

# James M Berger

## List of Publications by Year in descending order

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95  
papers

9,193  
citations

44069

48  
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46799

89  
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111  
all docs

111  
docs citations

111  
times ranked

7651  
citing authors

#	ARTICLE	IF	CITATIONS
1	Structure and mechanism of DNA topoisomerase II. <i>Nature</i> , 1996, 379, 225-232.	27.8	813
2	EVOLUTIONARY RELATIONSHIPS AND STRUCTURAL MECHANISMS OF AAA+ PROTEINS. <i>Annual Review of Biophysics and Biomolecular Structure</i> , 2006, 35, 93-114.	18.3	692
3	All tangled up: how cells direct, manage and exploit topoisomerase function. <i>Nature Reviews Molecular Cell Biology</i> , 2011, 12, 827-841.	37.0	527
4	DNA topoisomerases: harnessing and constraining energy to govern chromosome topology. <i>Quarterly Reviews of Biophysics</i> , 2008, 41, 41-101.	5.7	398
5	Structural basis for ATP-dependent DnaA assembly and replication-origin remodeling. <i>Nature Structural and Molecular Biology</i> , 2006, 13, 676-683.	8.2	291
6	The structural basis for MCM2â€™7 helicase activation by GINS and Cdc45. <i>Nature Structural and Molecular Biology</i> , 2011, 18, 471-477.	8.2	290
7	Running in Reverse: The Structural Basis for Translocation Polarity in Hexameric Helicases. <i>Cell</i> , 2009, 139, 523-534.	28.9	274
8	Structural basis for gate-DNA recognition and bending by type IIA topoisomerases. <i>Nature</i> , 2007, 450, 1201-1205.	27.8	261
9	Structure of the Rho Transcription Terminator. <i>Cell</i> , 2003, 114, 135-146.	28.9	234
10	Ancient Origin of cGAS-STING Reveals Mechanism of Universal 2â€™3â€™ cGAMP Signaling. <i>Molecular Cell</i> , 2015, 59, 891-903.	9.7	224
11	Structure and Function of Cdc6/Cdc18. <i>Molecular Cell</i> , 2000, 6, 637-648.	9.7	211
12	DNA stretching by bacterial initiators promotes replication origin opening. <i>Nature</i> , 2011, 478, 209-213.	27.8	172
13	Mechanisms for initiating cellular DNA replication. <i>Science</i> , 2017, 355, .	12.6	171
14	Crystal structure and stability of gyraseâ€™fluoroquinolone cleaved complexes from <i>Mycobacterium tuberculosis</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, 1706-1713.	7.1	164
15	Mechanisms for Initiating Cellular DNA Replication. <i>Annual Review of Biochemistry</i> , 2013, 82, 25-54.	11.1	161
16	The C-terminal domain of DNA gyrase A adopts a DNA-bending Å-pinwheel fold. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2004, 101, 7293-7298.	7.1	148
17	The Structural Basis for Substrate Specificity in DNA Topoisomerase IV. <i>Journal of Molecular Biology</i> , 2005, 351, 545-561.	4.2	147
18	Structure of a topoisomerase IIâ€™DNAâ€™nucleotide complex reveals a new control mechanism for ATPase activity. <i>Nature Structural and Molecular Biology</i> , 2012, 19, 1147-1154.	8.2	147

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19	The X-ray structure of the papillomavirus helicase in complex with its molecular matchmaker E2. <i>Genes and Development</i> , 2004, 18, 1981-1996.	5.9	145
20	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
21	Quaternary changes in topoisomerase II may direct orthogonal movement of two DNA strands. <i>Nature Structural Biology</i> , 1999, 6, 322-326.	9.7	137
22	The Structural Basis for Terminator Recognition by the Rho Transcription Termination Factor. <i>Molecular Cell</i> , 1999, 3, 487-493.	9.7	134
23	Replication Origin Recognition and Deformation by a Heterodimeric Archaeal Orc1 Complex. <i>Science</i> , 2007, 317, 1210-1213.	12.6	131
24	The nuts and bolts of ring-translocase structure and mechanism. <i>Current Opinion in Structural Biology</i> , 2011, 21, 240-248.	5.7	122
25	Structure-Guided Reprogramming of Human cGAS Dinucleotide Linkage Specificity. <i>Cell</i> , 2014, 158, 1011-1021.	28.9	111
26	Crystal structure of the eukaryotic origin recognition complex. <i>Nature</i> , 2015, 519, 321-326.	27.8	109
27	Structural Synergy and Molecular Crosstalk between Bacterial Helicase Loaders and Replication Initiators. <i>Cell</i> , 2008, 135, 623-634.	28.9	107
28	DNA binding polarity, dimerization, and ATPase ring remodeling in the CMG helicase of the eukaryotic replisome. <i>ELife</i> , 2014, 3, e03273.	6.0	103
29	Cell Cycle-Dependent Control and Roles of DNA Topoisomerase II. <i>Genes</i> , 2019, 10, 859.	2.4	101
30	Structure of the topoisomerase VI-B subunit: implications for type II topoisomerase mechanism and evolution. <i>EMBO Journal</i> , 2003, 22, 151-163.	7.8	98
31	Identification of Residues in Yeast Spo11p Critical for Meiotic DNA Double-Strand Break Formation. <i>Molecular and Cellular Biology</i> , 2002, 22, 1106-1115.	2.3	97
32	A new class of disordered elements controls DNA replication through initiator self-assembly. <i>ELife</i> , 2019, 8, .	6.0	92
33	The Bacterial DnaC Helicase Loader Is a DnaB Ring Breaker. <i>Cell</i> , 2013, 153, 438-448.	28.9	89
34	Holoenzyme assembly and ATP-mediated conformational dynamics of topoisomerase VI. <i>Nature Structural and Molecular Biology</i> , 2007, 14, 611-619.	8.2	86
35	Crystal structure of the N-terminal domain of the DnaB hexameric helicase. <i>Structure</i> , 1999, 7, 691-698.	3.3	81
36	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.	7.1	78

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37	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
38	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, 1987-1997.	2.5	73
39	Fluoroquinolone interactions with <i>Mycobacterium tuberculosis</i> 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.	7.1	73
40	Structural Dissection of ATP Turnover in the Prototypical GH1 ATPase TopoVI. <i>Structure</i> , 2005, 13, 873-882.	3.3	69
41	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
42	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, 11999-12004.	7.1	65
43	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
44	Capture and X-ray diffraction studies of protein microcrystals in a microfluidic trap array. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2015, 71, 928-940.	2.5	64
45	The ancestral role of ATP hydrolysis in type II topoisomerases: prevention of DNA double-strand breaks. <i>Nucleic Acids Research</i> , 2011, 39, 6327-6339.	14.5	62
46	ATP binding controls distinct structural transitions of <i>Escherichia coli</i> DNA gyrase in complex with DNA. <i>Nature Structural and Molecular Biology</i> , 2012, 19, 538-546.	8.2	61
47	Nucleotide and Partner-Protein Control of Bacterial Replicative Helicase Structure and Function. <i>Molecular Cell</i> , 2013, 52, 844-854.	9.7	57
48	Biochemical characterization of Cdc6/Orc1 binding to the replication origin of the euryarchaeon <i>Methanothermobacter thermoautotrophicus</i> . <i>Nucleic Acids Research</i> , 2004, 32, 4821-4832.	14.5	55
49	Structural frameworks for considering microbial protein- and nucleic acid-dependent motor ATPases. <i>Molecular Microbiology</i> , 2008, 69, 1071-1090.	2.5	52
50	Mechanisms for Defining Supercoiling Set Point of DNA Gyrase Orthologs. <i>Journal of Biological Chemistry</i> , 2012, 287, 18636-18644.	3.4	51
51	Divalent metal cofactor binding in the kinetic folding trajectory of <i>Escherichia coli</i> ribonuclease HI. <i>Protein Science</i> , 2000, 9, 1914-1921.	7.6	49
52	Physical Basis for the Loading of a Bacterial Replicative Helicase onto DNA. <i>Molecular Cell</i> , 2019, 74, 173-184.e4.	9.7	49
53	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
54	Mechanisms for Defining Supercoiling Set Point of DNA Gyrase Orthologs. <i>Journal of Biological Chemistry</i> , 2012, 287, 18645-18654.	3.4	46

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55	The role of DNA bending in type IIA topoisomerase function. <i>Nucleic Acids Research</i> , 2013, 41, 5444-5456.	14.5	46
56	Resveratrol: A novel type of topoisomerase II inhibitor. <i>Journal of Biological Chemistry</i> , 2017, 292, 21011-21022.	3.4	45
57	A Meier-Gorlin syndrome mutation in a conserved C-terminal helix of Orc6 impedes origin recognition complex formation. <i>ELife</i> , 2013, 2, e00882.	6.0	45
58	Synergistic Coordination of Chromatin Torsional Mechanics and Topoisomerase Activity. <i>Cell</i> , 2019, 179, 619-631.e15.	28.9	44
59	Molecular determinants of origin discrimination by Orc1 initiators in archaea. <i>Nucleic Acids Research</i> , 2011, 39, 3621-3631.	14.5	42
60	Structural and functional characterization of the Spo11 core complex. <i>Nature Structural and Molecular Biology</i> , 2021, 28, 92-102.	8.2	41
61	An Atypical AAA+ ATPase Assembly Controls Efficient Transposition through DNA Remodeling and Transposase Recruitment. <i>Cell</i> , 2015, 162, 860-871.	28.9	38
62	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
63	Loading strategies of ring-shaped nucleic acid translocases and helicases. <i>Current Opinion in Structural Biology</i> , 2014, 25, 16-24.	5.7	33
64	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
65	Lethal synergy involving bicyclomycin: an approach for reviving old antibiotics. <i>Journal of Antimicrobial Chemotherapy</i> , 2014, 69, 3227-3235.	3.0	29
66	Structural Mechanisms for Replicating DNA in Eukaryotes. <i>Annual Review of Biochemistry</i> , 2021, 90, 77-106.	11.1	29
67	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
68	A naturally chimeric type IIA topoisomerase in <i>Aquifex aeolicus</i> 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, 22055-22059.	7.1	20
69	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
70	Mechanisms of hexameric helicases. <i>Critical Reviews in Biochemistry and Molecular Biology</i> , 2021, 56, 621-639.	5.2	20
71	The role of ATP-dependent machines in regulating genome topology. <i>Current Opinion in Structural Biology</i> , 2016, 36, 85-96.	5.7	19
72	Topoisomerase VI senses and exploits both DNA crossings and bends to facilitate strand passage. <i>ELife</i> , 2018, 7, .	6.0	19

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73	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, 3029-3045.	4.2	18
74	Dynamic coupling between conformations and nucleotide states in DNA gyrase. <i>Nature Chemical Biology</i> , 2018, 14, 565-574.	8.0	18
75	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
76	A Primase-Induced Conformational Switch Controls the Stability of the Bacterial Replisome. <i>Molecular Cell</i> , 2020, 79, 140-154.e7.	9.7	18
77	Primus inter pares (first among equals). , 2001, 8, 2-4.		17
78	Recognition of DNA Supercoil Geometry by Mycobacterium tuberculosis Gyrase. <i>Biochemistry</i> , 2017, 56, 5440-5448.	2.5	17
79	IOTA: integration optimization, triage and analysis tool for the processing of XFEL diffraction images. <i>Journal of Applied Crystallography</i> , 2016, 49, 1057-1064.	4.5	17
80	Viral hijacking of a replicative helicase loader and its implications for helicase loading control and phage replication. <i>ELife</i> , 2016, 5, .	6.0	16
81	Enzymes that push DNA around. , 1999, 6, 900-902.		12
82	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
83	Tuning the sequence specificity of a transcription terminator. <i>Current Genetics</i> , 2019, 65, 729-733.	1.7	12
84	Synthesis and antimicrobial evaluation of new nitric oxide-donating fluoroquinolone/oxime hybrids. <i>Archiv Der Pharmazie</i> , 2021, 354, e2000180.	4.1	11
85	Molecular determinants of phase separation for Drosophila DNA replication licensing factors. <i>ELife</i> , 2021, 10, .	6.0	11
86	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
87	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
88	New fluoroquinolones/nitric oxide donor hybrids: design, synthesis and antitubercular activity. <i>Medicinal Chemistry Research</i> , 2019, 28, 1272-1283.	2.4	9
89	The molecular coupling between substrate recognition and ATP turnover in a AAA+ hexameric helicase loader. <i>ELife</i> , 2021, 10, .	6.0	7
90	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

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91	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
92	Mechanisms and Functional Diversity of Macromolecular Remodeling by ATP-Dependent Motors. <i>Journal of Molecular Biology</i> , 2016, 428, 1819-1821.	4.2	0
93	Caught in the Open: A Domain Insertion of M.Âtuberculosis Gyrase Suppresses ATPase Dimerization. <i>Structure</i> , 2019, 27, 561-563.	3.3	0
94	Building A Replication Fork: Structural Synergy And Molecular Crosstalk Between Bacterial Initiators And Helicase Loaders. <i>FASEB Journal</i> , 2010, 24, 196.1.	0.5	0
95	Biochemical methods to monitor loading and activation of hexameric helicases. <i>Methods in Enzymology</i> , 2022, , 143-152.	1.0	0