

Philipp Bayer

DECRA FELLOW

School of Biological Sciences, University of Western Australia

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About me

I use computers and large data sets to answer biological questions, especially in crops. I use genomics, pangenomics, k-mer/SNP/QTL-association studies, biostatistics, and interpretable machine learning to find new approaches to breed climate change-ready crops.

Education

University of Queensland

Brisbane, Australia

PHD 2012-2016

- Pure bioinformatics PhD in the Edwards group
- Developed computational pipeline SkimGBS for cheaper genotyping
- Worked extensively with industry (Bayer CropScience, later BASF)

Bond University

Gold Coast, Australia

MASTER OF IT 2010-2012

- 5x Top of class, 3x Vice-Chancellor List of Academic Excellence, 1x IT Award Academic Excellence
- Graduated with High Distinction. John Oglethorpe Medal for highest GPA of all IT students graduating

University of Muenster

Muenster, Germany

BACHELOR OF LIFE SCIENCES 2006-2009

- Studied general life sciences with a focus on microbiology
- In my final project I worked on EST-based differential gene expression in seagrasses

Employment

UWA

Perth

DECRA FELLOW 2021-2023

- My first step towards an independent lab with with AUD\$ 448k1 in government and AUD\$ 418k UWA funding
- I am modeling mechanisms of gene loss and birth in crops to learn where new genes come from, and how to avoid loss of agronomically important genes.

UWA

Perth

FORREST FELLOW 2017-2020

- One of three inaugural Forrest Fellows
- Work on genomics of complex plants with Forrest Foundation support
- Supervised three PhD students and four MSc students to completion.

UWA

Perth

POSTDOCTORAL RESEARCHER 2015-2017

- Researched genetics of complex plants with a focus on canola and wheat in Edwards lab
- Worked closely with industry partners to improve their breeding programs
- Supervised two interns, co-supervised four PhD students and one MSc student to completion

Experience

- 2021 **Host, ABACBS conference Perth Hub**
Hosted the Perth hub of the yearly ABACBS conference, chaired genomics session
- 2021-Now **Member, Scientific Advisory Panel Machine Learning**
Member of the scientific advisory panel for ongoing machine learning projects supported by the ARDC.
- 2012-2018 **Research Collaboration with Bayer CropScience, later BASF**
Continued collaboration with Bayer CropScience on their plant breeding projects.
- 2011-Now **Co-founder openSNP.org**
Partially wrote and maintain the site's uby on Rails code-base, interact and manage with the community of 5000 users, administration of the site's servers, and supervision of contributors
- 2013-Now **Certified Carpentries Instructor**
Certified Software Carpentry and Data Carpentry instructor. The Carpentries is a non-profit organization teaching programming to scientists around the world
- 2018 **Research Bazaar Organising Committee**
ResBaz is a world-wide three-day festival promoting digital literacy. As member of the organising committee I organised teachers, drafted the timeplan, designed the web page, raised funding, invited keynote speakers
- 2017-Now **Hacky Hour Founder**
A weekly get-together of researchers and staff working with programming and data, doubles as a help-desk for students with programming problems.
- 2017-2019 **Mozilla Open Science Leadership Mentor**
Mentored programmers and researchers on how to streamline and grow open science projects
- 2016-2019 **EMBL-ABR Head of Nodes member**
EMBL-ABR was an Australian-wide network supporting the technical needs of life sciences researchers
- 2016-2017 **COMBINE WA Representative**
As the local COMBINE representative I organise or help organise workshops and regular networking events

Awards and Funding

Grant: ARC Discovery Early Career Research Award

AWARDED DECRA FOR 2021-2023. TOTAL FUNDING: AUD\$ 448,781 AND AUD\$ 418,772 IN UWA FUNDING.

ARC
2021-2023

Grant: Identifying genetic contributors to canola blackleg resistance in the presence of environmental effects using Machine Learning

WITH PROF. DAVE EDWARDS, PROF. MOHAMMED BENNAMOUN, PROF. FARID BOUSSAID, PROF. JACQUELINE BATLEY. TOTAL FUNDING: AUD\$ 309,524.

GRDC
2020-2022

Grant: Machine Learning - Project E: Deep Learning for early detection and classification of crop disease and stress

WITH PROF. MOHAMMED BENNAMOUN, PROF. FARID BOUSSAID, PROF. DAVE EDWARDS, DR. NIC TAYLOR. TOTAL FUNDING: AUD\$ 344,971.

GRDC
2020-2022

Woodside Early Career Scientist of the Year, finalist

FINALIST IN PREMIER'S SCIENCE AWARDS 2019

WA
2019

Rising Stars nomination

TWO EARLY CAREER RESEARCHERS PER UWA RESEARCH SCHOOL WERE NOMINATED FOR RISING STARS, A UNIVERSITY-WIDE EVENT WHERE RESEARCHERS INTRODUCE A PUBLIC AUDIENCE TO THEIR RESEARCH.

UWA, Perth
2018

Forrest Research Foundation Non-stipendiary Fellowship

THREE YEAR FELLOWSHIP TO PURSUE RESEARCH AT UWA, PART OF THE THREE INAUGURAL FORREST FELLOWS

UWA, Perth
2018

UWA Research Collaboration Award

AUD\$ 28,100 TO FUND A SEAGRASS MICROBIOME SEQUENCING PROJECT.

UWA, Perth
2017

GRDC Travel Award

TRAVEL COST SCHOLARSHIP TO TRAVEL TO PAG, USA.

GRDC
2014

UQ SAFS Travel Award

TRAVEL COST SCHOLARSHIP TO TRAVEL TO PAG, USA.

UQ, Brisbane
2014

Bayer Grants4Apps

GRANT TO COVER OPENSNP RUNNING COSTS

Bayer

2013

Two postgraduate scholarships

MY PHD WAS SUPPORTED BY TWO SCHOLARSHIPS FROM UQ FOR TUITION FEES AND LIVING COSTS.

UQ, Brisbane

2011-2014

First place in PLOS/Mendeley Binary Challenge

WON FIRST PRICE IN A COMPETITION AIMED TOWARDS THE ADVANCEMENT OF OPEN SCIENCE

openSNP.org

2012

Teaching

University teaching

ORGANISED NEW MSc BIOINFORMATICS WITH NEW UNIT, SCIE5003 (ADVANCED BIOINFORMATICS). DEVELOPED CONTENT OF SCIE5003 AND SCIE4002, TAUGHT INTO BOTH UNITS.

UWA, Perth

2017-Now

Introduction to tidyverse and purrr

INTRODUCING RSTUDIO, PROJECT ORGANISATION, BASIC TIDYVERSE, LOOPS, FUNCTIONS, MAPS

ASI R Workshop

2021

Introduction to genomics on the command line

INTRODUCTION TO THE COMMAND LINE, BIOINFORMATICS ANALYSES AND PIPELINES, AND BASIC SNP ANALYSIS IN R.

ResBaz, Curtin

2019

Introduction to tidyverse and caret in R

INTRODUCTION TO R, TIDYVERSE, GGLOT2, CARET, AND BASIC STATISTICS IN R. TAUGHT OVER TWO DAYS.

School of Human Sciences, UWA

2019

Introduction to modern R

INTRODUCTION TO R, TIDYVERSE, GGLOT2, AND BASIC STATISTICS APPROACHES IN R. TAUGHT OVER TWO DAYS.

TKI, Perth

2018

Data Carpentry workshop

INTRODUCTION TO GENOMICS AND SHELL. PART OF THE PLANNING COMMITTEE.

ResBaz, UWA

2018

Software Carpentry workshop

INTRODUCTION TO DATA MANIPULATION USING PYTHON.

ResBaz, Curtin

2017

Data Carpentry workshop and host

HOSTED, PLANNED, AND SET UP THE FIRST DATA CARPENTRY WORKSHOP AT UWA, TAUGHT BEST DATA MANAGEMENT PRACTICES.

UWA, Perth

2016

Software Carpentry workshop

INTRODUCTION TO PYTHON AND GIT

ResBaz, Murdoch Uni

2016

Software Carpentry workshop

INTRODUCTION TO PYTHON AND GIT

Curtin Uni, Perth

2016

Software Carpentry workshop and host

HOSTED, PLANNED, AND TAUGHT INTO THE FIRST SOFTWARE CARPENTRY WORKSHOP AT UQ.

UQ, Brisbane

2016

Software Carpentry workshop

BASIC TO INTERMEDIATE PYTHON.

Sydney

2014

Software Carpentry workshop

BASIC TO INTERMEDIATE PYTHON

PyCon AU/UQ, Brisbane

2014

Software Carpentry workshop

BASIC TO INTERMEDIATE PYTHON AS ASSISTANT

Adelaide

2013

Programming tutor

TUTORED STUDENTS IN INTRO TO PROGRAMMING (JAVA), DATABASE MANAGEMENT (ORACLE/MYSQL) AND NETWORKS & APPLICATIONS, HELD SEVERAL ALL-DAY REFRESHER COURSES BEFORE EXAMS

Bond University

2009-2011

Presentations

Machine learning in bioinformatics – where are we and what's next?

INVITED TALK

CCDM/Curtin University

2021

Machine learning in plant breeding and bioinformatics

INVITED TALK

Cinvestav/online

2021

Future-ready crops for a changing climate: the role of bioinformatics	<i>UWA DVCR Forrest Fellow series</i>
INVITED TALK	2021
Bioinformatics at scale Q & A	<i>Pawsey Supercomputing Centre</i>
INVITED	2021
Interpretable Machine Learning in Bioinformatics	<i>ABACBS online seminars</i>
INVITED TALK	2021
Our machine learning technical stack	<i>GRDC Tech Seminars</i>
	2020
Predicting Gene Loss in Plants: Lessons Learned from Laptop-Scale Data	<i>PAG Conference, San Diego</i>
	2020
Eukaryotic pangenomics: where we've been, where we're going	<i>Bayliss Seminar Series</i>
INVITED	2019
Assembling complex plant genomes – things I wish someone would have told me earlier	<i>AGRF Seminar Series</i>
INVITED	2019
Helping Biologists Make Sense of Plant Variant and Annotation Data	<i>PAG Conference, San Diego</i>
	2019
Feeding the future world: safe-guarding Australia's food bowl in a changing climate	<i>Rising Stars UWA</i>
	2018
From QTLs to candidate genes, or: There and Back Again	<i>Institute of Ag seminars</i>
INVITED	2018
The path of least resistance (genes) - mining plant genomes for disease resistance	<i>COMBINE/Pawsey symposium</i>
INVITED	2018
Early Career Researcher Panel - What have I learnt at the beginning of my research career?	<i>Combined Biological Sciences Meeting</i>
	2018
ScienceCafe - STEM outreach aimed at year 10 students	<i>UWA</i>
	2018
The future of wheat research	<i>UWA</i>
	2017
Skippping the assembly step – what we can learn from looking at sequences directly	<i>Pawsey Roadshow</i>
INVITED	2017
The State of Bioinformatics in High Performance Computing in 2017	<i>HPCAC Conference, Perth</i>
	2017
Towards better plant breeding at UWA	<i>COMBINE, Perth</i>
	2017
Improving Plant Breeding using KNetMiner	<i>PAG, San Diego</i>
	2017
Towards a canola pan-genome: cautionary tales from the assembly bench	<i>CCDM, Curtin</i>
INVITED TALK	2016
Sharing Experience: What Can We Learn from Each Other Developing Plant Informatics Systems	<i>PAG, San Diego</i>
	2016
Assessing and validating the amphidiploid genome of Brassica napus using genotyping by sequencing	<i>PAG, San Diego</i>
	2015
Using skim-based genotyping by sequencing for trait association and QTL cloning in Brassica napus	<i>PAG, San Diego</i>
	2015

Publications

Machine learning in agriculture: from silos to marketplaces

PE BAYER, D EDWARDS

Plant Biotechnology Journal

2021

Current status of structural variation studies in plants

Y YUAN, PE BAYER, J BATLEY, D EDWARDS

Plant Biotechnology Journal

2021

Assembly of the non-heading pak choi genome and comparison with the genomes of heading Chinese cabbage and the oilseed yellow sarson

P LI, T SU, X ZHAO, W WANG, D ZHANG, Y YU, PE BAYER, D EDWARDS, S YU, ...

Plant biotechnology journal

2021

The application of pangenomics and machine learning in genomic selection in plants

PE BAYER, J PETEREIT, MF DANILEVICZ, R ANDERSON, J BATLEY, D EDWARDS

The Plant Genome

2021

Genotype-environment mismatch of kelp forests under climate change

S VRANKEN, T WERNBERG, A SCHEBEN, A SEVERN-ELLIS, J BATLEY, PE BAYER, ...

Molecular Ecology

2021

Genetic variation among 481 diverse soybean accessions, inferred from genomic re-sequencing

B VALLIYODAN, AV BROWN, J WANG, G PATIL, Y LIU, PI OTYAMA, RT NELSON, ...

Scientific data

2021

The pangenome of banana highlights differences between genera and genomes

H RIJZAANI, PE BAYER, M ROUARD, J DOLEŽEL, J BATLEY, D EDWARDS

The Plant Genome

2021

Resources for image-based high-throughput phenotyping in crops and data sharing challenges

MF DANILEVICZ, PE BAYER, BJ NESTOR, M BENNAMOUN, D EDWARDS

Plant physiology

2021

Sequencing the USDA core soybean collection reveals gene loss during domestication and breeding

PE BAYER, B VALLIYODAN, H HU, JI MARSH, Y YUAN, TD VUONG, G PATIL, ...

The Plant Genome (TSI)

2021

Fast-forward breeding for a food-secure world

RK VARSHNEY, A BOHRA, M ROORKIWAL, R BARMUKH, WA COWLING, ...

Trends in Genetics

2021

Genomic rearrangements have consequences for introgression breeding as revealed by genome assemblies of wild and cultivated lentil species

L RAMSAY, CS KOH, S KAGALE, D GAO, S KAUR, T HAILE, TS GELA, LA CHEN, ...

bioRxiv

2021

Amborella gene presence/absence variation is associated with abiotic stress responses that may contribute to environmental adaptation

H HU, A SCHEBEN, B VERPAALLEN, S TIRNAZ, PE BAYER, RGJ HODEL, J BATLEY, ...

New Phytologist

2021

Modelling of gene loss propensity in the pangenomes of three Brassica species suggests different mechanisms between polyploids and diploids

PE BAYER, A SCHEBEN, AA GOLICZ, Y YUAN, S FAURE, HT LEE, HS CHAWLA, ...

Plant Biotechnology Journal

2021

Marine heatwaves have minimal influence on the quality of adult Sydney rock oyster flesh

EE EWERE, N ROSIC, PE BAYER, A NGANGBAM, D EDWARDS, BP KELAHER, ...

Science of The Total Environment

2021

QTL Genetic Mapping Study for Traits Affecting Meal Quality in Winter Oilseed Rape (Brassica Napus L.)

K GACEK, PE BAYER, R ANDERSON, AA SEVERN-ELLIS, J WOLKO, A ŁOPATYŃSKA, ...

Genes

2021

Candidate Rlm6 resistance genes against Leptosphaeria. maculans identified through a genome-wide association study in Brassica juncea (L.) Czern

H YANG, NSM SAAD, MI IBRAHIM, PE BAYER, TX NEIK, AA SEVERN-ELLIS, ...

Theoretical and Applied Genetics

2021

Pangenomics in crop improvement—from coding structural variations to finding regulatory variants with pangenome graphs	<i>The Plant Genome</i> , e
SF ZANINI, PE BAYER, R WELLS, RJ SNOWDON, J BATLEY, RK VARSHNEY, ...	2021
Brassica napus genes Rlm4 and Rlm7, conferring resistance to Leptosphaeria maculans, are alleles of the Rlm9 wall-associated kinase-like resistance locus	<i>bioRxiv</i>
P HADDADI, NJ LARKAN, A VAN DE WOUW, Y ZHANG, TX NEIK, E BEYNON, ...	2021
Yield is negatively correlated with nucleotide-binding leucine-rich repeat gene content in soybean	<i>bioRxiv</i>
PE BAYER, H HU, J PETEREIT, RK VARSHNEY, B VALLIYODAN, HT NGUYEN, ...	2021
Haplotype mapping uncovers unexplored variation in wild and domesticated soybean at the major protein locus cqProt-003	<i>bioRxiv</i>
JI MARSH, H HU, J PETEREIT, PE BAYER, B VALLIYODAN, J BATLEY, HT NGUYEN, ...	2021
Maize yield prediction at an early developmental stage using multispectral images and genotype data for preliminary hybrid selection	<i>Remote Sensing</i>
MF DANILEVICZ, PE BAYER, F BOUSSAID, M BENNAMOUN, D EDWARDS	2021
High-Throughput Genotyping Technologies in Plant Taxonomy	<i>Molecular Plant Taxonomy</i>
MF DANILEVICZ, CGT FERNANDEZ, JI MARSH, PE BAYER, D EDWARDS	2021
Plant pan-genomes are the new reference	<i>Nature plants</i>
PE BAYER, AA GOLICZ, A SCHEBEN, J BATLEY, D EDWARDS	2020
Climate change and the need for agricultural adaptation	<i>Current opinion in plant biology</i>
R ANDERSON, PE BAYER, D EDWARDS	2020
Pangenomics comes of age: from bacteria to plant and animal applications	<i>Trends in Genetics</i>
AA GOLICZ, PE BAYER, PL BHALLA, J BATLEY, D EDWARDS	2020
Plant pangenomics: approaches, applications and advancements	<i>Current opinion in plant biology</i>
MF DANILEVICZ, CGT FERNANDEZ, JI MARSH, PE BAYER, D EDWARDS	2020
Characterization of disease resistance genes in the Brassica napus pangenome reveals significant structural variation	<i>Plant biotechnology journal</i>
A DOLATABADIAN, PE BAYER, S TIRNAZ, B HURGOBIN, D EDWARDS, J BATLEY	2020
Trait associations in the pangenome of pigeon pea (Cajanus cajan)	<i>Plant biotechnology journal</i>
J ZHAO, PE BAYER, P RUPERAO, RK SAXENA, AW KHAN, AA GOLICZ, ...	2020
Resistance gene analogs in the Brassicaceae: Identification, characterization, distribution, and evolution	<i>Plant physiology</i>
S TIRNAZ, PE BAYER, F INTURRISI, F ZHANG, H YANG, A DOLATABADIAN, TX NEIK, ...	2020
Induced methylation in plants as a crop improvement tool: progress and perspectives	<i>Agronomy</i>
C MERCÉ, PE BAYER, C TAY FERNANDEZ, J BATLEY, D EDWARDS	2020
Genome-wide identification and comparative analysis of resistance genes in Brassica juncea	<i>Molecular Breeding</i>
F INTURRISI, PE BAYER, H YANG, S TIRNAZ, D EDWARDS, J BATLEY	2020
Effect of Leptosphaeria maculans infection on promoter DNA methylation of defence genes in Brassica napus	<i>Agronomy</i>
S TIRNAZ, C MERCE, PE BAYER, AA SEVERN-ELLIS, D EDWARDS, J BATLEY	2020
Frontiers in dissecting and managing Brassica diseases: from reference-based RGA candidate identification to building pan-RGAomes	<i>International Journal of Molecular Sciences</i>
Y ZHANG, W THOMAS, PE BAYER, D EDWARDS, J BATLEY	2020
Genome-Wide Identification and Evolution of Receptor-Like Kinases (RLKs) and Receptor like Proteins (RLPs) in Brassica juncea. Biology 2021, 10, 17	<i>Agronomy</i>
H YANG, PE BAYER, S TIRNAZ, D EDWARDS, J BATLEY	2020
Legume pangenome construction using an iterative mapping and assembly approach	<i>Legume Genomics</i>
H HU, Y YUAN, PE BAYER, CT FERNANDEZ, A SCHEBEN, AA GOLICZ, ...	2020
Plant pangenomics: approaches, applications and advancements	
M FURASTE DANILEVICZ, MF DANILEVICZ, CG TAY FERNANDEZ, JI MARSH, ...	2020

RefKA: A fast and efficient long-read genome assembly approach for large and complex genomes	<i>bioRxiv</i>
Y YUAN, PE BAYER, R ANDERSON, HT LEE, CKK CHAN, R ZHAO, J BATLEY, ...	2020
Method for Genome-Wide Association Study: A Soybean Example	<i>Legume Genomics</i>
R ANDERSON, CT FERNANDEZ, Y YUAN, AA GOLICZ, D EDWARDS, PE BAYER	2020
A reference genome for pea provides insight into legume genome evolution	<i>Nature Genetics</i>
J KREPLAK, MA MADOU, P CÁPÁL, P NOVÁK, K LABADIE, G AUBERT, PE BAYER, ...	2019
Variation in abundance of predicted resistance genes in the Brassica oleracea pangenome	<i>Plant biotechnology journal</i>
PE BAYER, AA GOLICZ, S TIRNAZ, CKK CHAN, D EDWARDS, J BATLEY	2019
Adapting legume crops to climate change using genomic approaches	<i>Plant, cell & environment</i>
M MOUSAVI-DERAZMAHALLEH, PE BAYER, JK HANE, B VALLIYODAN, ...	2019
INDEL variation in the regulatory region of the major flowering time gene LanFTc1 is associated with vernalization response and flowering time in narrow-leaved lupin (Lupinus ...	<i>Plant, cell & environment</i>
CM TAYLOR, LG KAMPHUIS, W ZHANG, G GARG, JD BERGER, ...	2019
Construction and comparison of three reference-quality genome assemblies for soybean	<i>The Plant Journal</i>
B VALLIYODAN, SB CANNON, PE BAYER, S SHU, AV BROWN, L REN, J JENKINS, ...	2019
CropSNPdb: a database of SNP array data for Brassica crops and hexaploid bread wheat	<i>The Plant Journal</i>
A SCHEBEN, B VERPAALLEN, CT LAWLEY, CKK CHAN, PE BAYER, J BATLEY, ...	2019
High intraspecific diversity of Restorer-of-fertility-like genes in barley	<i>The Plant Journal</i>
J MELONEK, R ZHOU, PE BAYER, D EDWARDS, N STEIN, I SMALL	2019
Establishing a distributed national research infrastructure providing bioinformatics support to life science researchers in Australia	<i>Briefings in bioinformatics</i>
MV SCHNEIDER, PC GRIFFIN, S TYAGI, M FLANNERY, S DAYALAN, S GLADMAN, ...	2019
Genome-Wide Association Studies in Plants	<i>eLS</i>
R ANDERSON, D EDWARDS, J BATLEY, PE BAYER	2019
Genetic diversity linked to haplotype variation in the world core collection of Trifolium subterraneum for boron toxicity tolerance provides valuable markers for pasture breeding	<i>Frontiers in plant science</i>
H TAHGHIGHI, W ERSKINE, RG BENNETT, PE BAYER, M PAZOS-NAVARRO, P KAUR	2019
Genome-wide association to explore the genetic regulation of flowering time in narrow-leaved lupin (Lupinus angustifolius L.)	<i>Dissecting the genetic control of flowering time for improved phenological ...</i>
CM TAYLOR, LG KAMPHUIS, MN NELSON, JD BERGER, K STEFANOVA, ...	2019
W529: Walking on the wild side using pangenomics for accelerated crop improvement in chickpea	
AW KHAN, V GARG, M ROORKIWAL, PE BAYER, M THUDI, A CHITIKINENI, ...	2019
Poznanie genetyczne regulacji cech wpływających na wartość paszową białka w nasionach rzepaku ozimego przy użyciu mapowania genetycznego	<i>Biuletyn Instytutu Hodowli i Aklimatyzacji Roślin</i>
K GACEK, J WALKO, A DOBRZYCKA, L SZALA, I BARTKOWIAK-BRODA, ...	2019
Shifting the limits in wheat research and breeding using a fully annotated reference genome	<i>Science</i>
R APPELS, K EVERSOLE, N STEIN, C FEUILLET, B KELLER, J ROGERS, CJ POZNIAK, ...	2018
The transcriptional landscape of polyploid wheat	<i>Science</i>
RH RAMÍREZ-GONZÁLEZ, P BORRILL, D LANG, SA HARRINGTON, J BRINTON, ...	2018
Homoeologous exchange is a major cause of gene presence/absence variation in the amphidiploid Brassica napus	<i>Plant biotechnology journal</i>
B HURGOBIN, AA GOLICZ, PE BAYER, CKK CHAN, S TIRNAZ, A DOLATABADIAN, ...	2018
Genome wide identification and comparative analysis of NBS-LRR resistance genes in Brassica napus	<i>Crop and Pasture Science</i>
S ALAMERY, S TIRNAZ, P BAYER, R TOLLENAERE, B CHALHOUB, D EDWARDS, ...	2018

Exploring the genetic and adaptive diversity of a pan-Mediterranean crop wild relative: narrow-leaved lupin

M MOUSAVI-DERAZMAHALLEH, PE BAYER, B NEVADO, B HURGOBIN, D FILATOV, ...

Theoretical and Applied Genetics

2018

Bias in resistance gene prediction due to repeat masking

PE BAYER, D EDWARDS, J BATLEY

Nature plants

2018

The western Mediterranean region provided the founder population of domesticated narrow-leaved lupin

M MOUSAVI-DERAZMAHALLEH, B NEVADO, PE BAYER, DA FILATOV, JK HANE, ...

Theoretical and Applied Genetics

2018

Genomic comparison of two independent seagrass lineages reveals habitat-driven convergent evolution

HT LEE, AA GOLICZ, PE BAYER, AA SEVERN-ELLIS, CKK CHAN, J BATLEY, ...

Journal of experimental botany

2018

Genome-wide analysis of NBS-LRR genes in Indian mustard (Brassica juncea) and prediction of candidate disease resistance genes

FC INTURRISI, PE BAYER, H YANG, CKK CHAN, D EDWARDS, J BATLEY

Phytopathology

2018

Large-scale structural variation detection in subterranean clover subtypes using optical mapping

Y YUAN, Z MILEC, PE BAYER, J VRÁNA, J DOLEŽEL, D EDWARDS, W ERSKINE, ...

Frontiers in plant science

2018

Identification of the Single Nucleotide Polymorphisms Affecting Normal Phenotypic Variability in Human Craniofacial Morphology Using Candidate Gene Approach

M BARASH, PE BAYER, A VAN DAAL

J Genet Genome Res

2018

The pangenome of hexaploid bread wheat

JD MONTENEGRO, AA GOLICZ, PE BAYER, B HURGOBIN, HT LEE, CKK CHAN, ...

The Plant Journal

2017

A comprehensive draft genome sequence for lupin (Lupinus angustifolius), an emerging health food: insights into plant-microbe interactions and legume evolution

JK HANE, Y MING, LG KAMPHUIS, MN NELSON, G GARG, CA ATKINS, PE BAYER, ...

Plant biotechnology journal

2017

Assembly and comparison of two closely related Brassica napus genomes

PE BAYER, B HURGOBIN, AA GOLICZ, CKK CHAN, Y YUAN, HT LEE, M RENTON, ...

Plant biotechnology journal

2017

Improvements in genomic technologies: application to crop genomics

Y YUAN, PE BAYER, J BATLEY, D EDWARDS

Trends in Biotechnology

2017

Genome-wide association study of genetic control of seed fatty acid biosynthesis in Brassica napus

K GACEK, PE BAYER, I BARTKOWIAK-BRODA, L SZALA, J BOCIANOWSKI, ...

Frontiers in plant science

2017

An advanced reference genome of Trifolium subterraneum L. reveals genes related to agronomic performance

P KAUR, PE BAYER, Z MILEC, J VRÁNA, Y YUAN, R APPELS, D EDWARDS, ...

Plant Biotechnology Journal

2017

Climate clever clovers: New paradigm to reduce the environmental footprint of ruminants by breeding low methanogenic forages utilizing haplotype variation

P KAUR, R APPELS, PE BAYER, G KEEBLE-GAGNERE, J WANG, H HIRAKAWA, ...

Frontiers in Plant Science

2017

runBNG: a software package for BioNano genomic analysis on the command line

Y YUAN, PE BAYER, HT LEE, D EDWARDS

Bioinformatics

2017

BioNanoAnalyst: a visualisation tool to assess genome assembly quality using BioNano data

Y YUAN, PE BAYER, A SCHEBEN, CKK CHAN, D EDWARDS

BMC bioinformatics

2017

Large-scale structural variation detection in subterranean clover subtypes using optical mapping validated at nucleotide level

Y YUAN, Z MILEC, PE BAYER, J VRÁNA, J DOLEŽEL, D EDWARDS, W ERSKINE, ...

bioRxiv

2017

Constructing improved chickpea genome assemblies using skimGBS

P RUPERAO, P BAYER, CK KENNETH CHAN, S HAYASHI, M ROORKIWAL, ...

2017

The pangenome of an agronomically important crop plant Brassica oleracea

AA GOLICZ, PE BAYER, GC BARKER, PP EDGER, HR KIM, PA MARTINEZ, ...

Nature communications

2016

The Genome of a Southern Hemisphere Seagrass Species (Zostera muelleri)	<i>Plant physiology</i>
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