

# 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	Identification of Evolutionary Trajectories Associated with Antimicrobial Resistance Using Microfluidics. <i>ACS Infectious Diseases</i> , 2022, 8, 242-254.	3.8	10
2	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
3	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
4	Microfluidic platform for spatially segregated experimental evolution studies with <i>E. coli</i> . <i>STAR Protocols</i> , 2022, 3, 101332.	1.2	7
5	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
6	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
7	Pathogenic <i>Nocardia</i> : A diverse genus of emerging pathogens or just poorly recognized?. <i>PLoS Pathogens</i> , 2020, 16, e1008280.	4.7	54
8	Environment Shapes the Accessible Daptomycin Resistance Mechanisms in <i>Enterococcus faecium</i> . <i>Antimicrobial Agents and Chemotherapy</i> , 2019, 63, .	3.2	30
9	The Essential Role of Hypermutation in Rapid Adaptation to Antibiotic Stress. <i>Antimicrobial Agents and Chemotherapy</i> , 2019, 63, .	3.2	39
10	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
11	Antimicrobial sensing coupled with cell membrane remodeling mediates antibiotic resistance and virulence in <i>Enterococcus faecalis</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 26925-26932.	7.1	58
12	LiaR-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
13	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
14	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
15	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
16	Asymmetric Alkylation of Anthrones, Enantioselective Total Synthesis of (âˆ’)- and (+)-Viridicatumtoxins B and Analogues Thereof: Absolute Configuration and Potent Antibacterial Agents. <i>Journal of the American Chemical Society</i> , 2017, 139, 3736-3746.	13.7	32
17	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
18	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

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19	Differential Penicillin-Binding Protein 5 (PBP5) Levels in the Enterococcus faecium Clades with Different Levels of Ampicillin Resistance. <i>Antimicrobial Agents and Chemotherapy</i> , 2017, 61, .	3.2	42
20	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
21	An Adaptive Mutation in Enterococcus faecium LiaR Associated with Antimicrobial Peptide Resistance Mimics Phosphorylation and Stabilizes LiaR in an Activated State. <i>Journal of Molecular Biology</i> , 2016, 428, 4503-4519.	4.2	39
22	Targeting cell membrane adaptation as a novel antimicrobial strategy. <i>Current Opinion in Microbiology</i> , 2016, 33, 91-96.	5.1	20
23	Acinetobacter baumannii 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
24	A variable DNA recognition site organization establishes the LiaR-mediated cell envelope stress response of enterococci to daptomycin. <i>Nucleic Acids Research</i> , 2015, 43, 4758-4773.	14.5	47
25	Rampant Parasexuality Evolves in a Hospital Pathogen during Antibiotic Selection. <i>Molecular Biology and Evolution</i> , 2015, 32, 2585-2597.	8.9	31
26	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
27	Deletion of <i>liaR</i> Reverses Daptomycin Resistance in Enterococcus faecium Independent of the Genetic Background. <i>Antimicrobial Agents and Chemotherapy</i> , 2015, 59, 7327-7334.	3.2	41
28	A <i>liaR</i> Deletion Restores Susceptibility to Daptomycin and Antimicrobial Peptides in Multidrug-Resistant Enterococcus faecalis. <i>Journal of Infectious Diseases</i> , 2015, 211, 1317-1325.	4.0	80
29	Mutations in Global Regulators Lead to Metabolic Selection during Adaptation to Complex Environments. <i>PLoS Genetics</i> , 2014, 10, e1004872.	3.5	50
30	Adaptation of Enterococcus faecalis to Daptomycin Reveals an Ordered Progression to Resistance. <i>Antimicrobial Agents and Chemotherapy</i> , 2014, 58, 631-631.	3.2	0
31	Total Synthesis of Viridicatumtoxin B and Analogues Thereof: Strategy Evolution, Structural Revision, and Biological Evaluation. <i>Journal of the American Chemical Society</i> , 2014, 136, 12137-12160.	13.7	48
32	Structure analysis of free and bound states of an RNA aptamer against ribosomal protein S8 from Bacillus anthracis. <i>Nucleic Acids Research</i> , 2014, 42, 10795-10808.	14.5	26
33	Whole-Genome Analyses of Enterococcus faecium Isolates with Diverse Daptomycin MICs. <i>Antimicrobial Agents and Chemotherapy</i> , 2014, 58, 4527-4534.	3.2	119
34	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
35	Daptomycin-Resistant Enterococcus faecalis Diverts the Antibiotic Molecule from the Division Septum and Remodels Cell Membrane Phospholipids. <i>MBio</i> , 2013, 4, .	4.1	152
36	Whole-Genome Analysis of a Daptomycin-Susceptible Enterococcus faecium Strain and Its Daptomycin-Resistant Variant Arising during Therapy. <i>Antimicrobial Agents and Chemotherapy</i> , 2013, 57, 261-268.	3.2	101

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37	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
38	Small changes in enzyme function can lead to surprisingly large fitness effects during adaptive evolution of antibiotic resistance. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 21408-21413.	7.1	50
39	Daptomycin Resistance in Enterococci Is Associated with Distinct Alterations of Cell Membrane Phospholipid Content. <i>PLoS ONE</i> , 2012, 7, e43958.	2.5	126
40	Genetic Basis for In Vivo Daptomycin Resistance in Enterococci. <i>New England Journal of Medicine</i> , 2011, 365, 892-900.	27.0	324
41	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
42	Evolutionary fates within a microbial population highlight an essential role for protein folding during natural selection. <i>Molecular Systems Biology</i> , 2010, 6, 387.	7.2	38
43	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
44	Evolution of a single gene highlights the complexity underlying molecular descriptions of fitness. <i>Chaos</i> , 2010, 20, 026107.	2.5	6
45	Experimental Evolution of Adenylate Kinase Reveals Contrasting Strategies toward Protein Thermostability. <i>Biophysical Journal</i> , 2010, 99, 887-896.	0.5	26
46	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
47	Biophysical basis for TetX mediated antibiotic resistance. <i>FASEB Journal</i> , 2010, 24, 909.2.	0.5	1
48	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
49	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
50	An adaptive mutation in adenylate kinase that increases organismal fitness is linked to stability-activity trade-offs. <i>Protein Engineering, Design and Selection</i> , 2007, 21, 19-27.	2.1	32
51	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
52	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
53	In Vivo Molecular Evolution Reveals Biophysical Origins of Organismal Fitness. <i>Molecular Cell</i> , 2006, 22, 441-449.	9.7	92
54	Complex of Calmodulin with a Ryanodine Receptor Target Reveals a Novel, Flexible Binding Mode. <i>Structure</i> , 2006, 14, 1547-1556.	3.3	121

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55	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
56	Gene replacement of adenylate kinase in the gram-positive thermophile <i>Geobacillus stearothermophilus</i> disrupts adenine nucleotide homeostasis and reduces cell viability. <i>Extremophiles</i> , 2005, 9, 135-144.	2.3	31
57	Structural and Thermodynamic Analysis of Human PCNA with Peptides Derived from DNA Polymerase- $\beta$ p66 Subunit and Flap Endonuclease-1. <i>Structure</i> , 2004, 12, 2209-2219.	3.3	190
58	Human UP1 as a Model for Understanding Purine Recognition in the Family of Proteins Containing the RNA Recognition Motif (RRM). <i>Journal of Molecular Biology</i> , 2004, 342, 743-756.	4.2	41
59	Structural insights into BRCA2 function. <i>Current Opinion in Structural Biology</i> , 2003, 13, 206-211.	5.7	20
60	Structure-based Incorporation of 6-Methyl-8-(2-deoxy- $\beta$ -D-ribofuranosyl)isoxanthopterin into the Human Telomeric Repeat DNA as a Probe for UP1 Binding and Destabilization of G-tetrad Structures. <i>Journal of Biological Chemistry</i> , 2003, 278, 42300-42306.	3.4	44
61	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
62	Structure-based analysis of protein-RNA interactions using the program ENTANGLE. <i>Journal of Molecular Biology</i> , 2001, 311, 75-86.	4.2	241
63	Building a Replisome from Interacting Pieces. <i>Cell</i> , 1999, 99, 155-166.	28.9	368
64	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
65	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
66	Multiple RNA binding domains (RBDs) just don't add up. <i>Nucleic Acids Research</i> , 1995, 23, 725-728.	14.5	134
67	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
68	Translational Repression by the Bacteriophage T4 Gene 32 Protein Involves Specific Recognition of an RNA Pseudoknot Structure. <i>Journal of Molecular Biology</i> , 1993, 232, 89-104.	4.2	46
69	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. <i>Proteins: Structure, Function and Bioinformatics</i> , 1988, 4, 1-6.	2.6	40
70	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