

Manju M Hingorani

List of Publications by Year in descending order

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59
papers

2,193
citations

201674

27
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233421

45
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101
all docs

101
docs citations

101
times ranked

1604
citing authors

| # | ARTICLE | IF | CITATIONS |
|----|--|------|-----------|
| 1 | Mechanism of Processivity Clamp Opening by the Delta Subunit Wrench of the Clamp Loader Complex of <i>E. coli</i> DNA Polymerase III. <i>Cell</i> , 2001, 106, 417-428. | 28.9 | 236 |
| 2 | ATP Binding to the <i>Escherichia coli</i> Clamp Loader Powers Opening of the Ring-shaped Clamp of DNA Polymerase III Holoenzyme. <i>Journal of Biological Chemistry</i> , 1998, 273, 24550-24563. | 3.4 | 128 |
| 3 | Sliding clamps: A (tail)ored fit. <i>Current Biology</i> , 2000, 10, R25-R29. | 3.9 | 108 |
| 4 | Mismatch Recognition-Coupled Stabilization of Msh2-Msh6 in an ATP-Bound State at the Initiation of DNA Repair. <i>Biochemistry</i> , 2003, 42, 7682-7693. | 2.5 | 89 |
| 5 | The $\hat{\Gamma}$ Subunit of DNA Polymerase III Holoenzyme Serves as a Sliding Clamp Unloader in <i>Escherichia coli</i> . <i>Journal of Biological Chemistry</i> , 2000, 275, 34609-34618. | 3.4 | 79 |
| 6 | Overproduction and analysis of eukaryotic multiprotein complexes in <i>Escherichia coli</i> using a dual-vector strategy. <i>Analytical Biochemistry</i> , 2003, 319, 78-87. | 2.4 | 76 |
| 7 | A tale of toroids in DNA metabolism. <i>Nature Reviews Molecular Cell Biology</i> , 2000, 1, 22-30. | 37.0 | 74 |
| 8 | Large conformational changes in MutS during DNA scanning, mismatch recognition and repair signalling. <i>EMBO Journal</i> , 2012, 31, 2528-2540. | 7.8 | 73 |
| 9 | Replication Factor C Clamp Loader Subunit Arrangement within the Circular Pentamer and Its Attachment Points to Proliferating Cell Nuclear Antigen. <i>Journal of Biological Chemistry</i> , 2003, 278, 50744-50753. | 3.4 | 70 |
| 10 | Mechanism of Loading the <i>Escherichia coli</i> DNA Polymerase III $\hat{\Gamma}^2$ Sliding Clamp on DNA. <i>Journal of Biological Chemistry</i> , 2003, 278, 10033-10040. | 3.4 | 69 |
| 11 | Mechanism of MutS Searching for DNA Mismatches and Signaling Repair. <i>Journal of Biological Chemistry</i> , 2008, 283, 36646-36654. | 3.4 | 62 |
| 12 | Asymmetric ATP Binding and Hydrolysis Activity of the <i>Thermus aquaticus</i> MutS Dimer Is Key to Modulation of Its Interactions with Mismatched DNA. <i>Biochemistry</i> , 2004, 43, 13115-13128. | 2.5 | 61 |
| 13 | Mechanism of $\hat{\Gamma}^2$ Clamp Opening by the $\hat{\Gamma}$ Subunit of <i>Escherichia coli</i> DNA Polymerase III Holoenzyme. <i>Journal of Biological Chemistry</i> , 2001, 276, 19182-19189. | 3.4 | 59 |
| 14 | A Model for <i>Escherichia coli</i> DNA Polymerase III Holoenzyme Assembly at Primer/Template Ends. <i>Journal of Biological Chemistry</i> , 2000, 275, 3006-3015. | 3.4 | 58 |
| 15 | MutL traps MutS at a DNA mismatch. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 10914-10919. | 7.1 | 58 |
| 16 | Molecular Mechanism and Energetics of Clamp Assembly in <i>Escherichia coli</i> . <i>Journal of Biological Chemistry</i> , 2000, 275, 28413-28420. | 3.4 | 57 |
| 17 | Toroidal proteins: Running rings around DNA. <i>Current Biology</i> , 1998, 8, R83-R86. | 3.9 | 52 |
| 18 | Mechanism of ATP-Driven PCNA Clamp Loading by <i>S. cerevisiae</i> RFC. <i>Journal of Molecular Biology</i> , 2009, 388, 431-442. | 4.2 | 47 |

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|----|--|------|-----------|
| 19 | The Effects of Nucleotides on MutS-DNA Binding Kinetics Clarify the Role of MutS ATPase Activity in Mismatch Repair. <i>Journal of Molecular Biology</i> , 2007, 366, 1087-1098. | 4.2 | 45 |
| 20 | Single-molecule multiparameter fluorescence spectroscopy reveals directional MutS binding to mismatched bases in DNA. <i>Nucleic Acids Research</i> , 2012, 40, 5448-5464. | 14.5 | 44 |
| 21 | <scp>DnaN</scp> clamp zones provide a platform for spatiotemporal coupling of mismatch detection to <scp>DNA</scp> replication. <i>Molecular Microbiology</i> , 2013, 87, 553-568. | 2.5 | 44 |
| 22 | Contribution of Msh2 and Msh6 subunits to the asymmetric ATPase and DNA mismatch binding activities of <i>Saccharomyces cerevisiae</i> Msh2-Msh6 mismatch repair protein. <i>DNA Repair</i> , 2006, 5, 153-162. | 2.8 | 42 |
| 23 | Mismatch binding, ADP-ATP exchange and intramolecular signaling during mismatch repair. <i>DNA Repair</i> , 2016, 38, 24-31. | 2.8 | 39 |
| 24 | ATP Binding and Hydrolysis-Driven Rate-Determining Events in the RFC-Catalyzed PCNA Clamp Loading Reaction. <i>Journal of Molecular Biology</i> , 2012, 416, 176-191. | 4.2 | 38 |
| 25 | Missed cleavage opportunities by FEN1 lead to Okazaki fragment maturation via the long-flap pathway. <i>Nucleic Acids Research</i> , 2018, 46, 2956-2974. | 14.5 | 34 |
| 26 | On the Specificity of Interaction between the <i>Saccharomyces cerevisiae</i> Clamp Loader Replication Factor C and Primed DNA Templates during DNA Replication. <i>Journal of Biological Chemistry</i> , 2002, 277, 47213-47224. | 3.4 | 33 |
| 27 | Human MSH2 (hMSH2) Protein Controls ATP Processing by hMSH2-hMSH6. <i>Journal of Biological Chemistry</i> , 2011, 286, 40287-40295. | 3.4 | 33 |
| 28 | A Central Swivel Point in the RFC Clamp Loader Controls PCNA Opening and Loading on DNA. <i>Journal of Molecular Biology</i> , 2012, 416, 163-175. | 4.2 | 31 |
| 29 | Impact of Individual Proliferating Cell Nuclear Antigen-DNA Contacts on Clamp Loading and Function on DNA. <i>Journal of Biological Chemistry</i> , 2012, 287, 35370-35381. | 3.4 | 30 |
| 30 | Biochemical Analysis of the Human Mismatch Repair Proteins hMutS \pm MSH2G674A-MSH6 and MSH2-MSH6T1219D. <i>Journal of Biological Chemistry</i> , 2012, 287, 9777-9791. | 3.4 | 28 |
| 31 | Slow Conformational Changes in MutS and DNA Direct Ordered Transitions between Mismatch Search, Recognition and Signaling of DNA Repair. <i>Journal of Molecular Biology</i> , 2013, 425, 4192-4205. | 4.2 | 28 |
| 32 | Coordinated protein and DNA conformational changes govern mismatch repair initiation by MutS. <i>Nucleic Acids Research</i> , 2018, 46, 10782-10795. | 14.5 | 28 |
| 33 | <i>Saccharomyces cerevisiae</i> Msh2-Msh6 DNA binding kinetics reveal a mechanism of targeting sites for DNA mismatch repair. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 680-685. | 7.1 | 24 |
| 34 | MutS β -Induced DNA Conformational Changes Provide Insights into Its Role in Meiotic Recombination. <i>Biophysical Journal</i> , 2018, 115, 2087-2101. | 0.5 | 21 |
| 35 | Recurrent mismatch binding by MutS mobile clamps on DNA localizes repair complexes nearby. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 17775-17784. | 7.1 | 21 |
| 36 | Dynamical Allostereism in the Mechanism of Action of DNA Mismatch Repair Protein MutS. <i>Biophysical Journal</i> , 2011, 101, 1730-1739. | 0.5 | 20 |

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| 37 | Role of a Conserved Glutamate Residue in the Escherichia coli SecA ATPase Mechanism. Journal of Biological Chemistry, 2005, 280, 14611-14619. | 3.4 | 17 |
| 38 | Evolutionary Covariance Combined with Molecular Dynamics Predicts a Framework for Allostery in the MutS DNA Mismatch Repair Protein. Journal of Physical Chemistry B, 2017, 121, 2049-2061. | 2.6 | 17 |
| 39 | DNA Polymerase Structure and Mechanisms of Action. Current Organic Chemistry, 2000, 4, 887-913. | 1.6 | 16 |
| 40 | The ATPase mechanism of UvrA2 reveals the distinct roles of proximal and distal ATPase sites in nucleotide excision repair. Nucleic Acids Research, 2019, 47, 4136-4152. | 14.5 | 14 |
| 41 | Model-Based Global Analysis of Heterogeneous Experimental Data Using gfit. Methods in Molecular Biology, 2009, 500, 335-359. | 0.9 | 13 |
| 42 | The Variable Subdomain of Escherichia coli SecA Functions To Regulate SecA ATPase Activity and ADP Release. Journal of Bacteriology, 2012, 194, 2205-2213. | 2.2 | 12 |
| 43 | Interactions between avidin and graphene for development of a biosensing platform. Biosensors and Bioelectronics, 2017, 89, 326-333. | 10.1 | 12 |
| 44 | Dual Functions, Clamp Opening and Primer-Template Recognition, Define a Key Clamp Loader Subunit. Journal of Molecular Biology, 2004, 342, 1457-1469. | 4.2 | 11 |
| 45 | Linchpin DNA-binding residues serve as go/no-go controls in the replication factor C-catalyzed clamp-loading mechanism. Journal of Biological Chemistry, 2017, 292, 15892-15906. | 3.4 | 11 |
| 46 | Positioning the 5' flap junction in the active site controls the rate of flap endonuclease-1 catalyzed DNA cleavage. Journal of Biological Chemistry, 2018, 293, 4792-4804. | 3.4 | 11 |
| 47 | Conserved residues in the $\hat{\Gamma}$ subunit help the E. coli clamp loader, $\hat{\Gamma}^3$ complex, target primer-template DNA for clamp assembly. Nucleic Acids Research, 2008, 36, 3274-3286. | 14.5 | 7 |
| 48 | Application of Stopped-flow Kinetics Methods to Investigate the Mechanism of Action of a DNA Repair Protein. Journal of Visualized Experiments, 2010, , . | 0.3 | 7 |
| 49 | Mismatch Recognition by Saccharomyces cerevisiae Msh2-Msh6: Role of Structure and Dynamics. International Journal of Molecular Sciences, 2019, 20, 4271. | 4.1 | 4 |
| 50 | TIRF(ing) reveals Msh2-Msh6 surfing on DNA. Nature Structural and Molecular Biology, 2007, 14, 1124-1125. | 8.2 | 2 |
| 51 | Global and Local Conformational Studies of Mismatched Duplex DNA Upon Msh2-Msh6 Binding by Steady-State and Time-Resolved Fluorescence. Biophysical Journal, 2013, 104, 76a. | 0.5 | 0 |
| 52 | Msh4-Msh5 Induced DNA Conformational Changes Provide Insights into Its Role in Meiotic Recombination. Biophysical Journal, 2019, 116, 21a. | 0.5 | 0 |
| 53 | Examination of the ATPase Mechanism of <i>Saccharomyces cerevisiae</i> Replication Factor C. FASEB Journal, 2007, 21, A658. | 0.5 | 0 |
| 54 | Mopping up after messy polymerases and more. FASEB Journal, 2008, 22, 526.2. | 0.5 | 0 |

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|----|---|-----|-----------|
| 55 | Search and repair of bona fide base-pair mismatches in DNA. FASEB Journal, 2009, 23, . | 0.5 | 0 |
| 56 | A Sliding Scale Governs Mismatch Recognition and Initiation of DNA Mismatch Repair. FASEB Journal, 2010, 24, 876.5. | 0.5 | 0 |
| 57 | MutS and DNA dynamics during mismatch recognition and repair.. FASEB Journal, 2013, 27, . | 0.5 | 0 |
| 58 | Biochemical Analysis of <i>S. cerevisiae</i> Msh2-Msh3 Activity in Triplet Nucleotide Repeat Expansion. FASEB Journal, 2013, 27, 542.3. | 0.5 | 0 |
| 59 | Investigating the Link Between Mutations in MutS DNA Repair Protein and Lynch Cancer Syndrome. FASEB Journal, 2018, 32, . | 0.5 | 0 |