Curriculum Vitae
Geng Wu

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Education and Work Experience:

1992-1994: Strengthening class of mathematics and physics, University of Science and Technology of China
1994-1997: Department of Biology, University of Science and Technology of China, B.Sc. degree in Biology (thesis advisor: Prof. Haiyan Liu and Prof. Yunyu Shi)
1997: subsidiary B.Sc. degree in Chemical Physics, University of Science and Technology of China
1997-1999: Master's degree, Department of Chemistry, Princeton University, USA
1997-2001: Ph.D. degree, Department of Chemistry, Princeton University, USA (thesis advisor: Prof. Yigong Shi)
2001-2003: Research Associate, Memorial Sloan-Kettering Cancer Center, USA (advisor: Prof. Nikola Pavletich)
2003-2008: Research Associate, Children's Hospital Boston, Harvard Medial School, USA (Prof. Xi He)
2008-now: Professor, School of Life Sciences and Biotechnology, Shanghai Jiao Tong University, China

Honors and Awards:

2005-2008: Special Fellowship, Leukemia and Lymphoma Society, USA
2008: Eastern Scholar, Shanghai, China
2008: Dawn Scholar, Shanghai, China
2009: Pujiang Talent, Shanghai, China
2009: Excellent Talents of New Century, Ministry of Education, China
2014: My student, Zhenyi Zhang, was awarded Excellent PhD Thesis of Shanghai
2014: Eastern Scholar Tracking Program, Shanghai, China
2016: First Prize, Science Research Famous Achievement Award in Higher Institution, Ministry of Education, China

Present Research Interest:

Synthetic Biology & Biophysical Chemistry
Reconstruction of cellular life, proteinoid design and protein design, cellular delivery of tumor suppressor proteins, Cryo-EM structure of protein machines related to cancer

Selected Publications (*: corresponding author, $^{\#}$: co-first author):

1. Liu L, Jiang S, Xing M, Chen C, Lai C, Li N, Liu G, Wu D, Gao H, Hong L, Tan P, Chen S, Deng Z, **Wu G***, Wang L*. Structural analysis of an L-cysteine desulfurase from an Ssp DNA phosphorothioation system. ***mBio*** 11(2):e00488-20. (2020)

2. Xiong X$^{\#}$, **Wu G**$^{\#}$, Wei Y$^{\#}$, Liu L, Zhang Y, Su R, Jiang X, Li M, Gao H, Tian X, Zhang Y, Hu L, Chen S, Tang Y, Jiang S, Huang R, Li Z, Wang Y, Deng Z, Wang J, Dedon PC, Chen S, Wang L. SspABCD-SspE is a phosphorothioation-sensing bacterial defence system with broad anti-phage activities. ***Nature Microbiology*** 5(7):917-928. (2020)
3. Lin K, **Wu G***. Isothermal titration calorimetry assays to measure binging affinities in vitro. ***Methods in Molecular Biology*** 1893:257-272. (2019)
4. Liu G, Fu W, Zhang Z, He Y, Yu H, Wang Y, Wang X, Zhao YL, Deng Z, **Wu G***, He X*. Structural basis for the recognition of sulfur in phosphorothioated DNA. ***Nature Communications*** 9(1):4689. (2018)
5. Kulaberoglu Y, Lin K, Holder M, Gai Z, Gomez M, Shifa BA, Mavis M, Hua L, Sharif AAD, Lujan C, Smith EJ, Bjedov I, Tapon N, **Wu G***, Hergovich A*. Stable MOB1 interaction with Hippo/MST is not essential for development and tissue growth control. ***Nature Communications*** 8:695. (2017)
6. Mu Z, Wang L, Deng W, Wang J, **Wu G***. Structural insight into the Ragulator complex which anchors mTORC1 to the lysosomal membrane. ***Cell Discovery*** 3:17049. (2017) cited 10 times
7. Jiang H, Deng R, Yang X, Shang J, Lu S, Zhao Y, Song K, Liu X, Zhang Q, Chen Y, Chinn YE, **Wu G**, Li J, Chen G, Yu J, Zhang J. Peptidomimetic inhibitors of APC-Asef interaction block colorectal cancer migration. ***Nature Chemical Biology*** 13(9):994-1001. (2017) cited 36 times
8. Gai Z, Chu W, Deng W, Li W, Li H, He A, Nellist M, **Wu G***. Structure of the TBC1D7-TSC1 complex reveals that TBC1D7 stabilizes dimerization of the TSC1 C-terminal coiled coil region. ***Journal of Molecular Cell Biology*** 8:411-425. (2016) cited 11 times
9. Gai Z, Wang Q, Yang C, Wang L, Deng W, **Wu G***. Structural mechanism for the arginine sensing and regulation of CASTOR1 in the mTORC1 signaling pathway. ***Cell Discovery*** 2:16051. (2016) cited 14 times
10. Zhang Z, Akyildiz S, Xiao Y, Gai Z, An Y, Behrens J*, **Wu G***. Structures of the APC-ARM domain in complexes with discrete Amer1/WTX fragments reveal that it uses a consensus mode to recognize its binding partners. ***Cell Discovery*** 1:15016. (2015)
11. **Wu G**$^{\#}$, Chen D$^{\#}$, Tang H$^{\#}$, Ren Y, Chen Q, Lv Y, Zhang Z, Zhao YL*, Yao Y, Xu P*. Structural insights into the specific recognition of N-heterocycle biodenitrogenation-derived substrates by microbial amide hydrolases. ***Molecular Microbiology*** 91:1009-1021.（2014）
12. Zhao G$^{\#}$, **Wu G**$^{\#}$, Zhang Y, Liu G, Han T, Deng Z, He X*. Structure of the N-glycosidase MilB in complex with hydroxymethyl CMP reveals its Arg23 specifically recognizes the substrate and controls its entry. ***Nucleic Acids Research*** 42:8115-24.（2014）
13. Zhang Y, Fu L, Qi X, Zhang Z, Xia Y, Jia J, Jiang J, Zhao Y*, **Wu G***. Structural insight into the mutual recognition and regulation between Suppressor of Fused and Gli/Ci. ***Nature Communications*** 4:2608. (2013) cited 34 times

14. Chen D, Tang H, Lv Y, Zhang Z, Shen K, Lin K, Zhao YL, **Wu G***, Xu P*. Structural and computational studies of the maleate isomerase Iso from *Pseudomonas putida* S16 reveal a breathing motion wrapping the substrate inside. ***Molecular Microbiology*** 87:1237-1244. (2013) cited 10 times
15. Zhang Z, Chen L, Gao L, Lin K*, Zhu L, Lu Y, Shi X, Gao Y, Zhou J, Xu P, Zhang J*, **Wu G***. Structural basis for the recognition of Asef by Adenomatous Polyposis Coli. ***Cell Research*** 22:372-386. (2012, selected into the Faculty of 1000 database by Prof. Mariann Bienz, member of the Royal Society, UK) cited 21 times
16. **Wu G***, Huang H, Abreu JG, He X*. Inhibition of GSK3 phosphorylation of β-catenin via phosphorylated PPPSPXS motifs of Wnt coreceptor LRP6. ***PLoS One*** 4, e4926. (2009) cited 131 times
17. **Wu G**, He X*. Threonine 41 in β-catenin serves as a key phosphorylation relay residue in β-catenin degradation. ***Biochemistry*** 45, 5319-5323. (2006) cited 40 times
18. **Wu G**, Liu C, He X*. Ozz, a new name on the long list of β-Catenin's nemeses. ***Molecular Cell*** 13:451-3. (2004)
19. **Wu G**, Xu G, Schulman B, Jeffrey P, Harper JW, Pavletich NP*. Structure of a β-TrCP1–Skp1–β-catenin complex: destruction-motif binding and lysine specificity of the $\mathrm{SCF}^{\beta\text{-TrCP1}}$ ubiquitin ligase. ***Molecular Cell*** 11:1445-1456. (2003) cited 449 times
20. **Wu G**#, Chai J#, Suber T, Wu JW, Du C, Wang X, Shi Y*. Structural basis of IAP recognition by Smac/DIABLO. ***Nature*** 408:1008-1012. (2000) cited 667 times
21. **Wu G**#, Chen YG#, Ozdamar B, Gyuricza CA, Chong PA, Wrana JL, Massague J, Shi Y*. Structural basis of Smad2 recognition by the Smad Anchor for Receptor Activation. ***Science*** 287:92-97. (2000) cited 226 times

Other publications:

22. Yu H, Li J, Liu G, Zhao G, Wang Y, Hu W, Deng Z, **Wu G**, Gan J, Zhao YL, He X. DNA backbone interactions impact the sequence specificity of DNA sulfur-binding domains: revelations from structural analyses. ***Nucleic Acids Research*** gkaa574. (2020)
23. Li M, Hu X, Zhang S, Ho MS, **Wu G**, Zhang L. Traffic jam regulates the function of the ovarian germline stem cell progeny differentiation niche during pre-adult stage in *Drosophila*. ***Scientific Reports*** 9(1):10124. (2019)
24. Hu H, Wang L, Wang W, **Wu G**, Tao F, Xu P, Deng Z, Tang H. Regulatory Mechanism of Nicotine Degradation in *Pseudomonas putida*. ***mBio*** 10(3): e00602-19. (2019)
25. Shi M, Chen B, Mahajan D, Boh BK, Zhou Y, Dutta B, Tie HC, Sze SK, **Wu G**, Lu L. Amino acids stimulate the endosome-to-Golgi trafficking through Ragulator and small GTPase Arl5. ***Nature Communications*** 9(1):4987. (2018)
26. Yu H, Liu G, Zhao G, Hu W, **Wu G**, Deng Z, He X. Identification of a conserved DNA sulfur recognition domain by characterizing the phosphorothioate-specific endonuclease SprMcrA from *Streptomyces pristinaespiralis*. ***Molecular***

Microbiology 110(3):484-497. (2018)

27. Zhang K, **Wu G**, Tang H*, Hu C, Shi T, Xu P*. Structural basis for the transcriptional repressor NicR2 in nicotine degradation from *Pseudomonas*. ***Molecular Microbiology*** 103:165-180. (2017)
28. Qian T, Wo J, Zhang Y, Song Q, Feng G, Luo R, Lin S*, **Wu G***, Chen HF*. Crystal structure of StnA for the biosynthesis of antitumor drug streptonigrin reveals a unique substrate binding mode. ***Scientific Reports*** 7:40254. (2017)
29. Zhao G, Chen C, Xiong W, Gao T, Deng Z, **Wu G***, He X*. Structural basis of the substrate preference towards CMP for a thymidylate synthase MilA involved in mildiomycin biosynthesis. ***Scientific Reports*** 6:39675. (2016)
30. Jiang Y, Tang H*, **Wu G**, Xu P*. Functional identification of a novel gene, moaE, for 3-succinoylpyridine degradation in *Pseudomonas putida* S16. ***Scientific Reports*** 5:13464. (2015)
31. Zhang Y, An J, Yang G, Bai A, Zheng B, Lou Z, **Wu G**, Ye W, Chen HF, Feng Y*, Manco G*. Active site loop conformation regulates promiscuous activity in a lactonase from *Geobacillus kaustophilus* HTA426. ***PLoS One*** 10:e0115130. (2015)
32. Liu G, Zhang Z, Zhao G, Deng Z, **Wu G***, He X*. Crystallization and preliminary X-ray analysis of the type IV restriction endonuclease ScoMcrA from *Streptomyces coelicolor*, which cleaves both Dcm-methylated DNA and phosphorothioated DNA. ***Acta Crystallography Section F*** 71:57-60. (2015)
33. Xie Y, An J, Yang G, **Wu G**, Zhang Y, Cui L, Feng Y*. Enhanced enzyme kinetic stability by increasing rigidity within the active site. ***Journal of Biological Chemistry*** 289:7994-8006. (2014)
34. Wang H, Zhang Y, Zhang Z, Jin WL*, **Wu G***. Purification, crystallization and preliminary X-ray analysis of the inverse F-BAR domain of the human srGAP2 protein. ***Acta Crystallography Section F*** 70:123-126. (2014)
35. Li A, Zhang Y*, Wang C, **Wu G***, Wang Z. Purification, molecular cloning, and antimicrobial activity of peptides from the skin secretion of the black-spotted frog, *Rana nigromaculata*. ***World Journal of Microbiology and Biotechnology*** 29:1941-1949 (2013)
36. Chen F, Zhang Z, Lin K*, Qian T, Zhang Y, You D, He X, Wang Z, Liang J, Deng Z, **Wu G***. Crystal structure of the cysteine desulfurase DndA of *Streptomyces lividans* which is involved in DNA phosphorothioation. ***PLoS One*** 7:e36635. (2012)
37. Hu W, Wang C, Liang J, Zhang T, Hu Z, Wang Z, Lan W, Li F, Wu H, Ding J, **Wu G**, Deng Z, Cao C*. Structural insights into DndE from *Escherichia coli* B7A involved in DNA phosphorothioation modification. ***Cell Research*** 22:1203-1206. (2012)
38. Tang H, Yao Y, Wang L, Yu H, Ren Y, **Wu G**, Xu P*. Genomic analysis of *Pseudomonas putida*: genes in a genome island are crucial for nicotine degradation. ***Scientific Reports*** 2:377. (2012)
39. Li Q, Feng J, Gao C, Li F, Yu C, Meng L, Zhang Z, Ma C*, Gu L*, **Wu G**, Xu P. Purification and characterization of a flavin reductase from the biodesulfurizing

bacterium *Mycobacterium goodii* X7B. ***Process Biochemistry*** 47:1144-1149. (2012)

40. Tang H, Yu H, Tai C, Huang K, Liu Y, Wang L, Yao Y, **Wu G**, Xu P*. Genome sequence of a novel nicotine-degrading strain, *Pseudomonas geniculata* N1. ***Journal of Bacteriology*** 194:3553-3554. (2012)
41. Zhang Z, Li H, Chen L, Lu X, Zhang J, Xu P, Lin K*, **Wu G***. Molecular basis for the recognition of Adenomatous Polyposis Coli by the Discs Large 1 protein. ***PLoS One*** 6:e23507. (2011)
42. Zhang Z, Lin K*, Gao L, Chen L, Shi X, **Wu G***. Crystal structure of the armadillo repeat domain of adenomatous polyposis coli which reveals its inherent flexibility. ***Biochemical and Biophysical Research Communications*** 412:732-736. (2011)
43. Chen F, Lin K*, Zhang Z, Chen L, Shi X, Cao C, Wang Z, Liang J, Deng Z, **Wu G***. Purification, crystallization, and preliminary X-ray analysis of DndE protein from *Salmonella enterica* serovar Cerro 87 which is involved in DNA phosphorothioation. ***Acta Crystallography Section F*** 67:1440-1442. (2011)
44. Huang Z, Zhu L, Cao Y, **Wu G**, Liu X, Chen Y, Wang Q, Shi T, Zhao Y, Wang Y, Li W, Li Y, Chen H*, Chen G, Zhang J*. ASD: a comprehensive database of allosteric proteins and modulators. ***Nucleic Acids Research*** 39:D663-9. (2011)
45. Tao F, Zhao P, Li Q, Su F, Yu B, Ma C, Tang H, Tai C, **Wu G**, Xu P*. Genome sequence of *Rhodococcus erythropolis* XP, a biodesufurizing bacterium with industrial potential. ***Journal of Bacteriology*** 193:6422-6423. (2011)
46. Gai Z, Wang X, Tang H, Tai C, Tao F, **Wu G**, Xu P*. Genome sequence of *Sphingobium yanoikuyae* XLDN2-5, an efficient carbazole-degrading strain. ***Journal of Bacteriology*** 193:6404-6405. (2011)
47. Su F, Hua D, Zhang Z, Wang X, Tang H, Tao F, Tai C, Wu Q, **Wu G**, Xu P*. Genome sequence of *Bacillus pumilus* S-1, an efficient isoeugenol-utilizing producer for natural vanillin. ***Journal of Bacteriology*** 193:6400-6401. (2011)
48. Yu H, Tang H, Wang L, Yao Y, **Wu G**, Xu P*. Complete genome sequence of nicotine-degrading *Pseudomonas putida* strain S16. ***Journal of Bacteriology*** 193:5541-5542. (2011)
49. Gai Z, Wang X, Liu X, Tai C, Tang H, He X, **Wu G**, Deng Z, Xu P*. The genes coding for the conversion of carbazole to catechol are flanked by IS6100 elements in *Sphingomonas* sp. strain XLDN2-5. ***PLoS One*** 5:e10018. (2010)
50. Li J, Feng J, Li Q, Ma C, Yu B, Gao C, **Wu G**, Xu P*. Both FMNH2 and FADH2 can be utilized by the dibenzothiophene monooxygenase from a desulfurizing bacterium *Mycobacterium goodii* X7B. ***Bioresource Technology*** 100:2594-2599. (2009)
51. Tang H, Wang L, Meng X, Ma L, Wang S, He X, **Wu G**, Xu P*. Novel nicotine oxidoreductase-encoding gene involved in nicotine degradation by *Pseudomonas putida* strain S16. ***Applied and Environmental Microbiology*** 75:772-778. (2009)
52. Hao B, Zheng N, Schulman BA, **Wu G**, Miller JJ, Pagano M, Pavletich NP*. Structural basis of the Cks1-dependent recognition of p27Kip1 by the SCFSkp2 ubiquitin ligase. ***Molecular Cell*** 20:9-19. (2005)

53. Qin H, Srinivasula SM#, **Wu G#**, Fernandes-Alnemri T, Alnamri ES, Shi Y*. Structural basis of procaspase-9 recruitment by the apoptotic protease-activating factor 1. ***Nature*** 399:549-557. (1999)
54. Hua X, Miller Z, **Wu G**, Shi Y, Lodish HF*. Specificity in transforming growth factor β-induced transcription of the plasminogen activator inhibitor-1 gene: interactions of promoter DNA, transcription factor μE3 and Smad proteins. ***Proceedings of National Academy of Science USA*** 96:13130-13135. (1999)