Phoebe A Rice

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61 3,784 107 25 h-index g-index citations papers 117 4,294 13.9 5.34 L-index avg, IF ext. citations ext. papers

#	Paper	IF	Citations
107	Crystal structure of an IHF-DNA complex: a protein-induced DNA U-turn. <i>Cell</i> , 1996 , 87, 1295-306	56.2	688
106	Mechanisms of site-specific recombination. <i>Annual Review of Biochemistry</i> , 2006 , 75, 567-605	29.1	581
105	IHF and HU: flexible architects of bent DNA. Current Opinion in Structural Biology, 2004, 14, 28-35	8.1	308
104	A G-quadruplex-containing RNA activates fluorescence in a GFP-like fluorophore. <i>Nature Chemical Biology</i> , 2014 , 10, 686-91	11.7	213
103	Structure of the bacteriophage Mu transposase core: a common structural motif for DNA transposition and retroviral integration. <i>Cell</i> , 1995 , 82, 209-20	56.2	208
102	Flexible DNA bending in HU-DNA cocrystal structures. <i>EMBO Journal</i> , 2003 , 22, 3749-60	13	205
101	Comparative architecture of transposase and integrase complexes. <i>Nature Structural Biology</i> , 2001 , 8, 302-7		150
100	The crystal structure of the catalytic domain of the site-specific recombination enzyme gamma delta resolvase at 2.7 A resolution. <i>Cell</i> , 1990 , 63, 1323-9	56.2	110
99	The Itranspososome structure sheds light on DDE recombinase evolution. <i>Nature</i> , 2012 , 491, 413-7	50.4	99
98	Crystal structure of the Varkud satellite ribozyme. <i>Nature Chemical Biology</i> , 2015 , 11, 840-6	11.7	83
97	Cooperativity mutants of the gamma delta resolvase identify an essential interdimer interaction. <i>Cell</i> , 1990 , 63, 1331-8	56.2	81
96	Structure-based analysis of HU-DNA binding. Journal of Molecular Biology, 2007, 365, 1005-16	6.5	77
95	Integration host factor: putting a twist on protein-DNA recognition. <i>Journal of Molecular Biology</i> , 2003 , 330, 493-502	6.5	63
94	Shaping the Borrelia burgdorferi genome: crystal structure and binding properties of the DNA-bending protein Hbb. <i>Molecular Microbiology</i> , 2007 , 63, 1319-30	4.1	60
93	Architecture of a serine recombinase-DNA regulatory complex. <i>Molecular Cell</i> , 2008 , 30, 145-55	17.6	53
92	Moving DNA around: DNA transposition and retroviral integration. <i>Current Opinion in Structural Biology</i> , 2011 , 21, 370-8	8.1	48
91	Structural plasticity of the Flp-Holliday junction complex. <i>Journal of Molecular Biology</i> , 2003 , 326, 425-3	3 4 6.5	42

(2020-2003)

90	The role of the conserved Trp330 in Flp-mediated recombination. Functional and structural analysis. <i>Journal of Biological Chemistry</i> , 2003 , 278, 24800-7	5.4	36
89	ABHD10 is an S-depalmitoylase affecting redox homeostasis through peroxiredoxin-5. <i>Nature Chemical Biology</i> , 2019 , 15, 1232-1240	11.7	36
88	Roles of two large serine recombinases in mobilizing the methicillin-resistance cassette SCCmec. <i>Molecular Microbiology</i> , 2013 , 88, 1218-29	4.1	35
87	Structural basis for catalytic activation of a serine recombinase. <i>Structure</i> , 2011 , 19, 799-809	5.2	34
86	A proposed mechanism for IS607-family serine transposases. <i>Mobile DNA</i> , 2013 , 4, 24	4.4	30
85	Automated real-space refinement of protein structures using a realistic backbone move set. <i>Biophysical Journal</i> , 2011 , 101, 899-909	2.9	26
84	Regulatory mutations in Sin recombinase support a structure-based model of the synaptosome. <i>Molecular Microbiology</i> , 2009 , 74, 282-98	4.1	26
83	Arginine as a general acid catalyst in serine recombinase-mediated DNA cleavage. <i>Journal of Biological Chemistry</i> , 2013 , 288, 29206-14	5.4	24
82	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, 121-9		24
81	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	17.6	22
80	Mapping the transition state for DNA bending by IHF. Journal of Molecular Biology, 2012, 418, 300-15	6.5	22
79	Transposable phages, DNA reorganization and transfer. Current Opinion in Microbiology, 2017, 38, 88-94	17.9	21
78	Protein binding has a large effect on radical mediated DNA damage. <i>Journal of the American Chemical Society</i> , 2008 , 130, 12890-1	16.4	20
77	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, 19217-8	11.5	19
76	Serine Resolvases. <i>Microbiology Spectrum</i> , 2015 , 3, MDNA3-0045-2014	8.9	15
75	Sin resolvase catalytic activity and oligomerization state are tightly coupled. <i>Journal of Molecular Biology</i> , 2010 , 404, 16-33	6.5	14
74	Orchestrating serine resolvases. <i>Biochemical Society Transactions</i> , 2010 , 38, 384-7	5.1	14
73	Comment on "RNA-guided DNA insertion with CRISPR-associated transposases". <i>Science</i> , 2020 , 368,	33.3	12

72	Target DNA bending by the Mu transpososome promotes careful transposition and prevents its reversal. <i>ELife</i> , 2017 , 6,	8.9	12
71	Characterizing Watson-Crick versus Hoogsteen Base Pairing in a DNA-Protein Complex Using Nuclear Magnetic Resonance and Site-Specifically C- and N-Labeled DNA. <i>Biochemistry</i> , 2019 , 58, 1963-	·1974	11
70	The Influence of LINE-1 and SINE Retrotransposons on Mammalian Genomes 2015 , 1165-1208		11
69	Binding and catalytic contributions to site recognition by flp recombinase. <i>Journal of Biological Chemistry</i> , 2008 , 283, 11414-23	5.4	10
68	Target highlights in CASP13: Experimental target structures through the eyes of their authors. <i>Proteins: Structure, Function and Bioinformatics</i> , 2019 , 87, 1037-1057	4.2	9
67	A conserved RNA structural motif for organizing topology within picornaviral internal ribosome entry sites. <i>Nature Communications</i> , 2019 , 10, 3629	17.4	9
66	Inter-subunit interactions that coordinate Rad51's activities. <i>Nucleic Acids Research</i> , 2009 , 37, 557-67	20.1	9
65	Deciphering the Roles of Multicomponent Recognition Signals by the AAA+ Unfoldase ClpX. <i>Journal of Molecular Biology</i> , 2015 , 427, 2966-82	6.5	8
64	Everyman's Guide to Bacterial Insertion Sequences 2015 , 555-590		8
63	The Tn3-family of Replicative Transposons 2015 , 693-726		8
62	Mobile Bacterial Group II Introns at the Crux of Eukaryotic Evolution 2015 , 1209-1236		8
61	Phage-encoded Serine Integrases and Other Large Serine Recombinases253-272		8
60	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	3.4	8
59	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	20.1	7
	The state of the s		
58	Global analysis of ion dependence unveils hidden steps in DNA binding and bending by integration host factor. <i>Journal of Chemical Physics</i> , 2013 , 139, 121927	3.9	7
58 57	Global analysis of ion dependence unveils hidden steps in DNA binding and bending by integration	3.9	7
	Global analysis of ion dependence unveils hidden steps in DNA binding and bending by integration host factor. <i>Journal of Chemical Physics</i> , 2013 , 139, 121927	3.9	

54	Helitrons, the Eukaryotic Rolling-circle Transposable Elements891-924	6
53	Mammalian Endogenous Retroviruses 2015 , 1079-1100	5
52	Transposable Phage Mu669-691	5
51	Integration, Regulation, and Long-Term Stability of R2 Retrotransposons 2015 , 1125-1146	4
50	P Transposable Elements in Drosophila and other Eukaryotic Organisms 2015 , 727-752	4
49	Tn7 2015 , 647-667	4
48	The IS 200/IS605 Family and P eel and PastelSingle-strand Transposition Mechanism 2015 , 609-630	4
47	The Serine Recombinases73-89	4
46	Ty3, a Position-specific Retrotransposon in Budding Yeast965-996	4
45	Diversity-generating Retroelements in Phage and Bacterial Genomes1237-1252	4
44	The Integron: Adaptation On Demand139-161	4
43	Snapshots of a molecular swivel in action. <i>Nucleic Acids Research</i> , 2018 , 46, 5286-5296 20.1	3
42	Mu transpososome activity-profiling yields hyperactive MuA variants for highly efficient genetic and genome engineering. <i>Nucleic Acids Research</i> , 2018 , 46, 4649-4661	3
41	Cre Recombinase 2015 , 119-138	3
40	Adeno-associated Virus as a Mammalian DNA Vector 2015 , 827-849	2
39	The Integrase Site-specific Recombination Pathway 2015 , 91-118	2
38	The Long Terminal Repeat Retrotransposons Tf1 and Tf2 of Schizosaccharomyces pombe 2015 , 997-1010	2
37	Tyrosine Recombinase Retrotransposons and Transposons 2015 , 1271-1291	2

36	vls Antigenic Variation Systems of Lyme Disease Borrelia: Eluding Host Immunity through both Random, Segmental Gene Conversion and Framework Heterogeneity 2015 , 471-489	2
35	A Moveable Feast: An Introduction to Mobile DNA1-39	2
34	V(D)J Recombination: Mechanism, Errors, and Fidelity311-324	2
33	Mariner and the ITm Superfamily of Transposons753-772	2
32	Mutator and MULE Transposons801-826	2
31	Host Factors in Retroviral Integration and the Selection of Integration Target Sites1035-1050	2
30	Site-specific DNA Inversion by Serine Recombinases199-236	2
29	An Overview of Tyrosine Site-specific Recombination: From an Flp Perspective41-71	2
28	Xer Site-Specific Recombination: Promoting Vertical and Horizontal Transmission of Genetic Information 1	63-182
27	Mobile genetic elements: in silico, in vitro, in vivo. <i>Molecular Ecology</i> , 2016 , 25, 1027-31 5.7	7 1
27 26	Mobile genetic elements: in silico, in vitro, in vivo. <i>Molecular Ecology</i> , 2016 , 25, 1027-31 5.7 Sleeping Beauty Transposition 2015 , 851-872	7 1
26	Sleeping Beauty Transposition 2015 , 851-872	1
26 25	Sleeping Beauty Transposition 2015 , 851-872 Mobile DNA in the Pathogenic Neisseria 2015 , 451-469	1
26 25 24	Sleeping Beauty Transposition 2015 , 851-872 Mobile DNA in the Pathogenic Neisseria 2015 , 451-469 Site-specific non-LTR retrotransposons 2015 , 1147-1163	1 1
26 25 24 23	Sleeping Beauty Transposition 2015, 851-872 Mobile DNA in the Pathogenic Neisseria 2015, 451-469 Site-specific non-LTR retrotransposons 2015, 1147-1163 An Unexplored Diversity of Reverse Transcriptases in Bacteria 2015, 1253-1269	1 1 1
26 25 24 23 22	Sleeping Beauty Transposition 2015, 851-872 Mobile DNA in the Pathogenic Neisseria 2015, 451-469 Site-specific non-LTR retrotransposons 2015, 1147-1163 An Unexplored Diversity of Reverse Transcriptases in Bacteria 2015, 1253-1269 Serine Resolvases237-252	1 1 1 1

18	Transposons Tn10 and Tn5631-645	1
17	hATTransposable Elements773-800	1
16	Related Mechanisms of Antibody Somatic Hypermutation and Class Switch Recombination325-348	1
15	Reverse Transcription of Retroviruses and LTR Retrotransposons1051-1077	1
14	A Unique DNA Recombination Mechanism of the Mating/Cell-type Switching of Fission Yeasts: a Review	w515-528
13	Structure of the P element transpososome reveals new twists on the DD(E/D) theme. <i>Nature Structural and Molecular Biology</i> , 2019 , 26, 989-990	17.6 0
12	piggyBac Transposony 2015 , 873-890	0
11	Biology of Three ICE Families: SXT/R391, ICEBs1, and ICESt1/ICESt3 2015 , 289-309	O
10	Programmed Rearrangement in Ciliates: Paramecium369-388	0
9	Programmed Genome Rearrangements in the CiliateOxytricha389-407	O
8	DNA Recombination Strategies During Antigenic Variation in the African Trypanosome409-435	0
7	The protein-protein interactions required for assembly of the Tn3 resolution synapse. <i>Molecular Microbiology</i> , 2020 , 114, 952-965	4.1 0
6	Retroviral Integrase Structure and DNA Recombination Mechanism 2015 , 1011-1033	
5	Retroviral DNA Transposition: Themes and Variations1101-1123	
4	The Integration and Excision of CTnDOT183-198	
3	Hairpin Telomere Resolvases273-287	
2	Mating-type Gene Switching inSaccharomyces cerevisiae491-514	
1	The Ty1 LTR-Retrotransposon of Budding Yeast, Saccharomyces cerevisiae925-964	