Peter Friedhoff

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/9906593/publications.pdf

Version: 2024-02-01

59 papers	2,256 citations	201385 27 h-index	223531 46 g-index
63 all docs	63 docs citations	63 times ranked	2042 citing authors

#	Article	IF	Citations
1	Cryogenic electron microscopy structures reveal how ATP and DNA binding in MutS coordinates sequential steps of DNA mismatch repair. Nature Structural and Molecular Biology, 2022, 29, 59-66.	3.6	12
2	Reactive Acrylamide-Modified DNA Traps for Accurate Cross-Linking with Cysteine Residues in DNAâ€“Protein Complexes Using Mismatch Repair Protein MutS as a Model. Molecules, 2022, 27, 2438.	1.7	1
3	The selection process of licensing a DNA mismatch for repair. Nature Structural and Molecular Biology, 2021, 28, 373-381.	3.6	22
4	Probing the DNA-binding center of the MutL protein from the Escherichia coli mismatch repair system via crosslinking and FÃ¶rster resonance energy transfer. Biochimie, 2020, 171-172, 43-54.	1.3	9
5	The unstructured linker arms of MutL enable GATC site incision beyond roadblocks during initiation of DNA mismatch repair. Nucleic Acids Research, 2019, 47, 11667-11680.	6.5	26
6	Combinatorial recognition of clustered RNA elements by the multidomain RNA-binding protein IMP3. Nature Communications, 2019, 10, 2266.	5.8	53
7	Mechanism and Regulation of Co-transcriptional mRNP Assembly and Nuclear mRNA Export. Advances in Experimental Medicine and Biology, 2019, 1203, 1-31.	0.8	27
8	Use of Single-Cysteine Variants for Trapping Transient States in DNA Mismatch Repair. Methods in Enzymology, 2017, 592, 77-101.	0.4	4
9	Dual daughter strand incision is processive and increases the efficiency of DNA mismatch repair. Nucleic Acids Research, 2016, 44, 6770-6786.	6.5	18
10	Protein-protein interactions in DNA mismatch repair. DNA Repair, 2016, 38, 50-57.	1.3	38
11	Editorial: Alfred Pingoud (1945â€“2015). Nucleic Acids Research, 2015, 43, 7661-7663.	6.5	0
12	Chromatographic isolation of the functionally active MutS protein covalently linked to deoxyribonucleic acid. Journal of Chromatography A, 2015, 1389, 19-27.	1.8	12
13	MutS/MutL crystal structure reveals that the MutS sliding clamp loads MutL onto DNA. ELife, 2015, 4, e06744.	2.8	91
14	Is Thymidine Glycol Containing DNA a Substrate of E. coli DNA Mismatch Repair System?. PLoS ONE, 2014, 9, e104963.	1.1	4
15	Using stable MutS dimers and tetramers to quantitatively analyze DNA mismatch recognition and sliding clamp formation. Nucleic Acids Research, 2013, 41, 8166-8181.	6.5	36
16	Site- and strand-specific nicking of DNA by fusion proteins derived from MutH and I-SceI or TALE repeats. Nucleic Acids Research, 2013, 41, e83-e83.	6.5	31
17	Single-molecule multiparameter fluorescence spectroscopy reveals directional MutS binding to mismatched bases in DNA. Nucleic Acids Research, 2012, 40, 5448-5464.	6.5	44
18	Chemical Rescue of Active Site Mutants of S. pneumoniae Surface Endonuclease EndA and Other Nucleases of the HNH Family by Imidazole. ChemBioChem, 2012, 13, 713-721.	1.3	15

#	Article	IF	Citations
19	Covalently trapping MutS on DNA to study DNA mismatch recognition and signaling. Molecular BioSystems, 2012, 8, 1861.	2.9	10
20	Generation of DNA nanocircles containing mismatched bases. BioTechniques, 2011, 51, 259-265.	0.8	5
21	Changes in cytosolic Mg2+ levels can regulate the activity of the plasma membrane H+-ATPase in maize. Biochemical Journal, 2011, 435, 93-101.	1.7	26
22	Chemical Trapping of the Dynamic MutS-MutL Complex Formed in DNA Mismatch Repair in Escherichia coli. Journal of Biological Chemistry, 2011, 286, 17326-17337.	1.6	45
23	Native mass spectrometry provides direct evidence for DNA mismatch-induced regulation of asymmetric nucleotide binding in mismatch repair protein MutS. Nucleic Acids Research, 2011, 39, 8052-8064.	6.5	30
24	Chemical trapping of the dynamic MutS-MutL complex formed in DNA mismatch repair in Escherichia coli.. Journal of Biological Chemistry, 2011, 286, 22706.	1.6	0
25	Crosslinking of (Cytosine-5)-DNA Methyltransferase SsoII and its Complexes with Specific DNA Duplexes Provides an Insight into Their Structures. Nucleosides, Nucleotides and Nucleic Acids, 2011, 30, 632-650.	0.4	8
26	Identification of Lynch syndrome mutations in the MLH1-PMS2 interface that disturb dimerization and mismatch repair. Human Mutation, 2010, 31, 975-982.	1.1	52
27	The C-Terminal Domain of the MutL Homolog from Neisseria gonorrhoeae Forms an Inverted Homodimer. PLoS ONE, 2010, 5, e13726.	1.1	29
28	Maintaining a sense of direction during long-range communication on DNA. Biochemical Society Transactions, 2010, 38, 404-409.	1.6	24
29	Structure of the Endonuclease Domain of MutL: Unlicensed to Cut. Molecular Cell, 2010, 39, 145-151.	4.5	122
30	Physical and functional interactions between Escherichia coli MutL and the Vsr repair endonuclease. Nucleic Acids Research, 2009, 37, 4453-4463.	6.5	24
31	On the Divalent Metal Ion Dependence of DNA Cleavage by Restriction Endonucleases of the EcoRI Family. Journal of Molecular Biology, 2009, 393, 140-160.	2.0	59
32	The C-terminal domain is sufficient for endonuclease activity of Neisseria gonorrhoeae MutL. Biochemical Journal, 2009, 423, 265-277.	1.7	46
33	The PMS2 Subunit of Human MutLÎ± Contains a Metal Ion Binding Domain of the Iron-Dependent Repressor Protein Family. Journal of Molecular Biology, 2008, 382, 610-627.	2.0	55
34	Bioinformatics-Guided Experimental Characterization of Mismatch-Repair Enzymes and Their Relatives. Nucleic Acids and Molecular Biology, 2008, , 221-241.	0.2	0
35	Engineering Site-Specific Endonucleases. , 2007, 352, 111-124.		3
36	Mutations in the MutSÎ± interaction interface of MLH1 can abolish DNA mismatch repair. Nucleic Acids Research, 2006, 34, 6574-6586.	6.5	61

#	Article	IF	Citations
37	Structural and functional analysis of the MutS C-terminal tetramerization domain. Nucleic Acids Research, 2006, 34, 5270-5279.	6.5	32
38	Identifying an interaction site between MutH and the C-terminal domain of MutL by crosslinking, affinity purification, chemical coding and mass spectrometry. Nucleic Acids Research, 2006, 34, 3169-3180.	6.5	41
39	Mapping protein?protein interactions by bioinformatics and cross-linking. Analytical and Bioanalytical Chemistry, 2005, 381, 78-80.	1.9	21
40	Analysis of the Quaternary Structure of the MutL C-terminal Domain. Journal of Molecular Biology, 2005, 351, 895-909.	2.0	53
41	Mapping Protein-Protein Interactions between MutL and MutH by Cross-linking. Journal of Biological Chemistry, 2004, 279, 49338-49345.	1.6	49
42	Tyr212: A Key Residue Involved in Strand Discrimination by the DNA Mismatch Repair Endonuclease MutH. Journal of Molecular Biology, 2003, 325, 285-297.	2.0	27
43	Application of the C4'-Alkylated Deoxyribose Primer System (CAPS) in Allele-Specific Real-Time PCR for Increased Selectivity in Discrimination of Single Nucleotide Sequence Variants. Biological Chemistry, 2003, 384, 1533-41.	1.2	14
44	Site-specific protein modification to identify the MutL interface of MutH. Nucleic Acids Research, 2003, 31, 819-825.	6.5	18
45	Evolutionary Relationship between Different Subgroups of Restriction Endonucleases. Journal of Biological Chemistry, 2002, 277, 14306-14314.	1.6	53
46	An Efficient Method for the Preparation of Long Heteroduplex DNA as Substrate for Mismatch Repair by the Escherichia coli MutHLS System. Biological Chemistry, 2002, 383, 1459-1462.	1.2	17
47	Haemophilus influenzaeandVibrio choleraegenes formutHare able to fully complement amutHdefect inEscherichia coli. FEMS Microbiology Letters, 2002, 208, 123-128.	0.7	15
48	Sau3AI, a Monomeric Type II Restriction Endonuclease That Dimerizes on the DNA and Thereby Induces DNA Loops. Journal of Biological Chemistry, 2001, 276, 23581-23588.	1.6	55
49	Microtiter-Plate Assay and Related Assays for Nonspecific Endonucleases. , 2001, 160, 037-048.		2
50	Structure of tau protein and assembly into paired helical filaments. Biochimica Et Biophysica Acta - Molecular Basis of Disease, 2000, 1502, 122-132.	1.8	130
51	A similar active site for non-specific and specific endonucleases. Nature Structural Biology, 1999, 6, 112-113.	9.7	59
52	Cleavage experiments with deoxythymidine 3â€²,5â€²-bis-(p-nitrophenyl phosphate) suggest that the homing endonuclease I-PpoI follows the same mechanism of phosphodiester bond hydrolysis as the non-specificSerratianuclease1. FEBS Letters, 1999, 443, 209-214.	1.3	36
53	Application of Oligonucleoside Methylphosphonates in the Studies on Phosphodiester Hydrolysis bySerratiaEndonuclease. Nucleosides & Nucleotides, 1999, 18, 1945-1960.	0.5	4
54	Rapid Assembly of Alzheimer-like Paired Helical Filaments from Microtubule-Associated Protein Tau Monitored by Fluorescence in Solution. Biochemistry, 1998, 37, 10223-10230.	1.2	378

#	Article	IF	Citations
55	Analysis of the reaction mechanism of the non-specific endonuclease ofSerratia marcescensusing an artificial minimal substrate. FEBS Letters, 1996, 397, 343-346.	1.3	27
56	Kinetic Analysis of the Cleavage of Natural and Synthetic Substrates by the Serratia Nuclease. FEBS Journal, 1996, 241, 572-580.	0.2	47
57	A Quantitative Microtiter Plate Nuclease Assay Based on Ethidium/DNA Fluorescence. Analytical Biochemistry, 1996, 240, 283-288.	1.1	11
58	Sequence preferences in cleavage of dsDNA and ssDNA by the extracellular Serratia marcescens endonuclease. Biochemistry, 1995, 34, 11979-11988.	1.2	48
59	Identification of catalytically relevant amino acids of the extracellularSerratia marcescensendonuclease by alignment-guided mutagenesis. Nucleic Acids Research, 1994, 22, 3280-3287.	6.5	72