

Manju M Hingorani

List of Publications by Year in descending order

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59
papers

2,193
citations

201674

27
h-index

233421

45
g-index

101
all docs

101
docs citations

101
times ranked

1604
citing authors

#	ARTICLE	IF	CITATIONS
1	Recurrent mismatch binding by MutS mobile clamps on DNA localizes repair complexes nearby. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 17775-17784.	7.1	21
2	Mismatch Recognition by Saccharomyces cerevisiae Msh2-Msh6: Role of Structure and Dynamics. International Journal of Molecular Sciences, 2019, 20, 4271.	4.1	4
3	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
4	Msh4-Msh5 Induced DNA Conformational Changes Provide Insights into Its Role in Meiotic Recombination. Biophysical Journal, 2019, 116, 21a.	0.5	0
5	Missed cleavage opportunities by FEN1 lead to Okazaki fragment maturation via the long-flap pathway. Nucleic Acids Research, 2018, 46, 2956-2974.	14.5	34
6	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
7	MutS ³ -Induced DNA Conformational Changes Provide Insights into Its Role in Meiotic Recombination. Biophysical Journal, 2018, 115, 2087-2101.	0.5	21
8	Coordinated protein and DNA conformational changes govern mismatch repair initiation by MutS. Nucleic Acids Research, 2018, 46, 10782-10795.	14.5	28
9	Investigating the Link Between Mutations in MutS DNA Repair Protein and Lynch Cancer Syndrome. FASEB Journal, 2018, 32, .	0.5	0
10	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
11	Interactions between avidin and graphene for development of a biosensing platform. Biosensors and Bioelectronics, 2017, 89, 326-333.	10.1	12
12	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
13	Mismatch binding, ADP-ATP exchange and intramolecular signaling during mismatch repair. DNA Repair, 2016, 38, 24-31.	2.8	39
14	MutL traps MutS at a DNA mismatch. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 10914-10919.	7.1	58
15	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
16	Slow Conformational Changes in MutS and DNA Direct Ordered Transitions between Mismatch Search, Recognition and Signaling of DNA Repair. Journal of Molecular Biology, 2013, 425, 4192-4205.	4.2	28
17	<sc>DnaN</sc> clamp zones provide a platform for spatiotemporal coupling of mismatch detection to <sc>DNA</sc> replication. Molecular Microbiology, 2013, 87, 553-568.	2.5	44
18	MutS and DNA dynamics during mismatch recognition and repair.. FASEB Journal, 2013, 27, .	0.5	0

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19	Biochemical Analysis of <i>S. cerevisiae</i> Msh2-Msh3 Activity in Triplet Nucleotide Repeat Expansion. <i>FASEB Journal</i> , 2013, 27, 542.3.	0.5	0
20	The Variable Subdomain of <i>Escherichia coli</i> SecA Functions To Regulate SecA ATPase Activity and ADP Release. <i>Journal of Bacteriology</i> , 2012, 194, 2205-2213.	2.2	12
21	Biochemical Analysis of the Human Mismatch Repair Proteins hMutS± MSH2G674A-MSH6 and MSH2-MSH6T1219D. <i>Journal of Biological Chemistry</i> , 2012, 287, 9777-9791.	3.4	28
22	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
23	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
24	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
25	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
26	Large conformational changes in MutS during DNA scanning, mismatch recognition and repair signalling. <i>EMBO Journal</i> , 2012, 31, 2528-2540.	7.8	73
27	Dynamical Allostereism in the Mechanism of Action of DNA Mismatch Repair Protein MutS. <i>Biophysical Journal</i> , 2011, 101, 1730-1739.	0.5	20
28	Human MSH2 (hMSH2) Protein Controls ATP Processing by hMSH2-hMSH6. <i>Journal of Biological Chemistry</i> , 2011, 286, 40287-40295.	3.4	33
29	Application of Stopped-flow Kinetics Methods to Investigate the Mechanism of Action of a DNA Repair Protein. <i>Journal of Visualized Experiments</i> , 2010, , .	0.3	7
30	<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
31	A Sliding Scale Governs Mismatch Recognition and Initiation of DNA Mismatch Repair. <i>FASEB Journal</i> , 2010, 24, 876.5.	0.5	0
32	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
33	Model-Based Global Analysis of Heterogeneous Experimental Data Using gfit. <i>Methods in Molecular Biology</i> , 2009, 500, 335-359.	0.9	13
34	Search and repair of bona fide base-pair mismatches in DNA. <i>FASEB Journal</i> , 2009, 23, .	0.5	0
35	Conserved residues in the $\hat{\nu}$ subunit help the <i>E. coli</i> clamp loader, $\hat{\nu}^3$ complex, target primer-template DNA for clamp assembly. <i>Nucleic Acids Research</i> , 2008, 36, 3274-3286.	14.5	7
36	Mechanism of MutS Searching for DNA Mismatches and Signaling Repair. <i>Journal of Biological Chemistry</i> , 2008, 283, 36646-36654.	3.4	62

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37	Mopping up after messy polymerases and more. FASEB Journal, 2008, 22, 526.2.	0.5	0
38	The Effects of Nucleotides on MutS-DNA Binding Kinetics Clarify the Role of MutS ATPase Activity in Mismatch Repair. Journal of Molecular Biology, 2007, 366, 1087-1098.	4.2	45
39	TIRF(ing) reveals Msh2-Msh6 surfing on DNA. Nature Structural and Molecular Biology, 2007, 14, 1124-1125.	8.2	2
40	Examination of the ATPase Mechanism of <i>Saccharomyces cerevisiae</i> Replication Factor C. FASEB Journal, 2007, 21, A658.	0.5	0
41	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. DNA Repair, 2006, 5, 153-162.	2.8	42
42	Role of a Conserved Glutamate Residue in the Escherichia coli SecA ATPase Mechanism. Journal of Biological Chemistry, 2005, 280, 14611-14619.	3.4	17
43	Asymmetric ATP Binding and Hydrolysis Activity of the <i>Thermus aquaticus</i> MutS Dimer Is Key to Modulation of Its Interactions with Mismatched DNA. Biochemistry, 2004, 43, 13115-13128.	2.5	61
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	Overproduction and analysis of eukaryotic multiprotein complexes in Escherichia coli using a dual-vector strategy. Analytical Biochemistry, 2003, 319, 78-87.	2.4	76
46	Mismatch Recognition-Coupled Stabilization of Msh2-Msh6 in an ATP-Bound State at the Initiation of DNA Repair. Biochemistry, 2003, 42, 7682-7693.	2.5	89
47	Mechanism of Loading the Escherichia coli DNA Polymerase III Sliding Clamp on DNA. Journal of Biological Chemistry, 2003, 278, 10033-10040.	3.4	69
48	Replication Factor C Clamp Loader Subunit Arrangement within the Circular Pentamer and Its Attachment Points to Proliferating Cell Nuclear Antigen. Journal of Biological Chemistry, 2003, 278, 50744-50753.	3.4	70
49	On the Specificity of Interaction between the <i>Saccharomyces cerevisiae</i> Clamp Loader Replication Factor C and Primed DNA Templates during DNA Replication. Journal of Biological Chemistry, 2002, 277, 47213-47224.	3.4	33
50	Mechanism of Processivity Clamp Opening by the Delta Subunit Wrench of the Clamp Loader Complex of E. coli DNA Polymerase III. Cell, 2001, 106, 417-428.	28.9	236
51	Mechanism of Clamp Opening by the Subunit of Escherichia coli DNA Polymerase III Holoenzyme. Journal of Biological Chemistry, 2001, 276, 19182-19189.	3.4	59
52	A tale of toroids in DNA metabolism. Nature Reviews Molecular Cell Biology, 2000, 1, 22-30.	37.0	74
53	Sliding clamps: A (tail)ored fit. Current Biology, 2000, 10, R25-R29.	3.9	108
54	DNA Polymerase Structure and Mechanisms of Action. Current Organic Chemistry, 2000, 4, 887-913.	1.6	16

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55	The $\hat{\tau}$ Subunit of DNA Polymerase III Holoenzyme Serves as a Sliding Clamp Unloader in Escherichia coli. Journal of Biological Chemistry, 2000, 275, 34609-34618.	3.4	79
56	Molecular Mechanism and Energetics of Clamp Assembly in Escherichia coli. Journal of Biological Chemistry, 2000, 275, 28413-28420.	3.4	57
57	A Model for Escherichia coli DNA Polymerase III Holoenzyme Assembly at Primer/Template Ends. Journal of Biological Chemistry, 2000, 275, 3006-3015.	3.4	58
58	Toroidal proteins: Running rings around DNA. Current Biology, 1998, 8, R83-R86.	3.9	52
59	ATP Binding to the Escherichia coli Clamp Loader Powers Opening of the Ring-shaped Clamp of DNA Polymerase III Holoenzyme. Journal of Biological Chemistry, 1998, 273, 24550-24563.	3.4	128