

Mark J Banfield

List of Publications by Year in descending order

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99
papers

6,949
citations

53751

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69214

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124
all docs

124
docs citations

124
times ranked

7893
citing authors

#	ARTICLE	IF	CITATIONS
1	A divergent external loop confers antagonistic activity on floral regulators FT and TFL1. EMBO Journal, 2006, 25, 605-614.	3.5	445
2	Protein-folding location can regulate manganese-binding versus copper- or zinc-binding. Nature, 2008, 455, 1138-1142.	13.7	281
3	Structural basis of pathogen recognition by an integrated HMA domain in a plant NLR immune receptor. ELife, 2015, 4, .	2.8	246
4	Oomycetes, effectors, and all that jazz. Current Opinion in Plant Biology, 2012, 15, 483-492.	3.5	232
5	DETERMINATE and LATE FLOWERING Are Two TERMINAL FLOWER1/CENTRORADIALIS Homologs That Control Two Distinct Phases of Flowering Initiation and Development in Pea. Plant Cell, 2003, 15, 2742-2754.	3.1	221
6	An effector of the Irish potato famine pathogen antagonizes a host autophagy cargo receptor. ELife, 2016, 5, .	2.8	189
7	Function from structure? The crystal structure of human phosphatidylethanolamine-binding protein suggests a role in membrane signal transduction. Structure, 1998, 6, 1245-1254.	1.6	188
8	<i>Phytophthora infestans</i> RXLR Effector PexRD2 Interacts with Host MAPKKK1μ to Suppress Plant Immune Signaling. Plant Cell, 2014, 26, 1345-1359.	3.1	188
9	Effector Specialization in a Lineage of the Irish Potato Famine Pathogen. Science, 2014, 343, 552-555.	6.0	179
10	Structures of Phytophthora RXLR Effector Proteins. Journal of Biological Chemistry, 2011, 286, 35834-35842.	1.6	178
11	Effectors of Filamentous Plant Pathogens: Commonalities amid Diversity. Microbiology and Molecular Biology Reviews, 2017, 81, .	2.9	166
12	Sequence Divergent RXLR Effectors Share a Structural Fold Conserved across Plant Pathogenic Oomycete Species. PLoS Pathogens, 2012, 8, e1002400.	2.1	153
13	Single Amino Acid Mutations in the Potato Immune Receptor R3a Expand Response to <i>Phytophthora</i> Effectors. Molecular Plant-Microbe Interactions, 2014, 27, 624-637.	1.4	136
14	The structure of lactate dehydrogenase from Plasmodium falciparum reveals a new target for anti-malarial design. Nature Structural Biology, 1996, 3, 912-915.	9.7	134
15	The structure of Antirrhinum centroradialis protein (CEN) suggests a role as a kinase regulator ¹¹ Edited by I. A. Wilson. Journal of Molecular Biology, 2000, 297, 1159-1170.	2.0	133
16	Polymorphic residues in rice NLRs expand binding and response to effectors of the blast pathogen. Nature Plants, 2018, 4, 576-585.	4.7	127
17	Protein engineering expands the effector recognition profile of a rice NLR immune receptor. ELife, 2019, 8, .	2.8	118
18	Crystal Structure of Streptococcus pyogenes Sortase A. Journal of Biological Chemistry, 2009, 284, 6924-6933.	1.6	115

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19	Lessons in Effector and NLR Biology of Plant-Microbe Systems. <i>Molecular Plant-Microbe Interactions</i> , 2018, 31, 34-45.	1.4	109
20	Recent developments in effector biology of filamentous plant pathogens. <i>Cellular Microbiology</i> , 2010, 12, 705-715.	1.1	108
21	On the front line: structural insights into plant-pathogen interactions. <i>Nature Reviews Microbiology</i> , 2013, 11, 761-776.	13.6	101
22	Specificity in Trk Receptor:Neurotrophin Interactions. <i>Structure</i> , 2001, 9, 1191-1199.	1.6	96
23	Direct observation of the iron binding sites in a ferritin. <i>FEBS Letters</i> , 1994, 350, 258-262.	1.3	93
24	A molecular roadmap to the plant immune system. <i>Journal of Biological Chemistry</i> , 2020, 295, 14916-14935.	1.6	86
25	Recognition of structurally diverse substrates by type II 3-hydroxyacyl-CoA dehydrogenase (HADH) Tj ETQq1 1 0.784314 rgBT/Overlook	2.0	83
26	Distinct regions of the <i>Pseudomonas syringae</i> coiled-coil effector AvrRps4 are required for activation of immunity. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 16371-16376.	3.3	81
27	Tomato I2 Immune Receptor Can Be Engineered to Confer Partial Resistance to the Oomycete <i>Phytophthora infestans</i> in Addition to the Fungus <i>Fusarium oxysporum</i> . <i>Molecular Plant-Microbe Interactions</i> , 2015, 28, 1316-1329.	1.4	80
28	The Role of Hydrogen Bonding at the Active Site of a Cupredoxin: The Phe114Pro Azurin Variant,. <i>Biochemistry</i> , 2006, 45, 8812-8822.	1.2	78
29	The Æœsensor domainsÆ of plant NLR proteins: more than decoys?. <i>Frontiers in Plant Science</i> , 2015, 6, 134.	1.7	78
30	Crystal structure of the NADP(H)-dependent ketose reductase from <i>Bemisia argentifolii</i> at 2.3 Å... resolution11Edited by R. Huber. <i>Journal of Molecular Biology</i> , 2001, 306, 239-250.	2.0	76
31	The Plant ÆœResistosomeÆ: Structural Insights into Immune Signaling. <i>Cell Host and Microbe</i> , 2019, 26, 193-201.	5.1	76
32	A Highly Unusual Thioester Bond in a Pilus Adhesin Is Required for Efficient Host Cell Interaction*. <i>Journal of Biological Chemistry</i> , 2010, 285, 33858-33866.	1.6	74
33	Structural Basis of Host Autophagy-related Protein 8 (ATG8) Binding by the Irish Potato Famine Pathogen Effector Protein PexRD54. <i>Journal of Biological Chemistry</i> , 2016, 291, 20270-20282.	1.6	74
34	Taking the stage: effectors in the spotlight. <i>Current Opinion in Plant Biology</i> , 2017, 38, 25-33.	3.5	74
35	StructureÆ function analysis of the <i>Fusarium oxysporum</i> Avr2 effector allows uncoupling of its immune-suppressing activity from recognition. <i>New Phytologist</i> , 2017, 216, 897-914.	3.5	72
36	New <i>Listeria monocytogenes</i> prfA* mutants, transcriptional properties of PrfA* proteins and structure-function of the virulence regulator PrfA. <i>Molecular Microbiology</i> , 2004, 52, 1553-1565.	1.2	66

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37	<i>Pseudomonas syringae</i> type III effector HopAF1 suppresses plant immunity by targeting methionine recycling to block ethylene induction. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, E3577-86.	3.3	66
38	From pathogen genomes to host plant processes: the power of plant parasitic oomycetes. Genome Biology, 2013, 14, 211.	3.8	64
39	The crystal structure of PEBP-2, a homologue of the PEBP/RKIP family. Acta Crystallographica Section D: Biological Crystallography, 2002, 58, 1077-1080.	2.5	60
40	Uncoiling CNLs: Structure/function approaches to understanding CC domain function in plant NLRs. Plant and Cell Physiology, 2018, 59, 2398-2408.	1.5	59
41	Hop-on hop-off: importin- β -guided tours to the nucleus in innate immune signaling. Frontiers in Plant Science, 2013, 4, 149.	1.7	58
42	Perturbation of host ubiquitin systems by plant pathogen/pest effector proteins. Cellular Microbiology, 2015, 17, 18-25.	1.1	57
43	Multiple variants of the fungal effector AVR-Pik bind the HMA domain of the rice protein OsHIPP19, providing a foundation to engineer plant defense. Journal of Biological Chemistry, 2021, 296, 100371.	1.6	57
44	FutA2 Is a Ferric Binding Protein from Synechocystis PCC 6803. Journal of Biological Chemistry, 2008, 283, 12520-12527.	1.6	56
45	VL:VH domain rotations in engineered antibodies: Crystal structures of the Fab fragments from two murine antitumor antibodies and their engineered human constructs. , 1997, 29, 161-171.		52
46	Crystal Structure of SmcL, a Bacterial Neutral Sphingomyelinase C from Listeria. Journal of Biological Chemistry, 2005, 280, 35011-35017.	1.6	52
47	<i>Arabidopsis</i> downy mildew effector HaRxL106 suppresses plant immunity by binding to RADICAL-INDUCED CELL DEATH1. New Phytologist, 2018, 220, 232-248.	3.5	51
48	Cycle Inhibiting Factors (CIFs) Are a Growing Family of Functional Cyclomodulins Present in Invertebrate and Mammal Bacterial Pathogens. PLoS ONE, 2009, 4, e4855.	1.1	50
49	The RKIP (Raf-1 Kinase Inhibitor Protein) conserved pocket binds to the phosphorylated N-region of Raf-1 and inhibits the Raf-1-mediated activated phosphorylation of MEK. Cellular Signalling, 2008, 20, 935-941.	1.7	49
50	Roles of Minor Pilin Subunits Spy0125 and Spy0130 in the Serotype M1 <i>Streptococcus pyogenes</i> Strain SF370. Journal of Bacteriology, 2010, 192, 4651-4659.	1.0	48
51	Probing formation of cargo/importin- β transport complexes in plant cells using a pathogen effector. Plant Journal, 2015, 81, 40-52.	2.8	48
52	<i>Aegilops sharonensis</i> genome-assisted identification of stem rust resistance gene Sr62. Nature Communications, 2022, 13, 1607.	5.8	48
53	N-terminal β^2 -strand underpins biochemical specialization of an ATG8 isoform. PLoS Biology, 2019, 17, e3000373.	2.6	47
54	Engineering Copper Sites in Proteins: β Loops Confer Native Structures and Properties to Chimeric Cupredoxins. Journal of the American Chemical Society, 2007, 129, 709-718.	6.6	45

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55	Effector gene birth in plant parasitic nematodes: Neofunctionalization of a housekeeping glutathione synthetase gene. <i>PLoS Genetics</i> , 2018, 14, e1007310.	1.5	44
56	An internal thioester in a pathogen surface protein mediates covalent host binding. <i>ELife</i> , 2015, 4, .	2.8	43
57	Structural and biochemical studies of an NB-ARC domain from a plant NLR immune receptor. <i>PLoS ONE</i> , 2019, 14, e0221226.	1.1	43
58	Basic requirements for a metal-binding site in a protein: The influence of loop shortening on the cupredoxin azurin. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006, 103, 7258-7263.	3.3	40
59	Identification and Characterization of the Defensin-Like Gene Family of Grapevine. <i>Molecular Plant-Microbe Interactions</i> , 2012, 25, 1118-1131.	1.4	38
60	Two NLR immune receptors acquired high-affinity binding to a fungal effector through convergent evolution of their integrated domain. <i>ELife</i> , 2021, 10, .	2.8	38
61	Identification and Structure of the Nerve Growth Factor Binding Site on TrkA. <i>Biochemical and Biophysical Research Communications</i> , 2001, 282, 131-141.	1.0	37
62	The allelic rice immune receptor Pikh confers extended resistance to strains of the blast fungus through a single polymorphism in the effector binding interface. <i>PLoS Pathogens</i> , 2021, 17, e1009368.	2.1	37
63	Ï€-Interaction Tuning of the Active Site Properties of Metalloproteins. <i>Journal of the American Chemical Society</i> , 2008, 130, 15420-15428.	6.6	35
64	Gene Duplication and Mutation in the Emergence of a Novel Aggressive Allele of the <i>AVR-Pik</i> Effector in the Rice Blast Fungus. <i>Molecular Plant-Microbe Interactions</i> , 2019, 32, 740-749.	1.4	35
65	<i>Phytophthora infestans</i> effector <sc>Sf1</sc>3 targets potato <sc>UBK</sc> to suppress early immune transcriptional responses. <i>New Phytologist</i> , 2019, 222, 438-454.	3.5	33
66	A single amino acid polymorphism in a conserved effector of the multihost blast fungus pathogen expands host-target binding spectrum. <i>PLoS Pathogens</i> , 2021, 17, e1009957.	2.1	32
67	Perception of structurally distinct effectors by the integrated WRKY domain of a plant immune receptor. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	3.3	32
68	The rice NLR pair Pikp-1/Pikp-2 initiates cell death through receptor cooperation rather than negative regulation. <i>PLoS ONE</i> , 2020, 15, e0238616.	1.1	31
69	Exploring folds, evolution and host interactions: understanding effector structure/function in disease and immunity. <i>New Phytologist</i> , 2020, 227, 326-333.	3.5	31
70	Cross-reactivity of a rice NLR immune receptor to distinct effectors from the rice blast pathogen <i>Magnaporthe oryzae</i> provides partial disease resistance. <i>Journal of Biological Chemistry</i> , 2019, 294, 13006-13016.	1.6	29
71	Crystal Structures of Cif from Bacterial Pathogens <i>Photobacterium luminescens</i> and <i>Burkholderia pseudomallei</i> . <i>PLoS ONE</i> , 2009, 4, e5582.	1.1	28
72	The molecular basis of ubiquitin-like protein NEDD8 deamidation by the bacterial effector protein Cif. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, E1830-E1838.	3.3	28

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73	Functional diversification gave rise to allelic specialization in a rice NLR immune receptor pair. <i>ELife</i> , 2021, 10, .	2.8	28
74	Visualizing the Metal-Binding Versatility of Copper Trafficking Sites,. <i>Biochemistry</i> , 2010, 49, 7798-7810.	1.2	27
75	What a Difference a Dalton Makes: Bacterial Virulence Factors Modulate Eukaryotic Host Cell Signaling Systems via Deamidation. <i>Microbiology and Molecular Biology Reviews</i> , 2013, 77, 527-539.	2.9	25
76	Metal-binding loop length and not sequence dictates structure. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 5616-5621.	3.3	22
77	Intramolecular isopeptide but not internal thioester bonds confer proteolytic and significant thermal stability to the <i>S. pyogenes</i> pilus adhesin Spy0125. <i>Proteins: Structure, Function and Bioinformatics</i> , 2014, 82, 517-527.	1.5	22
78	Regulation of Protein Function: Crystal Packing Interfaces and Conformational Dimerization. <i>Biochemistry</i> , 2008, 47, 6583-6589.	1.2	20
79	A genetically linked pair of NLR immune receptors shows contrasting patterns of evolution. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022, 119, .	3.3	19
80	Hooked and Cooked: A Fish Killer Genome Exposed. <i>PLoS Genetics</i> , 2013, 9, e1003590.	1.5	16
81	Conformation of the EPEC Tir Protein in Solution: Investigating the Impact of Serine Phosphorylation at Positions 434/463. <i>Biophysical Journal</i> , 2007, 93, 586-596.	0.2	15
82	Metal-Binding Loop Length Is a Determinant of the pK_a of a Histidine Ligand at a Type 1 Copper Site. <i>Inorganic Chemistry</i> , 2011, 50, 482-488.	1.9	13
83	A new structural class of bacterial thioester domains reveals a slipknot topology. <i>Protein Science</i> , 2018, 27, 1651-1660.	3.1	13
84	Diversity and selection of the continuous-flowering gene, <i>RoKSN</i> , in rose. <i>Horticulture Research</i> , 2021, 8, 76.	2.9	12
85	Insertion of the Enteropathogenic <i>Escherichia coli</i> Tir Virulence Protein into Membranes in Vitro. <i>Journal of Biological Chemistry</i> , 2006, 281, 7842-7849.	1.6	11
86	Recent developments in effector biology of filamentous plant pathogens. <i>Cellular Microbiology</i> , 2010, 12, 1015-1015.	1.1	11
87	The Structure of an Ancient Conserved Domain Establishes a Structural Basis for Stable Histidine Phosphorylation and Identifies a New Family of Adenosine-specific Kinases. <i>Journal of Biological Chemistry</i> , 2006, 281, 22131-22141.	1.6	10
88	Structure of HisF, a histidine biosynthetic protein from <i>Pyrobaculum aerophilum</i> . <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2001, 57, 1518-1525.	2.5	9
89	Effect of Protein Kinase A-mediated Phosphorylation on the Structure and Association Properties of the Enteropathogenic <i>Escherichia coli</i> Tir Virulence Protein. <i>Journal of Biological Chemistry</i> , 2003, 278, 25839-25846.	1.6	9
90	Solution structure of the major (Spy0128) and minor (Spy0125 and Spy0130) pili subunits from <i>Streptococcus pyogenes</i> . <i>European Biophysics Journal</i> , 2010, 39, 469-480.	1.2	9

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91	The Importance of the Long Type-1 Copper-Binding Loop of Nitrite Reductase for Structure and Function. <i>Chemistry - A European Journal</i> , 2008, 14, 5820-5828.	1.7	7
92	Yet more intramolecular cross-links in Gram-positive surface proteins. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 1229-1230.	3.3	6
93	Structure of the Fab Fragment of a Monoclonal Antibody Specific for Carcinoembryonic Antigen. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 1996, 52, 1107-1113.	2.5	5
94	mADP-RTs: versatile virulence factors from bacterial pathogens of plants and mammals. <i>Frontiers in Plant Science</i> , 2012, 3, 142.	1.7	4
95	Crystallization and preliminary X-ray analysis of the RXLR-type effector RXLR3 from the oomycete pathogen <i>Hyaloperonospora arabidopsidis</i> . <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2011, 67, 1417-1420.	0.7	2
96	In vitro Assessment of Pathogen Effector Binding to Host Proteins by Surface Plasmon Resonance. <i>Bio-protocol</i> , 2020, 10, e3676.	0.2	2
97	Making the most of two crystals: structural analysis of a conserved hypothetical protein using native gel screening and SAD phasing. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2003, 59, 2242-2246.	2.5	1
98	Two-faced TIRs trip the immune switch. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, 2445-2446.	3.3	1
99	Production of RXLR Effector Proteins for Structural Analysis by X-Ray Crystallography. <i>Methods in Molecular Biology</i> , 2014, 1127, 231-253.	0.4	1