

Adam J Bogdanove

List of Publications by Year in descending order

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66
papers

11,953
citations

125106

35
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124990

64
g-index

77
all docs

77
docs citations

77
times ranked

11442
citing authors

| # | ARTICLE | IF | CITATIONS |
|----|--|-----|-----------|
| 1 | Efficient design and assembly of custom TALEN and other TAL effector-based constructs for DNA targeting. <i>Nucleic Acids Research</i> , 2011, 39, e82-e82. | 6.5 | 1,793 |
| 2 | A Simple Cipher Governs DNA Recognition by TAL Effectors. <i>Science</i> , 2009, 326, 1501-1501. | 6.0 | 1,710 |
| 3 | Targeting DNA Double-Strand Breaks with TAL Effector Nucleases. <i>Genetics</i> , 2010, 186, 757-761. | 1.2 | 1,618 |
| 4 | TAL Effectors: Customizable Proteins for DNA Targeting. <i>Science</i> , 2011, 333, 1843-1846. | 6.0 | 884 |
| 5 | <i>Xanthomonas oryzae</i> pathovars: model pathogens of a model crop. <i>Molecular Plant Pathology</i> , 2006, 7, 303-324. | 2.0 | 741 |
| 6 | TAL Effector-Nucleotide Targeter (TALE-NT) 2.0: tools for TAL effector design and target prediction. <i>Nucleic Acids Research</i> , 2012, 40, W117-W122. | 6.5 | 549 |
| 7 | The Crystal Structure of TAL Effector PthXo1 Bound to Its DNA Target. <i>Science</i> , 2012, 335, 716-719. | 6.0 | 505 |
| 8 | Transcription Activator-Like Effector Nucleases Enable Efficient Plant Genome Engineering. <i>Plant Physiology</i> , 2012, 161, 20-27. | 2.3 | 407 |
| 9 | TAL effectors: finding plant genes for disease and defense. <i>Current Opinion in Plant Biology</i> , 2010, 13, 394-401. | 3.5 | 383 |
| 10 | Genome sequence and rapid evolution of the rice pathogen <i>Xanthomonas oryzae</i> pv. <i>oryzae</i> PXO99A. <i>BMC Genomics</i> , 2008, 9, 204. | 1.2 | 327 |
| 11 | Unified nomenclature for broadly conserved hrp genes of phytopathogenic bacteria. <i>Molecular Microbiology</i> , 1996, 20, 681-683. | 1.2 | 232 |
| 12 | Host-Induced Gene Silencing in Barley Powdery Mildew Reveals a Class of Ribonuclease-Like Effectors. <i>Molecular Plant-Microbe Interactions</i> , 2013, 26, 633-642. | 1.4 | 190 |
| 13 | Two New Complete Genome Sequences Offer Insight into Host and Tissue Specificity of Plant Pathogenic <i>Xanthomonas</i> spp. <i>Journal of Bacteriology</i> , 2011, 193, 5450-5464. | 1.0 | 189 |
| 14 | TAL effector driven induction of a SWEET gene confers susceptibility to bacterial blight of cotton. <i>Nature Communications</i> , 2017, 8, 15588. | 5.8 | 144 |
| 15 | Code-Assisted Discovery of TAL Effector Targets in Bacterial Leaf Streak of Rice Reveals Contrast with Bacterial Blight and a Novel Susceptibility Gene. <i>PLoS Pathogens</i> , 2014, 10, e1003972. | 2.1 | 137 |
| 16 | <i>Erwinia amylovora</i> Secretes DspE, a Pathogenicity Factor and Functional AvrE Homolog, through the Hrp (Type III Secretion) Pathway. <i>Journal of Bacteriology</i> , 1998, 180, 2244-2247. | 1.0 | 128 |
| 17 | TAL effectors: highly adaptable phytobacterial virulence factors and readily engineered DNA-targeting proteins. <i>Trends in Cell Biology</i> , 2013, 23, 390-398. | 3.6 | 120 |
| 18 | Genome assembly and characterization of a complex zfBED-NLR gene-containing disease resistance locus in Carolina Gold Select rice with Nanopore sequencing. <i>PLoS Genetics</i> , 2020, 16, e1008571. | 1.5 | 112 |

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|----|---|-----|-----------|
| 19 | TAL effectors: function, structure, engineering and applications. <i>Current Opinion in Structural Biology</i> , 2013, 23, 93-99. | 2.6 | 105 |
| 20 | TAL effectors and activation of predicted host targets distinguish Asian from African strains of the rice pathogen <i>Xanthomonas oryzae</i> pv. <i>oryzicola</i> while strict conservation suggests universal importance of five TAL effectors. <i>Frontiers in Plant Science</i> , 2015, 6, 536. | 1.7 | 105 |
| 21 | Addition of transcription activator-like effector binding sites to a pathogen strain-specific rice bacterial blight resistance gene makes it effective against additional strains and against bacterial leaf streak. <i>New Phytologist</i> , 2012, 195, 883-893. | 3.5 | 103 |
| 22 | Transcription activator-like (TAL) effectors targeting <i>Oryza sativa</i> SWEET genes enhance virulence on diverse rice (<i>Oryza sativa</i>) varieties when expressed individually in a TAL effector-deficient strain of <i>Xanthomonas oryzae</i> . <i>New Phytologist</i> , 2012, 196, 1197-1207. | 3.5 | 91 |
| 23 | Suppression of Xo1-Mediated Disease Resistance in Rice by a Truncated, Non-DNA-Binding TAL Effector of <i>Xanthomonas oryzae</i> . <i>Frontiers in Plant Science</i> , 2016, 7, 1516. | 1.7 | 88 |
| 24 | Single molecule real-time sequencing of <i>Xanthomonas oryzae</i> genomes reveals a dynamic structure and complex TAL (transcription activator-like) effector gene relationships. <i>Microbial Genomics</i> , 2015, 1, . | 1.0 | 86 |
| 25 | Functional analysis of African <i>Xanthomonas oryzae</i> pv. <i>oryzae</i> TALomes reveals a new susceptibility gene in bacterial leaf blight of rice. <i>PLoS Pathogens</i> , 2018, 14, e1007092. | 2.1 | 86 |
| 26 | Novel Candidate Virulence Factors in Rice Pathogen <i>Xanthomonas oryzae</i> pv. <i>oryzicola</i> as Revealed by Mutational Analysis. <i>Applied and Environmental Microbiology</i> , 2007, 73, 8023-8027. | 1.4 | 82 |
| 27 | Effector Diversification Contributes to <i>Xanthomonas oryzae</i> pv. <i>oryzae</i> Phenotypic Adaptation in a Semi-Isolated Environment. <i>Scientific Reports</i> , 2016, 6, 34137. | 1.6 | 76 |
| 28 | A resistance locus in the American heirloom rice variety Carolina Gold Select is triggered by TAL effectors with diverse predicted targets and is effective against African strains of <i>Xanthomonas oryzae</i> pv. <i>oryzicola</i> . <i>Plant Journal</i> , 2016, 87, 472-483. | 2.8 | 76 |
| 29 | A Reference Genome Sequence for Giant Sequoia. <i>G3: Genes, Genomes, Genetics</i> , 2020, 10, 3907-3919. | 0.8 | 67 |
| 30 | Counting on Crossovers: Controlled Recombination for Plant Breeding. <i>Trends in Plant Science</i> , 2020, 25, 455-465. | 4.3 | 65 |
| 31 | Inhibition of Resistance Gene-Mediated Defense in Rice by <i>Xanthomonas oryzae</i> pv. <i>oryzicola</i> . <i>Molecular Plant-Microbe Interactions</i> , 2006, 19, 240-249. | 1.4 | 58 |
| 32 | Convergent Evolution of Effector Protease Recognition by <i>Arabidopsis</i> and Barley. <i>Molecular Plant-Microbe Interactions</i> , 2019, 32, 550-565. | 1.4 | 47 |
| 33 | The effect of increasing numbers of repeats on TAL effector DNA binding specificity. <i>Nucleic Acids Research</i> , 2017, 45, 6960-6970. | 6.5 | 41 |
| 34 | Protein-protein interactions in pathogen recognition by plants. <i>Plant Molecular Biology</i> , 2002, 50, 981-989. | 2.0 | 40 |
| 35 | TAL Effector Specificity for base 0 of the DNA Target Is Altered in a Complex, Effector- and Assay-Dependent Manner by Substitutions for the Tryptophan in Cryptic Repeat "1. <i>PLoS ONE</i> , 2013, 8, e82120. | 1.1 | 37 |
| 36 | Complete Genome Sequencing and Targeted Mutagenesis Reveal Virulence Contributions of Tal2 and Tal4b of <i>Xanthomonas translucens</i> pv. <i>undulosa</i> ICMP11055 in Bacterial Leaf Streak of Wheat. <i>Frontiers in Microbiology</i> , 2017, 8, 1488. | 1.5 | 37 |

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|----|--|-----|-----------|
| 37 | Engineering altered proteinâ€œDNA recognition specificity. <i>Nucleic Acids Research</i> , 2018, 46, 4845-4871. | 6.5 | 36 |
| 38 | Broadly Conserved Fungal Effector BEC1019 Suppresses Host Cell Death and Enhances Pathogen Virulence in Powdery Mildew of Barley (<i>Hordeum vulgare</i> L.) (Retracted). <i>Molecular Plant-Microbe Interactions</i> , 2015, 28, 968-983. | 1.4 | 33 |
| 39 | Spelling Changes and Fluorescent Tagging With Prime Editing Vectors for Plants. <i>Frontiers in Genome Editing</i> , 2021, 3, 617553. | 2.7 | 30 |
| 40 | A TAL effector-like protein of an endofungal bacterium increases the stress tolerance and alters the transcriptome of the host. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 17122-17129. | 3.3 | 29 |
| 41 | Tools for TAL effector design and target prediction. <i>Methods</i> , 2014, 69, 121-127. | 1.9 | 28 |
| 42 | An <i>ent</i> -kaurene-derived diterpenoid virulence factor from <i>Xanthomonas oryzae</i> pv. <i>oryzicola</i> . <i>New Phytologist</i> , 2015, 206, 295-302. | 3.5 | 28 |
| 43 | TAL Effectors Drive Transcription Bidirectionally in Plants. <i>Molecular Plant</i> , 2017, 10, 285-296. | 3.9 | 28 |
| 44 | Two ancestral genes shaped the <i>Xanthomonas campestris</i> TAL effector gene repertoire. <i>New Phytologist</i> , 2018, 219, 391-407. | 3.5 | 26 |
| 45 | The I-TevI Nuclease and Linker Domains Contribute to the Specificity of Monomeric TALENs. <i>G3: Genes, Genomes, Genetics</i> , 2014, 4, 1155-1165. | 0.8 | 23 |
| 46 | Genetic mapping of a major gene in triticale conferring resistance to bacterial leaf streak. <i>Theoretical and Applied Genetics</i> , 2018, 131, 649-658. | 1.8 | 23 |
| 47 | Cloning of the Rice <i>Xo1</i> Resistance Gene and Interaction of the Xo1 Protein with the Defense-Suppressing <i>Xanthomonas</i> Effector Tal2h. <i>Molecular Plant-Microbe Interactions</i> , 2020, 33, 1189-1195. | 1.4 | 23 |
| 48 | Transfer of <i>Xanthomonas campestris</i> pv. <i>arecae</i> and <i>X. campestris</i> pv. <i>musacearum</i> to <i>X. vasicola</i> (Vauterin) as <i>X. vasicola</i> pv. <i>arecae</i> comb. nov. and <i>X. vasicola</i> pv. <i>musacearum</i> comb. nov. and Description of <i>X. vasicola</i> pv. <i>vasculorum</i> pv. nov.. <i>Phytopathology</i> , 2020, 110, 1153-1160. | 1.1 | 23 |
| 49 | daTALbase: A Database for Genomic and Transcriptomic Data Related to TAL Effectors. <i>Molecular Plant-Microbe Interactions</i> , 2018, 31, 471-480. | 1.4 | 22 |
| 50 | A transcription activator-like effector from <i>Xanthomonas oryzae</i> pv. <i>oryzicola</i> elicits dose-dependent resistance in rice. <i>Molecular Plant Pathology</i> , 2017, 18, 55-66. | 2.0 | 20 |
| 51 | <i>Xanthomonas campestris</i> Pathovars. <i>Trends in Microbiology</i> , 2021, 29, 182-183. | 3.5 | 18 |
| 52 | Principles and applications of TAL effectors for plant physiology and metabolism. <i>Current Opinion in Plant Biology</i> , 2014, 19, 99-104. | 3.5 | 17 |
| 53 | A Strain of an Emerging Indian <i>Xanthomonas oryzae</i> pv. <i>oryzae</i> Pathotype Defeats the Rice Bacterial Blight Resistance Gene xa13 Without Inducing a Clade III SWEET Gene and Is Nearly Identical to a Recent Thai Isolate. <i>Frontiers in Microbiology</i> , 2018, 9, 2703. | 1.5 | 17 |
| 54 | Pto update: recent progress on an ancient plant defence response signalling pathway. <i>Molecular Plant Pathology</i> , 2002, 3, 283-288. | 2.0 | 12 |

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|----|---|-----|-----------|
| 55 | Complete Genome Sequences of <i>Xanthomonas axonopodis</i> pv. <i>glycines</i> Isolates from the United States and Thailand Reveal Conserved Transcription Activator-Like Effectors. <i>Genome Biology and Evolution</i> , 2019, 11, 1380-1384. | 1.1 | 11 |
| 56 | An xa5 Resistance Gene-Breaking Indian Strain of the Rice Bacterial Blight Pathogen <i>Xanthomonas oryzae</i> pv. <i>oryzae</i> Is Nearly Identical to a Thai Strain. <i>Frontiers in Microbiology</i> , 2020, 11, 579504. | 1.5 | 8 |
| 57 | Genomic insights advance the fight against black rot of crucifers. <i>Journal of General Plant Pathology</i> , 2021, 87, 127-136. | 0.6 | 3 |
| 58 | Online Tools for TALEN Design. <i>Methods in Molecular Biology</i> , 2016, 1338, 43-47. | 0.4 | 3 |
| 59 | An atypical class of non-coding small RNAs is produced in rice leaves upon bacterial infection. <i>Scientific Reports</i> , 2021, 11, 24141. | 1.6 | 3 |
| 60 | Complete Genome Resource of <i>Xanthomonas oryzae</i> pv. <i>oryzicola</i> GX01 Isolated in South China. <i>Molecular Plant-Microbe Interactions</i> , 2022, , MPMI10210259A. | 1.4 | 3 |
| 61 | Achieving Controlled Recombination with Targeted Cleavage and Epigenetic Modifiers. <i>Trends in Plant Science</i> , 2020, 25, 513-514. | 4.3 | 2 |
| 62 | A Confounding Effect of Bacterial Titer in a Type III Delivery-Based Assay of Eukaryotic Effector Function. <i>Molecular Plant-Microbe Interactions</i> , 2018, 31, 1115-1116. | 1.4 | 1 |
| 63 | TAL Effectors with Avirulence Activity in African Strains of <i>Xanthomonas oryzae</i> pv. <i>oryzae</i> . <i>Rice</i> , 2022, 15, 9. | 1.7 | 1 |
| 64 | Cruciferous Weed Isolates of <i>Xanthomonas campestris</i> Yield Insight into Pathovar Genomic Relationships and Genetic Determinants of Host and Tissue Specificity. <i>Molecular Plant-Microbe Interactions</i> , 2022, 35, 791-802. | 1.4 | 1 |
| 65 | Development of a Web Course on Gene Therapy by the International Consortium of Gene Therapy. <i>Molecular Therapy</i> , 2014, 22, 482. | 3.7 | 0 |
| 66 | Genome Sequence of <i>Xanthomonas campestris</i> Strain FDWSRU 18048, an Emerging Pathogen of Nonnative, Invasive Garlic Mustard (<i>Alliaria petiolata</i>). <i>Microbiology Resource Announcements</i> , 2022, 11, e0094221. | 0.3 | 0 |