

Christopher D Putnam

List of Publications by Year in descending order

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76
papers

6,462
citations

81900

39
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85541

71
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81
all docs

81
docs citations

81
times ranked

8441
citing authors

#	ARTICLE	IF	CITATIONS
1	Disease-associated mutations in topoisomerase II ^β result in defective NK cells. <i>Journal of Allergy and Clinical Immunology</i> , 2022, 149, 2171-2176.e3.	2.9	7
2	Ligation of newly replicated DNA controls the timing of DNA mismatch repair. <i>Current Biology</i> , 2021, 31, 1268-1276.e6.	3.9	19
3	Immunodeficiency and bone marrow failure with mosaic and germline TLR8 gain of function. <i>Blood</i> , 2021, 137, 2450-2462.	1.4	47
4	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
5	Strand discrimination in DNA mismatch repair. <i>DNA Repair</i> , 2021, 105, 103161.	2.8	31
6	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
7	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
8	Mechanisms underlying genome instability mediated by formation of foldback inversions in <i>Saccharomyces cerevisiae</i> . <i>ELife</i> , 2020, 9, .	6.0	10
9	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
10	Mutations in topoisomerase II ^β result in a B cell immunodeficiency. <i>Nature Communications</i> , 2019, 10, 3644.	12.8	37
11	Alternative splicing regulates stochastic NLRP3 activity. <i>Nature Communications</i> , 2019, 10, 3238.	12.8	44
12	Guidelines for DNA recombination and repair studies: Cellular assays of DNA repair pathways. <i>Microbial Cell</i> , 2019, 6, 1-64.	3.2	47
13	<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
14	Analyzing Genome Rearrangements in <i>Saccharomyces cerevisiae</i> . <i>Methods in Molecular Biology</i> , 2018, 1672, 43-61.	0.9	9
15	The properties of Msh2 ^Δ 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
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. <i>Nature Communications</i> , 2018, 9, 3680.	12.8	17
18	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

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19	Cdc73 suppresses genome instability by mediating telomere homeostasis. <i>PLoS Genetics</i> , 2018, 14, e1007170.	3.5	15
20	SUMO E3 ligase Mms21 prevents spontaneous DNA damage induced genome rearrangements. <i>PLoS Genetics</i> , 2018, 14, e1007250.	3.5	16
21	Pathways and Mechanisms that Prevent Genome Instability in <i>Saccharomyces cerevisiae</i> . <i>Genetics</i> , 2017, 206, 1187-1225.	2.9	49
22	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
23	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
24	Evolution of the methyl directed mismatch repair system in <i>Escherichia coli</i> . <i>DNA Repair</i> , 2016, 38, 32-41.	2.8	65
25	Exonuclease 1-dependent and independent mismatch repair. <i>DNA Repair</i> , 2015, 32, 24-32.	2.8	115
26	DNA Repair Pathway Selection Caused by Defects in TEL1, SAE2, and De Novo Telomere Addition Generates Specific Chromosomal Rearrangement Signatures. <i>PLoS Genetics</i> , 2014, 10, e1004277.	3.5	20
27	Mlh2 Is an Accessory Factor for DNA Mismatch Repair in <i>Saccharomyces cerevisiae</i> . <i>PLoS Genetics</i> , 2014, 10, e1004327.	3.5	36
28	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
29	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
30	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
31	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
32	Distinct SUMO Ligases Cooperate with Esc2 and Slx5 to Suppress Duplication-Mediated Genome Rearrangements. <i>PLoS Genetics</i> , 2013, 9, e1003670.	3.5	68
33	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
34	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
35	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
36	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

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37	A chemical-genetic screen to unravel the genetic network of CDC28/CDK1 links ubiquitin and Rad6-Bre1 to cell cycle progression. <i>FASEB Journal</i> , 2012, 26, 590.1.	0.5	0
38	Aneuploidy Drives a Mutator Phenotype in Cancer. <i>Science</i> , 2011, 333, 942-943.	12.6	45
39	Mismatch Repair, But Not Heteroduplex Rejection, Is Temporally Coupled to DNA Replication. <i>Science</i> , 2011, 334, 1713-1716.	12.6	109
40	A chemical-genetic screen to unravel the genetic network of CDC28/CDK1 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
41	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
42	Determination of Gross Chromosomal Rearrangement Rates. <i>Cold Spring Harbor Protocols</i> , 2010, 2010, pdb.prot5492.	0.3	39
43	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
44	Post-Replication Repair Suppresses Duplication-Mediated Genome Instability. <i>PLoS Genetics</i> , 2010, 6, e1000933.	3.5	39
45	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
46	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
47	Specific pathways prevent duplication-mediated genome rearrangements. <i>Nature</i> , 2009, 460, 984-989.	27.8	122
48	Inflammasome-Mediated Disease Animal Models Reveal Roles for Innate but Not Adaptive Immunity. <i>Immunity</i> , 2009, 30, 875-887.	14.3	305
49	<i>Escherichia coli</i> MutS Tetramerization Domain Structure Reveals That Stable Dimers but Not Tetramers Are Essential for DNA Mismatch Repair <i>In Vivo</i> . <i>Journal of Biological Chemistry</i> , 2007, 282, 16345-16354.	3.4	55
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	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
52	The N Terminus of <i>Saccharomyces cerevisiae</i> Msh6 Is an Unstructured Tether to PCNA. <i>Molecular Cell</i> , 2007, 26, 565-578.	9.7	110
53	The clinical continuum of cryopyrinopathies: Novel CIAS1 mutations in North American patients and a new cryopyrin model. <i>Arthritis and Rheumatism</i> , 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. <i>Quarterly Reviews of Biophysics</i> , 2007, 40, 191-285.	5.7	1,026

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55	Analysis of Gross Chromosomal Rearrangements in <i>Saccharomyces cerevisiae</i> . <i>Methods in Enzymology</i> , 2006, 409, 462-476.	1.0	50
56	Chromosome healing by de novo telomere addition in <i>Saccharomyces cerevisiae</i> . <i>Molecular Microbiology</i> , 2006, 59, 1357-1368.	2.5	85
57	Mutation in Rpa1 results in defective DNA double-strand break repair, chromosomal instability and cancer in mice. <i>Nature Genetics</i> , 2005, 37, 750-755.	21.4	141
58	<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
59	Protein mimicry of DNA and pathway regulation. <i>DNA Repair</i> , 2005, 4, 1410-1420.	2.8	63
60	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
61	Mechanism and energetics of green fluorescent protein chromophore synthesis revealed by trapped intermediate structures. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2003, 100, 12111-12116.	7.1	194
62	Maintenance of Genome Stability in <i>Saccharomyces cerevisiae</i> . <i>Science</i> , 2002, 297, 552-557.	12.6	442
63	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
64	DNA double-strand break repair from head to tail. <i>Current Opinion in Structural Biology</i> , 2002, 12, 115-122.	5.7	133
65	Structure and mechanism of the RuvB holliday junction branch migration motor. <i>Journal of Molecular Biology</i> , 2001, 311, 297-310.	4.2	157
66	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
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 Edited by R. Huber. <i>Journal of Molecular Biology</i> , 2000, 296, 295-309.	4.2	388
69	Lessons learned from structural results on uracil-DNA glycosylase. <i>Mutation Research DNA Repair</i> , 2000, 460, 183-199.	3.7	117
70	Evolution and mechanism from structures of an ADP-ribosylating toxin and NAD complex. <i>Nature Structural Biology</i> , 1999, 6, 932-936.	9.7	223
71	DNA REPAIR MECHANISMS FOR THE RECOGNITION AND REMOVAL OF DAMAGED DNA BASES. <i>Annual Review of Biophysics and Biomolecular Structure</i> , 1999, 28, 101-128.	18.3	170
72	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

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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 Edited by D. C. Rees. Journal of Molecular Biology, 1999, 287, 331-346.	4.2	120
74	Rational Design of a Functional Metalloenzyme: Introduction of a Site for Manganese Binding and Oxidation into a Heme Peroxidase. Biochemistry, 1998, 37, 16853-16862.	2.5	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.	14.5	101
76	Rad5 and Its Human Homologs, HLTF and SHPRH, Are Novel Interactors of Mismatch Repair. Frontiers in Cell and Developmental Biology, 0, 10, .	3.7	1