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www.bgitechsolutions.com www.bgiamericas.com info@bgitechsolutions.com
+86-(0)755-25273045

Effort of using whole genome sequencing to identify whole spectrum of *de novo* and rare inherited mutation in autism families

Venue: Harvard Medical School's New Research Building, Room 350, 77 Avenue Louis Pasteur, Boston.
Date: Monday, November 25, 2013, noon to 1:30 p.m

Speaker:

Xin JIN, Senior Research Scientist at BGI

Background for the speakers:

Xin Jin joined BGI in 2009. He has involved and been leading several important scientific research projects, including the Sino-Danish Diabetes Project (LUCAMP), building the human pan-genome project, high altitude adaptation project and Autism Genome 10K project. Now Xin is senior research scientist at BGI. He and his team mainly focus on sequencing based researches including complex disease, mendelian disorder and population genetics.

Selected Publication:

1. Yi X, Liang Y, Huerta-Sanchez E, #Jin X, … , et al. *Sequencing of 50 Human Exomes Reveals Adaptation to High Altitude.* ***Science*** (2010) vol. 329 (5987) pp. 75-78
2. #Jin X, He M, et al. *An effort to use human-based exome capture methods to analyze chimpanzee and macaque exomes.* ***PLoS ONE*** (2012) vol. 7 (7) pp. e40637
3. Michaelson J, Shi Y, Gujral M, Zheng H, Malhotra D, #Jin X, … , et al. *Whole-Genome Sequencing in Autism Identifies Hot Spots for De Novo Germline Mutation.* ***Cell*** (2012) vol. 151 (7) pp. 1431-1442
4. Jiang Y, Yuen RKC, #Jin X, M Wang, … , et al. *Detection of clinically relevant genetic variants in autism spectrum disorder by whole-genome sequencing.* ***AJHG*** (2013) 93 (2), 249-263

Local contact of BGI
Peter Russo
Business Development Manager
Peter.russo@bgiamericas.com
617-842-9625