Chuck S Farah

List of Publications by Year
in descending order

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82 papers	3,948 citations	201385 27 h-index	128067 60 g-index
88 all docs	88 docs citations	88 times ranked	3550 citing authors

#	Article	IF	Citations
1	Structural basis for effector recognition by an antibacterial type IV secretion system. Proceedings of the National Academy of Sciences of the United States of America, 2022, 119, .	3.3	9
2	Toxicity of spike fragments SARS-CoV-2 S protein for zebrafish: A tool to study its hazardous for human health?. Science of the Total Environment, 2022, 813, 152345.	3.9	19
3	An Extracytoplasmic Function Sigma Factor Required for Full Virulence in Xanthomonas citri pv. citri. Journal of Bacteriology, 2022, , e0062421.	1.0	0
4	Structural analysis of TrkA mutations in patients with congenital insensitivity to pain reveals PLCÎ³ as an analgesic drug target. Science Signaling, 2022, 15, eabm6046.	1.6	3
5	Secrete or perish: The role of secretion systems in Xanthomonas biology. Computational and Structural Biotechnology Journal, 2021, 19, 279-302.	1.9	38
6	The PilB-PilZ-FimX regulatory complex of the Type IV pilus from Xanthomonas citri. PLoS Pathogens, 2021, 17, e1009808.	2.1	6
7	A Novel Saliva RT-LAMP Workflow for Rapid Identification of COVID-19 Cases and Restraining Viral Spread. Diagnostics, 2021, 11, 1400.	1.3	18
8	Molecular Dynamics Reveals Complex Compensatory Effects of Ionic Strength on the Severe Acute Respiratory Syndrome Coronavirus 2 Spike/Human Angiotensin-Converting Enzyme 2 Interaction. Journal of Physical Chemistry Letters, 2020, 11, 10446-10453.	2.1	20
9	Substrate and Product-Assisted Catalysis: Molecular Aspects behind Structural Switches along Organic Hydroperoxide Resistance Protein Catalytic Cycle. ACS Catalysis, 2020, 10, 6587-6602.	5.5	4
10	Bactericidal type IV secretion system homeostasis in Xanthomonas citri. PLoS Pathogens, 2020, 16, e1008561.	2.1	15
11	Bactericidal type IV secretion system homeostasis in Xanthomonas citri. , 2020, 16, e1008561.		0
12	Bactericidal type IV secretion system homeostasis in Xanthomonas citri. , 2020, 16, e1008561.		0
13	Bactericidal type IV secretion system homeostasis in Xanthomonas citri. , 2020, 16, e1008561.		0
14	Bactericidal type IV secretion system homeostasis in Xanthomonas citri. , 2020, 16, e1008561.		0
15	Importance of the Î²5â^¼Î²6 Loop for the Structure, Catalytic Efficiency, and Stability of Carbapenem-Hydrolyzing Class D Î²-Lactamase Subfamily OXA-143. Biochemistry, 2019, 58, 3604-3616.	1.2	4
16	The Xanthomonas citri pv. citri Type VI Secretion System is Induced During Epiphytic Colonization of Citrus. Current Microbiology, 2019, 76, 1105-1111.	1.0	8
17	The opportunistic pathogen Stenotrophomonas maltophilia utilizes a type IV secretion system for interbacterial killing. PLoS Pathogens, 2019, 15, e1007651.	2.1	60
18	Distribution, Function and Regulation of Type 6 Secretion Systems of Xanthomonadales. Frontiers in Microbiology, 2019, 10, 1635.	1.5	39

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19	Bacteria-Killing Type IV Secretion Systems. Frontiers in Microbiology, 2019, 10, 1078.	1.5	108
20	Where do we aspire to publish? A position paper on scientific communication in biochemistry and molecular biology. Brazilian Journal of Medical and Biological Research, 2019, 52, e8935.	0.7	1
21	Xanthomonas citri T6SS mediates resistance to Dictyostelium predation and is regulated by an ECF Ïƒ factor and cognate Ser/Thr kinase. Environmental Microbiology, 2018, 20, 1562-1575.	1.8	47
22	Cryo-EM structure of the bacteria-killing type IV secretion system core complex from Xanthomonas citri. Nature Microbiology, 2018, 3, 1429-1440.	5.9	62
23	A bipartite periplasmic receptorâ€“diguanylate cyclase pair (XAC2383â€“XAC2382) in the bacterium Xanthomonas citri. Journal of Biological Chemistry, 2018, 293, 10767-10781.	1.6	2
24	Structural and Enzymatic Characterization of a cAMP-Dependent Diguanylate Cyclase from Pathogenic Leptospira Species. Journal of Molecular Biology, 2017, 429, 2337-2352.	2.0	24
25	Using the Amino Acid Network to Modulate the Hydrolytic Activity of Î²-Glycosidases. PLoS ONE, 2016, 11, e0167978.	1.1	14
26	VirB7 and VirB9 Interactions Are Required for the Assembly and Antibacterial Activity of a Type IV Secretion System. Structure, 2016, 24, 1707-1718.	1.6	14
27	The Xanthomonas type IV pilus. Current Opinion in Microbiology, 2016, 30, 88-97.	2.3	37
28	Cooperative Substrate Binding by a Diguanylate Cyclase. Journal of Molecular Biology, 2015, 427, 415-432.	2.0	22
29	Bacterial killing via a type IV secretion system. Nature Communications, 2015, 6, 6453.	5.8	197
30	The Post-transcriptional Regulator rsmA/csrA Activates T3SS by Stabilizing the 5â€² UTR of hrpG, the Master Regulator of hrp/hrc Genes, in Xanthomonas. PLoS Pathogens, 2014, 10, e1003945.	2.1	66
31	Xanthomonas citri subsp. citri Type IV Pilus Is Required for Twitching Motility, Biofilm Development, and Adherence. Molecular Plant-Microbe Interactions, 2014, 27, 1132-1147.	1.4	59
32	Structure of the PilZâ€“FimXEALâ€“c-di-GMP Complex Responsible for the Regulation of Bacterial Type IV Pilus Biogenesis. Journal of Molecular Biology, 2013, 425, 2174-2197.	2.0	49
33	Calcium Binding to Leptospira Outer Membrane Antigen LipL32 Is Not Necessary for Its Interaction with Plasma Fibronectin, Collagen Type IV, and Plasminogen. Journal of Biological Chemistry, 2012, 287, 4826-4834.	1.6	15
34	The 3D structure and function of digestive cathepsin L-like proteinases of Tenebrio molitor larval midgut. Insect Biochemistry and Molecular Biology, 2012, 42, 655-664.	1.2	33
35	Analysis of three Xanthomonas axonopodis pv. citri effector proteins in pathogenicity and their interactions with host plant proteins. Molecular Plant Pathology, 2012, 13, 865-876.	2.0	22
36	Structure-Function Analysis of the HrpB2-HrcU Interaction in the Xanthomonas citri Type III Secretion System. PLoS ONE, 2011, 6, e17614.	1.1	13

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37	A Component of the Xanthomonadaceae Type IV Secretion System Combines a VirB7 Motif with a N0 Domain Found in Outer Membrane Transport Proteins. PLoS Pathogens, 2011, 7, e1002031.	2.1	62
38	The Xanthomonas citri effector protein PthA interacts with citrus proteins involved in nuclear transport, protein folding and ubiquitination associated with DNA repair. Molecular Plant Pathology, 2010, 11, 663-675.	2.0	42
39	Cellâ€“cell signal-dependent dynamic interactions between HD-GYP and GGDEF domain proteins mediate virulence in Xanthomonas campestris. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 5989-5994.	3.3	133
40	A new member of the ribbon-helix-helix transcription factor superfamily from the plant pathogen Xanthomonas axonopodis pv. citri. Journal of Structural Biology, 2010, 170, 21-31.	1.3	6
41	Mg²⁺ ions bind at the Câ€terminal region of skeletal muscle Î±â€tropomyosin. Biopolymers, 2009, 91, 583-590.	1.2	4
42	Solution structure of the Câ€terminal domain of multiprotein bridging factor 1 (MBF1) of Trichoderma reesei. Proteins: Structure, Function and Bioinformatics, 2009, 75, 518-523.	1.5	12
43	Crystallization and preliminary X-ray analysis of LipL32 fromLeptospira interrogansserovar Copenhageni. Acta Crystallographica Section F: Structural Biology Communications, 2009, 65, 307-309.	0.7	2
44	Expression, crystallization and preliminary crystallographic analysis of PilZXAC1133fromXanthomonas axonopodispv.citri. Acta Crystallographica Section F: Structural Biology Communications, 2009, 65, 304-306.	0.7	2
45	Structure and Calcium-Binding Activity of LipL32, the Major Surface Antigen of Pathogenic Leptospira sp.. Journal of Molecular Biology, 2009, 390, 722-736.	2.0	41
46	PILZ Protein Structure and Interactions with PILB and the FIMX EAL Domain: Implications for Control of Type IV Pilus Biogenesis. Journal of Molecular Biology, 2009, 393, 848-866.	2.0	100
47	Skipping of exon 30 in C5 gene results in complete human C5 deficiency and demonstrates the importance of C5d and CUB domains for stability. Molecular Immunology, 2009, 46, 2116-2123.	1.0	17
48	Deciphering the role of the electrostatic interactions in the Î±â€tropomyosin headâ€toâ€tail complex. Proteins: Structure, Function and Bioinformatics, 2008, 73, 902-917.	1.5	7
49	Genetic analysis of complement C1s deficiency associated with systemic lupus erythematosus highlights alternative splicing of normal C1s gene. Molecular Immunology, 2008, 45, 1693-1702.	1.0	44
50	C1s deficiency associated with systemic lupus erythematosus highlights alternative splicing of normal C1s gene. Molecular Immunology, 2007, 44, 3961-3962.	1.0	0
51	Different Effects of Trifluoroethanol and Glycerol on the Stability of Tropomyosin Helices and the Head-to-Tail Complex. Biophysical Journal, 2007, 92, 2463-2475.	0.2	18
52	Solution structure of ApaG from Xanthomonas axonopodis pv. citri reveals a fibronectin-3 fold. Proteins: Structure, Function and Bioinformatics, 2007, 67, 490-500.	1.5	12
53	Structure of Xanthomonas axonopodis pv. citri YaeQ reveals a new compact protein fold built around a variation of the PDâ€(D/E)XK nuclease motif. Proteins: Structure, Function and Bioinformatics, 2007, 69, 644-651.	1.5	4
54	Identification of the flagellar chaperone FlgN in the phytopathogen Xanthomonas axonopodis pathovar citri by its interaction with hook-associated FlgK. Archives of Microbiology, 2007, 188, 243-250.	1.0	12

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55	Expression, crystallization and preliminary crystallographic analysis of SufE (XAC2355) fromXanthomonas axonopodispv.citri. Acta Crystallographica Section F: Structural Biology Communications, 2006, 62, 268-270.	0.7	3
56	The HD-GYP domain of RpfG mediates a direct linkage between the Rpf quorum-sensing pathway and a subset of diguanylate cyclase proteins in the phytopathogenXanthomonas axonopodispv citri. Molecular Microbiology, 2006, 62, 537-551.	1.2	124
57	The structural molecular biology network of the State of SÃ£o Paulo, Brazil. Anais Da Academia Brasileira De Ciencias, 2006, 78, 241-253.	0.3	3
58	Mapping contacts between regulatory domains of skeletal muscle TnC and TnI by analyses of single-chain chimeras. FEBS Journal, 2005, 272, 779-790.	2.2	8
59	Expression, purification, crystallization and preliminary X-ray analysis of YaeQ (XAC2396) fromXanthomonas axonopodispv.citri. Acta Crystallographica Section F: Structural Biology Communications, 2005, 61, 493-495.	0.7	4
60	Using 5-Hydroxytryptophan as a Probe to Follow Protein-Protein Interactions and Protein Folding Transitions. Protein and Peptide Letters, 2005, 12, 241-244.	0.4	9
61	Identification of New Protein-Protein Interactions Involving the Products of the Chromosome- and Plasmid-Encoded Type IV Secretion Loci of the Phytopathogen Xanthomonas axonopodis pv. citri. Journal of Bacteriology, 2005, 187, 2315-2325.	1.0	83
62	New Protein-Protein Interactions Identified for the Regulatory and Structural Components and Substrates of the Type III Secretion System of the Phytopathogen Xanthomonas axonopodis Pathovar citri. Journal of Bacteriology, 2004, 186, 6186-6197.	1.0	55
63	Ca2+-induced Rolling of Tropomyosin in Muscle Thin Filaments. Journal of Biological Chemistry, 2004, 279, 15204-15213.	1.6	36
64	A specific C-terminal deletion in tropomyosin results in a stronger head-to-tail interaction and increased polymerization. FEBS Journal, 2004, 271, 589-600.	0.2	11
65	Letter to the Editor:1H,15N and13C Resonance Assignments of the ApaG Protein of the Phytopathogen Xanthomonas Axonopodis pv. citri. Journal of Biomolecular NMR, 2004, 29, 423-424.	1.6	5
66	Cloning and expression of calglandulin, a new EF-hand protein from the venom glands of Bothrops insularis snake in E. coli. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2003, 1648, 90-98.	1.1	21
67	High-throughput screening of structural proteomics targets using NMR. FEBS Letters, 2003, 552, 207-213.	1.3	33
68	Parallel Measurement of Ca2+ Binding and Fluorescence Emission upon Ca2+ Titration of Recombinant Skeletal Muscle Troponin C. Journal of Biological Chemistry, 2003, 278, 11007-11014.	1.6	8
69	Quantitative Analysis of Tropomyosin Linear Polymerization Equilibrium as a Function of Ionic Strength. Journal of Biological Chemistry, 2002, 277, 2081-2088.	1.6	24
70	Specific Sequences Determine the Stability and Cooperativity of Folding of the C-terminal Half of Tropomyosin. Journal of Biological Chemistry, 2002, 277, 39574-39584.	1.6	26
71	Comparison of the genomes of two Xanthomonas pathogens with differing host specificities. Nature, 2002, 417, 459-463.	13.7	1,074
72	Homozygous hereditary C3 deficiency due to a premature stop codon. Journal of Clinical Immunology, 2002, 22, 321-330.	2.0	16

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73	Mapping the Domain of Troponin T Responsible for the Activation of Actomyosin ATPase Activity. Journal of Biological Chemistry, 2000, 275, 27513-27519.	1.6	41
74	Fluorescence Properties of Recombinant Tropomyosin Containing Tryptophan, 5-Hydroxytryptophan and 7-Azatryptophan. Photochemistry and Photobiology, 1999, 70, 719-730.	1.3	15
75	Regulatory Properties of Recombinant Tropomyosins Containing 5-Hydroxytryptophan:Â Ca2+-Binding to Troponin Results in a Conformational Change in a Region of Tropomyosin outside the Troponin Binding Siteâ€. Biochemistry, 1999, 38, 10543-10551.	1.2	27
76	Regulatory Properties of the NH2- and COOH-terminal Domains of Troponin T. Journal of Biological Chemistry, 1998, 273, 10594-10601.	1.6	97
77	Combined PCR/Gapped-Duplex Method for Site-Directed Mutagenesis. BioTechniques, 1998, 25, 758-762.	0.8	0
78	Distinct Regions of Troponin I Regulate Ca2+-dependent Activation and Ca2+ Sensitivity of the Acto-S1-TM ATPase Activity of the Thin Filament. Journal of Biological Chemistry, 1997, 272, 10529-10537.	1.6	70
79	The nonvitellogenic female protein of Musca domestica is an adultâ€specific hexamerin. Insect Molecular Biology, 1997, 6, 97-104.	1.0	14
80	Structural Interactions Responsible for the Assembly of the Troponin Complex on the Muscle Thin Filament.. Cell Structure and Function, 1997, 22, 219-223.	0.5	15
81	The troponin complex and regulation of muscle contraction. FASEB Journal, 1995, 9, 755-767.	0.2	517
82	Structural characterization of separated H DNA conformers. Biochemistry, 1990, 29, 11110-11115.	1.2	20