

Phoebe A Rice

List of Publications by Year in descending order

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111
papers

4,642
citations

236925

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h-index

175258

52
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117
all docs

117
docs citations

117
times ranked

4507
citing authors

#	ARTICLE	IF	CITATIONS
1	Crystal Structure of an IHF-DNA Complex: A Protein-Induced DNA U-Turn. <i>Cell</i> , 1996, 87, 1295-1306.	28.9	774
2	Mechanisms of Site-Specific Recombination. <i>Annual Review of Biochemistry</i> , 2006, 75, 567-605.	11.1	708
3	IHF and HU: flexible architects of bent DNA. <i>Current Opinion in Structural Biology</i> , 2004, 14, 28-35.	5.7	347
4	A G-quadruplex-containing RNA activates fluorescence in a GFP-like fluorophore. <i>Nature Chemical Biology</i> , 2014, 10, 686-691.	8.0	277
5	Flexible DNA bending in HU-DNA cocrystal structures. <i>EMBO Journal</i> , 2003, 22, 3749-3760.	7.8	239
6	Structure of the bacteriophage Mu transposase core: A common structural motif for DNA transposition and retroviral integration. <i>Cell</i> , 1995, 82, 209-220.	28.9	226
7	Comparative architecture of transposase and integrase complexes. <i>Nature</i> , 2001, 8, 302-307.		168
8	The Mu transpososome structure sheds light on DDE recombinase evolution. <i>Nature</i> , 2012, 491, 413-417.	27.8	135
9	The crystal structure of the catalytic domain of the site-specific recombination enzyme λ resolvase at 2.7 Å resolution. <i>Cell</i> , 1990, 63, 1323-1329.	28.9	121
10	Crystal structure of the Varkud satellite ribozyme. <i>Nature Chemical Biology</i> , 2015, 11, 840-846.	8.0	96
11	Structure-based Analysis of HU-DNA Binding. <i>Journal of Molecular Biology</i> , 2007, 365, 1005-1016.	4.2	87
12	Cooperativity mutants of the λ resolvase identify an essential interdimer interaction. <i>Cell</i> , 1990, 63, 1331-1338.	28.9	86
13	Integration Host Factor: Putting a Twist on Protein-DNA Recognition. <i>Journal of Molecular Biology</i> , 2003, 330, 493-502.	4.2	72
14	ABHD10 is an S-depalmitoylase affecting redox homeostasis through peroxiredoxin-5. <i>Nature Chemical Biology</i> , 2019, 15, 1232-1240.	8.0	72
15	Shaping the <i>Borrelia burgdorferi</i> genome: crystal structure and binding properties of the DNA-bending protein Hbb. <i>Molecular Microbiology</i> , 2007, 63, 1319-1330.	2.5	68
16	Moving DNA around: DNA transposition and retroviral integration. <i>Current Opinion in Structural Biology</i> , 2011, 21, 370-378.	5.7	64
17	Architecture of a Serine Recombinase-DNA Regulatory Complex. <i>Molecular Cell</i> , 2008, 30, 145-155.	9.7	55
18	Roles of two large serine recombinases in mobilizing the methicillin-resistance cassette <i>SCCmec</i> . <i>Molecular Microbiology</i> , 2013, 88, 1218-1229.	2.5	46

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19	Structural Plasticity of the Flp-Holliday Junction Complex. <i>Journal of Molecular Biology</i> , 2003, 326, 425-434.	4.2	43
20	The Role of the Conserved Trp330 in Flp-mediated Recombination. <i>Journal of Biological Chemistry</i> , 2003, 278, 24800-24807.	3.4	38
21	Structural Basis for Catalytic Activation of a Serine Recombinase. <i>Structure</i> , 2011, 19, 799-809.	3.3	37
22	A proposed mechanism for IS607-family serine transposases. <i>Mobile DNA</i> , 2013, 4, 24.	3.6	37
23	Holding damaged DNA together. , 1999, 6, 805-806.		36
24	Transposable phages, DNA reorganization and transfer. <i>Current Opinion in Microbiology</i> , 2017, 38, 88-94.	5.1	33
25	Comment on "CRNA-guided DNA insertion with CRISPR-associated transposases". <i>Science</i> , 2020, 368, .	12.6	32
26	Mapping the Transition State for DNA Bending by IHF. <i>Journal of Molecular Biology</i> , 2012, 418, 300-315.	4.2	31
27	Staphylococcal SCCmec elements encode an active MCM-like helicase and thus may be replicative. <i>Nature Structural and Molecular Biology</i> , 2016, 23, 891-898.	8.2	31
28	Copy-out-Paste-in Transposition of IS911: A Major Transposition Pathway. , 0, , 591-607.		30
29	Regulatory mutations in Sin recombinase support a structure-based model of the synaptosome. <i>Molecular Microbiology</i> , 2009, 74, 282-298.	2.5	28
30	Arginine as a General Acid Catalyst in Serine Recombinase-mediated DNA Cleavage. <i>Journal of Biological Chemistry</i> , 2013, 288, 29206-29214.	3.4	28
31	Automated Real-Space Refinement of Protein Structures Using a Realistic Backbone Move Set. <i>Biophysical Journal</i> , 2011, 101, 899-909.	0.5	26
32	The Influence of LINE-1 and SINE Retrotransposons on Mammalian Genomes. , 0, , 1165-1208.		25
33	Identification of a Potential General Acid/Base in the Reversible Phosphoryl Transfer Reactions Catalyzed by Tyrosine Recombinases: Flp H305. <i>Chemistry and Biology</i> , 2007, 14, 121-129.	6.0	24
34	Target DNA bending by the Mu transpososome promotes careful transposition and prevents its reversal. <i>ELife</i> , 2017, 6, .	6.0	24
35	An Overview of Tyrosine Site-specific Recombination: From an Flp Perspective. , 0, , 41-71.		24
36	Binding then bending: A mechanism for wrapping DNA. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006, 103, 19217-19218.	7.1	23

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37	Protein Binding Has a Large Effect on Radical Mediated DNA Damage. <i>Journal of the American Chemical Society</i> , 2008, 130, 12890-12891.	13.7	21
38	Serine Resolvases. <i>Microbiology Spectrum</i> , 2015, 3, MDNA3-0045-2014.	3.0	19
39	Characterizing Watson-Crick versus Hoogsteen Base Pairing in a DNA-Protein Complex Using Nuclear Magnetic Resonance and Site-Specifically ¹³ C- and ¹⁵ N-Labeled DNA. <i>Biochemistry</i> , 2019, 58, 1963-1974.	2.5	17
40	Sin Resolvase Catalytic Activity and Oligomerization State are Tightly Coupled. <i>Journal of Molecular Biology</i> , 2010, 404, 16-33.	4.2	16
41	Two-step interrogation then recognition of DNA binding site by Integration Host Factor: an architectural DNA-bending protein. <i>Nucleic Acids Research</i> , 2018, 46, 1741-1755.	14.5	15
42	A conserved RNA structural motif for organizing topology within picornaviral internal ribosome entry sites. <i>Nature Communications</i> , 2019, 10, 3629.	12.8	15
43	Orchestrating serine resolvases. <i>Biochemical Society Transactions</i> , 2010, 38, 384-387.	3.4	14
44	The Tn3-family of Replicative Transposons. , 0, , 693-726.		14
45	Static Kinks or Flexible Hinges: Multiple Conformations of Bent DNA Bound to Integration Host Factor Revealed by Fluorescence Lifetime Measurements. <i>Journal of Physical Chemistry B</i> , 2018, 122, 11519-11534.	2.6	14
46	Phage-encoded Serine Integrases and Other Large Serine Recombinases. , 0, , 253-272.		14
47	Tn7. , 0, , 647-667.		13
48	Binding and Catalytic Contributions to Site Recognition by Flp Recombinase. <i>Journal of Biological Chemistry</i> , 2008, 283, 11414-11423.	3.4	12
49	Everyman's Guide to Bacterial Insertion Sequences. , 0, , 555-590.		12
50	Mobile Bacterial Group II Introns at the Crux of Eukaryotic Evolution. , 2015, , 1209-1236.		12
51	Target highlights in CASP13: Experimental target structures through the eyes of their authors. <i>Proteins: Structure, Function and Bioinformatics</i> , 2019, 87, 1037-1057.	2.6	12
52	Inter-subunit interactions that coordinate Rad51's activities. <i>Nucleic Acids Research</i> , 2009, 37, 557-567.	14.5	11
53	Mechanisms of DNA Transposition. , 0, , 529-553.		11
54	Deciphering the Roles of Multicomponent Recognition Signals by the AAA + Unfoldase ClpX. <i>Journal of Molecular Biology</i> , 2015, 427, 2966-2982.	4.2	11

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55	Mammalian Endogenous Retroviruses. , 2015, , 1079-1100.		10
56	A novel DNA primase-helicase pair encoded by SCCmec elements. ELife, 2020, 9, .	6.0	9
57	Global analysis of ion dependence unveils hidden steps in DNA binding and bending by integration host factor. Journal of Chemical Physics, 2013, 139, 121927.	3.0	8
58	<i>Helitrons</i> , the Eukaryotic Rolling-circle Transposable Elements. , 0, , 891-924.		8
59	Diversity-generating Retroelements in Phage and Bacterial Genomes. , 0, , 1237-1252.		8
60	Control of transposase activity within a transpososome by the configuration of the flanking DNA segment of the transposon. Proceedings of the National Academy of Sciences of the United States of America, 2007, 104, 14622-14627.	7.1	7
61	Cre Recombinase. , 0, , 119-138.		7
62	Snapshots of a molecular swivel in action. Nucleic Acids Research, 2018, 46, 5286-5296.	14.5	7
63	The Integron: Adaptation On Demand. , 0, , 139-161.		7
64	Visualizing Mu transposition: assembling the puzzle pieces. Genes and Development, 2005, 19, 773-775.	5.9	6
65	piggyBac Transposony. , 2015, , 873-890.		6
66	P Transposable Elements in <i>Drosophila</i> and other Eukaryotic Organisms. , 0, , 727-752.		6
67	A Moveable Feast: An Introduction to Mobile DNA. , 0, , 1-39.		6
68	Transposable Phage Mu. , 0, , 669-691.		6
69	Tyrosine Recombinase Retrotransposons and Transposons. , 0, , 1271-1291.		5
70	The IS200/IS605 Family and "Peel and Paste" Single-strand Transposition Mechanism. , 2015, , 609-630.		5
71	The Serine Recombinases. , 0, , 73-89.		5
72	Ty3, a Position-specific Retrotransposon in Budding Yeast. , 0, , 965-996.		5

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73	Adeno-associated Virus as a Mammalian DNA Vector. , 0 , 827-849.		4
74	Integration, Regulation, and Long-Term Stability of R2 Retrotransposons. , 2015 , 1125-1146.		4
75	vlsAntigenic Variation Systems of Lyme DiseaseBorrelia: Eluding Host Immunity through both Random, Segmental Gene Conversion and Framework Heterogeneity. , 2015 , 471-489.		4
76	Mobile genetic elements: in silico<i>,</i> inÂvitro<i>,</i> inÂvivo. Molecular Ecology, 2016, 25, 1027-1031.	3.9	4
77	Mu transpososome activity-profiling yields hyperactive MuA variants for highly efficient genetic and genome engineering. Nucleic Acids Research, 2018, 46, 4649-4661.	14.5	4
78	V(D)J Recombination: Mechanism, Errors, and Fidelity. , 0 , 311-324.		4
79	Reverse Transcription of Retroviruses and LTR Retrotransposons. , 0 , 1051-1077.		4
80	Mobile DNA in the PathogenicNeisseria. , 2015 , 451-469.		3
81	The proteinâ€“protein interactions required for assembly of the Tn 3 resolution synapse. Molecular Microbiology, 2020, 114, 952-965.	2.5	3
82	Related Mechanisms of Antibody Somatic Hypermutation and Class Switch Recombination. , 0 , 325-348.		3
83	Xer Site-Specific Recombination: Promoting Vertical and Horizontal Transmission of Genetic Information. , 0 , 163-182.		3
84	The Î» Integrase Site-specific Recombination Pathway. , 0 , 91-118.		2
85	<i>Sleeping Beauty</i> Transposition. , 0 , 851-872.		2
86	The Long Terminal Repeat Retrotransposons Tf1 and Tf2 of Schizosaccharomyces pombe. , 2015 , 997-1010.		2
87	An Unexplored Diversity of Reverse Transcriptases in Bacteria. , 0 , 1253-1269.		2
88	A new twist on V(D)J recombination. Nature Structural and Molecular Biology, 2018, 25, 648-649.	8.2	2
89	Structure of the P element transpososome reveals new twists on the DD(E/D) theme. Nature Structural and Molecular Biology, 2019, 26, 989-990.	8.2	2
90	Programmed Rearrangement in Ciliates: <i>Paramecium</i>. , 0 , 369-388.		2

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91	Transposons Tn <i>10</i> and Tn <i>5</i> . , 0, , 631-645.		2
92	Mariner and the ITm Superfamily of Transposons. , 0, , 753-772.		2
93	<i>Mutator</i> and <i>MULE</i> Transposons. , 0, , 801-826.		2
94	Host Factors in Retroviral Integration and the Selection of Integration Target Sites. , 0, , 1035-1050.		2
95	Site-specific DNA Inversion by Serine Recombinases. , 0, , 199-236.		2
96	<i>hAT</i> Transposable Elements. , 0, , 773-800.		2
97	DNA Recombination Strategies During Antigenic Variation in the African Trypanosome. , 0, , 409-435.		2
98	A Unique DNA Recombination Mechanism of the Mating/Cell-type Switching of Fission Yeasts: a Review. , 0, , 515-528.		2
99	Biology of Three ICE Families: SXT/R391, ICEBs1, and ICESt1/ICESt3. , 2015, , 289-309.		1
100	Site-specific non-LTR retrotransposons. , 2015, , 1147-1163.		1
101	Serine Resolvases. , 0, , 237-252.		1
102	Programmed Genome Rearrangements in <i>Tetrahymena</i> . , 0, , 349-367.		1
103	Recombination and Diversification of the Variant Antigen Encoding Genes in the Malaria Parasite <i>Plasmodium falciparum</i> . , 0, , 437-449.		1
104	Programmed Genome Rearrangements in the Ciliate <i>Oxytricha</i> . , 0, , 389-407.		1
105	The Ty1 LTR-Retrotransposon of Budding Yeast, <i>Saccharomyces cerevisiae</i> . , 0, , 925-964.		1
106	Retroviral Integrase Structure and DNA Recombination Mechanism. , 2015, , 1011-1033.		0
107	Retroviral DNA Transposition: Themes and Variations. , 0, , 1101-1123.		0
108	The Integration and Excision of CTnDOT. , 0, , 183-198.		0

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109	Hairpin Telomere Resolvases. , 0, , 273-287.		0
110	Mating-type Gene Switching in <i>Saccharomyces cerevisiae</i> . , 0, , 491-514.		0
111	Crystal Structure of a New Single-Stranded DNA-Binding Protein Encoded by <i>Staphylococcal</i> Cassette Chromosome Elements. SSRN Electronic Journal, 0, , .	0.4	0