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 3. "The rice pan-genome derived from 3,010 diverse accessions", Invited talk, Network for Food Security (Net4FS), Shanghai, China, 7/19/2019
 4. "The rice pan-genome derived from 3,010 diverse accessions", Invited talk, the 13th Annual Meeting of the International Conference on Genomics, Shenzhen, China, 10/27/2018
 5. "Widespread of Horizontal Gene Transfer in the Human Genome", Invited talk, the 1st AsiaEvo Conference, Shenzhen, China, 4/19/2018
 6. "The rice pan-genome: gene presence/absence variation derived from >3000 rice genomes", Invited talk, Net4FS, Montpellier, France, 10/16/2017
 7. "RPAN: the rice pan-genome browser", Breakthrough Highlight Oral Presentation, ISMB 2017, Prague, Czech Republic, 7/24/2017
 8. "The rice pan-genome: gene presence/absence variation derived from >3000 rice genomes", Oral Presentation, the 15th Japan-Korea-China Bioinformatics Symposium, Seoul, Korea, 6/21/2017
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 11. "EUPAN: a large-scale pan-genome analysis pipeline for eukaryotic large genomes", Dublin, Ireland, 7/12/2015-7/14/2015
 12. "MOST+: A motif finding approach combining genomic sequence and heterogeneous genome-wide signatures", Poster, ISMB2013, Berlin, German, 7/23/2013

13. "Finding functional elements in genomes with statistical models", Lecture, the 11th Japan-Korea-China Bioinformatics Training Course, Suzhou, 6/18/2013
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16. "Regulatory element finding by integrating the genomic sequence and epigenetic information", Invited talk, International IRSES meeting, Shanghai, China, 9/10/2012
17. "Using GPUs to accelerate metagenomic sequence classification", Invited talk, ICB, Xi'an, China, 8/19/2012
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1.		ZL200910049555.4
2.	"	ZL201110125025.0
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30.	NeSSM	2010SR029333
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| 4 | RECOMB 2013 | 2012.10-2013.4 |
| 5 | ICIBM | 2014, 2015, 2016, 2018 |
| 6 | Genome Biology Bioinformatics | BMC Bioinformatics |
| 7 | ABI | 2010-2012 |
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| 9 | | 2009, 2010, 2011, 2013 |
| 10 | EMBO | 8/16-22/2009 |
| 11 | “Analysis of complex Biological Systems”, | 8/19/2009 |
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