



创新教育模式 培养一流人才



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四川大学 生命科学学院

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教职员工



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研究兴趣:

- 1) 药物分子设计算法与应用
- 2) 蛋白设计和三维结构预测
- 3) 序列分析与功能预测

主要成果:

- 1) 建立了 CYSCORE、CB-Dock、FitDock、LigMate、CIS-RR 等一系列分子模拟与设计算法与软件, 获广泛使用, 先后发现了针对 MDM2、HSP70、AChE、PB 等药物靶点的活性化合物。
- 2) 发展蛋白设计算法 EvoDesign, 成功设计出多个靶向 HER2、EGFR 等药物靶标的高稳定性、高亲和力、抗聚集的人工多肽、蛋白。
- 3) 建立 AbRSA、AbAlign 等抗体分析算法, 成功完成新冠抗体 R3P1-E4 的亲和力优化、肿瘤靶标 HMGB1、PrPc、PD1 抗体的人源化设计。

工作经历:

- 2014-今, 四川大学, 生命科学学院, 副教授
- 2011-2014, 四川大学, 生命科学学院, 讲师

教育经历:

- 2020-2021, 美国哈佛大学, 生物信息, X. Shirley Liu Lab
- 2016-2017, 美国密歇根大学, 生物信息, Yang Zhang Lab
- 2004-2010, 中科院生物物理所, 生物信息, 博士
- 2000-2004, 西南交通大学, 应用物理, 学士

主要论著:

1. Y Liu, X Yang, J Gan, S Chen, ZX Xiao, Y Cao*. CB-Dock2: improved protein-ligand blind docking by integrating cavity detection, docking and homologous template fitting. *Nucleic Acids Research*. In press, 2022.
2. X. Yang, Y Liu, J Gan, ZX Xiao, Y Cao*. FitDock: protein-ligand docking by template fitting. *Briefings in Bioinformatics*. doi.org/10.1093/bib/bba087, 2022
3. Y Liu, J Gan, R Wang, X Yang, Z Xiao, Y Cao*. DrugDevCovid19: An Atlas of Anti-COVID-19 Compounds Derived by Computer-Aided Drug Design. *Molecules* 27 (3), 683, 2022.
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10. Z Zhu, Y Fan, Y Liu, T Jiang, Y Cao*, Y Peng*. Prediction of antiviral drugs against African swine fever viruses based on protein-protein interaction analysis. *PeerJ*, 8, e8855, 2020
11. Y Liu#, M Grimm#, W Dai, M Hou, ZX Xiao, Y Cao*. CB-Dock: a web server for cavity detection-guided protein-ligand blind docking. *Acta Pharmacologica Sinica*. 41,138-144, 2020 (ESI高被引论文)
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13. Y Cao, W Dai, Z Miao. Evaluation of Protein-Ligand Docking by Cyscore. *Methods in molecular biology* 1762, 233-243, 2018
14. B Kong#, Y Cao#, D Wu, L An, F Ran, Y Lin, C Ye, H Wang*, H Hang*. Affinity maturation of an antibody for the UV-induced DNA lesions 6,4 pyrimidine-pyrimidones. *Applied Microbiology and Biotechnology*. 102(15) 6409-6424, 2018
15. C Li#, Z Wang#, Y Cao#, L Wang, J Ji, Z Chen, T Deng, T Jiang*, G Cheng*, F Qin*. Screening for Novel Small-Molecule Inhibitors Targeting the Assembly of Influenza Virus Polymerase Complex by a Bimolecular Luminescence Complementation-Based Reporter System. *J Virol*. 91(5): e02282-16, 2017
16. Z Miao* and Y Cao*. Quantifying side-chain conformational variations in protein structure. *Scientific Reports*. 6: 37024, 2016
17. J Liu#, Z Miao#, L Li, ZX Xiao*, Y Cao*. DRSP: A Structural Database for Single Residue Substitutions in PDB. *Progress in Biochemistry and Biophysics*. 43(8):810-816, 2016
18. J Guo#, Y Cao#, K Qin, X Zhao, D Wang, Z Li, L Xin, Y Shu, J Zhou*. Limited effect of recombinant human mannose-binding lectin on the infection of novel influenza A (H7N9) virus in vitro. *Biochem Biophys Res Commun*. 458(1):77-81, 2015
19. Y Cao*, L Li., Improved protein-ligand binding affinity prediction by using a curvature dependent surface area model. *Bioinformatics*, 30(12):1674-1680, 2014 (ESI高被引论文)
20. L Huang#, Y Cao#, J Zhou, K Qin, W Zhu, Y Zhu, L Yang, D Wang, H Wei*, Y Shu*. A conformational restriction in influenza A virus neuraminidase binding site by R152 caused the combinational effect of I222T with H274Y on oseltamivir resistance. *Antimicrob Agents Chemother*. 58(3), 1639-1645, 2014
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