2006, 124, 331-342.	13.5	94
47	Mechanism of a genetic glissando*: structural biology of indel mutations. Trends in Biochemical Sciences, 2006, 31, 206-214.	3.7	146
48	Promiscuous mismatch extension by human DNA polymerase lambda. Nucleic Acids Research, 2006, 34, 3259-3266.	6.5	38
49	A closed conformation for the Pol ϵ catalytic cycle. Nature Structural and Molecular Biology, 2005, 12, 97-98.	3.6	138
50	Biochemical Properties of Saccharomyces cerevisiae DNA Polymerase IV. Journal of Biological Chemistry, 2005, 280, 20051-20058.	1.6	56
51	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
52	Structure-function studies of DNA polymerase lambda. DNA Repair, 2005, 4, 1358-1367.	1.3	62
53	Implication of DNA Polymerase ϵ 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
54	A Structural Solution for the DNA Polymerase ϵ -Dependent Repair of DNA Gaps with Minimal Homology. Molecular Cell, 2004, 13, 561-572.	4.5	119

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55	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. <i>Journal of Molecular Biology</i> , 2003, 326, 1403-1412.	2.0	47
56	Lack of sugar discrimination by human Pol β requires a single glycine residue. <i>Nucleic Acids Research</i> , 2003, 31, 4441-4449.	6.5	87
57	The Frameshift Infidelity of Human DNA Polymerase β . <i>Journal of Biological Chemistry</i> , 2003, 278, 34685-34690.	1.6	101
58	Are There Mutator Polymerases?. <i>Scientific World Journal</i> , The, 2003, 3, 422-431.	0.8	2
59	DNA Polymerase β , a Novel DNA Repair Enzyme in Human Cells. <i>Journal of Biological Chemistry</i> , 2002, 277, 13184-13191.	1.6	166
60	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. <i>FEBS Journal</i> , 1995, 233, 442-447.	0.2	5
61	Alcohol esterification reactions and mechanisms of snake venom 5'-nucleotide phosphodiesterase. <i>FEBS Journal</i> , 1993, 213, 1139-1148.	0.2	17
62	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. <i>FEBS Journal</i> , 1991, 196, 451-457.	0.2	12
63	A specific, low K_m ADP-ribose pyrophosphatase from rat liver. <i>FEBS Letters</i> , 1989, 244, 123-126.	1.3	27