

Curriculum Vitae

Hong Sain OOI

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Date of birth: 28 September 1974

Education

Degree of Master of Science (M.Sc.) in Bioinformatics – 2004
National University of Singapore, Singapore

Degree of Bachelor of Science (B.Sc.) – 2000
University of Malaya, Kuala Lumpur, Malaysia
Major: Computational and Industrial Mathematics

Experiences

- Teaching Assistant, Institute of Mathematical Studies, University of Malaya, 2000 – 2002.
- Bioinformatics Specialist, Genome Institute of Singapore, Jan 2005 ~ March 2007
- Senior Bioinformatics Specialist, Genome Institute of Singapore, April 2007 ~ September 2007
- Research Associate, Bioinformatics Institute, October 2007 ~ March 2009
- Senior Research Associate, Bioinformatics Institute, April 2009 ~ March 2010
- Senior Research Officer, Bioinformatics Institute, April 2010 ~ August 2012
- Bioinformatics Consultant, September 2012 ~ September 2013
- Research Assistant, Department of Biomedicine, Aarhus University, Nov 2013 ~ March 2018
- Bioinformatics Consultant, ~ present

Computing Skills

- Various programming languages – mainly Python and Julia. I have used C, Java, Javascript, Perl in past projects and can pick up new tools quickly.
- Databases – moving toward NoSQL databases. I have used MySQL and PostgreSQL in previous projects.
- Others – Version Control System and bioinformatics tools.

Publications

- Genomic analyses of unique carbohydrate and phytohormone metabolism in the macroalga *Gracilariopsis lemaneiformis* (Rhodophyta). Sun X, Wu J, Wang G, Kang Y, **Ooi HS**, Shen T, Wang F, Yang R, Xu N, Zhao X. *BMC Plant Biol.* 2018 May 25;18(1):94. PMID: 29801464.
- Identification of the BRD1 interaction network and its impact on mental disorder risk. Fryland T, Christensen JH, Pallesen J, Mattheisen M, Palmfeldt J, Bak M, Grove J, Demontis D, Blechinger J, **Ooi HS**, Nyegaard M, Hauberg ME, Tommerup N, Gregersen N, Mors O, Corydon TJ, Nielsen AL, Børgeglum AD. *Genome Med.* 2016;8(1):53. PMID: 27142060.
- MALAT1 long ncRNA promotes gastric cancer metastasis by suppressing PCDH10. Qi Y, **Ooi HS**, Wu J, Chen J, Zhang X, Tan S, Yu Q, Li YY, Kang Y, Li H, Xiong Z, Zhu T, Liu B, Shao Z, Zhao X. *Oncotarget.* 2016;7(11):12693-703. PMID: 26871474.
- Genome-wide profiling of polyadenylation sites reveals a link between selective polyadenylation and cancer metastasis. Lai DP, Tan S, Kang YN, Wu J, **Ooi HS**, Chen J, Shen TT, Qi Y, Zhang X, Guo Y, Zhu T, Liu B, Shao Z, Zhao X. *Hum Mol Genet.* 2015;24(12):3410-7. PMID: 25759468.
- Genome-wide profiling of untranslated regions by paired-end ditag sequencing reveals unexpected transcriptome complexity in yeast. Kang YN, Lai DP, **Ooi HS**, Shen TT, Kou Y, Tian J, Czajkowsky DM, Shao Z, Zhao X. *Mol Genet Genomics.* 2015;290(1):217-24. PMID: 25213602.
- Parameterization of disorder predictors for large-scale applications requiring high specificity by using an extended benchmark dataset. Sirota FL, **Ooi HS**, Gattermayer T, Schneider G, Eisenhaber F, Maurer-Stroh S. *BMC Genomics.* 2010 Feb 10;11 Suppl 1:S15. PMID: 20158872
- ChIA-PET tool for comprehensive chromatin interaction analysis with paired-end tag sequencing. Li G, Fullwood MJ, Xu H, Mulawadi FH, Velkov S, Vega V, Ariyaratne PN, Mohamed YB, **Ooi HS**, Tennakoon C, Wei CL, Ruan Y, Sung WK. *Genome Biol.* 2010;11(2):R22. PMID: 20181287
- An oestrogen-receptor-alpha-bound human chromatin interactome. Fullwood MJ, Liu MH, Pan YF, Liu J, Xu H, Mohamed YB, Orlov YL, Velkov S, Ho A, Mei PH, Chew EG, Huang PY, Welboren WJ, Han Y, **Ooi HS**, Ariyaratne PN, Vega VB, Luo Y, Tan PY, Choy PY, Wansa KD, Zhao B, Lim KS, Leow SC, Yow JS, Joseph R, Li H, Desai KV, Thomsen JS, Lee YK, Karuturi RK, Herve T, Bourque G, Stunnenberg HG, Ruan X, Cacheux-Rataboul V, Sung WK, Liu ET, Wei CL, Cheung E, Ruan Y. *Nature.* 2009 Nov 5;462(7269):58-64. PMID: 19890323
- ANNIE: integrated de novo protein sequence annotation. **Ooi HS**, Kwo CY, Wildpaner M, Sirota FL, Eisenhaber B, Maurer-Stroh S, Wong WC, Schleiffer A, Eisenhaber F, Schneider G. *Nucleic Acids Res.* 2009 Jul 1;37(Web Server issue):W435-40. PMID: 19389726

- Identification and analysis of functional elements in 1% of the human genome by the ENCODE pilot project. ENCODE Project Consortium, Nature. 2007 Jun 14;447(7146):799-816. PMID: 17571346
- Fusion transcripts and transcribed retrotransposed loci discovered through comprehensive transcriptome analysis using Paired-End diTags (PETs). Ruan Y, *Ooi HS*, Choo SW, Chiu KP, Zhao XD, Srinivasan KG, Yao F, Choo CY, Liu J, Ariyaratne P, Bin WG, Kuznetsov VA, Shahab A, Sung WK, Bourque G, Palanisamy N, Wei CL. Genome Res. 2007 Jun;17(6):828-38. PMID: 17568001
- Global mapping of c-Myc binding sites and target gene networks in human B cells. Zeller KI, Zhao X, Lee CW, Chiu KP, Yao F, Yustein JT, *Ooi HS*, Orlov YL, Shahab A, Yong HC, Fu Y, Weng Z, Kuznetsov VA, Sung WK, Ruan Y, Dang CV, Wei CL. Proc Natl Acad Sci U S A. 2006 Nov 21;103(47):17834-9. PMID: 17093053
- PET-Tool: a software suite for comprehensive processing and managing of Paired-End diTag (PET) sequence data. Chiu KP, Wong CH, Chen Q, Ariyaratne P, *Ooi HS*, Wei CL, Sung WK, Ruan Y. BMC Bioinformatics. 2006 Aug 25;7:390. PMID: 16934139
- Multiplex sequencing of paired-end ditags (MS-PET): a strategy for the ultra-high-throughput analysis of transcriptomes and genomes. Ng P, Tan JJ, *Ooi HS*, Lee YL, Chiu KP, Fullwood MJ, Srinivasan KG, Perbost C, Du L, Sung WK, Wei CL, Ruan Y. Nucleic Acids Res. 2006 Jul 13;34(12):e84. PMID: 16840528

Book Chapters:

- Transcript profiling analysis through Paired-End Ditag (PET) approach coupled with deep sequencing reveals transcriptome complexity in yeast. Kang Y, *Ooi HS*, Xhao X. Methods Mol Biol. 2019; 2049:105-112. Article. PMID 31602607
- Databases of protein-protein interactions and complexes. *Ooi HS*, Schneider G, Chan YL, Lim TT, Eisenhaber B, Eisenhaber F. Methods Mol Biol. 2010;609:145-59. Review. PMID: 20221918
- Biomolecular pathway databases. *Ooi HS*, Schneider G, Lim TT, Chan YL, Eisenhaber B, Eisenhaber F. Methods Mol Biol. 2010;609:129-44. Review. PMID: 20221917

Posters:

- A framework for the construction of information maps. *Ooi HS*, Grove J, Schierup MH, Mors O, Børglum AD, Mattheisen M. American Society of Human Genetics Annual Meeting, Vancouver, Canada, 2016.
- A framework to evaluate the quality of protein interaction network. *Ooi HS*, Grove J, Schierup MH, Mors O, Børglum AD, Mattheisen M. World Congress of Psychiatric Genetics, Copenhagen, Denmark, 2014.