<table>
<tr><td>姓名</td><td>马英</td><td>职称</td><td>讲师</td><td>所在部门</td><td>药学院</td><td>研究方向</td><td>新型抗肿瘤药物研究</td><td rowspan="2">  </td></tr>
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<tr><td colspan="9">教育背景</td></tr>
<tr><td colspan="9">2010 年 9 月 – 2015 年 7 月天津医科大学，药理学专业，博士学位
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<tr><td colspan="9">工作经历</td></tr>
<tr><td colspan="9">2015 年 7 月至今　天津医科大学药学院，讲师</td></tr>
<tr><td colspan="9">研究成果（本人具有代表性的论著、论文及主持的科研项目）</td></tr>
<tr><td>论著及编著</td><td colspan="8"></td></tr>
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论文	1.Wu J, Li W, Zheng Z, Lu X, Zhang H, **Ma Y***, et al. Design, synthesis, biological evaluation, common feature pharmacophore model and molecular dynamics simulation studies of ethyl 4-(phenoxymethyl)-2-phenylthiazole-5-carboxylate as Src homology-2 domain containing protein tyrosine phosphatase-2 (SHP2) inhibitors. J Biomol Struct Dyn. 2021;39(4):1174-88. 2.Zhou L, Ma YC, Tang X, Li WY, **Ma Y***, Wang RL. Identification of the potential dual inhibitor of protein tyrosine phosphatase sigma and leukocyte common antigen-related phosphatase by virtual screen, molecular dynamic simulations and post-analysis. J Biomol Struct Dyn. 2021;39(1):45-62. 3.Li WY, **Ma Y***, Li HX, Lu XH, Du S, Ma YC, et al. Scaffold-based selective SHP2 inhibitors design using core hopping, molecular docking, biological evaluation and molecular simulation. Bioorg Chem. 2020;105:104391. 4.Liu WS, Yang B, Wang RR, Li WY, Ma YC, Zhou L, **Ma Y***,et al. Design, synthesis and biological evaluation of pyridine derivatives as selective SHP2 inhibitors. Bioorg Chem. 2020;100:103875. 5.Ma YC, Yang B, Wang X, Zhou L, Li WY, Liu WS,**Ma Y***,et al. Identification of novel inhibitor of protein tyrosine phosphatases delta: structure-based pharmacophore modeling, virtual screening, flexible docking, molecular dynamics simulation, and post-molecular dynamics analysis. J Biomol Struct Dyn.2020;38(15):4432-48. 6.Wu J, Sun Y, Zhou H,**Ma Y***, Wang R. Design, synthesis, biological evaluation and molecular dynamics simulation studies of (R)-5-methylthiazolidin-4-One derivatives as megakaryocyte protein tyrosine phosphatase 2 (PTP-MEG2) inhibitors for the treatment of type 2 diabetes. J Biomol Struct Dyn. 2020;38(11):3156-65. 7.Wu JW, Zhang H, Li WY, Tang X, Li HL, Lu XH,**Ma Y*** et al. Design potential selective inhibitors for human leukocyte common antigen-related (PTP-LAR) with fragment replace approach. J Biomol Struct Dyn. 2020;38(18):5338-48 8.Wu J, Sun Y, Zhou H, **Ma Y***, Wang R*. Design, synthesis, biological evaluation and molecular dynamics simulation studies of (R)-5-methylthiazolidin-4-One derivatives as megakaryocyte protein tyrosine phosphatase 2 (PTP-MEG2) inhibitors for the treatment of type 2 diabetes. J Biomol Struct Dyn. 2019:1-10. 9.Wei-Ya L, Yu-Qing D, Yang-Chun M, Xin-Hua L, **Ying M***, Wang R-L*. Exploring the cause of the inhibitor 4AX attaching to binding site disrupting protein tyrosine phosphatase 4A1 trimerization by molecular dynamic simulation.J Biomol Struct Dyn. 2019;37(18):4840-51. 10.Wang R-R, **Ma Y***, Du S, Li W-Y, Sun Y-Z, Zhou H, et al. Exploring the reason for increased activity of SHP2 caused by D61Y mutation through molecular dynamics. Comput Biol Chem. 2019;78:133-43. 11.Wang R-R, Liu W-S, Zhou L, **Ma Y***, Wang R-L*. Probing the acting mode and advantages of RMC-4550 as an Src-homology 2 domain-containing protein tyrosine phosphatase (SHP2) inhibitor at molecular level through molecular docking and molecular dynamics. J Biomol Struct Dyn. 2019:1-14. 12.Sun Y-Z, Wu J-W, Lu X-H, **Ma Y***, Wang R-L*. Exploring the effect of aplidin on low molecular weight protein tyrosine phosphatase by molecular docking and molecular dynamic simulation study. Comput Biol Chem. 2019;83:107123.

论文	13.Sun Y-Z, Chen X-B, Wang R-R, Li W-Y, **Ma Y***. Exploring the effect of N308D mutation on protein tyrosine phosphatase-2 cause gain-of-function activity by a molecular dynamics study. Journal of Cellular Biochemistry. 2019;120(4):5949-61. 14.Liu W-S, Wang R-R, Li W-Y, Rong M, Liu C-L, **Ma Y***, et al. Investigating the reason for loss-of-function of Src homology 2 domain-containing protein tyrosine phosphatase 2 (SHP2) caused by Y279C mutation through molecular dynamics simulation. J Biomol Struct Dyn. 2019:1-12. 15.Liu W-S, Jin W-Y, Zhou L, Lu X-H, Li W-Y, **Ma Y***, et al. Structure based design of selective SHP2 inhibitors by De novo design, synthesis and biological evaluation. Journal of Computer-Aided Molecular Design. 2019;33(8):759-74. 16.Liu WS, Wang RR, Sun YZ, Li WY, Li HL, Liu CL, **Ma Y***, et al. Exploring the effect of inhibitor AKB-9778 on VE-PTP by molecular docking and molecular dynamics simulation. Journal of Cellular Biochemistry. 2019. 17.Du S, Yang B, Wang X, Li W-Y, Lu X-H, Zheng Z-H, **Ma Y***, et al. Identification of potential leukocyte antigen-related protein (PTP-LAR) inhibitors through 3D QSAR pharmacophore-based virtual screening and molecular dynamics simulation.J Biomol Struct Dyn. 2019:1-14. 18.Zhu Y, Han Y, **Ma Y***, Yang P. ADME/toxicity prediction and antitumor activity of novel nitrogenous heterocyclic compounds designed by computer targeting of alkylglycerone phosphate synthase. Oncol Lett. 2018. 19.Ma Y, Li H-L, Chen X-B, Jin W-Y, Zhou H, **Ma Y***, et al. 3D QSAR Pharmacophore Based Virtual Screening for Identification of Potential Inhibitors for CDC25B. Comput Biol Chem. 2018;73:1-12. 20.Li W-Y, Wei H-Y, Sun Y-Z, Zhou H, **Ma Y***, Wang R-L*. Exploring the effect of E76K mutation on SHP2 cause gain-of-function activity by a molecular dynamics study. Journal of Cellular Biochemistry. 2018;119(12):9941-56. 21.Jin W-Y, **Ma Y***, Li W-Y, Li H-L, Wang R-L. Scaffold-based novel SHP2 allosteric inhibitors design using Receptor-Ligand pharmacophore model, virtual screening and molecular dynamics. Comput Biol Chem. 2018;73:179-88. 22.Liu X, Jing Z, Jia W-Q, Wang S-Q, **Ma Y***, Xu W-R, et al. Identification of novel PPARα/γ dual agonists by virtual screening, ADMET prediction and molecular dynamics simulations. Journal of Biomolecular Structure and Dynamics. 2017;36(11):2988-3002. 23.Li H-L, **Ma Y***, Zheng C-J, Jin W-Y, Liu W-S, Wang R-L. Exploring the effect of D61G mutation on SHP2 cause gain of function activity by a molecular dynamics study. Journal of Biomolecular Structure and Dynamics. 2017;36(14):3856-68. 24.**Ying Ma**[#], Hui-Yu Wei[#], Yu-Ze Zhang, Wen-Yan Jin, Hong-Lian Li, Hui Zhou, Xian-Chao Cheng, and Run-Ling Wang*. Synthesis, bioactivity, 3D-QSAR studies of novel dibenzofuran derivatives as PTP-MEG2 inhibitors [J]. Oncotarget, 2017, 8(24); 38466-38481. 25.Hong-Lian Li[#], **Ying Ma**[#], Ying Ma,Yu Li, Xiu-Bo Chen, Wei-Li Dong, and Run-Ling Wang*.The design of novel inhibitors for treating cancer by targeting CDC25B through disruption of CDC25B-CDK2/Cyclin A interaction using computational approaches [J]. Oncotarget, 2017, 8 (20); 33225-33240.

科研项目	1.天津市自然科学基金重点项目《选择性 SHP2 突变体 D61G、E76K 抑制剂研究》(16JCZDJC32500)；2016.04-2019.03；参与 2.国家自然科学基金国际（地区）合作与交流项目，81611130090 ，《以 SHP2 为靶点的抗白血病药物的设计、合成及活性筛选》；2016.1-2018.12；参与 3.国家自然科学基金项目《具有 PTP-1B、PPAR-α、PPAR-γ 三重作用的抗糖尿病先导物的设计、合成及活性研究》（20972112）； 2010.1-2012.12；参与 4.国家自然科学基金项目《高选择性蛋白酪氨酸磷酸酶 SHP2 抑制剂的研究》(81273361) ；2013.1-2016.12；参与 5. SHP2 变构抑制剂的设计、合成及活性筛选，天津市自然科学基金一般项目（18JCQNJC13700），项目主持人，2018.04-2022.03。
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