

Penny J Beuning

List of Publications by Citations

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

95
papers

911
citations

17
h-index

27
g-index

105
ext. papers

1,075
ext. citations

3.3
avg, IF

4.45
L-index

#	Paper	IF	Citations
95	Y-family DNA polymerases in Escherichia coli. <i>Trends in Microbiology</i> , 2007 , 15, 70-7	12.4	116
94	Identification, Characterization and Drug Discovery for Novel Target Sites for SARS-CoV-2 Proteins. <i>FASEB Journal</i> , 2021 , 35,	0.9	78
93	Biochemical functional predictions for protein structures of unknown or uncertain function. <i>Computational and Structural Biotechnology Journal</i> , 2015 , 13, 182-91	6.8	58
92	Characterization of Escherichia coli translesion synthesis polymerases and their accessory factors. <i>Methods in Enzymology</i> , 2006 , 408, 318-40	1.7	39
91	Escherichia coli processivity clamp β from DNA polymerase III is dynamic in solution. <i>Biochemistry</i> , 2011 , 50, 5958-68	3.2	34
90	Two processivity clamp interactions differentially alter the dual activities of UmuC. <i>Molecular Microbiology</i> , 2006 , 59, 460-74	4.1	33
89	A tale of two isomerases: compact versus extended active sites in ketosteroid isomerase and phosphoglucose isomerase. <i>Biochemistry</i> , 2011 , 50, 9283-95	3.2	28
88	Throwing Away the Cookbook: Implementing Course-Based Undergraduate Research Experiences (CUREs) in Chemistry. <i>ACS Symposium Series</i> , 2017 , 33-63	0.4	27
87	Distinct double- and single-stranded DNA binding of E. coli replicative DNA polymerase III alpha subunit. <i>ACS Chemical Biology</i> , 2008 , 3, 577-87	4.9	26
86	Progress against Escherichia coli with the Oxazolidinone Class of Antibacterials: Test Case for a General Approach To Improving Whole-Cell Gram-Negative Activity. <i>ACS Infectious Diseases</i> , 2016 , 2, 405-26	5.5	23
85	A non-cleavable UmuD variant that acts as a UmuD' mimic. <i>Journal of Biological Chemistry</i> , 2006 , 281, 9633-40	5.4	22
84	Conformational analysis of processivity clamps in solution demonstrates that tertiary structure does not correlate with protein dynamics. <i>Structure</i> , 2014 , 22, 572-581	5.2	21
83	Escherichia coli Y family DNA polymerases. <i>Frontiers in Bioscience - Landmark</i> , 2011 , 16, 3164-82	2.8	21
82	Conformational dynamics of the Escherichia coli DNA polymerase manager proteins UmuD and UmuD'. <i>Journal of Molecular Biology</i> , 2010 , 398, 40-53	6.5	20
81	Cryptocaryol Structure-Activity Relationship Study of Cancer Cell Cytotoxicity and Ability to Stabilize PDCD4. <i>ACS Medicinal Chemistry Letters</i> , 2014 , 5, 522-6	4.3	19
80	Prediction of distal residue participation in enzyme catalysis. <i>Protein Science</i> , 2015 , 24, 762-78	6.3	19
79	Multiple strategies for translesion synthesis in bacteria. <i>Cells</i> , 2012 , 1, 799-831	7.9	18

78	Engineering Polymerases for New Functions. <i>Trends in Biotechnology</i> , 2019 , 37, 1091-1103	15.1	16
77	Effects of non-catalytic, distal amino acid residues on activity of E. coli DinB (DNA polymerase IV). <i>Environmental and Molecular Mutagenesis</i> , 2012 , 53, 766-76	3.2	16
76	Single-molecule mechanochemical characterization of E. coli pol III core catalytic activity. <i>Protein Science</i> , 2017 , 26, 1413-1426	6.3	15
75	Steric gate variants of UmuC confer UV hypersensitivity on Escherichia coli. <i>Journal of Bacteriology</i> , 2009 , 191, 4815-23	3.5	15
74	The Roles of UmuD in Regulating Mutagenesis. <i>Journal of Nucleic Acids</i> , 2010 , 2010,	2.3	14
73	Characterization of novel alleles of the Escherichia coli umuDC genes identifies additional interaction sites of UmuC with the beta clamp. <i>Journal of Bacteriology</i> , 2009 , 191, 5910-20	3.5	14
72	Steric gate residues of Y-family DNA polymerases DinB and pol kappa are crucial for dNTP-induced conformational change. <i>DNA Repair</i> , 2015 , 29, 65-73	4.3	13
71	Discrimination against major groove adducts by Y-family polymerases of the DinB subfamily. <i>DNA Repair</i> , 2013 , 12, 713-22	4.3	13
70	The dimeric SOS mutagenesis protein UmuD is active as a monomer. <i>Journal of Biological Chemistry</i> , 2011 , 286, 3607-17	5.4	13
69	Selective disruption of the DNA polymerase III holo-complex by the umuD gene products. <i>Nucleic Acids Research</i> , 2012 , 40, 5511-22	20.1	13
68	Mammalian DNA Polymerase Kappa Activity and Specificity. <i>Molecules</i> , 2019 , 24,	4.8	12
67	Discrimination against the cytosine analog tC by Escherichia coli DNA polymerase IV DinB. <i>Journal of Molecular Biology</i> , 2011 , 409, 89-100	6.5	12
66	Compound design guidelines for evading the efflux and permeation barriers of Escherichia coli with the oxazolidinone class of antibacterials: Test case for a general approach to improving whole cell Gram-negative activity. <i>Bioorganic and Medicinal Chemistry Letters</i> , 2017 , 27, 5310-5321	2.9	11
65	Crystal structure of a metal-dependent phosphoesterase (YP_910028.1) from Bifidobacterium adolescentis: Computational prediction and experimental validation of phosphoesterase activity. <i>Proteins: Structure, Function and Bioinformatics</i> , 2011 , 79, 2146-60	4.2	11
64	Structure activity relationship study of Mezzettiasides natural products and their four new disaccharide analogues for anticancer/antibacterial activity. <i>MedChemComm</i> , 2014 , 5, 1138-1142	5	10
63	Dimer exchange and cleavage specificity of the DNA damage response protein UmuD. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2013 , 1834, 611-20	4	10
62	Prediction of Active Site and Distal Residues in E. coli DNA Polymerase III alpha Polymerase Activity. <i>Biochemistry</i> , 2018 , 57, 1063-1072	3.2	9
61	Polymerase manager protein UmuD directly regulates Escherichia coli DNA polymerase III binding to ssDNA. <i>Nucleic Acids Research</i> , 2013 , 41, 8959-68	20.1	9

60	Noncognate DNA damage prevents the formation of the active conformation of the Y-family DNA polymerases DinB and DNA polymerase η <i>FEBS Journal</i> , 2015 , 282, 2646-60	5.7	8
59	Characterization of Escherichia coli UmuC active-site loops identifies variants that confer UV hypersensitivity. <i>Journal of Bacteriology</i> , 2011 , 193, 5400-11	3.5	8
58	Visualizing the Nonhomogeneous Structure of RAD51 Filaments Using Nanofluidic Channels. <i>Langmuir</i> , 2016 , 32, 8403-12	4	8
57	Dynamics of the E. coli β Clamp Dimer Interface and Its Influence on DNA Loading. <i>Biophysical Journal</i> , 2019 , 117, 587-601	2.9	6
56	Electron spin labeling reveals the highly dynamic N-terminal arms of the SOS mutagenesis protein UmuD. <i>Molecular BioSystems</i> , 2011 , 7, 3183-6		6
55	Multiprotein E. coli SSB-ssDNA complex shows both stable binding and rapid dissociation due to interprotein interactions. <i>Nucleic Acids Research</i> , 2021 , 49, 1532-1549	20.1	6
54	Functional classification of protein structures by local structure matching in graph representation. <i>Protein Science</i> , 2018 , 27, 1125-1135	6.3	5
53	Identification of the Dimer Exchange Interface of the Bacterial DNA Damage Response Protein UmuD. <i>Biochemistry</i> , 2017 , 56, 4773-4785	3.2	5
52	Point mutations in Escherichia coli DNA pol V that confer resistance to non-cognate DNA damage also alter protein-protein interactions. <i>Mutation Research - Fundamental and Molecular Mechanisms of Mutagenesis</i> , 2015 , 780, 1-14	3.3	4
51	Local structure based method for prediction of the biochemical function of proteins: Applications to glycoside hydrolases. <i>Methods</i> , 2016 , 93, 51-63	4.6	4
50	The response of Escherichia coli to the alkylating agents chloroacetaldehyde and styrene oxide. <i>Mutation Research - Genetic Toxicology and Environmental Mutagenesis</i> , 2019 , 840, 1-10	3	4
49	Characterization of Nine Cancer-Associated Variants in Human DNA Polymerase η <i>Chemical Research in Toxicology</i> , 2018 , 31, 697-711	4	3
48	Human Y-Family DNA Polymerase η s More Tolerant to Changes in Its Active Site Loop than Its Ortholog Escherichia coli DinB. <i>Chemical Research in Toxicology</i> , 2017 , 30, 2002-2012	4	3
47	Functional Characterization of Structural Genomics Proteins in the Crotonase Superfamily.. <i>ACS Chemical Biology</i> , 2022 ,	4.9	3
46	Probing remote residues important for catalysis in Escherichia coli ornithine transcarbamoylase. <i>PLoS ONE</i> , 2020 , 15, e0228487	3.7	2
45	Altering the N-terminal arms of the polymerase manager protein UmuD modulates protein interactions. <i>PLoS ONE</i> , 2017 , 12, e0173388	3.7	2
44	NMR resonance assignments for the N-terminal domain of the β subunit of the E. coli β clamp loader complex. <i>Biomolecular NMR Assignments</i> , 2017 , 11, 169-173	0.7	1
43	Song: SOS (To the Tune of ABBA's "SOS"). <i>Biochemistry and Molecular Biology Education</i> , 2009 , 37, 316	1.3	1

42	Investigation of the Mechanism of Action of Oxazolidinones. <i>FASEB Journal</i> , 2015 , 29, 575.10	0.9	1
41	Complete enzymatic digestion of double-stranded RNA to nucleosides enables accurate quantification of dsRNA. <i>Analytical Methods</i> , 2021 , 13, 179-185	3.2	1
40	Polymerase Switching in Response to DNA Damage 2010 , 241-292		1
39	Versatile separation of nucleotides from bacterial cell lysates using strong anion exchange chromatography. <i>Journal of Chromatography B: Analytical Technologies in the Biomedical and Life Sciences</i> , 2021 , 1188, 123044	3.2	0
38	DNA Adductomics by mass tag prelabeling. <i>Rapid Communications in Mass Spectrometry</i> , 2021 , 35, e90952.2		0
37	Adapting Undergraduate Research to Remote Work to Increase Engagement. <i>The Biophysicist</i> , 2021 , 2, 28-32	1	0
36	A Professional Development Handbook for New Faculty. <i>ACS Symposium Series</i> , 2017 , 13-21	0.4	
35	A Non-cleavable UmuD variant that acts as a UmuD-mimic. <i>FASEB Journal</i> , 2006 , 20, LB55	0.9	
34	Active site mutations in the Y family DNA polymerase UmuC cause hypersensitivity to UV light and are dominant negative. <i>FASEB Journal</i> , 2007 , 21, A659	0.9	
33	Steric Gate Variants in a Y family DNA Polymerase Confer UV-Hypersensitivity. <i>FASEB Journal</i> , 2008 , 22, 990.3	0.9	
32	Dynamics of the polymerase manager protein UmuD: DNA damage tolerance in E. coli. <i>FASEB Journal</i> , 2008 , 22, 591.4	0.9	
31	Probing the role of distal residues in DinB and Pol Kappa in the extension step of DNA damage bypass. <i>FASEB Journal</i> , 2018 , 32, 646.3	0.9	
30	Understanding How Distal Residues Play a Role in Parkin Activity. <i>FASEB Journal</i> , 2018 , 32, 654.7	0.9	
29	Electrostatic interactions in natural enzymes: What can we learn for enzyme design?. <i>FASEB Journal</i> , 2018 , 32, 655.26	0.9	
28	Thinking Outside the Informatics Box: Computed Chemical Properties for Protein Function Annotation. <i>FASEB Journal</i> , 2019 , 33, 473.5	0.9	
27	Characterizing the conformational dynamics for DNA loading of the Escherichia coli DNA polymerase III subunit beta clamp. <i>FASEB Journal</i> , 2019 , 33, 776.4	0.9	
26	Remote Residues Affect Stability of Ornithine Transcarbamylase. <i>FASEB Journal</i> , 2015 , 29, 572.29	0.9	
25	Non-cognate DNA damage prevents formation of active conformation of Y-family DNA polymerases DinB and pol kappa. <i>FASEB Journal</i> , 2015 , 29, 561.8	0.9	

- 24 Characterization of the N-terminal Arms of the Polymerase Manager Protein UmuD. *FASEB Journal*, **2015**, 29, 561.10 0.9
- 23 Expression and purification of putative Y-family polymerase DinB from *Sinorhizobium meliloti*. *FASEB Journal*, **2015**, 29, 561.4 0.9
- 22 Directed Evolution of DinB in *Escherichia coli* by Hydroxylamine Mutagenesis and UV Selection. *FASEB Journal*, **2015**, 29, 560.5 0.9
- 21 Functional Characterization of Structural Genomics Proteins in the Crotonase Superfamily. *FASEB Journal*, **2015**, 29, 573.18 0.9
- 20 Regulation of DNA damage responses by the polymerase manager proteins UmuD and UmuD?. *FASEB Journal*, **2009**, 23, 837.1 0.9
- 19 Evidence for multiple active forms of the DNA damage response protein UmuD. *FASEB Journal*, **2010**, 24, 875.4 0.9
- 18 DNA damage response protein UmuD displays conformational dynamics. *FASEB Journal*, **2010**, 24, 880.2 0.9
- 17 Discrimination against the Fluorescent Cytosine Analog tC by *Escherichia coli* DNA Polymerase IV DinB. *FASEB Journal*, **2011**, 25, 880.11 0.9
- 16 Identification of critical residues in DNA polymerase III alpha through protein engineering. *FASEB Journal*, **2011**, 25, 880.4 0.9
- 15 Conformational and dynamic characterization of the *Escherichia coli* DNA polymerase III beta processivity clamp. *FASEB Journal*, **2011**, 25, 880.2 0.9
- 14 *E. coli* UmuD conformational dynamics in response to DNA damage. *FASEB Journal*, **2011**, 25, 500.11 0.9
- 13 Investigating the interaction between the alpha subunit of DNA polymerase III and UmuD. *FASEB Journal*, **2011**, 25, 880.9 0.9
- 12 Point mutations in *Escherichia coli* DNA pol V that confer resistance to non-cognate DNA damage. *FASEB Journal*, **2012**, 26, 539.14 0.9
- 11 Multiple forms of the *E. coli* SOS response protein UmuD. *FASEB Journal*, **2012**, 26, 539.7 0.9
- 10 Successful computational prediction of residues important for function in DNA polymerase III alpha subunit. *FASEB Journal*, **2012**, 26, 739.1 0.9
- 9 Point mutations in *Escherichia coli* DNA pol V that confer resistance to non-cognate DNA damage. *FASEB Journal*, **2013**, 27, 758.2 0.9
- 8 Conformational analysis of processivity clamps demonstrates that tertiary structure does not correlate with structural dynamics. *FASEB Journal*, **2013**, 27, 541.1 0.9
- 7 UmuD participates in a primitive DNA damage checkpoint by interacting with DNA pol III β and SSB. *FASEB Journal*, **2013**, 27, 538.3 0.9

- 6 Successful computational prediction of active site and distal residues essential for function in DNA polymerase III alpha subunit. *FASEB Journal*, **2013**, 27, 541.3 0.9
- 5 Computational prediction and validation of putative ketosteroid isomerase (KSI) structural genomics proteins. *FASEB Journal*, **2013**, 27, 811.5 0.9
- 4 Use of FRET to Study Dynamics of DNA Replication **2014**, 95-111
- 3 NMR resonance assignments for the nucleotide binding domains of the E. coli clamp loader complex β subunit. *Biomolecular NMR Assignments*, **2021**, 15, 281-285 0.7
- 2 DNA repair | UmuDC Lesion Bypass DNA Polymerase V **2021**, 334-344
- 1 DNA Recognition/Processing | DNA Polymerase III, Bacterial **2021**, 460-471