

Katrina T Forest

List of Publications by Year in descending order

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65
papers

4,390
citations

136950

32
h-index

128289

60
g-index

68
all docs

68
docs citations

68
times ranked

4398
citing authors

#	ARTICLE	IF	CITATIONS
1	A Surface Exposed, Two-Domain Lipoprotein Cargo of a Type XI Secretion System Promotes Colonization of Host Intestinal Epithelia Expressing Glycans. <i>Frontiers in Microbiology</i> , 2022, 13, 800366.	3.5	3
2	Structural interactions define assembly adapter function of a type II secretion system pseudopilin. <i>Structure</i> , 2021, 29, 1116-1127.e8.	3.3	20
3	Cryo-ET Characterization of Novel Cellular Extrusions in <i>Escherichia coli</i> Induced by the Major Subunit Protein of Type IV Pili, PilA, from <i>Pseudomonas aeruginosa</i> . <i>Microscopy and Microanalysis</i> , 2021, 27, 280-282.	0.4	0
4	A Widespread Bacterial Secretion System with Diverse Substrates. <i>MBio</i> , 2021, 12, e0195621.	4.1	30
5	Retention of Native Quaternary Structure in Racemic Melittin Crystals. <i>Journal of the American Chemical Society</i> , 2019, 141, 7704-7708.	13.7	19
6	Type IV pili: dynamics, biophysics and functional consequences. <i>Nature Reviews Microbiology</i> , 2019, 17, 429-440.	28.6	297
7	Light on the cell cycle of the non-photosynthetic bacterium <i>Ramlibacter tataouinensis</i> . <i>Scientific Reports</i> , 2019, 9, 16505.	3.3	8
8	A Hendecad Motif Is Preferred for Heterochiral Coiled-Coil Formation. <i>Journal of the American Chemical Society</i> , 2019, 141, 1583-1592.	13.7	19
9	Evaluation of α -Amino Acid Replacements in Protein Loops: Effects on Conformational Stability and Structure. <i>ChemBioChem</i> , 2018, 19, 604-612.	2.6	18
10	act Actinobacteria Assemble a Functional Actinorhodopsin with Natively Synthesized Retinal. <i>Applied and Environmental Microbiology</i> , 2018, 84, .	3.1	15
11	Reconstitution of a minimal machinery capable of assembling periplasmic type IV pili. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, E4978-E4986.	7.1	23
12	Conformational Control of UDP-Galactopyranose Mutase Inhibition. <i>Biochemistry</i> , 2017, 56, 3983-3992.	2.5	2
13	Metabolic Network Analysis and Metatranscriptomics Reveal Auxotrophies and Nutrient Sources of the Cosmopolitan Freshwater Microbial Lineage act. <i>MSystems</i> , 2017, 2, .	3.8	21
14	Stilbene Boronic Acids Form a Covalent Bond with Human Transthyretin and Inhibit Its Aggregation. <i>Journal of Medicinal Chemistry</i> , 2017, 60, 7820-7834.	6.4	25
15	Shearing and Enrichment of Extracellular Type IV Pili. <i>Methods in Molecular Biology</i> , 2017, 1615, 311-320.	0.9	5
16	Classic Spotlight: Crowd Sourcing Provided <i>Penicillium</i> Strains for the War Effort. <i>Journal of Bacteriology</i> , 2016, 198, 877-877.	2.2	2
17	Effects of Single \pm -to- \mp Residue Replacements on Structure and Stability in a Small Protein: Insights from Quasiracemic Crystallization. <i>Journal of the American Chemical Society</i> , 2016, 138, 6498-6505.	13.7	38
18	Structures of <i>Xenopus</i> Embryonic Epidermal Lectin Reveal a Conserved Mechanism of Microbial Glycan Recognition. <i>Journal of Biological Chemistry</i> , 2016, 291, 5596-5610.	3.4	33

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19	Arm-in-Arm Response Regulator Dimers Promote Intermolecular Signal Transduction. <i>Journal of Bacteriology</i> , 2016, 198, 1218-1229.	2.2	7
20	Removal of Chromophore-Proximal Polar Atoms Decreases Water Content and Increases Fluorescence in a Near Infrared Phytofluor. <i>Frontiers in Molecular Biosciences</i> , 2015, 2, 65.	3.5	24
21	Targeting diverse protein-protein interaction interfaces with β -peptides derived from the Z-domain scaffold. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 4552-4557.	7.1	93
22	Virtual Screening for UDP-Galactopyranose Mutase Ligands Identifies a New Class of Antimycobacterial Agents. <i>ACS Chemical Biology</i> , 2015, 10, 2209-2218.	3.4	34
23	Recognition of microbial glycans by human intelectin-1. <i>Nature Structural and Molecular Biology</i> , 2015, 22, 603-610.	8.2	133
24	High-resolution structures of a heterochiral coiled coil. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 13144-13149.	7.1	33
25	The non-detergent sulfobetaine-201 acts as a pharmacological chaperone to promote folding and crystallization of the type II TGF- β 2 receptor extracellular domain. <i>Protein Expression and Purification</i> , 2015, 115, 19-25.	1.3	5
26	Quasiracemate Crystal Structures of Magainin 2 Derivatives Support the Functional Significance of the Phenylalanine Zipper Motif. <i>Journal of the American Chemical Society</i> , 2015, 137, 11884-11887.	13.7	20
27	Editorial overview: Macromolecular machines and assemblies: Rise and fall at the molecular level. <i>Current Opinion in Structural Biology</i> , 2015, 31, vii-viii.	5.7	2
28	Evidence of a Bacterial Receptor for Lysozyme: Binding of Lysozyme to the Anti- β Factor RsiV Controls Activation of the ECF β Factor β V. <i>PLoS Genetics</i> , 2014, 10, e1004643.	3.5	40
29	Comparative single-cell genomics reveals potential ecological niches for the freshwater actinobacteria lineage. <i>ISME Journal</i> , 2014, 8, 2503-2516.	9.8	137
30	Vivid watercolor paintbox for eukaryotic algae. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 5448-5449.	7.1	5
31	Action at a distance in a light receptor. <i>Nature</i> , 2014, 509, 174-175.	27.8	1
32	Origins of Fluorescence in Evolved Bacteriophytochromes. <i>Journal of Biological Chemistry</i> , 2014, 289, 32144-32152.	3.4	59
33	A Polyketide Synthase Acyltransferase Domain Structure Suggests a Recognition Mechanism for Its Hydroxymalonyl-Acyl Carrier Protein Substrate. <i>PLoS ONE</i> , 2014, 9, e110965.	2.5	23
34	Evidence for Phenylalanine Zipper-Mediated Dimerization in the X-ray Crystal Structure of a Magainin 2 Analogue. <i>Journal of the American Chemical Society</i> , 2013, 135, 15738-15741.	13.7	34
35	Evidence for small-molecule-mediated loop stabilization in the structure of the isolated Pin1 WW domain. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2013, 69, 2506-2512.	2.5	10
36	Cell-free production of integral membrane aspartic acid proteases reveals zinc-dependent methyltransferase activity of the <i>Pseudomonas aeruginosa</i> prepilin peptidase PilD. <i>MicrobiologyOpen</i> , 2013, 2, 94-104.	3.0	21

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37	Structure-guided Engineering Enhances a Phytochrome-based Infrared Fluorescent Protein. <i>Journal of Biological Chemistry</i> , 2012, 287, 7000-7009.	3.4	109
38	Quasiracemic Crystallization as a Tool To Assess the Accommodation of Noncanonical Residues in Nativelike Protein Conformations. <i>Journal of the American Chemical Society</i> , 2012, 134, 2473-2476.	13.7	34
39	Structural insights into the Type II secretion nanomachine. <i>Current Opinion in Structural Biology</i> , 2012, 22, 208-216.	5.7	59
40	Bacterial phytochromes: More than meets the light. <i>Critical Reviews in Biochemistry and Molecular Biology</i> , 2011, 46, 67-88.	5.2	192
41	Structure of the minor pseudopilin XcpW from the <i>Pseudomonas aeruginosa</i> type II secretion system. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2011, 67, 124-130.	2.5	18
42	<i>P. aeruginosa</i> PilT Structures with and without Nucleotide Reveal a Dynamic Type IV Pilus Retraction Motor. <i>Journal of Molecular Biology</i> , 2010, 400, 1011-1021.	4.2	77
43	Structure-Based Design of a Periplasmic Binding Protein Antagonist that Prevents Domain Closure. <i>ACS Chemical Biology</i> , 2009, 4, 447-456.	3.4	25
44	Ligand Binding and Substrate Discrimination by UDP-Galactopyranose Mutase. <i>Journal of Molecular Biology</i> , 2009, 391, 327-340.	4.2	43
45	Tightening the Knot in Phytochrome by Single-Molecule Atomic Force Microscopy. <i>Biophysical Journal</i> , 2009, 96, 1508-1514.	0.5	69
46	X-ray Crystallography Reveals a Reduced Substrate Complex of UDP-Galactopyranose Mutase Poised for Covalent Catalysis by Flavin. <i>Biochemistry</i> , 2009, 48, 9171-9173.	2.5	46
47	Structure and Mechanism of Phytochrome. <i>FASEB Journal</i> , 2009, 23, 432.1.	0.5	0
48	The type II secretion arrowhead: the structure of GspL-GspJ-GspK. <i>Nature Structural and Molecular Biology</i> , 2008, 15, 428-430.	8.2	15
49	Mutational Analysis of <i>Deinococcus radiodurans</i> Bacteriophytochrome Reveals Key Amino Acids Necessary for the Photochromicity and Proton Exchange Cycle of Phytochromes. <i>Journal of Biological Chemistry</i> , 2008, 283, 12212-12226.	3.4	180
50	3D structure/function analysis of PilX reveals how minor pilins can modulate the virulence properties of type IV pili. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007, 104, 15888-15893.	7.1	105
51	High Resolution Structure of <i>Deinococcus</i> Bacteriophytochrome Yields New Insights into Phytochrome Architecture and Evolution. <i>Journal of Biological Chemistry</i> , 2007, 282, 12298-12309.	3.4	215
52	Crystal Structures of the Pilus Retraction Motor PilT Suggest Large Domain Movements and Subunit Cooperation Drive Motility. <i>Structure</i> , 2007, 15, 363-376.	3.3	120
53	Conformational changes of glucose/galactose-binding protein illuminated by open, unliganded, and ultra-high-resolution ligand-bound structures. <i>Protein Science</i> , 2007, 16, 1032-1041.	7.6	103
54	Type IV Pilin Structures: Insights on Shared Architecture, Fiber Assembly, Receptor Binding and Type II Secretion. <i>Journal of Molecular Microbiology and Biotechnology</i> , 2006, 11, 192-207.	1.0	70

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55	A light-sensing knot revealed by the structure of the chromophore-binding domain of phytochrome. <i>Nature</i> , 2005, 438, 325-331.	27.8	495
56	Functional Dissection of a Conserved Motif within the Pilus Retraction Protein PilT. <i>Journal of Bacteriology</i> , 2005, 187, 611-618.	2.2	37
57	The pilus-retraction protein PilT: ultrastructure of the biological assembly. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2004, 60, 978-982.	2.5	38
58	Type IV Pilin Structure and Assembly. <i>Molecular Cell</i> , 2003, 11, 1139-1150.	9.7	260
59	<i>Aquifex aeolicus</i> PilT, Homologue of a Surface Motility Protein, Is a Thermostable Oligomeric NTPase. <i>Journal of Bacteriology</i> , 2002, 184, 6465-6471.	2.2	61
60	Cu, Zn superoxide dismutase structure from a microbial pathogen establishes a class with a conserved dimer interface 1 Edited by D. C. Rees. <i>Journal of Molecular Biology</i> , 2000, 296, 145-153.	4.2	51
61	Crystallographic structure reveals phosphorylated pilin from <i>Neisseria</i> : phosphoserine sites modify type IV pilus surface chemistry and fibre morphology. <i>Molecular Microbiology</i> , 1999, 31, 743-752.	2.5	93
62	Consequences of the loss of O-linked glycosylation of meningococcal type IV pilin on piliation and pilus-mediated adhesion. <i>Molecular Microbiology</i> , 1998, 27, 705-715.	2.5	120
63	Structure of the fibre-forming protein pilin at 2.6 Å... resolution. <i>Nature</i> , 1995, 378, 32-38.	27.8	488
64	Structure and Assembly of Type IV Pilins. , 0, , 81-100.		4
65	Î²-Amino Acid Replacements in Protein Loops. <i>ChemistryViews</i> , 0, , .	0.0	0