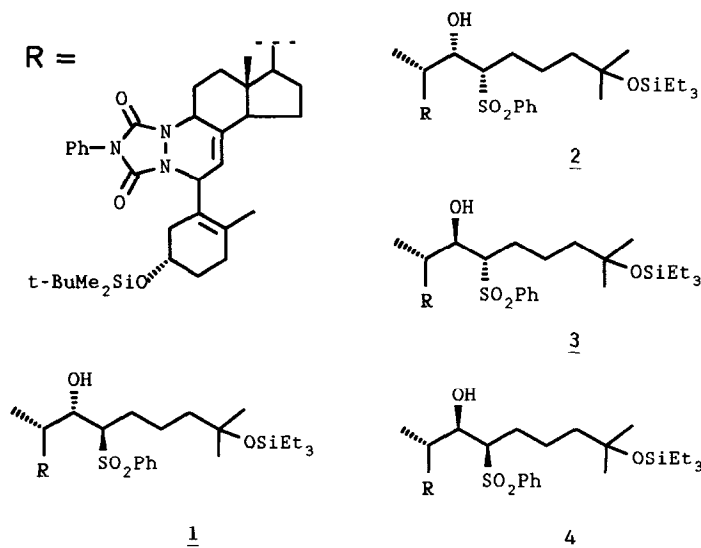


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Abstract: The least-energy conformers were determined for side-chain disubstituted analogs of vitamin D₃ by molecular mechanics modeling and semiempirical calculations based on a generalized Karplus equation.

The recently discovered immunosuppressive activity of some vitamin D analogs with an "unnatural" geometry of the side chain¹ gave another impulse to undertake conformational analysis of this part of the vitamin D molecule. The analyses performed by now were limited to the cholesterol-type unsubstituted side chain². Recent studies³ revealed, however, that side-chain substituted analogues might represent a class of analogues with highly specific activity profile. It was, therefore, a need to develop the conformational analysis of this class of compounds. For this purpose we selected a set of diastereomeric β -hydroxysulfones **1** - **4** as model compounds⁴ for which both crystallographic data of vitamin D nucleus⁵ and coupling constants for side-chain protons⁶ were available.



In order to determine the conformation of the side-chain part of compounds **1** - **4** we developed the methodology comprising molecular modeling⁷ and semiempirical calculations based on the generalized Karplus equation⁸. The starting coordinates for the vitamin D nucleus of compounds **1** - **4** were taken from X-ray crystal structure⁵ of the Diels-Alder adduct of 4-phenyl-1,2,4-triazoline-3,5-dione with the side-chain unsubstituted previtamin D₃. To this basic structure the respective side-chains of compounds **1** - **4** were attached and the resulting molecules were subjected to the energy minimization procedure. A systematic search was conducted for the conformation that corresponds to the minimum value of the total energy of the molecule, calculated by MMX force field in a standard molecular mechanics program⁹. Of a number of rotatable bonds in compounds examined only three bonds and the respective dihedral angles were taken into account as a first approximation. These included C4-C5-C6- C7 angle between A-ring and a relatively rigid tetrahydropyridazine moiety, C16-C17-C20-C22 angle between D-ring and the side chain, and an angle in the side-chain (H-C22-C23-H) for which the experimental vicinal coupling constants were available⁶. Successive non-rigid rotations around the selected bonds were carried out and several minimum energy conformations were identified. The population of the conformer was calculated from the following equation:

$$N_i/N_{st} = \exp (-\Delta E/RT)$$

where: ΔE is the difference of energy between a given conformer and the most stable one at $T = 300$ K and N_i/N_{st} is the respective molar ratio. The percentage population of a given conformer was calculated as follows:

$$P_i = \frac{N_i/N_{st}}{\sum N_i/N_{st}} * 100$$

and it is given for the least-energy conformers of compound **4** in Table I.

The vicinal coupling constants $J_{22,23}$ for compounds **1** - **4** were calculated on the basis of the generalized Karplus equation⁸. Electronegativity effects of both α and β substituents of C-22 and C- 23 carbons were included. Torsion angle H-C22-C23-H for each conformer was taken from the energy minimization procedure. The Karplus equation was obtained for each compound and it was shown for **4** in a graphic form in Figure 1. The values of calculated coupling constant for the least energy conformers of compound **4** are given in Table I.

The average coupling constant for each compound was calculated as follows:

$$J_{calcd} = \sum (P_i * J_i)/100$$

where P_i is defined above and J_i represents the vicinal coupling constant H-C22-C23-H of a given conformer. The calculated $J_{22,23}$ for **4** was 8.8 ± 0.4 Hz, while the experimental data was 10 ± 1 Hz. The stick model of 3D structure of the least-energy conformer **1** of compound **4** is shown in Fig. 2. Preliminary calculations indicate also a good correlation for other compounds (**1** - **3**) from the set examined. This

correlation might be considered as a partial validation of the conformation generated by this methodology for side-chain substituted analogs.

The use of the present conformational analysis for the selection of side-chain substituted vitamin D₃ analogs to be synthesized is under way in these laboratories.

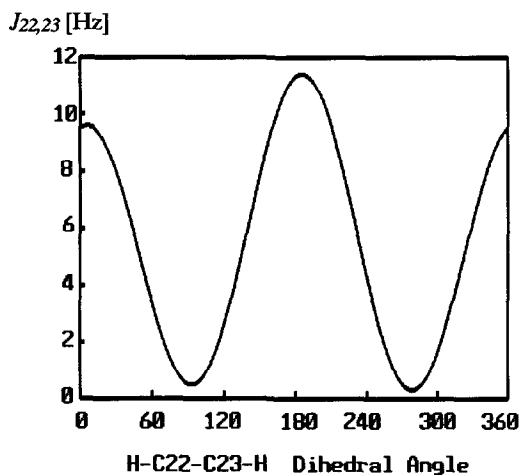


Fig. 1. Graphic presentation of the generalized Karplus equation for compound 4

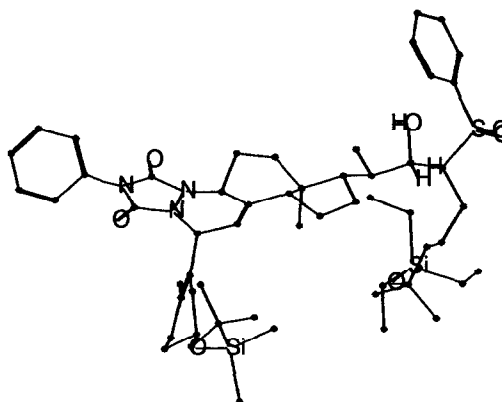


Fig. 2. Stick model of the least-energy conformer of compound 4

Table I. Least-energy conformers of β -hydroxysulfone 4

Conformer	1	2	3	4
Dihedral angle [°]:				
C4-C5-C6-C7	66.0	49.9	61.8	61.7
C16-C17-C20-C22	56.8	303.4	174.9	304.2
H-C22-C23-H	213.6	245.3	204.0	66.4
E [kJ/mol]	308.8	317.1	328.9	330.5
Δ E [kJ/mol]	0	8.3	20.1	21.7
Pi [%]	96.6	3.4	0.03	0.02
Ji [Hz]	9.0	3.4	10.3	2.4

Acknowledgment

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6. ¹H NMR (CDCl₃). **1**: δ 0.77 (3H, s, 18-CH₃), 0.94 (3H, d J = 6.5 Hz, 21-CH₃), 1.02, 1.11 (3H, s, 26,27-CH₃), 1.77 (3H, s, 19-CH₃), 2.55 (1H, m, 14-H), 2.79 (1H, d J = 2 Hz, 22-OH), 2.93 (1H, d J_{22,23} = 1Hz, 23-H), 3.13 (1H, m, 11-H), 3.73 (1H, m, 3-H), 4.31 (1H, m, 22-H), 4.44 (1H, d J = 12 Hz, 9-H), 5.16 (1H, m, 7-H), 5.30 (1H, m, 6-H).
2: δ 0.81 (3H, s, 18-CH₃), 1.06 (3H, d J = 6.5 Hz, 21-CH₃), 1.11, 1.12 (3H, s, 26,27-CH₃), 1.77 (3H, s, 19-CH₃), 2.58 (1H, m, 14-H), 3.15 (1H, m, 11-H), 3.33 (1H, m, J_{22,23} = 6Hz, 23-H), 3.56 (1H, d J = 6 Hz, 22-OH), 3.76 (1H, m, 3-H), 3.85 (1H, m, 22-H), 4.45 (1H, d J = 12.4 Hz, 9-H), 5.18 (1H, m, 7-H), 5.30 (1H, m, 6-H).
3: δ 0.73 (3H, s, 18-CH₃), 0.94 (3H, d J = 6.5 Hz, 21-CH₃), 1.05, 1.09 (3H, s, 26,27-CH₃), 1.77 (3H, s, 19-CH₃), 2.14 (1H, d J = 2Hz, 22-OH), 2.63 (1H, m, 14-H), 2.94 (1H, m, J_{22,23} = 3Hz, 23-H), 3.13 (1H, m, 11-H), 3.75 (1H, m, 3-H), 4.30 (1H, m, 22-H), 4.44 (1H, d J = 12 Hz, 9-H), 5.18 (1H, m, 7-H), 5.30 (1H, m, 6-H).
4: δ 0.77 (3H, s, 18-CH₃), 0.94 (3H, d J = 6.5 Hz, 21-CH₃), 1.09, 1.12 (3H, s, 26,27-CH₃), 1.77 (3H, s, 19-CH₃), 2.68 (1H, m, 14-H), 3.15 (1H, m, 11-H), 3.18 (1H, m, J_{22,23} = 10Hz, 23-H), 3.74 (1H, m, 3-H), 4.16 (1H, d J = 8.9Hz, 22-H), 4.47 (1H, d J = 10.6 Hz, 9-H), 5.18 (1H, m, 7-H), 5.30 (1H, m, 6-H).
7. The modeling procedure followed the methods outlined in *Computer Modeling of Carbohydrate Molecules*; French, A. D.; Brady, J. W. Eds; American Chemical Society: Washington, 1990. The description was made according to the guidelines for publications in molecular modeling related to medicinal chemistry.
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9. Serena Software, P.O.Box 307, Bloomington, IN 47402-3076. The option with a dielectric constant of the medium was used (CDCl₃, 4.7).