Penny J Beuning

List of Publications by Year in Descending Order

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	Functional Characterization of Structural Genomics Proteins in the Crotonase Superfamily.. *ACS Chemical Biology*, **2022**,	4.9	3
94	Versatile separation of nucleotides from bacterial cell lysates using strong anion exchange chromatography. *Journal of Chromatography B: Analytical Technologies in the Biomedical and Life Sciences*, **2021**, 1188, 123044	3.2	0
93	NMR resonance assignments for the nucleotide binding domains of the E. coli clamp loader complex □subunit. *Biomolecular NMR Assignments*, **2021**, 15, 281-285	0.7	
92	Identification, Characterization and Drug Discovery for Novel Target Sites for SARS-CoV-2 Proteins. *FASEB Journal*, **2021**, 35,	0.9	78
91	DNA Adductomics by mass tag prelabeling. *Rapid Communications in Mass Spectrometry*, **2021**, 35, e9095	2.2	0
90	DNA repair | UmuDC Lesion Bypass DNA Polymerase V **2021**, 334-344		
89	Complete enzymatic digestion of double-stranded RNA to nucleosides enables accurate quantification of dsRNA. *Analytical Methods*, **2021**, 13, 179-185	3.2	1
88	DNA Recognition/Processing | DNA Polymerase III, Bacterial **2021**, 460-471		
87	Adapting Undergraduate Research to Remote Work to Increase Engagement. *The Biophysicist*, **2021**, 2, 28-32	1	0
86	Multiprotein E. coli SSB-ssDNA complex shows both stable binding and rapid dissociation due to interprotein interactions. *Nucleic Acids Research*, **2021**, 49, 1532-1549	20.1	6
85	Probing remote residues important for catalysis in Escherichia coli ornithine transcarbamoylase. *PLoS ONE*, **2020**, 15, e0228487	3.7	2
84	Dynamics of the E.□coli □Clamp Dimer Interface and Its Influence on DNA Loading. *Biophysical Journal*, **2019**, 117, 587-601	2.9	6
83	Engineering Polymerases for New Functions. *Trends in Biotechnology*, **2019**, 37, 1091-1103	15.1	16
82	Mammalian DNA Polymerase Kappa Activity and Specificity. *Molecules*, **2019**, 24,	4.8	12
81	Thinking Outside the Informatics Box: Computed Chemical Properties for Protein Function Annotation. *FASEB Journal*, **2019**, 33, 473.5	0.9	
80	Characterizing the conformational dynamics for DNA loading of the Escherichia coli DNA polymerase III subunit beta clamp. *FASEB Journal*, **2019**, 33, 776.4	0.9	
79	The response of Escherichia coli to the alkylating agents chloroacetaldehyde and styrene oxide. *Mutation Research - Genetic Toxicology and Environmental Mutagenesis*, **2019**, 840, 1-10	3	4

78	Functional classification of protein structures by local structure matching in graph representation. *Protein Science*, **2018**, 27, 1125-1135	6.3	5
77	Prediction of Active Site and Distal Residues in E. coli DNA Polymerase III alpha Polymerase Activity. *Biochemistry*, **2018**, 57, 1063-1072	3.2	9
76	Characterization of Nine Cancer-Associated Variants in Human DNA Polymerase □*Chemical Research in Toxicology*, **2018**, 31, 697-711	4	3
75	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	0.9	
74	Understanding How Distal Residues Play a Role in Parkin Activity. *FASEB Journal*, **2018**, 32, 654.7	0.9	
73	Electrostatic interactions in natural enzymes: What can we learn for enzyme design?. *FASEB Journal* , **2018**, 32, 655.26	0.9	
72	Single-molecule mechanochemical characterization of E. coli pol III core catalytic activity. *Protein Science*, **2017**, 26, 1413-1426	6.3	15
71	NMR resonance assignments for the N-terminal domain of the □subunit of the E. coli □clamp loader complex. *Biomolecular NMR Assignments*, **2017**, 11, 169-173	0.7	1
70	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	2.9	11
69	Identification of the Dimer Exchange Interface of the Bacterial DNA Damage Response Protein UmuD. *Biochemistry*, **2017**, 56, 4773-4785	3.2	5
68	Human Y-Family DNA Polymerase □s More Tolerant to Changes in Its Active Site Loop than Its Ortholog Escherichia coli DinB. *Chemical Research in Toxicology*, **2017**, 30, 2002-2012	4	3
67	Throwing Away the Cookbook: Implementing Course-Based Undergraduate Research Experiences (CUREs) in Chemistry. *ACS Symposium Series*, **2017**, 33-63	0.4	27
66	A Professional Development Handbook for New Faculty. *ACS Symposium Series*, **2017**, 13-21	0.4	
65	Altering the N-terminal arms of the polymerase manager protein UmuD modulates protein interactions. *PLoS ONE*, **2017**, 12, e0173388	3.7	2
64	Local structure based method for prediction of the biochemical function of proteins: Applications to glycoside hydrolases. *Methods*, **2016**, 93, 51-63	4.6	4
63	Progress against Escherichia coli with the Oxazolidinone Class of Antibacterials: Test Case for a General Approach To Improving Whole-Cell Gram-Negative Activity. *ACS Infectious Diseases*, **2016**, 2, 405-26	5.5	23
62	Visualizing the Nonhomogeneous Structure of RAD51 Filaments Using Nanofluidic Channels. *Langmuir*, **2016**, 32, 8403-12	4	8
61	Point mutations in Escherichia coli DNA pol V that confer resistance to non-cognate DNA damage also alter protein-protein interactions. *Mutation Research - Fundamental and Molecular Mechanisms of Mutagenesis*, **2015**, 780, 1-14	3.3	4

60	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	4.3	13
59	Biochemical functional predictions for protein structures of unknown or uncertain function. *Computational and Structural Biotechnology Journal*, **2015**, 13, 182-91	6.8	58
58	Noncognate DNA damage prevents the formation of the active conformation of the Y-family DNA polymerases DinB and DNA polymerase *FEBS Journal*, **2015**, 282, 2646-60	5.7	8
57	Prediction of distal residue participation in enzyme catalysis. *Protein Science*, **2015**, 24, 762-78	6.3	19
56	Remote Residues Affect Stability of Ornithine Transcarbamylase. *FASEB Journal*, **2015**, 29, 572.29	0.9	
55	Non-cognate DNA damage prevents formation of active conformation of Y-family DNA polymerases DinB and pol kappa. *FASEB Journal*, **2015**, 29, 561.8	0.9	
54	Investigation of the Mechanism of Action of Oxazolidinones. *FASEB Journal*, **2015**, 29, 575.10	0.9	1
53	Characterization of the N-terminal Arms of the Polymerase Manager Protein UmuD. *FASEB Journal*, **2015**, 29, 561.10	0.9	
52	Expression and purification of putative Y-family polymerase DinB from Sinorhizobium meliloti. *FASEB Journal*, **2015**, 29, 561.4	0.9	
51	Directed Evolution of DinB in Escherichia coli by Hydroxylamine Mutagenesis and UV Selection. *FASEB Journal*, **2015**, 29, 560.5	0.9	
50	Functional Characterization of Structural Genomics Proteins in the Crotonase Superfamily. *FASEB Journal*, **2015**, 29, 573.18	0.9	
49	Structure activity relationship study of Mezzettiasides natural products and their four new disaccharide analogues for anticancer/antibacterial activity. *MedChemComm*, **2014**, 5, 1138-1142	5	10
48	Cryptocaryol Structure-Activity Relationship Study of Cancer Cell Cytotoxicity and Ability to Stabilize PDCD4. *ACS Medicinal Chemistry Letters*, **2014**, 5, 522-6	4.3	19
47	Conformational analysis of processivity clamps in solution demonstrates that tertiary structure does not correlate with protein dynamics. *Structure*, **2014**, 22, 572-581	5.2	21
46	Use of FRET to Study Dynamics of DNA Replication **2014**, 95-111		
45	Dimer exchange and cleavage specificity of the DNA damage response protein UmuD. *Biochimica Et Biophysica Acta - Proteins and Proteomics*, **2013**, 1834, 611-20	4	10
44	Discrimination against major groove adducts by Y-family polymerases of the DinB subfamily. *DNA Repair*, **2013**, 12, 713-22	4.3	13
43	Polymerase manager protein UmuD directly regulates Escherichia coli DNA polymerase III binding to ssDNA. *Nucleic Acids Research*, **2013**, 41, 8959-68	20.1	9

42	Point mutations in Escherichia coli DNA pol V that confer resistance to non-cognate DNA damage. *FASEB Journal*, **2013**, 27, 758.2	0.9	
41	Conformational analysis of processivity clamps demonstrates that tertiary structure does not correlate with structural dynamics. *FASEB Journal*, **2013**, 27, 541.1	0.9	
40	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	
39	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	
38	Computational prediction and validation of putative ketosteroid isomerase (KSI) structural genomics proteins. *FASEB Journal*, **2013**, 27, 811.5	0.9	
37	Effects of non-catalytic, distal amino acid residues on activity of E. coli DinB (DNA polymerase IV). *Environmental and Molecular Mutagenesis*, **2012**, 53, 766-76	3.2	16
36	Multiple strategies for translesion synthesis in bacteria. *Cells*, **2012**, 1, 799-831	7.9	18
35	Selective disruption of the DNA polymerase III β2 complex by the umuD gene products. *Nucleic Acids Research*, **2012**, 40, 5511-22	20.1	13
34	Point mutations in Escherichia coli DNA pol V that confer resistance to non-cognate DNA damage. *FASEB Journal*, **2012**, 26, 539.14	0.9	
33	Multiple forms of the E. coli SOS response protein UmuD. *FASEB Journal*, **2012**, 26, 539.7	0.9	
32	Successful computational prediction of residues important for function in DNA polymerase III alpha subunit. *FASEB Journal*, **2012**, 26, 739.1	0.9	
31	Discrimination against the cytosine analog tC by Escherichia coli DNA polymerase IV DinB. *Journal of Molecular Biology*, **2011**, 409, 89-100	6.5	12
30	Escherichia coli Y family DNA polymerases. *Frontiers in Bioscience - Landmark*, **2011**, 16, 3164-82	2.8	21
29	Crystal structure of a metal-dependent phosphoesterase (YP_910028.1) from Bifidobacterium adolescentis: Computational prediction and experimental validation of phosphoesterase activity. *Proteins: Structure, Function and Bioinformatics*, **2011**, 79, 2146-60	4.2	11
28	Electron spin labeling reveals the highly dynamic N-terminal arms of the SOS mutagenesis protein UmuD. *Molecular BioSystems*, **2011**, 7, 3183-6		6
27	Escherichia coli processivity clamp β from DNA polymerase III is dynamic in solution. *Biochemistry*, **2011**, 50, 5958-68	3.2	34
26	A tale of two isomerases: compact versus extended active sites in ketosteroid isomerase and phosphoglucose isomerase. *Biochemistry*, **2011**, 50, 9283-95	3.2	28
25	Characterization of Escherichia coli UmuC active-site loops identifies variants that confer UV hypersensitivity. *Journal of Bacteriology*, **2011**, 193, 5400-11	3.5	8

24	The dimeric SOS mutagenesis protein UmuD is active as a monomer. *Journal of Biological Chemistry*, **2011**, 286, 3607-17	5.4	13
23	Discrimination against the Fluorescent Cytosine Analog tC by Escherichia coli DNA Polymerase IV DinB. *FASEB Journal*, **2011**, 25, 880.11	0.9	
22	Identification of critical residues in DNA polymerase III alpha through protein engineering. *FASEB Journal*, **2011**, 25, 880.4	0.9	
21	Conformational and dynamic characterization of the Escherichia coli DNA polymerase III beta processivity clamp. *FASEB Journal*, **2011**, 25, 880.2	0.9	
20	E. coli UmuD conformational dynamics in response to DNA damage. *FASEB Journal*, **2011**, 25, 500.11	0.9	
19	Investigating the interaction between the alpha subunit of DNA polymerase III and UmuD. *FASEB Journal*, **2011**, 25, 880.9	0.9	
18	The Roles of UmuD in Regulating Mutagenesis. *Journal of Nucleic Acids*, **2010**, 2010,	2.3	14
17	Conformational dynamics of the Escherichia coli DNA polymerase manager proteins UmuD and UmuD'. *Journal of Molecular Biology*, **2010**, 398, 40-53	6.5	20
16	Evidence for multiple active forms of the DNA damage response protein UmuD. *FASEB Journal*, **2010**, 24, 875.4	0.9	
15	DNA damage response protein UmuD displays conformational dynamics. *FASEB Journal*, **2010**, 24, 880.2	0.9	
14	Polymerase Switching in Response to DNA Damage **2010**, 241-292		1
13	Steric gate variants of UmuC confer UV hypersensitivity on Escherichia coli. *Journal of Bacteriology*, **2009**, 191, 4815-23	3.5	15
12	Characterization of novel alleles of the Escherichia coli umuDC genes identifies additional interaction sites of UmuC with the beta clamp. *Journal of Bacteriology*, **2009**, 191, 5910-20	3.5	14
11	Song: SOS (To the Tune of ABBA's "SOS"). *Biochemistry and Molecular Biology Education*, **2009**, 37, 316	1.3	1
10	Regulation of DNA damage responses by the polymerase manager proteins UmuD and UmuD?. *FASEB Journal*, **2009**, 23, 837.1	0.9	
9	Distinct double- and single-stranded DNA binding of E. coli replicative DNA polymerase III alpha subunit. *ACS Chemical Biology*, **2008**, 3, 577-87	4.9	26
8	Steric Gate Variants in a Y family DNA Polymerase Confer UV-Hypersensitivity. *FASEB Journal*, **2008**, 22, 990.3	0.9	
7	Dynamics of the polymerase manager protein UmuD: DNA damage tolerance in E. coli. *FASEB Journal*, **2008**, 22, 591.4	0.9	

6	Y-family DNA polymerases in Escherichia coli. *Trends in Microbiology*, **2007**, 15, 70-7	12.4	116
5	Active site mutations in the Y family DNA polymerase UmuC cause hypersensitivity to UV light and are dominant negative. *FASEB Journal*, **2007**, 21, A659	0.9	
4	A non-cleavable UmuD variant that acts as a UmuD' mimic. *Journal of Biological Chemistry*, **2006**, 281, 9633-40	5.4	22
3	Characterization of Escherichia coli translesion synthesis polymerases and their accessory factors. *Methods in Enzymology*, **2006**, 408, 318-40	1.7	39
2	Two processivity clamp interactions differentially alter the dual activities of UmuC. *Molecular Microbiology*, **2006**, 59, 460-74	4.1	33
1	A Non-cleavable UmuD variant that acts as a UmuD′ mimic. *FASEB Journal*, **2006**, 20, LB55	0.9	