

A comparative study of the molecular structure, lipophilicity, solubility, acidity, absorption and polar surface area of coumarinic anticoagulants and direct thrombin inhibitors

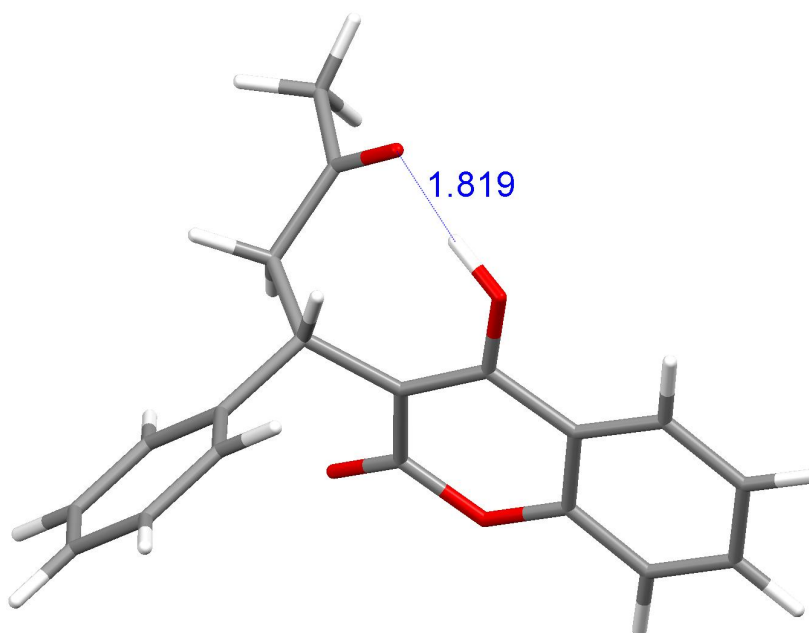
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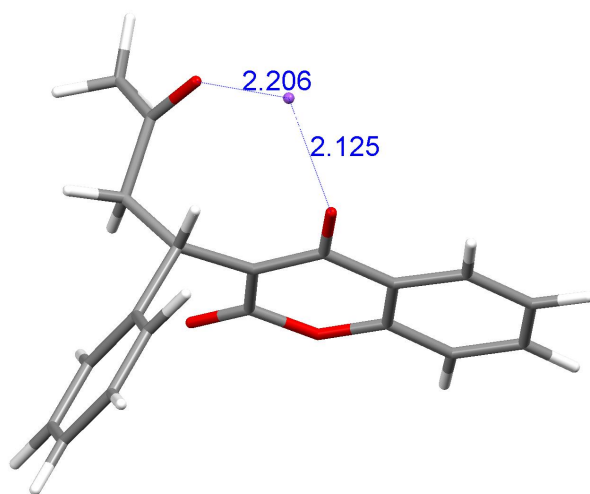
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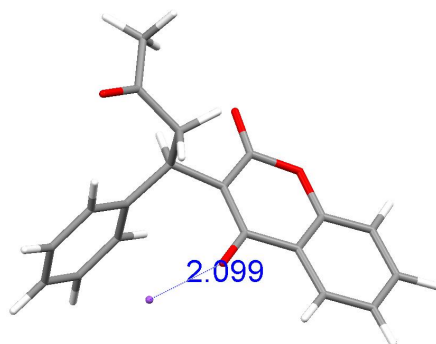
Supporting Material



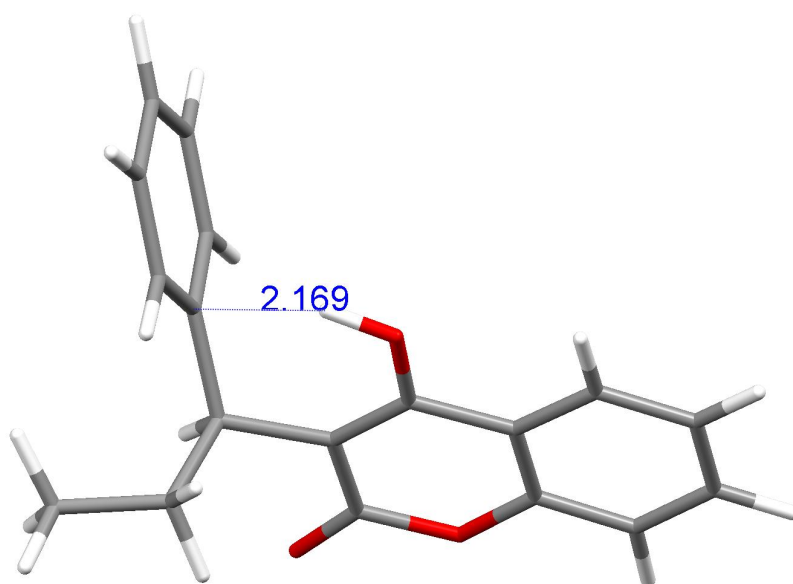
R-Warfarin, tautomer A



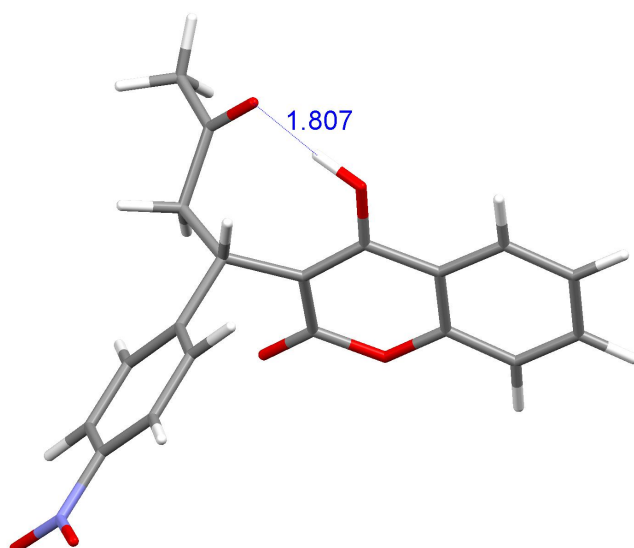
R-Warfarin sodium, tautomer A



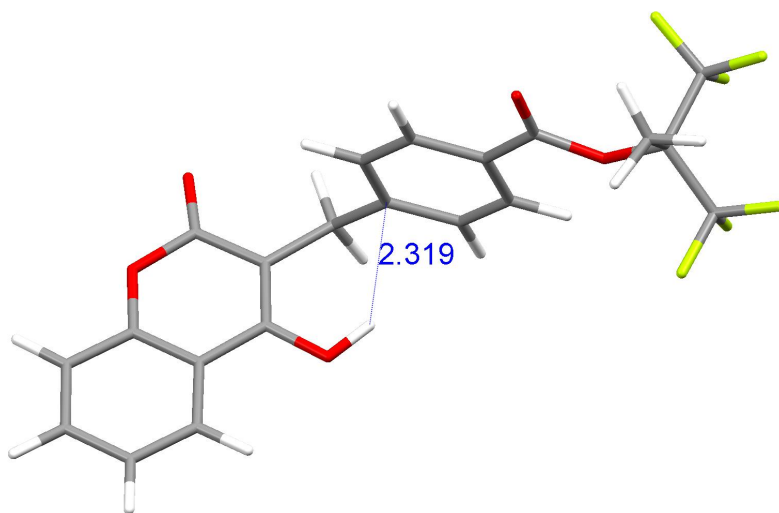
S-Warfarin sodium, tautomer A



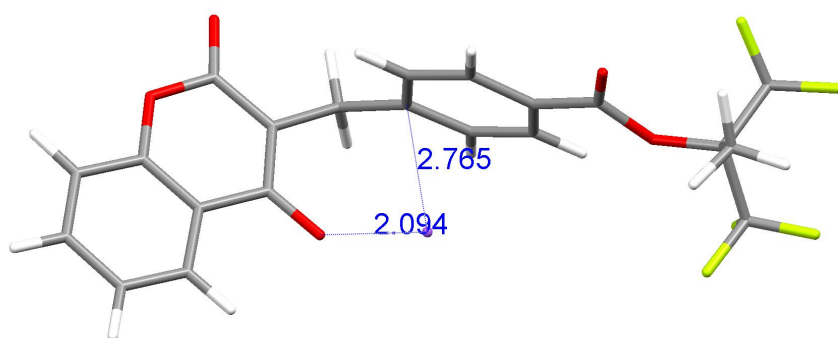
S-Phenprocoumon, tautomer A



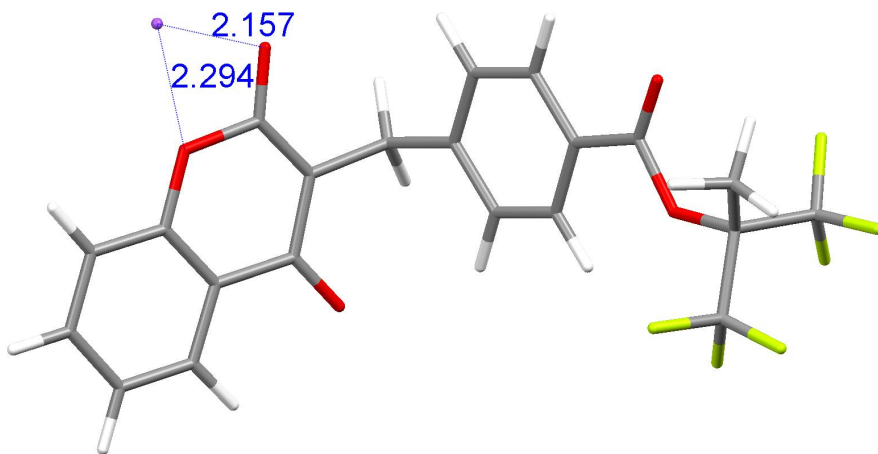
R-Acenocoumarol, tautomer A



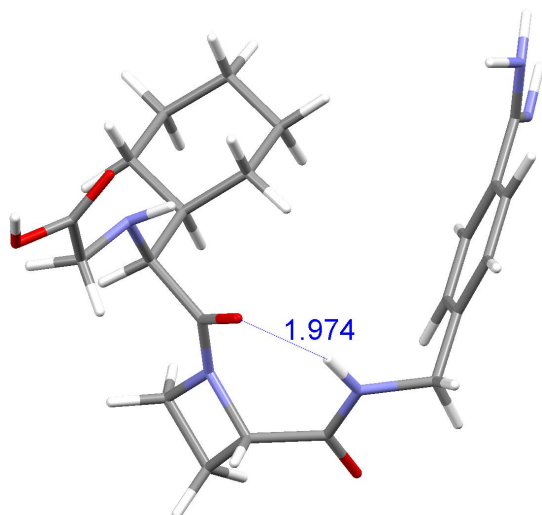
Tecarfarin, tautomer A



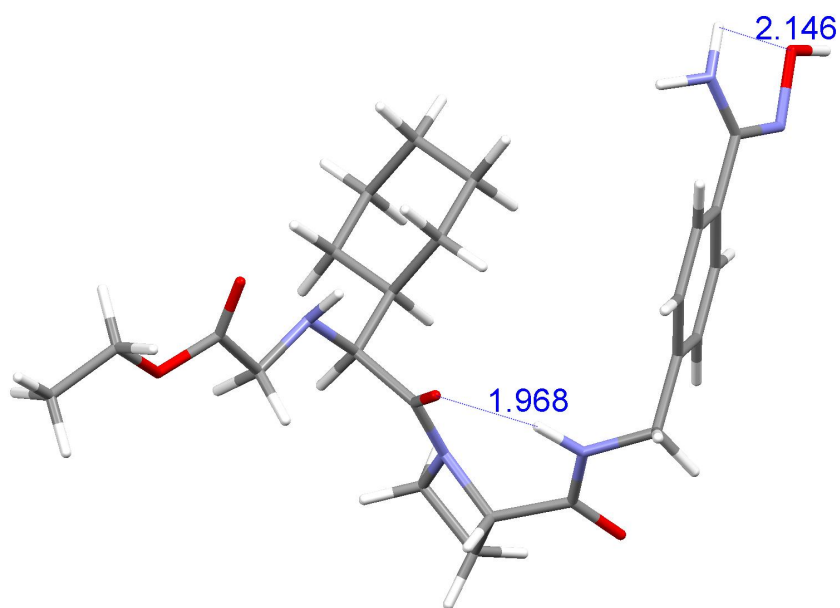
Tecarfarin sodium, tautomer A



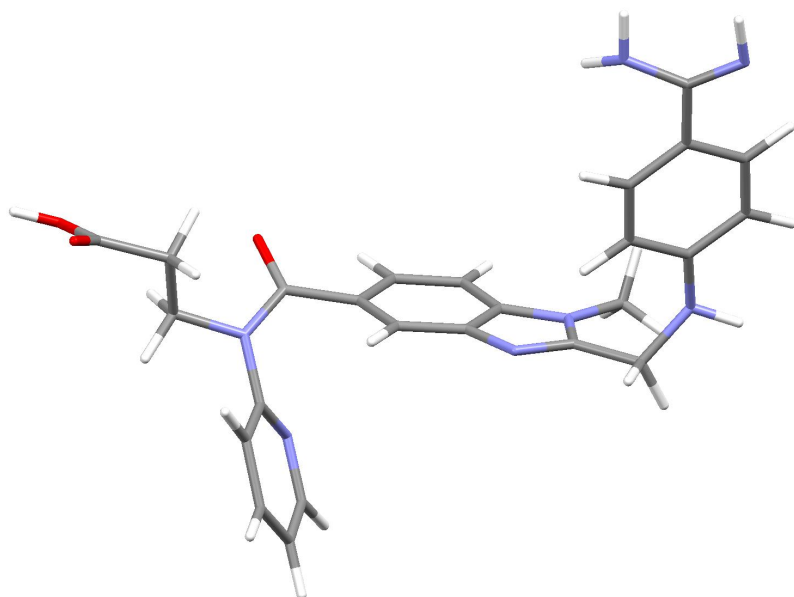
Tecarfarin sodium, tautomer B



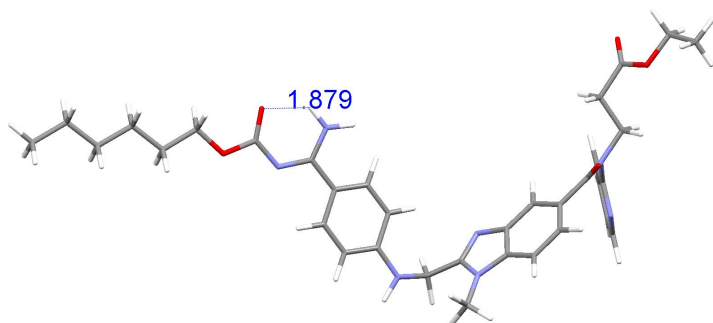
Melagatran



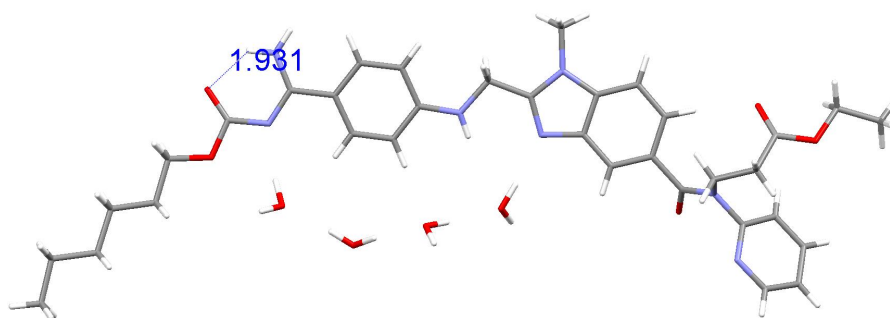
Ximelagatran



Dabigatran



Dabigatran etexilate



Dabigatran etexilate tetrahydrate, X-ray structure from ref. 24

Fig. 1A Overall shape of the most stable conformations of coumarinic anticoagulants and direct thrombin inhibitors (bond lengths are in Angstroms).

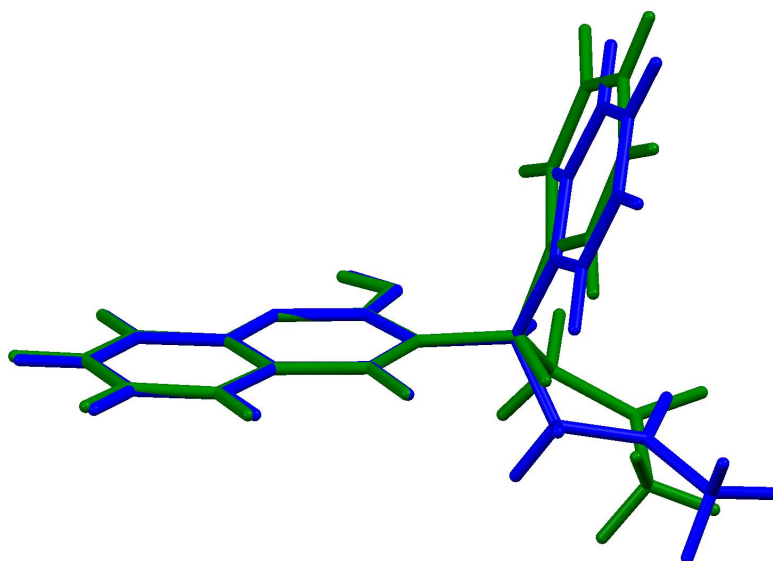


Fig. 2A Molecular superimposition of the *R*(+)-warfarin (blue) and *S*(-)-warfarin (green) from their cocrystals with human serum albumin myristate, PDB 1H9Z, 1HA2.

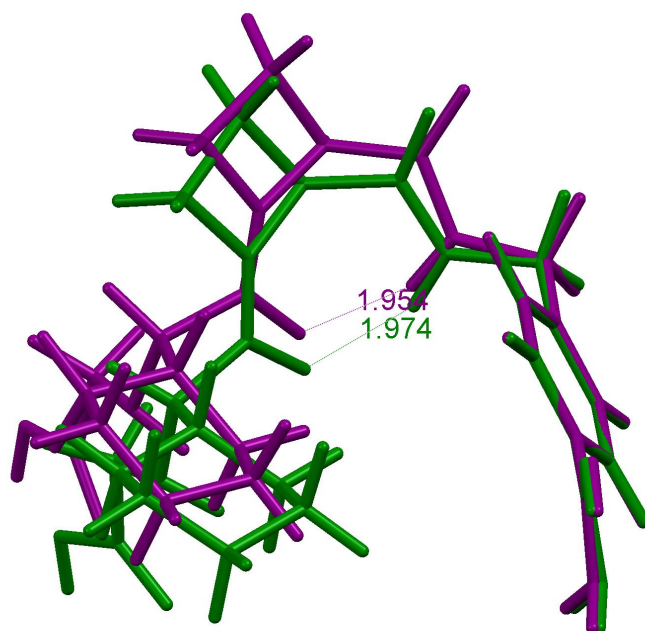


Fig. 3A Molecular superimposition of the DFT optimized melagatran (green) and in solution optimized melagatran (purple).

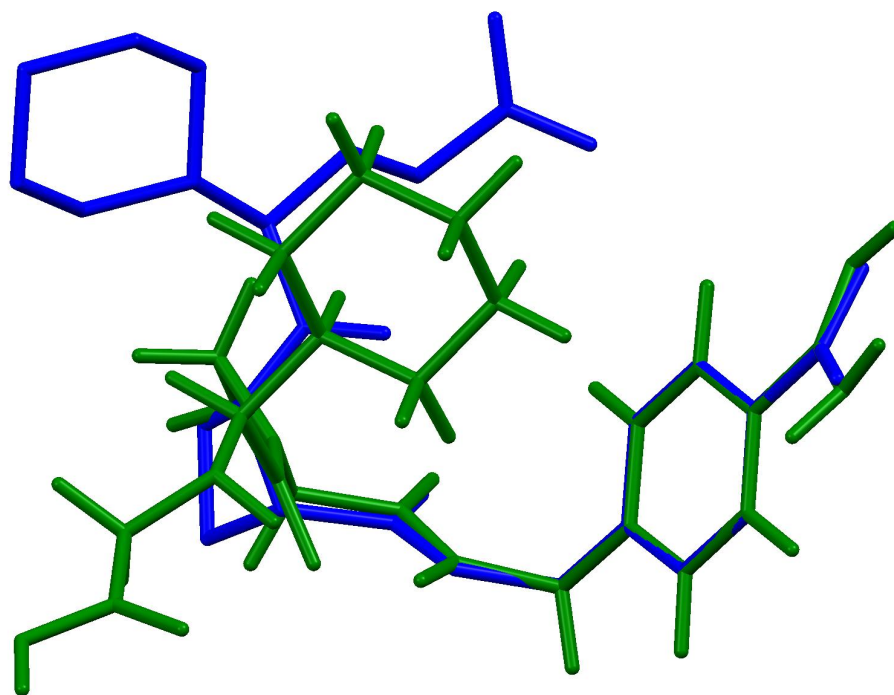


Fig. 4A Molecular superimposition of the DFT optimized melagatran (green) and melagatran from its cocrystal with thrombin (blue), PDB 1K1P.