Phoebe A Rice

List of Publications by Year
in descending order

111 papers	4,642 citations	236925 25 h-index	175258 52 g-index
117 all docs	117 docs citations	117 times ranked	4507 citing authors

#	Article	IF	Citations
1	The proteinâ€“protein interactions required for assembly of the Tn 3 resolution synapse. Molecular Microbiology, 2020, 114, 952-965.	2.5	3
2	Comment on â€œRNA-guided DNA insertion with CRISPR-associated transposasesâ€• Science, 2020, 368, .	12.6	32
3	A novel DNA primase-helicase pair encoded by SCCmec elements. ELife, 2020, 9, .	6.0	9
4	A conserved RNA structural motif for organizing topology within picornaviral internal ribosome entry sites. Nature Communications, 2019, 10, 3629.	12.8	15
5	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
6	Target highlights in CASP13: Experimental target structures through the eyes of their authors. Proteins: Structure, Function and Bioinformatics, 2019, 87, 1037-1057.	2.6	12
7	Characterizing Watsonâ€“Crick versus Hoogsteen Base Pairing in a DNAâ€–Protein Complex Using Nuclear Magnetic Resonance and Site-Specifically 13C- and 15N-Labeled DNA. Biochemistry, 2019, 58, 1963-1974.	2.5	17
8	ABHD10 is an S-depalmitoylase affecting redox homeostasis through peroxiredoxin-5. Nature Chemical Biology, 2019, 15, 1232-1240.	8.0	72
9	Snapshots of a molecular swivel in action. Nucleic Acids Research, 2018, 46, 5286-5296.	14.5	7
10	Two-step interrogation then recognition of DNA binding site by Integration Host Factor: an architectural DNA-bending protein. Nucleic Acids Research, 2018, 46, 1741-1755.	14.5	15
11	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
12	Static Kinks or Flexible Hinges: Multiple Conformations of Bent DNA Bound to Integration Host Factor Revealed by Fluorescence Lifetime Measurements. Journal of Physical Chemistry B, 2018, 122, 11519-11534.	2.6	14
13	A new twist on V(D)J recombination. Nature Structural and Molecular Biology, 2018, 25, 648-649.	8.2	2
14	Transposable phages, DNA reorganization and transfer. Current Opinion in Microbiology, 2017, 38, 88-94.	5.1	33
15	Target DNA bending by the Mu transpososome promotes careful transposition and prevents its reversal. ELife, 2017, 6, .	6.0	24
16	Staphylococcal SCCmec elements encode an active MCM-like helicase and thus may be replicative. Nature Structural and Molecular Biology, 2016, 23, 891-898.	8.2	31
17	Mobile genetic elements: in silico, inÂvitro, inÂvivo. Molecular Ecology, 2016, 25, 1027-1031.	3.9	4
18	Serine Resolvases. Microbiology Spectrum, 2015, 3, MDNA3-0045-2014.	3.0	19

#	Article	IF	Citations
19	piggyBac Transposony. , 2015, , 873-890.		6
20	Integration, Regulation, and Long-Term Stability of R2 Retrotransposons. , 2015, , 1125-1146.		4
21	Retroviral Integrase Structure and DNA Recombination Mechanism. , 2015, , 1011-1033.		0
22	The Long Terminal Repeat Retrotransposons Tf1 and Tf2 of Schizosaccharomyces pombe. , 2015, , 997-1010.		2
23	Biology of Three ICE Families: SXT/R391, ICEBs1, and ICESt1/ICESt3. , 2015, , 289-309.		1
24	Mammalian Endogenous Retroviruses. , 2015, , 1079-1100.		10
25	Mobile DNA in the PathogenicNeisseria. , 2015, , 451-469.		3
26	vlsAntigenic Variation Systems of Lyme DiseaseBorrelia: Eluding Host Immunity through both Random, Segmental Gene Conversion and Framework Heterogeneity. , 2015, , 471-489.		4
27	Site-specific non-LTR retrotransposons. , 2015, , 1147-1163.		1
28	Mobile Bacterial Group II Introns at the Crux of Eukaryotic Evolution. , 2015, , 1209-1236.		12
29	The IS200/IS605Family and â€œPeel and Pasteâ€•Single-strand Transposition Mechanism. , 2015, , 609-630.		5
30	Deciphering the Roles of Multicomponent Recognition Signals by the AAA + Unfoldase ClpX. Journal of Molecular Biology, 2015, 427, 2966-2982.	4.2	11
31	Crystal structure of the Varkud satellite ribozyme. Nature Chemical Biology, 2015, 11, 840-846.	8.0	96
32	A G-quadruplexâ€“containing RNA activates fluorescence in a GFP-like fluorophore. Nature Chemical Biology, 2014, 10, 686-691.	8.0	277
33	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
34	A proposed mechanism for IS607-family serine transposases. Mobile DNA, 2013, 4, 24.	3.6	37
35	Arginine as a General Acid Catalyst in Serine Recombinase-mediated DNA Cleavage. Journal of Biological Chemistry, 2013, 288, 29206-29214.	3.4	28
36	Roles of two large serine recombinases in mobilizing the methicillinâ€resistance cassette <scp>SCCmec</scp>. Molecular Microbiology, 2013, 88, 1218-1229.	2.5	46

#	Article	IF	Citations
37	Mapping the Transition State for DNA Bending by IHF. Journal of Molecular Biology, 2012, 418, 300-315.	4.2	31
38	The Mu transpososome structure sheds light on DDE recombinase evolution. Nature, 2012, 491, 413-417.	27.8	135
39	Automated Real-Space Refinement of Protein Structures Using a Realistic Backbone Move Set. Biophysical Journal, 2011, 101, 899-909.	0.5	26
40	Structural Basis for Catalytic Activation of a Serine Recombinase. Structure, 2011, 19, 799-809.	3.3	37
41	Moving DNA around: DNA transposition and retroviral integration. Current Opinion in Structural Biology, 2011, 21, 370-378.	5.7	64
42	Orchestrating serine resolvases. Biochemical Society Transactions, 2010, 38, 384-387.	3.4	14
43	Sin Resolvase Catalytic Activity and Oligomerization State are Tightly Coupled. Journal of Molecular Biology, 2010, 404, 16-33.	4.2	16
44	Inter-subunit interactions that coordinate Rad51's activities. Nucleic Acids Research, 2009, 37, 557-567.	14.5	11
45	Regulatory mutations in Sin recombinase support a structureâ€based model of the synaptosome. Molecular Microbiology, 2009, 74, 282-298.	2.5	28
46	Architecture of a Serine Recombinase-DNA Regulatory Complex. Molecular Cell, 2008, 30, 145-155.	9.7	55
47	Protein Binding Has a Large Effect on Radical Mediated DNA Damage. Journal of the American Chemical Society, 2008, 130, 12890-12891.	13.7	21
48	Binding and Catalytic Contributions to Site Recognition by Flp Recombinase. Journal of Biological Chemistry, 2008, 283, 11414-11423.	3.4	12
49	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
50	Structure-based Analysis of HUâ€“DNA Binding. Journal of Molecular Biology, 2007, 365, 1005-1016.	4.2	87
51	Identification of a Potential General Acid/Base in the Reversible Phosphoryl Transfer Reactions Catalyzed by Tyrosine Recombinases: Flp H305. Chemistry and Biology, 2007, 14, 121-129.	6.0	24
52	Shaping the Borrelia burgdorferi genome: crystal structure and binding properties of the DNA-bending protein Hbb. Molecular Microbiology, 2007, 63, 1319-1330.	2.5	68
53	Mechanisms of Site-Specific Recombination. Annual Review of Biochemistry, 2006, 75, 567-605.	11.1	708
54	Binding then bending: A mechanism for wrapping DNA. Proceedings of the National Academy of Sciences of the United States of America, 2006, 103, 19217-19218.	7.1	23

#	Article	IF	Citations
55	Visualizing Mu transposition: assembling the puzzle pieces. Genes and Development, 2005, 19, 773-775.	5.9	6
56	IHF and HU: flexible architects of bent DNA. Current Opinion in Structural Biology, 2004, 14, 28-35.	5.7	347
57	Flexible DNA bending in HU-DNA cocrystal structures. EMBO Journal, 2003, 22, 3749-3760.	7.8	239
58	Structural Plasticity of the Flpâ€“Holliday Junction Complex. Journal of Molecular Biology, 2003, 326, 425-434.	4.2	43
59	Integration Host Factor: Putting a Twist on Proteinâ€“DNA Recognition. Journal of Molecular Biology, 2003, 330, 493-502.	4.2	72
60	The Role of the Conserved Trp330 in Flp-mediated Recombination. Journal of Biological Chemistry, 2003, 278, 24800-24807.	3.4	38
61	Comparative architecture of transposase and integrase complexes. , 2001, 8, 302-307.		168
62	Holding damaged DNA together. , 1999, 6, 805-806.		36
63	Crystal Structure of an IHF-DNA Complex: A Protein-Induced DNA U-Turn. Cell, 1996, 87, 1295-1306.	28.9	774
64	Structure of the bacteriophage Mu transposase core: A common structural motif for DNA transposition and retroviral integration. Cell, 1995, 82, 209-220.	28.9	226
65	The crystal structure of the catalytic domain of the site-specific recombination enzyme Î³Î´ resolvase at 2.7 Ã... resolution. Cell, 1990, 63, 1323-1329.	28.9	121
66	Cooperativity mutants of the Î³Î´ resolvase identify an essential interdimer interaction. Cell, 1990, 63, 1331-1338.	28.9	86
67	Adeno-associated Virus as a Mammalian DNA Vector. , 0, , 827-849.		4
68	The Î» Integrase Site-specific Recombination Pathway. , 0, , 91-118.		2
69	Sleeping Beauty Transposition. , 0, , 851-872.		2
70	Cre Recombinase. , 0, , 119-138.		7
71	Mechanisms of DNA Transposition. , 0, , 529-553.		11
72	Everyman's Guide to Bacterial Insertion Sequences. , 0, , 555-590.		12

#	Article	IF	Citations
73	P Transposable Elements in Drosophila and other Eukaryotic Organisms. , 0, , 727-752.		6
74	Tyrosine Recombinase Retrotransposons and Transposons. , 0, , 1271-1291.		5
75	The Tn3-family of Replicative Transposons. , 0, , 693-726.		14
76	The Influence of LINE-1 and SINE Retrotransposons on Mammalian Genomes. , 0, , 1165-1208.		25
77	Tn7. , 0, , 647-667.		13
78	An Unexplored Diversity of Reverse Transcriptases in Bacteria. , 0, , 1253-1269.		2
79	A Moveable Feast: An Introduction to Mobile DNA. , 0, , 1-39.		6
80	Serine Resolvases. , 0, , 237-252.		1
81	Phage-encoded Serine Integrases and Other Large Serine Recombinases. , 0, , 253-272.		14
82	V(D)J Recombination: Mechanism, Errors, and Fidelity. , 0, , 311-324.		4
83	Programmed Genome Rearrangements inTetrahymena. , 0, , 349-367.		1
84	Programmed Rearrangement in Ciliates: Paramecium. , 0, , 369-388.		2
85	Recombination and Diversification of the Variant Antigen Encoding Genes in the Malaria Parasite Plasmodium falciparum. , 0, , 437-449.		1
86	Copy-out-Paste-in Transposition of IS911: A Major Transposition Pathway. , 0, , 591-607.		30
87	Transposons Tn10 and Tn5. , 0, , 631-645.		2
88	The Serine Recombinases. , 0, , 73-89.		5
89	Transposable Phage Mu. , 0, , 669-691.		6
90	Mariner and the ITm Superfamily of Transposons. , 0, , 753-772.		2

#	Article	IF	Citations
91	Mutator and MULE Transposons. , 0, , 801-826.		2
92	Helitrons, the Eukaryotic Rolling-circle Transposable Elements. , 0, , 891-924.		8
93	Ty3, a Position-specific Retrotransposon in Budding Yeast. , 0, , 965-996.		5
94	Host Factors in Retroviral Integration and the Selection of Integration Target Sites. , 0, , 1035-1050.		2
95	Diversity-generating Retroelements in Phage and Bacterial Genomes. , 0, , 1237-1252.		8
96	The Integron: Adaptation On Demand. , 0, , 139-161.		7
97	Site-specific DNA Inversion by Serine Recombinases. , 0, , 199-236.		2
98	hAT Transposable Elements. , 0, , 773-800.		2
99	Programmed Genome Rearrangements in the CiliateOxytricha. , 0, , 389-407.		1
100	DNA Recombination Strategies During Antigenic Variation in the African Trypanosome. , 0, , 409-435.		2
101	Retroviral DNA Transposition: Themes and Variations. , 0, , 1101-1123.		0
102	The Integration and Excision of CTnDOT. , 0, , 183-198.		0
103	An Overview of Tyrosine Site-specific Recombination: From an Flp Perspective. , 0, , 41-71.		24
104	Hairpin Telomere Resolvases. , 0, , 273-287.		0
105	Related Mechanisms of Antibody Somatic Hypermutation and Class Switch Recombination. , 0, , 325-348.		3
106	Reverse Transcription of Retroviruses and LTR Retrotransposons. , 0, , 1051-1077.		4
107	Mating-type Gene Switching in Saccharomyces cerevisiae. , 0, , 491-514.		0
108	A Unique DNA Recombination Mechanism of the Mating/Cell-type Switching of Fission Yeasts: a Review. , 0, , 515-528.		2

#	Article	IF	Citations
109	The Ty1 LTR-Retrotransposon of Budding Yeast,Saccharomyces cerevisiae. , 0, , 925-964.		1
110	Xer Site-Specific Recombination: Promoting Vertical and Horizontal Transmission of Genetic Information. , 0, , 163-182.		3
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