

Journal publications: (from Pubmed: <http://paed.hku.hk/genome>)

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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.
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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., Fürtrohr, 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)

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