

Sylvie Doublie

List of Publications by Year in descending order

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87
papers

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109321

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times ranked

5717
citing authors

#	ARTICLE	IF	CITATIONS
1	Mouse Embryonic Fibroblasts Isolated From Nthl1 D227Y Knockin Mice Exhibit Defective DNA Repair and Increased Genome Instability. <i>DNA Repair</i> , 2022, 109, 103247.	2.8	0
2	Probing the structure and function of polymerase $\hat{\iota}$, helicase-like domain. <i>DNA Repair</i> , 2022, 116, 103358.	2.8	2
3	Unique Structural Features of Mammalian NEIL2 DNA Glycosylase Prime Its Activity for Diverse DNA Substrates and Environments. <i>Structure</i> , 2021, 29, 29-42.e4.	3.3	19
4	Human DNA polymerase $\hat{\iota}$, harbors DNA end-trimming activity critical for DNA repair. <i>Molecular Cell</i> , 2021, 81, 1534-1547.e4.	9.7	25
5	A lipoprotein allosterically activates the Cwld amidase during <i>Clostridioides difficile</i> spore formation. <i>PLoS Genetics</i> , 2021, 17, e1009791.	3.5	8
6	When DNA Polymerases Multitask: Functions Beyond Nucleotidyl Transfer. <i>Frontiers in Molecular Biosciences</i> , 2021, 8, 815845.	3.5	8
7	Caught in motion: human NTHL1 undergoes interdomain rearrangement necessary for catalysis. <i>Nucleic Acids Research</i> , 2021, 49, 13165-13178.	14.5	11
8	The CspC pseudoprotease regulates germination of <i>Clostridioides difficile</i> spores in response to multiple environmental signals. <i>PLoS Genetics</i> , 2019, 15, e1008224.	3.5	32
9	I260Q DNA polymerase $\hat{\iota}^2$ highlights precatalytic conformational rearrangements critical for fidelity. <i>Nucleic Acids Research</i> , 2018, 46, 10740-10756.	14.5	8
10	The nature of the DNA substrate influences pre-catalytic conformational changes of DNA polymerase $\hat{\iota}^2$. <i>Journal of Biological Chemistry</i> , 2018, 293, 15084-15094.	3.4	7
11	Remote Mutations Induce Functional Changes in Active Site Residues of Human DNA Polymerase $\hat{\iota}^2$. <i>Biochemistry</i> , 2017, 56, 2363-2371.	2.5	9
12	The A-Rule and Deletion Formation During Abasic and Oxidized Abasic Site Bypass by DNA Polymerase $\hat{\iota}$. <i>ACS Chemical Biology</i> , 2017, 12, 1584-1592.	3.4	10
13	Defective Nucleotide Release by DNA Polymerase $\hat{\iota}^2$ Mutator Variant E288K Is the Basis of Its Low Fidelity. <i>Biochemistry</i> , 2017, 56, 5550-5559.	2.5	11
14	Expression and Structural Analyses of Human DNA Polymerase $\hat{\iota}$ (POLQ). <i>Methods in Enzymology</i> , 2017, 592, 103-121.	1.0	13
15	The NEIL1 G83D germline DNA glycosylase variant induces genomic instability and cellular transformation. <i>Oncotarget</i> , 2017, 8, 85883-85895.	1.8	17
16	Destabilization of the PCNA trimer mediated by its interaction with the NEIL1 DNA glycosylase. <i>Nucleic Acids Research</i> , 2016, 45, gkw1282.	14.5	11
17	DNA polymerase $\hat{\iota}$ (POLQ), double-strand break repair, and cancer. <i>DNA Repair</i> , 2016, 44, 22-32.	2.8	158
18	Phosphorylation Sites Identified in the NEIL1 DNA Glycosylase Are Potential Targets for the JNK1 Kinase. <i>PLoS ONE</i> , 2016, 11, e0157860.	2.5	16

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19	Base Excision Repair in the Mitochondria. <i>Journal of Cellular Biochemistry</i> , 2015, 116, 1490-1499.	2.6	111
20	Human DNA polymerase $\hat{\epsilon}$, grasps the primer terminus to mediate DNA repair. <i>Nature Structural and Molecular Biology</i> , 2015, 22, 304-311.	8.2	109
21	Fluorescence Resonance Energy Transfer Studies of DNA Polymerase $\hat{\epsilon}$. <i>Journal of Biological Chemistry</i> , 2014, 289, 16541-16550.	3.4	23
22	Look Ma, no PCNA: how DNA polymerase $\hat{\mu}$ synthesizes long stretches of DNA without a processivity factor. <i>Nature Structural and Molecular Biology</i> , 2014, 21, 12-14.	8.2	2
23	A Germline Polymorphism of Thymine DNA Glycosylase Induces Genomic Instability and Cellular Transformation. <i>PLoS Genetics</i> , 2014, 10, e1004753.	3.5	16
24	Mechanism of Suppression of Chromosomal Instability by DNA Polymerase POLQ. <i>PLoS Genetics</i> , 2014, 10, e1004654.	3.5	214
25	Structural insights into eukaryotic DNA replication. <i>Frontiers in Microbiology</i> , 2014, 5, 444.	3.5	34
26	Genome and cancer single nucleotide polymorphisms of the human NEIL1 DNA glycosylase: Activity, structure, and the effect of editing. <i>DNA Repair</i> , 2014, 14, 17-26.	2.8	38
27	Crystal Structure of DNA Polymerase $\hat{\epsilon}$ with DNA Containing the Base Lesion Spiroiminodihydroantoin in a Templating Position. <i>Biochemistry</i> , 2014, 53, 2075-2077.	2.5	18
28	Crystal Structure of Human Poly(A) Polymerase Gamma Reveals a Conserved Catalytic Core for Canonical Poly(A) Polymerases. <i>Journal of Molecular Biology</i> , 2014, 426, 43-50.	4.2	18
29	The E295K Cancer Variant of Human Polymerase $\hat{\epsilon}$ Favors the Mismatch Conformational Pathway during Nucleotide Selection. <i>Journal of Biological Chemistry</i> , 2013, 288, 34850-34860.	3.4	15
30	Structural investigation of a viral ortholog of human NEIL2/3 DNA glycosylases. <i>DNA Repair</i> , 2013, 12, 1062-1071.	2.8	21
31	Neil3, the final frontier for the DNA glycosylases that recognize oxidative damage. <i>Mutation Research - Fundamental and Molecular Mechanisms of Mutagenesis</i> , 2013, 743-744, 4-11.	1.0	72
32	Structural Characterization of a Mouse Ortholog of Human NEIL3 with a Marked Preference for Single-Stranded DNA. <i>Structure</i> , 2013, 21, 247-256.	3.3	51
33	Structural and Functional Analysis of the CspB Protease Required for Clostridium Spore Germination. <i>PLoS Pathogens</i> , 2013, 9, e1003165.	4.7	99
34	Structural Studies of a Bacterial tRNA ^{HIS} Guanylyltransferase (Thg1)-Like Protein, with Nucleotide in the Activation and Nucleotidyl Transfer Sites. <i>PLoS ONE</i> , 2013, 8, e67465.	2.5	15
35	8-Oxoguanine DNA Glycosylases: One Lesion, Three Subfamilies. <i>International Journal of Molecular Sciences</i> , 2012, 13, 6711-6729.	4.1	36
36	Structural Characterization of Viral Ortholog of Human DNA Glycosylase NEIL1 Bound to Thymine Glycol or 5-Hydroxyuracil-containing DNA. <i>Journal of Biological Chemistry</i> , 2012, 287, 4288-4298.	3.4	48

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37	Structural and biochemical studies of a plant formamidopyrimidine-DNA glycosylase reveal why eukaryotic Fpg glycosylases do not excise 8-oxoguanine. <i>DNA Repair</i> , 2012, 11, 714-725.	2.8	46
38	Consequences and Repair of Oxidative DNA Damage. <i>Issues in Toxicology</i> , 2012, , 115-159.	0.1	10
39	The Fpg/Nei Family of DNA Glycosylases. <i>Progress in Molecular Biology and Translational Science</i> , 2012, 110, 71-91.	1.7	78
40	The Miscoding Potential of 5-Hydroxycytosine Arises Due to Template Instability in the Replicative Polymerase Active Site. <i>Biochemistry</i> , 2011, 50, 10350-10358.	2.5	18
41	Lesion Bypass Activity of DNA Polymerase η (POLQ) Is an Intrinsic Property of the Pol Domain and Depends on Unique Sequence Inserts. <i>Journal of Molecular Biology</i> , 2011, 405, 642-652.	4.2	81
42	A Crystallographic Study of the Role of Sequence Context in Thymine Glycol Bypass by a Replicative DNA Polymerase Serendipitously Sheds Light on the Exonuclease Complex. <i>Journal of Molecular Biology</i> , 2011, 412, 22-34.	4.2	25
43	Crystal Structure of a Human Cleavage Factor CFI _{m25} /CFI _{m68} /RNA Complex Provides an Insight into Poly(A) Site Recognition and RNA Looping. <i>Structure</i> , 2011, 19, 368-377.	3.3	127
44	DNA polymerases provide a canon of strategies for translesion synthesis past oxidatively generated lesions. <i>Current Opinion in Structural Biology</i> , 2011, 21, 358-369.	5.7	34
45	Structural biology of poly(A) site definition. <i>Wiley Interdisciplinary Reviews RNA</i> , 2011, 2, 732-747.	6.4	45
46	Purification, crystallization and preliminary X-ray diffraction of a disulfide cross-linked complex between bovine poly(A) polymerase and a chemically modified 15-mer oligo(A) RNA. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2011, 67, 241-244.	0.7	4
47	The structure of human Cleavage Factor I _m hints at functions beyond UGUA-specific RNA binding. <i>RNA Biology</i> , 2011, 8, 748-753.	3.1	56
48	Phosphonoformic Acid Inhibits Viral Replication by Trapping the Closed Form of the DNA Polymerase. <i>Journal of Biological Chemistry</i> , 2011, 286, 25246-25255.	3.4	48
49	Structural basis of UGUA recognition by the Nudix protein CFI _m 25 and implications for a regulatory role in mRNA 3' processing. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 10062-10067.	7.1	123
50	tRNA ^{His} guanylyltransferase (THG1), a unique 3'→5' nucleotidyl transferase, shares unexpected structural homology with canonical 5'→3' DNA polymerases. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 20305-20310.	7.1	47
51	Crystal Structure of a Replicative DNA Polymerase Bound to the Oxidized Guanine Lesion Guanidinohydantoin. <i>Biochemistry</i> , 2010, 49, 2502-2509.	2.5	37
52	The C-terminal Lysine of Ogg2 DNA Glycosylases is a Major Molecular Determinant for Guanine/8-Oxoguanine Distinction. <i>Journal of Molecular Biology</i> , 2010, 397, 46-56.	4.2	21
53	Kinetics of Mismatch Formation opposite Lesions by the Replicative DNA Polymerase from Bacteriophage RB69. <i>Biochemistry</i> , 2010, 49, 2317-2325.	2.5	19
54	Structural Characterization of a Viral NEIL1 Ortholog Unliganded and Bound to Abasic Site-containing DNA. <i>Journal of Biological Chemistry</i> , 2009, 284, 26174-26183.	3.4	41

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55	Crystal Structures of Two Archaeal 8-Oxoguanine DNA Glycosylases Provide Structural Insight into Guanine/8-Oxoguanine Distinction. <i>Structure</i> , 2009, 17, 703-712.	3.3	20
56	Structural basis for the lack of opposite base specificity of <i>Clostridium acetobutylicum</i> 8-oxoguanine DNA glycosylase. <i>DNA Repair</i> , 2009, 8, 1283-1289.	2.8	13
57	Structural Characterization of <i>Clostridium acetobutylicum</i> 8-Oxoguanine DNA Glycosylase in Its Apo Form and in Complex with 8-Oxodeoxyguanosine. <i>Journal of Molecular Biology</i> , 2009, 387, 669-679.	4.2	14
58	The Soul of a New Structure-Function Machine. <i>Structure</i> , 2008, 16, 3-4.	3.3	1
59	Determinants of substrate specificity in RNA-dependent nucleotidyl transferases. <i>Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms</i> , 2008, 1779, 206-216.	1.9	21
60	Crystal structure of the 25 kDa subunit of human cleavage factor I m. <i>Nucleic Acids Research</i> , 2008, 36, 3474-3483.	14.5	39
61	Crystallographic Software: A Sustainable Resource for the Community. , 2007, 364, 273-278.		1
62	Structural and Biochemical Investigation of the Role in Proofreading of a \hat{I}^2 Hairpin Loop Found in the Exonuclease Domain of a Replicative DNA Polymerase of the B Family. <i>Journal of Biological Chemistry</i> , 2007, 282, 1432-1444.	3.4	67
63	A structural rationale for stalling of a replicative DNA polymerase at the most common oxidative thymine lesion, thymine glycol. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007, 104, 814-818.	7.1	91
64	Caught Bending the A-Rule:â€™ Crystal Structures of Translesion DNA Synthesis with a Non-Natural Nucleotide. <i>Biochemistry</i> , 2007, 46, 10551-10561.	2.5	40
65	Production of Selenomethionyl Proteins in Prokaryotic and Eukaryotic Expression Systems. <i>Methods in Molecular Biology</i> , 2007, 363, 91-108.	0.9	116
66	Bumps in the road: how replicative DNA polymerases see DNA damage. <i>Current Opinion in Structural Biology</i> , 2005, 15, 86-93.	5.7	46
67	Activation of the Hetero-octameric ATP Phosphoribosyl Transferase through Subunit Interface Rearrangement by a tRNA Synthetase Paralog. <i>Journal of Biological Chemistry</i> , 2005, 280, 34096-34104.	3.4	30
68	The crystal structure of human endonuclease VIII-like 1 (NEIL1) reveals a zincless finger motif required for glycosylase activity. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2004, 101, 10284-10289.	7.1	132
69	Crystallographic snapshots of a replicative DNA polymerase encountering an abasic site. <i>EMBO Journal</i> , 2004, 23, 1483-1493.	7.8	134
70	Structural basis for the dual coding potential of 8-oxoguanosine by a high-fidelity DNA polymerase. <i>EMBO Journal</i> , 2004, 23, 3452-3461.	7.8	200
71	Nucleotide insertion opposite a cis-syn thymine dimer by a replicative DNA polymerase from bacteriophage T7. <i>Nature Structural and Molecular Biology</i> , 2004, 11, 784-790.	8.2	66
72	Infidelity Out in the Open. <i>Structure</i> , 2004, 12, 1749-1750.	3.3	1

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73	Overproduction, crystallization and preliminary crystallographic analysis of a novel human DNA-repair enzyme that recognizes oxidative DNA damage. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2004, 60, 1142-1144.	2.5	28
74	Biochemical and Structural Insights into Substrate Binding and Catalytic Mechanism of Mammalian Poly(A) Polymerase. <i>Journal of Molecular Biology</i> , 2004, 341, 911-925.	4.2	42
75	Cryocooling of Macromolecular Crystals: Optimization Methods. <i>Methods in Enzymology</i> , 2003, 368, 188-216.	1.0	33
76	The Motif D Loop of Human Immunodeficiency Virus Type 1 Reverse Transcriptase Is Critical for Nucleoside 5'-Triphosphate Selectivity. <i>Journal of Biological Chemistry</i> , 1999, 274, 35768-35776.	3.4	19
77	An open and closed case for all polymerases. <i>Structure</i> , 1999, 7, R31-R35.	3.3	292
78	Crystal structure of a bacteriophage T7 DNA replication complex at 2.2 Å resolution. <i>Nature</i> , 1998, 391, 251-258.	27.8	1,207
79	The mechanism of action of T7 DNA polymerase. <i>Current Opinion in Structural Biology</i> , 1998, 8, 704-712.	5.7	185
80	Chemical modifications of <i>Bacillus subtilis</i> tryptophanyl-tRNA synthetase. <i>Biochemistry and Cell Biology</i> , 1997, 75, 709-715.	2.0	2
81	[29] Preparation of selenomethionyl proteins for phase determination. <i>Methods in Enzymology</i> , 1997, 276, 523-530.	1.0	801
82	Crystallization and preliminary crystallographic analysis of the signal recognition particle SRP14-9 fusion protein. <i>FEBS Letters</i> , 1996, 384, 215-218.	2.8	4
83	Crystallization and preliminary X-ray analysis of the 9 kDa protein of the mouse signal recognition particle and the selenomethionyl-SRP9. <i>FEBS Letters</i> , 1996, 384, 219-221.	2.8	52
84	A Concerted Tryptophanyl-adenylate-dependent Conformational Change in <i>Bacillus subtilis</i> Tryptophanyl-tRNA Synthetase Revealed by the Fluorescence of Trp92. <i>Journal of Molecular Biology</i> , 1996, 260, 446-466.	4.2	21
85	Tryptophanyl-tRNA synthetase crystal structure reveals an unexpected homology to tyrosyl-tRNA synthetase. <i>Structure</i> , 1995, 3, 17-31.	3.3	181
86	Quantitative Analysis of Crystal Growth. <i>Journal of Molecular Biology</i> , 1994, 238, 346-365.	4.2	32
87	Production of Selenomethionyl Proteins in Prokaryotic and Eukaryotic Expression Systems. , 0, , 91-108.		3