

CONFORMATIONAL ANALYSIS—II†

A LANTHANIDE-INDUCED SHIFT NMR AND THEORETICAL STUDY OF BICYCLO [3.1.0] HEXAN-3-ONE AND ADAMANTANONE

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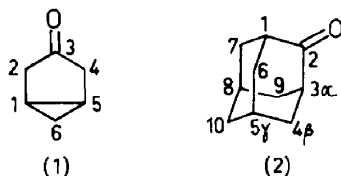
(Received in UK 4 August 1980)

Abstract—The solution conformation of bicyclo [3.1.0] hexan-3-one has been obtained by the use of the shifts induced in its ^1H and ^{13}C NMR by $\text{Yb}(\text{fod})_3$. Refinement of the angle of pucker, α , of the 5-membered ring indicates that the molecule adopts a flattened boat conformation with $\alpha = 195^\circ$. This prediction is supported by *ab initio*, STO-3G, calculations on the isolated molecule. Use of a two- or four-site model for lanthanide-substrate complexing adequately reproduces the experimental data whereas a one-site binding model is unsatisfactory. The importance of multi-site binding is further emphasised by results for the C_{2v} -symmetric ketone, adamantanone, where only a four-site model gives satisfactory agreement between observed and calculated lanthanide-induced shifts.

INTRODUCTION

In a recent paper,¹ we have shown that by the simultaneous use of ^1H - and ^{13}C -lanthanide-induced NMR shifts (L.I.S.'s), combined with a chemically reasonable model for lanthanide ion binding, it is possible to determine, reliably, the solution conformations of cyclohexanone and 4-*t*-butylcyclohexanone.

In this paper, we present a full account‡ of a similar study of bicyclo [3.1.0] hexan-3-one (1), including a detailed investigation of the dependence of the outcome of the analyses on the lanthanide binding model. Additional light is shed on the question of the correct choice of binding model by our results on adamantanone (2). We also take this opportunity to publish detailed geometries for 1 and 2, since these are not readily available elsewhere.



The bicyclo [3.1.0] hexane skeleton occurs in nature in a wide range of monoterpenes of the thujane series. The parent hydrocarbon is calculated to be *ca.* 134 kJ M^{-1} more strained than cyclohexane.³ Qualitative and semiquantitative studies of NMR coupling constants in a range of thujane derivatives⁴ demonstrate that the 6-membered ring exists in a boat conformation. Microwave studies on bicyclo [3.1.0] hexane⁵ and the X-ray structure determination of *N*'-isopropylidenebicyclo [3.1.0] hex-

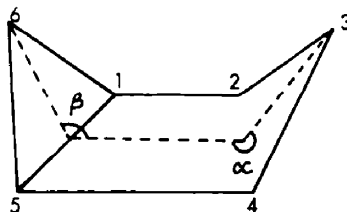


Fig. 1. Definitions of angles of pucker in bicyclo[3.1.0]hexane.

ane-6-*exo*-carbohydrazide⁶ indicate angles of pucker (Fig. 1) $\alpha = 218^\circ$, $\beta = 117^\circ (\pm 5^\circ)$ and $\alpha = 209.8^\circ$, $\beta = 110.5^\circ$ (errors not given, but may be estimated approximately as $\pm 2-3^\circ$).

The results of the microwave analyses are rendered somewhat controversial by a high correlation between α and β making the values dependent, to some extent, on the chosen method of calculation.

The preference for a boat conformation presumably arises from the staggered arrangement of H atoms bonded to carbons 1 and 5 with respect to the methylene H atoms on carbons 2 and 4. In a chair conformation, the equatorial H atoms on these latter atoms approximately eclipse those on carbons 1 and 5 (contrary to the situation in cyclohexane); in addition, repulsive 1, 3-H...H interactions between the *quasi*-axial hydrogen atom on carbon 6 and axial H atoms on carbons 2 and 4 are replaced by a single, less severe 1,4-H...H interaction (between *quasi*-axial H atoms on carbons 6 and 3) on chair to boat ring inversion.

At the outset of this work, there was no accurate information available for the geometry of the analogous bicyclic ketone (1), important as the basic skeleton for the commonly-occurring monoterpenes thujone and isothujone. We therefore undertook the refinement of the conformation of ketone (1) in solution. This, in turn,

†Ref. 1 is considered to be Part I of this series.

‡Preliminary accounts of this work have been published previously.²

raised questions about the choice of shift reagent-substrate binding model, requiring additional exploratory work on lanthanide ion binding to the rigid, symmetric ketone adamantanone (2). As a final comment on the correctness of the geometry found experimentally for 1, we present the results of an *ab initio* quantum mechanical study of the variation of its potential energy with the angle of pucker of the 5-membered ring.

EXPERIMENTAL

Bicyclo [3.1.0] hexane-3-one (1)⁷ was purified by distillation *in vacuo*; commercial adamantanone (2) and Yb(fod)₃ (dried over P₄O₁₀ *in vacuo* for 24 hr) were used as supplied. Solvent CDCl₃ was stored over molecular sieves and passed through an alumina column immediately before use. ¹H and ¹³C NMR spectra were recorded on Perkin-Elmer R-34 (220 MHz) and Varian XL-100 (25.2 MHz) spectrometers with probe temperatures *ca* 30°.

L.I.S.'s were measured for all carbon and H atoms (on the same solns) by incremental addition of Yb(fod)₃ to 0.89 M (1) and 0.92 M (2) solns of the ketones in CDCl₃. (We prefer this approach, for reasons of convenience and reproducibility, to the

incremental dilution method. Use of Yb(fod)₃, in preference to Eu or Pr complexes, serves to minimise contact contributions to the ¹³C L.I.S.'s.) The slopes of the least-squares linear plots of induced shifts *versus* the molar ratios of shift reagent to substrate were assumed to correspond to the bound shifts, ΔM values; results are summarised for 1 and 2 in Tables 1 and 2.

Computations were performed on ICL 1906S and CDC 7600 computers.

RESULTS AND DISCUSSION

Whereas in single-crystal X-ray diffraction experiments several thousand data points are customarily measured, permitting simultaneous refinement of often hundreds of atomic coordinates, the amount of data available in the L.I.S. experiment is strictly limited. Thus, in ketone (1), there are only nine NMR observables; of these, the L.I.S. at the carbonyl C atom C(3) is unreliable, being vulnerable to contact and complex-formation contributions,⁸ and must therefore be excluded from the analysis. In addition, the computations are conducted on bound shift *ratios*, and the

Table 1. Observed, bound (ΔM) and calculated L.I.S.'s for (1)

$\rho \times 10^{-2},^a$	H _{2,4} ^{endo}	H _{2,4} ^{exo}	H _{1,5}	H ₆ ^{endo}	H ₆ ^{exo}	C ₃	C _{2,4}	C _{1,5}	C ₆	R-factor
0.00 ^b	2.148	2.594	1.539	-0.060	0.908	218.26	41.06	12.22	13.30	
3.58	3.376	3.720	1.968	0.576	1.225	222.48	42.67	12.99	13.93	
9.71	5.128	5.304	2.561	1.456	1.666	228.25	44.93	14.07	14.72	
12.58	5.929	6.019	2.831	1.867	1.867	-	-	-	-	
15.66	6.816	6.816	3.123	2.302	2.080	-	-	-	-	
M ^c	29.50	26.67	10.01	14.93	7.42	97.8 ⁸	37.9	18.1	13.9	
correlation	.999	.999	.999	.999	.999	.998	.999	.998	.997	
one-site ^d	29.5	28.0	12.0	13.7	7.4	85.5	36.9	18.8	13.5	.049
two-site	29.5	27.0	10.4	15.8	7.1	84.9	38.0	18.0	13.6	.015
four-site	29.5	26.5	10.5	15.2	7.4	88.7	38.0	18.2	13.7	.011

^a $\rho = [\text{shift reagent}] / [\text{substrate}]_0$

^b shifts are in p.p.m. relative to internal tms

^c carbon data normalised to H_{2,4}^{exo} (three points) ΔM = 27.69

^d calculated ΔM's for lanthanide ion positions with best R-factors at a pucker angle of 195°

^e excluded from the analysis (see text)

Table 2. Observed, bound (ΔM) and calculated L.I.S.'s for (2)

$\rho \times 10^{-2},^a$	C _{CO}	C _α	C _β	C _γ	C _δ	H _α	H _{βⁿ} ^c	H _{β^x} ^c	H _γ	H _δ	R-factor
0.00 ^b	217.85	46.93	39.23	27.45	36.26	2.540	2.000	2.092	2.038	1.947	
3.96	223.76	49.29	40.41	28.36	36.95	4.535	3.023	2.730	2.544	2.396	
8.26	228.87	51.35	41.48	29.14	37.51	6.323	3.926	3.295	2.991	2.790	
ΔM	133.2 ⁸	53.5	27.2	20.5	15.1	45.74	23.28	14.54	11.52	10.19	
correlation	.998	.998	.999	.998	.997	.999	.998	.998	.998	.998	
one-site ^d	134.2	53.5	27.7	21.4	16.1	41.9	24.7	16.1	13.2	11.8	.065
two-site	116.9	53.5	26.9	20.6	14.9	44.4	25.7	14.1	12.4	10.5	.045
four-site	118.6	53.5	26.8	20.2	14.9	45.9	23.8	14.5	11.8	10.5	.011

^a $\rho = [\text{shift reagent}] / [\text{substrate}]_0$

^b shifts are in p.p.m. relative to internal tms

^c H_{βⁿ}^{syn} to C=O; H_{β^x}^{anti} to C=O

^d calculated ΔM's for lanthanide ion positions with best R-factors

^e excluded from the analysis (see text)

ΔM values thus require normalisation with respect to a reliable data point. There are therefore only seven independent L.I.S. data available for the exploration of 1's conformation. Clearly, then, the amount of structural information derivable from the L.I.S. experiment is very limited. Nonetheless, if it is possible to recognise, in a particular structure under study, a small number of variables whose values effectively define the conformation and to fix all other geometric parameters at reasonable values derived from the literature, then useful solution conformational information is easily obtained from L.I.S. data.

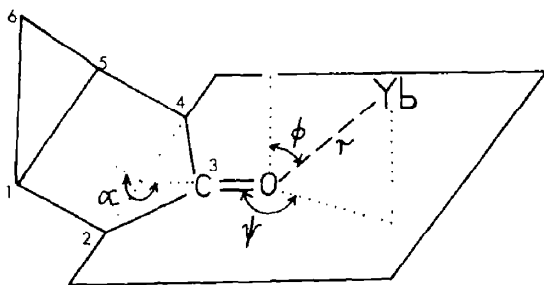


Fig. 2. Definitions of angle of pucker in bicyclo[3.1.0]hexane-3-one, and of lanthanide polar variables.

In the case of bicyclo [3.1.0] hexan-3-one [1, Fig. 2], for example, the bond lengths and majority of bond angles can readily be estimated given the availability in the literature of reliable geometries for the bicyclo [3.1.0] hexane⁶ and cyclopropane⁹ skeletons. Far more difficult, however, is the determination of a reliable value for the angle of pucker α (Fig. 2), given that in cyclohexanone, for example, the carbonyl-containing region of the ring is known to be more flexible than cyclohexane; α might well, therefore, be affected by change of phase or solvent. Our approach to the study of the conformation of 1 in solution has therefore been to concentrate on the refinement of the angle of pucker α .

The starting geometry for 1 was based on X-ray diffraction data for a 6-*exo*-derivative of bicyclo [3.1.0] hexane.⁶ Bond lengths and bond angles are listed in Table 6. The molecule was constructed to have approximate mirror symmetry with respect to a plane bisecting the C(2)-C(3)-C(4) angle and orthogonal to the ketonic plane. Although this symmetry is absent from the bicyclohexane, its assumption for the ketone seems reasonable in view of the absence of the 1,4-H...H interaction in the latter. In any case, even if the ketone is skewed slightly with respect to the assumed mirror plane, the barrier to interconversion between the skew isomers would be very low, and an averaged picture identical to the mirror-symmetric case would be observed in the NMR experiment. Cartesian coordinates for 1 were subsequently calculated within the programme LIRAS¹, which accepts as input a matrix of bond lengths, bond angles and torsion angles, the "Z-matrix".¹⁰ These coordinates were then used directly by the L.I.S. section of the programme.

For any substrate geometry, the position of the complexed lanthanide ion was varied incrementally by scanning of three polar variables (r , ϕ , ψ , Fig. 2) in the ranges 2.00–4.00 Å (in 0.10 Å steps), 10–170° and 90–180° (in 10° steps) respectively. For each position of the lanthanide, ratios of ΔM values were calculated from the one-term McConnell–Robertson eqn (1), where R_i is the distance

from the

$$\Delta M_i = K \cdot (3 \cos^2 \theta_i - 1)/R_i^3 \quad (1)$$

bound ion to the i th nucleus and θ_i is the angle subtended by this distance vector with the principal symmetry axis of the complex (assumed to be along the lanthanide-co-ordinating O bond). Effective axial symmetry of the complex as implied by this treatment, although questioned,¹¹ is generally accepted;¹² certainly, we have no evidence to encourage the inclusion of a second, "non-axial" term into (1), and such inclusion would further degrade the degree of determination of the system by the introduction of additional variables. For each position of the lanthanide ion, calculated and observed ΔM ratios (Δ 's) were compared by calculation of an agreement (R) factor [eqn (2)].

$$R = \sqrt{\left\{ \sum_i (\Delta_i, \text{obs.} - \Delta_i, \text{calc.})^2 / \sum_i \Delta_i^2, \text{obs.} \right\}} \quad (2)$$

We prefer this global search of lanthanide space to the steepest descent or allied minimisation methods since it avoids the problem of distinguishing between local minima and global minimum. In addition, the fineness of the scan can be tuned to suit the particular problem in hand.

The angle of pucker α in ketone 1 (Fig. 2) was varied systematically by the inclusion in the Z-matrix defining (1)'s geometry of variable "torsion" angles involving non-bonded atoms: C(1)-C(2)-C(4)-C(3) and C(5)-C(4)-C(2)-C(3), the sum of these always being 360° (or 0°). The disadvantage of this geometric construction is that changes in α induce small changes in bond angles C(3)-C(2)-C(1) and H-C(2)-H [and the mirror symmetric angles C(3)-C(4)-C(5) and H-C(4)-H]; for example, for a variation in α of 10° (from 190 to 200°), the bond angles change by 1.5 (from 108.2 to 106.7°) and 1.4° (from 110.7 to 112.1°) respectively. Such small changes would not be expected to affect the L.I.S. analyses appreciably, and attempts to relax the geometries for any particular value of α would only serve to introduce further arbitrariness into the treatment.

For each value of α , in the range 175–210°, the best lanthanide ion position (with minimum R-factor) was located. Comparison of the R-factors between geometries should indicate the true geometry (with an overall minimum R-value).

Three models for lanthanide ion binding were explored: one site, two site equal populations (the sites being related by the molecular mirror plane), and four site equal populations [the sites being related by the molecular mirror plane and the local plane defined by the carbonyl group, i.e. C(2,4)-C(3)-O]. The results are summarised in Fig. 3, in which the variation in best R-factors with pucker α is plotted for the three binding models. It must be stressed that the two-dimensional curves of Fig. 3 are drawn through minima on hypersurfaces (for any particular value of α) of R as a function of r , ϕ and ψ , the lanthanide polar coordinates.

It is immediately apparent from Fig. 3 that the one-site binding model is inadequate. No convergence to a minimum is found, indeed quite the reverse. This observation is entirely in accord with results previously obtained by us for cyclohexanone and 4-*t*-butylcyclohexanone.¹ By contrast, the two- and four-site binding models show good convergence to well-defined minima,

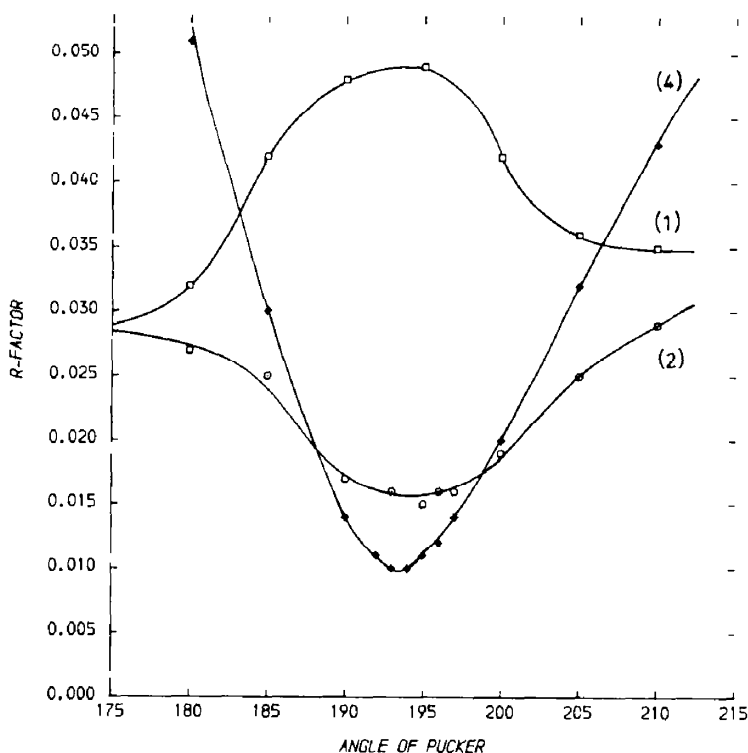


Fig. 3. The agreement factor (R) versus the angle of pucker α for bicyclo [3.1.0] hexan-3-one, one-, two- and four-site binding models (curves labelled in parentheses).

predicting an angle of pucker of *ca* 194.2° (2-site) and 193.5° (4-site). They are in encouraging agreement with each other and with the value of 198.8° obtained by studies based on gas-phase, microwave spectroscopy¹³ and published shortly before our preliminary communication.^{2a}

It is probably not profitable to speculate too widely on

the significance of the improvement in R -factor on change of model from two- to four-site binding in the region of the minima in the R -factor vs pucker curves. The atom by atom agreement between observed and calculated L.I.S.'s is excellent in both cases (specimen data are in Table 1). Both models, after all, represent comparatively crude attempts to simulate what must in

Table 3. Bicyclo [3.1.0] hexan-3-one. Ytterbium ion polar coordinates at positions with minimum R -factors for each angle of pucker and binding model

α°	r (Å)	φ°	ψ°	site-occupancy	R
175	2.58-2.64	130	180	1	.025
	2.58-2.74	125-130	155, 205-180 ^a	2	.025
180	2.80-2.82	135	180	1	.032
	2.98-3.02	120-125	140, 220	2	.027
	3.38-3.46	75, 105-90 ^b	125, 235-130, 230	4	.051
185	2.98-3.00	140	175-180	1	.042
	3.18-3.22	110	130, 230	2	.025
	3.38	90 ^b	125, 235	4	.030
190	3.28-3.30	150	180	1	.048
	3.30	90	125, 235	2	.017
	3.22-3.24	70, 110	125, 235	4	.014
195	2.70-2.76	65	180	1	.049
	3.18-3.20	80	130, 230	2	.015
	3.00-3.10	60, 120	135, 225 - 140, 220	4	.011
200	2.50-2.66	65-70	180	1	.042
	3.08-3.16	70-75	130, 230 - 135, 225	2	.019
	2.86	55, 125	145, 215	4	.020
205	2.44-2.46	70	180	1	.036
	2.96-3.04	70	135, 225 - 140, 220	2	.025
	2.70-2.80	55, 125	145, 215 - 150, 210	4	.032
210	2.36-2.50	65-70	180	1	.035
	2.76	65	150, 210	2	.029
	2.40-2.54	55, 125	155, 205 - 165, 195	4	.043

^a When $\psi = 180^{\circ}$, the two-site model is identical to the one-site model

^b When $\varphi = 90^{\circ}$, the four-site model is identical to the two-site model

fact be a complex set of solution equilibria. In addition, given the flexibility of the cyclohexanone skeleton, it is unrealistic to expect a totally rigid geometry for the bicyclic ketone: it may be that the four-site model is better able to compensate for the consequent thermal libration. It is not surprising that the four-site model gives poorer R-factors than the other models in regions remote from the minimum. Inspection of Table 3, in which the lanthanide polar coordinates at minimum R are listed against angle of pucker, shows that an inaccurate substrate geometry is, to some extent, compensated for by adjustments in "r" and " ϕ " (and, to a lesser extent, " ψ " in the two- and four-site models). The possibilities for ϕ -compensation in the four-site model are, of course, limited by the constraint that the lanthanide ion populates equally sites with coordinates " ϕ " and " $180-\phi$ ".

If it were possible to identify a "true" lanthanide ion binding site with respect to a CO group, it would then no longer be necessary to refine the polar coordinates, and the compensation for inaccurate substrate geometry would be eliminated. The curves of Fig. 3 would then be much steeper, particularly for the two-site model. That this is indeed the case is shown in Fig. 4, in which the polar radius is constrained for the two- and four-site models to roughly its value for solutions with overall minimum R-values (two-site 3.20 Å, four-site 3.10 Å). It is not straightforward to extend this analysis to the one-site model since there is no minimum in the corresponding R-factor vs pucker curve (Fig. 3). We have therefore examined the dependence of the form of the curve on polar radius "r" for a range of r-values (2.4–3.4 Å); results for r = 2.5, 2.9 and 3.3 Å are given as representative examples in Fig. 5. It is striking that as

"r" in the one-site case approaches the values found to yield optimum results in the two- and four-site cases, a minimum develops in the same general region (in terms of pucker angle) as in other models. It might then be argued that this analysis provides us with an indication of the value of the polar radius most appropriate to the one-site model. It is certainly encouraging that this is close to the values found for the two- and four-site models. More important, perhaps, is that all three models predict very similar values for the angle of pucker (albeit with varying degrees of confidence). Bond lengths, bond angles and torsion angles for a pucker of 195° are given in Table 4, cartesian coordinates are listed in Table 5 and a stereo-structure is drawn in Fig. 6.

A search of the Cambridge Crystallographic Data File (containing approximately 27,000 organic compounds for which structural information from X-ray or neutron diffraction experiments is available) retrieved 64 entries for compounds of europium, praseodymium, ytterbium and dysprosium (the elements most commonly used in lanthanide shift reagents). In none of the retrieved structures is there a complex between the lanthanide ion and the oxygen of a simple ketone (as distinct from chelated complexes of the β -diketonate and related kinds). In most cases, the lanthanide ion is coordinated to three bidentate ligands and, in addition, to water or organic Lewis bases (e.g. pyridine¹⁴ or quinuclidine¹⁵) leading to 7- (and, less commonly 8-) coordination; the average lanthanide... nitrogen separation is ca 2.64 Å. On this basis, the polar radii which our binding models predict are not unreasonable. Until such time as X-ray diffraction data on simple ketone complexes become available, we leave this problem, bearing in mind the usual *caveat*

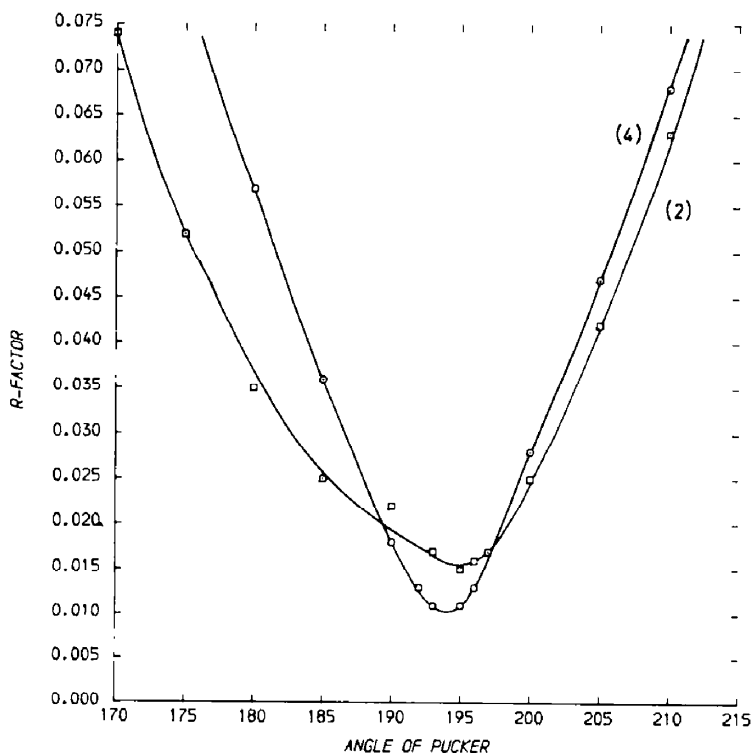


Fig. 4. The agreement factor (R) versus the angle of pucker α for bicyclo [3.1.0] hexan-3-one: two- and four-site binding models with ytterbium polar radius constrained to 3.20 and 3.10 Å respectively (curves labelled in parentheses).

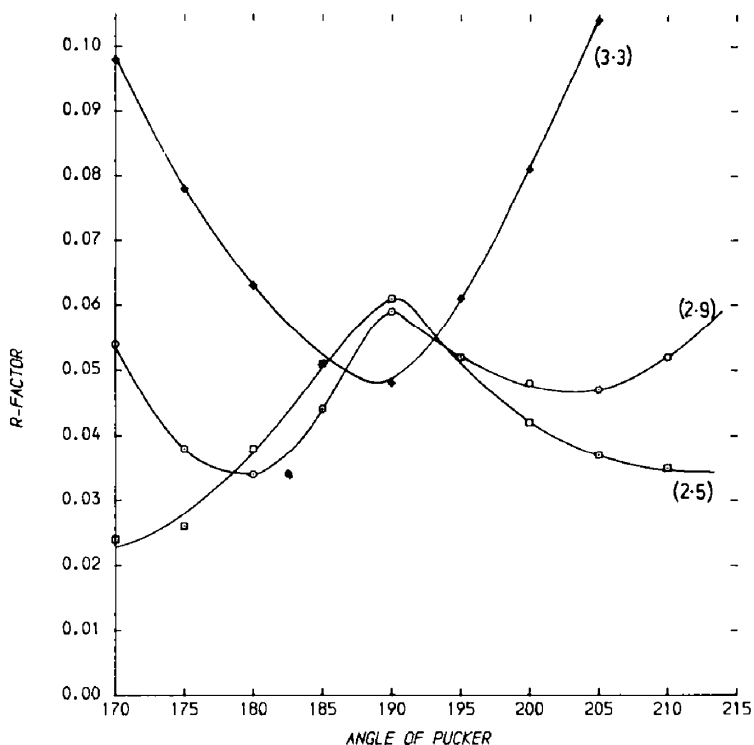


Fig. 5. The agreement factor (R) versus the angle of pucker α for bicyclo[3.1.0]hexan-3-one: one-site binding model with yttrium polar radius constrained to 2.5, 2.9 and 3.3 Å respectively (curves labelled in parentheses).

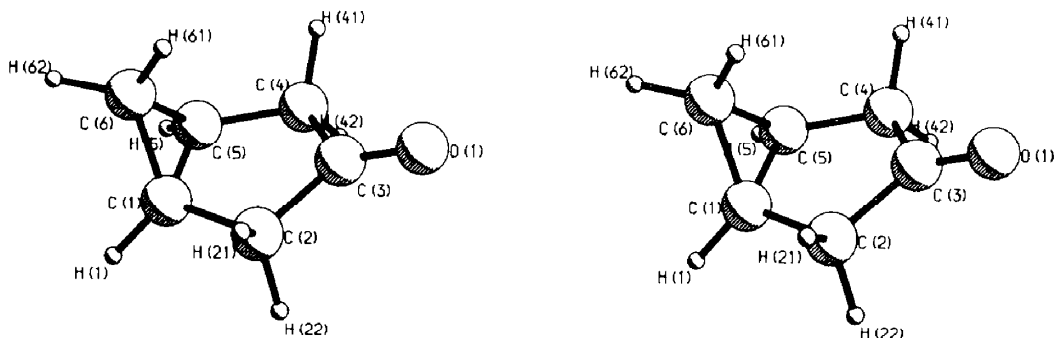


Fig. 6. Stereoscopic view of a molecule of (1), pucker = 195°, drawn with programme PLUTO 78 (Cambridge Crystallographic Data Centre, Cambridge, England).

on the dangers of extrapolating geometries from solid to solution phases.

After the preliminary publication of our results on 1, and in the absence of structural information from other physical techniques, we embarked upon an analysis by *ab initio*, quantum mechanical methods of the dependence of 1's potential energy on the angle of pucker α . The results of the calculations (GAUSSIAN 70 programme,¹⁷ STO-3G basis set) are summarised in Fig. 7. Comfortingly, the predicted minimum energy conformation with 197° pucker is very close to the recently-published structure (gas-phase, microwave data¹³) with 198.8° pucker and close to that derived from our L.I.S. analyses. Since the geometric construction that we use in buckling the ring induces some angle strain at extreme values of α , and because the *ab initio* calculations were carried out on unrelaxed structures, the slope of the curve in Fig. 7 is expected to be too steep in those

regions where α is remote from the minimum.

As in our previous work on cyclohexanone and 4-*t*-butylcyclohexanone,¹ we are driven by the experimental results to the conclusion that the one-site lanthanide ion binding model inadequately reproduces the experimental L.I.S. data and leads to inaccurate prediction of substrate conformation (unless constraints are applied to the lanthanide ion-binding site separation). This conclusion differs from that of Földesi and Hofer,¹⁸ based on a theoretical comparison of one- and two-site models employing a cuboidal network of "atoms" as an artificial substrate molecule. These authors stress the similar geometry of the dipolar magnetic fields for the two binding models. As a final comment on this important aspect of the work, however, we present our L.I.S. results for adamantanone (2) which strongly support a multi-site binding model

In the absence of X-ray diffraction data, a geometry

Table 4. Bond lengths (Å), bond angles and torsion angles (°) for (1),^a $\alpha = 195^\circ$

O(1)	C(3)	1.208	C(3)	C(2)	1.510	C(3)	C(4)	1.510			
C(2)	C(1)	1.510	C(2)	H(21)	1.100	C(2)	H(22)	1.100			
C(4)	C(5)	1.510	C(4)	H(41)	1.100	C(4)	H(42)	1.100			
C(1)	C(5)	1.471	C(1)	C(6)	1.520	C(1)	H(1)	1.100			
C(5)	C(6)	1.516	C(5)	H(5)	1.100	C(6)	H(61)	1.100			
C(6)	H(62)	1.100									
O(1)	C(3)	C(2)	126.9	O(1)	C(3)	C(4)	126.9	C(2)	C(3)	C(4)	106.1
C(3)	C(2)	C(1)	107.6	C(3)	C(2)	H(21)	109.5	C(3)	C(2)	H(22)	109.5
C(1)	C(2)	H(21)	109.5	C(1)	C(2)	H(22)	109.5	H(21)	C(2)	H(22)	111.3
C(3)	C(4)	C(5)	107.6	C(3)	C(4)	H(41)	109.5	C(3)	C(4)	H(42)	109.5
C(5)	C(4)	H(41)	109.5	C(5)	C(4)	H(42)	109.5	H(41)	C(4)	H(42)	111.3
C(2)	C(1)	C(5)	108.2	C(2)	C(1)	C(6)	116.3	C(2)	C(1)	H(1)	120.9
C(5)	C(1)	C(6)	68.9	C(5)	C(1)	H(1)	117.7	C(6)	C(1)	H(1)	117.7
C(4)	C(5)	C(1)	108.2	C(4)	C(5)	C(6)	116.3	C(4)	C(5)	H(5)	120.8
H(1)	C(5)	C(6)	61.2	C(1)	C(5)	H(5)	117.7	C(6)	C(5)	H(5)	117.7
C(1)	C(6)	C(5)	57.9	C(1)	C(6)	H(61)	117.7	C(1)	C(6)	H(62)	117.7
L(5)	C(6)	H(61)	117.7	C(5)	C(6)	H(62)	117.7	H(61)	C(6)	H(62)	115.8
O(1)	C(3)	C(2)	C(1)	165.1	O(1)	C(3)	C(2)	H(21)	46.2		
O(1)	C(3)	C(2)	H(22)	-76.1	C(4)	C(3)	C(2)	C(1)	-14.9		
C(4)	C(3)	C(2)	H(21)	-133.8	C(4)	C(3)	C(2)	H(22)	103.9		
O(1)	C(3)	C(4)	C(5)	-165.1	O(1)	C(3)	C(4)	H(41)	-46.2		
O(1)	C(3)	C(4)	H(42)	76.1	C(2)	C(3)	C(4)	C(5)	14.9		
C(2)	C(3)	C(4)	H(41)	133.8	C(2)	C(3)	C(4)	H(42)	-103.9		
C(3)	C(2)	C(1)	C(5)	9.4	C(3)	C(2)	C(1)	C(6)	-56.5		
C(3)	C(2)	C(1)	H(1)	149.4	H(21)	C(2)	C(1)	C(5)	128.2		
H(21)	C(2)	C(1)	C(6)	62.4	H(21)	C(2)	C(1)	H(1)	-91.7		
H(22)	C(2)	C(1)	C(5)	-109.5	H(22)	C(2)	C(1)	C(6)	-175.4		
H(22)	C(2)	C(1)	H(1)	30.6	C(3)	C(4)	C(5)	C(1)	-9.4		
C(3)	C(4)	C(5)	C(6)	56.8	C(3)	C(4)	C(5)	H(5)	-149.4		
H(41)	C(4)	C(5)	C(1)	-128.2	H(41)	C(4)	C(5)	C(6)	-62.1		
H(41)	C(4)	C(5)	H(5)	91.8	H(42)	C(4)	C(5)	C(1)	109.5		
H(42)	C(4)	C(5)	C(6)	175.6	H(42)	C(4)	C(5)	H(5)	-30.5		
C(2)	C(1)	C(5)	C(4)	0.0	C(2)	C(1)	C(5)	C(6)	-110.5		
C(2)	C(1)	C(5)	H(5)	141.4	C(6)	C(1)	C(5)	C(4)	110.5		
C(6)	C(1)	C(5)	C(6)	0.0	C(6)	C(1)	C(5)	H(5)	-108.1		
H(1)	C(1)	C(5)	C(4)	-141.5	H(1)	C(1)	C(5)	C(6)	108.0		
H(1)	C(1)	C(5)	H(5)	-1.1	C(2)	C(1)	C(6)	C(5)	97.1		
C(2)	C(1)	C(6)	H(61)	-9.0	C(2)	C(1)	C(6)	H(62)	-156.0		
C(5)	C(1)	C(6)	C(5)	-1.0	C(5)	C(1)	C(6)	H(61)	-106.9		
C(5)	C(1)	C(6)	H(62)	106.9	H(1)	C(1)	C(6)	C(5)	-108.0		
H(1)	C(1)	C(6)	H(61)	145.1	H(1)	C(1)	C(6)	H(62)	-1.1		
C(4)	C(5)	C(6)	C(1)	-97.2	C(4)	C(5)	C(6)	H(61)	9.7		
C(4)	C(5)	C(6)	H(62)	155.9	C(1)	C(5)	C(6)	C(1)	-0.0		
C(1)	C(5)	C(6)	H(61)	106.9	C(1)	C(5)	C(6)	H(62)	-106.9		
H(5)	C(5)	C(6)	C(1)	108.1	H(5)	C(5)	C(6)	H(61)	-145.0		
H(5)	C(5)	C(6)	H(62)	1.2							

^aValues calculated by programme GEOM, Cambridge Crystallographic Data Centre, Cambridge, England.

Table 5. Cartesian coordinates for (1),^a $\alpha = 195^\circ$

Atom	X	Y	Z
O(1)	0.000	0.000	0.000
C(1)	3.501	0.735	0.371
C(2)	2.115	1.207	0.000
C(3)	1.208	0.000	0.000
C(6)	3.629	-0.004	1.693
H(1)	4.394	1.247	-0.017
H(21)	1.762	1.931	0.748
H(22)	2.136	1.650	-1.007
H(61)	2.758	-0.005	2.365
H(62)	4.613	-0.005	2.185

^a Coordinates given only for the asymmetric unit. The remainder of the molecule may be generated by transformation of the appropriate coordinates from X, Y, Z to X, -Y, Z.

for 2 was derived from molecular mechanics calculations on adamantane¹⁹ (with subsequent geometry manipulation to furnish the CO group and hydrogen atom positions), methylene adamantane and adamantanone.²⁰ Differences between the three geometries and results derived therefrom are not significant. Bond lengths, bond

angles and torsion angles are given in Table 6 and cartesian coordinates are listed in Table 7.

The C_{2v} symmetry of 2 necessarily requires that the lanthanide ion be located along the axis of the CO group in a one-site binding model. Indeed, the lanthanide coordinates corresponding to a minimum R-factor ($r =$

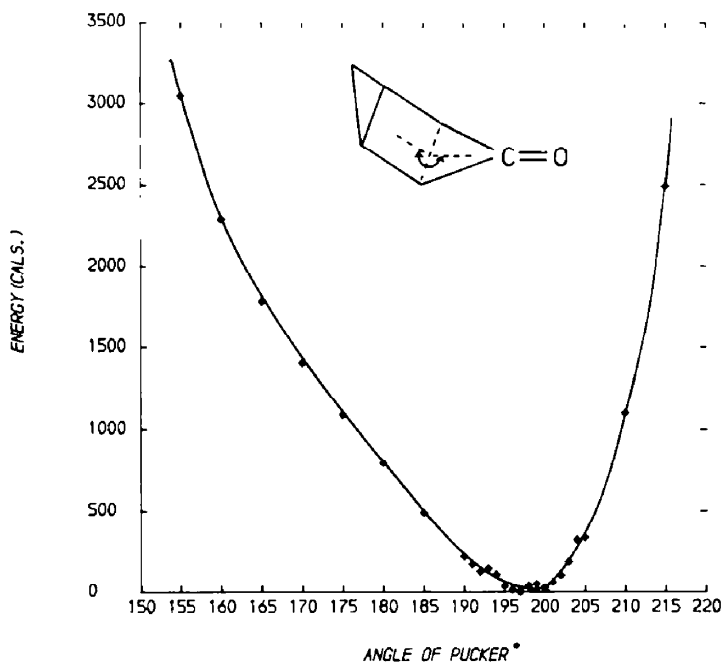


Fig. 7. Variation in potential energy with angle of pucker for (1) as estimated by *ab initio*, STO-3G calculations.

2.15–2.20 Å, $\phi = 90^\circ$, $\psi = 180^\circ$) support this view. The resulting polar radius is too short, and the R-factor (0.065) is poor. Because 2 possesses two mirror planes of symmetry, the lanthanide ion is constrained into the ketonic plane in the two-site binding model: the best-fit, lanthanide ion positions ($r = 3.05$ – 3.20 Å, $\phi = 90^\circ$, $\psi = 130$ – 135° and 230 – 225°) again support this view. Although the resulting polar radius is reasonable, the R-factor at minimum disagreement between observed and calculated L.I.S.'s (0.045) is still disquietingly large compared with the values routinely expected (see Fig. 3 and 4). Only in the four-site model is the lanthanide ion position truly variable in three dimensions. The resulting lanthanide coordinates ($r = 2.80$ – 3.00 Å, $\phi = 55$ – 60° and 125 – 120° , $\psi = 155$ – 145° and 205 – 215°) and R-factor (0.011) at minimum disagreement, and improvement over the other

models in atom by atom agreement between observed and calculated L.I.S.'s (Table 2) demonstrate convincingly the appropriateness of the four-site model in this case. The lanthanide ion adopts chemically reasonable positions, balancing the attractive interactions with the oxygen lone-pair electron density and repulsive interactions with the ketone α -H atoms. The importance of steric effects in influencing the *strength* of binding between shift reagents and Lewis bases is widely recognised.²¹ our present work implies a similar importance in relation to the *stereochemistry* of binding.

CONCLUSIONS

The results of this combined L.I.S. and *ab initio*, quantum mechanical study demonstrate that reliable, accurate information about solution molecular structure

Table 6. Bond lengths (Å), bond angles and torsion angles ($^\circ$) for (2)^a

C(1)	C(2)	1.212	C(2)	C(1)	1.513	C(2)	C(3)	1.513			
C(1)	H(1)	1.102	C(1)	C(7)	1.534	C(1)	C(6)	1.534			
C(3)	H(3)	1.102	C(3)	C(9)	1.534	C(3)	C(4)	1.534			
C(7)	C(8)	1.536	C(7)	H(71)	1.101	C(7)	H(72)	1.101			
C(6)	C(5)	1.536	C(6)	H(61)	1.101	C(6)	H(62)	1.101			
C(9)	C(8)	1.536	C(9)	H(91)	1.101	C(9)	H(92)	1.101			
C(4)	C(5)	1.536	C(4)	H(41)	1.101	C(4)	H(42)	1.101			
C(8)	C(10)	1.535	C(8)	H(8)	1.101	C(8)	C(10)	1.534			
C(5)	C(5)	1.101	C(10)	H(101)	1.101	C(10)	H(102)	1.101			
C(1)	C(2)	C(11)	122.4	C(1)	C(2)	C(3)	122.4	C(1)	C(2)	C(3)	115.2
C(2)	C(1)	H(1)	112.3	C(2)	C(1)	C(7)	107.4	C(2)	C(1)	C(6)	107.4
H(1)	C(1)	C(7)	110.0	H(1)	C(1)	C(6)	110.0	C(7)	C(1)	C(6)	109.8
C(1)	C(3)	H(3)	112.3	C(2)	C(3)	C(9)	107.4	C(2)	C(3)	C(4)	107.4
H(3)	C(3)	C(9)	110.0	H(3)	C(3)	C(4)	110.0	C(9)	C(3)	C(4)	109.8
C(1)	C(7)	C(8)	109.8	C(1)	C(7)	H(71)	109.9	C(1)	C(7)	H(72)	109.6
C(8)	C(7)	H(71)	109.7	C(8)	C(7)	H(72)	109.7	H(71)	C(7)	H(72)	108.2
C(1)	C(6)	C(5)	109.8	C(1)	C(6)	H(61)	109.6	C(1)	C(6)	H(62)	109.9
C(5)	C(6)	H(61)	109.7	C(5)	C(6)	H(62)	109.7	H(61)	C(6)	H(62)	108.2
C(3)	C(9)	C(8)	109.8	C(3)	C(9)	H(91)	109.6	C(3)	C(9)	H(92)	109.8
C(8)	C(9)	H(91)	109.7	C(8)	C(9)	H(92)	109.7	H(91)	C(9)	H(92)	108.2
C(3)	C(4)	C(5)	109.8	C(3)	C(4)	H(41)	109.9	C(3)	C(4)	H(42)	109.6
C(5)	C(4)	H(41)	109.7	C(5)	C(4)	H(42)	109.7	H(41)	C(4)	H(42)	108.2
C(7)	C(8)	C(9)	110.2	C(7)	C(8)	C(10)	109.2	C(7)	C(8)	H(8)	109.4
C(9)	C(8)	C(10)	109.2	C(9)	C(8)	H(8)	109.4	C(10)	C(8)	H(8)	109.5
C(6)	C(5)	C(4)	110.2	C(6)	C(5)	C(10)	109.2	C(6)	C(5)	H(5)	109.4
C(4)	C(5)	C(10)	109.2	C(4)	C(5)	H(5)	109.4	C(10)	C(5)	H(5)	109.5
C(8)	C(10)	C(5)	109.8	C(8)	C(10)	H(101)	109.7	C(8)	C(10)	H(102)	109.7
C(5)	C(10)	H(101)	109.7	C(5)	C(10)	H(102)	109.6	H(101)	C(10)	H(102)	108.2

Table 6 (Contd.).

O(1)	C(2)	C(1)	H(1)	0.0	O(1)	C(2)	C(1)	C(7)	-121.0
O(1)	C(2)	C(1)	C(6)	121.0	C(3)	C(2)	C(1)	H(1)	180.0
C(3)	C(2)	C(1)	C(7)	59.0	C(3)	C(2)	C(1)	C(6)	-59.0
O(1)	C(2)	C(3)	H(3)	0.0	O(1)	C(2)	C(3)	C(9)	121.0
O(1)	C(2)	C(3)	C(4)	-121.0	C(1)	C(2)	C(3)	H(3)	180.0
C(1)	C(2)	C(3)	C(9)	-59.0	C(1)	C(2)	C(3)	C(4)	59.0
C(2)	C(1)	C(7)	C(8)	-57.1	C(2)	C(1)	C(7)	H(71)	63.6
C(2)	C(1)	C(7)	H(72)	-177.7	H(1)	C(1)	C(7)	C(8)	-179.6
H(1)	C(1)	C(7)	H(71)	-58.9	H(1)	C(1)	C(7)	H(72)	59.8
C(6)	C(1)	C(7)	C(8)	59.3	C(6)	C(1)	C(7)	H(71)	180.0
C(6)	C(1)	C(7)	H(72)	-61.3	C(2)	C(1)	C(6)	C(5)	57.1
C(2)	C(1)	C(6)	H(61)	177.7	C(2)	C(1)	C(6)	H(62)	-63.6
H(1)	C(1)	C(6)	C(5)	179.6	H(1)	C(1)	C(6)	H(61)	-59.8
H(1)	C(1)	C(6)	H(62)	58.9	C(7)	C(1)	C(6)	C(5)	-59.3
C(7)	C(1)	C(6)	H(61)	61.3	C(7)	C(1)	C(6)	H(62)	-180.0
C(2)	C(3)	C(9)	C(8)	57.1	C(2)	C(3)	C(9)	H(91)	177.7
C(2)	C(3)	C(9)	H(92)	-63.6	H(3)	C(3)	C(9)	C(8)	179.6
H(3)	C(3)	C(9)	H(91)	-59.8	H(3)	C(3)	C(9)	H(92)	58.9
C(4)	C(3)	C(9)	C(8)	-59.2	C(4)	C(3)	C(9)	H(91)	61.3
C(4)	C(3)	C(9)	H(92)	-180.0	C(2)	C(3)	C(4)	C(5)	-57.1
C(2)	C(3)	C(4)	H(41)	63.6	C(2)	C(3)	C(4)	H(42)	-177.7
H(3)	C(3)	C(4)	C(5)	-179.6	H(3)	C(3)	C(4)	H(41)	-58.9
H(3)	C(3)	C(4)	H(42)	59.8	C(9)	C(3)	C(4)	C(5)	59.2
C(9)	C(3)	C(4)	H(41)	180.0	C(9)	C(3)	C(4)	H(42)	-61.3
C(1)	C(7)	C(8)	C(9)	60.4	C(1)	C(7)	C(8)	C(10)	-59.6
C(1)	C(7)	C(8)	H(8)	-179.3	H(71)	C(7)	C(8)	C(9)	-60.4
H(71)	C(7)	C(8)	C(10)	179.6	H(71)	C(7)	C(8)	H(8)	59.9
H(72)	C(7)	C(8)	C(9)	-179.1	H(72)	C(7)	C(8)	C(10)	61.0
H(72)	C(7)	C(8)	H(8)	-58.8	C(11)	C(6)	C(5)	C(4)	-60.4
C(1)	C(6)	C(5)	C(10)	59.6	C(1)	C(6)	C(5)	H(5)	179.3
H(61)	C(6)	C(5)	C(4)	179.1	H(61)	C(6)	C(5)	C(10)	-60.9
H(61)	C(6)	C(5)	H(5)	58.8	H(62)	C(6)	C(5)	C(4)	60.4
H(62)	C(6)	C(5)	C(10)	-179.6	H(62)	C(6)	C(5)	H(5)	-59.9
C(3)	C(9)	C(8)	C(7)	-60.4	C(3)	C(9)	C(8)	C(10)	59.5
C(3)	C(9)	C(8)	H(8)	179.3	H(91)	C(9)	C(8)	C(7)	179.1
H(91)	C(9)	C(8)	C(10)	-61.0	H(91)	C(9)	C(8)	H(8)	58.0
H(92)	C(9)	C(8)	C(7)	60.4	H(92)	C(9)	C(8)	C(10)	-179.7
H(92)	C(9)	C(8)	H(8)	-59.9	C(3)	C(4)	C(5)	C(6)	60.4
C(3)	C(4)	C(5)	C(10)	-59.6	C(3)	C(4)	C(5)	H(5)	-179.3
H(41)	C(4)	C(5)	C(6)	-60.4	H(41)	C(4)	C(5)	C(10)	179.6
H(41)	C(4)	C(5)	H(5)	59.9	H(42)	C(4)	C(5)	C(6)	-179.1
H(42)	C(4)	C(5)	C(10)	61.0	H(42)	C(4)	C(5)	H(5)	-58.8
C(7)	C(8)	C(10)	C(5)	60.3	C(7)	C(8)	C(10)	H(101)	-60.4
C(7)	C(8)	C(10)	H(102)	-179.1	C(9)	C(8)	C(10)	C(5)	-60.2
C(9)	C(8)	C(10)	H(101)	179.1	C(9)	C(8)	C(10)	H(102)	60.3
H(8)	C(8)	C(10)	C(5)	-180.0	H(8)	C(8)	C(10)	H(101)	59.3
H(8)	C(8)	C(10)	H(102)	-59.4	C(6)	C(5)	C(10)	C(8)	-60.3
C(6)	C(5)	C(10)	H(101)	60.4	C(6)	C(5)	C(10)	H(102)	179.1
C(4)	C(5)	C(10)	C(8)	60.3	C(4)	C(5)	C(10)	H(101)	-179.1
C(4)	C(5)	C(10)	H(102)	-60.4	H(5)	C(5)	C(10)	C(8)	180.0
H(5)	C(5)	C(10)	H(101)	-59.3	H(5)	C(5)	C(10)	H(102)	59.4

^aValues calculated as in Table 4.

Table 7. Cartesian coordinates for (2)^a

Atom	X	Y	Z
O(1)	0.000	0.000	0.000
C(1)	2.022	1.278	0.000
C(2)	1.212	0.000	0.000
C(4)	2.904	-1.260	1.255
C(5)	3.783	0.000	1.255
C(10)	4.665	0.000	0.000
H(1)	1.386	2.177	0.000
H(41)	2.272	-1.272	2.156
H(42)	3.542	-2.157	1.271
H(5)	4.421	0.000	2.153
H(101)	5.310	0.892	0.000

^aCoordinates given only for the asymmetric unit. The remainder of the molecule may be generated by transformation of the appropriate coordinates from X, Y, Z to X, \pm Y, \pm Z.

may be derived by this approach. Features essential to the success of the work are (i) obtention of precise L.I.S. data on ^1H and ^{13}C nuclei; (ii) adoption of a reasonable starting geometry for the conformational refinement, and (iii) selection of a lanthanide ion-substrate binding model appropriate to the problem in hand.

Acknowledgements—We thank the British Council for a substantive academic link between Liverpool and Genoa and the Science Research Council for grants towards the purchase of NMR spectrometers. We are grateful for helpful discussions with Dr. Lee Griffiths.

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