Date of preparation: 9th January 2022

Curriculum Vitae

Personal information

Name: Kwok Shing Ng 'Patrick'
Personal email: patrickn.hk@gmail.com
Mobile: 832-278-7203

Academic qualifications

2001-2007	Doctor of Philosophy in Molecular Biology (City University of Hong Kong)
1998-2001	Bachelor of Science (Hons) in Applied Biology with **First Class Honors** (City University of Hong Kong)

Training and Experiences

July 2020 – present	Research Scientist, The Jackson Laboratory for Genomic Medicine
July 2021 – present	Assistant Professor, Department of Pediatrics, School of Medicine, University of Connecticut
Dec 2019 – Jun 2020	Scientific Manager, Institute of Personalized Cancer Therapy, MD Anderson Cancer Center, The University of Texas
Nov 2018 – Nov 2019	Senior Research Scientist, Institute of Personalized Cancer Therapy, MD Anderson Cancer Center, The University of Texas
Apr 2014 – Oct 2018	Research Scientist, Institute of Personalized Cancer Therapy, MD Anderson Cancer Center, The University of Texas
Sep 2011 – Apr 2014	Postdoctoral Fellow, Department of Systems Biology, MD Anderson Cancer Center (MDACC), The University of Texas
Dec 2008 – Jun 2011	Postdoctoral Fellow, School of Biomedical Sciences, The Chinese University of Hong Kong
Jun 2007 – Nov 2008	Research Associate, Department of Biochemistry (Medicine), The Chinese University of Hong Kong
Jul 2006 – May 2007	Research Assistant, Department of Biology and Chemistry, City University of Hong Kong

Research summary

My current research focuses are (1) to better understand the tumor microenvironment and heterogeneity of osteosarcoma using single cell RNA sequencing and spatial transcriptomic analyses, and (2) to investigate alternative splicing events in osteosarcoma using hybrid RNA sequencing. The goal is to

identify new biomarkers predicting treatment response, metastasis and survival and new therapeutic target for new treatment development.

In my previous positions, I led the development and operation of a platform testing the functional effect (i.e. transforming potential) of mutations which were identified by large-scale tumor sequencing projects (e.g. TCGA) and routine molecular profiling of cancer patients using 2 cell models, Ba/F3 and MCF10A. With the collaborative effort, we constructed >1,600 mutation clones with HiTTMoB technique and tested the function of those mutations platform. We also constructed a data portal and published the result to Cancer Cell journal providing a great resource for research community to facilitate the development of biomarker and drug for novel cancer treatments. Apart from carrying out basic research, my team and I also are part of Precision Oncology Decision Support (PODS) team of Institute for Personalized Cancer Therapy (IPCT) in MDACC coordinating and test the mutations with unknown significant identified in MDACC patients. Our result is used by the PODS team for annotation of mutations in patient reports requested by physicians.

In addition, I worked with bioinformatics team on analyses of the proteomic data and classified the tumors into different subtypes at protein level in lung adenocarcinoma and Head and neck squamous cell carcinoma under The Cancer Genome Atlas (TCGA). We also carried out a Pan-Cancer proteomic analysis across 11 cancer types aiming to better understand biology of various tumor types with multiple levels analyses on DNA, mRNA and signaling pathway. Our finding improved the understanding of individual cancer types, hence provided foundation for development of new biomarkers and targets for personalized medicine for cancer patients.

Skills/Experience

- Extensive Hands-on experience in molecular and *in vitro* cellular techniques: PCR, cloning (restriction enzyme-based and Gateway), DNA/RNA extraction, qPCR, cell culture, lentivirus production and transduction, proliferation assay and drug testing assay
- Hands-on experience in molecular and *in vitro* cellular techniques: qPCR, western blot, immunoprecipitation, GST-pull down assay, shRNA/RNAi knock-down, CRISPR-mediated knock-out, flow cytometry and reporter assay
- Extensive Data mining computational experience: use of web-based interface on public cancer genome database, e.g., cBio, TCGA, COSMIC, TCPA and oncoKB
- Simple statistical software: GraphPad and R-studio
- Basic computation skill: MS-office and Google doc, sheet and slide
- Collaboration experience with statisticians and informaticians on Reverse Phase Protein Array analysis on TCGA and cell line databases

Research-related Experiences

- Established and oversaw the functional genomic platform
    a. Direct supervised a team of 1 research scientist, 1 senior research assistant and 2 research assistants
    b. Established the workflow and data tracking system to keep track of the platform
    c. Coordinated the materials and information sharing among collaborators within and across institutes
    d. Prepared reports, presentations and manuscripts regarding the functional genomics platform

- Coordinated the collaboration between of multiple research groups within or across institutes on multiple projects.

- Reviewed 3 manuscripts in Peer-reviewed journals

- Prepared funding proposal of a developmental research project, entitled "Identification of "driver" mutations and effective targeted therapy in durggable cancer genes in Head and Neck Cancers." UT MD Anderson SPORE in Head and Neck Cancer, UT MD Anderson Cancer Center, Houston, TX. April 20, 2012.

- Provided technical training and mentoring
    a. Trained and supervised 6 research assistants and senior research assistant
    b. Mentored 3 postgraduate students on experimental planning and trouble shooting
    c. Trained and supervised >10 undergraduate students and high school-er on their final year research projects and summer projects, respectively.

- Provided laboratory management, such as arranging meetings, ordering and keeping inventory, maintenance of specific equipment, laboratory relocation, coordinating lab member schedules on shared space and equipment.

Publications (* indicates Co-first authorship)

Bagheri-Yarmand R, Busaidy NL, McBeath E, Danysh BP, Evans KW, Moss TJ, Akcakanat A, **Ng PKS**, Knippler CM, Golden JA, Williams MD, Multani AS, Cabanillas ME, Shaw KR, Meric-Bernstam F, Shah MH, Ringel MD, Hofmann MC. RAC1 Alterations Induce Acquired Dabrafenib Resistance in Association with Anaplastic Transformation in a Papillary Thyroid Cancer Patient. **Cancers (Basel)**. 2021 Sep 30;13(19):4950. doi: 10.3390/cancers13194950. PMID: 34638434; PMCID: PMC8507731.

Li X, Lau AYT, Ng ASN, Aldehaiman A, Zhou Y, **Ng PKS**, Arold ST, Cheung LWT. Cancer-associated mutations in the p85α N-terminal SH2 domain activate a spectrum of receptor tyrosine kinases. **Proc Natl Acad Sci U S A**. 2021 Sep 14;118(37):e2101751118. doi: 10.1073/pnas.2101751118. PMID: 34507989; PMCID: PMC8449365.

Loree JM, Wang Y, Syed MA, Sorokin AV, Coker O, Xiu J, Weinberg BA, Vanderwalde AM, Tesfaye A, Raymond VM, Miron B, Tarcic G, Zelichov O, Broaddus RR, **Ng PKS**, Jeong KJ, Tsang YH, Mills GB, Overman MJ, Grothey A, Marshall JL, Kopetz S. Clinical and Functional Characterization of Atypical KRAS/NRAS Mutations in Metastatic Colorectal Cancer. **Clin Cancer Res**. 2021 Aug 15;27(16):4587-4598. doi: 10.1158/1078-0432.CCR-21-0180. Epub 2021 Jun 11. PMID: 34117033; PMCID: PMC8364867.

Shariati M, Evans KW, Zheng X, Bristow CA, **Ng PK**, Rizvi YQ, Tapia C, Yang F, Carugo A, Heffernan TP, Peoples MD, Tripathy D, Meric-Bernstam F. Combined inhibition of DDR1 and CDK4/6 induces synergistic effects in ER-positive, HER2-negative breast cancer with PIK3CA/AKT1 mutations. **Oncogene**. 2021 Jul;40(26):4425-4439. doi: 10.1038/s41388-021-01819-0. Epub 2021 Jun 9. PMID: 34108622.

Negrao MV, Raymond VM, Lanman RB, Robichaux JP, He J, Nilsson MB, **Ng PKS**, Amador BE, Roarty EB, Nagy RJ, Banks KC, Zhu VW, Ng C, Chae YK, Clarke JM, Crawford JA, Meric-Bernstam F, Ignatius Ou SH, Gandara DR, Heymach JV, Bivona TG, McCoach CE. Molecular Landscape of BRAF-Mutant NSCLC Reveals an Association Between Clonality and Driver Mutations and Identifies Targetable Non-V600 Driver Mutations. **J Thorac Oncol**. 2020 Oct;15(10):1611-1623. doi: 10.1016/j.jtho.2020.05.021. Epub 2020 Jun 13. PMID: 32540409; PMCID: PMC7529990.

Chen H, Li J, Wang Y, **Ng PKS**, Tsang YH, Shaw KR, Mills GB, Liang H. Comprehensive assessment of computational algorithms in predicting cancer driver mutations. **Genome Biol** 21, 43 (2020). https://doi.org/10.1186/s13059-020-01954-z

Wang J, Zhao W, Guo H, Fang Y, Stockman SE, Bai S, **Ng PK**, Li Y, Yu Q, Lu Y, Jeong KJ, Chen X, Gao M, Liang J, Li W, Tian X, Jonasch E, Mills GB, Ding Z. AKT isoform-specific expression and activation across cancer lineages. **BMC Cancer**. 2018 Jul 16;18(1):742. doi: 10.1186/s12885-018-4654-5. PubMed PMID: 30012111; PubMed Central PMCID: PMC6048698.

Ip CKM, **Ng PKS**, Jeong KJ, Shao SH, Ju Z, Leonard PG, Hua X, Vellano CP, Woessner R, Sahni N, Scott KL, Mills GB. Neomorphic PDGFRA extracellular domain driver mutations are resistant to PDGFRA targeted therapies. **Nat Commun**. 2018 Nov 2;9(1):4583. doi: 10.1038/s41467-018-06949-w. PubMed PMID: 30389923; PubMed Central PMCID: PMC6214970

Wang Y, Xu X, Maglic D, Dill MT, Mojumdar K, **Ng PK**, Jeong KJ, Tsang YH, Moreno D, Bhavana VH, Peng X, Ge Z, Chen H, Li J, Chen Z, Zhang H, Han L, Du D, Creighton CJ, Mills GB, Cancer Genome Atlas Research Network, Camargo F, Liang H. Comprehensive Molecular Characterization of the Hippo Signaling Pathway in Cancer. **Cell Rep**. 2018 Oct 30;25(5):1304-1317.e5. doi: 10.1016/j.celrep.2018.10.001. PubMed PMID: 30380420.

Bailey MH, Tokheim C, Porta-Pardo E, Sengupta S, Bertrand D, Weerasinghe A, Colaprico A, Wendl MC, Kim J, Reardon B, **Ng PKS**, Jeong KJ, Cao S, Wang Z, Gao J, Gao Q, Wang F, Liu EM, Mularoni L, Rubio-Perez C, Nagarajan N, Cortés-Ciriano I, Zhou DC, Liang WW, Hess JM, Yellapantula VD, Tamborero D, Gonzalez-Perez A, Suphavilai C, Ko JY, Khurana E, Park PJ, Van Allen EM, Liang H; MC3 Working Group; Cancer Genome Atlas Research Network, Lawrence MS, Godzik A, Lopez-Bigas N, Stuart J, Wheeler D, Getz G, Chen K, Lazar AJ, Mills GB, Karchin R, Ding L. Comprehensive Characterization of Cancer Driver Genes and Mutations. **Cell**. 2018 Aug 9;174(4):1034-1035. doi: 10.1016/j.cell.2018.07.034. PubMed PMID: 30096302.

Ng PK*, Li J*, Jeong KJ*, Shao S, Chen H, Tsang YH, Sengupta S, Wang Z, Bhavana VH, Tran R, Soewito S, Minussi DC, Moreno D, Kong K, Dogruluk T, Lu H, Gao J, Tokheim C, Zhou DC, Johnson AM, Zeng J, Ip CKM, Ju Z, Wester M, Yu S, Li Y, Vellano CP, Schultz N, Karchin R, Ding L, Lu Y, Cheung LWT, Chen K, Shaw KR, Meric-Bernstam F, Scott KL, Yi S, Sahni N, Liang H, Mills GB. Systematic Functional Annotation of Somatic Mutations in Cancer. **Cancer Cell**. 2018 Mar 12;33(3):450-462.e10. doi: 10.1016/j.ccell.2018.01.021. PubMed PMID: 29533785.

Ng PKS, Lau CPY, Lam EKY, Li SSK, Lui VWY, Yeo W, Ng YK, Lai PBS, Tsui SKW. Hypermethylation of NF-κB-Activating Protein-Like (NKAPL) Promoter in Hepatocellular Carcinoma Suppresses Its Expression and Predicts a Poor Prognosis. **Dig Dis Sci**. 2018 Mar;63(3):676-686. doi: 10.1007/s10620-018-4929-3. Epub 2018 Jan 20. PubMed PMID: 29353445.

Wang Z, **Ng KS**, Chen T, Kim TB, Wang F, Shaw K, Scott KL, Meric-Bernstam F, Mills GB, Chen K. Cancer driver mutation prediction through Bayesian integration of multi-omic data. **PLoS One**. 2018 May 8;13(5):e0196939. doi: 10.1371/journal.pone.0196939. PMID: 29738578; PMCID: PMC5940219.

Han G, Zhao W, Song X, **Ng PKS**, Karam JA, Jonasch E, Mills GB, Zhao Z, Ding Z, Jia P. Unique protein expression signatures of survival time in kidney renal clear cell carcinoma through a pan-cancer screening. **BMC Genomics**. 2017 Oct 3;18(Suppl 6):678. doi: 10.1186/s12864-017-4026-6. PubMed PMID: 28984208; PubMed Central PMCID: PMC5629613.

Zhang Y*, **Ng PKS***, Kucherlapati M, Chen F, Liu Y, Tsang YH, de Velasco G, Jeong KJ, Akbani R, Hadjipanayis A, Pantazi A, Bristow CA, Lee E, Mahadeshwar HS, Tang J, Zhang J, Yang L, Seth S, Lee S, Ren X, Song X, Sun H, Seidman J, Luquette LJ, Xi R, Chin L, Protopopov A, Westbrook TF, Shelley CS, Choueiri TK, Ittmann M, Van Waes C, Weinstein JN, Liang H, Henske EP, Godwin AK, Park PJ, Kucherlapati R, Scott KL, Mills GB, Kwiatkowski DJ, Creighton CJ. A Pan-Cancer Proteogenomic Atlas of PI3K/AKT/mTOR Pathway Alterations. **Cancer Cell**. 2017 Jun 12;31(6):820-832.e3. doi: 10.1016/j.ccell.2017.04.013. Epub 2017 May 18. PubMed PMID: 28528867; PubMed Central PMCID: PMC5502825.

Sun C, Fang Y, Yin J, Chen J, Ju Z, Zhang D, Chen X, Vellano CP, Jeong KJ, **Ng PK**, Eterovic AKB, Bhola NH, Lu Y, Westin SN, Grandis JR, Lin SY, Scott KL, Peng G, Brugge J, Mills GB. Rational combination therapy with PARP and MEK inhibitors capitalizes on therapeutic liabilities in RAS mutant cancers. **Sci Transl Med**. 2017 May 31;9(392). pii: eaal5148. doi: 10.1126/scitranslmed.aal5148. PubMed PMID: 28566428; PubMed Central PMCID: PMC5919217.

Kong K, **Ng PK**, Scott KL. Ba/F3 transformation assays. **Oncotarget**. 2017 May 30;8(22):35488-35489. doi: 10.18632/oncotarget.17828. PMID: 28500277; PMCID: PMC5482591.

Wang C, Gu C, Jeong KJ, Zhang D, Guo W, Lu Y, Ju Z, Panupinthu N, Yang JY, Gagea MM, **Ng PK**, Zhang F, Mills GB. YAP/TAZ-Mediated Upregulation of GAB2 Leads to Increased Sensitivity to Growth Factor-Induced Activation of the PI3K Pathway. **Cancer Res**. 2017 Apr 1;77(7):1637-1648. doi: 10.1158/0008-5472.CAN-15-3084. Epub 2017 Feb 15. PubMed PMID: 28202507; PubMed Central PMCID: PMC6026015.

Ip CKM, Yin J, **Ng PKS**, Lin SY, Mills GB. Genomic-Glycosylation Aberrations in Tumor Initiation, Progression and Management. **AIMS Med Sci**. 2016 Dec 23;3(4): 386-416. doi: 10.3934/medsci.2016.4.386

Yang KY, Chen Y, Zhang Z, **Ng PK**, Zhou WJ, Zhang Y, Liu M, Chen J, Mao B, Tsui SK. Transcriptome analysis of different developmental stages of amphioxus reveals dynamic changes of distinct classes of genes during development. **Sci Rep**. 2016 Mar 16;6:23195. doi: 10.1038/srep23195. PubMed PMID: 26979494; PubMed Central PMCID: PMC4793263.

Cancer Genome Atlas Network. Comprehensive genomic characterization of head and neck squamous cell carcinomas. **Nature**. 2015 Jan 29;517(7536):576-82. doi: 10.1038/nature14129. PubMed PMID: 25631445; PubMed Central PMCID: PMC4311405. (**One of the authors in Cancer Genome Atlas Research Network**)

Grubbs EG, **Ng PK**, Bui J, Busaidy NL, Chen K, Lee JE, Lu X, Lu H, Meric-Bernstam F, Mills GB, Palmer G, Perrier ND, Scott KL, Shaw KR, Waguespack SG, Williams MD, Yelensky R, Cote GJ. RET fusion as a novel driver of medullary thyroid carcinoma. **J Clin Endocrinol Metab**. 2014 Dec 29:jc20144153. [Epub ahead of print] PubMed PMID: 25546157.

Chan TF, Ji KM, Yim AK, Liu XY, Zhou JW, Li RQ, Yang KY, Li J, Li M, Law PT, Wu YL, Cai ZL, Qin H, Bao Y, Leung RK, **Ng PK**, Zou J, Zhong XJ, Ran PX, Zhong NS, Liu ZG, Tsui SK. The draft genome, transcriptome, and microbiome of Dermatophagoides farinae reveal a broad spectrum of dust mite allergens. **J Allergy Clin Immunol**. 2014 Oct 31. pii: S0091-6749(14)01366-9. doi: 10.1016/j.jaci.2014.09.031. [Epub ahead of print] PubMed PMID: 25445830.

Cheung LW, Yu S, Zhang D, Li J, **Ng PK**, Panupinthu N, Mitra S, Ju Z, Yu Q, Liang H, Hawke DH, Lu Y, Broaddus RR, Mills GB. Naturally occurring neomorphic PIK3R1 mutations activate the MAPK pathway, dictating therapeutic response to MAPK pathway inhibitors. **Cancer Cell**. 2014 Oct 13;26(4):479-94. doi: 10.1016/j.ccell.2014.08.017. Epub 2014 Oct 2. PubMed PMID: 25284480; PubMed Central PMCID: PMC4198486.

Mazumdar T, Byers LA, **Ng PK**, Mills GB, Peng S, Diao L, Fan YH, Stemke-Hale K, Heymach JV, Myers JN, Glisson BS, Johnson FM. A comprehensive evaluation of biomarkers predictive of response to PI3K inhibitors and of resistance mechanisms in head and neck squamous cell carcinoma. **Mol Cancer Ther**. 2014 Nov;13(11):2738-50. doi: 10.1158/1535-7163.MCT-13-1090. Epub 2014 Sep 5. PubMed PMID: 25193510; PubMed Central PMCID: PMC4221385.

Cancer Genome Atlas Research Network. Comprehensive molecular profiling of lung adenocarcinoma. **Nature**. 2014 Jul 31;511(7511):543-50. doi: 10.1038/nature13385. Epub 2014 Jul 9. Erratum in: Nature. 2014 Oct 9;514(7521):262. Rogers, K [corrected to Rodgers, K]. PubMed PMID: 25079552; PubMed Central PMCID: PMC4231481. (**One of the authors in Cancer Genome Atlas Research Network**)

Akbani R*, **Ng PK***, Werner HM*, Shahmoradgoli M, Zhang F, Ju Z, Liu W, Yang JY, Yoshihara K, Li J, Ling S, Seviour EG, Ram PT, Minna JD, Diao L, Tong P, Heymach JV, Hill SM, Dondelinger F, Städler N, Byers LA, Meric-Bernstam F, Weinstein JN, Broom BM, Verhaak RG, Liang H, Mukherjee S, Lu Y, Mills GB. A pan-cancer proteomic perspective on The Cancer Genome Atlas. **Nat Commun**. 2014 May 29;5:3887. doi: 10.1038/ncomms4887. PubMed PMID: 24871328; PubMed Central PMCID: PMC4109726.

Lui VW, Peyser ND, **Ng PK**, Hritz J, Zeng Y, Lu Y, Li H, Wang L, Gilbert BR, General IJ, Bahar I, Ju Z, Wang Z, Pendleton KP, Xiao X, Du Y, Vries JK, Hammerman PS, Garraway LA, Mills GB, Johnson DE, Grandis JR. Frequent mutation of receptor protein tyrosine phosphatases provides a mechanism for STAT3 hyperactivation in head and neck cancer. **Proc Natl Acad Sci U S A**. 2014 Jan 21;111(3):1114-9. doi: 10.1073/pnas.1319551111. Epub 2014 Jan 6. PubMed PMID: 24395800; PubMed Central PMCID: PMC3903220.

Lui VW, Hedberg ML, Li H, Vangara BS, Pendleton K, Zeng Y, Lu Y, Zhang Q, Du Y, Gilbert BR, Freilino M, Sauerwein S, Peyser ND, Xiao D, Diergaarde B, Wang L, Chiosea S, Seethala R, Johnson JT, Kim S, Duvvuri U, Ferris RL, Romkes M, Nukui T, **Ng PKS**, Garraway LA, Hammerman PS, Mills GB, Grandis JR. Frequent Mutation of the PI3K Pathway in Head and Neck Cancer Defines Predictive Biomarkers. **Cancer Discov**. 2013 Jul;3(7):761-9. doi: 10.1158/2159-8290.CD-13-0103. Epub 2013 Apr 25. PubMed PMID: 23619167; PubMed Central PMCID: PMC3710532.

Ng YK, Lau WS, Lui VW, Cheng AS, **Ng PK**, Tsui SK, Cheung YS, Lai PB. Full-length Mst1 exhibits growth promoting function in human hepatocellular carcinoma cells. **FEBS Lett**. 2013 Mar 1;587(5):496-503. doi: 10.1016/j.febslet.2013.01.018. Epub 2013 Jan 21. PubMed PMID: 23347832.

Lau CP, **Ng PK**, Li MS, Tsui SK, Huang L, Kumta SM. p63 regulates cell proliferation and cell cycle progression associated genes in stromal cells of giant cell tumor of the bone. **Int J Oncol**. 2013 Feb;42(2):437-43. doi: 10.3892/ijo.2012.1727. Epub 2012 Dec 3. PubMed PMID: 23229819; PubMed Central PMCID: PMC3583652.

Ma BB, Lui VW, Cheung CS, Lau CP, Ho K, Hui EP, Tsui SK, Ng MH, Cheng SH, **Ng PK**, Tsao SW, Chan AT. Activity of the MEK inhibitor selumetinib (AZD6244; ARRY-142886) in nasopharyngeal cancer cell lines. **Invest New Drugs**. 2013 Feb;31(1):30-8. doi: 10.1007/s10637-012-9828-4. Epub 2012 May 8. PubMed PMID: 22565394.

Li SK*, **Ng PK***, Qin H, Lau JK, Lau JP, Tsui SK, Chan TF, Lau TC. Identification of small RNAs in Mycobacterium smegmatis using heterologous Hfq. **RNA**. 2013 Jan;19(1):74-84. doi: 10.1261/rna.034116.112. Epub 2012 Nov 20. PubMed PMID: 23169799; PubMed Central PMCID: PMC3527728.

Wilkins S, Zhang KW, Mahfuz I, Quantin R, D'Cruz N, Hutson J, Ee M, Bagli D, Aitken K, Fong FN, **Ng PK**, Tsui SK, Fung WY, Banu T, Thakre A, Johar K, Jaureguizar E, Li L, Cheng W. Insertion/deletion polymorphisms in the ΔNp63 promoter are a risk factor for bladder exstrophy epispadias complex.

PLoS Genet. 2012;8(12):e1003070. doi: 10.1371/journal.pgen.1003070. Epub 2012 Dec 20. PubMed PMID: 23284286; PubMed Central PMCID: PMC3527294.

Li MS, Lau TC, Chan SK, Wong CH, **Ng PK**, Sung JJ, Chan HL, Tsui SK. The G1613A mutation in the HBV genome affects HBeAg expression and viral replication through altered core promoter activity. **PLoS One**. 2011;6(7):e21856. doi: 10.1371/journal.pone.0021856. Epub 2011 Jul 21. PubMed PMID: 21814558; PubMed Central PMCID: PMC3140978.

Ng CF, Zhou WJ, **Ng PK**, Li MS, Ng YK, Lai PB, Tsui SK. Characterization of human FHL2 transcript variants and gene expression regulation in hepatocellular carcinoma. **Gene**. 2011 Jul 15;481(1):41-7. doi: 10.1016/j.gene.2011.04.005. Epub 2011 Apr 22. PubMed PMID: 21540083.
Yang Q, Xue HM, Wong WT, Tian XY, Huang Y, Tsui SK, **Ng PK**, Wohlfart P, Li H, Xia N, Tobias S, Underwood MJ, He GW. AVE3085, an enhancer of endothelial nitric oxide synthase, restores endothelial function and reduces blood pressure in spontaneously hypertensive rats. **Br J Pharmacol**. 2011 Jul;163(5):1078-85. doi: 10.1111/j.1476-5381.2011.01308.x. PubMed PMID: 21385179; PubMed Central PMCID: PMC3130953.

Ng CF, **Ng PK**, Lui VW, Li J, Chan JY, Fung KP, Ng YK, Lai PB, Tsui SK. FHL2 exhibits anti-proliferative and anti-apoptotic activities in liver cancer cells. **Cancer Lett**. 2011 May 28;304(2):97-106. doi: 10.1016/j.canlet.2011.02.001. Epub 2011 Mar 5. PubMed PMID: 21377781.

Lui VW, Yau DM, Cheung CS, Wong SC, Chan AK, Zhou Q, Wong EY, Lau CP, Lam EK, Hui EP, Hong B, Hui CW, Chan AS, **Ng PK**, Ng YK, Lo KW, Tsang CM, Tsui SK, Tsao SW, Chan AT. FGF8b oncogene mediates proliferation and invasion of Epstein-Barr virus-associated nasopharyngeal carcinoma cells: implication for viral-mediated FGF8b upregulation. **Oncogene**. 2011 Mar 31;30(13):1518-30. doi: 10.1038/onc.2010.529. Epub 2010 Nov 29. PubMed PMID: 21119603.

Law CS, Leung PY, **Ng PK**, Kou CY, Au KK, Zhou J, Tsui SK. The involvement of N-G,N-G-dimethyarginine dimethylhydrolase 1 in the proliferative effect of Astragali radix on cardiac cells. **J Ethnopharmacol**. 2011 Mar 8;134(1):130-5. doi: 10.1016/j.jep.2010.11.072. Epub 2010 Dec 3. PubMed PMID: 21130852.

Lui VW, Wong EY, Ho K, **Ng PK**, Lau CP, Tsui SK, Tsang CM, Tsao SW, Cheng SH, Ng MH, Ng YK, Lam EK, Hong B, Lo KW, Mok TS, Chan AT, Mills GB. Inhibition of c-Met downregulates TIGAR expression and reduces NADPH production leading to cell death. **Oncogene**. 2011 Mar 3;30(9):1127-34. doi: 10.1038/onc.2010.490. Epub 2010 Nov 8. PubMed PMID: 21057531; PubMed Central PMCID: PMC3428712.

Lau CP, Huang L, Tsui SK, **Ng PK**, Leung PY, Kumta SM. Pamidronate, farnesyl transferase, and geranylgeranyl transferase-I inhibitors affects cell proliferation, apoptosis, and OPG/RANKL mRNA expression in stromal cells of giant cell tumor of bone. **J Orthop Res**. 2011 Mar;29(3):403-13. doi: 10.1002/jor.21249. Epub 2010 Sep 30. PubMed PMID: 20886653.

Ng PK*, Yu RM*, Kwong TF, Wong MM, Kong RY. Transcriptional regulation and functional implication of the grass carp CITED1 (gcCITED1) in the negative regulation of HIF-1. **Int J Biochem Cell Biol**. 2010 Sep;42(9):1544-52. doi: 10.1016/j.biocel.2010.06.007. Epub 2010 Jun 12. PubMed PMID: 20547241.

Ng PK, Tsui SK, Lau CP, Wong CH, Wong WH, Huang L, Kumta SM. CCAAT/enhancer binding protein beta is up-regulated in giant cell tumor of bone and regulates RANKL expression. **J Cell Biochem**. 2010 May 15;110(2):438-46. doi: 10.1002/jcb.22556. PubMed PMID: 20225273.

Ng PK*, Chiu SK*, Kwong TF, Yu RM, Wong MM, Kong RY. Functional characterization of two CITED3 homologs (gcCITED3a and gcCITED3b) in the hypoxia-tolerant grass carp, Ctenopharyngodon idellus. **BMC Mol Biol**. 2009 Nov 3;10:101. doi: 10.1186/1471-2199-10-101. PubMed PMID: 19883516; PubMed Central PMCID: PMC2780419.

Yu RM, **Ng PK**, Tan T, Chu DL, Wu RS, Kong RY. Enhancement of hypoxia-induced gene expression in fish liver by the aryl hydrocarbon receptor (AhR) ligand, benzo[a]pyrene (BaP). **Aquat Toxicol**. 2008 Nov 21;90(3):235-42. doi: 10.1016/j.aquatox.2008.09.004. Epub 2008 Sep 12. PubMed PMID: 18945501.

Wong MM, Yu RM, **Ng PK**, Law SH, Tsang AK, Kong RY. Characterization of a hypoxia-responsive leptin receptor (omLepR(L)) cDNA from the marine medaka (Oryzias melastigma). **Mar Pollut Bull**. 2007 Jun;54(6):797-803. Epub 2007 Mar 23. PubMed PMID: 17382971.

Yu RM, Chen EX, Kong RY, **Ng PK**, Mok HO, Au DW. Hypoxia induces telomerase reverse transcriptase (TERT) gene expression in non-tumor fish tissues in vivo: the marine medaka (Oryzias melastigma) model. **BMC Mol Biol**. 2006 Sep 11;7:27. PubMed PMID: 16961934; PubMed Central PMCID: PMC1578579.

Law SH, Wu RS, **Ng PK**, Yu RM, Kong RY. Cloning and expression analysis of two distinct HIF-alpha isoforms--gcHIF-1alpha and gcHIF-4alpha--from the hypoxia-tolerant grass carp, Ctenopharyngodon idellus. **BMC Mol Biol**. 2006 Apr 20;7:15. PubMed PMID: 16623959; PubMed Central PMCID: PMC1473195.

Ng PK, Wu RS, Zhang ZP, Mok HO, Randall DJ, Kong RY. Molecular cloning and characterization of a hypoxia-responsive CITED3 cDNA from grass carp. Comp **Biochem Physiol B Biochem Mol Biol**. 2003 Oct;136(2):163-72. PubMed PMID: 14529742.