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## Associate Professor (With Tenure)

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## EDUCATION:

- Ph.D., Pharmacology (minor in Bioinformatics), University of Minnesota, Minneapolis, USA (2002)
- Master of Medicine, Jiamusi Medical College, China (1989)

## Research interest:

1. Association studies of complex diseases, especially autoimmune diseases
2. Genetic studies of Mendelian disorders using next generation sequencing (NGS) tools
3. Comprehensive and integrative analyses of various types of omics data and databases to understand the disturbances of signal transduction pathways and interaction networks underlying human diseases

## RESEARCH AND TEACHING EXPERIENCE:

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| July 2014 – Present | Associate Professor, Department of Paediatrics and Adolescent Medicine, The University of Hong Kong |
| Sep. 2008 – June 2014 | Assistant ProfessorDepartment of Paediatrics and Adolescent Medicine, The University of Hong Kong |
| Jan. 2006 – Aug. 2008 | Research Assistant Professor and Honorary Assistant Professor Department of Paediatrics and Adolescent Medicine, The University of Hong Kong |
| Jul. 2002 – Jan. 2006 | Postdoctoral Research Fellow (with John D. Hildebrandt) Department of Pharmacology, Medical University of South Carolina, Charleston, South Carolina, USA |
| May 1995 – Jan. 1997 | WHO Fellow in Neurobiology Department of Pharmacology, University of Minnesota, Minneapolis, Minnesota, USA |
| Jul. 1989 – Apr. 1995 | Lecturer, Jiamusi Medical College, China |

## PUBLICATIONS:

**Book chapter:**

**Yang W**, and Hildebrandt, J.D. (2013) Gq Family. In: Lennarz, W.J. and Lane, M.D. (eds.) The Encyclopedia of Biological Chemistry, Vol. 2, pp. 496-500. Waltham, MA: Academic Press, invited and editor-reviewed.

**Journal publications: (from Pubmed:** http://paed.hku.hk/genome)
(*: Corresponding or co-corresponding author. #: Equal contribution/co-first author.)

1. Yeung KS, Chung BH, Choufani S, Mok MY, Wong WL, Mak CC, **Yang W**, Lee PP, Wong WH, Chen YA, Grafodatskaya D, Wong RW, Lau CS, Chan DT, Weksberg R, Lau YL.Genome-Wide DNA Methylation Analysis of Chinese Patients with Systemic Lupus Erythematosus Identified Hypomethylation in Genes Related to the Type I Interferon Pathway. **PLoS One.** 2017 Jan 13;12(1):e0169553.

2. Zhou XJ, Nath SK, Qi YY, Sun C, Hou P, Zhang YM, Lv JC, Shi SF, Liu LJ, Chen R, **Yang W**, He KZ, Li Y, Zhang H. Novel identified associations of RGS1 and RASGRP1 variants in IgA Nephropathy. **Sci Rep.** 2016 Nov 2;6:35781.

3. Kwok J, Guo M, **Yang W**, Lee CK, Ho J, Tang WH, Chan YS, Middleton D, Lu LW, Chan GC. HLA-A, -B, -C, and -DRB1 genotyping and haplotype frequencies for a Hong Kong Chinese population of 7595 individuals. **Hum Immunol**. 2016 Dec;77(12):1111-1112.

4. Kwok J, Guo M, **Yang W**, Lee CK, Chan NK, Ho J, Tang WH, Chan YS, Middleton D, Lu LW, Chan GC. HLA-A, -B and -DRB1 genotyping and haplotype frequencies of 3892 cord blood units in the Hong Kong Chinese Cord Blood Registry. **Hum Immunol**. 2016 Dec;77(12):1109-1110.

5. Chen R, Lau YL, Zhang Y, **Yang W**. SRinversion: a tool for detecting short inversions by splitting and re-aligning poorly mapped and unmapped sequencing reads. **Bioinformatics.** 2016 Dec 1;32(23):3559-3565.

6. Zhang F, Wu L, Qian J, Qu B, Xia S, La T, Wu Y, Ma J, Zeng J, Guo Q, Cui Y, **Yang W**, Huang J, Zhu W, Yao Y, Shen N, Tang Y. Identification of the long noncoding RNA NEAT1 as a novel inflammatory regulator acting through MAPK pathway in human lupus**. J Autoimmun**. 2016 Dec;75:96-104.

7. Jiang S, Tang L, Zhao N, **Yang W**, Qiu Y, Chen HZ. A Systems View of the Differences between APOE ε4 Carriers and Non-carriers in Alzheimer's Disease. **Front Aging Neurosci**. 2016 Jul 12;8:171.

8. #Morris, D.L., #Sheng, Y., #Zhang, Y., #Wang, Y.F., #Zhu, Z., #Tombleson, P., Chen, L., Graham D.S.C., Bentham, J., Chen, R., Zuo, X., Wen, L., Yang, C., Liu, L., Yang, L., Li, F., Huang, Y., Yang, S., Rönnblom, L., Fürnrohr, B.G., Voll, R.E., Schett, G., Costedoat–Chalumeau, N., Gaffney P.M., Lau, Y.L., Zhang, X., **#Yang, W.**, #Cui, Y., & #Vyse, T.J. Meta-analysis of Chinese and European GWAS identifies 10 novel SLE associated loci and provides evidence for increased genetic risk of disease in Chinese. **Nature Genetics** (in press 2016) (co-corresponding author)

9. Chiu YT, Wong JK, Choi SW, Sze KM, Ho DW, Chan LK, Lee JM, Man K, Cherny S, **Yang W**, Wong CM, Sham PC, Ng IO. Novel pre-mRNA splicing of intronically integrated HBV generates oncogenic chimera in hepatocellular carcinoma. **J Hepatol.** 2016 Feb 8. pii: S0168-8278(16)00084-2. doi: 10.1016/j.jhep.2016.02.005.

10. Leng RX, Pan HF, Liu J, Yang XK, Zhang C, Tao SS, Wang DG, Li XM, Li XP, **Yang W**, Ye DQ. Evidence for genetic association of TBX21 and IFNG with systemic lupus erythematosus in a Chinese Han population. **Sci Rep.** 2016 Feb 26;6:22081.

11. Zhu Z, Liang Z, Liany H, Yang C, Wen L, Lin Z, Sheng Y, Lin Y, Ye L, Cheng Y, Chang Y, Liu L, Yang L, Shi Y, Shen C, Zhou F, Zheng X, Zhu J, Liang B, Ding Y, Zhou Y, Yin X, Tang H, Zuo X, Sun L, Bei JX, Liu J, Yang S, *__Yang W__, *Cui Y, *Zhang
X. Discovery of a novel genetic susceptibility locus on X chromosome for systemic lupus erythematosus. **Arthritis Res Ther.** 2015 Dec 3;17:349.

12. Jing Zhang, Lu Zhang, Yan Zhang, Jing Yang, Mengbiao Guo, Liangdan Sun, Hai-Feng Pan, Nattiya Hirankarn, Dingge Ying, Shuai Zeng, Tsz Leung Lee, Chak Sing Lau, Tak Mao Chan, Alexander Moon Ho Leung, Chi Chiu Mok, Sik Nin Wong, Ka Wing Lee, Marco Hok Kung Ho, Pamela Pui Wah Lee, Brian Hon-Yin Chung, Chun Yin Chong, Raymond Woon Sing Wong, Mo Yin Mok, Wilfred Hing Sang Wong, Kwok Lung Tong, Niko Kei Chiu Tse, Xiang-Pei Li, Yingyos Avihingsanon, Pornpimol Rianthavorn, Thavatchai Deekajorndej, Kanya Suphapeetiporn, Vorasuk Shotelersuk, Shirley King Yee Ying, Samuel Ka Shun Fung, Wai Ming Lai, Maria-Mercè Garcia-Barceló, Stacey S. Cherny, Pak Chung Sham, Yong Cui, Sen Yang, Dong Qing Ye, Xue-Jun Zhang, *Yu Lung Lau, ***Yang W**, Gene-based meta-analysis of GWAS data identifies independent SNPs in ANXA6 as associated with SLE in Asian populations, **Arthritis Rheumatol**. 2015 Nov;67(11):2966-77. doi: 10.1002/art.39275.

13. Tam RC, Lee AL, **Yang W**, Lau CS, Chan VS. Systemic Lupus Erythematosus Patients Exhibit Reduced Expression of CLEC16A Isoforms in Peripheral Leukocytes. Int J Mol Sci. 2015 Jun 25;16(7):14428-40. doi: 10.3390/ijms160714428. PubMed PMID: 26121298.

14. Ying D, Sham PC, Smith DK, Zhang L, Lau YL, *__Yang W__. HaploShare: identification of extended haplotypes shared by cases and evaluation against controls. Genome Biol. 2015 May 9;16:92. doi: 10.1186/s13059-015-0662-9. PubMed PMID: 25956955; PubMed Central PMCID: PMC4432975.

15. Huang Y, Yang J, Ying D, Zhang Y, Shotelersuk V, Hirankarn N, Sham PC, Lau YL, *__Yang W__. HLAreporter: a tool for HLA typing from next generation sequencing data. Genome Med. 2015 Mar 16;7(1):25. doi: 10.1186/s13073-015-0145-3. eCollection 2015. PubMed PMID: 25908942; PubMed Central PMCID: PMC4407542.

16. Zhang Y, Wang Y, Yang J, Zhang J, Sun L, Hirankarn N, Pan HF, Lau CS, Chan TM, Lee TL, Leung AM, Mok CC, Zhang L, Shen JJ, Wong SN, Lee KW, Ho MH, Lee PP, Chung BH, Chong CY, Wong RW, Mok MY, Wong WH, Tong KL, Tse NK, Li XP,

Avihingsanon Y, Rianthavorn P, Deekajorndej T, Suphapeetiporn K, Shotelersuk V, Ying SK, Fung SK, Lai WM, Wong CM, Ng IO, Garcia-Barcelo MM, Cherny SS, Tam PK, Sham PC, Yang S, Ye DQ, Cui Y, Zhang XJ, **Yang W**, Lau YL. Meta-analysis of two Chinese populations identifies an autoimmune disease risk allele in 22q11.21 as associated with systemic lupus erythematosus. Arthritis Res Ther. 2015 Mar 20;17(1):67. [Epub ahead of print] PubMed PMID: 25880549; PubMed Central PMCID: PMC4404227.

17. Zhang Y, Yang J, Zhang J, Sun L, Hirankarn N, Pan HF, Lau CS, Chan TM, Lee TL, Leung AM, Mok CC, Zhang L, Wang Y, Shen JJ, Wong SN, Lee KW, Ho MH, Lee PP, Chung BH, Chong CY, Wong RW, Mok MY, Wong WH, Tong KL, Tse NK, Li XP, Avihingsanon Y, Rianthavorn P, Deekajorndej T, Suphapeetiporn K, Shotelersuk V, Ying SK, Fung SK, Lai WM, Wong CM, Ng IO, Garcia-Barcelo MM, Cherny SS, Cui Y, Sham PC, Yang S, Ye DQ, Zhang XJ, Lau YL, *__Yang W__. Genome-wide search followed by replication reveals genetic interaction of CD80 and ALOX5AP associated with systemic lupus erythematosus in Asian populations. Ann Rheum Dis. 2015 Apr 10. pii: annrheumdis-2014-206367. doi: 10.1136/annrheumdis-2014-206367. [Epub ahead of print] PubMed PMID: 25862617.

18. Tu X, Chong WP, Zhai Y, Zhang H, Zhang F, Wang S, Liu W, Wei M, Siu NH, Yang H, **Yang W**, Cao W, Lau YL, He F, Zhou G. Functional polymorphisms of the CCL2 and MBL genes cumulatively increase susceptibility to severe acute respiratory syndrome coronavirus infection. J Infect. 2015 Jul;71(1):101-9. doi: 10.1016/j.jinf.2015.03.006. Epub 2015 Mar 27. PubMed PMID: 25818534.

19. Jiang S, **Yang W**, Qiu Y, Chen HZ; Alzheimer's Disease Neuroimaging Initiative (ADNI). Identification of novel quantitative traits-associated susceptibility loci for APOE ε 4 non-carriers of Alzheimer's disease. Curr Alzheimer Res. 2015;12(3):218-27. PubMed PMID: 25731621.

20. Li MJ, Deng J, Wang P, **Yang W**, Ho SL, Sham PC, Wang J, Li M. wKGGSeq: A Comprehensive Strategy-Based and Disease-Targeted Online Framework to Facilitate Exome Sequencing Studies of Inherited Disorders. Hum Mutat. 2015 May;36(5):496-503. doi: 10.1002/humu.22766. Epub 2015 Apr 4. PubMed PMID: 25676918.

21. **Yang W**, Lee PP, Thong MK, Ramanujam TM, Shanmugam A, Koh MT, Chan KW, Ying D, Wang Y, Shen JJ, Yang J, Lau YL. Compound heterozygous mutations in TTC7A cause familial multiple intestinal atresias and severe combined immunodeficiency. Clin Genet. 2014 Dec 23. doi: 10.1111/cge.12553. [Epub ahead of print] PubMed PMID: 25534311.

22. Tao VQ, Chan KY, Chu YW, Mok GT, Tan TY, **Yang W**, Lee SL, Tang WF, Tso WW, Lau ET, Kan AS, Tang MH, Lau YL, Chung BH. The clinical impact of chromosomal microarray on paediatric care in Hong Kong. PLoS One. 2014 Oct 15;9(10):e109629.

doi: 10.1371/journal.pone.0109629. eCollection 2014. PubMed PMID: 25333781; PubMed Central PMCID: PMC4198120.

23. **Yang W**, Lau YL. Solving the genetic puzzle of systemic lupus erythematosus. Pediatr Nephrol. 2014 Sep 20. [Epub ahead of print] PubMed PMID: 25239301.

24. Zhang Y, Zhang J, Yang J, Wang Y, Zhang L, Zuo X, Sun L, Pan HF, Hirankarn N, Wang T, Chen R, Ying D, Zeng S, Shen JJ, Lee TL, Lau CS, Chan TM, Leung AM, Mok CC, Wong SN, Lee KW, Ho MH, Lee PP, Chung BH, Chong CY, Wong RW, Mok MY, Wong WH, Tong KL, Tse NK, Li XP, Avihingsanon Y, Rianthavorn P, Deekajorndej T, Suphapeetiporn K, Shotelersuk V, Ying SK, Fung SK, Lai WM, Wong CM, Ng IO, Garcia-Barcelo MM, Cherny SS, Tam PK, Sham PC, Yang S, Ye DQ, Cui Y, Zhang XJ, Lau YL, *__Yang W__. Meta-analysis of GWAS on two Chinese populations followed by replication identifies novel genetic variants on the X chromosome associated with systemic lupus erythematosus. Hum Mol Genet. 2015 Jan 1;24(1):274-84. doi: 10.1093/hmg/ddu429. Epub 2014 Aug 22. PubMed PMID: 25149475.

25. International League Against Epilepsy Consortium on Complex Epilepsies. Electronic address: epilepsy-austin@unimelb.edu.au. Genetic determinants of common epilepsies: a meta-analysis of genome-wide association studies. Lancet Neurol. 2014 Sep;13(9):893-903. doi: 10.1016/S1474-4422(14)70171-1. Epub 2014 Jul 30. PubMed PMID: 25087078; PubMed Central PMCID: PMC4189926.

26. Zhou XJ, Nath SK, Qi YY, Cheng FJ, Yang HZ, Zhang Y, **Yang W**, Ma JY, Zhao MH, Shen N, Zhang H. Brief Report: identification of MTMR3 as a novel susceptibility gene for lupus nephritis in northern Han Chinese by shared-gene analysis with IgA nephropathy. Arthritis Rheumatol. 2014 Oct;66(10):2842-8. doi: 10.1002/art.38749. PubMed PMID: 24943867; PubMed Central PMCID: PMC4180767.

27. Zeng S, Yang J, Chung BH, Lau YL, *__Yang W__. EFIN: predicting the functional impact of nonsynonymous single nucleotide polymorphisms in human genome. BMC Genomics. 2014 Jun 10;15:455. doi: 10.1186/1471-2164-15-455. PubMed PMID: 24916671; PubMed Central PMCID: PMC4061446.

28. Lee PP, Mao H, **Yang W**, Chan KW, Ho MH, Lee TL, Chan JF, Woo PC, Tu W, Lau YL. Penicillium marneffei infection and impaired IFN-γ immunity in humans with autosomal-dominant gain-of-phosphorylation STAT1 mutations. J Allergy Clin Immunol. 2014 Mar;133(3):894-6.e5. doi: 10.1016/j.jaci.2013.08.051. Epub 2013 Nov PubMed PMID: 24188975.

29. Zhang J, Zhang Y, Yang J, Zhang L, Sun L, Pan HF, Hirankarn N, Ying D, Zeng S, Lee TL, Lau CS, Chan TM, Leung AM, Mok CC, Wong SN, Lee KW, Ho MH, Lee PP, Chung BH, Chong CY, Wong RW, Mok MY, Wong WH, Tong KL, Tse NK, Li XP, Avihingsanon Y, Rianthavorn P, Deekajorndej T, Suphapeetiporn K, Shotelersuk V, Ying SK, Fung SK, Lai WM, Garcia-Barceló MM, Cherny SS, Tam PK, Cui Y, Sham PC,

Yang S, Ye DQ, Zhang XJ, Lau YL, *__Yang W__. Three SNPs in chromosome 11q23.3 are independently associated with systemic lupus erythematosus in Asians. Hum Mol Genet. 2014 Jan 15;23(2):524-33. doi: 10.1093/hmg/ddt424. Epub 2013 Sep 2. PubMed PMID: 24001599.

30. Zhang J, Zhang Y, Zhang L, Yang J, Ying D, Zeng S, Lee TL, Lau CS, Chan TM, Leung AM, Mok CC, Wong SN, Lee KW, Ho MH, Lee PP, Chung BH, Chong CY, Wong RW, Mok MY, Wong WH, Lau YL, *__Yang W__. Epistatic interaction between genetic variants in susceptibility gene ETS1 correlates with IL-17 levels in SLE patients. Ann Hum Genet. 2013 Jul;77(4):344-50. doi: 10.1111/ahg.12018. Epub 2013 Apr 24. PubMed PMID: 23614478.

31. Li MX, Kwan JS, Bao SY, __Yang W__, Ho SL, Song YQ, Sham PC. Predicting mendelian disease-causing non-synonymous single nucleotide variants in exome sequencing studies. PLoS Genet. 2013;9(1):e1003143. doi: 10.1371/journal.pgen.1003143. Epub 2013 Jan 17. PubMed PMID: 23341771; PubMed Central PMCID: PMC3547823.

32. __Yang W__, Tang H, Zhang Y, Tang X, Zhang J, Sun L, Yang J, Cui Y, Zhang L, Hirankarn N, Cheng H, Pan HF, Gao J, Lee TL, Sheng Y, Lau CS, Li Y, Chan TM, Yin X, Ying D, Lu Q, Leung AM, Zuo X, Chen X, Tong KL, Zhou F, Diao Q, Tse NK, Xie H, Mok CC, Hao F, Wong SN, Shi B, Lee KW, Hui Y, Ho MH, Liang B, Lee PP, Cui H, Guo Q, Chung BH, Pu X, Liu Q, Zhang X, Zhang C, Chong CY, Fang H, Wong RW, Sun Y, Mok MY, Li XP, Avihingsanon Y, Zhai Z, Rianthavorn P, Deekajorndej T, Suphapeetiporn K, Gao F, Shotelersuk V, Kang X, Ying SK, Zhang L, Wong WH, Zhu D, Fung SK, Zeng F, Lai WM, Wong CM, Ng IO, Garcia-Barceló MM, Cherny SS, Shen N, Tam PK, Sham PC, Ye DQ, Yang S, Zhang X, Lau YL. Meta-analysis followed by replication identifies loci in or near CDKN1B, TET3, CD80, DRAM1, and ARID5B as associated with systemic lupus erythematosus in Asians. Am J Hum Genet. 2013 Jan 10;92(1):41-51. doi:10.1016/j.ajhg.2012.11.018. Epub 2012 Dec 27. PubMed PMID: 23273568; PubMed Central PMCID: PMC3542470.

33. Kaiser R, Taylor KE, Deng Y, Zhao J, Li Y, Nititham J, Chang M, Catanese J, Begovich AB, Brown EE, Edberg JC, McGwin G, Alarcón GS, Ramsey-Goldman R, Reveille JD, Vila LM, Petri M, Kimberly RP, Feng X, Sun L, Shen N, Li W, Lu JX, Wakeland EK, Li QZ, __Yang W__, Lau YL, Liu FL, Chang DM, Yu CY, Song YW, Tsao BP,Criswell LA; Hwee Siew Howe and the Tan Tock Seng Hospital Systemic Lupus Erythematosus Study Group. Brief Report: Single-nucleotide polymorphisms in VKORC1 are risk factors for systemic lupus erythematosus in Asians. Arthritis Rheum. 2013 Jan;65(1):211-5. doi: 10.1002/art.37751. PubMed PMID: 23124848; PubMed Central PMCID: PMC3670944.

34. Wong EH, Cui L, Ng CL, Tang CS, Liu XL, So MT, Yip BH, Cheng G, Zhang R, Tang WK, __Yang W__, Lau YL, Baum L, Kwan P, Sun LD, Zuo XB, Ren YQ, Yin XY, Miao XP, Liu J, Lui VC, Ngan ES, Yuan ZW, Zhang SW, Xia J, Wang H, Sun XB, Wang R, Chang T,Chan IH, Chung PH, Zhang XJ, Wong KK, Cherny SS, Sham PC, Tam PK, Garcia-Barcelo MM. Genome-wide copy number variation study in anorectal

malformations. Hum Mol Genet. 2013 Feb 1;22(3):621-31. doi: 10.1093/hmg/dds451. Epub 2012 Oct 29. PubMed PMID: 23108157.

35. Zhang L, Zhang J, Yang J, Ying D, Lau YL, *__Yang W__. PriVar: a toolkit for prioritizing SNVs and indels from next-generation sequencing data. Bioinformatics. 2013 Jan 1;29(1):124-5. doi: 10.1093/bioinformatics/bts627. Epub 2012 Oct 25. PubMed PMID: 23104884.

36. Li PH, Wong WH, Lee TL, Lau CS, Chan TM, Leung AM, Tong KL, Tse NK, Mok CC, Wong SN, Lee KW, Ho MH, Lee PP, Chong CY, Wong RW, Mok MY, Ying SK, Fung SK, Lai WM, __Yang W__, Lau YL. Relationship between autoantibody clustering and clinical subsets in SLE: cluster and association analyses in Hong Kong Chinese. Rheumatology (Oxford). 2013 Feb;52(2):337-45. doi: 10.1093/rheumatology/kes261. Epub 2012 Oct 4. PubMed PMID: 23038697.

37. Zhao H, __Yang W__, Qiu R, Li J, Xin Q, Wang X, Feng Y, Shan S, Liu Y, Gong Y, Liu Q. An intronic variant associated with systemic lupus erythematosus changes the binding affinity of Yinyang1 to downregulate WDFY4. Genes Immun. 2012 Oct;13(7):536-42. doi: 10.1038/gene.2012.33. Epub 2012 Sep 13. PubMed PMID: 22972472.

38. Mao H, #__Yang W__, Lee PP, Ho MH, Yang J, Zeng S, Chong CY, Lee TL, Tu W, Lau YL. Exome sequencing identifies novel compound heterozygous mutations of IL-10 receptor 1 in neonatal-onset Crohn's disease. Genes Immun. 2012 Jul;13(5):437-42. doi: 10.1038/gene.2012.8. Epub 2012 Apr 5. PubMed PMID: 22476154.

39. Guo Y, Baum LW, Sham PC, Wong V, Ng PW, Lui CH, Sin NC, Tsoi TH, Tang CS, Kwan JS, Yip BH, Xiao SM, Thomas GN, Lau YL, __Yang W__, Cherny SS, Kwan P. Two-stage genome-wide association study identifies variants in CAMSAP1L1 as susceptibility loci for epilepsy in Chinese. Hum Mol Genet. 2012 Mar 1;21(5):1184-9. doi: 10.1093/hmg/ddr550. Epub 2011 Nov 24. PubMed PMID: 22116939.

40. Khor CC, Davila S, Breunis WB, Lee YC, Shimizu C, Wright VJ, Yeung RS, Tan DE, Sim KS, Wang JJ, Wong TY, Pang J, Mitchell P, Cimaz R, Dahdah N, Cheung YF, Huang GY, __Yang W__, Park IS, Lee JK, Wu JY, Levin M, Burns JC, Burgner D, Kuijpers TW, Hibberd ML; Hong Kong–Shanghai Kawasaki Disease Genetics Consortium; Korean Kawasaki Disease Genetics Consortium; Taiwan Kawasaki Disease Genetics Consortium; International Kawasaki Disease Genetics Consortium; US Kawasaki Disease Genetics Consortium; Blue Mountains Eye Study. Genome-wide association study identifies FCGR2A as a susceptibility locus for Kawasaki disease. Nat Genet. 2011 Nov 13;43(12):1241-6. doi: 10.1038/ng.981. PubMed PMID: 22081228.

41. Li R, #__Yang W__, Zhang J, Hirankarn N, Pan HF, Mok CC, Chan TM, Wong RW, Mok MY, Lee KW, Wong SN, Leung AM, Li XP, Avihingsanon Y, Lee TL, Ho MH, Lee PP,

Wong WH, Wong CM, Ng IO, Yang J, Li PH, Zhang Y, Zhang L, Li W, Baum L, Kwan P, Rianthavorn P, Deekajorndej T, Suphapeetiporn K, Shotelersuk V, Garcia-Barceló MM, Cherny SS, Tam PK, Sham PC, Lau CS, Shen N, Lau Yl, Ye DQ. Association of CD247 with systemic lupus erythematosus in Asian populations. Lupus. 2012 Jan;21(1):75-83. doi: 10.1177/0961203311422724. Epub 2011 Oct 17. PubMed PMID: 22004975.

42. Luo X, #**Yang W**, Ye DQ, Cui H, Zhang Y, Hirankarn N, Qian X, Tang Y, Lau YL, de Vries N, Tak PP, Tsao BP, Shen N. A functional variant in microRNA-146a promoter modulates its expression and confers disease risk for systemic lupus erythematosus. PLoS Genet. 2011 Jun;7(6):e1002128. doi: 10.1371/journal.pgen.1002128. Epub 2011 Jun 30. PubMed PMID: 21738483; PubMed Central PMCID: PMC3128113.

43. Zhang Y, #**Yang W**, Mok CC, Chan TM, Wong RW, Mok MY, Lee KW, Wong SN, Leung AM, Lee TL, Ho MH, Lee PP, Wong WH, Yang J, Zhang J, Wong CM, Ng IO, Garcia-Barceló MM, Cherny SS, Tam PK, Sham PC, Lau CS, Lau YL. Two missense variants in UHRF1BP1 are independently associated with systemic lupus erythematosus in Hong Kong Chinese. Genes Immun. 2011 Apr;12(3):231-4. doi: 10.1038/gene.2010.66. Epub 2011 Feb 17. PubMed PMID: 21326321.

44. Zhang L, #*Yang W, Ying D, Cherny SS, Hildebrandt F, Sham PC, Lau YL. Homozygosity mapping on a single patient: identification of homozygous regions of recent common ancestry by using population data. Hum Mutat. 2011 Mar;32(3):345-53. doi: 10.1002/humu.21432. PubMed PMID: 21309031; PubMed Central PMCID: PMC3357498.

45. Lin P, Mao F, Liu Q, **Yang W**, Shao C, Yan C, Gong Y. A novel deletion mutation in GJB1 causes X-linked Charcot-Marie-Tooth disease in a Han Chinese family. Muscle Nerve. 2010 Dec;42(6):922-6. doi: 10.1002/mus.21790. PubMed PMID: 21104867.

46. Yang J, #**Yang W**, Hirankarn N, Ye DQ, Zhang Y, Pan HF, Mok CC, Chan TM, Wong RW, Mok MY, Lee KW, Wong SN, Leung AM, Li XP, Avihingsanon Y, Rianthavorn P, Deekajorndej T, Suphapeetiporn K, Shotelersuk V, Baum L, Kwan P, Lee TL, Ho MH, Lee PP, Wong WH, Zeng S, Zhang J, Wong CM, Ng IO, Garcia-Barceló MM, Cherny SS, Tam PK, Sham PC, Lau CS, Lau YL. ELF1 is associated with systemic lupus erythematosus in Asian populations. Hum Mol Genet. 2011 Feb 1;20(3):601-7. doi: 10.1093/hmg/ddq474. Epub 2010 Nov 2. PubMed PMID: 21044949.

47. Shen N, Fu Q, Deng Y, Qian X, Zhao J, Kaufman KM, Wu YL, Yu CY, Tang Y, Chen JY, **Yang W**, Wong M, Kawasaki A, Tsuchiya N, Sumida T, Kawaguchi Y, Howe HS, Mok MY, Bang SY, Liu FL, Chang DM, Takasaki Y, Hashimoto H, Harley JB, Guthridge JM, Grossman JM, Cantor RM, Song YW, Bae SC, Chen S, Hahn BH, Lau YL, Tsao BP. Sex-specific association of X-linked Toll-like receptor 7 (TLR7) with male systemic lupus erythematosus. Proc Natl Acad Sci U S A. 2010 Sep

7;107(36):15838-43. doi: 10.1073/pnas.1001337107. Epub 2010 Aug 23. PubMed PMID: 20733074; PubMed Central PMCID: PMC2936646.

48. Yu F, Chen MH, Kuo L, Huang P, **Yang W**. Bayesian hierarchical modeling and selection of differentially expressed genes for the EST data. Biometrics. 2011 Mar;67(1):142-50. doi: 10.1111/j.1541-0420.2010.01447.x. PubMed PMID: 20560937; PubMed Central PMCID: PMC4171397.

49. Niederer HA, Willcocks LC, Rayner TF, **Yang W**, Lau YL, Williams TN, Scott JA, Urban BC, Peshu N, Dunstan SJ, Hien TT, Phu NH, Padyukov L, Gunnarsson I, Svenungsson E, Savage CO, Watts RA, Lyons PA, Clayton DG, Smith KG. Copy number, linkage disequilibrium and disease association in the FCGR locus. Hum Mol Genet. 2010 Aug 15;19(16):3282-94. doi: 10.1093/hmg/ddq216. Epub 2010 May 27. PubMed PMID: 20508037; PubMed Central PMCID: PMC2908468.

50. Willcocks LC, Carr EJ, Niederer HA, Rayner TF, Williams TN, **Yang W**, Scott JA, Urban BC, Peshu N, Vyse TJ, Lau YL, Lyons PA, Smith KG. A defunctioning polymorphism in FCGR2B is associated with protection against malaria but susceptibility to systemic lupus erythematosus. Proc Natl Acad Sci U S A. 2010 Apr 27;107(17):7881-5. doi: 10.1073/pnas.0915133107. Epub 2010 Apr 12. PubMed PMID: 20385827; PubMed Central PMCID: PMC2867866.

51. **Yang W**, Shen N, Ye DQ, Liu Q, Zhang Y, Qian XX, Hirankarn N, Ying D, Pan HF, Mok CC, Chan TM, Wong RW, Lee KW, Mok MY, Wong SN, Leung AM, Li XP, Avihingsanon Y, Wong CM, Lee TL, Ho MH, Lee PP, Chang YK, Li PH, Li RJ, Zhang L, Wong WH, Ng IO, Lau CS, Sham PC, Lau YL; Asian Lupus Genetics Consortium. Genome-wide association study in Asian populations identifies variants in ETS1 and WDFY4 associated with systemic lupus erythematosus. PLoS Genet. 2010 Feb 12;6(2):e1000841. doi: 10.1371/journal.pgen.1000841. PubMed PMID: 20169177; PubMed Central PMCID: PMC2820522.

52. Lee PP, Chen TX, Jiang LP, Chan KW, **Yang W**, Lee BW, Chiang WC, Chen XY, Fok SF, Lee TL, Ho MH, Yang XQ, Lau YL. Clinical characteristics and genotype-phenotype correlation in 62 patients with X-linked agammaglobulinemia. J Clin Immunol. 2010 Jan;30(1):121-31. doi: 10.1007/s10875-009-9341-5. Epub 2009 Nov 11. PubMed PMID: 19904586.

53. Wang L, Wang Z, *__Yang W__. Linked region detection using high-density SNP genotype data via the minimum recombinant model of pedigree haplotype inference. BMC Bioinformatics. 2009 Jul 15;10:216. doi: 10.1186/1471-2105-10-216. PubMed PMID: 19604391; PubMed Central PMCID: PMC2723091.

54. *__Yang W__, Ying D, Lau YL. In-depth cDNA library sequencing provides quantitative gene expression profiling in cancer biomarker discovery. Genomics Proteomics Bioinformatics. 2009 Jun;7(1-2):1-12. doi:

10.1016/S1672-0229(09)00003-5. PubMed PMID: 19591787.

55. Chung BH, Lam ST, Tong TM, Li SY, Lun KS, Chan DH, Fok SF, Or JS, Smith DK, **Yang W**, Lau YL. Identification of novel FBN1 and TGFBR2 mutations in 65 probands with Marfan syndrome or Marfan-like phenotypes. Am J Med Genet A. 2009 Jul;149A(7):1452-9. doi: 10.1002/ajmg.a.32918. PubMed PMID: 19533785.

56. Chang YK, **Yang W**, Zhao M, Mok CC, Chan TM, Wong RW, Lee KW, Mok MY, Wong SN, Ng IO, Lee TL, Ho MH, Lee PP, Wong WH, Lau CS, Sham PC, Lau YL. Association of BANK1 and TNFSF4 with systemic lupus erythematosus in Hong Kong Chinese. Genes Immun. 2009 Jul;10(5):414-20. doi: 10.1038/gene.2009.16. Epub 2009 Apr 9. PubMed PMID: 19357697; PubMed Central PMCID: PMC2834352.

57. **Yang W**, Zhao M, Hirankarn N, Lau CS, Mok CC, Chan TM, Wong RW, Lee KW, Mok MY, Wong SN, Avihingsanon Y, Lin IO, Lee TL, Ho MH, Lee PP, Wong WH, Sham PC, Lau YL. ITGAM is associated with disease susceptibility and renal nephritis of systemic lupus erythematosus in Hong Kong Chinese and Thai. Hum Mol Genet. 2009 Jun 1;18(11):2063-70. doi: 10.1093/hmg/ddp118. Epub 2009 Mar 13. PubMed PMID: 19286673; PubMed Central PMCID: PMC2678927.

58. **Yang W**, Ng P, Zhao M, Hirankarn N, Lau CS, Mok CC, Chan TM, Wong RW, Lee KW, Mok MY, Wong SN, Avihingsanon Y, Lee TL, Ho MH, Lee PP, Wong WH, Lau YL. Population differences in SLE susceptibility genes: STAT4 and BLK, but not PXK, are associated with systemic lupus erythematosus in Hong Kong Chinese. Genes Immun. 2009 Apr;10(3):219-26. doi: 10.1038/gene.2009.1. Epub 2009 Feb 19. PubMed PMID: 19225526.

59. Lin P, Li J, Liu Q, Mao F, Li J, Qiu R, Hu H, Song Y, Yang Y, Gao G, Yan C, **Yang W**, Shao C, Gong Y. A missense mutation in SLC33A1, which encodes the acetyl-CoA transporter, causes autosomal-dominant spastic paraplegia (SPG42). Am J Hum Genet. 2008 Dec;83(6):752-9. doi: 10.1016/j.ajhg.2008.11.003. PubMed PMID: 19061983; PubMed Central PMCID: PMC2668077.

60. Wong TK, Lam TW, **Yang W**, Yiu SM. Finding alternative splicing patterns with strong support from expressed sequences on individual exons/introns. J Bioinform Comput Biol. 2008 Oct;6(5):1021-33. PubMed PMID: 18942164.

61. **Yang W**, Ng P, Zhao M, Wong TK, Yiu SM, Lau YL. Promoter-sharing by different genes in human genome--CPNE1 and RBM12 gene pair as an example. BMC Genomics. 2008 Oct 3;9:456. doi: 10.1186/1471-2164-9-456. PubMed PMID: 18831769; PubMed Central PMCID: PMC2568002.

62. **Yang W**, Wang Z, Wang L, Sham PC, Huang P, Lau YL. Predicting the number and sizes of IBD regions among family members and evaluating the family size

requirement for linkage studies. Eur J Hum Genet. 2008 Dec;16(12):1535-43. doi: 10.1038/ejhg.2008.116. Epub 2008 Jun 25. PubMed PMID: 18575462.

63. Willcocks LC, Lyons PA, Clatworthy MR, Robinson JI, **Yang W**, Newland SA, Plagnol V, McGovern NN, Condliffe AM, Chilvers ER, Adu D, Jolly EC, Watts R, Lau YL, Morgan AW, Nash G, Smith KG. Copy number of FCGR3B, which is associated with systemic lupus erythematosus, correlates with protein expression and immune complex uptake. J Exp Med. 2008 Jul 7;205(7):1573-82. doi: 10.1084/jem.20072413. Epub 2008 Jun 16. PubMed PMID: 18559452; PubMed Central PMCID: PMC2442635.

64. Siu HO, **Yang W**, Lau CS, Chan TM, Wong RW, Wong WH, Lau YL, Alarcon-Riquelme ME. Association of a haplotype of IRF5 gene with systemic lupus erythematosus in Chinese. J Rheumatol. 2008 Feb;35(2):360-2. PubMed PMID: 18260169.

65. Lin G, Wang Z, Wang L, Lau YL, ***Yang W**. Identification of linked regions using high-density SNP genotype data in linkage analysis. Bioinformatics. 2008 Jan 1;24(1):86-93. Epub 2007 Nov 17. PubMed PMID: 18024969.

66. **Yang W**, Hildebrandt JD. Genomic analysis of G protein gamma subunits in human and mouse - the relationship between conserved gene structure and G protein betagamma dimer formation. Cell Signal. 2006 Feb;18(2):194-201. Epub 2005 Jul 11. PubMed PMID: 16006100.

67. **Yang W**, White B, Spicer EK, Weinstein BL, Hildebrandt JD. Complex haplotype structure of the human GNAS gene identifies a recombination hotspot centred on a single nucleotide polymorphism widely used in association studies. Pharmacogenetics. 2004 Nov;14(11):741-7. PubMed PMID: 15564881.

68. **Yang W**, Law PY, Guo X, Loh HH. In vivo activation of a mutant mu-opioid receptor by antagonist: future direction for opiate pain treatment paradigm that lacks undesirable side effects. Proc Natl Acad Sci U S A. 2003 Feb 18;100(4):2117-21. Epub 2003 Jan 13. Erratum in: Proc Natl Acad Sci U S A. 2003 Feb 18;100(4):2163. PubMed PMID: 12525693; PubMed Central PMCID: PMC149968.

69. Loh HH, Liu HC, Cavalli A, **Yang W**, Chen YF, Wei LN. mu Opioid receptor knockout in mice: effects on ligand-induced analgesia and morphine lethality. Brain Res Mol Brain Res. 1998 Mar 1;54(2):321-6. PubMed PMID: 9555078.

70. Chakrabarti S, **Yang W**, Law PY, Loh HH. The mu-opioid receptor down-regulates differently from the delta-opioid receptor: requirement of a high affinity receptor/G protein complex formation. Mol Pharmacol. 1997 Jul;52(1):105-13. PubMed PMID: 9224819.

**SUMMARY and Research Plan**

**Research:**
My research is on genetic studies of complex diseases and Mendelian disorders, and development of methodologies in analyzing genetics and genomics data, two parallel tracks involving genomics and bioinformatics.

**Research on Complex diseases:**
I have been working on the genetics of systemic lupus erythematosus (SLE), an autoimmune disease that mainly affects women of child-bearing age. We have performed genome-wide association study (GWAS) on SLE and uncovered 8 novel susceptibility loci for this disease, some of which are likely to be population-specific. I have published more than a dozen papers on lupus, depicting genetic factors particularly relevant to Asian populations. I have on-going collaborations with renowned researchers world-wide including Dr. Mark Lathrop from McGill, and Dr. Tim Vyse from KCL. I would like to continue this research on complex diseases including but not limited to SLE depending on collaborations.

**Rare diseases and NGS data analysis:**
I have also worked on single gene disorders diagnosed in the Department of Paediatrics and Adolescent Medicine and other departments in Queen Mary Hospital, Hong Kong, such as primary immunodeficiency, using next-generation sequencing (NGS). We are among the first to identify IL10RA mutations causal to infant-onset Crohn's disease and have made molecular diagnosis for a number of patients using this cutting-edge technology. We also published tools in facilitating whole exome sequencing data analysis (PriVar, Zhang et al, Bioinformatics). I would like to continue to work on perfecting analysis for NGS data, combining genetics, molecular biology, population databases and population genetics, pathway analysis and gene expression profiles etc. to help make a comprehensive analysis and understanding of the data. This is very much a multidisciplinary field and my expertise in genetics and genomics and experience in collaborating with statisticians and computer scientists will definitely help to make headways in this field.

**Development of bioinformatics tools**
My laboratory has developed two programs, HRRA (*Hum Mut*, 2011) and HaploShare (in revision with *Genome Biology*), to help detect recent founder mutations that are difficult to detect using linkage analysis or association studies. We also developed software packages such as EFIN and PriVar to facilitate analysis of whole exome sequencing data. Cancer genomics is also an interest for me if suitable collaborators can be found in this area.

**Applicational genomics:**
We also work to apply genomics to clinical diagnosis, testing and screening and have developed a barcoding system that is particularly suitable to screen a number of genes on thousands of samples using NGS technology. We made progress on calling HLA types using NGS data and are developing a novel method on HLA typing using NGS sequencing. Genomics is both for research and clinical application. I will continue to work on applying genomics to clinical diagnosis and population screening, to make genomics really translational.

I have limited bioinformatics training myself but have been able to assemble a laboratory composed of a number of bioinformatics students, and we are able to use/modify tools for genetic and genomic data analysis and to develop tools ourselves in this field. I have been collaborating with research scientists from computer science and statistics in my own research and tool development. I also have a broad range of collaborations with molecular biologists and clinician scientists to help their data analysis and research. I believe I am in the best position for genomics, bioinformatics and interdisciplinary research, being a biologist with in-depth understanding of the questions but also with a good understanding of different languages, and am able to collaborate and interact with scientists from different disciplines.

**Research interest:**

Dr. Yang's research focuses on genetic studies of complex diseases such as SLE using GWAS and of single gene disorders using whole exome sequencing (WES), and on developing bioinformatics tools to improve analysis of genomic data. His laboratory, in collaboration with others, identified *ETS1*, *WDFY4*, *CDKN1B*, *CD80*, *ARID5B*, *TET3*, *DRAM1* and *ELF1* as associated with SLE, and many of these susceptibility genes are believed to be specific to Asians, pointing to the necessity of developing population-based approaches in risk prediction and personalized treatment of complex diseases. His lab also developed tools for detecting recent founder mutations based on GWAS data (HRRA, HaploShare) and facilitating mutation identification from whole exome sequencing (PriVar, EFIN). His recent focus is on developing tools for applying genomics to clinical diagnosis and population screening, such as HLAtyping using next generation sequencing.

**Editorship and Referee of scholarly journals**

Served as *ad hoc* referee for the following international peer-review journals in the last 4 years (ad hoc, multiple times for most of the listed journals):

1. **American Journal of Human Genetics**
2. Annals of Human Genetics
3. Arthritis Research and Therapy
4. Artificial intelligence in Medicine
5. Autoimmunity
6. Briefings in Bioinformatics
7. Behavior Genetics
8. BMC Bioinformatics
9. Clinica Chimica Acta
10. DNA and Cell Biology
11. **Human Molecular Genetics**
12. Human Genetics
13. Immunologic Research (IMRE)
14. International Journal of Immunogenetics
15. International Journal of Rheumatic Diseases
16. Journal of Cellular and Molecular Medicine
17. Journal of Human Genetics
18. Journal of Rheumatology
19. Molecular Biology Reports
20. Mutation Research/Fundamental and Molecular Mechanisms of Mutagenesis
21. **Nature Genetics**
22. **PLoS Genetics**
23. PLoS One
24. Tissue Antigens
25. Tumor Biology

## Invited Presentations:

1. Seoul 2015 invited speaker, 2015 International Symposium on Statistical Genetics, Seoul, May 27-28, 2015 Integrative Analysis of GWAS data to Understand Disease Mechanism for Systemic Lupus Erythematosus
2. Kyoto Course and Symposium on Bioinformatics for NGS with Applications in Human Genetics "Target sequencing analysis of HLA loci (course)" and "GWAS and Beyond: understanding the disease mechanisms of SLE through integrative data analysis (symposium)"
3. Susceptibility genes for SLE: what do we know and what do they mean. 4th International Symposium on Frontiers in Cardiovascular Diseases, June 4th, 2013 Wuhan, China
4. Lupus genetics. International Dermatogenetics Workshop, June 19-20, 2013 Chengdu, China
5. SLE: what do we know and what do they mean. NPG Asia-Pacific: From GWAS to Precision Medicine Workshop, May 16-18, 2013, Shanghai, China
6. Genomics and Bioinformatics in Clinical Diagnostics: the Present and the Future, May 15, KinMed Diagnostics, Guangzhou, China
7. Teaching week: Genetics, Genomics, and Bioinformatics and the Future of the Personalized Medicine. College of Life Sciences, Fujian University of Agriculture and Forestry, April 14-19, 2013
8. Data analysis in a geneticist's eye. International Society on Computational Biology (ISCB)-Asia 2012, Shenzhen, China, Dec 19th, 2012
9. Data analysis in modern genetic studies. Shandong University Medical School, Oct 18-19th, 2012
10. Medical Genetics and Genetic data analysis. Southeastern University, Nanjing China, Oct. 10th-11st, 2012
11. Bioinformatics, genomics and the future of genomic medicine. 5th International Workshop and Summer School on Crops, Chips and Computers, Sep 9th, 2012, Fuzhou, China
12. Invited Lecture Series: Application of new sequencing technologies and bioinformatic data analysis to clinical genetics, Dec 2011-jan. 2012 (Invited teacher of a commissioned training course), Clinical Genetics Service, Department of Health, the Government of Hong Kong
13. The 12th International Congress of Human Genetics, Montreal Canada, Nov 2011, Selected for Platform Oral Presentation: Finding rare variants in GWAS and exome sequencing data by making use of recent common founder information
14. Asia Pacific Conference in Medical Genetics, Hong Kong, Nov 4th, 2010: Identification of compound heterozygous mutations in an early onset Crohn's disease patient using whole exome sequencing technology, invited presentation
15. Frontiers in Biomedical Research HKU2010, Mendelian diseases, complex diseases and those in between—and their study approaches, invited presentation
16. The International Conference on BioMedical Engineering and Informatics; 2008, Sanya, Hainan, China, Biomarker identification for early tumor detection aided by bioinformatics gene expression analysis, invited presentation
17. Joint Symposium on "New paradigms in Medical Genetics", Nov. 24-26, 2006, Hong Kong, Linkage analysis with dense SNP genotyping, invited presentation
18. Genomics Symposium at Experimental Biology 2005 by FASEB MARC program on April 4th , 2005, Characterization of a recombination hotspot in the GNAS locus previously associated with hypertension, invited presentation

## Memberships:

- Member, Strategic Research Theme of University Research Committee, HKU, Genomics
- Member, American Society of Human Genetics

**Honors and Awards:**

- World Health Organization Fellowship, Neurobiology (1995);
- LM. Nutter Research Award, Dept of Pharmacology, University of Minnesota (2001)
- Buccaneer Research Award, Minnesota Medical Foundation (2002).

## Research Grants:

**General Research Fund (major funding form in Hong Kong, externally peer reviewed, in a PI's capacity):**

- 17146616 Unravelling the genetic puzzle of systemic lupus erythematosus (SLE) through comprehensive analyses of genetic association by functional annotation of genes, variants, and genomic regions, $1,016,800， Oct 2016-Oct 2019
- 17125114 Meta-Analysis of three GWAS datasets from Hong Kong, Anhui China and UK followed by replication in independent cohorts in Asia and UK for identification of novel susceptibility genes associated with SLE, $1,098,000
- Mapping Susceptibility Genes for Systemic Lupus Erythematosus (SLE) through a Genome-Wide Association Study, 2009-2011, HKU781709 M, $755,760.
- Meta-Analysis of two Asian GWAS datasets for identification of novel genetic variants associated with systemic lupus erythematosus, 2011-2013, HKU784611M, $650,000.
- Identifying susceptibility genes in the human MHC region independently associated with systemic lupus erythematosus (SLE) in Chinese populations. HKU783813M, 2013-2015, $ 822,731

**General Research Fund in a co-I's capacity:**

- HKU 770411- Identification of coding variants associated with early-onset and familial systemic lupus erythematosus through whole exome sequencing and replication, 2011-2013, $747,500.
- HKU777511M-Method and Software for Personal Risk Profiling of Complex Diseases, 2011-2013, $1086, 750. This is a study that proposes to make use of available GWAS findings to predict disease risks for the general population. (PI: Prof Pak Sham).
- HKU 765311M, Genome-wide DNA methylation profiling in Chinese patients with Systemic Lupus Erythematosus (SLE), 2011-2013, $805,000. This project proposes to study the role of methylation on disease risk of SLE, trying to bridge the effect of genetics and environmental factors. (PI: Dr. Brian Chung).
- Design and Analysis of Algorithms for Finding the Maximum Quasi-Biclique, Perfect Duplication History and Identification of Linked Regions, HK$ 497,084 2009-2011 (PI: Prof. Wang LS, Department of Computer science, City U HK).
- HKU 776412M -Bioinformatics tools for identifying disease loci from exome sequencing data, 2012-2014, HK$1,098,000 (PI: Prof Pak Sham).
- Cell-lineage specific differential DNA methylation in Chinese patients with early-onset systemic lupus erythematosus (SLE): implications for disease susceptibility. 2013-2015 (PI: Dr. Brian Chung)

**Other Peer Reviewed Grants as PI:**

- HMRF Molecular diagnosis for severe combined immunodeficiencies (SCID) using whole exome sequencing, PI, External, peer-reviewed grant. (project no.: 01120846), $980, 000, 01/02/2014—31/01/2016
- 12133701 HMRF, Meta-analysis of SLE GWAS followed by replication on X chromosome in cross-ethnic populations $395,000.00 1/03/2015----28/02/2017

## CURRICULUM DEVELOPMENT:

- Genome Bioinformatics, Bioinformatics Program 2009 and 2010
- Common Core Course: Genetics and Human Nature
- BBMS2003 Human Genetics, 2014, 2015, 2016, 2017
- BBMS3009 Genome Science, 2015, 2016, 2017