

James L Keck

List of Publications by Year in descending order

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107
papers

5,025
citations

76326

40
h-index

98798

67
g-index

114
all docs

114
docs citations

114
times ranked

4140
citing authors

#	ARTICLE	IF	CITATIONS
1	Natural Transformation Protein ComFA Exhibits Single-Stranded DNA Translocase Activity. <i>Journal of Bacteriology</i> , 2022, 204, JB0051821.	2.2	2
2	Use of an unnatural amino acid to map helicase/DNA interfaces via photoactivated crosslinking. <i>Methods in Enzymology</i> , 2022, , .	1.0	1
3	Mismatch discrimination and sequence bias during end-joining by DNA ligases. <i>Nucleic Acids Research</i> , 2022, 50, 4647-4658.	14.5	12
4	X-ray crystal structure of the Escherichia coli RadD DNA repair protein bound to ADP reveals a novel zinc ribbon domain. <i>PLoS ONE</i> , 2022, 17, e0266031.	2.5	5
5	The molecular coupling between substrate recognition and ATP turnover in a ⁺ hexameric helicase loader. <i>ELife</i> , 2021, 10, .	6.0	7
6	Examination of the roles of a conserved motif in the PriA helicase in structure-specific DNA unwinding and processivity. <i>PLoS ONE</i> , 2021, 16, e0255409.	2.5	2
7	Escherichia coli Δ 12 has two distinguishable PriA \rightarrow PriB replication restart pathways. <i>Molecular Microbiology</i> , 2021, 116, 1140-1150.	2.5	9
8	Minor Alterations in Core Promoter Element Positioning Reveal Functional Plasticity of a Bacterial Transcription Factor. <i>MBio</i> , 2021, 12, e0275321.	4.1	1
9	Interaction with single-stranded DNA-binding protein localizes ribonuclease HI to DNA replication forks and facilitates R-loop removal. <i>Molecular Microbiology</i> , 2020, 114, 495-509.	2.5	14
10	Development of a single-stranded DNA-binding protein fluorescent fusion toolbox. <i>Nucleic Acids Research</i> , 2020, 48, 6053-6067.	14.5	16
11	Molecular Mechanism of Regulation of the Purine Salvage Enzyme XPRT by the Alarmones pppGpp, ppGpp, and pGpp. <i>Journal of Molecular Biology</i> , 2020, 432, 4108-4126.	4.2	31
12	Antigenic Variation in <i>Neisseria gonorrhoeae</i> Occurs Independently of RecQ-Mediated Unwinding of the <i>pilE</i> G Quadruplex. <i>Journal of Bacteriology</i> , 2020, 202, .	2.2	9
13	E. coli Rep helicase and RecA recombinase unwind G4 DNA and are important for resistance to G4-stabilizing ligands. <i>Nucleic Acids Research</i> , 2020, 48, 6640-6653.	14.5	24
14	Function of a strand-separation pin element in the PriA DNA replication restart helicase. <i>Journal of Biological Chemistry</i> , 2019, 294, 2801-5614.	3.4	19
15	Structural Mechanisms of Cooperative DNA Binding by Bacterial Single-Stranded DNA-Binding Proteins. <i>Journal of Molecular Biology</i> , 2019, 431, 178-195.	4.2	31
16	Practical Model Selection for Prospective Virtual Screening. <i>Journal of Chemical Information and Modeling</i> , 2019, 59, 282-293.	5.4	46
17	Evolution of (p)ppGpp-HPRT regulation through diversification of an allosteric oligomeric interaction. <i>ELife</i> , 2019, 8, .	6.0	40
18	A Potential Specificity Code for B. subtilis SsbA and SsbB Quaternary Structures. <i>FASEB Journal</i> , 2019, 33, 493.7.	0.5	0

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19	Mechanisms of bacterial DNA replication restart. <i>Nucleic Acids Research</i> , 2018, 46, 504-519.	14.5	67
20	A High-Throughput Screening Strategy to Identify Inhibitors of SSB Protein-Protein Interactions in an Academic Screening Facility. <i>SLAS Discovery</i> , 2018, 23, 94-101.	2.7	23
21	A guanine-flipping and sequestration mechanism for G-quadruplex unwinding by RecQ helicases. <i>Nature Communications</i> , 2018, 9, 4201.	12.8	46
22	Structure-specific DNA replication-fork recognition directs helicase and replication restart activities of the PriA helicase. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, E9075-E9084.	7.1	30
23	Development of Protein-Protein Interaction Inhibitors for the Treatment of Infectious Diseases. <i>Advances in Protein Chemistry and Structural Biology</i> , 2018, 111, 197-222.	2.3	15
24	Single molecule kinetics uncover roles for E. coli RecQ DNA helicase domains and interaction with SSB. <i>Nucleic Acids Research</i> , 2018, 46, 8500-8515.	14.5	30
25	Structural and Cellular Mechanisms of DNA Replication Restart in <i>Escherichia coli</i> . <i>FASEB Journal</i> , 2018, 32, 786.9.	0.5	0
26	An aromatic-rich loop couples DNA binding and ATP hydrolysis in the PriA DNA helicase. <i>Nucleic Acids Research</i> , 2016, 44, gkw690.	14.5	13
27	Structure and Function of the PriC DNA Replication Restart Protein. <i>Journal of Biological Chemistry</i> , 2016, 291, 18384-18396.	3.4	17
28	A High-Throughput Screening Strategy to Identify Protein-Protein Interaction Inhibitors That Block the Fanconi Anemia DNA Repair Pathway. <i>Journal of Biomolecular Screening</i> , 2016, 21, 626-633.	2.6	29
29	Structural and Functional Studies of <i>H. seropedicae</i> RecA Protein - Insights into the Polymerization of RecA Protein as Nucleoprotein Filament. <i>PLoS ONE</i> , 2016, 11, e0159871.	2.5	7
30	Molecular Mechanism and Evolution of Guanylate Kinase Regulation by (p)ppGpp. <i>Molecular Cell</i> , 2015, 57, 735-749.	9.7	88
31	Interaction with Single-stranded DNA-binding Protein Stimulates <i>Escherichia coli</i> Ribonuclease HI Enzymatic Activity. <i>Journal of Biological Chemistry</i> , 2015, 290, 14626-14636.	3.4	61
32	Structural mechanisms of DNA binding and unwinding in bacterial RecQ helicases. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 4292-4297.	7.1	58
33	Structural mechanisms of PriA-mediated DNA replication restart. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 1373-1378.	7.1	94
34	RecD2 Helicase Limits Replication Fork Stress in <i>Bacillus subtilis</i> . <i>Journal of Bacteriology</i> , 2014, 196, 1359-1368.	2.2	27
35	Grip it and rip it: Structural mechanisms of DNA helicase substrate binding and unwinding. <i>Protein Science</i> , 2014, 23, 1498-1507.	7.6	20
36	The BLM dissolvasome in DNA replication and repair. <i>Cellular and Molecular Life Sciences</i> , 2013, 70, 4067-4084.	5.4	92

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37	<i>Neisseria gonorrhoeae</i> RecQ Helicase HRDC Domains Are Essential for Efficient Binding and Unwinding of the <i>pilE</i> Guanine Quartet Structure Required for Pilin Antigenic Variation. <i>Journal of Bacteriology</i> , 2013, 195, 2255-2261.	2.2	29
38	PriC-mediated DNA Replication Restart Requires PriC Complex Formation with the Single-stranded DNA-binding Protein. <i>Journal of Biological Chemistry</i> , 2013, 288, 17569-17578.	3.4	47
39	The <i>Deinococcus radiodurans</i> DR1245 Protein, a DdrB Partner Homologous to YbjN Proteins and Reminiscent of Type III Secretion System Chaperones. <i>PLoS ONE</i> , 2013, 8, e56558.	2.5	23
40	Protein Interactions in Genome Maintenance as Novel Antibacterial Targets. <i>PLoS ONE</i> , 2013, 8, e58765.	2.5	37
41	Indispensable Replication Restart Helicase PriA Aids Bacterial Survival: A SMART Team Story. <i>FASEB Journal</i> , 2013, 27, lb201.	0.5	0
42	Genetic recombination in <i>Bacillus subtilis</i> : a division of labor between two single-strand DNA-binding proteins. <i>Nucleic Acids Research</i> , 2012, 40, 5546-5559.	14.5	90
43	Structure and Cellular Dynamics of <i>Deinococcus radiodurans</i> Single-stranded DNA (ssDNA)-binding Protein (SSB)-DNA Complexes. <i>Journal of Biological Chemistry</i> , 2012, 287, 22123-22132.	3.4	49
44	Defining the molecular interface that connects the Fanconi anemia protein FANCM to the Bloom syndrome dissolvosome. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 4437-4442.	7.1	56
45	Binding Mechanism of Metal-Dependent NTP Substrates and Stringent-Response Alarmones to Bacterial DnaG-Type Primases. <i>Structure</i> , 2012, 20, 1478-1489.	3.3	73
46	Structural and Kinetic Isotope Effect Studies of Nicotinamidase (Pnc1) from <i>Saccharomyces cerevisiae</i> . <i>Biochemistry</i> , 2012, 51, 243-256.	2.5	18
47	Structural basis for the interaction between <i>E. coli</i> RNase HI and SSB. <i>FASEB Journal</i> , 2012, 26, lb87.	0.5	0
48	Molecular Interactions in PriC-Mediated DNA Replication Restart. <i>FASEB Journal</i> , 2012, 26, lb88.	0.5	0
49	The primase domain of PfPrex is a proteolytically matured, essential enzyme of the apicoplast. <i>Molecular and Biochemical Parasitology</i> , 2011, 180, 69-75.	1.1	21
50	Mechanism of Exonuclease I stimulation by the single-stranded DNA-binding protein. <i>Nucleic Acids Research</i> , 2011, 39, 6536-6545.	14.5	20
51	Structure and Biochemical Activities of <i>Escherichia coli</i> MgsA. <i>Journal of Biological Chemistry</i> , 2011, 286, 12075-12085.	3.4	29
52	Creating Directed Double-strand Breaks with the Ref Protein. <i>Journal of Biological Chemistry</i> , 2011, 286, 8240-8251.	3.4	16
53	Structure of the SSB-DNA polymerase III interface and its role in DNA replication. <i>EMBO Journal</i> , 2011, 30, 4236-4247.	7.8	132
54	Primase: a SMART team adventure through DNA replication. <i>FASEB Journal</i> , 2011, 25, lb164.	0.5	0

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55	Structure and Cellular Roles of the RMI Core Complex from the Bloom Syndrome Dissolvasome. <i>Structure</i> , 2010, 18, 1149-1158.	3.3	33
56	X-ray Crystal Structure of the Bacterial Conjugation Factor PsiB, a Negative Regulator of RecA. <i>Journal of Biological Chemistry</i> , 2010, 285, 30615-30621.	3.4	8
57	Small-molecule tools for dissecting the roles of SSB/protein interactions in genome maintenance. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 633-638.	7.1	29
58	Catalytic activation of histone acetyltransferase Rtt109 by a histone chaperone. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 20275-20280.	7.1	42
59	Rising from the Ashes: DNA Repair in <i>Deinococcus radiodurans</i> . <i>PLoS Genetics</i> , 2010, 6, e1000815.	3.5	54
60	Structural Determinants of DNA Binding by a <i>P. falciparum</i> ApiAP2 Transcriptional Regulator. <i>Journal of Molecular Biology</i> , 2010, 395, 558-567.	4.2	59
61	Werner Helicase Wings DNA Binding. <i>Structure</i> , 2010, 18, 149-151.	3.3	7
62	The missing piece: Structural identification of the SSB binding site on the Chi/Psi clamp loader subassembly. <i>FASEB Journal</i> , 2010, 24, lb47.	0.5	0
63	The structure of the RMI core complex resembles the RPA interface. <i>FASEB Journal</i> , 2010, 24, lb44.	0.5	0
64	Structural mechanisms of ssDNA/SSB processing enzymes. <i>FASEB Journal</i> , 2010, 24, 196.3.	0.5	0
65	3D rapid prototyping to model DNA replication and engage students in the scientific process. <i>FASEB Journal</i> , 2010, 24, lb45.	0.5	0
66	RecQ DNA helicase HRDC domains are critical determinants in <i>Neisseria gonorrhoeae</i> pilin antigenic variation and DNA repair. <i>Molecular Microbiology</i> , 2009, 71, 158-171.	2.5	11
67	Slip sliding on DNA. <i>Nature</i> , 2009, 461, 1067-1068.	27.8	3
68	Peptide Inhibitors Identify Roles for SSB C-Terminal Residues in SSB/Exonuclease I Complex Formation. <i>Biochemistry</i> , 2009, 48, 6764-6771.	2.5	31
69	Identification of the SSB Binding Site on <i>E. coli</i> RecQ Reveals a Conserved Surface for Binding SSB's C Terminus. <i>Journal of Molecular Biology</i> , 2009, 386, 612-625.	4.2	84
70	Insights into tumor suppressor protein p53 using three-dimensional modeling and rapid prototyping technology. <i>FASEB Journal</i> , 2009, 23, LB310.	0.5	0
71	Molecular functions of the histone acetyltransferase chaperone complex Rtt109-Vps75. <i>Nature Structural and Molecular Biology</i> , 2008, 15, 948-956.	8.2	104
72	SSB as an Organizer/Mobilizer of Genome Maintenance Complexes. <i>Critical Reviews in Biochemistry and Molecular Biology</i> , 2008, 43, 289-318.	5.2	487

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73	Influences of the N700S Thrombospondin-1 Polymorphism on Protein Structure and Stability. <i>Journal of Biological Chemistry</i> , 2008, 283, 20069-20076.	3.4	22
74	Structure and function of the regulatory C-terminal HRDC domain from <i>Deinococcus radiodurans</i> RecQ. <i>Nucleic Acids Research</i> , 2008, 36, 3139-3149.	14.5	28
75	Structural basis of <i>Escherichia coli</i> single-stranded DNA-binding protein stimulation of exonuclease I. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008, 105, 9169-9174.	7.1	109
76	SSB: Organizational center and Achilles heel. <i>FASEB Journal</i> , 2008, 22, 592.3.	0.5	0
77	Magic Spots Cast a Spell on DNA Primase. <i>Cell</i> , 2007, 128, 823-824.	28.9	12
78	A Hand-Off Mechanism for Primosome Assembly in Replication Restart. <i>Molecular Cell</i> , 2007, 26, 781-793.	9.7	72
79	A Central Role for SSB in <i>Escherichia coli</i> RecQ DNA Helicase Function. <i>Journal of Biological Chemistry</i> , 2007, 282, 19247-19258.	3.4	130
80	Helix Bundle Quaternary Structure from β -Peptide Foldamers. <i>Journal of the American Chemical Society</i> , 2007, 129, 4178-4180.	13.7	191
81	Sit down, relax and unwind: structural insights into RecQ helicase mechanisms. <i>Nucleic Acids Research</i> , 2006, 34, 4098-4105.	14.5	56
82	Structure of the Sir3 protein bromo adjacent homology (BAH) domain from <i>S. cerevisiae</i> at 1.95 Å resolution. <i>Protein Science</i> , 2006, 15, 1182-1186.	7.6	25
83	Three HRDC Domains Differentially Modulate <i>Deinococcus radiodurans</i> RecQ DNA Helicase Biochemical Activity. <i>Journal of Biological Chemistry</i> , 2006, 281, 12849-12857.	3.4	32
84	Structure of the calcium-rich signature domain of human thrombospondin-2. <i>Nature Structural and Molecular Biology</i> , 2005, 12, 910-914.	8.2	81
85	The HRDC domain of BLM is required for the dissolution of double Holliday junctions. <i>EMBO Journal</i> , 2005, 24, 2679-2687.	7.8	150
86	Conferring Substrate Specificity to DNA Helicases: Role of the RecQ HRDC Domain. <i>Structure</i> , 2005, 13, 1173-1182.	3.3	81
87	Structural basis of the Sir1-origin recognition complex interaction in transcriptional silencing. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005, 102, 8489-8494.	7.1	80
88	PriB Stimulates PriA Helicase via an Interaction with Single-stranded DNA. <i>Journal of Biological Chemistry</i> , 2005, 280, 39693-39700.	3.4	59
89	Coupling DNA-binding and ATP hydrolysis in <i>Escherichia coli</i> RecQ: role of a highly conserved aromatic-rich sequence. <i>Nucleic Acids Research</i> , 2005, 33, 6982-6991.	14.5	36
90	Structure of the Calcium-Rich Signature Domain of Human Thrombospondin-2. <i>Blood</i> , 2005, 106, 3679-3679.	1.4	0

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91	Crystal structure of the <i>Deinococcus radiodurans</i> single-stranded DNA-binding protein suggests a mechanism for coping with DNA damage. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2004, 101, 8575-8580.	7.1	100
92	The Origin Recognition Complex and Sir4 Protein Recruit Sir1p to Yeast Silent Chromatin through Independent Interactions Requiring a Common Sir1p Domain. <i>Molecular and Cellular Biology</i> , 2004, 24, 774-786.	2.3	64
93	Crystal Structure of PriB, a Component of the <i>Escherichia coli</i> Replication Restart Primosome. <i>Structure</i> , 2004, 12, 1967-1975.	3.3	33
94	Structure and Function of RecQ DNA Helicases. <i>Critical Reviews in Biochemistry and Molecular Biology</i> , 2004, 39, 79-97.	5.2	89
95	High-resolution structure of the <i>E.coli</i> RecQ helicase catalytic core. <i>EMBO Journal</i> , 2003, 22, 4910-4921.	7.8	220
96	Domain mapping of <i>Escherichia coli</i> RecQ defines the roles of conserved N- and C-terminal regions in the RecQ family. <i>Nucleic Acids Research</i> , 2003, 31, 2778-2785.	14.5	77
97	Primus inter pares (first among equals)., 2001, 8, 2-4.		17
98	DNA replication at high resolution. <i>Chemistry and Biology</i> , 2000, 7, R63-R71.	6.0	13
99	Divalent metal cofactor binding in the kinetic folding trajectory of <i>Escherichia coli</i> ribonuclease H1. <i>Protein Science</i> , 2000, 9, 1914-1921.	7.6	49
100	Structure of the RNA Polymerase Domain of <i>E. coli</i> Primase. <i>Science</i> , 2000, 287, 2482-2486.	12.6	160
101	Enzymes that push DNA around. , 1999, 6, 900-902.		12
102	Structure and function of an archaeal topoisomerase VI subunit with homology to the meiotic recombination factor Spo11. <i>EMBO Journal</i> , 1999, 18, 6177-6188.	7.8	152
103	Binding specificity determines polarity of DNA unwinding by the Sgs1 protein of <i>S. cerevisiae</i> . <i>Journal of Molecular Biology</i> , 1999, 289, 235-248.	4.2	122
104	Activation/Attenuation Model for RNase H. <i>Journal of Biological Chemistry</i> , 1998, 273, 34128-34133.	3.4	84
105	Metal activation and regulation of <i>E. coli</i> RNase H. <i>Techniques in Protein Chemistry</i> , 1997, , 409-416.	0.3	3
106	The Putative Substrate Recognition Loop of <i>Escherichia coli</i> Ribonuclease H Is Not Essential for Activity. <i>Journal of Biological Chemistry</i> , 1996, 271, 19883-19887.	3.4	31
107	Substitution of a highly basic helix/loop sequence into the RNase H domain of human immunodeficiency virus reverse transcriptase restores its Mn(2+)-dependent RNase H activity.. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1995, 92, 2740-2744.	7.1	55