

Christopher D Putnam

List of Publications by Year in descending order

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76
papers

6,462
citations

81900

39
h-index

85541

71
g-index

81
all docs

81
docs citations

81
times ranked

8441
citing authors

| # | ARTICLE | IF | CITATIONS |
|----|--|------|-----------|
| 1 | X-ray solution scattering (SAXS) combined with crystallography and computation: defining accurate macromolecular structures, conformations and assemblies in solution. Quarterly Reviews of Biophysics, 2007, 40, 191-285. | 5.7 | 1,026 |
| 2 | Maintenance of Genome Stability in <i>Saccharomyces cerevisiae</i> . Science, 2002, 297, 552-557. | 12.6 | 442 |
| 3 | Active and inhibited human catalase structures: ligand and NADPH binding and catalytic mechanism 1 Edited by R. Huber. Journal of Molecular Biology, 2000, 296, 295-309. | 4.2 | 388 |
| 4 | The clinical continuum of cryopyrinopathies: Novel CIAS1 mutations in North American patients and a new cryopyrin model. Arthritis and Rheumatism, 2007, 56, 1273-1285. | 6.7 | 362 |
| 5 | Inflammasome-Mediated Disease Animal Models Reveal Roles for Innate but Not Adaptive Immunity. Immunity, 2009, 30, 875-887. | 14.3 | 305 |
| 6 | Evolution and mechanism from structures of an ADP-ribosylating toxin and NAD complex. Nature Structural Biology, 1999, 6, 932-936. | 9.7 | 223 |
| 7 | Mechanism and energetics of green fluorescent protein chromophore synthesis revealed by trapped intermediate structures. Proceedings of the National Academy of Sciences of the United States of America, 2003, 100, 12111-12116. | 7.1 | 194 |
| 8 | DNA REPAIR MECHANISMS FOR THE RECOGNITION AND REMOVAL OF DAMAGED DNA BASES. Annual Review of Biophysics and Biomolecular Structure, 1999, 28, 101-128. | 18.3 | 170 |
| 9 | Structure and mechanism of the RuvB holliday junction branch migration motor. Journal of Molecular Biology, 2001, 311, 297-310. | 4.2 | 157 |
| 10 | Mutation in Rpa1 results in defective DNA double-strand break repair, chromosomal instability and cancer in mice. Nature Genetics, 2005, 37, 750-755. | 21.4 | 141 |
| 11 | DNA double-strand break repair from head to tail. Current Opinion in Structural Biology, 2002, 12, 115-122. | 5.7 | 133 |
| 12 | Specific pathways prevent duplication-mediated genome rearrangements. Nature, 2009, 460, 984-989. | 27.8 | 122 |
| 13 | Protein mimicry of DNA from crystal structures of the uracil-DNA glycosylase inhibitor protein and its complex with <i>Escherichia coli</i> uracil-DNA glycosylase 1 Edited by D. C. Rees. Journal of Molecular Biology, 1999, 287, 331-346. | 4.2 | 120 |
| 14 | Lessons learned from structural results on uracil-DNA glycosylase. Mutation Research DNA Repair, 2000, 460, 183-199. | 3.7 | 117 |
| 15 | Exonuclease 1-dependent and independent mismatch repair. DNA Repair, 2015, 32, 24-32. | 2.8 | 115 |
| 16 | The N Terminus of <i>Saccharomyces cerevisiae</i> Msh6 Is an Unstructured Tether to PCNA. Molecular Cell, 2007, 26, 565-578. | 9.7 | 110 |
| 17 | Mismatch Repair, But Not Heteroduplex Rejection, Is Temporally Coupled to DNA Replication. Science, 2011, 334, 1713-1716. | 12.6 | 109 |
| 18 | The RNA polymerase I transcription factor UBF is a sequence-tolerant HMG-box protein that can recognize structured nucleic acids. Nucleic Acids Research, 1994, 22, 2651-2657. | 14.5 | 101 |

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|----|---|-----|-----------|
| 19 | PCNA and Msh2-Msh6 Activate an Mlh1-Pms1 Endonuclease Pathway Required for Exo1-Independent Mismatch Repair. <i>Molecular Cell</i> , 2014, 55, 291-304. | 9.7 | 89 |
| 20 | Chromosome healing by de novo telomere addition in <i>Saccharomyces cerevisiae</i> . <i>Molecular Microbiology</i> , 2006, 59, 1357-1368. | 2.5 | 85 |
| 21 | Structure and function correlation in histone H2A peptide-mediated gene transfer. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2002, 99, 7467-7471. | 7.1 | 72 |
| 22 | A conserved MutS homolog connector domain interface interacts with MutL homologs. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 22223-22228. | 7.1 | 69 |
| 23 | Perspectives on the DNA damage and replication checkpoint responses in <i>Saccharomyces cerevisiae</i> . <i>DNA Repair</i> , 2009, 8, 974-982. | 2.8 | 68 |
| 24 | Distinct SUMO Ligases Cooperate with Esc2 and Slx5 to Suppress Duplication-Mediated Genome Rearrangements. <i>PLoS Genetics</i> , 2013, 9, e1003670. | 3.5 | 68 |
| 25 | Evolution of the methyl directed mismatch repair system in <i>Escherichia coli</i> . <i>DNA Repair</i> , 2016, 38, 32-41. | 2.8 | 65 |
| 26 | Rational Design of a Functional Metalloenzyme: Introduction of a Site for Manganese Binding and Oxidation into a Heme Peroxidase. <i>Biochemistry</i> , 1998, 37, 16853-16862. | 2.5 | 63 |
| 27 | Protein mimicry of DNA and pathway regulation. <i>DNA Repair</i> , 2005, 4, 1410-1420. | 2.8 | 63 |
| 28 | Guinier peak analysis for visual and automated inspection of small-angle X-ray scattering data. <i>Journal of Applied Crystallography</i> , 2016, 49, 1412-1419. | 4.5 | 56 |
| 29 | <i>Escherichia coli</i> MutS Tetramerization Domain Structure Reveals That Stable Dimers but Not Tetramers Are Essential for DNA Mismatch Repair in Vivo. <i>Journal of Biological Chemistry</i> , 2007, 282, 16345-16354. | 3.4 | 55 |
| 30 | DNA conformations in mismatch repair probed in solution by X-ray scattering from gold nanocrystals. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 17308-17313. | 7.1 | 53 |
| 31 | FEN1 endonuclease as a therapeutic target for human cancers with defects in homologous recombination. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 19415-19424. | 7.1 | 53 |
| 32 | Dominant Mutations in <i>S. cerevisiae</i> PMS1 Identify the Mlh1-Pms1 Endonuclease Active Site and an Exonuclease 1-Independent Mismatch Repair Pathway. <i>PLoS Genetics</i> , 2013, 9, e1003869. | 3.5 | 52 |
| 33 | Chromosome healing through terminal deletions generated by de novo telomere additions in <i>Saccharomyces cerevisiae</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2004, 101, 13262-13267. | 7.1 | 51 |
| 34 | <i>Saccharomyces cerevisiae</i> as a Model System To Define the Chromosomal Instability Phenotype. <i>Molecular and Cellular Biology</i> , 2005, 25, 7226-7238. | 2.3 | 51 |
| 35 | <i>EPCAM</i> mutation update: Variants associated with congenital tufting enteropathy and Lynch syndrome. <i>Human Mutation</i> , 2019, 40, 142-161. | 2.5 | 51 |
| 36 | Analysis of Chromosomal Rearrangements in <i>Saccharomyces cerevisiae</i> . <i>Methods in Enzymology</i> , 2006, 409, 462-476. | 1.0 | 50 |

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|----|---|------|-----------|
| 37 | Pathways and Mechanisms that Prevent Genome Instability in <i>Saccharomyces cerevisiae</i> . <i>Genetics</i> , 2017, 206, 1187-1225. | 2.9 | 49 |
| 38 | Guidelines for DNA recombination and repair studies: Cellular assays of DNA repair pathways. <i>Microbial Cell</i> , 2019, 6, 1-64. | 3.2 | 47 |
| 39 | Immunodeficiency and bone marrow failure with mosaic and germline TLR8 gain of function. <i>Blood</i> , 2021, 137, 2450-2462. | 1.4 | 47 |
| 40 | A <i>Saccharomyces cerevisiae</i> RNase H2 Interaction Network Functions To Suppress Genome Instability. <i>Molecular and Cellular Biology</i> , 2014, 34, 1521-1534. | 2.3 | 46 |
| 41 | Aneuploidy Drives a Mutator Phenotype in Cancer. <i>Science</i> , 2011, 333, 942-943. | 12.6 | 45 |
| 42 | Alternative splicing regulates stochastic NLRP3 activity. <i>Nature Communications</i> , 2019, 10, 3238. | 12.8 | 44 |
| 43 | Coupling distant sites in DNA during DNA mismatch repair. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007, 104, 12953-12954. | 7.1 | 41 |
| 44 | Probing DNA- and ATP-mediated Conformational Changes in the MutS Family of Mismatch Recognition Proteins Using Deuterium Exchange Mass Spectrometry. <i>Journal of Biological Chemistry</i> , 2010, 285, 13170-13182. | 3.4 | 40 |
| 45 | Determination of Cross Chromosomal Rearrangement Rates. <i>Cold Spring Harbor Protocols</i> , 2010, 2010, pdb.prot5492. | 0.3 | 39 |
| 46 | Post-Replication Repair Suppresses Duplication-Mediated Genome Instability. <i>PLoS Genetics</i> , 2010, 6, e1000933. | 3.5 | 39 |
| 47 | Mutations in topoisomerase $\text{I}\beta^2$ result in a B cell immunodeficiency. <i>Nature Communications</i> , 2019, 10, 3644. | 12.8 | 37 |
| 48 | Mlh2 Is an Accessory Factor for DNA Mismatch Repair in <i>Saccharomyces cerevisiae</i> . <i>PLoS Genetics</i> , 2014, 10, e1004327. | 3.5 | 36 |
| 49 | A genetic network that suppresses genome rearrangements in <i>Saccharomyces cerevisiae</i> and contains defects in cancers. <i>Nature Communications</i> , 2016, 7, 11256. | 12.8 | 36 |
| 50 | Chimeric <i>Saccharomyces cerevisiae</i> Msh6 protein with an Msh3 mismatch-binding domain combines properties of both proteins. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007, 104, 10956-10961. | 7.1 | 35 |
| 51 | Identification of Exo1-Msh2 interaction motifs in DNA mismatch repair and new Msh2-binding partners. <i>Nature Structural and Molecular Biology</i> , 2018, 25, 650-659. | 8.2 | 35 |
| 52 | Mutations of Complement Factor I and Potential Mechanisms of Neuroinflammation in Acute Hemorrhagic Leukoencephalitis. <i>Journal of Clinical Immunology</i> , 2013, 33, 162-171. | 3.8 | 34 |
| 53 | Functional Studies and Homology Modeling of Msh2-Msh3 Predict that Mismatch Recognition Involves DNA Bending and Strand Separation. <i>Molecular and Cellular Biology</i> , 2010, 30, 3321-3328. | 2.3 | 33 |
| 54 | A chemical-genetic screen to unravel the genetic network of <i>CDC28/CDK1</i> links ubiquitin and Rad6-Bre1 to cell cycle progression. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 18748-18753. | 7.1 | 31 |

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|----|---|------|-----------|
| 55 | Strand discrimination in DNA mismatch repair. <i>DNA Repair</i> , 2021, 105, 103161. | 2.8 | 31 |
| 56 | DNA damage recognition and repair pathway coordination revealed by the structural biochemistry of DNA repair enzymes. <i>Progress in Molecular Biology and Translational Science</i> , 2001, 68, 315-347. | 1.9 | 30 |
| 57 | Mutation of an Active Site Residue in <i>Escherichia coli</i> Uracil-DNA Glycosylase: Effect on DNA Binding, Uracil Inhibition and Catalysis. <i>Biochemistry</i> , 1999, 38, 4834-4845. | 2.5 | 28 |
| 58 | Bioinformatic identification of genes suppressing genome instability. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, E3251-9. | 7.1 | 25 |
| 59 | The properties of Msh2-Msh6 ATP binding mutants suggest a signal amplification mechanism in DNA mismatch repair. <i>Journal of Biological Chemistry</i> , 2018, 293, 18055-18070. | 3.4 | 24 |
| 60 | DNA Repair Pathway Selection Caused by Defects in TELL1, SAE2, and De Novo Telomere Addition Generates Specific Chromosomal Rearrangement Signatures. <i>PLoS Genetics</i> , 2014, 10, e1004277. | 3.5 | 20 |
| 61 | Ligation of newly replicated DNA controls the timing of DNA mismatch repair. <i>Current Biology</i> , 2021, 31, 1268-1276.e6. | 3.9 | 19 |
| 62 | The Swr1 chromatin-remodeling complex prevents genome instability induced by replication fork progression defects. <i>Nature Communications</i> , 2018, 9, 3680. | 12.8 | 17 |
| 63 | SUMO E3 ligase Mms21 prevents spontaneous DNA damage induced genome rearrangements. <i>PLoS Genetics</i> , 2018, 14, e1007250. | 3.5 | 16 |
| 64 | Cdc73 suppresses genome instability by mediating telomere homeostasis. <i>PLoS Genetics</i> , 2018, 14, e1007170. | 3.5 | 15 |
| 65 | The food of sweet and bitter fancy. , 2000, 7, 17-18. | | 13 |
| 66 | Engineered Disulfide-forming Amino Acid Substitutions Interfere with a Conformational Change in the Mismatch Recognition Complex Msh2-Msh6 Required for Mismatch Repair. <i>Journal of Biological Chemistry</i> , 2012, 287, 41232-41244. | 3.4 | 13 |
| 67 | Mechanisms underlying genome instability mediated by formation of foldback inversions in <i>Saccharomyces cerevisiae</i> . <i>ELife</i> , 2020, 9, . | 6.0 | 10 |
| 68 | Analyzing Genome Rearrangements in <i>Saccharomyces cerevisiae</i> . <i>Methods in Molecular Biology</i> , 2018, 1672, 43-61. | 0.9 | 9 |
| 69 | Rad27 and Exo1 function in different excision pathways for mismatch repair in <i>Saccharomyces cerevisiae</i> . <i>Nature Communications</i> , 2021, 12, 5568. | 12.8 | 9 |
| 70 | Essential <i>Saccharomyces cerevisiae</i> genome instability suppressing genes identify potential human tumor suppressors. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 17377-17382. | 7.1 | 8 |
| 71 | Disease-associated mutations in topoisomerase III ² result in defective NK cells. <i>Journal of Allergy and Clinical Immunology</i> , 2022, 149, 2171-2176.e3. | 2.9 | 7 |
| 72 | MutS sliding clamps on an uncertain track to DNA mismatch repair. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 20351-20353. | 7.1 | 3 |

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|----|---|-----|-----------|
| 73 | DNA Mismatch Repair: Mechanisms and Cancer Genetics. , 2018, , . | | 1 |
| 74 | Rad5 and Its Human Homologs, HLTF and SHPRH, Are Novel Interactors of Mismatch Repair. <i>Frontiers in Cell and Developmental Biology</i> , 0, 10, . | 3.7 | 1 |
| 75 | A chemicalâ€genetic screen to unravel the genetic network of CDC28/CDK1 links ubiquitin and Rad6â€Bre1 to cell cycle progression. <i>FASEB Journal</i> , 2012, 26, 590.1. | 0.5 | 0 |
| 76 | Template homology determines the genetics and mechanisms of gross chromosomal rearrangements in <i>S. cerevisiae</i> (736.11). <i>FASEB Journal</i> , 2014, 28, 736.11. | 0.5 | 0 |