

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	<i>Aegilops sharonensis</i> genome-assisted identification of stem rust resistance gene Sr62. <i>Nature Communications</i> , 2022, 13, 1607.	5.8	48
2	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
3	Multiple variants of the fungal effector AVR-Pik bind the HMA domain of the rice protein OsHIPP19, providing a foundation to engineer plant defense. <i>Journal of Biological Chemistry</i> , 2021, 296, 100371.	1.6	57
4	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
5	Diversity and selection of the continuous-flowering gene, RoKSN, in rose. <i>Horticulture Research</i> , 2021, 8, 76.	2.9	12
6	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
7	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
8	Functional diversification gave rise to allelic specialization in a rice NLR immune receptor pair. <i>ELife</i> , 2021, 10, .	2.8	28
9	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
10	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
11	A molecular roadmap to the plant immune system. <i>Journal of Biological Chemistry</i> , 2020, 295, 14916-14935.	1.6	86
12	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
13	In vitro Assessment of Pathogen Effector Binding to Host Proteins by Surface Plasmon Resonance. <i>Bio-protocol</i> , 2020, 10, e3676.	0.2	2
14	The Plant "Resistosome": Structural Insights into Immune Signaling. <i>Cell Host and Microbe</i> , 2019, 26, 193-201.	5.1	76
15	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
16	N-terminal β^2 -strand underpins biochemical specialization of an ATG8 isoform. <i>PLoS Biology</i> , 2019, 17, e3000373.	2.6	47
17	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
18	Gene Duplication and Mutation in the Emergence of a Novel Aggressive Allele of the AVR-Pik Effector in the Rice Blast Fungus. <i>Molecular Plant-Microbe Interactions</i> , 2019, 32, 740-749.	1.4	35

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19	<i>Phytophthora infestans</i> effector SFI3 targets potato UBK to suppress early immune transcriptional responses. <i>New Phytologist</i> , 2019, 222, 438-454.	3.5	33
20	Protein engineering expands the effector recognition profile of a rice NLR immune receptor. <i>ELife</i> , 2019, 8, .	2.8	118
21	Uncoiling CNLs: Structure/function approaches to understanding CC domain function in plant NLRs. <i>Plant and Cell Physiology</i> , 2018, 59, 2398-2408.	1.5	59
22	<i>Arabidopsis</i> downy mildew effector HaRxL106 suppresses plant immunity by binding to RADICAL-INDUCED CELL DEATH1. <i>New Phytologist</i> , 2018, 220, 232-248.	3.5	51
23	A new structural class of bacterial thioester domains reveals a slipknot topology. <i>Protein Science</i> , 2018, 27, 1651-1660.	3.1	13
24	Polymorphic residues in rice NLRs expand binding and response to effectors of the blast pathogen. <i>Nature Plants</i> , 2018, 4, 576-585.	4.7	127
25	Effector gene birth in plant parasitic nematodes: Neofunctionalization of a housekeeping glutathione synthetase gene. <i>PLoS Genetics</i> , 2018, 14, e1007310.	1.5	44
26	Lessons in Effector and NLR Biology of Plant-Microbe Systems. <i>Molecular Plant-Microbe Interactions</i> , 2018, 31, 34-45.	1.4	109
27	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
28	Taking the stage: effectors in the spotlight. <i>Current Opinion in Plant Biology</i> , 2017, 38, 25-33.	3.5	74
29	Effectors of Filamentous Plant Pathogens: Commonalities amid Diversity. <i>Microbiology and Molecular Biology Reviews</i> , 2017, 81, .	2.9	166
30	Structure-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
31	An effector of the Irish potato famine pathogen antagonizes a host autophagy cargo receptor. <i>ELife</i> , 2016, 5, .	2.8	189
32	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
33	<i>Pseudomonas syringae</i> type III effector HopAF1 suppresses plant immunity by targeting methionine recycling to block ethylene induction. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, E3577-86.	3.3	66
34	Probing formation of cargo/importin transport complexes in plant cells using a pathogen effector. <i>Plant Journal</i> , 2015, 81, 40-52.	2.8	48
35	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
36	An internal thioester in a pathogen surface protein mediates covalent host binding. <i>ELife</i> , 2015, 4, .	2.8	43

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37	The "sensor domains" of plant NLR proteins: more than decoys?. <i>Frontiers in Plant Science</i> , 2015, 6, 134.	1.7	78
38	Perturbation of host ubiquitin systems by plant pathogen/pest effector proteins. <i>Cellular Microbiology</i> , 2015, 17, 18-25.	1.1	57
39	Structural basis of pathogen recognition by an integrated HMA domain in a plant NLR immune receptor. <i>ELife</i> , 2015, 4, .	2.8	246
40	<i>Phytophthora infestans</i> RXLR Effector PexRD2 Interacts with Host MAPKKK1 to Suppress Plant Immune Signaling. <i>Plant Cell</i> , 2014, 26, 1345-1359.	3.1	188
41	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
42	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
43	Effector Specialization in a Lineage of the Irish Potato Famine Pathogen. <i>Science</i> , 2014, 343, 552-555.	6.0	179
44	Single Amino Acid Mutations in the Potato Immune Receptor R3a Expand Response to <i>Phytophthora</i> Effectors. <i>Molecular Plant-Microbe Interactions</i> , 2014, 27, 624-637.	1.4	136
45	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
46	On the front line: structural insights into plant-pathogen interactions. <i>Nature Reviews Microbiology</i> , 2013, 11, 761-776.	13.6	101
47	From pathogen genomes to host plant processes: the power of plant parasitic oomycetes. <i>Genome Biology</i> , 2013, 14, 211.	3.8	64
48	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
49	Hooked and Cooked: A Fish Killer Genome Exposed. <i>PLoS Genetics</i> , 2013, 9, e1003590.	1.5	16
50	Hop-on hop-off: importin- α -guided tours to the nucleus in innate immune signaling. <i>Frontiers in Plant Science</i> , 2013, 4, 149.	1.7	58
51	Sequence Divergent RXLR Effectors Share a Structural Fold Conserved across Plant Pathogenic Oomycete Species. <i>PLoS Pathogens</i> , 2012, 8, e1002400.	2.1	153
52	mADP-RTs: versatile virulence factors from bacterial pathogens of plants and mammals. <i>Frontiers in Plant Science</i> , 2012, 3, 142.	1.7	4
53	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
54	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

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55	Identification and Characterization of the Defensin-Like Gene Family of Grapevine. <i>Molecular Plant-Microbe Interactions</i> , 2012, 25, 1118-1131.	1.4	38
56	Oomycetes, effectors, and all that jazz. <i>Current Opinion in Plant Biology</i> , 2012, 15, 483-492.	3.5	232
57	Metal-Binding Loop Length Is a Determinant of the p <i>K</i> of a Histidine Ligand at a Type 1 Copper Site. <i>Inorganic Chemistry</i> , 2011, 50, 482-488.	1.9	13
58	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
59	Structures of Phytophthora RXLR Effector Proteins. <i>Journal of Biological Chemistry</i> , 2011, 286, 35834-35842.	1.6	178
60	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
61	Recent developments in effector biology of filamentous plant pathogens. <i>Cellular Microbiology</i> , 2010, 12, 705-715.	1.1	108
62	Recent developments in effector biology of filamentous plant pathogens. <i>Cellular Microbiology</i> , 2010, 12, 1015-1015.	1.1	11
63	Roles of Minor Pilin Subunits Spy0125 and Spy0130 in the Serotype M1 <i>Streptococcus pyogenes</i> Strain SF370. <i>Journal of Bacteriology</i> , 2010, 192, 4651-4659.	1.0	48
64	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
65	Visualizing the Metal-Binding Versatility of Copper Trafficking Sites. <i>Biochemistry</i> , 2010, 49, 7798-7810.	1.2	27
66	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
67	Crystal Structure of <i>Streptococcus pyogenes</i> Sortase A. <i>Journal of Biological Chemistry</i> , 2009, 284, 6924-6933.	1.6	115
68	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
69	Cycle Inhibiting Factors (CIFs) Are a Growing Family of Functional Cyclomodulins Present in Invertebrate and Mammal Bacterial Pathogens. <i>PLoS ONE</i> , 2009, 4, e4855.	1.1	50
70	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
71	Protein-folding location can regulate manganese-binding versus copper- or zinc-binding. <i>Nature</i> , 2008, 455, 1138-1142.	13.7	281
72	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. <i>Cellular Signalling</i> , 2008, 20, 935-941.	1.7	49

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73	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
74	Regulation of Protein Function: Crystal Packing Interfaces and Conformational Dimerization. <i>Biochemistry</i> , 2008, 47, 6583-6589.	1.2	20
75	FutA2 Is a Ferric Binding Protein from <i>Synechocystis</i> PCC 6803. <i>Journal of Biological Chemistry</i> , 2008, 283, 12520-12527.	1.6	56
76	Engineering Copper Sites in Proteins: Å Loops Confer Native Structures and Properties to Chimeric Cupredoxins. <i>Journal of the American Chemical Society</i> , 2007, 129, 709-718.	6.6	45
77	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
78	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
79	A divergent external loop confers antagonistic activity on floral regulators FT and TFL1. <i>EMBO Journal</i> , 2006, 25, 605-614.	3.5	445
80	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
81	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
82	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
83	Crystal Structure of SmcL, a Bacterial Neutral Sphingomyelinase C from <i>Listeria</i> . <i>Journal of Biological Chemistry</i> , 2005, 280, 35011-35017.	1.6	52
84	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
85	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
86	DETERMINATE and LATE FLOWERING Are Two TERMINAL FLOWER1/CENTRORADIALIS Homologs That Control Two Distinct Phases of Flowering Initiation and Development in Pea. <i>Plant Cell</i> , 2003, 15, 2742-2754.	3.1	221
87	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
88	The crystal structure of PEBP-2, a homologue of the PEBP/RKIP family. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2002, 58, 1077-1080.	2.5	60
89	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
90	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

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91	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
92	Specificity in Trk Receptor: Neurotrophin Interactions. <i>Structure</i> , 2001, 9, 1191-1199.	1.6	96
93	The structure of Antirrhinum centroradialis protein (CEN) suggests a role as a kinase regulator 11 Edited by I. A. Wilson. <i>Journal of Molecular Biology</i> , 2000, 297, 1159-1170.	2.0	133
94	Recognition of structurally diverse substrates by type II 3-hydroxyacyl-CoA dehydrogenase (HADH) Tj ETQq0 0 0 rgBT/Overlock 10 Tf 50	2.0	83
95	Function from structure? The crystal structure of human phosphatidylethanolamine-binding protein suggests a role in membrane signal transduction. <i>Structure</i> , 1998, 6, 1245-1254.	1.6	188
96	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
97	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
98	The structure of lactate dehydrogenase from <i>Plasmodium falciparum</i> reveals a new target for anti-malarial design. <i>Nature Structural Biology</i> , 1996, 3, 912-915.	9.7	134
99	Direct observation of the iron binding sites in a ferritin. <i>FEBS Letters</i> , 1994, 350, 258-262.	1.3	93