

Finbarr Hayes

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/12148260/publications.pdf>

Version: 2024-02-01

54
papers

3,062
citations

201385

27
h-index

182168

51
g-index

56
all docs

56
docs citations

56
times ranked

2655
citing authors

#	ARTICLE	IF	CITATIONS
1	Characterization of permissive and non-permissive peptide insertion sites in chloramphenicol acetyltransferase. <i>Microbial Pathogenesis</i> , 2020, 149, 104395.	1.3	3
2	Genome Segregation by the Venus Flytrap Mechanism: Probing the Interaction Between the ParF ATPase and the ParG Centromere Binding Protein. <i>Frontiers in Molecular Biosciences</i> , 2020, 7, 108.	1.6	6
3	A three-dimensional ParF meshwork assembles through the nucleoid to mediate plasmid segregation. <i>Nucleic Acids Research</i> , 2017, 45, gkw1302.	6.5	21
4	Emerging Roles of Toxin-Antitoxin Modules in Bacterial Pathogenesis. <i>Molecules</i> , 2016, 21, 790.	1.7	116
5	Terminator Operon Reporter: combining a transcription termination switch with reporter technology for improved gene synthesis and synthetic biology applications. <i>Scientific Reports</i> , 2016, 6, 26572.	1.6	4
6	Disentangling gene networks. <i>Nature Chemical Biology</i> , 2016, 12, 3-4.	3.9	1
7	Breaking and Restoring the Hydrophobic Core of a Centromere-binding Protein. <i>Journal of Biological Chemistry</i> , 2015, 290, 9273-9283.	1.6	1
8	RapGene: a fast and accurate strategy for synthetic gene assembly in <i>Escherichia coli</i> . <i>Scientific Reports</i> , 2015, 5, 11302.	1.6	9
9	Regulating Toxin-Antitoxin Expression: Controlled Detonation of Intracellular Molecular Timebombs. <i>Toxins</i> , 2014, 6, 337-358.	1.5	87
10	The Axe-Txe Complex of <i>Enterococcus faecium</i> Presents a Multilayered Mode of Toxin-Antitoxin Gene Expression Regulation. <i>PLoS ONE</i> , 2013, 8, e73569.	1.1	15
11	Amino acid residues crucial for specificity of toxin-antitoxin interactions in the homologous $\langle \text{scp} \rangle \text{A} \langle / \text{scp} \rangle$ - $\langle \text{scp} \rangle \text{T} \langle / \text{scp} \rangle$ and $\langle \text{scp} \rangle \text{Y} \langle / \text{scp} \rangle$ - $\langle \text{scp} \rangle \text{M} \langle / \text{scp} \rangle$ - $\langle \text{scp} \rangle \text{Y} \langle / \text{scp} \rangle$ - $\langle \text{scp} \rangle \text{B} \langle / \text{scp} \rangle$ complexes. <i>FEBS Journal</i> , 2013, 280, 5906-5918.	2.2	15
12	Uncoupling of Nucleotide Hydrolysis and Polymerization in the ParA Protein Superfamily Disrupts DNA Segregation Dynamics. <i>Journal of Biological Chemistry</i> , 2012, 287, 42545-42553.	1.6	11
13	Structural Mechanism of ATP-induced Polymerization of the Partition Factor ParF. <i>Journal of Biological Chemistry</i> , 2012, 287, 26146-26154.	1.6	31
14	Combinatorial targeting of ribbon-helix artificial transcription factors to chimeric recognition sites. <i>Nucleic Acids Research</i> , 2012, 40, 6673-6682.	6.5	4
15	Moving in for the Kill: Activation of an Endoribonuclease Toxin by a Quorum-Sensing Peptide. <i>Molecular Cell</i> , 2011, 41, 617-618.	4.5	5
16	Toxins-antitoxins: diversity, evolution and function. <i>Critical Reviews in Biochemistry and Molecular Biology</i> , 2011, 46, 386-408.	2.3	254
17	Segrosome assembly at the pliable parH centromere. <i>Nucleic Acids Research</i> , 2011, 39, 5082-5097.	6.5	14
18	The Centromere Site of the Segregation Cassette of Broad-Host-Range Plasmid RA3 Is Located at the Border of the Maintenance and Conjugative Transfer Modules. <i>Applied and Environmental Microbiology</i> , 2011, 77, 2414-2427.	1.4	15

#	ARTICLE	IF	CITATIONS
19	Extrachromosomal Components of the Nucleoid: Recent Developments in Deciphering the Molecular Basis of Plasmid Segregation. , 2010, , 49-70.		8
20	Influence of Operator Site Geometry on Transcriptional Control by the YefM-YoeB Toxin-Antitoxin Complex. Journal of Bacteriology, 2009, 191, 762-772.	1.0	31
21	Recruitment of the ParG Segregation Protein to Different Affinity DNA Sites. Journal of Bacteriology, 2009, 191, 3832-3841.	1.0	11
22	Centromere anatomy in the multidrug-resistant pathogen Enterococcus faecium. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 2151-2156.	3.3	17
23	Genomic and Functional Characterization of the Modular Broad-Host-Range RA3 Plasmid, the Archetype of the IncU Group. Applied and Environmental Microbiology, 2008, 74, 4119-4132.	1.4	43
24	The tail of the ParG DNA segregation protein remodels ParF polymers and enhances ATP hydrolysis via an arginine finger-like motif. Proceedings of the National Academy of Sciences of the United States of America, 2007, 104, 1811-1816.	3.3	78
25	Promiscuous Stimulation of ParF Protein Polymerization by Heterogeneous Centromere Binding Factors. Journal of Molecular Biology, 2007, 374, 1-8.	2.0	35
26	Toxin-antitoxin regulation: bimodal interaction of YefM-YoeB with paired DNA palindromes exerts transcriptional autorepression. Nucleic Acids Research, 2006, 35, 325-339.	6.5	78
27	The bacterial segrosome: a dynamic nucleoprotein machine for DNA trafficking and segregation. Nature Reviews Microbiology, 2006, 4, 133-143.	13.6	127
28	Assembling the bacterial segrosome. Trends in Biochemical Sciences, 2006, 31, 247-250.	3.7	33
29	Bacterial DNA segregation dynamics mediated by the polymerizing protein ParF. EMBO Journal, 2005, 24, 1453-1464.	3.5	129
30	The Unstructured N-terminal Tail of ParG Modulates Assembly of a Quaternary Nucleoprotein Complex in Transcription Repression. Journal of Biological Chemistry, 2005, 280, 28683-28691.	1.6	25
31	Protein Diversity Confers Specificity in Plasmid Segregation. Journal of Bacteriology, 2005, 187, 2651-2661.	1.0	18
32	ParG, a protein required for active partition of bacterial plasmids, has a dimeric ribbon-helix-helix structure. Molecular Microbiology, 2003, 50, 1141-1153.	1.2	76
33	Axe-Txe, a broad-spectrum proteic toxin-antitoxin system specified by a multidrug-resistant, clinical isolate of Enterococcus faecium. Molecular Microbiology, 2003, 47, 1419-1432.	1.2	210
34	Architecture of the ParF-ParG protein complex involved in prokaryotic DNA segregation. Molecular Microbiology, 2003, 49, 487-499.	1.2	39
35	Transposon-Based Strategies for Microbial Functional Genomics and Proteomics. Annual Review of Genetics, 2003, 37, 3-29.	3.2	164
36	Toxins-Antitoxins: Plasmid Maintenance, Programmed Cell Death, and Cell Cycle Arrest. Science, 2003, 301, 1496-1499.	6.0	515

#	ARTICLE	IF	CITATIONS
37	The Function and Organization of Plasmids. , 2003, 235, 1-18.		22
38	Identification of XcpZ Domains Required for Assembly of the Secreton of <i>Pseudomonas aeruginosa</i> . <i>Journal of Bacteriology</i> , 2002, 184, 1779-1782.	1.0	21
39	The partition system of multidrug resistance plasmid TP228 includes a novel protein that epitomizes an evolutionarily distinct subgroup of the ParA superfamily. <i>Molecular Microbiology</i> , 2002, 37, 528-541.	1.2	89
40	Pentapeptide scanning mutagenesis: encouraging old proteins to execute unusual tricks. <i>Trends in Microbiology</i> , 2000, 8, 571-577.	3.5	47
41	A newly identified, essential catalytic residue in a critical secondary structure element in the integrase family of site-specific recombinases is conserved in a similar element in eucaryotic type IB topoisomerases. <i>Journal of Molecular Biology</i> , 1999, 289, 517-527.	2.0	29
42	A Family of Stability Determinants in Pathogenic Bacteria. <i>Journal of Bacteriology</i> , 1998, 180, 6415-6418.	1.0	60
43	Pentapeptide scanning mutagenesis: random insertion of a variable five amino acid cassette in a target protein. <i>Nucleic Acids Research</i> , 1997, 25, 1866-1867.	6.5	86
44	Insertion Mutagenesis as a Tool in the Modification of Protein Function. <i>Journal of Biological Chemistry</i> , 1997, 272, 28833-28836.	1.6	37
45	Recombinase binding specificity at the chromosome dimer resolution site dif of <i>Escherichia coli</i> 1 Edited by I. B. Holland. <i>Journal of Molecular Biology</i> , 1997, 266, 525-537.	2.0	37
46	Structure-function correlations in the XerD site-specific recombinase revealed by pentapeptide scanning mutagenesis. <i>Journal of Molecular Biology</i> , 1997, 274, 39-53.	2.0	29
47	<i>Salmonella typhimurium</i> specifies a circular chromosome dimer resolution system which is homologous to the Xer site-specific recombination system of <i>Escherichia coli</i> . <i>Gene</i> , 1997, 198, 105-110.	1.0	13
48	The homologous operons for P1 and P7 plasmid partition are autoregulated from dissimilar operator sites. <i>Molecular Microbiology</i> , 1994, 11, 249-260.	1.2	67
49	Topological Scanning of the P1 Plasmid Partition Site. <i>Journal of Molecular Biology</i> , 1994, 243, 190-198.	2.0	43
50	Physical analysis of in vivo pCI301 fusion plasmids in <i>Lactococcus lactis</i> subsp. <i>lactis</i> . <i>FEMS Microbiology Letters</i> , 1993, 106, 295-300.	0.7	0
51	Molecular organization of the minimal replicon of novel, narrow-host-range, lactococcal plasmid pCI305. <i>Plasmid</i> , 1991, 25, 16-26.	0.4	66
52	Integration and excision of plasmid DNA in <i>Lactococcus lactis</i> subsp. <i>lactis</i> . <i>Plasmid</i> , 1990, 24, 81-89.	0.4	13
53	pAM ¹ 21-Associated Mobilization of Proteinase Plasmids from <i>Lactococcus lactis</i> subsp. <i>lactis</i> UC317 and <i>L. lactis</i> subsp. <i>cremoris</i> UC205. <i>Applied and Environmental Microbiology</i> , 1990, 56, 195-201.	1.4	21
54	Identification of the Minimal Replicon of <i>Lactococcus lactis</i> subsp. <i>lactis</i> UC317 Plasmid pCI305. <i>Applied and Environmental Microbiology</i> , 1990, 56, 202-209.	1.4	131