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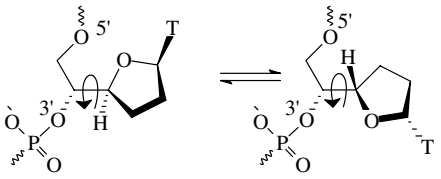
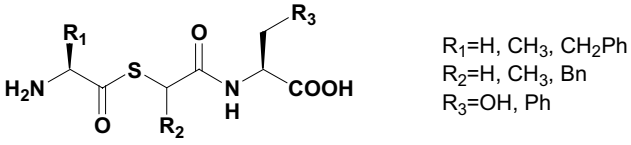
Contents

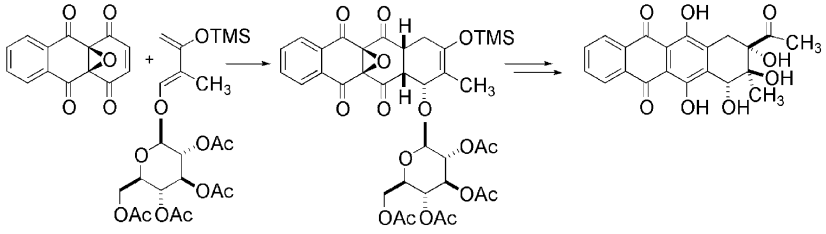
ARTICLES

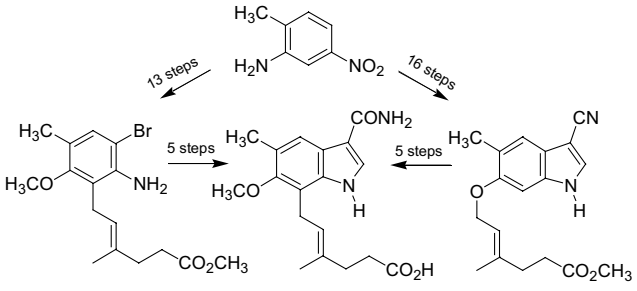


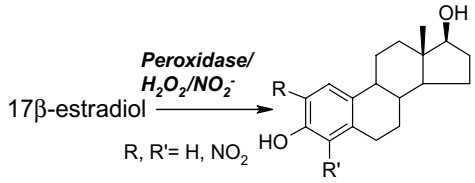
A new type of nucleosides is considered as an acyclic nucleoside, which is conformationally restricted by a linking furanose ring. Thermal stability of its oligonucleotides with DNA/RNA complements and RNase H activity were studied.

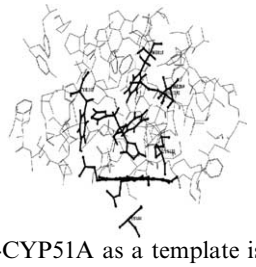


21 Chromogenic thiopeptolide substrates

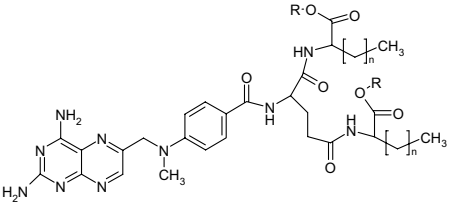






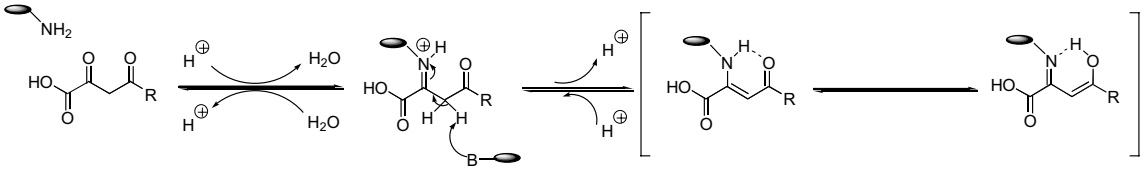


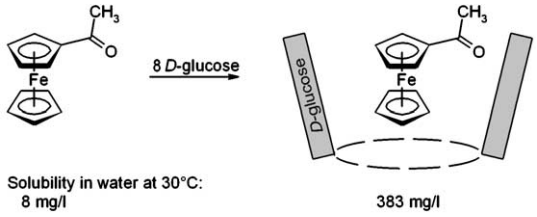
A homology model of AF-CYP51A built using MT-CYP51A as a template is described. This model was used to dock known azole antifungals such as fluconazole into the active site.

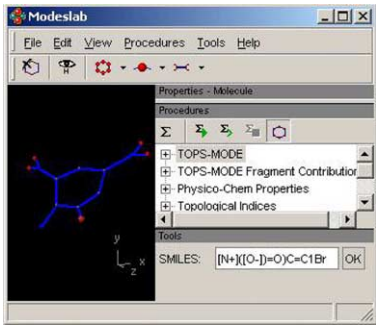


A new series of lipophilic α,γ-bis(amide) conjugates of the anticancer drug methotrexate (MTX) with short-chain 2-alkylamino acids (4–6 carbon atoms) was described.

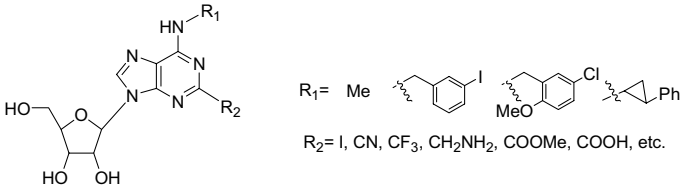
The aim of these derivatives was to increase the uptake of the drug into transport-resistant tumor cell lines toward the uptake of MTX. The inhibitory activity of these compounds against the target enzyme, dihydrofolate reductase (DHFR), and a sensitive (CCRF-CEM) and a transport-resistant tumor cell subline (CEM-MTX) was assessed. The α,γ-bis(hexyl) derivative was the most active term of the series, showing the ability of retaining the same inhibitory activity also against the resistant cell subline, against which the parent drug was much less active than against the wild one. Docking studies combined with a conformational NMR analysis of MTX conjugates in solution are in agreement with the experimental biological data and the proposed binding mode.



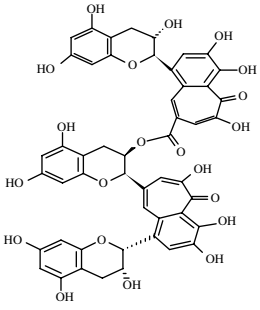




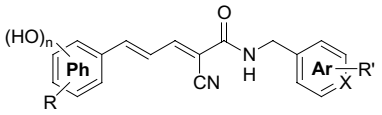
The TOPological Sub-Structural Molecular Design (TOPS-MODE) approach has been applied to the study of the A_1 adenosine receptors. A model able to describe closed to 79% of the variance in the values for binding experiments of 32 analogues of these compounds was developed with the use of the mentioned approach.



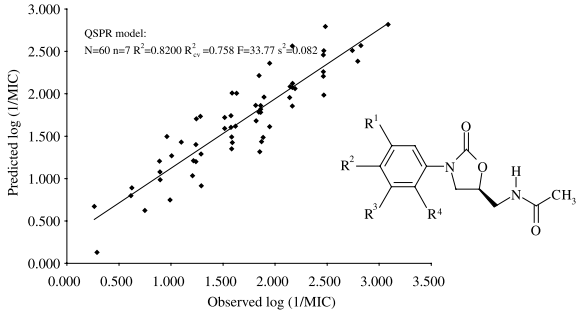
We have studied the structural determinants of binding affinity and efficacy of adenosine receptor (AR) agonists. Substituents at the 2-position of adenosine have been combined with N^6-substitutions known to enhance human A_3AR affinity. The environment surrounding the 2-position within the putative A_3AR binding site was explored using rhodopsin-based homology modeling and ligand docking.



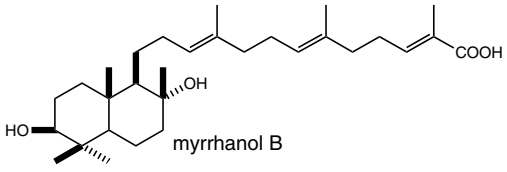
Three new dibenzotropolone, theadibenzotropolone **A**, **B** and **C**, together with one new tribenzotropolone, theatribenzotropolone **A** were formed by the reaction of theaflavins and tea catechins with horseradish peroxidase in the presence of H_2O_2. The structures of these new benzotropolone derivatives were elucidated on the basis of MS and 2D NMR spectroscopic analyses. The existence of these compounds in black tea was characterized by LC/ESI-MS/MS. Theadibenzotropolone **A** and **B** were the first benzotropolone-type trimers of catechins found in the black tea extract.



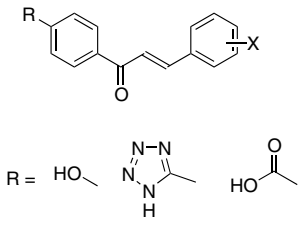
A series of substituted styryl-acrylonitriles was synthesized and tested for the ability to inhibit acute lymphocytic leukemia cancer cell growth. The compounds revealed great potency as antitumor agents.

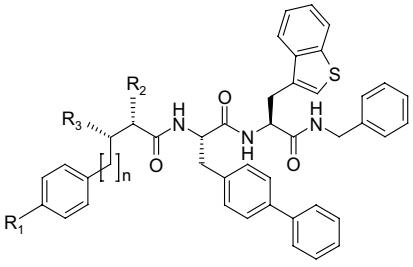


A QSPR treatment has been applied to a data set consisting of 60 3-aryloxazolidin-2-one antibacterials to relate the in vitro minimum inhibitory concentration (MIC) (required for inhibiting growth of *Staphylococcuc aureus*) with theoretical molecular and fragment descriptors. The treatment using CODESSA PRO descriptors leads to a seven-parameter model with $r^2 = 0.820$ and $r^2_{cv} = 0.758$.

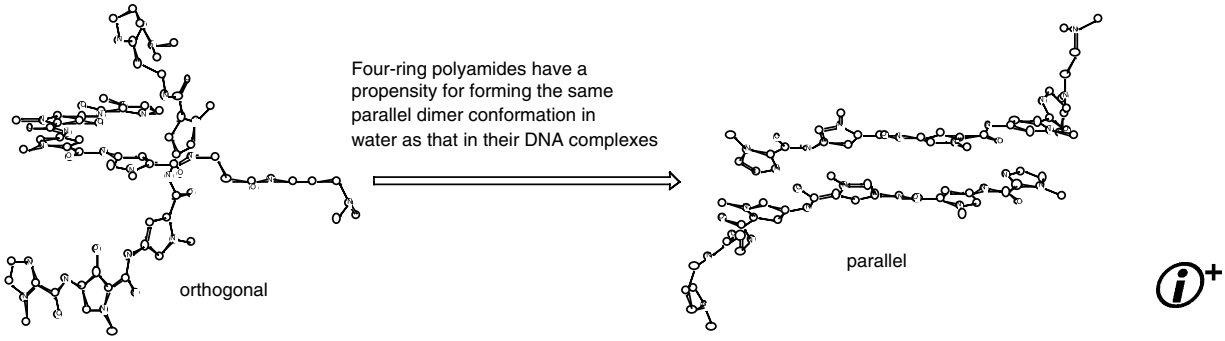


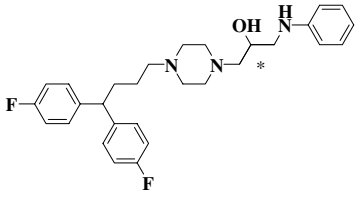
The MeOH ext. from guggul-gum resin was found to inhibit NO production in LPS-activated mouse peritoneal macrophages. From the MeOH ext., three new polypodane-type triterpenes, myrrhanol B and myrrhanones B and A acetate, and a new octanordammarane-type triterpene, epimansumbinol, were isolated. The several constituents showed inhibitory effects on NO production and iNOS induction.

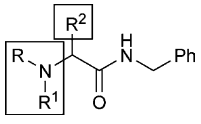


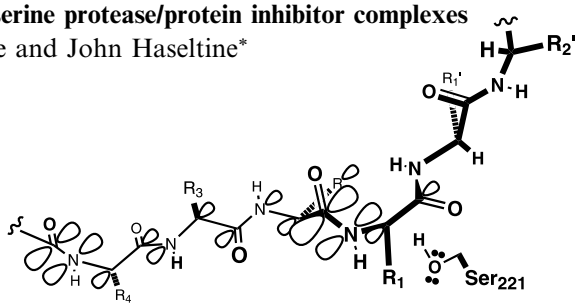


$R_{1\text{-}3}$ = various substituents,
n = 0 or 1









An analysis of complexes between serine proteases and their protein inhibitors reveals extensive alignments of atomic orbitals in the bound strand and the active-serine-bearing strand. This implies that some kind of long-range backbone electronics are involved in the proteolytic mechanism.

OTHER CONTENTS

*Corresponding author
ⓘ+ Supplementary data available via ScienceDirect

COVER

2004: Overlaps of the eight known aldolase alpha-beta barrels in 2-deoxyribose-5-phosphate aldolase (DERA). Ribbon model for DERA is shown in green, with key Lys residues capable of Schiff base formation highlighted in stick figure. Reactive Lys167 is shown in yellow. DeSantis, G.; Liu, J.; Clark, D. P.; Heine, A.; Wilson, I. A.; and Wong, C.-H. *Bioorganic & Medicinal Chemistry* **2003**, *11*, 43–52.

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