

# Nilesh K Banavali

## List of PR Articles by Year in descending order

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44

PR articles

1,936

PR citations

262009

22

PR h-index

215727

43

g-index

45

documents

2158

doc citations

299426

22

h-index

2546

citing authors

| #  | ARTICLE  | IF   | PR CITATIONS |
|----|--|------|--------------|
| 1  | Starvation sensing by mycobacterial RelA/SpoT homologue through constitutive surveillance of translation. Proceedings of the National Academy of Sciences of the United States of America, 2023, 120, .  | 7.6  | 6            |
| 2  | The structure of a hibernating ribosome in a Lyme disease pathogen. Nature Communications, 2023, 14, .   | 13.9 | 6            |
| 3  | Ribosome hibernation: a new molecular framework for targeting nonreplicating persisters of mycobacteria. Microbiology (United Kingdom), 2021, 167, .   | 3.0  | 17           |
| 4  | Distinct mechanisms of the human mitoribosome recycling and antibiotic resistance. Nature Communications, 2021, 12, .  | 13.9 | 20           |
| 5  | The Mechanism of Cholesterol Modification of Hedgehog Ligand. Journal of Computational Chemistry, 2020, 41, 520-527.   | 4.9  | 12           |
| 6  | Structures of the human mitochondrial ribosome bound to EF-G1 reveal distinct features of mitochondrial translation elongation. Nature Communications, 2020, 11, .                                       | 13.9 | 47           |
| 7  | Spliceosomal Prp8 intein at the crossroads of protein and RNA splicing. PLoS Biology, 2019, 17, e3000104.  | 5.0  | 40           |
| 8  | General Base Swap Preserves Activity and Expands Substrate Tolerance in Hedgehog Autoprocessing. Journal of the American Chemical Society, 2019, 141, 18380-18384.                                       | 15.0 | 8            |
| 9  | Sterol A-ring plasticity in hedgehog protein cholesterolysis supports a primitive substrate selectivity mechanism. Chemical Communications, 2019, 55, 1829-1832.   | 3.4  | 10           |
| 10 | Conditional Protein Splicing Switch in Hyperthermophiles through an Intein-Extein Partnership. MBio, 2018, 9, .  | 4.4  | 33           |
| 11 | Structural Articulation of Biochemical Reactions Using Restrained Geometries and Topology Switching. Journal of Chemical Information and Modeling, 2018, 58, 453-463.                                    | 4.5  | 3            |
| 12 | Mycobacterial DnaB helicase intein as oxidative stress sensor. Nature Communications, 2018, 9, .   | 13.9 | 34           |
| 13 | Geometric Patterns for Neighboring Bases Near the Stacked State in Nucleic Acid Strands. Biochemistry, 2017, 56, 1426-1443.  | 2.4  | 8            |
| 14 | Chemical activation of adenylyl cyclase Rv1625c inhibits growth of <i>Mycobacterium tuberculosis</i> on cholesterol and modulates intramacrophage signaling. Molecular Microbiology, 2017, 105, 294-308. | 2.6  | 39           |
| 15 | Maintenance of electrostatic stabilization in altered tubulin lateral contacts may facilitate formation of helical filaments in foraminifera. Scientific Reports, 2016, 6, .                             | 3.5  | 6            |
| 16 | RNA approaches the B-form in stacked single strand dinucleotide contexts. Biopolymers, 2016, 105, 65-82.   | 2.9  | 8            |
| 17 | Novel Broad Spectrum Inhibitors Targeting the Flavivirus Methyltransferase. PLoS ONE, 2015, 10, e0130062.  | 2.4  | 64           |
| 18 | Identification and Characterization of Novel Broad-Spectrum Inhibitors of the Flavivirus Methyltransferase. ACS Infectious Diseases, 2015, 1, 340-349.   | 3.7  | 60           |

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|----|---|------|--------------|
| 19 | Post-translational environmental switch of RadA activity by exteinâ€“intein interactions in protein splicing. <i>Nucleic Acids Research</i> , 2015, 43, 6631-6648.  | 15.7 | 60           |
| 20 | Cytosine Unstacking and Strand Slippage at an Insertionâ€“Deletion Mutation Sequence in an Overhang-Containing DNA Duplex. <i>Biochemistry</i> , 2014, 53, 3807-3816.   | 2.4  | 5            |
| 21 | Analyzing the Relationship between Single Base Flipping and Strand Slippage near DNA Duplex Termini. <i>Journal of Physical Chemistry B</i> , 2013, 117, 14320-14328.   | 2.7  | 4            |
| 22 | Partial Base Flipping Is Sufficient for Strand Slippage near DNA Duplex Termini. <i>Journal of the American Chemical Society</i> , 2013, 135, 8274-8282.  | 15.0 | 16           |
| 23 | Molecular Evidence for $\beta$ -tubulin Neofunctionalization in Retaria (Foraminifera and Radiolarians). <i>Molecular Biology and Evolution</i> , 2013, 30, 2487-2493.  | 4.7  | 20           |
| 24 | Modeling a Ryanodine Receptor N-terminal Domain Connecting the Central Vestibule and the Corner Clamp Region. <i>Journal of Biological Chemistry</i> , 2013, 288, 903-914.  | 2.2  | 10           |
| 25 | Insertion domain within mammalian mitochondrial translation initiation factor 2 serves the role of eubacterial initiation factor 1. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 3918-3923.  | 7.6  | 59           |
| 26 | Computational Exploration of Structural Hypotheses for an Additional Sequence in a Mammalian Mitochondrial Protein. <i>PLoS ONE</i> , 2011, 6, e21871.  | 2.4  | 5            |
| 27 | A Low Affinity Ground State Conformation for the Dynein Microtubule Binding Domain. <i>Journal of Biological Chemistry</i> , 2010, 285, 15994-16002.  | 2.2  | 12           |
| 28 | Mapping the conformational transition in Src activation by cumulating the information from multiple molecular dynamics trajectories. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 3776-3781. | 7.6  | 113          |
| 29 | Flexibility and charge asymmetry in the activation loop of Src tyrosine kinases. <i>Proteins: Structure, Function and Bioinformatics</i> , 2009, 74, 378-389.   | 2.6  | 39           |
| 30 | Characterizing Structural Transitions Using Localized Free Energy Landscape Analysis. <i>PLoS ONE</i> , 2009, 4, e5525.   | 2.4  | 7            |
| 31 | DNA bending induced by carbocyclic sugar analogs constrained to the north conformation. <i>Biopolymers</i> , 2007, 85, 438-449.   | 2.9  | 5            |
| 32 | Anatomy of a structural pathway for activation of the catalytic domain of Src kinase Hck. <i>Proteins: Structure, Function and Bioinformatics</i> , 2007, 67, 1096-1112.  | 2.6  | 39           |
| 33 | Conserved Patterns in Backbone Torsional Changes Allow for Single Base Flipping from Duplex DNA with Minimal Distortion of the Double Helix. <i>Journal of Physical Chemistry B</i> , 2006, 110, 10997-11004.                                       | 2.7  | 12           |
| 34 | The N-Terminal End of the Catalytic Domain of Src Kinase Hck Is a Conformational Switch Implicated in Long-Range Allosteric Regulation. <i>Structure</i> , 2005, 13, 1715-1723.   | 3.8  | 46           |
| 35 | Free Energy Landscape of A-DNA to B-DNA Conversion in Aqueous Solution. <i>Journal of the American Chemical Society</i> , 2005, 127, 6866-6876.   | 15.0 | 125          |
| 36 | Caught in the act: visualization of an intermediate in the DNA base-flipping pathway induced by HhaI methyltransferase. <i>Nucleic Acids Research</i> , 2004, 32, 3877-3886.  | 15.7 | 44           |

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|----|--|------|--------------|
| 37 | Protein-facilitated base flipping in DNA by cytosine-5-methyltransferase. Proceedings of the National Academy of Sciences of the United States of America, 2003, 100, 68-73.   | 7.6  | 132          |
| 38 | Atomic Radii for Continuum Electrostatics Calculations on Nucleic Acids. Journal of Physical Chemistry B, 2002, 106, 11026-11035.  | 2.7  | 70           |
| 39 | Electrostatic free energy calculations using the generalized solvent boundary potential method. Journal of Chemical Physics, 2002, 117, 7381-7388.   | 2.8  | 38           |
| 40 | Free Energy and Structural Pathways of Base Flipping in a DNA GCGC Containing Sequence. Journal of Molecular Biology, 2002, 319, 141-160.  | 4.2  | 159          |
| 41 | INHIBITION OF (CYTOSINE C5)-METHYLTRANSFERASE BY OLIGONUCLEOTIDES CONTAINING FLEXIBLE (CYCLOPENTANE) AND CONFORMATIONALLY CONSTRAINED (BICYCLO[3.1.0]HEXANE) ABASIC SITES. Nucleosides, Nucleotides and Nucleic Acids, 2001, 20, 451-459.      | 1.6  | 22           |
| 42 | Reevaluation of Stereoelectronic Contributions to the Conformational Properties of the Phosphodiester and N3 <sup>-</sup> -Phosphoramidate Moieties of Nucleic Acids. Journal of the American Chemical Society, 2001, 123, 6747-6755.          | 15.0 | 36           |
| 43 | All-atom empirical force field for nucleic acids: II. Application to molecular dynamics simulations of DNA and RNA in solution. Journal of Computational Chemistry, 2000, 21, 105-120.   | 4.9  | 723          |
| 44 | Use of Oligodeoxyribonucleotides with Conformationally Constrained Abasic Sugar Targets To Probe the Mechanism of Base Flipping by HhaI DNA (Cytosine C5)-methyltransferase. Journal of the American Chemical Society, 2000, 122, 12422-12434. | 15.0 | 51           |