preparations of $(PPTA)Cr(CO)_3$ (fully and partially complexed) and $(PPTA)Cr(CO)_2P(CH_3)_3$, and polarized light optical micrograph of $(PPTA)Cr(CO)_3$ (5 pages). Ordering information is given on any current masthead page.

Molecular Reception Catalysis of the Decarboxylation of *N*-Carboxyimidazolidinone. A Model for Activation by Distortion of *N*-Carboxybiotin

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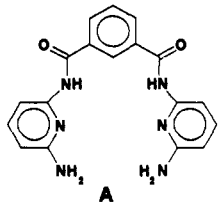
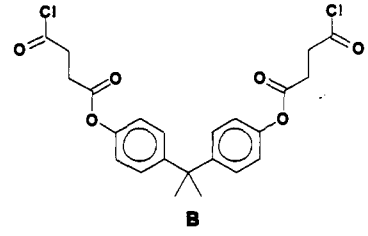
It has been proposed that the observed substrate-induced decarboxylation of enzyme-bound *N*-carboxybiotin[1] can result from movement of the exocyclic carboxyl group out of the plane of the imidazolidinone ring upon binding to an enzymic receptor[2,3] (Scheme I). On the basis of this proposal, we designed a synthetic host (**H**) to induce distortion of a functional model of *N*-carboxybiotin. Hamilton's methodology provides a convenient route to appropriate hosts.[4-9] While host-guest chemistry has been used to promote decarboxylation reactions by electrostatic and nucleophilic catalysis,[10,11] binding that distorts a substrate toward a transition-state structure has not previously been tested.

High-dilution coupling of diamine **A** with diacid dichloride **B** (THF, 2 equiv of triethylamine) produces **H** (chromatography, neutral alumina (2% $MeOH/CH_2Cl_2$); HPLC, C8 reverse phase, eluted with acetonitrile; recrystallization, THF/heptane). Relative concentrations of complexed and uncomplexed **H** with imidazolidinone derivatives in THF solutions were determined by changes in UV spectra. Spectral titration gave data which were used to derive association constants (Table I).



A



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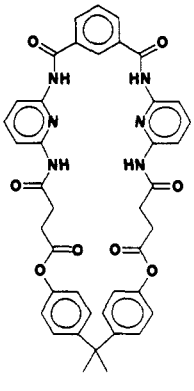
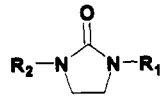


H



1 , $R_1 = R_2 = H$
2 , $R_1 = H$, $R_2 = CH_3$
3 , $R_1 = R_2 = CH_3$
4 , $R_1 = H$, $R_2 = C(O)OCH_3$
5 , $R_1 = H$, $R_2 = COO^- NBu_4^+$

Scheme I

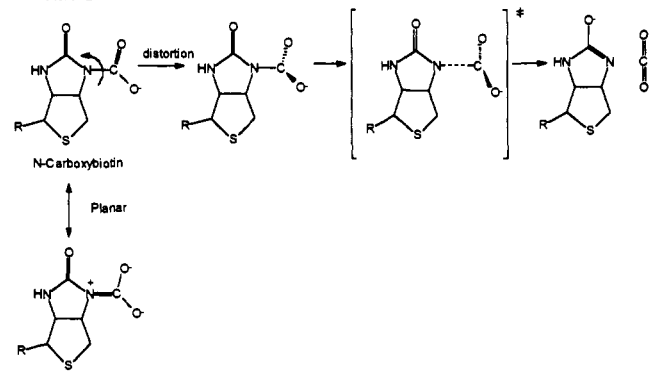


Table I. Association Constants (K_1) for Host H with Cyclic Ureas[a]

guest	K, M^{-1} (25 °C, THF)
imidazolidinone (**1**)	5.7×10^4
N-methylimidazolidinone (**2**)	9.0×10^2
N,*N*-dimethylimidazolidinone (**3**)	0
N-carbomethoxyimidazolidinone (**4**)	8.5×10^2

[a] Concentration of **H** is 10^{-5}-10^{-6} M. Titration curves show a 1:1 stoichiometry and were fit to ligand-association expressions by nonlinear regression.

The affinity of **H** for **1**, **2**, and **3** parallels the number of possible hydrogen bonds between the host and the guest according to the mode proposed by Hamilton.[6-8] *N*-Carbomethoxyimidazolidinone (**4**) is stable in the presence of **H** and was used to estimate the binding affinity of **5** for **H**. The affinity of **H** for **5** is lower than that of **H** for **1**, presumably due to a combination of steric effects and one fewer hydrogen bonding sites in **5**. Since the transition state for decarboxylation of **5** will have lower bond order to the carboxyl group and partial formation of a hydrogen bond, the host should bind it with a greater affinity than it does the reactant. Stabilization of the transition state upon binding is the requirement for catalysis of decarboxylation by the host, paralleling the proposal for distortion of *N*-carboxybiotin in Scheme I. Molecular modeling of **5** (with the program Insight II using a Silicon Graphics system) shows that the stable conformation is the expected coplanar arrangement of all heavy atoms. Docking of **5** onto **H** gives a minimized structure in which the carboxyl group of **5** moves out of the plane of the imidazolidinone ring while the ring associates with the hydrogen bond donors of the host (which is in a twisted conformation accommodating the carboxylate group). Thus, it is expected that the association of host and guest will direct the guest toward the conformation predicted for the transition state for decarboxylation.

The rate of decarboxylation of **5** in anhydrous THF at 25 °C was followed at 228 nm (over 3 half-lives). The product is the conjugate base of imidazolidinone, which was converted to imidazolidinone by a trace of methanol and analyzed (GC-MS: 50 °C, 2 min, 20 °C/min to 250 °C; retention time = 8:33 min, MH^+ 87; HPLC (C_{18} Novapak, CH_3CN) 9.05 min). The host was unchanged during the course of the reaction. In the absence of **H**, reaction of **5** was too slow to observe over 3 days. Controls which cause no reaction of **5** included addition of benzamide, 2,6-diaminopyridine, and *N*-methylbenzamide (which have the functionality of **H** but are not expected to be receptors). *N*,*N*'-

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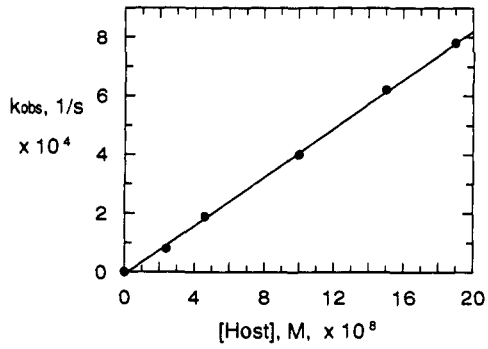
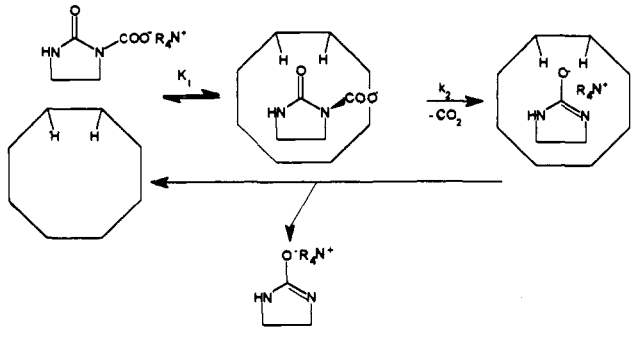
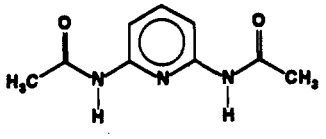


Figure 1. Observed first-order rate constant for decarboxylation of *N*-carboxyimidazolidinone (**5**) as a function of the concentration of host **H**.

Scheme II



2,6-Pyridinediylbis(acetamide) (**6**)[12] binds both **5** and **1**, but there is no decarboxylation of **5** detected (3 days, THF).



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Addition of aqueous base leads to hydrolytic decomposition, presumably via an addition intermediate.[13] Concentrations of **5** above 10^{-7} M produce nonlinear response in UV absorbance, indicating that aggregation is occurring. The observed first-order rate constant for decarboxylation of **5** was measured as a function of the concentration of **H** (Figure 1). The slope gives an apparent second-order rate constant ($k_{obs}/[H]$) of $4.15 \pm 0.05 \times 10^3$ M^{-1} s^{-1}. Kinetic saturation could not be observed under conditions where **5** does not aggregate.

A schematic mechanism of decarboxylation of **1** in the presence of **H** is shown in Scheme II based on the array seen using computer modeling of the host–guest complex. The rate expression for the reaction is

$$v = k_{obs}[5] = k_2[\text{complex}] = K_1k_2[H][5]$$

and

$$k_{obs}/[H] = k_2K_1$$

If $K_1 \approx 10^3$ M^{-1} (see Table I), then $k_2 = 4$ s^{-1}.

Since decarboxylation of **5** was too slow to detect in the absence of **H**, its half-life must be at least 10 days under the reaction conditions, giving an upper limit for the rate constant of the uncatalyzed process of 10^{-6} s^{-1}, corresponding to an acceleration in the complex of over 10^6. The actual acceleration could be much larger. The results are consistent with the proposal of distortion upon binding as a means of altering the biochemical reactivity of *N*-carboxybiotin.[2,3]

Acknowledgment. We thank the Natural Sciences and Engineering Research Council of Canada for continued support through an operating grant.

Supplementary Material Available: Spectral data for **H** (1 page). Ordering information is given on any current masthead page.

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Book Reviews

Advances in Chromatography. Volume 31. Edited by J. Calvin Giddings (University of Utah), Eli Grushka (Hebrew University of Jerusalem), and Phyllis R. Brown (University of Rhode Island). Marcel Dekker, Inc.: New York. 1992. xix + 393. $150.00 (U.S. and Canada), $172.50 (elsewhere). ISBN 0-8247-8568-1.

This series, initiated in 1965, reviews topics which are important to separation scientists. Authors are encouraged to be selective of material, evaluate information, and be critical as their experience dictates. Reviewers are not encouraged to merely assemble an annotated bibliography. The editors have accomplished this goal very well for nearly three decades, and this volume continues the tradition.

Elution gas–liquid and liquid–liquid chromatographies have dominated separation methods, largely due to the linearity of the solute distribution; that is, the distribution coefficient is constant over an appreciable range of solute concentration and the solute species are independent of one another in both phases. Groups intent on establishing standard nomenclature and preferred methods of reporting data such as the retention index, number of theoretical plates, and plate height have based their recommendations on linear systems. If a system is non-linear, efforts are made to make it linear or a different system is sought which is linear. In so doing, powerful gas–solid and liquid–solid separation systems and techniques such as frontal and displacement analysis became obscure diversions. The review (188 pages, 220 references) by A. Katti and G. Guiochon (University of Tennessee) attacks the subject. The review, which is highly mathematical, selects the most successful models and presents those equations which best describe solute behavior in the system, for example, Langmuir-type sorption isotherms and solute competition for sorption sites. Results and conclusions based on the mathematics are presented in more easily understood graphical form to give a balance between mathematical formalism and interpretation. Frontal and displacement methods are discussed. Applications include displacement separations of nucleotides and proteins. The review ends with a discussion of remaining mysteries. This is an excellent review of a difficult subject prepared by knowledgable and experienced workers. It is not light reading, however.

P. L. Dubin (Indiana-Purdue University) treats problems in aqueous size exclusion chromatography (32 pages, 95 references). The author presents valuable tables of commercial packings which include the number of theoretical plates to be expected, upper molecular weight limits, and maximum mobile flow rates. Aqueous solutions of high molecular weight compounds are complicated by both solvation and charge interactions, as these depend on the ionic strength. Dubin treats both effects and presents some dramatic graphs summarizing the dependence of retention on ionic strength and possible explanations. The search for a universal calibration curve is the Holy Grail of the polymer chemist. There is an excellent section devoted to this problem. The chapter should also interest those doing hydrodynamic chromatography and field-flow fractionation with aqueous solutions where ionic strength also plays a part.

Too often high performance liquid column chromatography with ex-