

Dapeng Wang

Contact information

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Education

PhD, Bioinformatics 09/2006-07/2011

Beijing Institute of Genomics, Chinese Academy of Sciences Beijing, China

- Develop approaches and a package for the measurement of sequence variations
- Devise a novel research scheme using InDels (Insertion/Deletion) data from 3 major human populations (African, European and Asian) including 179 human individuals to examine the role of natural selection on the size and GC content of minimal introns (50nt-150nt)
- Generate expressed sequence tags to identify 136 immune-related genes from head kidney tissues in Grass carp.
- Use Illumina Human Expression BeadChip to discover 5197 genes in blood and 243 genes in placenta which have altered expressions as a result of gestational diabetes mellitus (GDM).
- Use Illumina Human DNA Analysis BeadChip to investigate the difference in copy number variations (CNVs) between low-grade and high-grade gliomas from 18 patients.

B.S., Information and Computational Science 09/2002-07/2006

School of Mathematics and System Sciences, Shandong University Jinan, China

Training Certificates

Data Carpentry instructor	12/2020
Fundamentals of Deep Learning, NVIDIA Deep Learning Institute	12/2020
Software Carpentry, ARCHER2	11/2020
Data Carpentry, ARCHER2	10/2020
Metagenomics, metatranscriptomics, and multi'omics for microbial community studies, Physalia-courses	06/2020
An Introduction to Machine Learning, University of Cambridge	10/2019
Practical Software Development, ARCHER, University of Leeds	07/2019
Analysis of single cell RNA-seq data, University of Cambridge	05/2019
HPC Carpentry, ARCHER, University of Leeds	07/2018
An introduction to metabolomics and its application in life-sciences, University of Cambridge	07/2018
Analysis of DNA Methylation using Sequencing, University of Cambridge	06/2018

Professional Experience

Senior Bioinformatician in Integrative Analysis

01/2021-present

Wellcome Centre for Human Genetics, University of Oxford

Oxford, UK

- Act as a point of contact for the COVID-19 Multi-omics Blood ATlas (COMBAT) consortium
- Manage the data deposition and new user registration for COMBAT data warehouse
- Develop and maintain the COMBATdb to integrate various types of omics data with support of data visualization
- Develop and maintain the COMBAT consortium website
- Support the data integration work on multiple modalities such as bulk RNA-Seq, single-cell transcriptomics and proteomics, repertoire sequencing, SNP typing, cytometry and clinical phenotyping.

Senior Bioinformatics Research Officer

02/2018-12/2020

LeedsOmics, University of Leeds

Leeds, UK

- Lead the LeedsOmics bioinformatician team.
- Manage the LeedsOmics computing infrastructure.
- Provide multi-omics or bioinformatics data analysis support for over 30 research groups.
- Construct a series of pipelines and standard operating procedures for multi-omics data analysis.
- Obtain research grants with collaborators from MRC, BBSRC, Royal Society, BHF and Cancer Research UK.
- Organise LeedsOmics events and activities such as research seminars, annual symposiums, coding clubs and training workshops.
- Use DNA-Seq to mine SNPs in ethyl methanesulfonate (EMS)-mutagenised Arabidopsis lines which display early flowering phenotype.
- Use RNA-Seq to determine common RELA-target genes identified individually in the 3 multiple myeloma cell lines (JJN3, KMS18 and U266) from the knock-down experiment.
- Use RNA-Seq to explore the gene expression changes affected by the treatment of retinal pigment epithelium with a drug, hydroxychloroquine.
- Use proteomics to identify phosphopeptides that change in abundance in response to X-irradiation (100 Gy over 100 min) in callus cell populations of wild-type and atm-3 Arabidopsis plants.
- Use 16S rRNA gene sequencing and whole genome shotgun metagenomic sequencing to determine the effect of trehalose and glucose on the human microbiome and the effect of sugar supplementation on Clostridioides difficile growth kinetics using an in vitro gut model.
- Use the data from 10289 individuals from UK Biobank to perform the association analysis between the variants in EFCAB4B and COVID-19 status.

Postdoctoral Research Assistant

02/2016-01/2018

Department of Plant Sciences, University of Oxford

Oxford, UK

- Use RNA-Seq to conduct de-novo reference transcriptome assembly for 6 conifer species.
- Use RNA-Seq to explore the underlying gene expression networks of ABA (abscisic acid)-independent and ABA-dependent drought resistance mechanisms for 4 conifer species.
- Develop a Snakemake-based handy parameter-free pipeline for RNA-Seq analysis of numerous samples with the functionality to work with fusion genes, single nucleotide polymorphisms, messenger RNAs, long noncoding RNAs and circular RNAs.
- Construct an evolution-based database for GC content in eukaryotic genomes which houses compositional and size related data from 1118 genomes.

- Build a database for eukaryotic intron features which characterizes the intronic parameters of ~50 000 000 introns from over 1000 genomes.

Research Associate

03/2014-01/2016

UCL Cancer Institute, University College London

London, UK

- Use RNA-Seq and ChIP-Seq to identify direct targets of the ETV6/RUNX1 and examine the competition between the RUNX1 and the ETV6/RUNX1 on patients with childhood acute lymphoblastic leukaemia (ALL) as well as cell lines (REH, NALM6 and BA/F3).
- Use RNA-Seq to measure the transcriptomic similarity between hPSC- and fetal liver-derived B cell hierarchies and investigate both IL-7R progenitor and proB cell populations.

Associate Professor

01/2014-02/2014

Beijing Institute of Genomics, Chinese Academy of Sciences

Beijing, China

- Construct the evolutionary theoretical model of human minimal intron during the course of vertebrate evolution

Assistant Professor

07/2011-12/2013

Beijing Institute of Genomics, Chinese Academy of Sciences

Beijing, China

- Build an annotation database for rice comparative genomics and evolutionary biology which includes multi-omics data, user-friendly viewers and bioinformatic tools.
- Construct a K-mer based database for genome-wide phylogeny and complexity evaluation for ~8,000 genomes.
- Create 3 databases and 1 webserver to visualise the conservative and dynamic features of gene orders along the eukaryotic genomes within and across species.
- Study the evolutionary features of transposable elements (TEs) and satellite sequences (SSs) in the intronic sequences of 12 selected mammalian genomes and 4 non-mammalian vertebrate species.
- Characterize the functional networks and modules of human divergently paired genes (DPGs).

Skills

- Programming languages: R, Python, Perl
- Omics data analysis: DNA-Seq, Exome-Seq, bulk RNA-Seq, single-cell RNA-Seq, ChIP-Seq, BS-Seq, RAD-Seq, Ribo-Seq, proteomics, metabolomics
- Array data analysis: Gene expression array, SNP array
- Sample type: Patients, Cell lines, Animals, Plants, Microbes

Awards and Honors

Member, Youth Innovation Promotion Association, Chinese Academy of Sciences	2013
President Awarding, Chinese Academy of Sciences	2011
Excellent Graduate, Graduate University of Chinese Academy of Sciences	2011
Hao Bailin Scholarship, Beijing Institute of Genomics, Chinese Academy of Sciences	2011
Pivot of Merit Student, Graduate University of Chinese Academy of Sciences	2010
Zhu Li Yue Hua Doctorial Scholarship, Chinese Academy of Sciences	2010

Excellent Student Leader, Graduate University of Chinese Academy of Sciences	2010
Excellent Graduate, Shandong Province, China	2006
First prize, Shandong Province Senior High School Mathematics Contest, China	2001
Grand prize, Shandong Province Junior High School Biology Contest, China	1998

Expert Peer Reviewers for Journals

<i>BMC Evolutionary Biology</i> (2013:1)
<i>Bioinformatics</i> (2011:1, 2017:1)
<i>Bioinformatics and Biology Insights</i> (2011:1, 2012:1, 2015:3, 2016:2)
<i>Biomedical Engineering and Computational Biology</i> (2013:1, 2015:2, 2016:1)
<i>Cancer Informatics</i> (2013:1, 2014:9, 2015:2, 2018:1)
<i>Evolutionary Bioinformatics</i> (2011:6, 2012:12, 2013:10, 2014:4, 2015:1, 2016:1, 2017:2, 2018:1, 2020:1)
<i>Frontiers in Plant Science</i> (2016:2, 2017:5, 2018:5)
<i>Frontiers in Genetics</i> (2013:1, 2014:1, 2016:1, 2017:3, 2018:11)
<i>Frontiers in Microbiology</i> (2017:1)
<i>Gene Regulation and Systems Biology</i> (2016:1)
<i>GigaScience</i> (2020:2)
<i>Genomics Proteomics & Bioinformatics</i> (2014:1, 2015:1)
<i>Nucleic Acids Research</i> (2014:1)
<i>OMICS: A Journal of Integrative Biology</i> (2015:1)
<i>PLoS ONE</i> (2008:1, 2012:1, 2013:2)
<i>Reproduction</i> (2020:1)
<i>Scientific Reports</i> (2016:1)

Editorial Services

Editorial Board Member, <i>BMC Genomic Data</i>	03/2021-present
Editorial Board Member, <i>BMC Research Notes</i>	03/2021-present
Academic Editor, <i>PeerJ</i>	05/2020-present
Associate Editor, <i>Gene</i>	05/2020-present
Associate Editor, Phylogenetics, Phylogenomics, and Systematics section of <i>Frontiers in Ecology and Evolution</i>	04/2020-present
Editorial Board Member, <i>Scientific Reports</i>	01/2019-present
Editorial Board Member, <i>Evolutionary Bioinformatics</i>	12/2018-present
Associate Editor, Computational Genomics section of <i>Frontiers in Genetics</i>	11/2018-present
Editorial Board Member, <i>PLOS ONE</i>	11/2018-present
Review Editor, Evolutionary and Population Genetics section of <i>Frontiers in Genetics</i> and <i>Frontiers in Ecology and Evolution</i>	10/2013-present
Review Editor, <i>Frontiers in Bioinformatics and Computational Biology</i>	04/2013-11/2018
Editorial Board Member, <i>Biomedical Engineering and Computational Biology</i>	07/2012-09/2021

Professional Services

Member of Organising Committee for NBUG6 (Northern Bioinformatics User Group meeting 6)	24/01/2020
Member of Organizing Committee for LeedsOmics Research Symposium	13/05/2019
Member of Organizing Committee for LeedsOmics Research Symposium	21/05/2018
Member of LeedsOmics Management Board	02/2018-present

Other Services

President of Post Graduate's Union in Beijing Institute of Genomics, Chinese Academy of Sciences	2008-2010
President of Post Graduate's Union in Beijing Institutes of Life Science, Chinese Academy of Sciences	2009-2010
City Volunteer of Beijing Olympics Games	2008

Memberships

Research Member of Common Room, Kellogg College, University of Oxford	2021-present
Associate Fellow of the Higher Education Academy	2020-present
Society for Molecular Biology and Evolution	2020-present
Genetics Society	2020-present
Royal Society of Biology	2020-present
Biochemical Society	2020-present
Society of Research Software Engineering	2020-present
Northern Bioinformatics User Group (Northern BUG)	2020-present

Professional activities

Grant reviewer for UK Biotechnology and Biological Sciences Research Council
Grant reviewer for UK Medical Research Council
Grant reviewer for The National Natural Science Foundation of China
Evaluator in Phase I for Biological sciences B panel, Research Evaluation 2020: Czech Academy of Sciences

Grants

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- APEX Awards 2020 (APX\R1\201174), Primary applicant: Douglas Stewart, £78,346.06, 01/09/2020-31/05/2022
Title: Probing bio-geochemistry of alkaline waste impacted systems
Role: Co-applicant
 - AWS (Amazon Web Services) Proof of Concept Program, \$300 credit, 04/30/2020-10/31/2020
 - Cancer Research UK Clinical Careers Committee - Postdoctoral Research Bursary (C46675/A30258), Principal Investigator: Vinton Cheng, £29,386.97, 01/02/2020
Title: *Elucidating the pre-metastatic vascular niche in the brain using a pre-clinical breast cancer model*
Role: Collaborator
 - MRC Research Grant (MR/T004134/1), Principal Investigator: Lynn McKeown, £191,938, 12/2019 - 11/2021

Title: *The role of Rab46 in immune-mediated inflammatory diseases*

Role: Researcher

- BBSRC Research Grant (BB/P020488/1), Principal Investigator: John MacKay, £784,409, 01/07/2017 - 30/09/2020

Title: *Next generation Sitka spruce breeding informed by predictive and comparative genomics*

Role: Researcher

- National Natural Science Foundation of China (31301030), ¥240,000, 01/2014 –12/2016

Title: *Research on functional network and evolution of vertebrate genes with minimal introns and construction of related database*

Role: Principal Investigator

- The membership grant of CAS Youth Innovation Promotion Association, ¥400,000, 01/2013

Role: Principal Investigator

- National Natural Science Foundation of China (81000220), Principal Investigator: Fuhong He, ¥200,000, 01/2011-12/2013

Title: *The role of specific recruitment of Histone-Modifying Enzymes MLL by transcription factor AML1 in the Pathogenesis of Leukemia*

Role: Participant

- National Natural Science Foundation of China (81170033), Principal Investigator: Mingliang Gu, ¥140,000, 01/2012-12/2012

Title: *The study of asthma susceptible genes based on signal transduction network of cascade and activation of mast cells*

Role: Participant

- CAS Strategic Priority Research Programs A (Designer Breeding by Molecular Modules), Principal Investigator: Jun Yu, 01/2013-12/2017

Title: *Analyze on Pig Fat Deposition and Other High-yield Molecular Module*

Role: Participant

- Undergraduate technology innovation project grant of Shandong University, 05/2005 - 05/2006

Title: *The study on evaluation system of different groups of people*

Role: Principal Investigator

- Undergraduate technology innovation project grant of Shandong University, 05/2005 - 05/2006

Title: *The study on the investigation of university students experiencing setbacks and coping strategies*

Role: Co-Investigator

Talks

“Standardization of omics data analysis workflow”, a special full-day event for National Measurement Laboratory (NML) visit at University of Leeds 20/01/2020

“How to build the integrated bioinformatics framework”, Mini-workshop on statistical machine learning and biosciences, Beijing Institute of Genomics, Chinese Academy of Sciences 18/07/2013

Mini-Workshop, Beijing Institute of Genomics, Chinese Academy of Sciences 30/05/2012

Poster Presentations

Plant and Animal Genome XXII Conference, San Diego, USA 13/01/2014

SMBE (annual conference for the Society of Molecular Biology and Evolution), Chicago, USA	09/07/2013
RECOMB (17th Annual International Conference on Research in Computational Molecular Biology), Beijing, China	07/04/2013
ICG-8 (The 8th International Conference on Genomics), Shenzhen, China	30/10/2013

Teaching

LeedsOmics introduction to RNA-Seq data analysis workshop (18 students)	20/02/2019-21/02/2019
LeedsOmics introduction to RNA-Seq data analysis workshop (14 students)	26/06/2019-27/06/2019
LeedsOmics introduction to RNA-Seq data analysis workshop (9 students)	31/10/2019-01/11/2019
LeedsOmics R for Omics workshop (18 students)	20/02/2020-21/02/2020
LeedsOmics Coding Club	2019-2020
LeedsOmics bioinformatics support session	2018-2020

Supervision of postdocs and postgraduate students

Postdoctoral researchers at the Beijing Institute of Genomics, Chinese Academy of Sciences

Kejing Wu (2013-2014), co-supervised with Jun Yu

Ph.D. students at the Beijing Institute of Genomics, Chinese Academy of Sciences

Yao Su (2011-2012), co-supervised with Hongxing Lei and Jun Yu

Bin Xie (2012-2014), co-supervised with Hongxing Lei and Jun Yu

Yubin Zhang (2011-2013), co-supervised with Jun Yu

Jiayue Xu (2014-2016), co-supervised with Jun Yu

Master’s students at the Beijing Institute of Genomics, Chinese Academy of Sciences

Yan Xia (2011-2013), co-supervised with Jun Yu

Personal tutor for the MSc Cancer Programme at the UCL Cancer Institute, University College London

Thanabodee Yeh (2014-2015)

Laila Khazendar (2014-2015)

Staff management and supervision

Team member at the University of Leeds

Elton Rosas de Vasconcelos (02/2019-present), Bioinformatics Research Officer at LeedsOmics

Team member at the Beijing Institute of Genomics, Chinese Academy of Sciences

Lixia Hou (09/2012-02/2014), Assistant Engineer

Publications

1. RNASeq analysis of a Pax3-expressing myoblast clone *in-vitro* and effect of culture surface stiffness on differentiation. Louise Richardson, [Dapeng Wang](#), Ruth Hughes, Colin A Johnson, Michelle Peckham. bioRxiv 2021.09.05.459022; doi: <https://doi.org/10.1101/2021.09.05.459022>
2. COvid-19 Multi-omics Blood ATlas (COMBAT) Consortium. A blood atlas of COVID-19 defines hallmarks of disease severity and specificity. medRxiv 2021.05.11.21256877; doi: <https://doi.org/10.1101/2021.05.11.21256877>
3. Alysha S. Taylor, Haidee Tinning, Vladimir Ovchinnikov, William Smith, Anna L. Pullinger, Ruth A. Sutton, Bede Constantinides, [Dapeng Wang](#), Niamh Forde, Mary J O'Connell. An ancestral burst of regulatory and protein innovation drives divergent implantation in eutherian mammals. bioRxiv 2021.07.22.453388; doi: <https://doi.org/10.1101/2021.07.22.453388>
4. Buckley AM, Moura IB, Arai N, Spittal W, Clark E, Nishida Y, Harris HC, Bentley K, Davis G, [Wang D](#), Mitra S, Higashiyama T, Wilcox MH. Trehalose-Induced Remodelling of the Human Microbiota Affects Clostridioides difficile Infection Outcome in an In Vitro Colonic Model: A Pilot Study. **Front Cell Infect Microbiol.** 2021;11:670935. doi: 10.3389/fcimb.2021.670935. eCollection 2021.
5. Douka K, Birds I, [Wang D](#), Kosteleto A, Clayton S, Byford A, Vasconcelos EJR, O'Connell MJ, Deuchars J, Whitehouse A, Aspden JL. Cytoplasmic long non-coding RNAs are differentially regulated and translated during human neuronal differentiation. **RNA.** 2021 Jun 30; doi: 10.1261/rna.078782.121.
6. De Bem THC, Tinning H, Vasconcelos EJR, [Wang D](#), Forde N. Endometrium On-a-Chip Reveals Insulin- and Glucose-induced Alterations in the Transcriptome and Proteomic Secretome. **Endocrinology.** 2021 Jun 1;162(6). doi: 10.1210/endo/bqab054.
7. Wang M, [Wang D](#), Yu J, Huang S. Enrichment in conservative amino acid changes among fixed and standing missense variations in slowly evolving proteins. **PeerJ.** 2020;8:e9983. doi: 10.7717/peerj.9983. eCollection 2020.
8. Tinning H, Taylor A, [Wang D](#), Constantinides B, Sutton R, Oikonomou G, Velazquez MA, Thompson P, Treumann A, O'Connell MJ, Forde N. The role of CAPG in molecular communication between the embryo and the uterine endometrium: Is its function conserved in species with different implantation strategies?. **FASEB J.** 2020 Aug;34(8):11015-11029. doi: 10.1096/fj.202000882RR.
9. Waterworth WM, Wilson M, [Wang D](#), Nuhse T, Warward S, Selley J, West CE. Phosphoproteomic analysis reveals plant DNA damage signalling pathways with a functional role for histone H2AX phosphorylation in plant growth under genotoxic stress. **Plant J.** 2019 Dec;100(5):1007-1021. doi: 10.1111/tpj.14495.
10. [Wang D](#). IntronDB: a database for eukaryotic intron features. **Bioinformatics.** 2019 Nov 1;35(21):4400-4401. doi: 10.1093/bioinformatics/btz242.
11. [Wang D](#). hppRNA-a Snakemake-based handy parameter-free pipeline for RNA-Seq analysis of numerous samples. **Brief Bioinform.** 2018 Jul 20;19(4):622-626. doi: 10.1093/bib/bbw143.
12. [Wang D](#). GCevobase: an evolution-based database for GC content in eukaryotic genomes. **Bioinformatics.** 2018 Jun 15;34(12):2129-2131. doi: 10.1093/bioinformatics/bty068.
13. Böiers C, Richardson SE, Laycock E, Zriwil A, Turati VA, Brown J, Wray JP, [Wang D](#), James C, Herrero J, Sitnicka E, Karlsson S, Smith AJH, Jacobsen SEW, Enver T. A Human IPS Model Implicates Embryonic B-Myeloid Fate Restriction as Developmental Susceptibility to B Acute Lymphoblastic Leukemia-Associated ETV6-RUNX1. **Dev Cell.** 2018 Feb 5;44(3):362-377.e7. doi: 10.1016/j.devcel.2017.12.005.
14. Kato I, Nishinaka Y, Nakamura M, Akarca AU, Niwa A, Ozawa H, Yoshida K, Mori M, [Wang D](#), Morita M, Ueno H, Shiozawa Y, Shiraishi Y, Miyano S, Gupta R, Umeda K, Watanabe K, Koh K, Adachi S, Heike T, Saito MK, Sanada M, Ogawa S, Marafioti T, Watanabe A, Nakahata T, Enver T. Hypoxic adaptation of leukemic cells infiltrating the CNS affords a therapeutic strategy targeting VEGFA. **Blood.** 2017 Jun 8;129(23):3126-3129. doi: 10.1182/blood-2016-06-721712.
15. [Wang D](#). DLGP: A database for lineage-conserved and lineage-specific gene pairs in animal and plant genomes. **Biochem Biophys Res Commun.** 2016 Jan 15;469(3):542-5. doi: 10.1016/j.bbrc.2015.12.039.
16. [Wang D](#), Xu J, Yu J. KGCAK: a K-mer based database for genome-wide phylogeny and complexity evaluation. **Biol Direct.** 2015 Sep 16;10:53. doi: 10.1186/s13062-015-0083-4.

17. Wang D, Yu J. LCGserver: A Webserver for Exploring Evolutionary Trajectory of Gene Orders in a Large Number of Genomes. *OMICS*. 2015 Sep;19(9):574-7. doi: 10.1089/omi.2015.0060.
18. Pina C, Teles J, Fugazza C, May G, Wang D, Guo Y, Soneji S, Brown J, Edén P, Ohlsson M, Peterson C, Enver T. Single-Cell Network Analysis Identifies DDIT3 as a Nodal Lineage Regulator in Hematopoiesis. *Cell Rep*. 2015 Jun 16;11(10):1503-10. doi: 10.1016/j.celrep.2015.05.016.
19. Wang D, Yu J. Plastid-LCGbase: a collection of evolutionarily conserved plastid-associated gene pairs. *Nucleic Acids Res*. 2015 Jan;43(Database issue):D990-5. doi: 10.1093/nar/gku1070.
20. Wang L, Zhang XW, Pan LL, Liu WF, Wang DP, Zhang GY, Yin YX, Yin A, Jia SG, Yu XG, Sun GY, Hu SN, Al-Mssallem IS, Yu J. A large-scale gene discovery for the red palm weevil *Rhynchophorus ferrugineus* (Coleoptera: Curculionidae). *Insect Sci*. 2013 Dec;20(6):689-702. doi: 10.1111/j.1744-7917.2012.01561.x.
21. Xie B, Wang D, Duan Y, Yu J, Lei H. Functional networking of human divergently paired genes (DPGs). *PLoS One*. 2013;8(10):e78896. doi: 10.1371/journal.pone.0078896. eCollection 2013. (co-first author)
22. Li Y, Wang D, Wang L, Yu J, Du D, Chen Y, Gao P, Wang DM, Yu J, Zhang F, Fu S. Distinct genomic aberrations between low-grade and high-grade gliomas of Chinese patients. *PLoS One*. 2013;8(2):e57168. doi: 10.1371/journal.pone.0057168. (co-first author) (Highlighted in GenomeWeb Daily Scan)
23. Wang D, Xia Y, Li X, Hou L, Yu J. The Rice Genome Knowledgebase (RGKbase): an annotation database for rice comparative genomics and evolutionary biology. *Nucleic Acids Res*. 2013 Jan;41(Database issue):D1199-205. doi: 10.1093/nar/gks1225.
24. Wang D, Su Y, Wang X, Lei H, Yu J. Transposon-derived and satellite-derived repetitive sequences play distinct functional roles in Mammalian intron size expansion. *Evol Bioinform Online*. 2012;8:301-19. doi: 10.4137/EBO.S9758.
25. Wang D, Zhang Y, Fan Z, Liu G, Yu J. LCGbase: A Comprehensive Database for Lineage-Based Co-regulated Genes. *Evol Bioinform Online*. 2012;8:39-46. doi: 10.4137/EBO.S8540.
26. Wang D, Yu J. Both size and GC-content of minimal introns are selected in human populations. *PLoS One*. 2011 Mar 17;6(3):e17945. doi: 10.1371/journal.pone.0017945. (Highlighted in GenomeWeb Daily Scan)
27. Wang D, Liu F, Wang L, Huang S, Yu J. Nonsynonymous substitution rate (Ka) is a relatively consistent parameter for defining fast-evolving and slow-evolving protein-coding genes. *Biol Direct*. 2011 Feb 22;6:13. doi: 10.1186/1745-6150-6-13.
28. Zhao YH, Wang DP, Zhang LL, Zhang F, Wang DM, Zhang WY. Genomic expression profiles of blood and placenta reveal significant immune-related pathways and categories in Chinese women with gestational diabetes mellitus. *Diabet Med*. 2011 Feb;28(2):237-46. doi: 10.1111/j.1464-5491.2010.03140.x. (co-first author)
29. Liu F, Wang D, Fu J, Sun G, Shen Y, Dong L, Zhang B, Hu S, Li J. Identification of immune-relevant genes by expressed sequence tag analysis of head kidney from grass carp (*Ctenopharyngodon idella*). *Comp Biochem Physiol Part D Genomics Proteomics*. 2010 Jun;5(2):116-23. doi: 10.1016/j.cbd.2010.02.003. (co-first author)
30. Zhu J, He F, Wang D, Liu K, Huang D, Xiao J, Wu J, Hu S, Yu J. A novel role for minimal introns: routing mRNAs to the cytosol. *PLoS One*. 2010 Apr 12;5(4):e10144. doi: 10.1371/journal.pone.0010144.
31. Wang D, Zhang Y, Zhang Z, Zhu J, Yu J. KaKs_Calculator 2.0: a toolkit incorporating gamma-series methods and sliding window strategies. *Genomics Proteomics Bioinformatics*. 2010 Mar;8(1):77-80. doi: 10.1016/S1672-0229(10)60008-3. (Distinguished articles published in *Genomics, Proteomics & Bioinformatics* 2003–2011)
32. Wang D, Zhang S, He F, Zhu J, Hu S, Yu J. How do variable substitution rates influence Ka and Ks calculations?. *Genomics Proteomics Bioinformatics*. 2009 Sep;7(3):116-27. doi: 10.1016/S1672-0229(08)60040-6.
33. Wang DP, Wan HL, Zhang S, Yu J. Gamma-MYN: a new algorithm for estimating Ka and Ks with consideration of variable substitution rates. *Biol Direct*. 2009 Jun 16;4:20. doi: 10.1186/1745-6150-4-20.