Chatgilialoglu et al.[7] have found that at 300 K the cis isomer is 2.4 times more reactive than the trans isomer, the respective absolute k values being 2.1×10^7 and 8.9×10^6 M^{-1} s^{-1}. Table IV lists relative addition rate data for the reaction of these two compounds with various radicals. It can be seen that in all the reactions the trans isomer is more reactive than the cis isomer. The observation that this order of reactivity is reversed in the reactions with triethylsilyl radicals can be rationalized if it is assumed that the cis isomer reacts mainly by Cl transfer and that in this reaction it is much more reactive than the trans isomer of dichloroethylene.

Registry No. C_2Cl_4, 127-18-4; Et_3SiH, 617-86-7; Et_3SiCl, 994-30-9; C_2Cl_3H, 79-01-6; *t*-BuCl, 507-20-0; *t*-BuH, 1320-76-9.

Pyramidalization of Carbonyl Carbons in Asymmetric Environments: Carboxylates, Amides, and Amino Acids

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Abstract: Ab initio molecular orbital calculations, in some cases using unusually stringent convergence criteria for both SCF and geometry optimizations, predict that pyramidalization of the sp^2 carbon atoms will occur in the asymmetric conformers of acetamide, acetic acid, acetaldehyde, propionaldehyde, and the acetate anion. This pyramidalization is small, $\approx 2°$, such that the displacement of the apex of the pyramid is anti to the direction of the bond on the adjacent carbon atom which is most nearly normal to the mean plane of the sp^2 C bonds. This produces partial staggering about the bond to the carbonyl carbon. A survey of 49 neutron diffraction crystal structure analyses of amino acids and dipeptides provides experimental evidence in qualitative support of these theoretical predictions.

Theoretical studies of a variety of alkenes[2-4] and acetaldehyde[2b] led to the prediction that doubly bonded carbon atoms will pyramidalize toward a staggered geometry when the local molecular environment is asymmetrical with respect to the formal plane of the sp^2-hybridized orbitals of the alkene carbons. Dramatic examples of pyramidalization have been found in X-ray crystal structures of polycyclic alkenes.[5,7] These distortions are also obtained in molecular mechanics (force-field) calculations and have been interpreted to be the consequence of torsional strain.[4,6,7]

We now report a systematic study of pyramidalization in carboxylates, amides, and amino acids, based on theoretical ab initio calculations and a survey of some relevant crystal structural data. This work was prompted by the observation of pyramidalization in the molecule of acetamide in its rhombohedral crystalline form.[8] Although acetamide has C_s symmetry in the gas phase and solution, in the trigonal form of crystalline acetamide, the molecules have the asymmetric conformation, **1**, in an asymmetric crystal structure, space group $R3c$. One of the three methyl C–H bonds is almost normal to the molecular plane of the non-hydrogen atoms, as in **1**. This alteration of conformation about the C–C(O) bond of amides and peptides is well-

Chart I

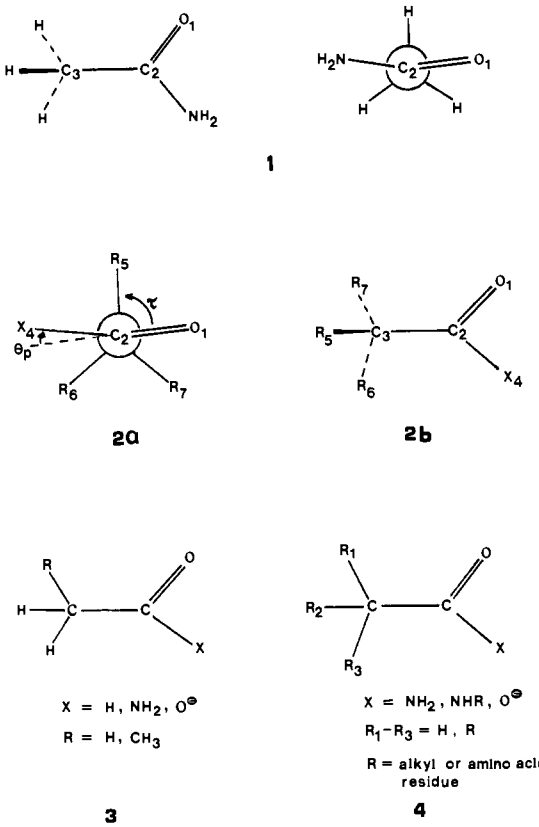

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Table I. 3-21G Optimized Structures and Energies of Molecules Shown in Figure 1

Acetaldehyde

	5	6	6		5	6	6
optimization	DEFAULT	DEFAULT	TIGHT				
$\angle HC_3C_2O_1$, deg	0.0	90.0	90.0				
			Bond Lengths (Å)				
C_2O_1	1.209	1.209	1.209	C_3H_5	1.080	1.087	1.087
C_2C_3	1.507	1.509	1.510	C_3H_6	1.086	1.082	1.082
C_2H_4	1.086	1.086	1.086	C_3H_7	1.086	1.082	1.082
			Bond Angles (deg)				
$C_3C_2O_1$	124.8	124.3	124.3	$H_6C_3C_2$	109.9	111.0	111.0
$H_4C_2C_3$	114.3	114.8	114.8	$H_7C_3C_2$	109.9	109.9	109.9
$H_5C_3C_2$	110.0	109.2	109.2				
			Dihedral Angles (deg)				
$H_6C_3C_2H_5$	120.9	119.5	119.6	θ_d	0.0	1.8	1.8
$H_7C_3C_2H_5$	−120.9	−118.2	−118.1	θ_p	0.0	1.6	1.6
$H_4C_2C_3O_1$	180.0	181.8	181.8	E, au	−152.05525		−155.05439

Propionaldehyde

	7	8	8	9	9	10	10
$\angle C_5C_3C_2O_1$, deg	0.0	124.2	127.8	210.9	210.8	90.0	90.0
optimization	DEFAULT	DEFAULT	TIGHT	DEFAULT	TIGHT	DEFAULT	TIGHT
			Bond Lengths (Å)				
C_2O_1	1.209	1.209	1.208	1.208	1.208	1.209	1.209
C_2C_3	1.508	1.508	1.508	1.512	1.512	1.509	1.509
C_2H_4	1.087	1.087	1.089	1.089	1.089	1.088	1.088
C_3C_5	1.534	1.546	1.545	1.539	1.539	1.551	1.551
C_3H_6	1.087	1.087	1.087	1.082	1.082	1.083	1.083
C_3H_7	1.087	1.081	1.081	1.088	1.088	1.082	1.082
			Bond Angles (deg)				
$C_3C_2O_1$	124.4	125.3	125.3	124.8	124.8	124.4	124.4
$C_3C_2H_4$	114.8	113.8	113.8	114.3	114.3	114.6	114.6
$C_5C_3C_2$	111.9	110.4	110.5	111.5	111.5	109.3	109.4
$H_6C_3C_2$	108.0	108.5	108.3	108.4	108.4	109.8	109.9
$H_7C_3C_2$	108.0	108.6	108.6	107.9	107.9	108.8	108.8
			Dihedral Angles (deg)				
$H_6C_3C_2C_5$	122.5	119.7	119.8	123.2	123.3	120.7	120.8
$H_7C_3C_2C_5$	−122.5	−122.2	−122.4	−120.9	−120.8	−119.5	−119.4
$H_4C_2C_3O_1$	180.0	180.4	180.1	181.4	181.4	183.2	183.1
θ_d	0.0	0.4	0.1	1.4	1.4	3.2	3.1
θ_p	0.0	0.3	0.1	1.2	1.2	2.9	2.9
E, au	−190.87779	−190.87505		−190.87464		−190.87381	

Acetamide

	11	12	12		11	12	12
optimization	DEFAULT	DEFAULT	TIGHT				
$\angle H_5C_3C_3O_1$, deg	0.0	90.0	90.0				
			Bond Lengths (Å)				
C_2O_1	1.215	1.216	1.216	C_3H_6	1.084	1.082	1.082
C_2C_3	1.515	1.517	1.517	C_3H_7	1.084	1.080	1.080
C_2N_4	1.360	1.358	1.358	N_4H_8	0.997	0.998	0.998
C_3H_5	1.079	1.085	1.085	N_4H_9	0.994	0.994	0.994
			Bond Angles (deg)				
$C_3C_2O_1$	123.5	122.9	122.9	$H_7C_3C_2$	110.3	108.7	108.6
$N_4C_2C_3$	113.8	114.4	114.4	$H_8N_4C_2$	118.8	118.7	118.6
$H_5C_3C_2$	108.7	109.0	109.0	$H_9N_4C_2$	122.5	122.8	122.7
$H_6C_3C_2$	110.3	112.2	112.2				
			Dihedral Angles (deg)				
$H_6C_3C_2H_5$		120.7	120.8	$H_9N_4C_2O_1$	180.0	180.5	180.5
$H_7C_3C_2H_5$		−117.6	−117.5	θ_d	0.0	1.9	2.0
$N_4C_2C_3H_5$	180.0	181.9	182.0	θ_p	0.0	1.7	1.8
$H_8N_4C_2O_1$	0.0	−0.6	−0.1		−206.81594		−206.81531

Acetic Acid

	13	14	14		13	14	14
optimization	DEFAULT	DEFAULT	TIGHT				
$\angle H_5C_3C_2O_1$, deg	0.0	90.0	90.0				
			Bond Lengths (Å)				
C_2O_1	1.202	1.202	1.202	C_3H_6	1.083	1.078	1.078
C_2C_3	1.498	1.499	1.499	C_3H_7	1.083	1.079	1.079
C_2O_4	1.360	1.359	1.359	C_4H_8	0.969	0.969	0.969

Table I (*Continued*)

	13	14	14		13	14	14
			Bond Lengths (Å)				
C_3H_5	1.078	1.085	1.085				
			Bond Angles (deg)				
$C_3C_2O_1$	127.4	127.0	127.0	$H_6C_3C_2$	111.8	110.2	110.2
$O_4C_2C_3$	110.5	110.9	110.9	$H_7C_3C_2$	111.8	109.5	109.5
$H_5C_3C_2$	109.6	108.9	108.9	$H_5O_4C_2$	111.8	111.7	111.7
			Dihedral Angle (deg)				
$H_6C_3C_2H_5$	121.1	119.2	119.2	θ_d	0.0	1.9	1.9
$H_7C_3C_2H_5$	−121.1	−118.3	−118.3	θ_p	0.0	1.7	1.7
$O_4C_2C_3O_1$	180.0	181.9	181.9	E, au	−226.53423	−226.53362	
$H_5O_4C_2O_1$	0.0	−0.1	0.0				
			Acetate Anion				
	15	16	16		15	16	16
optimization	DEFAULT	DEFAULT	TIGHT				
$\angle H_5C_3C_2O_1$, deg	0.0	90.0	90.0				
C_2O_1	1.248	1.250	1.250	C_3H_5	1.082	1.089	1.089
C_2C_3	1.575	1.576	1.575	C_3H_6	1.087	1.083	1.083
C_2O_4	1.251	1.250	1.250	C_3H_7	1.087	1.083	1.083
			Bond Angles (deg)				
$C_3C_2O_1$	115.8	115.1	115.1	$H_6C_3C_2$	109.2	110.0	110.0
$O_4C_2C_3$	114.4	115.1	115.1	$H_7C_3C_2$	109.2	110.0	110.0
$H_5C_3C_2$	110.4	108.9	108.9				
			Dihedral Angles (deg)				
$H_6C_3C_2H_5$	121.4	118.5	118.5	θ_d	0.0	1.8	1.8
$H_7C_3C_2H_5$	−121.4	−118.5	−118.5	θ_p	0.0	1.6	1.6
$O_4C_2C_3O_1$	180.0	181.8	181.8	E, au	−225.93308	−225.93310	

known and has been shown to be the result of crystal lattice forces.[9] The carbonyl carbon, C_1, is observed to be pyramidalized by 1.5 (1)° in a neutron diffraction crystal structure analysis at 20 K.[8]

In this paper we refer to the degree of pyramidalization in terms of two related parameters, θ_p and θ_d, the definition of which can be understood with reference to drawings **1**, **2a**, and **2b**. θ_p is the out-of-plane angle made by the bond vector C_2X_4 with the plane defined by atoms $O_1C_2C_3$. It measures the angular amount by which atom X_4 moves out of the $O_1C_2C_3$ plane. θ_d is defined as $(180° - \angle X_4C_2C_3O_1)$. It is the dihedral angle by which X moves away from planarity. Both θ_p and θ_d are 0° for a perfectly planar system. θ_p and θ_d are related by the following equation: $\theta_p = \sin^{-1}(\sin\theta_d \sin\angle X_4C_2C_3)$. A positive value for θ_p and θ_d means that the C_2X_4 bond vector in projection **2b** bends upward toward R_5.

The direction of pyramidalization in acetamide is the same as that predicted by theory,[2b] such that the apex of the pyramid at C_2 is anti to the bond which is most nearly normal to the C_2 sp^2 plane. In other words, there is partial staggering about the C_2C_3 bond. In contrast, in the molecule of monofluoroacetamide, which has almost *m* symmetry in its monoclinic crystal structure, with the CF bond in the $O_1C_2C_3$ plane, the experimentally observed pyramidalization at C_2 is negligible, 0.25 (6)°.[10]

Theoretical calculations using ab initio molecular orbital methods with the 3-21G basis set gave nearly the same degree of pyramidalization, 1.7°, for the conformer **1** of acetamide[11] as found experimentally, 1.5°.[8] This suggests that the distortion from planarity of the non-hydrogen atoms is an intrinsic molecular property, rather than a crystal-field effect, as was originally assumed.[8] To be sure, the alignment of the allylic CH bonds in the asymmetric conformation, **1**, must arise from crystal-field effects,[9] but the simultaneous pyramidalization of the carbonyl carbon is suggested by theory to be a natural consequence of the methyl rotation, and not a result of crystal-field effects acting directly on the carbonyl group. In this paper we have extended these theoretical calculations to some related simple molecules containing carbonyl groups of the general type shown in **3**. In particular, we have investigated whether the pyramidalization calculated (and observed) for **1** is an inherent feature of carbonyls in an asymmetric environment or whether the degree and direction of pyramidalization is merely a random event in the gas phase, or produced only by crystal field effects in the solid state.

Molecular distortions from planarity of this order of magnitude are difficult to study experimentally. Acetamide is too large a molecule for structure determination by microwave spectroscopy, and the distortions from planarity in question are too small to be measured by gas-phase electron diffraction. Accurate crystal structure analysis at low temperatures is the only method available, but the observations may be obscured by, or confused with, the consequences of crystal-field effects, which are believed to result in distortions of the same order of magnitude. Neutron diffraction is preferred to X-ray diffraction because reliable location of the hydrogen atoms is relevant to the interpretation of the results. The only group of molecules containing sp^2 carbon atoms for which the crystal structures have been systematically studied by neutron diffraction are the amino acids. It was to this data set,[12] which gives data on carbonyl compounds of the general formula **4**, that we turned for further experimental evidence.

Theoretical Calculations of Carbonyl Structures

Calculations were performed at the Hartree–Fock level with the 3-21G basis set[13] with use of the GAUSSIAN 80 series of programs.[14] Initial investigations used standard convergence criteria, but at the suggestion of one of the referees, we reoptimized eight structures with more stringent convergence criteria than the default

(9) Caillet, J.; Claverio, P.; Pullman, B. *Theor. Chim. Acta* **1978**, *47*, 17 and references therein.

(10) Jeffrey, G. A.; Ruble, J. R.; McMullan, R. K.; DeFrees, D. J.; Pople, J. A. *Acta Crystallogr., Sect. B* **1981**, *37*, 1885.

(11) Whiteside, R. A.; Binkley, J. S.; Krishnan, R.; DeFrees, D. J.; Schlegel, H. B.; Pople, J. A. "Carnegie-Mellon Quantum Chemistry Archive"; Carnegie-Mellon University: Pittsburgh, PA 15213. This conformer is calculated to be 0.4 kcal/mol higher in energy than that with *m* symmetry in the gas phase.

(12) The 49 neutron diffraction crystal structure analyses of amino acids in the Cambridge Crystallographic Data Base (January, 1982 release) were used.

(13) Binkley, J. S.; Pople, J. A.; Hehre, W. J. *J. Am. Chem. Soc.* **1980**, *102*, 939.

(14) Binkley, J. S.; Whiteside, R. A.; Krishnan, R.; Seeger, R.; DeFrees, D. J.; Schlegel, H. B.; Topiol, S.; Kahn, L. R.; Pople, J. A., GAUSSIAN 80, Quantum Chemistry Program Exchange, Indiana University. The TIGHT optimizations were carried out with GAUSSIAN 82.

Table II. Comparisons of Geometries of 6 and 8 with Different Basis Sets

	6 3-21G	6 4-31G	8 3-21G	8 6-31G*
	Bond Lengths (Å)			
C_2O_1	1.209	1.210	1.208	1.188
C_2C_3	1.509	1.496	1.508	1.507
C_2H_4	1.086	1.085	1.089	1.097
C_3H_5	1.087	1.086		
C_3H_6	1.082	1.080	1.087	1.089
C_3H_7	1.082	1.081	1.081	1.083
C_3H_5			1.545	1.532
	Bond Angles (deg)			
$C_3C_2O_1$	124.3	123.7	125.3	124.7
$H_4C_2C_3$	114.8	116.5	113.8	115.1
$H_5C_3C_2$	109.2	109.4		
$H_6C_3C_2$	111.1	111.4	108.3	107.6
$H_7C_3C_2$	109.9	110.2	108.6	108.3
$C_5C_3C_2$			110.5	111.8
	Dihedral Angles (deg)			
$H_5C_3C_2H_4$	-88.2	-88.3		
$H_6C_3C_2H_5$	119.6	119.5		
H_7C-(3)C_2H_5	-118.1	-118.2		
$H_4C_2C_3O_1$	181.8	181.7	180.1	180.1
$H_7C_3C_2O_1$			5.4	2.7
θ_d	1.8	1.7	0.1	0.1
θ_p	1.6	1.5	0.1	0.1

values. The more stringent thresholds (TIGHT optimizations) used for SCF convergence, maximum force, root-mean-square force, maximum displacement, and root-mean-square displacement are 10^{-9}, 1.5×10^{-5}, 1.0×10^{-5}, 6.0×10^{-5}, and 4.0×10^{-5}, respectively. For comparison, the default values in GAUSSIAN 80 are 10^{-7}, 4.5×10^{-4}, 3.0×10^{-4}, 1.8×10^{-3}, and 1.2×10^{-3}, respectively. All geometrical parameters were fully optimized, except for the constraint of one dihedral angle, $RC_3C_2O_1$ (R = H or Me), as noted below. The results of the theoretical calculations on various conformers of acetaldehyde, propionaldehyde, acetamide, acetic acid, and the acetate anion are shown in Figure 1 and Table I. The C_1 structure of acetaldehyde was reoptimized by using the 4-31G basis set in order to test the authenticity of the nonplanar behavior of the carbonyl center. Dr. J. S. Binkley kindly provided us with the fully optimized 6-31G* structure of the second most stable conformation of propanal. The results of the 4-31G and 6-31G* calculations are summarized in Table II, along with the fully optimized 3-21G structures. From Table II it is apparent that the pyramidalization of the carbonyl group is not basis set dependent. In addition, we found that this pyramidalization survives even if more rigorous optimization criteria are used, as can be seen by the geometries summarized in Table I. The energies obtained in both DEFAULT and TIGHT optimizations are identical to within 10^{-6} au.

Acetaldehyde prefers the eclipsed conformation (∠HCCO = 0° and ≃ 120°). The conformation in which one HCCO is constrained to 90° is calculated to be 0.5 kcal/mol higher in energy. This conformation has a slightly pyramidal carbonyl carbon, since the aldehyde hydrogen moves out-of-plane toward the perpendicular CH bond by 1.6°.

Propionaldehyde has two different eclipsed geometries which are local minima, and we also calculated geometries of conformations in which either a CH or CCH_3 bond is fixed perpendicular to the CCO plane. These were optimized in order to assess the relative importance of perpendicular CH and CC bonds in inducing pyramidalization. As shown in Figure 1, there is little difference in the pyramidalization in the two cases, suggesting that for these conformations the strain due to partial eclipsing of either CC with CH or of CH with CH is similar.

The structure of acetamide has been optimized previously by Schafer et al., using the 4-21G basis set.[15] These authors found

(15) Klimkowksi, V. J.; Sellers, H. J.; Schafer, L. *J. Mol. Struct.* **1979**, *54*, 299.

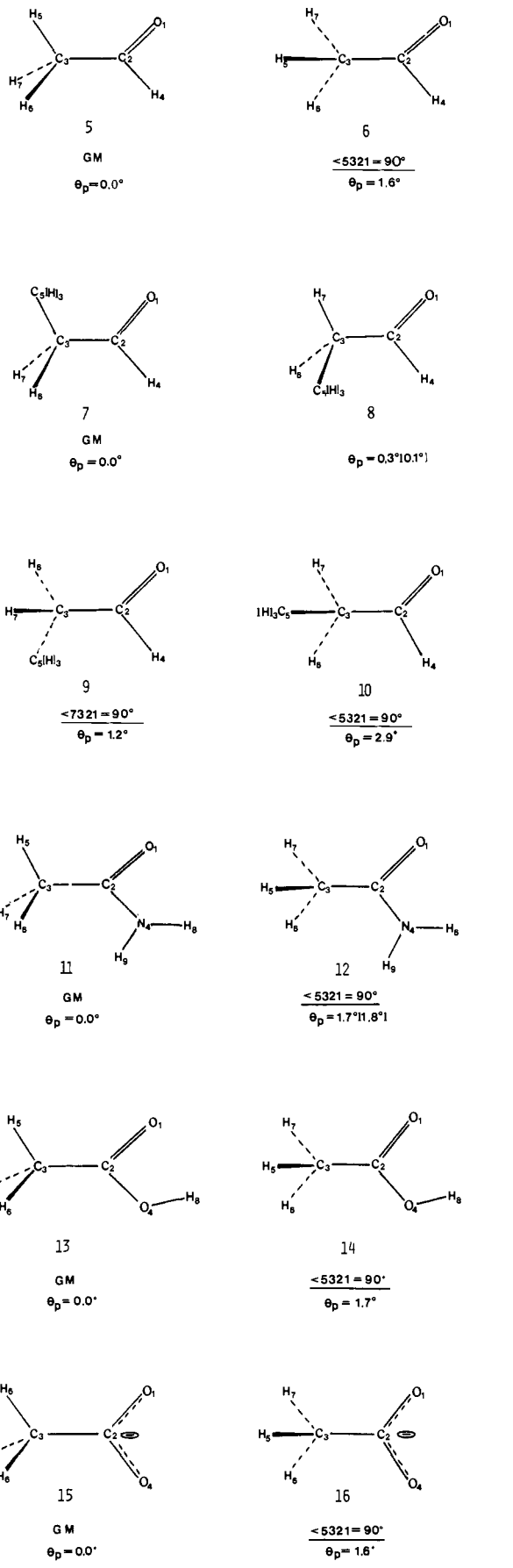

Figure 1. 3-21G pyramidalizations for optimized structures of carbonyl compounds using DEFAULT or, in brackets (if different), TIGHT convergence and optimization criteria. Underlined parameters were fixed in the optimizations. Additional geometrical parameters are given in Table I. GM designates global minimum.

Table III. Neutron Diffraction Data from Acetamide, Amino Acids, and Dipeptides

compound	θ_p,[a] deg	$\perp$,[a] Å	τ,[a] deg	refcode[b]
acetamide (**1**)	1.50	0.012	92.3	*c*
acetamide·$^1/_2$HCl (**2**)	1.09	0.009	−114.2	*d*
N-acetylglycine (**3**)	0.37	0.003	105.1	ACYGLY11
L-asparagine·H_2O (**4**)	0.50	0.004	−118.0	ASPARM02
L-asparagine·H_2O (**4′**)[e]	0.65	0.005	−116.4	ASPARM03
L-glutamine (**5**)	0.47	0.004	107.5	GLUTAM01
glycylglycine·HCl·H_2O (**6**)	2.04	0.016	99.3	GLCICH01
α-glycylglycine (82 K) (**7**)	2.92	0.023	−91.6	GLYGLY04
perdeuterioglycylglycine (α-form) (**8**)	2.90	0.023	90.3	GLYGLD
perdeuterioglycylglycine (α-form) (**8′**)	2.41	0.019	−90.4	GLYGLD02
N-acetylglycine (9)	0.22	0.002	−119.9	ACYGLY11
L-asparagine·H_2O (**10**)	4.30	0.033	70.4	ASPARM02
L-asparagine·H_2O (**10′**)	4.82	0.045	67.8	ASPARM03
L-cysteic acid·H_2O (**11**)	1.43	0.011	76.2	CYSTAC01
L-cystine·2HCl (**12**)	0.71	0.005	−106.1	CYSTCL02
L-cystine·2HCl (**12′**)	0.66	0.005	−106.5	CYSTCL01
diglycine nitrate (ferro form) (**13**)	1.56	0.012	63.7	DGLYCN01
diglycine nitrate (ferro form) (**14**)	−1.62	−0.012	−65.7	DGLYCN01
diglycine nitrate (para form) (**15**)	4.06	0.031	−66.4	DGLYCN10
diglycine nitrate (para form) (**16**)	5.92	0.046	74.6	DGLYCN10
L-glutamic acid (β-form) (**17**)	−0.40	−0.003	−107.9	LGLUAC11
L-glutamic acid·HCl (**18**)	1.70	0.013	−105.3	LGLUTA
α-glycine (**19**)	0.58	0.004	78.4	GLYCIN03
α-glycine (**19′**)	0.78	0.006	78.5	GLYCIN05
γ-glycine (298 K) (**20**)	2.27	0.017	−74.3	GLYCIN15
γ-glycine (83 K) (**21**)	2.23	0.017	−74.2	GLYCIN16
glycine·HCl (**22**)	−0.38	−0.003	59.7	GLYHCL
glycylglycine·HCl·H_2O (**23**)	0.60	0.005	119.2	GLCICH01
α-glycylglycine (82 K) (**24**)	0.27	0.002	−111.5	GLYGLY04
triglycine·sulfate (ferro form, room temp) (**25**)	1.13	0.009	−76.0	TGLYSU11
triglycine·sulfate (ferro form, room temp) (**26**)	2.46	0.019	−56.0	TGLYSU11
triglycine·sulfate (ferro form, room temp) (**27**)	−0.19	−0.001	64.6	TGLYSU11
hippuric acid (**28**)	−2.38	−0.018	65.5	HIPPAC02
L-histidine·HCl·H_2O (29)	−1.13	−0.009	−116.9	HISTCM12
iminodiacetic acid·HBr (**30**)	0.00	0.000	−120.1	IMDACB11
deuterioiminodiacetic acid·HBr (**31**)	0.00	0.000	−120.5	DIMDAB01
perdeuterioglycylglycine (α-form) (**32**)	−0.23	−0.002	111.9	GLYGLD
perdeuterioglycylglycine (α-form) (**32′**)	−0.02	0.000	−112.0	GLYGLD02
L-phenylalanine·HCl (**33**)	0.97	0.007	−116.8	PHALNC01
L-serine·H_2O (**34**)	1.16	0.009	−114.6	LSERMH10
DL-serine (**35**)	1.31	0.009	−114.7	DLSERN11
L-alanine (**36**)	−0.06	0.000	−76.9	LALNIN12
L-arginine·$2H_2O$ (**37**)	0.84	0.006	110.1	ARGIND11
L-cysteine (**38**)	0.44	0.003	107.1	LCYSTN12
L-glutamic acid (α-form) (39)	0.57	0.004	−110.5	LGLUAC03
L-glutamic acid (α-form) (**40**)	1.08	0.008	74.2	LGLUAC03
L-glutamic acid (β-form) (**41**)	3.20	0.025	−97.2	LGLUAC11
L-glutamic acid·HCl (**42**)	2.20	0.017	−76.4	LGLUTA
L-histidine (**43**)	0.54	0.004	95.4	LHISTD13
4-hydroxyl-L-proline (**44**)	1.77	0.014	113.6	HOPROL12
L-lysine·HCl·$2H_2O$ (**45**)	0.85	0.007	75.6	LYSCHL02
L-lysine·HCl·$2H_2O$ (**45′**)	1.70	0.013	75.6	LYSCLH11
L-threonine (**46**)	0.96	0.007	95.9	LTHREO01
L-tyrosine (**47**)	0.39	0.003	108.2	LTYROS11
L-tyrosine·HCl (**48**)	2.68	0.021	−89.0	LTYRHC10
L-valine·HCl (**49**)	0.23	0.002	112.0	VALEHC11

[a] Defined in the text. [b] From the Cambridge Crystallographic Data Base (ref 12). [c] Reference 8. [d] Reference 10. [e] Primed numbers are second determinations of the same crystal structure. Identical entries under different numbers refer to different sp^2 C atoms.

that the amino group is planar in such molecules, but with very low out-of-plane bending force constants. These results are mimicked by the 3-21G results. The amino group slightly pyramidalizes in the conformation having one HCCO angle fixed at 90°, presumably in response to the carbonyl pyramidalization of 1.7°. The pyramidalization here is comparable to that found for acetaldehyde and propionaldehyde.

Acetic acid prefers the eclipsed conformation, and the 90° conformation is 0.4 kcal/mol higher in energy and has a pyramidalization of 1.7°. By contrast, acetate ion has essentially free rotation about the CC bond, since in this molecule the rotational potential is sixfold. The pyramidalization of the 90° conformation is again comparable to that found in the other carbonyl compounds. An X-ray crystal structure of ammonium acetate indicates that an eclipsed conformation is preferred, with a planar carbonyl group, within experimental error.[16]

In summary, the theoretical calculations indicate that carbonyl compounds lacking a plane of symmetry should pyramidalize, and the direction of pyramidalization is always that which results in a partially staggered conformation around the C_2–C_3 bond. The degree of pyramidalization is similar for different carbonyl compounds and reaches a maximum of 1.5–1.7° for conformations in which one allylic bond is perpendicular to the $O_1C_2C_3$ plane.

As we have described earlier,[7] this direction of pyramidalization is exactly what is expected if the pyramidalization occurs so as to relieve closed-shell repulsions between vicinal bonds. In short, the molecules investigated are all predicted to have partially staggered conformations when allylic bonds are arranged unsymmetrically. Of course the molecules studied are all predicted

(16) Nahringbauer, I. *Acta Crystallogr.* **1967**, *23*, 956.

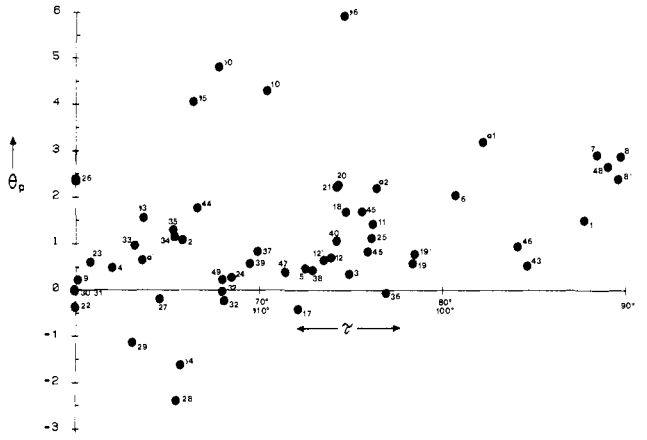

Figure 2. Plot of pyramidalization of amino acids or dipeptide carbonyl groups, θ_p, vs. the torsional angle, τ, which measures the asymmetry of allylic bonds with respect to the carbonyl plane. Data are from neutron crystal structures.[12] The points on the left axis have the following values of θ_p and τ (**22**: −0.38, 59.7; **26**: 2.46, 56.0; **30**: 0.00, 59.9; **31**: 0.00, 59.5). The structures correspond to **4**, with X = NH_2, R_1 = H for numbers **1**, **4**, **4′**, and **5**; X = NHC (amino acid), R_1 = H for numbers **3**, **6**, **7**, **8**, and **8′**; X = $O^{-1/2}$ in CO_2^- or OH in CO_2H, R_1 = H in numbers **9**–**35**; and X = $O^{-1/2}$ in CO_2^- or OH in CO_2H, R_1 = alkyl in numbers **36**–**49**. Number 2 is O-protonated acetamide.

to have a plane of symmetry, or to have one allylic bond nearly eclipsed with the carbonyl group, in the gas phase. The solution conformations are expected to be identical. In such cases, no pyramidalizaton of the carbonyl carbon is expected. Why then are we making much ado over a few degrees of pyramidalization in geometries which are expected to be energy maxima or near-maxima? When these functional groups are incorporated into cyclic or rigid polycyclic skeletons, or into proteins, an asymmetric arrangement of allylic bonds may be enforced, and pyramidalization will result. More generally, in solids, crystal forces may rotate allylic bonds away from gas-phase minima, and pyramidalization in the sense predicted above is expected. In the following section, we provide experimental evidence that supports this conclusion.

Experimental Data on Pyramidalization of Amino Acids and Dipeptides

Table III summarizes the relevant experimental data for 49 amides, amino acids, or dipeptides that have been analyzed by means of single-crystal neutron diffraction. In Figure 2, the pyramidalization, θ_p, of each sp^2 carbon atom, C_1, in each of these structures is plotted against the $R_5C_3C_2O_1$ torsion angle, τ, for which $120° > \tau > 60°$. The definition of τ is given in **2**. It is that dihedral angle closest to 90° between the CO bond and an allylic bond. The approximate relationships between τ and the torsional angles involving R_6 and R_7 are $\tau_6 = \tau_5 + 120°$ and $\tau_7 = \tau_5 + 240°$. Positive pyramidalization is defined as in **2a** as that in which the apex of the pyramid at C_2 is anti to the C_3–R_5 bond. That is, a positive value of θ_p implies partial staggering about C_2C_3, while a negative value implies partial eclipsing.

The data show a well-defined distortion from planarity of the sp^2 carbon atoms in the amino acids, reaching a maximum nearly double that predicted by theory. The force constants obtained from 3-21G calculations are 10–30% too large.[13] The degree of pyramidalization is related to the force constant of the planar symmetrical species, which will tend to restore the carbonyl to planarity, and to the asymmetric pyramidalizing force, identified here as torsional effects. Theory at this level is expected to underestimate the pyramidalization, since the out-of-plane bending force constants are overestimated relative to torsional (closed-shell repulsion) factors.

The non-planar distortion is predominantly in the staggered direction about C_2C_3, as predicted by our theoretical calculations. Seven of these structure analyses were duplicated by independent investigators. In all of the analyses, with two possible exceptions, these distortions are significant.[17] The data in Figure 2 suggest that there is a relationship between θ and τ such that the pyramidalization is a maximum when $\tau = 90°$.

Those examples where the pyramidalization is the reverse of that expected occur at values of τ of less than 70° or greater than 110°, suggesting that crystal-field effects which result in distortions from planarity opposed to the pyramidalization are only large enough to overcome the inherent electronic preference when one of the C_3–R bonds is within 10° of the C_2 sp^2 plane.

The experimental data taken alone cannot distinguish between two possible interpretations. One is that sp^2 C_2 bonds in the isolated or gas-phase molecule are planar, but distort more readily on one side of the molecule than on the other under the influence of asymmetric crystal-field forces. The second is that pyramidalization is an intrinsic property of the isolated molecule, when forced into an asymmetric conformation; this tendency persists in the crystalline state and produces the bias shown in Figure 2. The theoretical results strongly support the second interpretation.

These pyramidalizations are clearly related to the phenomenon of addition selectivity[2] and to hypotheses concerning "orbital distortion".[7] Although the effects are small, they are cumulative in polypeptides and could influence the overall conformations of macromolecules, which do not have local symmetry at each carbonyl group. More significantly, they imply that reactions involving additions to peptide or carbonyl bonds in polypeptides may take place more easily from one side of the peptide plane than from the other, depending upon the conformation at the adjacent sp^3 carbon atom.[7] We have shown earlier that the torsional effects which induce pyramidalization are more pronounced in the transition states for addition reactions.[7,18]

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Registry No. Acetamide, 60-35-5; acetic acid, 64-19-7; acetaldehyde, 75-07-0; propionaldehyde, 123-38-6; acetate anion, 71-50-1.

(17) The estimated standard deviations of θ range from 0.03° for structure **19** to 0.62° for structure **14**. The values of $\sigma(\theta)$ were calculated from those given for the atomic coordinates σ_j by $\sigma(\theta) = \sum (d\theta/d\sigma_j)^2 \sigma_j^2$. The values of 3.03 $\sigma(\theta)$, i.e., 99.9% significance level, for the outliers in Figure 2 are 1.3° for structure **16**, 0.8° for **10′**, 0.1° for **10**, 1.9° for **15**, 0.1° for **41**, 0.9° for **28**, and 0.2° for **29**. There were no particular aspects of these crystal structures suggestive of exceptionally large crystal field distortions. However, the paramagnetic crystal structure of diglycine nitrate (**14**, **16**) is disordered. As a consequence, the final agreement factors were high ($R = 0.13$), and the model used for the final refinement may be incorrect in detail.

(18) Rondan, N. G.; Paddon-Row, M. N.; Caramella, P.; Mareda, J.; Mueller, P. H.; Houk, K. N. *J. Am. Chem. Soc.* **1982**, *104*, 4974. Paddon-Row, M. N.; Rondan, N. G.; Houk, K. N. *J. Am. Chem. Soc.* **1982**, *104*, 7162.