

Maria Spies

List of Publications by Year in descending order

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Version: 2024-02-01

67
papers

2,850
citations

186265
28
h-index

197818
49
g-index

85
all docs

85
docs citations

85
times ranked

2616
citing authors

#	ARTICLE	IF	CITATIONS
1	Gain-of-function mutations in RPA1 cause a syndrome with short telomeres and somatic genetic rescue. <i>Blood</i> , 2022, 139, 1039-1051.	1.4	29
2	Making choices: DNA replication fork recovery mechanisms. <i>Seminars in Cell and Developmental Biology</i> , 2021, 113, 27-37.	5.0	30
3	KERA: analysis tool for multi-process, multi-state single-molecule data. <i>Nucleic Acids Research</i> , 2021, 49, e53-e53.	14.5	9
4	Switch-like control of helicase processivity by single-stranded DNA binding protein. <i>ELife</i> , 2021, 10, .	6.0	7
5	Construction of a Three-Color Prism-Based TIRF Microscope to Study the Interactions and Dynamics of Macromolecules. <i>Biology</i> , 2021, 10, 571.	2.8	6
6	Getting swept off your toe(hold)s: Single-molecule DNA fission analysis offers glimpse into kinetics of branch migration. <i>Biophysical Journal</i> , 2021, 120, 2367-2369.	0.5	0
7	RPA complexes in <i>Caenorhabditis elegans</i> meiosis; unique roles in replication, meiotic recombination and apoptosis. <i>Nucleic Acids Research</i> , 2021, 49, 2005-2026.	14.5	14
8	DSS1 interacts with and stimulates RAD52 to promote the repair of DSBs. <i>Nucleic Acids Research</i> , 2020, 48, 694-708.	14.5	24
9	Dynamic elements of replication protein A at the crossroads of DNA replication, recombination, and repair. <i>Critical Reviews in Biochemistry and Molecular Biology</i> , 2020, 55, 482-507.	5.2	70
10	RAD51 discrimination between single- and double-strand DNA : a matter of flexibility and enthalpy. <i>EMBO Journal</i> , 2020, 39, e104547.	7.8	2
11	Physiological and Pathological Roles of RAD52 at DNA Replication Forks. <i>Cancers</i> , 2020, 12, 402.	3.7	20
12	Dynamics and selective remodeling of the DNA-binding domains of RPA. <i>Nature Structural and Molecular Biology</i> , 2019, 26, 129-136.	8.2	94
13	Rad52 prevents excessive replication fork reversal and protects from nascent strand degradation. <i>Nature Communications</i> , 2019, 10, 1412.	12.8	60
14	Observation and Analysis of RAD51 Nucleation Dynamics at Single-Monomer Resolution. <i>Methods in Enzymology</i> , 2018, 600, 201-232.	1.0	15
15	Preface. <i>Methods in Enzymology</i> , 2018, 601, xv-xvi.	1.0	0
16	A structural and dynamic model for the assembly of Replication Protein A on single-stranded DNA. <i>Nature Communications</i> , 2018, 9, 5447.	12.8	110
17	Expression, Purification, and Biochemical Evaluation of Human RAD51 Protein. <i>Methods in Enzymology</i> , 2018, 600, 157-178.	1.0	9
18	Single-Molecule Sorting of Human DNA Repair Enzymes. <i>Biophysical Journal</i> , 2017, 112, 5a-6a.	0.5	0

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19	Small-Molecule Inhibitors Targeting DNA Repair and DNA Repair Deficiency in Research and Cancer Therapy. <i>Cell Chemical Biology</i> , 2017, 24, 1101-1119.	5.2	111
20	Helicase SPRNTing through the nanopore. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, 11809-11811.	7.1	12
21	Protein–nucleic acids interactions: new ways of connecting structure, dynamics and function. <i>Biophysical Reviews</i> , 2017, 9, 289-291.	3.2	5
22	The Tiam1 guanine nucleotide exchange factor is auto-inhibited by its pleckstrin homology coiled-coil extension domain. <i>Journal of Biological Chemistry</i> , 2017, 292, 17777-17793.	3.4	19
23	A time for promiscuity in a eukaryotic recombinase. <i>Journal of Biological Chemistry</i> , 2017, 292, 11136-11137.	3.4	2
24	Preface. <i>Methods in Enzymology</i> , 2017, 582, xv-xvi.	1.0	1
25	PCNA tool belts and polymerase bridges form during translesion synthesis. <i>Nucleic Acids Research</i> , 2016, 44, 8250-8260.	14.5	49
26	G-quadruplex recognition and remodeling by the FANCD1 helicase. <i>Nucleic Acids Research</i> , 2016, 44, 8742-8753.	14.5	80
27	Insights into the Autoinhibition Mechanism of the Tiam1 Guanine Nucleotide Exchange Factor. <i>Biophysical Journal</i> , 2016, 110, 206a.	0.5	0
28	Dynamic binding of replication protein a is required for DNA repair. <i>Nucleic Acids Research</i> , 2016, 44, 5758-5772.	14.5	82
29	Tyrosine phosphorylation stimulates activity of human RAD51 recombinase through altered nucleoprotein filament dynamics. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, E6045-E6054.	7.1	47
30	Single-molecule sorting of DNA helicases. <i>Methods</i> , 2016, 108, 14-23.	3.8	19
31	Preface. <i>Methods in Enzymology</i> , 2016, 581, xvii-xviii.	1.0	0
32	Quantifying the Assembly of Multicomponent Molecular Machines by Single-Molecule Total Internal Reflection Fluorescence Microscopy. <i>Methods in Enzymology</i> , 2016, 581, 105-145.	1.0	16
33	The Proliferating Cell Nuclear Antigen (PCNA)-interacting Protein (PIP) Motif of DNA Polymerase δ Mediates Its Interaction with the C-terminal Domain of Rev1. <i>Journal of Biological Chemistry</i> , 2016, 291, 8735-8744.	3.4	44
34	Small-molecule inhibitors identify the RAD52-ssDNA interaction as critical for recovery from replication stress and for survival of BRCA2 deficient cells. <i>ELife</i> , 2016, 5, .	6.0	64
35	Mismatch Repair during Homologous and Homeologous Recombination. <i>Cold Spring Harbor Perspectives in Biology</i> , 2015, 7, a022657.	5.5	146
36	Two steps forward, one step back: Determining XPD helicase mechanism by single-molecule fluorescence and high-resolution optical tweezers. <i>DNA Repair</i> , 2014, 20, 58-70.	2.8	25

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37	Mismatch repair protein hMSH2â€”hMSH6 recognizes mismatches and forms sliding clamps within a D-loop recombination intermediate. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, E316-25.	7.1	37
38	Direct Correlation of DNA Binding and Single Protein Domain Motion via Dual Illumination Fluorescence Microscopy. Nano Letters, 2014, 14, 5920-5931.	9.1	37
39	Fulfilling the dream of a perfect genome editing tool. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 10029-10030.	7.1	1
40	There and back again: new single-molecule insights in the motion of DNA repair proteins. Current Opinion in Structural Biology, 2013, 23, 154-160.	5.7	17
41	Single-Molecule Analysis of Conformational Transitions in XPD Helicase. Biophysical Journal, 2013, 104, 61a.	0.5	0
42	Overview: What Are Helicases?. Advances in Experimental Medicine and Biology, 2013, 767, 1-16.	1.6	18
43	DNA Repair: Trust but Verify. Current Biology, 2013, 23, R115-R117.	3.9	2
44	Structure and Mechanisms of SF2 DNA Helicases. Advances in Experimental Medicine and Biology, 2013, 767, 47-73.	1.6	31
45	Survival of the Replication Checkpoint Deficient Cells Requires MUS81-RAD52 Function. PLoS Genetics, 2013, 9, e1003910.	3.5	68
46	Single-molecule study of the CUG repeatâ€”MBNL1 interaction and its inhibition by small molecules. Nucleic Acids Research, 2013, 41, 6687-6697.	14.5	27
47	Contributions of the RAD51 N-terminal domain to BRCA2-RAD51 interaction. Nucleic Acids Research, 2013, 41, 9020-9032.	14.5	37
48	Single-molecule sorting reveals how ubiquitylation affects substrate recognition and activities of FBH1 helicase. Nucleic Acids Research, 2013, 41, 3576-3587.	14.5	28
49	Sequence-dependent base pair stepping dynamics in XPD helicase unwinding. ELife, 2013, 2, e00334.	6.0	72
50	Regulation of translocation polarity by helicase domain 1 in SF2B helicases. EMBO Journal, 2012, 31, 503-514.	7.8	58
51	Tyrosine phosphorylation enhances RAD52-mediated annealing by modulating its DNA binding. EMBO Journal, 2011, 30, 3368-3382.	7.8	56
52	FRET-Based Assays to Monitor DNA Binding and Annealing by Rad52 Recombination Mediator Protein. Methods in Molecular Biology, 2011, 745, 463-483.	0.9	20
53	Human Rad52 binds and wraps single-stranded DNA and mediates annealing via two hRad52â€”ssDNA complexes. Nucleic Acids Research, 2010, 38, 2917-2930.	14.5	121
54	Inching over hurdles: How DNA helicases move on crowded lattices. Cell Cycle, 2010, 9, 1742-1749.	2.6	11

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55	Ensemble and single-molecule fluorescence-based assays to monitor DNA binding, translocation, and unwinding by iron-sulfur cluster containing helicases. <i>Methods</i> , 2010, 51, 313-321.	3.8	16
56	Single-Molecule Analysis Reveals Differential Effect of ssDNA-Binding Proteins on DNA Translocation by XPD Helicase. <i>Molecular Cell</i> , 2009, 35, 694-703.	9.7	73
57	Ferroplasma acidarmanus RPA2 Facilitates Efficient Unwinding of Forked DNA Substrates by Monomers of FacXPD Helicase. <i>Journal of Molecular Biology</i> , 2008, 383, 982-998.	4.2	32
58	Human Rad52-mediated homology search and annealing occurs by continuous interactions between overlapping nucleoprotein complexes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008, 105, 20274-20279.	7.1	80
59	Engineering of Functional Replication Protein A Homologs Based on Insights into the Evolution of Oligonucleotide/ Oligosaccharide-Binding Folds. <i>Journal of Bacteriology</i> , 2008, 190, 5766-5780.	2.2	19
60	The Iron-containing Domain Is Essential in Rad3 Helicases for Coupling of ATP Hydrolysis to DNA Translocation and for Targeting the Helicase to the Single-stranded DNA-Double-stranded DNA Junction. <i>Journal of Biological Chemistry</i> , 2008, 283, 1732-1743.	3.4	88
61	RecBCD Enzyme Switches Lead Motor Subunits in Response to γ -Recognition. <i>Cell</i> , 2007, 131, 694-705.	28.9	120
62	The RecA Binding Locus of RecBCD Is a General Domain for Recruitment of DNA Strand Exchange Proteins. <i>Molecular Cell</i> , 2006, 21, 573-580.	9.7	99
63	Translocation by the RecB Motor Is an Absolute Requirement for γ -Recognition and RecA Protein Loading by RecBCD Enzyme. <i>Journal of Biological Chemistry</i> , 2005, 280, 37078-37087.	3.4	40
64	RecBCD enzyme is a bipolar DNA helicase. <i>Nature</i> , 2003, 423, 893-897.	27.8	196
65	A Molecular Throttle. <i>Cell</i> , 2003, 114, 647-654.	28.9	176
66	Homologous Recombination by the RecBCD and RecF Pathways. , 0, , 389-403.		40
67	RAD52 Prevents Excessive Replication Fork Reversal and Protects from Nascent Strand Degradation. <i>SSRN Electronic Journal</i> , 0, , .	0.4	0