

Supporting Information

Molecular docking, pharmacophore based virtual screening and molecular dynamics studies towards the identification of potential leads for the management of *H. pylori*

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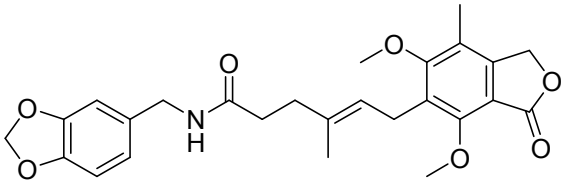
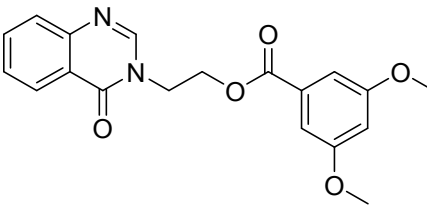
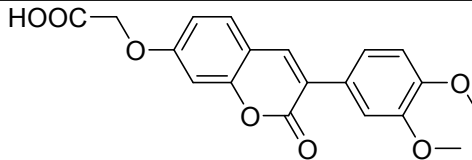
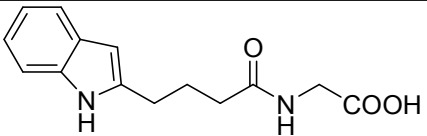
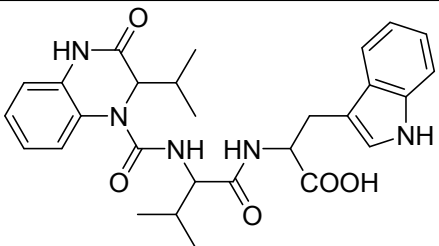
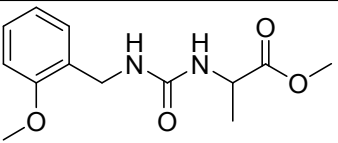
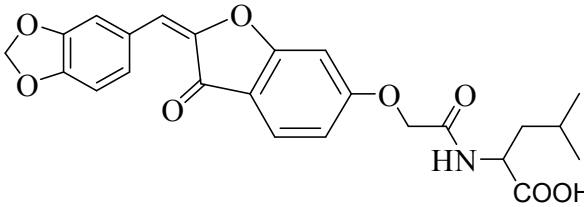
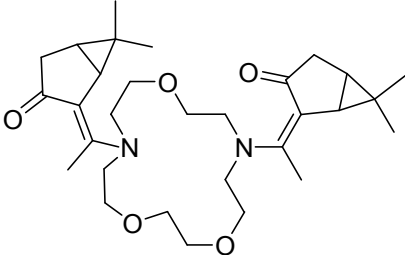
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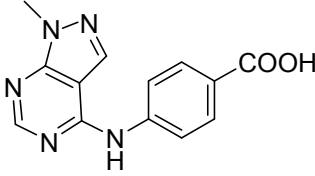
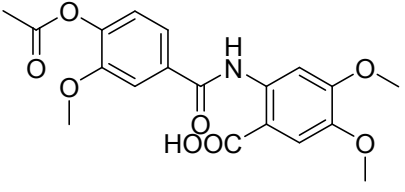
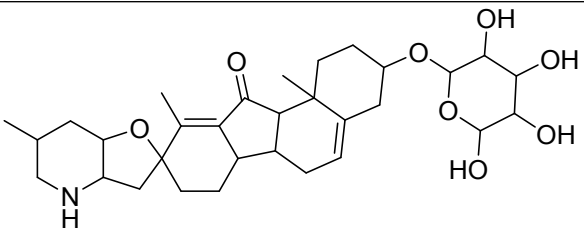
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1. Table S1	2-4
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Table S1. Structures of the virtual hits

Structure ID		Structure ID	
STOCK1N - 76518		STOCK1N-74127	
STOCK1N-71293		STOCK1N-68553	
STOCK1N-67377		STOCK1N-64449	
STOCK1N-59730		STOCK1N-26126	

STOCK1N-28765		STOCK1N-32864	
STOCK1N-36335		STOCK1N-45539	