Front part of the example document 'test.txt'

Background

Recently there has been increased interest in pancreatic cholesterol esterase due to correlation between enzymatic activity in vivo and absorption of dietary cholesterol.

Results

Our analysis indicates that the current set of nearest neigh-bough energy parameters in conjunction with the Mfold folding algorithm are unable to consistently and reliably predict an RNA's correct secondary structure.

Conclusion

We are the first to report that the acyl chain binding site of cholesterol esterase shows stereoselectivity for the four diastereomers of 1.

Body part of the example document 'test.txt'

Background

There has been increased interest in pancreatic cholesterol esterase (CEase, EC 3.1.1.13) due to correlation between enzymatic activity in vivo and absorption of dietary cholesterol [1,2]. Figure 2 Structures of the four diastereomers of carbamates 1 and two atropisomers of 2.

Results

The inhibition data for CEase by the four diastereomers of 1 and the two enantiomers of 2 are summarized (Table 1). The stereochemical preference of CEase for the binaphthyl moiety of 1 (R > S, ca. 10 times) is the same as that for 2 [20,22]. The stereoselectivity of CEase for the α-methylbenzyl moiety of 1 is also the R-form (2-3 times over S-form).

Table 1. Inhibition constants for CEase-catalyzed hydrolysis of PNPB in the presence of the four diastereomers of 1 and the two enantiomers of 2

Inhibitor	Ki (μM)	K2 (10-3s-1)	Ki (103 M-1s-1)
(1R, αR) - 1	0.20 ± 0.01	2.0 ± 0.2	10.0 ± 1
(1R, gαS) - 1	0.50 ± 0.03	2.0 ± 0.2	4.0 ± 0.4

Conclusion

The enzyme stereospecificity toward the 1, 1'-bi-napthyl moiety of the inhibitors is the R-form and is the same as that for 2.

Acknowledgement

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References

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XML format for example document 'test.txt'

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            <results>
            Our analysis indicates that the current set of nearest neighbour energy parameters in conjunction with the mfold folding algorithm are unable to consistently and reliably predict an rna's correct secondary structure.
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