# Christopher D Putnam

List of Publications by Year
in descending order

Source: https://exaly.com/author-pdf/5336628/publications.pdf

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|---|---|---|---|
| 76 papers | 6,462 citations | 81743 39 h-index | 85405 71 g-index |
| 81 all docs | 81 docs citations | 81 times ranked | 8441 citing authors |

| # | Article | IF | Citations |
|---|---|---|---|
| 1 | Disease-associated mutations in topoisomerase IIÎ² result in defective NK cells. Journal of Allergy and Clinical Immunology, 2022, 149, 2171-2176.e3. | 1.5 | 7 |
| 2 | Ligation of newly replicated DNA controls the timing of DNA mismatch repair. Current Biology, 2021, 31, 1268-1276.e6. | 1.8 | 19 |
| 3 | Immunodeficiency and bone marrow failure with mosaic and germline TLR8 gain of function. Blood, 2021, 137, 2450-2462. | 0.6 | 47 |
| 4 | Rad27 and Exo1 function in different excision pathways for mismatch repair in Saccharomyces cerevisiae. Nature Communications, 2021, 12, 5568. | 5.8 | 9 |
| 5 | Strand discrimination in DNA mismatch repair. DNA Repair, 2021, 105, 103161. | 1.3 | 31 |
| 6 | MutS sliding clamps on an uncertain track to DNA mismatch repair. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 20351-20353. | 3.3 | 3 |
| 7 | FEN1 endonuclease as a therapeutic target for human cancers with defects in homologous recombination. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 19415-19424. | 3.3 | 53 |
| 8 | Mechanisms underlying genome instability mediated by formation of foldback inversions in Saccharomyces cerevisiae. ELife, 2020, 9, . | 2.8 | 10 |
| 9 | Essential Saccharomyces cerevisiae genome instability suppressing genes identify potential human tumor suppressors. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 17377-17382. | 3.3 | 8 |
| 10 | Mutations in topoisomerase IIÎ² result in a B cell immunodeficiency. Nature Communications, 2019, 10, 3644. | 5.8 | 37 |
| 11 | Alternative splicing regulates stochastic NLRP3 activity. Nature Communications, 2019, 10, 3238. | 5.8 | 44 |
| 12 | Guidelines for DNA recombination and repair studies: Cellular assays of DNA repair pathways. Microbial Cell, 2019, 6, 1-64. | 1.4 | 47 |
| 13 | EPCAMmutation update: Variants associated with congenital tufting enteropathy and Lynch syndrome. Human Mutation, 2019, 40, 142-161. | 1.1 | 51 |
| 14 | Analyzing Genome Rearrangements in Saccharomyces cerevisiae. Methods in Molecular Biology, 2018, 1672, 43-61. | 0.4 | 9 |
| 15 | The properties of Msh2â€“Msh6 ATP binding mutants suggest a signal amplification mechanism in DNA mismatch repair. Journal of Biological Chemistry, 2018, 293, 18055-18070. | 1.6 | 24 |
| 16 | DNA Mismatch Repair: Mechanisms and Cancer Genetics. , 2018, , . | | 1 |
| 17 | The Swr1 chromatin-remodeling complex prevents genome instability induced by replication fork progression defects. Nature Communications, 2018, 9, 3680. | 5.8 | 17 |
| 18 | Identification of Exo1-Msh2 interaction motifs in DNA mismatch repair and new Msh2-binding partners. Nature Structural and Molecular Biology, 2018, 25, 650-659. | 3.6 | 35 |

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|---|---|---|---|
| 19 | Cdc73 suppresses genome instability by mediating telomere homeostasis. PLoS Genetics, 2018, 14, e1007170. | 1.5 | 15 |
| 20 | SUMO E3 ligase Mms21 prevents spontaneous DNA damage induced genome rearrangements. PLoS Genetics, 2018, 14, e1007250. | 1.5 | 16 |
| 21 | Pathways and Mechanisms that Prevent Genome Instability in Saccharomyces cerevisiae. Genetics, 2017, 206, 1187-1225. | 1.2 | 49 |
| 22 | Guinier peak analysis for visual and automated inspection of small-angle X-ray scattering data. Journal of Applied Crystallography, 2016, 49, 1412-1419. | 1.9 | 56 |
| 23 | A genetic network that suppresses genome rearrangements in Saccharomyces cerevisiae and contains defects in cancers. Nature Communications, 2016, 7, 11256. | 5.8 | 36 |
| 24 | Evolution of the methyl directed mismatch repair system in Escherichia coli. DNA Repair, 2016, 38, 32-41. | 1.3 | 65 |
| 25 | Exonuclease 1-dependent and independent mismatch repair. DNA Repair, 2015, 32, 24-32. | 1.3 | 115 |
| 26 | DNA Repair Pathway Selection Caused by Defects in TEL1, SAE2, and De Novo Telomere Addition Generates Specific Chromosomal Rearrangement Signatures. PLoS Genetics, 2014, 10, e1004277. | 1.5 | 20 |
| 27 | Mlh2 Is an Accessory Factor for DNA Mismatch Repair in Saccharomyces cerevisiae. PLoS Genetics, 2014, 10, e1004327. | 1.5 | 36 |
| 28 | A Saccharomyces cerevisiae RNase H2 Interaction Network Functions To Suppress Genome Instability. Molecular and Cellular Biology, 2014, 34, 1521-1534. | 1.1 | 46 |
| 29 | PCNA and Msh2-Msh6 Activate an Mlh1-Pms1 Endonuclease Pathway Required for Exo1-Independent Mismatch Repair. Molecular Cell, 2014, 55, 291-304. | 4.5 | 89 |
| 30 | Template homology determines the genetics and mechanisms of gross chromosomal rearrangements in S. cerevisiae (736.11). FASEB Journal, 2014, 28, 736.11. | 0.2 | 0 |
| 31 | Mutations of Complement Factor I and Potential Mechanisms of Neuroinflammation in Acute Hemorrhagic Leukoencephalitis. Journal of Clinical Immunology, 2013, 33, 162-171. | 2.0 | 34 |
| 32 | Distinct SUMO Ligases Cooperate with Esc2 and Slx5 to Suppress Duplication-Mediated Genome Rearrangements. PLoS Genetics, 2013, 9, e1003670. | 1.5 | 68 |
| 33 | Dominant Mutations in S. cerevisiae PMS1 Identify the Mlh1-Pms1 Endonuclease Active Site and an Exonuclease 1-Independent Mismatch Repair Pathway. PLoS Genetics, 2013, 9, e1003869. | 1.5 | 52 |
| 34 | DNA conformations in mismatch repair probed in solution by X-ray scattering from gold nanocrystals. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 17308-17313. | 3.3 | 53 |
| 35 | Engineered Disulfide-forming Amino Acid Substitutions Interfere with a Conformational Change in the Mismatch Recognition Complex Msh2-Msh6 Required for Mismatch Repair. Journal of Biological Chemistry, 2012, 287, 41232-41244. | 1.6 | 13 |
| 36 | Bioinformatic identification of genes suppressing genome instability. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, E3251-9. | 3.3 | 25 |

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|---|---|---|---|
| 37 | A chemicalâ€genetic screen to unravel the genetic network of CDC28/CDK1 links ubiquitin and Rad6â€“Bre1 to cell cycle progression. FASEB Journal, 2012, 26, 590.1. | 0.2 | 0 |
| 38 | Aneuploidy Drives a Mutator Phenotype in Cancer. Science, 2011, 333, 942-943. | 6.0 | 45 |
| 39 | Mismatch Repair, But Not Heteroduplex Rejection, Is Temporally Coupled to DNA Replication. Science, 2011, 334, 1713-1716. | 6.0 | 109 |
| 40 | A chemical-genetic screen to unravel the genetic network of CDC28/CDK1 links ubiquitin and Rad6â€“Bre1 to cell cycle progression. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 18748-18753. | 3.3 | 31 |
| 41 | Functional Studies and Homology Modeling of Msh2-Msh3 Predict that Mispair Recognition Involves DNA Bending and Strand Separation. Molecular and Cellular Biology, 2010, 30, 3321-3328. | 1.1 | 33 |
| 42 | Determination of Gross Chromosomal Rearrangement Rates. Cold Spring Harbor Protocols, 2010, 2010, pdb.prot5492. | 0.2 | 39 |
| 43 | Probing DNA- and ATP-mediated Conformational Changes in the MutS Family of Mispair Recognition Proteins Using Deuterium Exchange Mass Spectrometry. Journal of Biological Chemistry, 2010, 285, 13170-13182. | 1.6 | 40 |
| 44 | Post-Replication Repair Suppresses Duplication-Mediated Genome Instability. PLoS Genetics, 2010, 6, e1000933. | 1.5 | 39 |
| 45 | A conserved MutS homolog connector domain interface interacts with MutL homologs. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 22223-22228. | 3.3 | 69 |
| 46 | Perspectives on the DNA damage and replication checkpoint responses in Saccharomyces cerevisiae. DNA Repair, 2009, 8, 974-982. | 1.3 | 68 |
| 47 | Specific pathways prevent duplication-mediated genome rearrangements. Nature, 2009, 460, 984-989. | 13.7 | 122 |
| 48 | Inflammasome-Mediated Disease Animal Models Reveal Roles for Innate but Not Adaptive Immunity. Immunity, 2009, 30, 875-887. | 6.6 | 305 |
| 49 | Escherichia coli MutS Tetramerization Domain Structure Reveals That Stable Dimers but Not Tetramers Are Essential for DNA Mismatch Repair in Vivo. Journal of Biological Chemistry, 2007, 282, 16345-16354. | 1.6 | 55 |
| 50 | Chimeric Saccharomyces cerevisiae Msh6 protein with an Msh3 mispair-binding domain combines properties of both proteins. Proceedings of the National Academy of Sciences of the United States of America, 2007, 104, 10956-10961. | 3.3 | 35 |
| 51 | Coupling distant sites in DNA during DNA mismatch repair. Proceedings of the National Academy of Sciences of the United States of America, 2007, 104, 12953-12954. | 3.3 | 41 |
| 52 | The N Terminus of Saccharomyces cerevisiae Msh6 Is an Unstructured Tether to PCNA. Molecular Cell, 2007, 26, 565-578. | 4.5 | 110 |
| 53 | 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 |
| 54 | 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. | 2.4 | 1,026 |

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|---|---|---|---|
| 55 | Analysis of Grossâ€Chromosomal Rearrangements in Saccharomyces cerevisiae. Methods in Enzymology, 2006, 409, 462-476. | 0.4 | 50 |
| 56 | Chromosome healing byde novotelomere addition inSaccharomyces cerevisiae. Molecular Microbiology, 2006, 59, 1357-1368. | 1.2 | 85 |
| 57 | Mutation in Rpa1 results in defective DNA double-strand break repair, chromosomal instability and cancer in mice. Nature Genetics, 2005, 37, 750-755. | 9.4 | 141 |
| 58 | Saccharomyces cerevisiae as a Model System To Define the Chromosomal Instability Phenotype. Molecular and Cellular Biology, 2005, 25, 7226-7238. | 1.1 | 51 |
| 59 | Protein mimicry of DNA and pathway regulation. DNA Repair, 2005, 4, 1410-1420. | 1.3 | 63 |
| 60 | Chromosome healing through terminal deletions generated by de novo telomere additions in Saccharomyces cerevisiae. Proceedings of the National Academy of Sciences of the United States of America, 2004, 101, 13262-13267. | 3.3 | 51 |
| 61 | 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. | 3.3 | 194 |
| 62 | Maintenance of Genome Stability in Saccharomyces cerevisiae. Science, 2002, 297, 552-557. | 6.0 | 442 |
| 63 | Structure and function correlation in histone H2A peptide-mediated gene transfer. Proceedings of the National Academy of Sciences of the United States of America, 2002, 99, 7467-7471. | 3.3 | 72 |
| 64 | DNA double-strand break repair from head to tail. Current Opinion in Structural Biology, 2002, 12, 115-122. | 2.6 | 133 |
| 65 | Structure and mechanism of the RuvB holliday junction branch migration motor. Journal of Molecular Biology, 2001, 311, 297-310. | 2.0 | 157 |
| 66 | DNA damage recognition and repair pathway coordination revealed by the structural biochemistry of DNA repair enzymes. Progress in Molecular Biology and Translational Science, 2001, 68, 315-347. | 1.9 | 30 |
| 67 | The food of sweet and bitter fancy. , 2000, 7, 17-18. | | 13 |
| 68 | Active and inhibited human catalase structures: ligand and NADPH binding and catalytic mechanism 1 1Edited by R. Huber. Journal of Molecular Biology, 2000, 296, 295-309. | 2.0 | 388 |
| 69 | Lessons learned from structural results on uracil-DNA glycosylase. Mutation Research DNA Repair, 2000, 460, 183-199. | 3.8 | 117 |
| 70 | Evolution and mechanism from structures of an ADP-ribosylating toxin and NAD complex. Nature Structural Biology, 1999, 6, 932-936. | 9.7 | 223 |
| 71 | 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 |
| 72 | Mutation of an Active Site Residue inEscherichia coliUracil-DNA Glycosylase:Â Effect on DNA Binding, Uracil Inhibition and Catalysisâ€. Biochemistry, 1999, 38, 4834-4845. | 1.2 | 28 |

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|---|---|---|---|
| 73 | Protein mimicry of DNA from crystal structures of the uracil-DNA glycosylase inhibitor protein and its complex with Escherichia coli uracil-DNA glycosylase 1 1Edited by D. C. Rees. Journal of Molecular Biology, 1999, 287, 331-346. | 2.0 | 120 |
| 74 | Rational Design of a Functional Metalloenzyme:â€‰ Introduction of a Site for Manganese Binding and Oxidation into a Heme Peroxidase. Biochemistry, 1998, 37, 16853-16862. | 1.2 | 63 |
| 75 | 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. | 6.5 | 101 |
| 76 | Rad5 and Its Human Homologs, HLTF and SHPRH, Are Novel Interactors of Mismatch Repair. Frontiers in Cell and Developmental Biology, 0, 10, . | 1.8 | 1 |