

James M Berger

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

94
papers

7,306
citations

45
h-index

85
g-index

111
ext. papers

8,428
ext. citations

16.3
avg, IF

6.31
L-index

#	Paper	IF	Citations
94	Molecular determinants of phase separation for DNA replication licensing factors.. <i>ELife</i> , 2021 , 10,	8.9	2
93	A Fluorescent Assay to Monitor Ligand-Dependent Closure of the Hexameric Rho Helicase Ring. <i>Methods in Molecular Biology</i> , 2021 , 2209, 133-142	1.4	1
92	The molecular coupling between substrate recognition and ATP turnover in a[AAA+ hexameric helicase loader. <i>ELife</i> , 2021 , 10,	8.9	2
91	Structural Mechanisms for Replicating DNA in Eukaryotes. <i>Annual Review of Biochemistry</i> , 2021 , 90, 77-106.	106.1	3
90	Synthesis and antimicrobial evaluation of new nitric oxide-donating fluoroquinolone/oxime hybrids. <i>Archiv Der Pharmazie</i> , 2021 , 354, e2000180	4.3	5
89	Structural and functional characterization of the Spo11 core complex. <i>Nature Structural and Molecular Biology</i> , 2021 , 28, 92-102	17.6	12
88	Mechanisms of hexameric helicases. <i>Critical Reviews in Biochemistry and Molecular Biology</i> , 2021 , 56, 621-639	639	1
87	Control of topoisomerase II activity and chemotherapeutic inhibition by TCA cycle metabolites. <i>Cell Chemical Biology</i> , 2021 ,	8.2	5
86	A Primase-Induced Conformational Switch Controls the Stability of the Bacterial Replisome. <i>Molecular Cell</i> , 2020 , 79, 140-154.e7	17.6	9
85	Modulated control of DNA supercoiling balance by the DNA-wrapping domain of bacterial gyrase. <i>Nucleic Acids Research</i> , 2020 , 48, 2035-2049	20.1	1
84	Molecular Basis for ATP-Hydrolysis-Driven DNA Translocation by the CMG Helicase of the Eukaryotic Replisome. <i>Cell Reports</i> , 2019 , 28, 2673-2688.e8	10.6	32
83	Synthesis, molecular docking, antimicrobial evaluation, and DNA cleavage assay of new thiadiazole/oxadiazole ciprofloxacin derivatives. <i>Monatshefte Für Chemie</i> , 2019 , 150, 1809-1824	1.4	4
82	New fluoroquinolones/nitric oxide donor hybrids: design, synthesis and antitubercular activity. <i>Medicinal Chemistry Research</i> , 2019 , 28, 1272-1283	2.2	6
81	Design, synthesis and molecular docking of new N-4-piperazinyl ciprofloxacin-triazole hybrids with potential antimicrobial activity. <i>Bioorganic Chemistry</i> , 2019 , 88, 102952	5.1	9
80	Caught in the Open: A Domain Insertion of M. Tuberculosis Gyrase Suppresses ATPase Dimerization. <i>Structure</i> , 2019 , 27, 561-563	5.2	
79	Tuning the sequence specificity of a transcription terminator. <i>Current Genetics</i> , 2019 , 65, 729-733	2.9	7
78	A complex suite of loci and elements in eukaryotic type II topoisomerases determine selective sensitivity to distinct poisoning agents. <i>Nucleic Acids Research</i> , 2019 , 47, 8163-8179	20.1	6

77	Garcinol and Related Polyisoprenylated Benzophenones as Topoisomerase II Inhibitors: Biochemical and Molecular Modeling Studies. <i>Journal of Natural Products</i> , 2019 , 82, 2768-2779	4.9	11
76	Synergistic Coordination of Chromatin Torsional Mechanics and Topoisomerase Activity. <i>Cell</i> , 2019 , 179, 619-631.e15	56.2	26
75	Cell Cycle-Dependent Control and Roles of DNA Topoisomerase II. <i>Genes</i> , 2019 , 10,	4.2	46
74	A new class of disordered elements controls DNA replication through initiator self-assembly. <i>ELife</i> , 2019 , 8,	8.9	46
73	Physical Basis for the Loading of a Bacterial Replicative Helicase onto DNA. <i>Molecular Cell</i> , 2019 , 74, 1731-1744.e45	17.8	45
72	Dynamic coupling between conformations and nucleotide states in DNA gyrase. <i>Nature Chemical Biology</i> , 2018 , 14, 565-574	11.7	8
71	Topoisomerase VI senses and exploits both DNA crossings and bends to facilitate strand passage. <i>ELife</i> , 2018 , 7,	8.9	10
70	Mechanism of Action of Mycobacterium tuberculosis Gyrase Inhibitors: A Novel Class of Gyrase Poisons. <i>ACS Infectious Diseases</i> , 2018 , 4, 1211-1222	5.5	13
69	Mechanism for the Regulated Control of Bacterial Transcription Termination by a Universal Adaptor Protein. <i>Molecular Cell</i> , 2018 , 71, 911-922.e4	17.6	41
68	Conformational control and DNA-binding mechanism of the metazoan origin recognition complex. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018 , 115, E5906-E5915	11.5	25
67	Mechanisms and regulation of DNA replication initiation in eukaryotes. <i>Critical Reviews in Biochemistry and Molecular Biology</i> , 2017 , 52, 107-144	8.7	93
66	Interdomain Communication of the Chd1 Chromatin Remodeler across the DNA Gyres of the Nucleosome. <i>Molecular Cell</i> , 2017 , 65, 447-459.e6	17.6	51
65	Mechanisms for initiating cellular DNA replication. <i>Science</i> , 2017 , 355,	33.3	115
64	Resveratrol: A novel type of topoisomerase II inhibitor. <i>Journal of Biological Chemistry</i> , 2017 , 292, 21011-21022.e8	5.4	28
63	Recognition of DNA Supercoil Geometry by Mycobacterium tuberculosis Gyrase. <i>Biochemistry</i> , 2017 , 56, 5440-5448	3.2	11
62	Molecular mechanisms of substrate-controlled ring dynamics and substepping in a nucleic acid-dependent hexameric motor. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016 , 113, E7691-E7700	11.5	34
61	Ligand-induced and small-molecule control of substrate loading in a hexameric helicase. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016 , 113, 13714-13719	11.5	26
60	Crystal structure and stability of gyrase-fluoroquinolone cleaved complexes from Mycobacterium tuberculosis. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016 , 113, 1706-13	11.5	112

59	Fluoroquinolone interactions with Mycobacterium tuberculosis gyrase: Enhancing drug activity against wild-type and resistant gyrase. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016 , 113, E839-46	11.5	56
58	The role of ATP-dependent machines in regulating genome topology. <i>Current Opinion in Structural Biology</i> , 2016 , 36, 85-96	8.1	18
57	: integration optimization, triage and analysis tool for the processing of XFEL diffraction images. <i>Journal of Applied Crystallography</i> , 2016 , 49, 1057-1064	3.8	17
56	Viral hijacking of a replicative helicase loader and its implications for helicase loading control and phage replication. <i>ELife</i> , 2016 , 5,	8.9	10
55	Crystal structure of the eukaryotic origin recognition complex. <i>Nature</i> , 2015 , 519, 321-6	50.4	90
54	Capture and X-ray diffraction studies of protein microcrystals in a microfluidic trap array. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2015 , 71, 928-40		51
53	An Atypical AAA+ ATPase Assembly Controls Efficient Transposition through DNA Remodeling and Transposase Recruitment. <i>Cell</i> , 2015 , 162, 860-71	56.2	26
52	A high-transparency, micro-patternable chip for X-ray diffraction analysis of microcrystals under native growth conditions. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2015 , 71, 1987-97		59
51	Ancient Origin of cGAS-STING Reveals Mechanism of Universal 2'5'-pppAmp Signaling. <i>Molecular Cell</i> , 2015 , 59, 891-903	17.6	144
50	Cdc45 (cell division cycle protein 45) guards the gate of the Eukaryote Replisome helicase stabilizing leading strand engagement. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015 , 112, E249-58	11.5	64
49	Structure-guided reprogramming of human cGAS dinucleotide linkage specificity. <i>Cell</i> , 2014 , 158, 1011-1021	19.2	81
48	Lethal synergy involving bicyclomycin: an approach for reviving old antibiotics. <i>Journal of Antimicrobial Chemotherapy</i> , 2014 , 69, 3227-35	5.1	21
47	Loading strategies of ring-shaped nucleic acid translocases and helicases. <i>Current Opinion in Structural Biology</i> , 2014 , 25, 16-24	8.1	26
46	DNA binding polarity, dimerization, and ATPase ring remodeling in the CMG helicase of the eukaryotic replisome. <i>ELife</i> , 2014 , 3, e03273	8.9	89
45	Distinct regions of the Escherichia coli ParC C-terminal domain are required for substrate discrimination by topoisomerase IV. <i>Journal of Molecular Biology</i> , 2013 , 425, 3029-45	6.5	15
44	Nucleotide and partner-protein control of bacterial replicative helicase structure and function. <i>Molecular Cell</i> , 2013 , 52, 844-54	17.6	37
43	The bacterial DnaC helicase loader is a DnaB ring breaker. <i>Cell</i> , 2013 , 153, 438-48	56.2	65
42	Mechanisms for initiating cellular DNA replication. <i>Annual Review of Biochemistry</i> , 2013 , 82, 25-54	29.1	144

41	The role of DNA bending in type IIA topoisomerase function. <i>Nucleic Acids Research</i> , 2013 , 41, 5444-56	20.1	35
40	A Meier-Gorlin syndrome mutation in a conserved C-terminal helix of Orc6 impedes origin recognition complex formation. <i>ELife</i> , 2013 , 2, e00882	8.9	37
39	Structure of a topoisomerase II-DNA-nucleotide complex reveals a new control mechanism for ATPase activity. <i>Nature Structural and Molecular Biology</i> , 2012 , 19, 1147-54	17.6	96
38	ATP binding controls distinct structural transitions of Escherichia coli DNA gyrase in complex with DNA. <i>Nature Structural and Molecular Biology</i> , 2012 , 19, 538-46, S1	17.6	50
37	Mechanisms for defining supercoiling set point of DNA gyrase orthologs: II. The shape of the GyrA subunit C-terminal domain (CTD) is not a sole determinant for controlling supercoiling efficiency. <i>Journal of Biological Chemistry</i> , 2012 , 287, 18645-54	5.4	41
36	Mechanisms for defining supercoiling set point of DNA gyrase orthologs: I. A nonconserved acidic C-terminal tail modulates Escherichia coli gyrase activity. <i>Journal of Biological Chemistry</i> , 2012 , 287, 18636-44	5.4	42
35	ATP-dependent conformational dynamics underlie the functional asymmetry of the replicative helicase from a minimalist eukaryote. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012 , 109, 11999-2004	11.5	57
34	All tangled up: how cells direct, manage and exploit topoisomerase function. <i>Nature Reviews Molecular Cell Biology</i> , 2011 , 12, 827-41	48.7	401
33	The structural basis for MCM2-7 helicase activation by GINS and Cdc45. <i>Nature Structural and Molecular Biology</i> , 2011 , 18, 471-7	17.6	255
32	The nuts and bolts of ring-translocase structure and mechanism. <i>Current Opinion in Structural Biology</i> , 2011 , 21, 240-8	8.1	98
31	DNA stretching by bacterial initiators promotes replication origin opening. <i>Nature</i> , 2011 , 478, 209-13	50.4	144
30	Molecular determinants of origin discrimination by Orc1 initiators in archaea. <i>Nucleic Acids Research</i> , 2011 , 39, 3621-31	20.1	40
29	The ancestral role of ATP hydrolysis in type II topoisomerases: prevention of DNA double-strand breaks. <i>Nucleic Acids Research</i> , 2011 , 39, 6327-39	20.1	48
28	A naturally chimeric type IIA topoisomerase in Aquifex aeolicus highlights an evolutionary path for the emergence of functional paralogs. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010 , 107, 22055-9	11.5	19
27	Building A Replication Fork: Structural Synergy And Molecular Crosstalk Between Bacterial Initiators And Helicase Loaders. <i>FASEB Journal</i> , 2010 , 24, 196.1	0.9	
26	Running in reverse: the structural basis for translocation polarity in hexameric helicases. <i>Cell</i> , 2009 , 139, 523-34	56.2	232
25	Structural frameworks for considering microbial protein- and nucleic acid-dependent motor ATPases. <i>Molecular Microbiology</i> , 2008 , 69, 1071-90	4.1	44
24	DNA topoisomerases: harnessing and constraining energy to govern chromosome topology. <i>Quarterly Reviews of Biophysics</i> , 2008 , 41, 41-101	7	344

23	Structural synergy and molecular crosstalk between bacterial helicase loaders and replication initiators. <i>Cell</i> , 2008 , 135, 623-34	56.2	94
22	Holoenzyme assembly and ATP-mediated conformational dynamics of topoisomerase VI. <i>Nature Structural and Molecular Biology</i> , 2007 , 14, 611-9	17.6	64
21	Structural basis for gate-DNA recognition and bending by type IIA topoisomerases. <i>Nature</i> , 2007 , 450, 1201-5	50.4	221
20	Replication origin recognition and deformation by a heterodimeric archaeal Orc1 complex. <i>Science</i> , 2007 , 317, 1210-3	33.3	122
19	Evolutionary relationships and structural mechanisms of AAA+ proteins. <i>Annual Review of Biophysics and Biomolecular Structure</i> , 2006 , 35, 93-114		571
18	Structural basis for ATP-dependent DnaA assembly and replication-origin remodeling. <i>Nature Structural and Molecular Biology</i> , 2006 , 13, 676-83	17.6	234
17	The structural basis for substrate specificity in DNA topoisomerase IV. <i>Journal of Molecular Biology</i> , 2005 , 351, 545-61	6.5	133
16	Structural dissection of ATP turnover in the prototypical GHL ATPase TopoVI. <i>Structure</i> , 2005 , 13, 873-82	5.2	63
15	Biochemical characterization of Cdc6/Orc1 binding to the replication origin of the euryarchaeon <i>Methanothermobacter thermoautotrophicus</i> . <i>Nucleic Acids Research</i> , 2004 , 32, 4821-32	20.1	48
14	The C-terminal domain of DNA gyrase A adopts a DNA-bending beta-pinwheel fold. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2004 , 101, 7293-8	11.5	131
13	The X-ray structure of the papillomavirus helicase in complex with its molecular matchmaker E2. <i>Genes and Development</i> , 2004 , 18, 1981-96	12.6	130
12	Micro-Crystallization. <i>Methods and Principles in Medicinal Chemistry</i> , 2003 , 235-255	0.4	
11	Structure of the topoisomerase VI-B subunit: implications for type II topoisomerase mechanism and evolution. <i>EMBO Journal</i> , 2003 , 22, 151-63	13	82
10	Structure of the Rho transcription terminator: mechanism of mRNA recognition and helicase loading. <i>Cell</i> , 2003 , 114, 135-46	56.2	206
9	Identification of residues in yeast Spo11p critical for meiotic DNA double-strand break formation. <i>Molecular and Cellular Biology</i> , 2002 , 22, 1106-15	4.8	84
8	Divalent metal cofactor binding in the kinetic folding trajectory of <i>Escherichia coli</i> ribonuclease HI. <i>Protein Science</i> , 2000 , 9, 1914-21	6.3	42
7	Structure and function of Cdc6/Cdc18: implications for origin recognition and checkpoint control. <i>Molecular Cell</i> , 2000 , 6, 637-48	17.6	193
6	Quaternary changes in topoisomerase II may direct orthogonal movement of two DNA strands. <i>Nature Structural Biology</i> , 1999 , 6, 322-6		123

5	Crystal structure of the N-terminal domain of the DnaB hexameric helicase. <i>Structure</i> , 1999 , 7, 691-8	5.2	72
4	The structural basis for terminator recognition by the Rho transcription termination factor. <i>Molecular Cell</i> , 1999 , 3, 487-93	17.6	120
3	Structure and mechanism of DNA topoisomerase II. <i>Nature</i> , 1996 , 379, 225-32	50.4	723
2	A new class of disordered elements controls DNA replication through initiator self-assembly		1
1	Structural and functional characterization of the Spo11 core complex		2