# Sung Sam Gong, PhD

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## Employment History

1. Apr, 2014 – Current: Senior Research Associate in Bioinformatics, Department of Obstetrics and Gynaecology, School of Clinical Science, University of Cambridge, Cambridge, UK
2. Feb, 2015 – Current: Visiting Researcher, Wellcome Trust Sanger Institute, Hinxton, UK
3. Sep, 2010 – Mar, 2014: Lead Bioinformatician, Cardiovascular Genetics and Genomics, NIHR Cardiovascular Biomedical Research Unit, Royal Brompton and Harefield NHS Foundation Trust and Imperial College, London, UK
4. Oct, 2010 – Sep, 2011: Visiting Scientist, MRC Clinical Science Centre, Hammersmith, London, UK
5. Sep, 2005 – Sep, 2006: Research Scientist, KOBIC (Korean Bioinformation Centre), KRIBB (Korea Research Institute of Bioscience and Biotechnology), Daejeon, Korea

## Education

1. Oct, 2006 – Aug, 2010: PhD, Department of Biochemistry, University of Cambridge, Cambridge, UK (supervisor: Professor Sir Tom Blundell) Thesis title: Structural and Functional Analysis of Single Amino Acid Replacement in Proteins: Insights from Protein Evolution into the Disease Aetiology
2. Sep, 2003 – Aug, 2005: MSc, KAIST (Korea Advanced Institute of Science and Technology), Department of BioSystems, Daejeon, Korea (supervisor: Dr. Jong Bhak) Thesis title: PSIbase and interpare : systems for studying protein structural interactomics
3. Mar, 2002 – Aug, 2003: BSc, Department of Computer Science, Korea University, Seoul, Korea.
4. Mar, 1995 – Feb, 2002: BSc, Department of Biology, Korea University, Seoul, Korea

## Honours and Awards

1. 2013 KSEAUK (The Korean Scientists and Engineers Association in the UK) Early Career Scientist and Engineering Award
2. 2009 Travel Bursary (the Sanger fund) from the Dept. Biochemistry, University of Cambridge
3. 2009 Travel Bursary from Hughes Hall, University of Cambridge, Cambridge, UK
4. 2009 KSEAUK (The Korean Scientists and Engineers Association in the UK) Travel Award
5. 2007 Mogam Science Scholarship of Korea

# Publications

1. **Placental polyamine metabolism is enhanced via SMS escape from X-inactivation and protects from fetal growth restriction but predisposes to preeclampsia. Gong S,** Sovio U, Aye ILMH, Gaccioli F, Johnson MD, Dopierala J, Wood AM, Cook E, Jenkins B, Koulman A, Casero R, Constância M, Charnock-Jones DS, Smith GCS, ***Cell Metabolism, IN REVIEW.***
2. **Screening for fetal growth restriction using ultrasound and the sFLT1:PlGF ratio**, Gaccioli F, Sovio U, Dopierala J, **Gong S**, Kirk P, Cook E, Richardson S, Hund M, Charnock-Jones DS, Smith G, ***Lancet, SUBMITTED***
3. **Genome-wide oxidative bisulfite sequencing identifies sex-specific methylation differences in the human placenta. Gong S,** Johnson MD, Dopierala J, Gaccioli F, Sovio U, Constância M, Smith GCS, Charnock-Jones DS, ***Epigenetics, IN REVISION***.
4. **RNA-Seq reveals conservation of function among the yolk sacs of human, mouse and chicken.** Cindrova-Davies T, Jauniaux E, Elliot MG, **Gong S**, Burton GJ, Charnock-Jones DS. ***Proc Natl Acad Sci U S A. 2017*** Jun 13;114(24):E4753-E4761. doi: 10.1073/pnas.1702560114.
5. **MANORAA (Mapping Analogous Nuclei Onto Residue And Affinity) for identifying protein-ligand fragment interaction, pathways and SNPs.** Tanramluk D, Narupiyakul L, Akavipat R, **Gong S**, Charoensawan V. ***Nucleic Acids Res. 2016*** Jul 8;44(W1):W514-21. doi: 10.1093/nar/gkw314.
6. **Integrated allelic, transcriptional, and phenomic dissection of the cardiac effects of titin truncations in health and disease.** Roberts AM, Ware JS, Herman DS, Schafer S, Baksi J, Bick AG, Buchan RJ, Walsh R, John S, Wilkinson S, Mazzarotto F, Felkin LE, **Gong S**, MacArthur JA, Cunningham F, Flannick J, Gabriel SB, Altshuler DM, Macdonald PS, Heinig M, Keogh AM, Hayward CS, Banner NR, Pennell DJ, O'Regan DP, San TR, de Marvao A, Dawes TJ, Gulati A, Birks EJ, Yacoub MH, Radke M, Gotthardt M, Wilson JG, O'Donnell CJ, Prasad SK, Barton PJ, Fatkin D, Hubner N, Seidman JG, Seidman CE, Cook SA. ***Sci Transl Med. 2015*** Jan 14;7(270):270ra6. doi: 10.1126/scitranslmed.3010134.
7. **NECTAR: a database of codon-centric missense variant annotations. Gong S**, Ware J, Walsh R. Cook S. ***Nucleic Acids Res. 2014*** Jan 1;42(1):D1013-9. doi: 10.1093/nar/gkt1245.
8. **Next generation diagnostics in inherited arrhythmia syndromes: a comparison of two approaches.** Ware JS, John S, Roberts AM, Buchan R, **Gong S**, Peters NS, Robinson DO, Lucassen A, Behr ER, Cook SA. ***J Cardiovasc Transl Res. 2013*** Feb;6(1):94-103. doi: 10.1007/s12265-012-9401-8.
9. **MetaBase--the wiki-database of biological databases.** Bolser DM, Chibon PY, Palopoli N, **Gong S**, Jacob D, Del Angel VD, Swan D, Bassi S, González V, Suravajhala P, Hwang S, Romano P, Edwards R, Bishop B, Eargle J, Shtatland T, Provart NJ, Clements D, Renfro DP, Bhak D, Bhak J. ***Nucleic Acids Res. 2012*** Jan;40(Database issue):D1250-4. doi: 10.1093/nar/gkr1099.
10. **Meet me halfway: when genomics meets structural bioinformatics. Gong S**, Worth CL, Cheng TM, Blundell TL. ***J Cardiovasc Transl Res. 2011*** Jun;4(3):281-303. doi: 10.1007/s12265-011-9259-1.
11. **Structural and Functional Restraints on the Occurrence of Single Amino Acid Variations in Human Proteins. Gong S**, Blundell TL. ***PLoS One.*** **2010** Feb 12;5(2):e9186. doi: 10.1371/journal.pone.0009186.

12. **MitoInteractome: mitochondrial protein interactome database, and its application in 'aging network' analysis.** Reja R, Venkatakrishnan AJ, Lee J, Kim BC, Ryu JW, **Gong S**, Bhak J, Park D. ***BMC Genomics. 2009*** Dec 3;10 Suppl 3:S20. doi: 10.1186/1471-2164-10-S3-S20.
13. **Structural and functional constraints in the evolution of protein families**. Worth CL, **Gong S**, Blundell TL. ***Nat Rev Mol Cell Biol. 2009*** Oct;10(10):709-20. doi: 10.1038/nrm2762. Epub 2009 Sep 16. Review
14. **Structural interactomics: informatics approaches to aid the interpretation of genetic variation and the development of novel therapeutics**. Lee S, Brown A, Pitt WR, Perez Higueruelo A, **Gong S**, Bickerton GR, Schreyer A, Tanramluk D, Baylay A, Blundell TL. ***Mol Biosyst.* 2009** Dec;5(12):1456-72. doi: 10.1039/B906402h. Epub 2009 Aug 6. Review
15. **Structural and functional restraints in the evolution of protein families and superfamilies. Gong S**, Worth CL, Bickerton GR, Lee S, Tanramluk D, Blundell TL. ***Biochem Soc Trans. 2009*** Aug;37(Pt 4):727-33. doi: 10.1042/BST0370727. Review.
16. **Discarding functional residues from the substitution table improves predictions of active sites within three-dimensional structures. Gong S**, Blundell TL. ***PLoS Comput Biol. 2008*** Oct 3;4(10):e1000179. doi: 10.1371/journal.pcbi.1000179.
17. **A structural bioinformatics approach to the analysis of nonsynonymous single nucleotide polymorphisms (nsSNPs) and their relation to disease.** Worth CL, Bickerton GR, Schreyer A, Forman JR, Cheng TM, Lee S, **Gong S**, Burke DF, Blundell TL. J ***Bioinform Comput Biol. 2007*** Dec;5(6):1297-318.
18. **SNP@Domain: a web resource of single nucleotide polymorphisms (SNPs) within protein domain structures and sequences.** Han A, Kang HJ, Cho Y, Lee S, Kim YJ, **Gong S**. ***Nucleic Acids Res. 2006*** Jul 1;34(Web Server issue):W642-4.
19. **A protein domain interaction interface database: InterPare. Gong S**, Park C, Choi H, Ko J, Jang I, Lee J, Bolser DM, Oh D, Kim DS, Bhak J. ***BMC Bioinformatics. 2005*** Aug 25;6:207.
20. **PSIbase: a database of Protein Structural Interactome map (PSIMAP). Gong S**, Yoon G, Jang I, Bolser D, Dafas P, Schroeder M, Choi H, Cho Y, Han K, Lee S, Choi H, Lappe M, Holm L, Kim S, Oh D, Bhak J. ***Bioinformatics. 2005*** May 15;21(10):2541-3.

## Patent

1. System and Method for Analysis of Interfaces Based on Protein Domain and their ligands and Recording Medium Therefore (KOR:2005-0121684)
2. System and Method for Searching Materials Interfacing with Proteins Based on Interfaceome and Recording Medium Therefore, (KOR:2006-0062631)

## Peer Review Records

1. A regular invited reviewer of *Nucleic Acids Research*, Oxford University Press
2. Invited reviewer for *PLoS ONE* (Public Library of Science) and *Journal of Evolutionary Biology* (Wiley)
3. See the list of review record verified from Publons: https://publons.com/author/1225687/sungsam-gong#profile

## Research Interests

1. Computational epigenomics and epitranscriptomics

2. Non-invasive prenatal diagnostics via cell-free fetus DNA/RNA
3. Developmental origin of health and disease
4. Computational assessment of structural and functional effect of genetic variations
5. Different promoter usage and its effect on transcriptome and proteome diversity at the single-cell resolution
6. Splice variants and protein isoforms diversity by transcriptome reconstruction

# Transferable Skills

## Computer programming & system administration

1. Various programming languages
    a. Perl, Python, Java, C, SQL, HTML, Bash, R etc.
2. Unix system administration
    a. File system, DBMS, storage, web, FTP, DHCP, and DNS server
3. High performance computing
    a. PBS-based linux cluster
    b. Ganglia to monitor distributed system
4. Cloud-computing
    a. Use of EC2 and S3 from Amazon Web Service
5. Software versioning and revision control
    a. Git and SVN

## Bioinformatics

1. Structural bioinformatics
    a. Protein sequence analysis
    b. Three-dimensional structure modelling
    c. Protein-protein interaction prediction
    d. Functional residue prediction
2. Next generation sequencing data analysis
    a. Variant calling and assessment
    b. De-novo assembly
    c. Differentially expressed gene analysis from RNA-Seq
    d. Allele specific expression and methylation
    e. Differentially methylated region detection from (ox)BS-Seq
    f. Peak calling from ChIP-Seq

# Referees

1. Professor Sir Tom Blundell
    Relation: PhD supervisor
    Position: Professor
    Address: Department of Biochemistry, University of Cambridge, Sanger Building, 80 Tennis Court Road, Cambridge, CB2 1GA
    Email: tom@cryst.bioc.cam.ac.uk
    Telephone: +44 (0)1223 333628

2. Professor Jong Bhak (aka. Jong Park)
   Relation: MSc. supervisor
   Position: Professor
   Address: Department of Biomedical Engineering, School of Life Sciences, Ulsan National Institute of Science and Technology (UNIST), 50 UNIST-gil, Ulju-gun, Ulsan, 689-798, Republic of Korea
   Email: j@bio.cc, jongbhak@genomics.org
   Telephone: +82 (0)10 9944 6754

3. Professor Gordon Smith
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   Telephone: +44 (0)1223 336871

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   Email:dscj1@cam.ac.uk
   Telephone: +44 (0)1223 336875

5. Professor Stuart Cook
   Relation: Former group head
   Position: Group head
   Address: Cardiovascular Genetics and Genomics, NIHR Cardiovascular Biomedical Research Unit, Royal Brompton Hospital, Sydney Street, London, SW3 6NP
   Email: stuart.cook@imperial.ac.uk

6. Dr. Paul Barton
   Relation: Former line manager
   Position: Genetics research manager
   Address: Cardiovascular Genetics and Genomics, NIHR Cardiovascular Biomedical Research Unit, Royal Brompton Hospital, Sydney Street, London, SW3 6NP
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