

Yousif Shamoo

List of Publications by Year in descending order

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70
papers

4,004
citations

136950

32
h-index

128289

60
g-index

76
all docs

76
docs citations

76
times ranked

4101
citing authors

#	ARTICLE	IF	CITATIONS
1	Building a Replisome from Interacting Pieces. <i>Cell</i> , 1999, 99, 155-166.	28.9	368
2	Genetic Basis for In Vivo Daptomycin Resistance in Enterococci. <i>New England Journal of Medicine</i> , 2011, 365, 892-900.	27.0	324
3	Crystal structure of a replication fork single-stranded DNA binding protein (T4 gp32) complexed to DNA. <i>Nature</i> , 1995, 376, 362-366.	27.8	252
4	Structure-based analysis of protein-RNA interactions using the program ENTANGLE. <i>Journal of Molecular Biology</i> , 2001, 311, 75-86.	4.2	241
5	Structural and Thermodynamic Analysis of Human PCNA with Peptides Derived from DNA Polymerase- γ p66 Subunit and Flap Endonuclease-1. <i>Structure</i> , 2004, 12, 2209-2219.	3.3	190
6	Daptomycin-Resistant <i>Enterococcus faecalis</i> Diverts the Antibiotic Molecule from the Division Septum and Remodels Cell Membrane Phospholipids. <i>MBio</i> , 2013, 4, .	4.1	152
7	Multiple RNA binding domains (RBDs) just don't add up. <i>Nucleic Acids Research</i> , 1995, 23, 725-728.	14.5	134
8	Daptomycin Resistance in Enterococci Is Associated with Distinct Alterations of Cell Membrane Phospholipid Content. <i>PLoS ONE</i> , 2012, 7, e43958.	2.5	126
9	Complex of Calmodulin with a Ryanodine Receptor Target Reveals a Novel, Flexible Binding Mode. <i>Structure</i> , 2006, 14, 1547-1556.	3.3	121
10	Whole-Genome Analyses of <i>Enterococcus faecium</i> Isolates with Diverse Daptomycin MICs. <i>Antimicrobial Agents and Chemotherapy</i> , 2014, 58, 4527-4534.	3.2	119
11	The Ribosomal S10 Protein Is a General Target for Decreased Tigecycline Susceptibility. <i>Antimicrobial Agents and Chemotherapy</i> , 2015, 59, 5561-5566.	3.2	106
12	Adaptation of <i>Enterococcus faecalis</i> to Daptomycin Reveals an Ordered Progression to Resistance. <i>Antimicrobial Agents and Chemotherapy</i> , 2013, 57, 5373-5383.	3.2	102
13	Whole-Genome Analysis of a Daptomycin-Susceptible <i>Enterococcus faecium</i> Strain and Its Daptomycin-Resistant Variant Arising during Therapy. <i>Antimicrobial Agents and Chemotherapy</i> , 2013, 57, 261-268.	3.2	101
14	In Vivo Molecular Evolution Reveals Biophysical Origins of Organismal Fitness. <i>Molecular Cell</i> , 2006, 22, 441-449.	9.7	92
15	A <i>liaR</i> Deletion Restores Susceptibility to Daptomycin and Antimicrobial Peptides in Multidrug-Resistant <i>Enterococcus faecalis</i> . <i>Journal of Infectious Diseases</i> , 2015, 211, 1317-1325.	4.0	80
16	Both RNA-Binding Domains in Heterogeneous Nuclear Ribonucleoprotein A1 Contribute Toward Single-Stranded-RNA Binding. <i>Biochemistry</i> , 1994, 33, 8272-8281.	2.5	71
17	Biochemical Characterization of Cardiolipin Synthase Mutations Associated with Daptomycin Resistance in Enterococci. <i>Antimicrobial Agents and Chemotherapy</i> , 2013, 57, 289-296.	3.2	71
18	<i>Acinetobacter baumannii</i> Repeatedly Evolves a Hypermutator Phenotype in Response to Tigecycline That Effectively Surveys Evolutionary Trajectories to Resistance. <i>PLoS ONE</i> , 2015, 10, e0140489.	2.5	59

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19	Antimicrobial sensing coupled with cell membrane remodeling mediates antibiotic resistance and virulence in <i>Enterococcus faecalis</i> . Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 26925-26932.	7.1	58
20	Pathogenic Nocardia: A diverse genus of emerging pathogens or just poorly recognized?. PLoS Pathogens, 2020, 16, e1008280.	4.7	54
21	Small changes in enzyme function can lead to surprisingly large fitness effects during adaptive evolution of antibiotic resistance. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 21408-21413.	7.1	50
22	Mutations in Global Regulators Lead to Metabolic Selection during Adaptation to Complex Environments. PLoS Genetics, 2014, 10, e1004872.	3.5	50
23	Total Synthesis of Viridicatumtoxin B and Analogues Thereof: Strategy Evolution, Structural Revision, and Biological Evaluation. Journal of the American Chemical Society, 2014, 136, 12137-12160.	13.7	48
24	A variable DNA recognition site organization establishes the LiaR-mediated cell envelope stress response of enterococci to daptomycin. Nucleic Acids Research, 2015, 43, 4758-4773.	14.5	47
25	Translational Repression by the Bacteriophage T4 Gene 32 Protein Involves Specific Recognition of an RNA Pseudoknot Structure. Journal of Molecular Biology, 1993, 232, 89-104.	4.2	46
26	Structure-based Incorporation of 6-Methyl-8-(2-deoxy- β -D-ribofuranosyl)isoxanthopterin into the Human Telomeric Repeat DNA as a Probe for UP1 Binding and Destabilization of G-tetrad Structures. Journal of Biological Chemistry, 2003, 278, 42300-42306.	3.4	44
27	Differential Penicillin-Binding Protein 5 (PBP5) Levels in the <i>Enterococcus faecium</i> Clades with Different Levels of Ampicillin Resistance. Antimicrobial Agents and Chemotherapy, 2017, 61, .	3.2	42
28	Human UP1 as a Model for Understanding Purine Recognition in the Family of Proteins Containing the RNA Recognition Motif (RRM). Journal of Molecular Biology, 2004, 342, 743-756.	4.2	41
29	Deletion of <i>liaR</i> Reverses Daptomycin Resistance in <i>Enterococcus faecium</i> Independent of the Genetic Background. Antimicrobial Agents and Chemotherapy, 2015, 59, 7327-7334.	3.2	41
30	Photochemical crosslinking of bacteriophage T4 single-stranded DNA-binding protein (gp32) to oligo-p(dT)8: Identification of phenylalanine-183 as the site of crosslinking. Proteins: Structure, Function and Bioinformatics, 1988, 4, 1-6.	2.6	40
31	An Adaptive Mutation in <i>Enterococcus faecium</i> LiaR Associated with Antimicrobial Peptide Resistance Mimics Phosphorylation and Stabilizes LiaR in an Activated State. Journal of Molecular Biology, 2016, 428, 4503-4519.	4.2	39
32	The Essential Role of Hypermutation in Rapid Adaptation to Antibiotic Stress. Antimicrobial Agents and Chemotherapy, 2019, 63, .	3.2	39
33	Evolutionary fates within a microbial population highlight an essential role for protein folding during natural selection. Molecular Systems Biology, 2010, 6, 387.	7.2	38
34	An adaptive mutation in adenylate kinase that increases organismal fitness is linked to stability-activity trade-offs. Protein Engineering, Design and Selection, 2007, 21, 19-27.	2.1	32
35	Asymmetric Alkylation of Anthrones, Enantioselective Total Synthesis of (âˆ’)- and (+)-Viridicatumtoxins B and Analogues Thereof: Absolute Configuration and Potent Antibacterial Agents. Journal of the American Chemical Society, 2017, 139, 3736-3746.	13.7	32
36	Gene replacement of adenylate kinase in the gram-positive thermophile <i>Geobacillus stearothermophilus</i> disrupts adenine nucleotide homeostasis and reduces cell viability. Extremophiles, 2005, 9, 135-144.	2.3	31

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37	Rampant Parasexuality Evolves in a Hospital Pathogen during Antibiotic Selection. <i>Molecular Biology and Evolution</i> , 2015, 32, 2585-2597.	8.9	31
38	Mutation of E1-CONJUGATING ENZYME-RELATED1 Decreases RELATED TO UBIQUITIN Conjugation and Alters Auxin Response and Development. <i>Plant Physiology</i> , 2007, 144, 976-987.	4.8	30
39	Environment Shapes the Accessible Daptomycin Resistance Mechanisms in <i>Enterococcus faecium</i> . <i>Antimicrobial Agents and Chemotherapy</i> , 2019, 63, .	3.2	30
40	Phase Improvement by Multi-Start Simulated Annealing Refinement and Structure-Factor Averaging. <i>Journal of Applied Crystallography</i> , 1998, 31, 798-805.	4.5	28
41	Experimental Evolution of Adenylate Kinase Reveals Contrasting Strategies toward Protein Thermostability. <i>Biophysical Journal</i> , 2010, 99, 887-896.	0.5	26
42	Structure analysis of free and bound states of an RNA aptamer against ribosomal protein S8 from <i>Bacillus anthracis</i> . <i>Nucleic Acids Research</i> , 2014, 42, 10795-10808.	14.5	26
43	Using experimental evolution to identify druggable targets that could inhibit the evolution of antimicrobial resistance. <i>Journal of Antibiotics</i> , 2018, 71, 279-286.	2.0	26
44	Lia-Independent pathways to daptomycin resistance in <i>Enterococcus faecalis</i> reveal a multilayer defense against cell envelope antibiotics. <i>Molecular Microbiology</i> , 2019, 111, 811-824.	2.5	26
45	A Novel Phosphodiesterase of the GdpP Family Modulates Cyclic di-AMP Levels in Response to Cell Membrane Stress in Daptomycin-Resistant <i>Enterococci</i> . <i>Antimicrobial Agents and Chemotherapy</i> , 2017, 61, .	3.2	24
46	Structural insights into BRCA2 function. <i>Current Opinion in Structural Biology</i> , 2003, 13, 206-211.	5.7	20
47	Biochemical Characterization of Interactions between DNA Polymerase and Single-stranded DNA-binding Protein in Bacteriophage RB69. <i>Journal of Biological Chemistry</i> , 2003, 278, 3876-3881.	3.4	20
48	Targeting cell membrane adaptation as a novel antimicrobial strategy. <i>Current Opinion in Microbiology</i> , 2016, 33, 91-96.	5.1	20
49	Enantioselective Total Synthesis of Antibiotic CJ-16,264, Synthesis and Biological Evaluation of Designed Analogues, and Discovery of Highly Potent and Simpler Antibacterial Agents. <i>Journal of the American Chemical Society</i> , 2017, 139, 15868-15877.	13.7	19
50	Structure and enzymatic properties of a chimeric bacteriophage RB69 DNA polymerase and single-stranded DNA binding protein with increased processivity. <i>Proteins: Structure, Function and Bioinformatics</i> , 2006, 65, 231-238.	2.6	18
51	Structure and biochemical characterization of an adenylate kinase originating from the psychrophilic organism <i>Marinibacillus marinus</i> . <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2009, 65, 751-756.	0.7	18
52	A 60-Kilodalton Protein Component of the Counting Factor Complex Regulates Group Size in <i>Dictyostelium discoideum</i> . <i>Eukaryotic Cell</i> , 2006, 5, 1532-1538.	3.4	17
53	Crystal structure of <i>Bacteroides thetaiotaomicron</i> TetX2: A tetracycline degrading monooxygenase at 2.8 Å resolution. <i>Proteins: Structure, Function and Bioinformatics</i> , 2011, 79, 2335-2340.	2.6	16
54	Protein chemistry-nuclear magnetic resonance approach to mapping functional domains in single-stranded DNA binding proteins. <i>Journal of Cellular Biochemistry</i> , 1986, 32, 305-326.	2.6	14

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55	EfgA is a conserved formaldehyde sensor that leads to bacterial growth arrest in response to elevated formaldehyde. <i>PLoS Biology</i> , 2021, 19, e3001208.	5.6	13
56	Two Mutations Commonly Associated with Daptomycin Resistance in <i>Enterococcus faecium</i> LiaST120A and LiaRW73C Appear To Function Epistatically in LiaFSR Signaling. <i>Biochemistry</i> , 2018, 57, 6797-6805.	2.5	12
57	Crystal structure of a trimeric archaeal adenylate kinase from the mesophile <i>Methanococcus maripaludis</i> with an unusually broad functional range and thermal stability. <i>Proteins: Structure, Function and Bioinformatics</i> , 2010, 78, 357-364.	2.6	11
58	Daptomycin Resistance in <i>Enterococcus faecium</i> Can Be Delayed by Disruption of the LiaFSR Stress Response Pathway. <i>Antimicrobial Agents and Chemotherapy</i> , 2021, 65, .	3.2	10
59	Identification of Evolutionary Trajectories Associated with Antimicrobial Resistance Using Microfluidics. <i>ACS Infectious Diseases</i> , 2022, 8, 242-254.	3.8	10
60	Pseudosymmetry, high copy number and twinning complicate the structure determination of <i>Desulfovibrio desulfuricans</i> (ATCC 29577) flavodoxin. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2009, 65, 523-534.	2.5	7
61	Microfluidic platform for spatially segregated experimental evolution studies with <i>E. coli</i> . <i>STAR Protocols</i> , 2022, 3, 101332.	1.2	7
62	Evolution of a single gene highlights the complexity underlying molecular descriptions of fitness. <i>Chaos</i> , 2010, 20, 026107.	2.5	6
63	Experimental Evolution of Diverse Strains as a Method for the Determination of Biochemical Mechanisms of Action for Novel Pyrrolizidinone Antibiotics. <i>ACS Infectious Diseases</i> , 2017, 3, 854-865.	3.8	6
64	Using cellular fitness to map the structure and function of a major facilitator superfamily effluxer. <i>Molecular Systems Biology</i> , 2017, 13, 964.	7.2	6
65	Disrupting Membrane Adaptation Restores In Vivo Efficacy of Antibiotics Against Multidrug-Resistant <i>Enterococci</i> and Potentiates Killing by Human Neutrophils. <i>Journal of Infectious Diseases</i> , 2019, 220, 494-504.	4.0	6
66	Evolution of <i>Enterococcus faecium</i> in Response to a Combination of Daptomycin and Fosfomycin Reveals Distinct and Diverse Adaptive Strategies. <i>Antimicrobial Agents and Chemotherapy</i> , 2022, 66, e0233321.	3.2	6
67	Mutational Switch-Backs Can Accelerate Evolution of <i>Francisella</i> to a Combination of Ciprofloxacin and Doxycycline. <i>Frontiers in Microbiology</i> , 2022, 13, .	3.5	5
68	Biophysical basis for TetX mediated antibiotic resistance. <i>FASEB Journal</i> , 2010, 24, 909.2.	0.5	1
69	Adaptation of <i>Enterococcus faecalis</i> to Daptomycin Reveals an Ordered Progression to Resistance. <i>Antimicrobial Agents and Chemotherapy</i> , 2014, 58, 631-631.	3.2	0
70	Structural studies of an RNA aptamer with high affinity for the <i>B. anthracis</i> ribosomal protein S8.. <i>FASEB Journal</i> , 2010, 24, 499.1.	0.5	0