Anna Bebenek

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/179192/publications.pdf

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	1039406	1125271	
327	9	13	
citations	h-index	g-index	
13	13	300	
docs citations	times ranked	citing authors	
	citations 13	327 9 citations h-index 13 13	

#	Article	IF	CITATIONS
1	Fidelity of DNA replication—a matter of proofreading. Current Genetics, 2018, 64, 985-996.	0.8	109
2	Interacting Fidelity Defects in the Replicative DNA Polymerase of Bacteriophage RB69. Journal of Biological Chemistry, 2001, 276, 10387-10397.	1.6	54
3	Dissecting the Fidelity of Bacteriophage RB69 DNA Polymerase: Site-Specific Modulation of Fidelity by Polymerase Accessory Proteins. Genetics, 2002, 162, 1003-1018.	1.2	40
4	Fidelity consequences of the impaired interaction between DNA polymerase epsilon and the GINS complex. DNA Repair, 2015, 29, 23-35.	1.3	29
5	The L561A Substitution in the Nascent Base-Pair Binding Pocket of RB69 DNA Polymerase Reduces Base Discrimination. Biochemistry, 2006, 45, 2211-2220.	1.2	27
6	Processivity Clamp gp45 and ssDNA-Binding-Protein gp32 Modulate the Fidelity of Bacteriophage RB69 DNA Polymerase in a Sequence-Specific Manner, Sometimes Enhancing and Sometimes Compromising Accuracy. Genetics, 2005, 169, 1815-1824.	1.2	16
7	The Roles of Tyr391 and Tyr619 in RB69 DNA Polymerase Replication Fidelity. Journal of Molecular Biology, 2007, 368, 18-29.	2.0	14
8	Different Behaviors In Vivo of Mutations in the \hat{l}^2 Hairpin Loop of the DNA Polymerases of the Closely Related Phages T4 and RB69. Journal of Molecular Biology, 2009, 389, 797-807.	2.0	10
9	Reversal of a Mutator Activity by a Nearby Fidelity-Neutral Substitution in the RB69 DNA Polymerase Binding Pocket. Journal of Molecular Biology, 2010, 404, 778-793.	2.0	10
10	TheisfA mutation inhibits mutator activity and processing of UmuD protein inEscherichia coli recA730 strains. Molecular Genetics and Genomics, 1996, 250, 674-680.	2.4	7
11	A Remote Palm Domain Residue of RB69 DNA Polymerase Is Critical for Enzyme Activity and Influences the Conformation of the Active Site. PLoS ONE, 2013, 8, e76700.	1.1	7
12	The isfA mutation specifically inhibits the SOS-dependent mutagenic pathway and does not selectively affect any particular base substitution. Mutagenesis, 1999, 14, 295-300.	1.0	2