

James M Berger

List of Publications by Year in descending order

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95
papers

9,193
citations

44069

48
h-index

46799

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111
all docs

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docs citations

111
times ranked

7651
citing authors

#	ARTICLE	IF	CITATIONS
1	Control of topoisomerase II activity and chemotherapeutic inhibition by TCA cycle metabolites. <i>Cell Chemical Biology</i> , 2022, 29, 476-489.e6.	5.2	10
2	Biochemical methods to monitor loading and activation of hexameric helicases. <i>Methods in Enzymology</i> , 2022, , 143-152.	1.0	0
3	Synthesis and antimicrobial evaluation of new nitric oxide-donating fluoroquinolone/oxime hybrids. <i>Archiv Der Pharmazie</i> , 2021, 354, e2000180.	4.1	11
4	Structural and functional characterization of the Spo11 core complex. <i>Nature Structural and Molecular Biology</i> , 2021, 28, 92-102.	8.2	41
5	The molecular coupling between substrate recognition and ATP turnover in a ⁺ hexameric helicase loader. <i>ELife</i> , 2021, 10, .	6.0	7
6	Structural Mechanisms for Replicating DNA in Eukaryotes. <i>Annual Review of Biochemistry</i> , 2021, 90, 77-106.	11.1	29
7	Mechanisms of hexameric helicases. <i>Critical Reviews in Biochemistry and Molecular Biology</i> , 2021, 56, 621-639.	5.2	20
8	A Fluorescent Assay to Monitor Ligand-Dependent Closure of the Hexameric Rho Helicase Ring. <i>Methods in Molecular Biology</i> , 2021, 2209, 133-142.	0.9	2
9	Molecular determinants of phase separation for <i>Drosophila</i> DNA replication licensing factors. <i>ELife</i> , 2021, 10, .	6.0	11
10	A Primase-Induced Conformational Switch Controls the Stability of the Bacterial Replisome. <i>Molecular Cell</i> , 2020, 79, 140-154.e7.	9.7	18
11	Modulated control of DNA supercoiling balance by the DNA-wrapping domain of bacterial gyrase. <i>Nucleic Acids Research</i> , 2020, 48, 2035-2049.	14.5	3
12	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.	14.5	10
13	Garcinol and Related Polyisoprenylated Benzophenones as Topoisomerase II Inhibitors: Biochemical and Molecular Modeling Studies. <i>Journal of Natural Products</i> , 2019, 82, 2768-2779.	3.0	20
14	Synergistic Coordination of Chromatin Torsional Mechanics and Topoisomerase Activity. <i>Cell</i> , 2019, 179, 619-631.e15.	28.9	44
15	Cell Cycle-Dependent Control and Roles of DNA Topoisomerase II. <i>Genes</i> , 2019, 10, 859.	2.4	101
16	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.	6.4	74
17	Synthesis, molecular docking, antimicrobial evaluation, and DNA cleavage assay of new thiadiazole/oxadiazole ciprofloxacin derivatives. <i>Monatshefte Für Chemie</i> , 2019, 150, 1809-1824.	1.8	12
18	New fluoroquinolones/nitric oxide donor hybrids: design, synthesis and antitubercular activity. <i>Medicinal Chemistry Research</i> , 2019, 28, 1272-1283.	2.4	9

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19	Design, synthesis and molecular docking of new N-4-piperazinyl ciprofloxacin-triazole hybrids with potential antimicrobial activity. <i>Bioorganic Chemistry</i> , 2019, 88, 102952.	4.1	18
20	Caught in the Open: A Domain Insertion of M.Âtuberculosis Gyrase Suppresses ATPase Dimerization. <i>Structure</i> , 2019, 27, 561-563.	3.3	0
21	Tuning the sequence specificity of a transcription terminator. <i>Current Genetics</i> , 2019, 65, 729-733.	1.7	12
22	Physical Basis for the Loading of a Bacterial Replicative Helicase onto DNA. <i>Molecular Cell</i> , 2019, 74, 173-184.e4.	9.7	49
23	A new class of disordered elements controls DNA replication through initiator self-assembly. <i>ELife</i> , 2019, 8, .	6.0	92
24	Dynamic coupling between conformations and nucleotide states in DNA gyrase. <i>Nature Chemical Biology</i> , 2018, 14, 565-574.	8.0	18
25	Topoisomerase VI senses and exploits both DNA crossings and bends to facilitate strand passage. <i>ELife</i> , 2018, 7, .	6.0	19
26	Mechanism of Action of <i>Mycobacterium tuberculosis</i> Gyrase Inhibitors: A Novel Class of Gyrase Poisons. <i>ACS Infectious Diseases</i> , 2018, 4, 1211-1222.	3.8	23
27	Mechanism for the Regulated Control of Bacterial Transcription Termination by a Universal Adaptor Protein. <i>Molecular Cell</i> , 2018, 71, 911-922.e4.	9.7	65
28	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.	7.1	34
29	Mechanisms and regulation of DNA replication initiation in eukaryotes. <i>Critical Reviews in Biochemistry and Molecular Biology</i> , 2017, 52, 107-144.	5.2	140
30	Interdomain Communication of the Chd1 Chromatin Remodeler across the DNA Gyres of the Nucleosome. <i>Molecular Cell</i> , 2017, 65, 447-459.e6.	9.7	67
31	Mechanisms for initiating cellular DNA replication. <i>Science</i> , 2017, 355, .	12.6	171
32	Resveratrol: A novel type of topoisomerase II inhibitor. <i>Journal of Biological Chemistry</i> , 2017, 292, 21011-21022.	3.4	45
33	Recognition of DNA Supercoil Geometry by <i>Mycobacterium tuberculosis</i> Gyrase. <i>Biochemistry</i> , 2017, 56, 5440-5448.	2.5	17
34	Mechanisms and Functional Diversity of Macromolecular Remodeling by ATP-Dependent Motors. <i>Journal of Molecular Biology</i> , 2016, 428, 1819-1821.	4.2	0
35	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.	7.1	48
36	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.	7.1	33

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37	Crystal structure and stability of gyrase-fluoroquinolone cleaved complexes from <i>Mycobacterium tuberculosis</i> . Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, 1706-1713.	7.1	164
38	Fluoroquinolone interactions with <i>Mycobacterium tuberculosis</i> gyrase: Enhancing drug activity against wild-type and resistant gyrase. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, E839-46.	7.1	73
39	The role of ATP-dependent machines in regulating genome topology. Current Opinion in Structural Biology, 2016, 36, 85-96.	5.7	19
40	IOTA: integration optimization, triage and analysis tool for the processing of XFEL diffraction images. Journal of Applied Crystallography, 2016, 49, 1057-1064.	4.5	17
41	Viral hijacking of a replicative helicase loader and its implications for helicase loading control and phage replication. ELife, 2016, 5, .	6.0	16
42	Cdc45 (cell division cycle protein 45) guards the gate of the Eukaryote Replisome helicase stabilizing leading strand engagement. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, E249-58.	7.1	78
43	Crystal structure of the eukaryotic origin recognition complex. Nature, 2015, 519, 321-326.	27.8	109
44	Capture and X-ray diffraction studies of protein microcrystals in a microfluidic trap array. Acta Crystallographica Section D: Biological Crystallography, 2015, 71, 928-940.	2.5	64
45	An Atypical AAA+ ATPase Assembly Controls Efficient Transposition through DNA Remodeling and Transposase Recruitment. Cell, 2015, 162, 860-871.	28.9	38
46	A high-transparency, micro-patternable chip for X-ray diffraction analysis of microcrystals under native growth conditions. Acta Crystallographica Section D: Biological Crystallography, 2015, 71, 1987-1997.	2.5	73
47	Ancient Origin of cGAS-STING Reveals Mechanism of Universal cGAMP Signaling. Molecular Cell, 2015, 59, 891-903.	9.7	224
48	Loading strategies of ring-shaped nucleic acid translocases and helicases. Current Opinion in Structural Biology, 2014, 25, 16-24.	5.7	33
49	Structure-Guided Reprogramming of Human cGAS Dinucleotide Linkage Specificity. Cell, 2014, 158, 1011-1021.	28.9	111
50	Lethal synergy involving bicyclomycin: an approach for reviving old antibiotics. Journal of Antimicrobial Chemotherapy, 2014, 69, 3227-3235.	3.0	29
51	DNA binding polarity, dimerization, and ATPase ring remodeling in the CMG helicase of the eukaryotic replisome. ELife, 2014, 3, e03273.	6.0	103
52	Distinct Regions of the Escherichia coli ParC C-Terminal Domain Are Required for Substrate Discrimination by Topoisomerase IV. Journal of Molecular Biology, 2013, 425, 3029-3045.	4.2	18
53	Nucleotide and Partner-Protein Control of Bacterial Replicative Helicase Structure and Function. Molecular Cell, 2013, 52, 844-854.	9.7	57
54	The Bacterial DnaC Helicase Loader Is a DnaB Ring Breaker. Cell, 2013, 153, 438-448.	28.9	89

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55	Mechanisms for Initiating Cellular DNA Replication. Annual Review of Biochemistry, 2013, 82, 25-54.	11.1	161
56	The role of DNA bending in type IIA topoisomerase function. Nucleic Acids Research, 2013, 41, 5444-5456.	14.5	46
57	A Meier-Gorlin syndrome mutation in a conserved C-terminal helix of Orc6 impedes origin recognition complex formation. ELife, 2013, 2, e00882.	6.0	45
58	Mechanisms for Defining Supercoiling Set Point of DNA Gyrase Orthologs. Journal of Biological Chemistry, 2012, 287, 18636-18644.	3.4	51
59	ATP-dependent conformational dynamics underlie the functional asymmetry of the replicative helicase from a minimalist eukaryote. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 11999-12004.	7.1	65
60	Structure of a topoisomerase IIâ€“DNAâ€“nucleotide complex reveals a new control mechanism for ATPase activity. Nature Structural and Molecular Biology, 2012, 19, 1147-1154.	8.2	147
61	ATP binding controls distinct structural transitions of Escherichia coli DNA gyrase in complex with DNA. Nature Structural and Molecular Biology, 2012, 19, 538-546.	8.2	61
62	Mechanisms for Defining Supercoiling Set Point of DNA Gyrase Orthologs. Journal of Biological Chemistry, 2012, 287, 18645-18654.	3.4	46
63	DNA stretching by bacterial initiators promotes replication origin opening. Nature, 2011, 478, 209-213.	27.8	172
64	All tangled up: how cells direct, manage and exploit topoisomerase function. Nature Reviews Molecular Cell Biology, 2011, 12, 827-841.	37.0	527
65	The structural basis for MCM2â€“7 helicase activation by GINS and Cdc45. Nature Structural and Molecular Biology, 2011, 18, 471-477.	8.2	290
66	The nuts and bolts of ring-translocase structure and mechanism. Current Opinion in Structural Biology, 2011, 21, 240-248.	5.7	122
67	Molecular determinants of origin discrimination by Orc1 initiators in archaea. Nucleic Acids Research, 2011, 39, 3621-3631.	14.5	42
68	The ancestral role of ATP hydrolysis in type II topoisomerases: prevention of DNA double-strand breaks. Nucleic Acids Research, 2011, 39, 6327-6339.	14.5	62
69	A naturally chimeric type IIA topoisomerase in <i>Aquifex aeolicus</i> highlights an evolutionary path for the emergence of functional paralogs. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 22055-22059.	7.1	20
70	Building A Replication Fork: Structural Synergy And Molecular Crosstalk Between Bacterial Initiators And Helicase Loaders. FASEB Journal, 2010, 24, 196.1.	0.5	0
71	Running in Reverse: The Structural Basis for Translocation Polarity in Hexameric Helicases. Cell, 2009, 139, 523-534.	28.9	274
72	Structural frameworks for considering microbial proteinâ€“and nucleic acidâ€“dependent motor ATPases. Molecular Microbiology, 2008, 69, 1071-1090.	2.5	52

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73	DNA topoisomerases: harnessing and constraining energy to govern chromosome topology. Quarterly Reviews of Biophysics, 2008, 41, 41-101.	5.7	398
74	Structural Synergy and Molecular Crosstalk between Bacterial Helicase Loaders and Replication Initiators. Cell, 2008, 135, 623-634.	28.9	107
75	Replication Origin Recognition and Deformation by a Heterodimeric Archaeal Orc1 Complex. Science, 2007, 317, 1210-1213.	12.6	131
76	Holoenzyme assembly and ATP-mediated conformational dynamics of topoisomerase VI. Nature Structural and Molecular Biology, 2007, 14, 611-619.	8.2	86
77	Structural basis for gate-DNA recognition and bending by type IIA topoisomerases. Nature, 2007, 450, 1201-1205.	27.8	261
78	EVOLUTIONARY RELATIONSHIPS AND STRUCTURAL MECHANISMS OF AAA+ PROTEINS. Annual Review of Biophysics and Biomolecular Structure, 2006, 35, 93-114.	18.3	692
79	Structural basis for ATP-dependent DnaA assembly and replication-origin remodeling. Nature Structural and Molecular Biology, 2006, 13, 676-683.	8.2	291
80	Structural Dissection of ATP Turnover in the Prototypical GHL ATPase TopoVI. Structure, 2005, 13, 873-882.	3.3	69
81	The Structural Basis for Substrate Specificity in DNA Topoisomerase IV. Journal of Molecular Biology, 2005, 351, 545-561.	4.2	147
82	Biochemical characterization of Cdc6/Orc1 binding to the replication origin of the euryarchaeon Methanothermobacter thermoautotrophicus. Nucleic Acids Research, 2004, 32, 4821-4832.	14.5	55
83	The C-terminal domain of DNA gyrase A adopts a DNA-bending \hat{A} -pinwheel fold. Proceedings of the National Academy of Sciences of the United States of America, 2004, 101, 7293-7298.	7.1	148
84	The X-ray structure of the papillomavirus helicase in complex with its molecular matchmaker E2. Genes and Development, 2004, 18, 1981-1996.	5.9	145
85	Structure of the topoisomerase VI-B subunit: implications for type II topoisomerase mechanism and evolution. EMBO Journal, 2003, 22, 151-163.	7.8	98
86	Structure of the Rho Transcription Terminator. Cell, 2003, 114, 135-146.	28.9	234
87	Identification of Residues in Yeast Spo11p Critical for Meiotic DNA Double-Strand Break Formation. Molecular and Cellular Biology, 2002, 22, 1106-1115.	2.3	97
88	Primus inter pares (first among equals)., 2001, 8, 2-4.		17
89	Divalent metal cofactor binding in the kinetic folding trajectory of <i>Escherichia coli</i> ribonuclease HI. Protein Science, 2000, 9, 1914-1921.	7.6	49
90	Structure and Function of Cdc6/Cdc18. Molecular Cell, 2000, 6, 637-648.	9.7	211

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91	Enzymes that push DNA around. , 1999, 6, 900-902.		12
92	Quaternary changes in topoisomerase II may direct orthogonal movement of two DNA strands. Nature Structural Biology, 1999, 6, 322-326.	9.7	137
93	Crystal structure of the N-terminal domain of the DnaB hexameric helicase. Structure, 1999, 7, 691-698.	3.3	81
94	The Structural Basis for Terminator Recognition by the Rho Transcription Termination Factor. Molecular Cell, 1999, 3, 487-493.	9.7	134
95	Structure and mechanism of DNA topoisomerase II. Nature, 1996, 379, 225-232.	27.8	813