Phoebe A Rice

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

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

| # | Paper | IF | Citations |
|-----|--|-----------------|-----------|
| 107 | Comment on "RNA-guided DNA insertion with CRISPR-associated transposases". <i>Science</i> , 2020 , 368, | 33.3 | 12 |
| 106 | The protein-protein interactions required for assembly of the Tn3 resolution synapse. <i>Molecular Microbiology</i> , 2020 , 114, 952-965 | 4.1 | O |
| 105 | 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 |
| 104 | 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, 1963-1 | 37 4 | 11 |
| 103 | A conserved RNA structural motif for organizing topology within picornaviral internal ribosome entry sites. <i>Nature Communications</i> , 2019 , 10, 3629 | 17.4 | 9 |
| 102 | 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 | О |
| 101 | ABHD10 is an S-depalmitoylase affecting redox homeostasis through peroxiredoxin-5. <i>Nature Chemical Biology</i> , 2019 , 15, 1232-1240 | 11.7 | 36 |
| 100 | Snapshots of a molecular swivel in action. <i>Nucleic Acids Research</i> , 2018 , 46, 5286-5296 | 20.1 | 3 |
| 99 | 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 |
| 98 | Mu transpososome activity-profiling yields hyperactive MuA variants for highly efficient genetic and genome engineering. <i>Nucleic Acids Research</i> , 2018 , 46, 4649-4661 | 20.1 | 3 |
| 97 | 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 |
| 96 | Transposable phages, DNA reorganization and transfer. Current Opinion in Microbiology, 2017, 38, 88-94 | 7.9 | 21 |
| 95 | Target DNA bending by the Mu transpososome promotes careful transposition and prevents its reversal. <i>ELife</i> , 2017 , 6, | 8.9 | 12 |
| 94 | 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 |
| 93 | Mobile genetic elements: in silico, in vitro, in vivo. <i>Molecular Ecology</i> , 2016 , 25, 1027-31 | 5.7 | 1 |
| 92 | 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 |
| 91 | Crystal structure of the Varkud satellite ribozyme. <i>Nature Chemical Biology</i> , 2015 , 11, 840-6 | 11.7 | 83 |

(2015-2015)

| 90 | Serine Resolvases. <i>Microbiology Spectrum</i> , 2015 , 3, MDNA3-0045-2014 | 8.9 | 15 |
|----|---|-----|----|
| 89 | Adeno-associated Virus as a Mammalian DNA Vector 2015 , 827-849 | | 2 |
| 88 | piggyBac Transposony 2015 , 873-890 | | О |
| 87 | The Integrase Site-specific Recombination Pathway 2015 , 91-118 | | 2 |
| 86 | Integration, Regulation, and Long-Term Stability of R2 Retrotransposons 2015 , 1125-1146 | | 4 |
| 85 | Sleeping Beauty Transposition 2015 , 851-872 | | 1 |
| 84 | Retroviral Integrase Structure and DNA Recombination Mechanism 2015, 1011-1033 | | |
| 83 | Cre Recombinase 2015 , 119-138 | | 3 |
| 82 | The Long Terminal Repeat Retrotransposons Tf1 and Tf2 of Schizosaccharomyces pombe 2015 , 997-10 | 10 | 2 |
| 81 | Biology of Three ICE Families: SXT/R391, ICEBs1, and ICESt1/ICESt3 2015 , 289-309 | | Ο |
| 80 | Mechanisms of DNA Transposition 2015 , 529-553 | | 6 |
| 79 | Everyman's Guide to Bacterial Insertion Sequences 2015 , 555-590 | | 8 |
| 78 | P Transposable Elements in Drosophila and other Eukaryotic Organisms 2015 , 727-752 | | 4 |
| 77 | Mammalian Endogenous Retroviruses 2015 , 1079-1100 | | 5 |
| 76 | Tyrosine Recombinase Retrotransposons and Transposons 2015 , 1271-1291 | | 2 |
| 75 | Mobile DNA in the Pathogenic Neisseria 2015 , 451-469 | | 1 |
| 74 | The Tn3-family of Replicative Transposons 2015 , 693-726 | | 8 |
| 73 | The Influence of LINE-1 and SINE Retrotransposons on Mammalian Genomes 2015 , 1165-1208 | | 11 |

| 72 | vls Antigenic Variation Systems of Lyme Disease Borrelia: Eluding Host Immunity through both Random, Segmental Gene Conversion and Framework Heterogeneity 2015 , 471-489 | | 2 |
|----|--|------|-----|
| 71 | Site-specific non-LTR retrotransposons 2015 , 1147-1163 | | 1 |
| 70 | Mobile Bacterial Group II Introns at the Crux of Eukaryotic Evolution 2015 , 1209-1236 | | 8 |
| 69 | Tn7 2015 , 647-667 | | 4 |
| 68 | An Unexplored Diversity of Reverse Transcriptases in Bacteria 2015 , 1253-1269 | | 1 |
| 67 | The IS 200/IS605 Family and Peel and PastelSingle-strand Transposition Mechanism 2015, 609-630 | | 4 |
| 66 | A G-quadruplex-containing RNA activates fluorescence in a GFP-like fluorophore. <i>Nature Chemical Biology</i> , 2014 , 10, 686-91 | 11.7 | 213 |
| 65 | 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 |
| 64 | A proposed mechanism for IS607-family serine transposases. <i>Mobile DNA</i> , 2013 , 4, 24 | 4.4 | 30 |
| 63 | 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 |
| 62 | Roles of two large serine recombinases in mobilizing the methicillin-resistance cassette SCCmec. <i>Molecular Microbiology</i> , 2013 , 88, 1218-29 | 4.1 | 35 |
| 61 | Mapping the transition state for DNA bending by IHF. <i>Journal of Molecular Biology</i> , 2012 , 418, 300-15 | 6.5 | 22 |
| 60 | The Itranspososome structure sheds light on DDE recombinase evolution. <i>Nature</i> , 2012 , 491, 413-7 | 50.4 | 99 |
| 59 | Automated real-space refinement of protein structures using a realistic backbone move set. <i>Biophysical Journal</i> , 2011 , 101, 899-909 | 2.9 | 26 |
| 58 | Structural basis for catalytic activation of a serine recombinase. <i>Structure</i> , 2011 , 19, 799-809 | 5.2 | 34 |
| 57 | Moving DNA around: DNA transposition and retroviral integration. <i>Current Opinion in Structural Biology</i> , 2011 , 21, 370-8 | 8.1 | 48 |
| 56 | Sin resolvase catalytic activity and oligomerization state are tightly coupled. <i>Journal of Molecular Biology</i> , 2010 , 404, 16-33 | 6.5 | 14 |
| 55 | Orchestrating serine resolvases. <i>Biochemical Society Transactions</i> , 2010 , 38, 384-7 | 5.1 | 14 |

(2001-2009)

| 54 | Inter-subunit interactions that coordinate Rad51's activities. <i>Nucleic Acids Research</i> , 2009 , 37, 557-67 | 20.1 | 9 |
|----|--|-------|-----|
| 53 | Regulatory mutations in Sin recombinase support a structure-based model of the synaptosome. <i>Molecular Microbiology</i> , 2009 , 74, 282-98 | 4.1 | 26 |
| 52 | Architecture of a serine recombinase-DNA regulatory complex. <i>Molecular Cell</i> , 2008 , 30, 145-55 | 17.6 | 53 |
| 51 | 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 |
| 50 | Binding and catalytic contributions to site recognition by flp recombinase. <i>Journal of Biological Chemistry</i> , 2008 , 283, 11414-23 | 5.4 | 10 |
| 49 | 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 |
| 48 | 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 |
| 47 | Control of transposase activity within a transpososome by the configuration of the flanking DNA segment of the transposon. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007 , 104, 14622-7 | 11.5 | 6 |
| 46 | Structure-based analysis of HU-DNA binding. Journal of Molecular Biology, 2007, 365, 1005-16 | 6.5 | 77 |
| 45 | 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 |
| 44 | Mechanisms of site-specific recombination. Annual Review of Biochemistry, 2006, 75, 567-605 | 29.1 | 581 |
| 43 | Visualizing Mu transposition: assembling the puzzle pieces. <i>Genes and Development</i> , 2005 , 19, 773-5 | 12.6 | 6 |
| 42 | IHF and HU: flexible architects of bent DNA. Current Opinion in Structural Biology, 2004, 14, 28-35 | 8.1 | 308 |
| 41 | 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 |
| 40 | Flexible DNA bending in HU-DNA cocrystal structures. <i>EMBO Journal</i> , 2003 , 22, 3749-60 | 13 | 205 |
| 39 | Structural plasticity of the Flp-Holliday junction complex. <i>Journal of Molecular Biology</i> , 2003 , 326, 425-3 | 346.5 | 42 |
| 38 | Integration host factor: putting a twist on protein-DNA recognition. <i>Journal of Molecular Biology</i> , 2003 , 330, 493-502 | 6.5 | 63 |
| 37 | Comparative architecture of transposase and integrase complexes. <i>Nature Structural Biology</i> , 2001 , 8, 302-7 | | 150 |

| 36 | Crystal structure of an IHF-DNA complex: a protein-induced DNA U-turn. <i>Cell</i> , 1996 , 87, 1295-306 | 56.2 | 688 |
|----|---|------|-----|
| 35 | 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 |
| 34 | 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 |
| 33 | Cooperativity mutants of the gamma delta resolvase identify an essential interdimer interaction. <i>Cell</i> , 1990 , 63, 1331-8 | 56.2 | 81 |
| 32 | A Moveable Feast: An Introduction to Mobile DNA1-39 | | 2 |
| 31 | Serine Resolvases237-252 | | 1 |
| 30 | Phage-encoded Serine Integrases and Other Large Serine Recombinases253-272 | | 8 |
| 29 | V(D)J Recombination: Mechanism, Errors, and Fidelity311-324 | | 2 |
| 28 | Programmed Genome Rearrangements in Tetrahymena349-367 | | 1 |
| 27 | Programmed Rearrangement in Ciliates: Paramecium369-388 | | O |
| 26 | Recombination and Diversification of the Variant Antigen Encoding Genes in the Malaria Parasite Plasmodium falciparum437-449 | | 1 |
| 25 | Copy-out P aste-in Transposition of IS911: A Major Transposition Pathway591-607 | | 1 |
| 24 | Transposons Tn10 and Tn5631-645 | | 1 |
| 23 | The Serine Recombinases73-89 | | 4 |
| 22 | Transposable Phage Mu669-691 | | 5 |
| 21 | Mariner and the ITm Superfamily of Transposons753-772 | | 2 |
| 20 | Mutator and MULE Transposons801-826 | | 2 |
| 19 | Helitrons, the Eukaryotic Rolling-circle Transposable Elements891-924 | | 6 |

| 18 | Ty3, a Position-specific Retrotransposon in Budding Yeast965-996 | 4 |
|----|---|------------|
| 17 | Host Factors in Retroviral Integration and the Selection of Integration Target Sites1035-1050 | 2 |
| 16 | Diversity-generating Retroelements in Phage and Bacterial Genomes1237-1252 | 4 |
| 15 | The Integron: Adaptation On Demand139-161 | 4 |
| 14 | Site-specific DNA Inversion by Serine Recombinases199-236 | 2 |
| 13 | hATTransposable Elements773-800 | 1 |
| 12 | Programmed Genome Rearrangements in the CiliateOxytricha389-407 | Ο |
| 11 | DNA Recombination Strategies During Antigenic Variation in the African Trypanosome409-435 | О |
| 10 | Retroviral DNA Transposition: Themes and Variations1101-1123 | |
| 9 | The Integration and Excision of CTnDOT183-198 | |
| 8 | An Overview of Tyrosine Site-specific Recombination: From an Flp Perspective41-71 | 2 |
| 7 | Hairpin Telomere Resolvases273-287 | |
| 6 | Related Mechanisms of Antibody Somatic Hypermutation and Class Switch Recombination325-348 | 1 |
| 5 | Reverse Transcription of Retroviruses and LTR Retrotransposons1051-1077 | 1 |
| 4 | Mating-type Gene Switching inSaccharomyces cerevisiae491-514 | |
| 3 | A Unique DNA Recombination Mechanism of the Mating/Cell-type Switching of Fission Yeasts: a Review515-52 | 2 <u>8</u> |
| 2 | The Ty1 LTR-Retrotransposon of Budding Yeast, Saccharomyces cerevisiae925-964 | |
| 1 | Xer Site-Specific Recombination: Promoting Vertical and Horizontal Transmission of Genetic Information163-1 | 182 |