

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

PHD Brisbane, Australia

2012-2016

Bond University

MASTER OF IT Gold Coast, Australia

2010-2012

University of Muenster

BACHELOR OF LIFE SCIENCES Muenster, Germany

2006-2009

Employment

DECRA Fellow

MY FIRST STEP TOWARDS AN INDEPENDENT LAB WITH FUNDING FOR THE FIRST PHD-STUDENT PRIMARILY SUPERVISED BY ME AND WITH AUD\$ 448,781 IN GOVERNMENT AND AUD\$ 418,772 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. Perth, UWA

2021-2023

Forrest Fellow

ONE OF THREE INAUGURAL FORREST FELLOWS. CONTINUED WORK ON GENOMICS OF COMPLEX PLANTS WITH FORREST FOUNDATION SUPPORT. SUPERVISED THREE PHD STUDENTS AND FOUR MSc STUDENTS TO COMPLETION. Perth, UWA

2017-2020

Postdoctoral researcher

EDWARDS LAB. RESEARCHED GENETICS OF COMPLEX PLANTS WITH A FOCUS ON CANOLA AND WHEAT. WORKED CLOSELY WITH INDUSTRY PARTNERS TO IMPROVE THEIR BREEDING PROGRAMS. SUPERVISED TWO INTERNS, CO-SUPERVISED FOUR PHD STUDENTS AND ONE MSc STUDENT, SYSTEM ADMINISTRATOR FOR THE LOCAL COMPUTATIONAL INFRASTRUCTURE AND GROUP DATA MANAGER. Perth, UWA

2015-2017

Experience

Host, ABACBS conference Perth Hub

HOSTED THE PERTH HUB OF THE YEARLY ABACBS CONFERENCE, CHAIRED GENOMICS SESSION Perth

2021

Member, Scientific Advisory Panel Machine Learning

MEMBER OF THE SCIENTIFIC ADVISORY PANEL FOR ONGOING MACHINE LEARNING PROJECTS SUPPORTED BY THE ARDC. ARDC

2021-Current

Research Collaboration with Bayer CropScience, later BASF

CONTINUED COLLABORATION WITH BAYER CROPSCIENCE ON THEIR PLANT BREEDING PROJECTS. Ghent, Belgium

2012-2018

Co-founder openSNP.org

A PROJECT FOR CUSTOMERS OF GENOTYPING COMPANIES LIKE 23ANDME TO SHARE THEIR DATA WITH SCIENTISTS AROUND THE WORLD, FOR FREE. 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 Germany/Australia

2011-Current

Certified Carpentries Instructor

CERTIFIED SOFTWARE CARPENTRY AND DATA CARPENTRY INSTRUCTOR. THE CARPENTRIES IS A NON-PROFIT ORGANIZATION TEACHING PROGRAMMING TO SCIENTISTS AROUND THE WORLD. Australia

2013-Current

Research Bazaar Organising Committee

RESBAZ IS A WORLD-WIDE THREE-DAY FESTIVAL PROMOTING DIGITAL LITERACY. AS MEMBER OF THE ORGANISING COMMITTEE I SEARCHED FOR HELPERS AND TEACHERS, DRAFTED THE TIMEPLAN, DESIGNED THE WEB PAGE, RAISED FUNDING, SUCCEEDED IN GETTING GOVERNMENT MP TO HOLD THE KEYNOTE

UWA, Perth

2018

Hacky Hour Funder

FOUNDED THE HACKY HOUR AT UWA, A WEEKLY GET-TOGETHER OF RESEARCHERS AND STAFF WORKING WITH PROGRAMMING AND DATA, DOUBLES AS A HELP-DESK FOR STUDENTS WITH PROGRAMMING PROBLEMS.

UWA, Perth

2017-Current

Mozilla Open Science Leadership Mentor

MENTORED OPEN SOURCE PROGRAMMERS AND RESEARCHERS ON HOW TO STREAMLINE AND GROW OPEN SOURCE AND OPEN SCIENCE PROJECTS UNDER THE UMBRELLA OF MOZILLA

Online

2017-2019

EMBLR-ABR Head of Nodes member, Open Science Special Interest Group member

EMBL-ABR WAS AN AUSTRALIAN-WIDE NETWORK SUPPORTING THE TECHNICAL NEEDS OF LIFE SCIENCES RESEARCHERS.

UWA, Perth

2016-2019

COMBINE WA Representative

COMBINE IS THE STUDENT AND EARLY CAREER RESEARCHER SUBCOMMITTEE OF THE AUSTRALIAN BIOINFORMATICS AND COMPUTATIONAL BIOLOGY SOCIETY (ABACBS). AS THE LOCAL REPRESENTATIVE I ORGANISE OR HELP ORGANISE WORKSHOPS AND REGULAR NETWORKING EVENTS.

UWA, Perth

2016-2017

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 PRIZE IN A COMPETITION AIMED TOWARDS THE ADVANCEMENT OF OPEN SCIENCE

openSNP.org

2012

Master IT

5X TOP OF CLASS, 3X VICE-CHANCELLOR'S LIST FOR ACADEMIC EXCELLENCE, 1X IT AWARD ACADEMIC EXCELLENCE. GRADUATED WITH HIGH DISTINCTION. JOHN OGLETHORPE MEDAL FOR HIGHEST GPA OF ALL IT STUDENTS GRADUATING.

Bond University

2009-2001

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-Current

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

INVITED TALK

UWA DVCR Forrest Fellow series

2021

Bioinformatics at scale Q & A

INVITED

Pawsey Supercomputing Centre

2021

Interpretable Machine Learning in Bioinformatics

INVITED TALK

ABACBS online seminars

2021

Our machine learning technical stack

GRDC Tech Seminars

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
Assembling and validating the genome of the Brassica napus using skim-based genotyping by sequencing	<i>UQ, GenGen Seminars</i>
	2014
openSNP: Crowdsourcing Genome Wide Association Studies	<i>Chaos Communication Congress, Berlin</i>
	2012

Publications

Machine learning in agriculture: from silos to marketplaces	<i>Plant Biotechnology Journal</i>
PE BAYER, D EDWARDS	2021

Current status of structural variation studies in plants	<i>Plant Biotechnology Journal</i>
Y YUAN, PE BAYER, J BATLEY, D EDWARDS	2021
Assembly of the non-heading pak choi genome and comparison with the genomes of heading Chinese cabbage and the oilseed yellow sarson	<i>Plant biotechnology journal</i>
P LI, T SU, X ZHAO, W WANG, D ZHANG, Y YU, PE BAYER, D EDWARDS, S YU, ...	2021
The application of pangenomics and machine learning in genomic selection in plants	<i>The Plant Genome</i>
PE BAYER, J PETEREIT, MF DANILEVICZ, R ANDERSON, J BATLEY, D EDWARDS	2021
Genotype-environment mismatch of kelp forests under climate change	<i>Molecular Ecology</i>
S VRANKEN, T WERNBERG, A SCHEBEN, A SEVERN-ELLIS, J BATLEY, PE BAYER, ...	2021
Genetic variation among 481 diverse soybean accessions, inferred from genomic re-sequencing	<i>Scientific data</i>
B VALLIYODAN, AV BROWN, J WANG, G PATIL, Y LIU, PI OTYAMA, RT NELSON, ...	2021
The pangenome of banana highlights differences between genera and genomes	<i>The Plant Genome</i>
H RIJZAANI, PE BAYER, M ROUARD, J DOLEŽEL, J BATLEY, D EDWARDS	2021
Resources for image-based high-throughput phenotyping in crops and data sharing challenges	<i>Plant physiology</i>
MF DANILEVICZ, PE BAYER, BJ NESTOR, M BENNAMOUN, D EDWARDS	2021
Sequencing the USDA core soybean collection reveals gene loss during domestication and breeding	<i>The Plant Genome (TSI)</i>
PE BAYER, B VALLIYODAN, H HU, JI MARSH, Y YUAN, TD VUONG, G PATIL, ...	2021
Fast-forward breeding for a food-secure world	<i>Trends in Genetics</i>
RK VARSHNEY, A BOHRA, M ROORKIWAL, R BARMUKH, WA COWLING, ...	2021
Genomic rearrangements have consequences for introgression breeding as revealed by genome assemblies of wild and cultivated lentil species	<i>bioRxiv</i>
L RAMSAY, CS KOH, S KAGALE, D GAO, S KAUR, T HAILE, TS GELA, LA CHEN, ...	2021
Amborella gene presence/absence variation is associated with abiotic stress responses that may contribute to environmental adaptation	<i>New Phytologist</i>
H HU, A SCHEBEN, B VERPAALLEN, S TIRNAZ, PE BAYER, RGJ HODEL, J BATLEY, ...	2021
Modelling of gene loss propensity in the pangenomes of three Brassica species suggests different mechanisms between polyploids and diploids	<i>Plant Biotechnology Journal</i>
PE BAYER, A SCHEBEN, AA GOLICZ, Y YUAN, S FAURE, HT LEE, HS CHAWLA, ...	2021
Marine heatwaves have minimal influence on the quality of adult Sydney rock oyster flesh	<i>Science of The Total Environment</i>
EE EWERE, N ROSIC, PE BAYER, A NGANGBAM, D EDWARDS, BP KELAHER, ...	2021
QTL Genetic Mapping Study for Traits Affecting Meal Quality in Winter Oilseed Rape (Brassica Napus L.)	<i>Genes</i>
K GACEK, PE BAYER, R ANDERSON, AA SEVERN-ELLIS, J WOLKO, A ŁOPATYŃSKA, ...	2021
Candidate Rlm6 resistance genes against Leptosphaeria. maculans identified through a genome-wide association study in Brassica juncea (L.) Czern	<i>Theoretical and Applied Genetics</i>
H YANG, NSM SAAD, MI IBRAHIM, PE BAYER, TX NEIK, AA SEVERN-ELLIS, ...	2021
Pangenomics in crop improvement—from coding structural variations to finding regulatory variants with pangenome graphs	<i>The Plant Genome, e</i>
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
Łopatynska	<i>Seed</i>
K GACEK, PE BAYER, R ANDERSON, AA SEVERN-ELLIS, J WOLKO	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-leafed 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
Identyfikacja genetycznych podstaw procesu kielkowania w nasionach rzepaku (Brassica napus L.) z wykorzystaniem mapowania genetycznego	<i>Biuletyn Instytutu Hodowli i Aklimatyzacji Roślin</i>
K GACEK, I BARTKOWIAK-BRODA, L SZALA, T CEGIELSKA-TARAS, PE BAYER, ...	2019
Genome-wide association to explore the genetic regulation of flowering time in narrow-leafed 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-leafed lupin	<i>Theoretical and Applied Genetics</i>
M MOUSAVI-DERAZMAHALLEH, PE BAYER, B NEVADO, B HURGOBIN, D FILATOV, ...	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

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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, ...

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Improvements in genomic technologies: application to crop genomics

Y YUAN, PE BAYER, J BATLEY, D EDWARDS

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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, ...

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

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

Y YUAN, PE BAYER, HT LEE, D EDWARDS

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

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Centromere Locations in Brassica A and C Genomes Revealed Through Half-Tetrad Analysis	<i>Genetics</i>
AS MASON, M ROUSSEAU-GUEUTIN, J MORICE, PE BAYER, N BESHARAT, ...	2016
An efficient approach to BAC based assembly of complex genomes	<i>Plant Methods</i>
P VISENDI, PJ BERKMAN, S HAYASHI, AA GOLICZ, PE BAYER, P RUPERAO, ...	2016
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J BATLEY, A DOLATABADIAN, H YANG, A SEVERN-ELLIS, S ALAMERY, ...	2016
Candidate gene scan for Single Nucleotide Polymorphisms involved in the determination of normal variability in human craniofacial morphology	<i>bioRxiv</i>
M BARASH, PE BAYER, A VAN DAAL	2016
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A DOLATABADIAN, J BATLEY, D EDWARDS, MJ BARBETTI, B HURGOBIN, P BAYER	2016
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B GRESHAKE, PE BAYER, H RAUSCH, J REDA	2014
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