

Penny J Beuning

List of Publications by Year in descending order

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105
papers

1,104
citations

394286

19
h-index

477173

29
g-index

105
all docs

105
docs citations

105
times ranked

1157
citing authors

#	ARTICLE	IF	CITATIONS
1	Y-family DNA polymerases in <i>Escherichia coli</i> . <i>Trends in Microbiology</i> , 2007, 15, 70-77.	3.5	137
2	Biochemical functional predictions for protein structures of unknown or uncertain function. <i>Computational and Structural Biotechnology Journal</i> , 2015, 13, 182-191.	1.9	77
3	Characterization of <i>Escherichia coli</i> Translesion Synthesis Polymerases and Their Accessory Factors. <i>Methods in Enzymology</i> , 2006, 408, 318-340.	0.4	46
4	<i>Escherichia coli</i> Processivity Clamp $\hat{\tau}^2$ from DNA Polymerase III Is Dynamic in Solution. <i>Biochemistry</i> , 2011, 50, 5958-5968.	1.2	40
5	Throwing Away the Cookbook: Implementing Course-Based Undergraduate Research Experiences (CUREs) in Chemistry. <i>ACS Symposium Series</i> , 2017, , 33-63.	0.5	37
6	Two processivity clamp interactions differentially alter the dual activities of UmuC. <i>Molecular Microbiology</i> , 2006, 59, 460-474.	1.2	36
7	Distinct Double- and Single-Stranded DNA Binding of <i>E. coli</i> Replicative DNA Polymerase III $\hat{\tau}$ Subunit. <i>ACS Chemical Biology</i> , 2008, 3, 577-587.	1.6	32
8	A Tale of Two Isomerases: Compact versus Extended Active Sites in Ketosteroid Isomerase and Phosphoglucose Isomerase. <i>Biochemistry</i> , 2011, 50, 9283-9295.	1.2	32
9	Conformational Analysis of Processivity Clamps in Solution Demonstrates that Tertiary Structure Does Not Correlate with Protein Dynamics. <i>Structure</i> , 2014, 22, 572-581.	1.6	30
10	Progress against <i>Escherichia coli</i> 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, 405-426.	1.8	29
11	Mammalian DNA Polymerase Kappa Activity and Specificity. <i>Molecules</i> , 2019, 24, 2805.	1.7	28
12	Engineering Polymerases for New Functions. <i>Trends in Biotechnology</i> , 2019, 37, 1091-1103.	4.9	28
13	Multiple Strategies for Translesion Synthesis in Bacteria. <i>Cells</i> , 2012, 1, 799-831.	1.8	25
14	A Non-cleavable UmuD Variant That Acts as a UmuD $\hat{\epsilon}^2$ Mimic. <i>Journal of Biological Chemistry</i> , 2006, 281, 9633-9640.	1.6	24
15	<i>Escherichia coli</i> Y family DNA polymerases. <i>Frontiers in Bioscience - Landmark</i> , 2011, 16, 3164.	3.0	24
16	Cryptocaryol Structure-Activity Relationship Study of Cancer Cell Cytotoxicity and Ability to Stabilize PDCD4. <i>ACS Medicinal Chemistry Letters</i> , 2014, 5, 522-526.	1.3	23
17	Prediction of distal residue participation in enzyme catalysis. <i>Protein Science</i> , 2015, 24, 762-778.	3.1	23
18	Multiprotein <i>E. coli</i> SSB-ssDNA complex shows both stable binding and rapid dissociation due to interprotein interactions. <i>Nucleic Acids Research</i> , 2021, 49, 1532-1549.	6.5	22

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19	Conformational Dynamics of the Escherichia coli DNA Polymerase Manager Proteins UmuD and UmuC. Journal of Molecular Biology, 2010, 398, 40-53.	2.0	20
20	Effects of non-catalytic, distal amino acid residues on activity of <i>E. coli</i> DinB (DNA polymerase) Tj ETQq0 0.0 rgt /Overlock 10	0.9	20
21	Single-molecule mechanochemical characterization of <i>E. coli</i> pol III core catalytic activity. Protein Science, 2017, 26, 1413-1426.	3.1	20
22	Steric Gate Variants of UmuC Confer UV Hypersensitivity on <i>Escherichia coli</i> . Journal of Bacteriology, 2009, 191, 4815-4823.	1.0	18
23	Discrimination against major groove adducts by Y-family polymerases of the DinB subfamily. DNA Repair, 2013, 12, 713-722.	1.3	18
24	Characterization of Novel Alleles of the <i>Escherichia coli</i> umuDC Genes Identifies Additional Interaction Sites of UmuC with the Beta Clamp. Journal of Bacteriology, 2009, 191, 5910-5920.	1.0	16
25	Prediction of Active Site and Distal Residues in <i>E. coli</i> DNA Polymerase III alpha Polymerase Activity. Biochemistry, 2018, 57, 1063-1072.	1.2	16
26	The Roles of UmuD in Regulating Mutagenesis. Journal of Nucleic Acids, 2010, 2010, 1-12.	0.8	15
27	Steric gate residues of Y-family DNA polymerases DinB and pol kappa are crucial for dNTP-induced conformational change. DNA Repair, 2015, 29, 65-73.	1.3	15
28	Identification of the Dimer Exchange Interface of the Bacterial DNA Damage Response Protein UmuD. Biochemistry, 2017, 56, 4773-4785.	1.2	15
29	Discrimination against the Cytosine Analog tC by Escherichia coli DNA Polymerase IV DinB. Journal of Molecular Biology, 2011, 409, 89-100.	2.0	14
30	Selective disruption of the DNA polymerase III β - η complex by the umuD gene products. Nucleic Acids Research, 2012, 40, 5511-5522.	6.5	14
31	The Dimeric SOS Mutagenesis Protein UmuD Is Active as a Monomer. Journal of Biological Chemistry, 2011, 286, 3607-3617.	1.6	13
32	Structure activity relationship study of mezzettiasides natural products and their four new disaccharide analogues for anticancer/antibacterial activity. MedChemComm, 2014, 5, 1138-1142.	3.5	13
33	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. Bioorganic and Medicinal Chemistry Letters, 2017, 27, 5310-5321.	1.0	13
34	Characterization of Escherichia coli UmuC Active-Site Loops Identifies Variants That Confer UV Hypersensitivity. Journal of Bacteriology, 2011, 193, 5400-5411.	1.0	12
35	Noncognate β -DNA damage prevents the formation of the active conformation of the β -family β -DNA polymerases DinB and β -DNA polymerase η . FEBS Journal, 2015, 282, 2646-2660.	2.2	12
36	Dynamics of the <i>E. coli</i> β -Clamp Dimer Interface and Its Influence on DNA Loading. Biophysical Journal, 2019, 117, 587-601.	0.2	12

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37	Crystal structure of a metalâ€dependent phosphoesterase (YP_910028.1) from <i>Bifidobacterium adolescentis</i> : Computational prediction and experimental validation of phosphoesterase activity. <i>Proteins: Structure, Function and Bioinformatics</i> , 2011, 79, 2146-2160.	1.5	11
38	Visualizing the Nonhomogeneous Structure of RAD51 Filaments Using Nanofluidic Channels. <i>Langmuir</i> , 2016, 32, 8403-8412.	1.6	11
39	Dimer exchange and cleavage specificity of the DNA damage response protein UmuD. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2013, 1834, 611-620.	1.1	10
40	Polymerase manager protein UmuD directly regulates Escherichia coli DNA polymerase III binding to ssDNA. <i>Nucleic Acids Research</i> , 2013, 41, 8959-8968.	6.5	9
41	Local structure based method for prediction of the biochemical function of proteins: Applications to glycoside hydrolases. <i>Methods</i> , 2016, 93, 51-63.	1.9	9
42	Functional classification of protein structures by local structure matching in graph representation. <i>Protein Science</i> , 2018, 27, 1125-1135.	3.1	8
43	Characterization of Nine Cancer-Associated Variants in Human DNA Polymerase Î². <i>Chemical Research in Toxicology</i> , 2018, 31, 697-711.	1.7	8
44	Electron spin labeling reveals the highly dynamic N-terminal arms of the SOS mutagenesis protein UmuD. <i>Molecular BioSystems</i> , 2011, 7, 3183.	2.9	7
45	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.	0.9	7
46	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> , 2022, 1188, 123044.	1.2	6
47	Functional Characterization of Structural Genomics Proteins in the Crotonase Superfamily. <i>ACS Chemical Biology</i> , 2022, 17, 395-403.	1.6	6
48	Novel Mobile Phase to Control Charge States and Metal Adducts in the LC/MS for mRNA Characterization Assays. <i>ACS Omega</i> , 2022, 7, 22181-22191.	1.6	6
49	Point mutations in Escherichia coli DNA pol V that confer resistance to non-cognate DNA damage also alter proteinâ€protein interactions. <i>Mutation Research - Fundamental and Molecular Mechanisms of Mutagenesis</i> , 2015, 780, 1-14.	0.4	5
50	Human Y-Family DNA Polymerase Î² Is 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.	1.7	5
51	Research skills and ethics: the 20-year evolution of a professional development graduate course. <i>Analytical and Bioanalytical Chemistry</i> , 2017, 409, 859-862.	1.9	4
52	Probing remote residues important for catalysis in Escherichia coli ornithine transcarbamoylase. <i>PLoS ONE</i> , 2020, 15, e0228487.	1.1	4
53	Complete enzymatic digestion of double-stranded RNA to nucleosides enables accurate quantification of dsRNA. <i>Analytical Methods</i> , 2021, 13, 179-185.	1.3	3
54	Polymerase Switching in Response to DNA Damage. <i>Biological and Medical Physics Series</i> , 2010, , 241-292.	0.3	3

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55	Jettison-MS of Nucleic Acid Species. <i>Journal of the American Society for Mass Spectrometry</i> , 2020, 31, 1641-1646.	1.2	2
56	DNA Adductomics by mass tag prelabeling. <i>Rapid Communications in Mass Spectrometry</i> , 2021, 35, e9095.	0.7	2
57	Adapting Undergraduate Research to Remote Work to Increase Engagement. <i>The Biophysicist</i> , 2021, 2, 28-32.	0.1	2
58	Altering the N-terminal arms of the polymerase manager protein UmuD modulates protein interactions. <i>PLoS ONE</i> , 2017, 12, e0173388.	1.1	2
59	Song: SOS (To the Tune of ABBA's "SOS"). <i>Biochemistry and Molecular Biology Education</i> , 2009, 37, 316-316.	0.5	1
60	NMR resonance assignments for the N-terminal domain of the $\hat{\Gamma}$ subunit of the <i>E. coli</i> $\hat{\Gamma}$ clamp loader complex. <i>Biomolecular NMR Assignments</i> , 2017, 11, 169-173.	0.4	1
61	DNA Polymerases: From Molecular Mechanisms to Human Disease, a Special Issue. <i>Chemical Research in Toxicology</i> , 2017, 30, 1921-1921.	1.7	1
62	Investigation of the Mechanism of Action of Oxazolidinones. <i>FASEB Journal</i> , 2015, 29, 575.10.	0.2	1
63	ILV methyl NMR resonance assignments of the 81 kDa <i>E. coli</i> $\hat{\Gamma}$ -clamp. <i>Biomolecular NMR Assignments</i> , 0, .	0.4	1
64	A Professional Development Handbook for New Faculty. <i>ACS Symposium Series</i> , 2017, , 13-21.	0.5	0
65	DNA repair UmuDC Lesion Bypass DNA Polymerase V. , 2021, , 334-344.		0
66	DNA Recognition/Processing DNA Polymerase III, Bacterial. , 2021, , 460-471.		0
67	NMR resonance assignments for the nucleotide binding domains of the <i>E. coli</i> clamp loader complex $\hat{\Gamma}$ subunit. <i>Biomolecular NMR Assignments</i> , 2021, 15, 281-285.	0.4	0
68	Identification, Characterization and Drug Discovery for Novel Target Sites for SARS-CoV-2 Proteins. <i>FASEB Journal</i> , 2021, 35, .	0.2	0
69	Division of Chemical Toxicology Program at the American Chemical Society National Meeting: Celebrating 25 Years!. <i>Chemical Research in Toxicology</i> , 2021, 34, 2167-2168.	1.7	0
70	A Non-releasable UmuD variant that acts as a UmuD TM mimic. <i>FASEB Journal</i> , 2006, 20, LB55.	0.2	0
71	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.	0.2	0
72	Steric Gate Variants in a Y family DNA Polymerase Confer UV-Hypersensitivity. <i>FASEB Journal</i> , 2008, 22, 990.3.	0.2	0

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73	Dynamics of the polymerase manager protein UmuD: DNA damage tolerance in <i>E. coli</i> . <i>FASEB Journal</i> , 2008, 22, 591.4.	0.2	0
74	Regulation of DNA damage responses by the polymerase manager proteins UmuD and UmuD ^{Δ2} . <i>FASEB Journal</i> , 2009, 23, 837.1.	0.2	0
75	Evidence for multiple active forms of the DNA damage response protein UmuD. <i>FASEB Journal</i> , 2010, 24, 875.4.	0.2	0
76	DNA damage response protein UmuD displays conformational dynamics. <i>FASEB Journal</i> , 2010, 24, 880.2.	0.2	0
77	Discrimination against the Fluorescent Cytosine Analog tC by <i>Escherichia coli</i> DNA Polymerase IV DinB. <i>FASEB Journal</i> , 2011, 25, 880.11.	0.2	0
78	Identification of critical residues in DNA polymerase III alpha through protein engineering. <i>FASEB Journal</i> , 2011, 25, 880.4.	0.2	0
79	Conformational and dynamic characterization of the <i>Escherichia coli</i> DNA polymerase III beta processivity clamp. <i>FASEB Journal</i> , 2011, 25, 880.2.	0.2	0
80	<i>E. coli</i> UmuD conformational dynamics in response to DNA damage. <i>FASEB Journal</i> , 2011, 25, 500.11.	0.2	0
81	Investigating the interaction between the alpha subunit of DNA polymerase III and UmuD. <i>FASEB Journal</i> , 2011, 25, 880.9.	0.2	0
82	Point mutations in <i>Escherichia coli</i> DNA pol V that confer resistance to non-cognate DNA damage. <i>FASEB Journal</i> , 2012, 26, 539.14.	0.2	0
83	The <i>Escherichia coli</i> SOS-induced umuD gene products interact with single-stranded DNA binding protein. <i>FASEB Journal</i> , 2012, 26, .	0.2	0
84	Multiple forms of the <i>E. coli</i> SOS response protein UmuD. <i>FASEB Journal</i> , 2012, 26, 539.7.	0.2	0
85	Successful computational prediction of residues important for function in DNA polymerase III alpha subunit. <i>FASEB Journal</i> , 2012, 26, 739.1.	0.2	0
86	Point mutations in <i>Escherichia coli</i> DNA pol V that confer resistance to non-cognate DNA damage. <i>FASEB Journal</i> , 2013, 27, 758.2.	0.2	0
87	Conformational analysis of processivity clamps demonstrates that tertiary structure does not correlate with structural dynamics. <i>FASEB Journal</i> , 2013, 27, 541.1.	0.2	0
88	UmuD participates in a primitive DNA damage checkpoint by interacting with DNA pol III ϵ and SSB. <i>FASEB Journal</i> , 2013, 27, 538.3.	0.2	0
89	Successful computational prediction of active site and distal residues essential for function in DNA polymerase III alpha subunit. <i>FASEB Journal</i> , 2013, 27, 541.3.	0.2	0
90	Computational prediction and validation of putative ketosteroid isomerase (KSI) structural genomics proteins. <i>FASEB Journal</i> , 2013, 27, 811.5.	0.2	0

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91	Use of FRET to Study Dynamics of DNA Replication. , 2014, , 95-111.		0
92	Remote Residues Affect Stability of Ornithine Transcarbamylase. FASEB Journal, 2015, 29, 572.29.	0.2	0
93	Specificity and Activity of γ -family DNA Polymerases DinB and Pol Kappa. FASEB Journal, 2015, 29, .	0.2	0
94	Non-cognate DNA damage prevents formation of active conformation of γ -family DNA polymerases DinB and pol kappa. FASEB Journal, 2015, 29, 561.8.	0.2	0
95	Characterization of the N-terminal Arms of the Polymerase Manager Protein UmuD. FASEB Journal, 2015, 29, 561.10.	0.2	0
96	Expression and purification of putative γ -family polymerase DinB from <i>Sinorhizobium meliloti</i> . FASEB Journal, 2015, 29, 561.4.	0.2	0
97	Directed Evolution of DinB in <i>Escherichia coli</i> by Hydroxylamine Mutagenesis and UV Selection. FASEB Journal, 2015, 29, 560.5.	0.2	0
98	Functional Characterization of Structural Genomics Proteins in the Crotonase Superfamily. FASEB Journal, 2015, 29, 573.18.	0.2	0
99	The LexA-regulated gene ybfE plays a role in DNA metabolism in <i>E. coli</i> . FASEB Journal, 2018, 32, .	0.2	0
100	Probing the role of distal residues in DinB and Pol Kappa in the extension step of DNA damage bypass. FASEB Journal, 2018, 32, 646.3.	0.2	0
101	Understanding How Distal Residues Play a Role in Parkin Activity. FASEB Journal, 2018, 32, 654.7.	0.2	0
102	Electrostatic interactions in natural enzymes: What can we learn for enzyme design?. FASEB Journal, 2018, 32, 655.26.	0.2	0
103	Thinking Outside the Informatics Box: Computed Chemical Properties for Protein Function Annotation. FASEB Journal, 2019, 33, 473.5.	0.2	0
104	Characterizing the conformational dynamics for DNA loading of the <i>Escherichia coli</i> DNA polymerase III subunit beta clamp. FASEB Journal, 2019, 33, 776.4.	0.2	0
105	Stereoselective Synthesis of β^2 -Glycinamide Ribonucleotide. Molecules, 2022, 27, 2528.	1.7	0