

# Drugs of the Future

Volume 32, Suppl. A, July 2007



ABSTRACTS FROM THE  
**6<sup>th</sup> AFMC International  
Medicinal Chemistry  
Symposium**

July 8-11, 2007, Istanbul, Turkey



**PROUS SCIENCE**  
BARCELONA PHILADELPHIA

## PB-49

### Thermodynamic Analysis for Interaction of n-Alkyl Sulfates with Insulin

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Binding Isotherms, for the interaction of a homologous series of sodium n – alkyl sulfates (chain lengths 8-9-10 and 12) on interaction with bovine insulin at 25°C, and pH = 3.2 have been previously reported by Jones. The Isotherms show two unusual features, first the binding ranges up to 60 – 70 surfactant molecules per insulin molecule. And secondly it is only slightly dependent on the n – alkyl chain length. In the present study, we introduced a new thermodynamic approach for analysis of these binding isotherms. The plots of  $RT \ln K_d$  vs.  $1/C_n$  represent a two sites for binding sites for these systems. The estimation of binding parameters is becomes more reliable by these plots. The intrinsic binding free energy were calculated at various surfactant concentration using formula which introduced previously. The results certifies previous results respect to slightly dependent on n – alkyl chain length, more over, shows that this dependency (for  $C_8$  and  $C_9$  is less than the others.) Resolution of electrostatic and hydrophobic contributions in intrinsic Gibbs free energy of binding. Represents the higher role of electrostatic interaction in first binding set. However, the increasing of electrostatic interaction at the first binding set may be due to unfolding of insulin and exposure of more positive charged aminoacids. An Isoaffinitic point was observed at  $c_n = 7.8$ , in the plot of  $\Delta G_{b,v}^{(2)}$  vs  $C_n$  at various  $\text{Log}[s]$ . This point can revealed a special feature of insulin structure. The extent of interaction between sites have been increased by increasing of chain length of surfactant, especially in the first binding set. The high binding levels coupled with the slight chain length dependence suggest a miscellar - based structure for the insulin. Surfactant complexes.

## Recent Approaches in Anticancer Therapy

### PB-50

#### Cyclodextrin Encapsulation of Biomimetic Organometallic Cancer Drug Candidates

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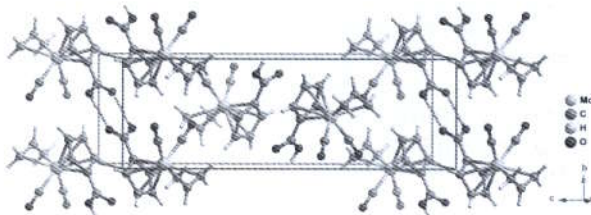
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To develop tailored methods for obtaining beta-cyclodextrin ( $\beta$ -CD) and permethylated  $\beta$ -CD (TRIMEB) inclusion compounds of the molybdenum carbonyl biomimetic compound  $\text{Mo}(\text{Cp-COO-Phe-O-Me})(\text{allyl})(\text{CO})_2$  (**2**) and its precursor  $\text{Mo}(\text{CpCOOH})(\text{allyl})(\text{CO})_2$  (**1**); to study the chemical structure of the inclusion compounds, and to evaluate the influence of cyclodextrins on the cytostatic and antiproliferative activity of the molybdenum compounds.

Methods: Mixing a dichloromethane solution of **1** with an aqueous solution of the host  $\beta$ -CD allowed the isolation of the inclusion compound **3**. The same host in aqueous solution was treated with an ethanol solution of **2** and the mixture was freeze-dried to obtain the inclusion compound **5**. Inclusion of compounds **1** and **2** in TRIMEB was performed by co-dissolution in dichloromethane followed by vacuum-drying to isolate the adducts **4** and **6**, respectively. Compounds **1** – **6** were studied in the solid state by powder X-ray diffraction,  $^{13}\text{C}\{^1\text{H}\}$  CP/MAS NMR and FTIR spectroscopies, and thermogravimetry (TG).

Complex **1** was re-crystallised and its structure was determined using single-crystal X-ray diffraction (see Figure).



TG results support the formation of true inclusion compounds for **3** to **6**, pointing to a strong host-guest interaction, in particular for the  $\beta$ -CD adducts. Powder X-ray diffraction studies were used to qualitatively identify the molecular packing of inclusion compounds **3** and **5**; adducts with complex **2** are significantly less crystalline with diffraction data being inconclusive. NMR results support, on the one hand, the expected crystal arrangement of inclusion compounds **3** and **5** and, on the other, the low crystallinity of **4** and **6**. FTIR confirmed that guest integrity was preserved during inclusion. Conclusion: Compound **3** has  $\beta$ -CD molecules aligned so as to form infinite channels which host the guest molecules **1**; in **5** TRIMEB molecules form distorted columns in a zig-zag pattern, as found for TRIMEB-CpMo(CO)<sub>3</sub>Cl [Braga, SS]. Compounds **4** and **6** are mainly amorphous, most likely due to the bulky nature of guest **2**. Cytostatic and antiproliferative tests are underway.

References: SS Braga, FA Almeida Paz, M Pillinger, JD Seixas, CC Romão, IS Gonçalves, Eur. J. Inorg. Chem. 2006, 1662-1669.

The authors are grateful to FCT, OE and FEDER for funding (Project POCI//QUI/56109/2004).